Biomek Software

Version 3.2 User's Manual

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Beckman Coulter, Inc
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Indianapolis, Indiana
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Warranty and Returned Goods Requirements

All standard Beckman Coulter, Inc. policies governing returned goods apply to this product. Subject to the exceptions and upon the conditions stated below, the Company warrants that the products sold under this sales agreement shall be free from defects in workmanship and materials for one year after delivery of the products to the original Purchaser by the Company, and if any such product should prove to be defective within such one year period, the Company agrees, at its option, either (1) to correct by repair or at the Company's election by replacement, any such defective product provided that investigation and factory inspection discloses that such defect developed under normal and proper use, or (2) to refund the purchase price. The exceptions and conditions mentioned above are as follows:

a. Components or accessories manufactured by the Company which by their nature are not intended to and will not function for one year are warranted only to reasonable service for a reasonable time. What constitutes a reasonable time and a reasonable service shall be determined solely by the Company. A complete list of such components and accessories is maintained at the factory.

b. The Company makes no warranty with respect to components or accessories not manufactured by it. In the event of defect in any such component or accessory, the Company will give reasonable assistance to Purchaser in obtaining from the manufacturer's own warranty.

c. Any product claimed to be defective must, if required by the Company, be returned to the factory, transportation charges prepaid, and will be returned to Purchaser with transportation charges collect unless the product is found to be defective, in which case the product must be properly decontaminated of any chemical, biological, or radioactive hazardous material.

d. The Company shall be released from all obligations under all warranties, either expressed or implied, if any product covered hereby is repaired or modified by persons other than its own authorized service personnel, unless such repair by others is made with the written consent of the Company.

e. If the product is a reagent or the like, it is warranted only to conform to the quantity and content and for the period (but not in excess of one year) stated on the label at the time of delivery.

It is expressly agreed that the above warranty shall be in lieu of all warranties of fitness and of the warranty of merchantability, and that the company shall have no liability for special or consequential damages of any kind or from any cause whatsoever arising out of the manufacture, use, sale, handling, repair, maintenance, or replacement of any of the products sold under the sales agreement.

Representatives and warranties made by any person, including dealers and representatives of the Company, which are consistent or in conflict with the terms of this warranty, shall not be binding upon the Company unless reduced in writing and approved by an expressly authorized officer of the Company.

Parts replaced during the warranty period are warranted to the end of the instrument warranty.

Note: Performance characteristics and specifications are only warranted when Beckman Coulter replacement parts are used.

Safety Information

All Warnings and Cautions in this document include an exclamation point, a lightning bolt, or a light burst symbol framed within a triangle. Please pay special attention to the specific safety information associated with these symbols.

WARNING: If the equipment is used in a manner not specified by Beckman Coulter, Inc., the protection provided by the equipment may be impaired.

Warning and Caution Definitions

The exclamation point symbol is an international symbol which serves as a reminder that all safety instructions should be read and understood before installation, use, maintenance, and servicing is attempted.

When this symbol is displayed in this manual, pay special attention to the specific safety information associated with the symbol.

WARNING

A WARNING calls attention to a condition or possible situation that could cause injury to the operator.

CAUTION

A CAUTION calls attention to a condition or possible situation that could damage or destroy the product or the operator's work.

Electrical Safety

To prevent electrically related injuries and property damage, properly inspect all electrical equipment prior to use and immediately report any electrical deficiencies. Contact a Beckman Coulter Service Representative for any servicing of equipment requiring the removal of covers or panels.

High Voltage

This symbol indicates the potential of an electrical shock hazard existing from a high voltage source and that all safety instructions should be read and understood before proceeding with the installation, maintenance, and servicing of all modules.

Do not remove system covers. To avoid electrical shock, use supplied power cords only and connect to properly grounded (three-holed) wall outlets. Do not use multiplug power strips.

Laser Light

This symbol indicates that a potential hazard to personal safety exists from a laser source. When this symbol is displayed in this manual, pay special attention to the specific safety information associated with the symbol.

Laser Specifications

Laser Type:	Class II Laser Diode
Maximum Output:	1mW
Wavelength:	670 nm

Chemical and Biological Safety

Normal operation of laboratory equipment may involve the use of materials that are toxic, flammable, or otherwise biologically harmful. When using such materials, observe the following precautions:

- Handle infectious samples according to good laboratory procedures and methods to prevent the spread of disease.
- Observe all cautionary information printed on the original solutions containers prior to their use.
- Dispose of all waste solutions according to your facility's waste disposal procedures.
- Operate the Biomek instrument in accordance with the instructions outlined in this manual, and take all the necessary precautions when using pathological, toxic, or radioactive materials.
- Objects dropped onto plates, accidental tool release, or other accidental collisions may result in splashing of liquids; therefore, take appropriate safety precautions, such as using safety glasses and wearing protective clothing, when working with potentially hazardous liquids.
- Use an appropriately contained environment when using hazardous materials.
- Observe the appropriate cautionary procedures as defined by your safety officer when using flammable solvents in or near a powered-up instrument.
- Observe the appropriate cautionary procedures as defined by your safety officer when using toxic, pathological, or radioactive materials.

Note: Observe all warnings and cautions listed for the Biomek instrument and any external devices attached or used during operation of the instrument. Refer to the applicable instrument and external device user's manuals for operating procedures of that device.

Moving Parts

To avoid injury due to moving parts, observe the following:

- Never attempt to exchange labware, reagents, or tools while the instrument is operating.
- Never attempt to physically restrict any of the moving components of the Biomek instrument.
- Keep the Biomek instrument work area clear to prevent obstruction of the movement.

Cleaning

Observe the cleaning procedures outlined in the user's manual for the Biomek instrument, automated labware positioner (ALP), or external device. Prior to cleaning equipment that has been exposed to hazardous material:

- Appropriate Chemical and Biological Safety personnel should be contacted.
- The Chemical and Biological Safety information contained in this user's manual should be reviewed.

Maintenance

Perform only the maintenance described in this manual or the user's manual for the Biomek instrument. Maintenance other than that specified in these manuals should be performed only by Beckman Coulter Service Representatives.

Important

It is your responsibility to decontaminate the Biomek instrument or any of its accessories before requesting service by a Beckman Coulter Service Representative or returning parts to Beckman Coulter for repair. Beckman Coulter will NOT accept any items which have not been decontaminated where it is appropriate to do so. If any parts are returned, they must be enclosed in a sealed plastic bag stating that the contents are safe to handle and are not contaminated.

Warnings and Cautions Found in this Manual

Please read and observe all cautions and instructions. Remember, the most important key to safety is to operate the Biomek instrument and accessories with care.

The WARNINGs and CAUTIONs found within this document are listed below.

Note: Also refer to the warnings and cautions in the applicable Biomek instrument user's manual for additional safety information.

WARNING: If the equipment is used in a manner not specified by Beckman Coulter, Inc., the protection provided by the equipment may be impaired.

CAUTION: Make sure the correct ALP is chosen when configuring the deck setup in the Deck Editor. ALPs vary in height and failure to choose the correct ALP in the Deck Editor may result in collisions between pod(s) and ALPs during operation.

CAUTION: After new tips are added, the correct properties must be defined in the Tip Type Editor according to the manufacturer's specifications. Inaccurate specifications may lead to hardware crashes.

CAUTION: The correct well properties must be defined in Labware Types according to the manufacturer's specifications. Inaccurate specifications may lead to inaccurate pipetting.

CAUTION: Make sure the correct ALP is chosen when configuring the deck setup in the Deck Editor. ALPs vary in height and failure to choose each ALP correctly in the software may result in collisions between pod(s) and ALPs during operation.

CAUTION: No changes to the Biomek state are permitted while a method is paused. Changes can be made to the labware contents, but not the deck or the devices.

WARNING: The light curtain is a safety device. Use it to stop a method only in an emergency.

CAUTION: An inaccurate Instrument Setup may result in pod and labware collisions, or in inappropriate pipetting.

CAUTION: To make sure the Biomek pod avoids all obstacles during its travel, always specify the labware, ALPs, and devices that are on the deck, and the deck position each occupies.

CAUTION: Do not place labware other than a tip box on a tip loader position (TL#).

CAUTION: Do not purge the system without mandrels installed and tubing attached to disposable or fixed tips. Purging the system without the mandrels installed and the tubing attached to tips may cause corrosion in the tip interface.

CAUTION: Do not attempt to access a 96-Channel or 384-Channel Tip Wash ALP with a Multichannel Pod equipped with an HDR Tool Body. The gripper may crash and damage the pod, HDR Tool Body, or Tip Wash ALP.

CAUTION: Do not access labware positioned on a 1 x 5 Passive ALP with the HDR Tool Body. The gripper may crash into the ALP.

CAUTION: Do not access labware on a Stirring ALP with the HDR Tool Body. The magnetic stirrer may bend the pins or interfere with the liquid transfer performance of the pins.

CAUTION: When setting the height for pipetting operations on the Stirring ALP, the presence of the stir bar must be taken into consideration. Pipetting operations that do not account for the height of the stir bar could damage the tips.

WARNING: The Ignore error recovery option is potentially dangerous since almost every action depends upon the successful completion of previous actions. Choose Ignore at your own risk.

CAUTION: Resuming a method assumes that the Biomek instrument is in the same state as when the error occurred. The pod may be moved to deal with a problem, but no changes can be made to the Biomek instrument deck.

CAUTION: The partially completed steps assume the pods are in the same position they were in when the method was halted. Removing the Recovery step without also removing these partially completed steps could result in a crash.

WARNING: To eliminate the possibility of replacing a Continuation method before corrections are made, it is recommended that a Continuation method be edited and run as soon as it is created.

CAUTION: A Continuation method assumes that the instrument is in the same state as when the Continuation was snapped. If this is not true, the Continuation method must be edited to account for the changes.

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1 Biomek Software Introduction

1.1 About Biomek Software

Biomek Software is used to control the Beckman Coulter Biomek line of laboratory automation workstations. Biomek Software consists of a method editor and other tools and editors for configuring the system to perform desired operations.

Configuring the Biomek instrument is necessary to achieve the desired results from automated methods. The software must have information on the deck layout, labware and tips utilized in the method, liquid types to pipette, and how to perform pipetting operations.

Biomek Software comes with a default set of parameters suitable for many applications; many opportunities are presented for customization to achieve a wide variety of desired results.

Information about the liquid-handling system is stored in two separate files. The instrument file includes information specific to an instrument, including additional components installed, deck layout, and framing information. A project file stores information about labware, tip, and liquid types, and pipetting techniques and templates.

Effectively using Biomek Software includes using the method editor for method building and the various tools and editors to appropriately configure the instrument and project files for the desired task or application.

1.1.1 Instrument Files

An instrument file contains all pertinent information relating to the physical hardware. This includes:

- instrument type and configuration.
- devices installed on the instrument deck.
- external devices integrated with the instrument.
- deck layout and framing information.

The instrument configuration must accurately represent the Biomek instrument hardware to prevent collisions between the instrument and any on-deck components. All instrument configuration is done using Hardware Setup and the Deck Editor.

Hardware Setup is used to configure the heads, devices, and accessories available to the instrument. The Deck Editor is used to configure the precise location of all labware positions on the deck and associate any devices or accessories to those positions. The pod must then be precisely aligned to each deck position by framing the deck.

Refer to Chapter 3, *Using Instrument Files and Settings*, for more information on instrument files.

1.1.2 Project Files

A project file stores custom information about liquid types, labware and tip types, and pipetting techniques and templates that are used to configure the actions of the instrument in a database. Project files store a history of all changes, additions, and deletions from the project file.

Project items are configured using the following editors:

- Labware Type Editor
- Tip Type Editor
- Liquid Type Editor
- Technique Editor
- Pipetting Template Editor
- Well Patterns Editor

Project items may be checked in, which creates a revision of the project item. Checked in revisions can always be recovered and reused, ensuring that checked in or validated methods are reproducible even if project items are subsequently modified or deleted. Refer to Chapter 6, *Understanding and Using Project Files*, for more information on project files.

1.1.3 Methods

Methods contain the precise information for performing a specific sequence of actions to complete a task, and utilize information from the project and instrument files to configure and customize those actions.

The Biomek method editor is used to create methods that control the Biomek liquid-handling system. Methods comprise a series of steps that together perform various operations, such as liquid transfers or labware moves using the gripper. Additional operations, such as microplate shaking, can be performed in a Biomek method through active ALPs or integrated devices that are controlled through the Biomek instrument via serial communications. Refer to Chapter 12, *Creating and Using Methods*, for more information on building and working with methods.

Note: ALPs (Automated Labware Positioners) are removable and interchangeable platform structures installed on the Biomek deck to allow automated assays to be performed.

1.2 About this Manual

The information in this manual on Biomek Software generally refers to all Biomek instruments; however, the following conventions present specific conditions or information that apply to one or more, but not all, Biomek instruments:

- ***FX*** — Biomek FX Laboratory Automation Workstation
- ***3000*** — Biomek 3000 Laboratory Automation Workstation
- ***NX-MC*** — Biomek NX Multichannel Laboratory Automation Workstation
- ***NX-S8*** — Biomek NX Span-8 Laboratory Automation Workstation

This manual should be used in conjunction with the appropriate hardware manual for the specific instrument.

An index and glossary are also provided. The glossary contains terms and definitions relating to the Biomek instruments, ALPs, and Biomek Software. It is a separate .pdf file that may be accessed from this manual or any of the related manuals.

1.2.1 Related Manuals

The following related user's manuals for accessing more in-depth information on the Biomek instruments and ALPs are included as specific cross-referenced links to this manual:

- *Biomek® FX Laboratory Automation Workstation User's Manual*
- *Biomek® 3000 Laboratory Automation Workstation User's Manual*
- *Biomek® NX Multichannel Laboratory Automation Workstation User's Manual*
- *Biomek® NX Span-8 Laboratory Automation Workstation User's Manual*
- *ALPs User's Manual*

2 Using Accounts & Permissions

2.1 Overview

Beckman Coulter Accounts & Permissions is an integrated set of features built into Beckman Coulter software that assists users in complying with electronic signature requirements (such as 21 CFR Part 11) for closed systems. With Biomek Software, support is extended only for the Biomek instrument; devices integrated with the Biomek instrument are not supported unless specified in separate documentation.

Accounts & Permissions only provides support for closed systems; networked systems are not supported. In a location where several Beckman Coulter systems are present, Accounts & Permissions must be installed and enabled separately for each system where compliance is desired. Users require a separate account for each system they need to access.

For each Beckman Coulter system, a single administrator sets up the level of support provided by Accounts & Permissions, creates, manages, and sets permissions for user accounts, and configures system parameters relating to Accounts & Permissions.

This chapter covers:

- *Installing and Setting the Level of Support For Accounts & Permissions* (Section 2.2).
- *Administering User Accounts and Permissions* (Section 2.3).
- *Restoring the Administrator Password* (Section 2.4).
- *Viewing the Audit Log* (Section 2.5).
- *Using the Biomek Software With Accounts & Permissions Enabled* (Section 2.6).

2.2 Installing and Setting the Level of Support For Accounts & Permissions

Some Accounts & Permissions functionality is built into Biomek Software; however, additional options that allow Accounts & Permissions to be enabled and configured are installed separately. This section covers:

- *Installing Accounts & Permissions* (Section 2.2.1).
- *Setting the Level of Support For Accounts & Permissions* (Section 2.2.2).

2.2.1 Installing Accounts & Permissions

Beckman Coulter Accounts & Permissions support may be installed before or after Biomek Software is installed on the system.

Note: Site processes should be in place to ensure that access to the Accounts & Permissions installation CD is controlled.

To install support for Accounts & Permissions:

1. Close all open applications on the computer.
2. Place the Beckman Coulter Accounts & Permissions Installer CD in the drive, and browse to the contents of the CD.
3. Double-click **Beckman Coulter Accounts & Permissions.exe**. Beckman Coulter Accounts & Permissions Setup appears.

   Note: If Accounts & Permissions is already installed, options to repair, modify, and remove the application appear.

4. Follow the steps in the setup wizard.
5. Restart the computer.
6. After the computer is restarted, set the level of Accounts & Permissions support desired (refer to Section 2.2.2, *Setting the Level of Support For Accounts & Permissions*).

2.2.2 Setting the Level of Support For Accounts & Permissions

The administrator may change the level of support for Accounts & Permissions at any time.

Note: The site must have processes in place to govern all system administration activities, as specified in the 21 CFR Part 11 regulation.

To set the level of support for Accounts & Permissions:

1. Log off and close Biomek Software and any other Beckman Coulter software applications using Accounts & Permissions, if necessary.
2. Place the Beckman Coulter Accounts & Permissions Installer CD in the drive, and browse to the contents of the CD.
3. Double-click **Beckman Coulter Accounts & Permissions - Support Options.exe**.
4. When prompted, enter the **Administration Password** and choose **OK**. Support Options appears (Figure 2-1). A series of tabs displays all installed software applications compatible with Beckman Coulter Accounts & Permissions.

   Note: If the Administration Password is lost, forgotten, or not known, follow the steps in Section 2.4, *Restoring the Administrator Password*.

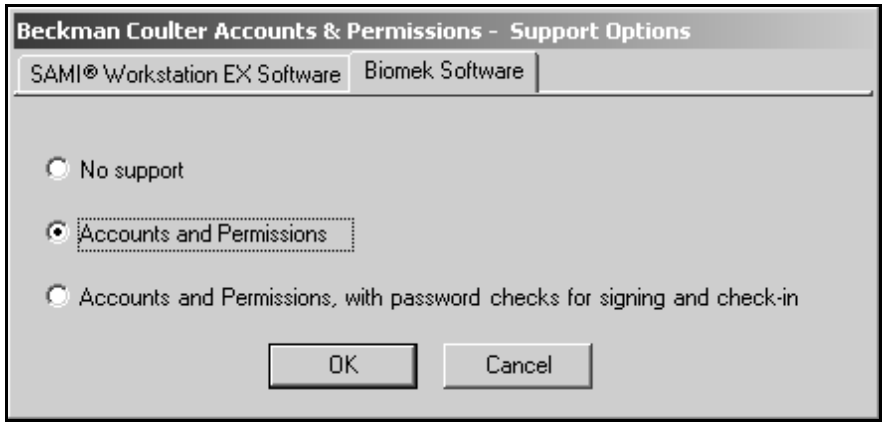


Figure 2-1. Support Options

5. Choose the **Biomek Software** tab, if multiple Beckman Coulter software applications supporting Accounts & Permissions are installed on the system.

6. Select the level of support. When several Beckman Coulter software applications are installed on the same system, the level of support selected must be the same for each application.

    - **No support** — User accounts are not required to access Biomek Software. Users have access to all software operations and functionality.

      Note: System activity, such as creating, editing, or running methods, is still logged in the audit trail and can be viewed in the Audit Log (refer to Section 2.5, *Viewing the Audit Log*).

    - **Accounts and Permissions** — Enables the use of user accounts and permissions for Biomek Software. Users must log in to use the software and may access only features and operations for which they have permission. Operations such as checking in, validating, or signing methods do not require password confirmation.

      Note: Accounts and Permissions without password checks may not provide adequate support for 21 CFR Part 11 compliance. Each site must evaluate the level of support required for a given system.

    - **Accounts and Permissions, with password checks for signing and check-in** — Enables the use of user accounts and permissions with electronic signatures for Biomek Software. Users must log in to use the software and may access only features and operations for which they have permission. Support for 21 CFR Part 11 is provided by requiring password checks for operations such as checking in, validating, and signing methods.

    Note: Compliance with 21 CFR Part 11 requires implementing site processes beyond the control of the software.

7. Choose **OK** to activate the level of support chosen and close Support Options.

    OR

    Choose **Cancel** to close Support Options without changing the level of support.

2.3 Administering User Accounts and Permissions

System administration tasks for Beckman Coulter Accounts & Permissions are performed in Account Management, a separate application from Biomek Software. The system administrator sets up and configures user accounts, passwords, and permissions, and configures system settings such as automatic password expiration and system logout time.

A single system administrator password is used on a system. System administration tasks may be performed only on the computer where Account Management is installed; access to Account Management over a network is not supported.

Note: The administrator is not automatically given a user account on the system. If the administrator requires an account, one must be created in Account Management.

Note: The 21 CFR Part 11 regulation contains additional requirements for account management beyond the control of the software.

This section covers opening Account Management and provides an overview of permissions available for Biomek Software users (refer to Section 2.3.1, *Assigning Biomek Software Permissions*). Refer to the Account Management online help for detailed information about administering user accounts and permissions.

To open Account Management:

1. Log off and close Biomek Software and any other Beckman Coulter software applications using Accounts & Permissions.
2. In the Windows® Start menu, choose **Settings>Control Panel**. Control Panel appears.
3. In Control Panel, double-click **Administrative Tools**. Administrative Tools appears.
4. In Administrative Tools, double-click **Beckman Coulter Accounts & Permissions Administrator**. Beckman Coulter Accounts & Permissions appears.
5. In Beckman Coulter Accounts & Permissions, enter the administrator password and choose **OK**. Account Management appears (Figure 2-2).

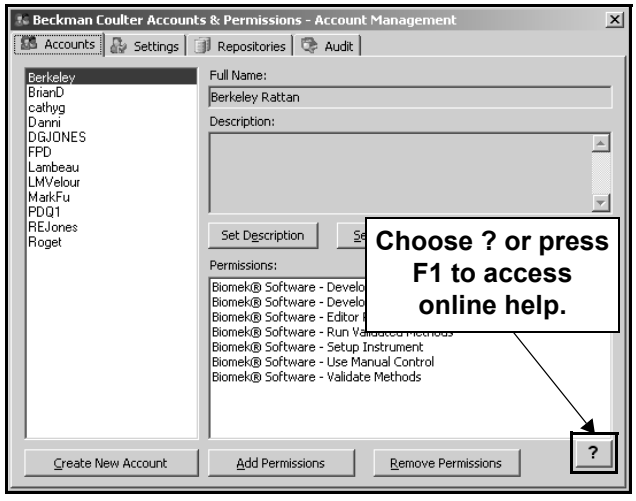


Figure 2-2. Account Management

2.3.1 Assigning Biomek Software Permissions

Permissions provide the ability to control user access to program operations. The administrator assigns permissions for each user in Account Management. Table 2-1 describes the permissions available for Biomek Software users.

Note: Refer to Account Management online help for detailed information about assigning permissions.

Table 2-1. Biomek Software Permissions

Permission	Description
Develop Methods	Allows the user to open and run methods that have not been validated, develop new methods and edit existing methods (refer to Chapter 12, *Creating and Using Methods*).
Develop Projects	Allows the user to create and edit project files (refer to Chapter 6, *Understanding and Using Project Files*).
Editor Preferences	Allows the user to modify Preferences and Log Configurations (refer to Section 29.2, *Changing Display Preferences* and Chapter 26, *Generating and Using Log Data*).
Run Validated Methods	Allows the user to open and run validated methods. A validated method is a revision of a method that cannot be modified or associated with a different instrument (refer to Section 12.15, *Checking Out a Method*).
Setup Instrument	Allows the user to configure instrument settings in Hardware Setup (refer to Chapter 4, *Configuring Hardware Setup*), the Deck Editor (refer to Chapter 5, *Preparing and Managing the Deck*), the Device Editor (refer to Section 22.4.1, *Configuring Devices Using the Device Editor*), and the Import/Export Utility (refer to Section 3.4, *Sharing Instrument Settings Using the Import/Export Utility*).
Use Manual Control	Allows the user to control instrument actions outside a method using Manual Control (refer to Chapter 27, *Using Manual Control*).
Validate Methods	Allows the user to validate a revision of a method. Once validated, that revision of the method cannot be modified or associated with a different instrument (refer to Section 12.15, *Checking Out a Method*).

2.4 Restoring the Administrator Password

Only one administrator account exists on a system with Accounts & Permissions installed. If the administrator password is lost or forgotten, Beckman Coulter Customer Technical Support must be contacted to restore access to the Account Management application.

To restore the administrator password:

1. Place the Beckman Coulter Accounts & Permissions Installer CD in the drive, and browse to the contents of the CD.
2. Double-click **Beckman Coulter Accounts & Permissions Admin Password Restore.exe**. Password Restore appears (Figure 2-3).

Figure 2-3. Password Restore

3. Contact Beckman Coulter Customer Technical Support and provide the code displayed in the upper field of Password Restore.

Note: Leave Password Restore open until Beckman Coulter Customer Technical Support supplies a new code. The new code is based on the code displayed in the upper field, which changes each time Password Restore is opened.

4. In the lower field of Password Restore, enter the new code provided by Beckman Coulter Customer Technical Support.
5. Choose **OK** to close Password Restore and accept the new code.

   OR

   Choose **Cancel** to close Password Restore without accepting the new code.
6. Follow any additional instructions provided by Beckman Coulter Customer Technical Support.

2.5 Viewing the Audit Log

Audit Log displays the audit trail for all user activity in software applications that support Beckman Coulter Accounts & Permissions. System activity is logged, even when Accounts & Permissions is set to No Support (refer to Section 2.2.2, *Setting the Level of Support For Accounts & Permissions*).

Note: Administrator activity other than changing the level of support for Accounts & Permissions is not available in the Audit Log. However, all administrator activity is logged and may be viewed in Account Management.

To view the Audit Log:

1. In the Windows® Start menu, choose **Settings>Control Panel**. Control Panel appears.
2. In Control Panel, double-click **Administrative Tools**. Administrative Tools appears.
3. In Administrative Tools, double-click **Beckman Coulter Accounts & Permissions Audit Log**. The Audit Log appears (Figure 2-4).

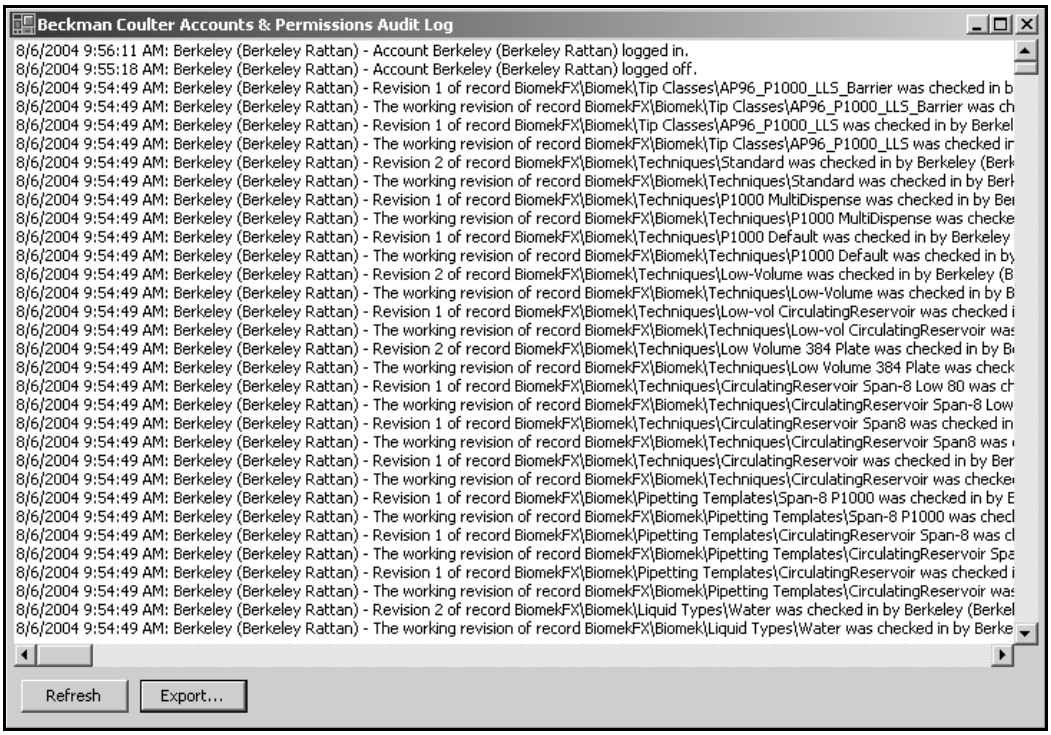


Figure 2-4. Accounts & Permissions Audit Log

4. Choose **Export** to export the entire audit log to a text file, if desired. The exported file may be opened, read, and printed in any application that supports text files.

Note: When the Audit Log is open while Biomek Software is running, system activity is logged, but not refreshed automatically in the Audit Log. Choose **Refresh** to to view system activity logged since the Audit Log was opened or the last time displayed data was refreshed.

2.6 Using the Biomek Software With Accounts & Permissions Enabled

When Beckman Coulter Accounts & Permissions is enabled, all users must log on to use Biomek Software. Only one user may be logged on at a time. Users are permitted to perform only the operations for which the administrator has assigned them permission.

Note: This section covers logging on and off Biomek Software. Refer to Chapter 12, *Creating and Using Methods* for information about checking in, validating, and signing methods when Accounts & Permissions is enabled. Refer to Section 6.4, *Deleting and Restoring Project Files* for information about checking in projects.

2.6.1 Logging Onto the Biomek Software

To log onto Biomek Software:

1. On the toolbar, choose the log on/off button (Figure 2-5). Logon appears (Figure 2-6).

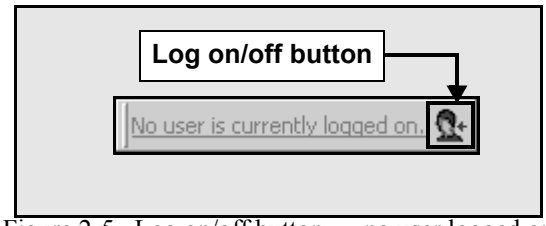


Figure 2-5. Log on/off button — no user logged on

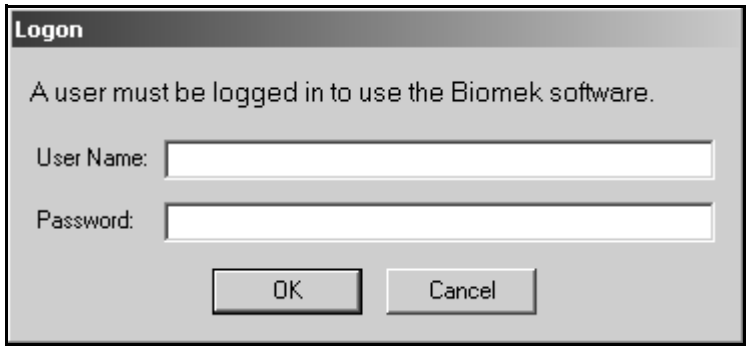


Figure 2-6. Logon

2. Enter the account **User Name** and **Password**.

   Note: The first time a user logs on using a new account, or after having the password changed by the administrator, Biomek Software automatically prompts for the password to be changed.

   The new password must be different from the original and may include alphanumeric characters and spaces and be up to 250 characters in length. Accounts & Permissions passwords are case insensitive.

3. Choose **OK** to log onto Biomek Software. The name of the user logged on appears to the left of the log on/off button (Figure 2-8).

2.6.1.1 Handling Disabled Accounts

User accounts may be disabled by the administrator, or automatically after a number of logon attempts for the account fail. Allowing accounts to be automatically disabled after a number of failed logon attempts is optional, and configured by the administrator.

When an account is automatically disabled, Administrator Notification appears (Figure 2-7). The administrator password must be entered before Biomek Software can be accessed by users.

Figure 2-7. Administrator Notification

2.6.1.2 Viewing the Logged On User's Permissions

To view the permissions of the user currently logged onto Biomek Software:

1. On the toolbar, choose the user name displayed next to the log on/off button (Figure 2-8). Current Permissions appears (Figure 2-9).

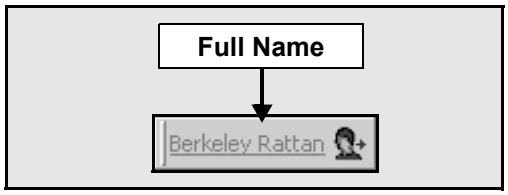


Figure 2-8. Log on/off button — user logged on

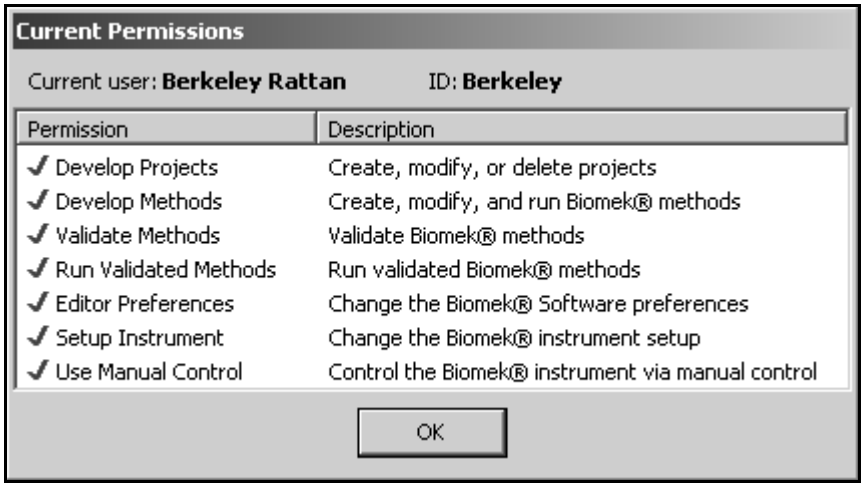


Figure 2-9. Current Permissions

2. Choose **OK** to close Current Permissions.

2.6.2 Logging Off the Biomek Software

To log off Biomek Software:

On the toolbar, choose the log on/off button (Figure 2-10). The user is logged off the system.

Note: Closing Biomek Software will not automatically log a user off. The current user will remain logged on until the software is reopened and the account is logged off, or until the login times out automatically.

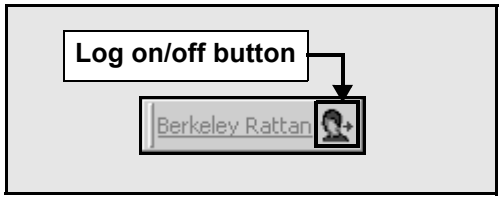


Figure 2-10. Log on/off button — user logged on

3 Using Instrument Files and Settings

3.1 Overview

An instrument file stores information about the hardware configuration and deck layout of the Biomek instrument. Instrument files can represent different Biomek instruments, or different hardware configurations for the same instrument.

The instrument configuration must accurately represent the Biomek instrument hardware to prevent collisions between pods and any on-deck components. All instrument configuration is done using Hardware Setup (refer to Chapter 4, *Configuring Hardware Setup*)and the Deck Editor (refer to Chapter 5, *Preparing and Managing the Deck*).

The Instrument menu contains options to open and save instrument files, as well as provide access to the editors to configure the instrument file.

The sections in this chapter include:

- *Saving and Opening Instrument Files* (Section 3.2) — Save the current configuration of an instrument or open an existing instrument file.
- *Restoring Instrument Settings from Backup Files* (Section 3.3) — If settings are deleted or lost, workspace settings or an entire workspace can be restored from one of the automatic daily, weekly, or monthly backup files created by Biomek Software.
- *Sharing Instrument Settings Using the Import/Export Utility* (Section 3.4) — Settings may be shared with another host computer or sent to Beckman Coulter Technical Support for analysis using the Import/Export Utility. This utility allows instrument settings (decks, framing tools, pod settings) to be imported and exported as import files (.imp).

3.1.1 Instrument Display in Method Editor

The active instrument file and project file are displayed in the status bar of the Biomek method editor (Figure 3-1). Any instrument file can be used with any project file and method. Validated methods, however, are validated for a specific instrument and are no longer validated when used with a different instrument file, even if the instrument file is equivalent to the one on which the method is validated (refer to Section 12.11, *Validating a Method*).

Note: A validated method for a specific instrument is not the same as validating a method before a run to internally test the method for errors before it is actually run. To validate a method to test for errors before it is run, check **Validate the current method before running it** in Preferences (refer to Section 29.2, *Changing Display Preferences*).

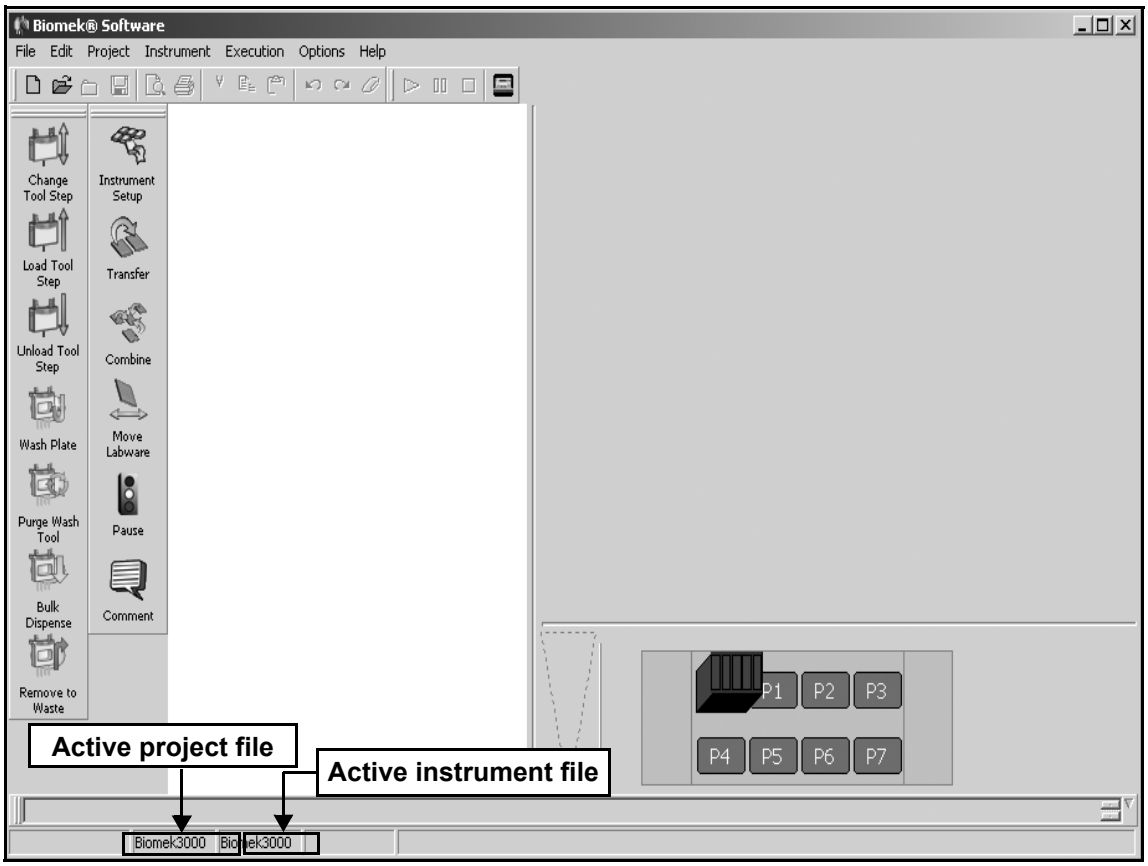


Figure 3-1. Biomek method editor

3.1.2 Contents of an Instrument File

An instrument file contains all:

- Hardware configurations — information about the instrument and integrated ALPs or devices as configured in Hardware Setup.
- Pod settings — axis limit values and other settings for the pod(s).
- Deck layouts and framing information — layout of ALPs and devices on the instrument deck as configured in the Deck Editor.

Note: When an instrument file is loaded or imported, the deck framing is reset to Unframed and the deck must be framed again.

3.2 Saving and Opening Instrument Files

Instrument files are saved as *.bif files that may be opened on any system in Biomek Software.

Instrument files can represent different Biomek instruments, or different hardware configurations for the same instrument. These instrument files can be used to:

- quickly change the instrument configuration between two or more commonly used configurations for an instrument.
- change instruments when developing methods in simulation mode for multiple instruments on one computer.
- share the instrument configuration with other users or Beckman Coulter Technical Support to ensure a method is being run using an equivalent instrument.

3.2.1 Saving an Instrument File

An instrument file may be saved at any time. The instrument file is automatically saved when another instrument file is opened or Biomek Software is closed; however, to save the current instrument file without closing it, use Save Instrument.

To save changes made to an instrument file:

From the Instrument menu, choose **Save Instrument**. The active instrument file is saved.

3.2.2 Creating a New Instrument File

A new instrument file is created by saving the current active instrument file with a new file name. The new instrument file has the same settings as the active instrument when it was saved; however, any changes made to the original instrument file are saved as the new instrument and not with the original instrument file.

To create a new instrument file:

1. From the Instrument menu, choose **Save Instrument As**. Save Instrument appears (Figure 3-2).

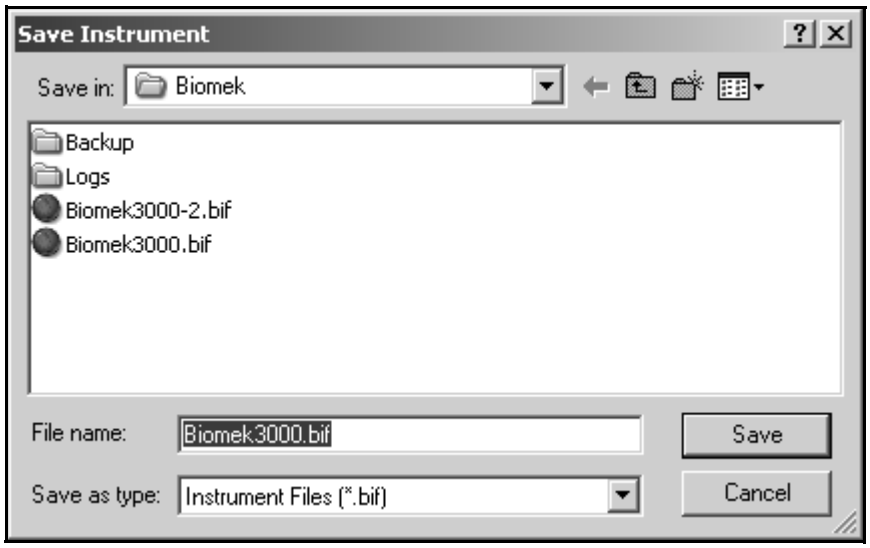


Figure 3-2. Save Instrument

2. In Save Instrument, browse to the desired drive and directory in which to save the instrument file.
3. In File Name, enter the desired file name for the instrument file.
4. Choose **Save**. The instrument file is saved in the selected drive and directory with the specified file name and opened as the active instrument file.

3.2.3 Opening an Existing Instrument File

Any existing instrument file may be opened at any time to develop methods using a specific instrument configuration.

To open an existing instrument file:

1. From the Instrument menu, choose **Open**. Open Instrument appears.

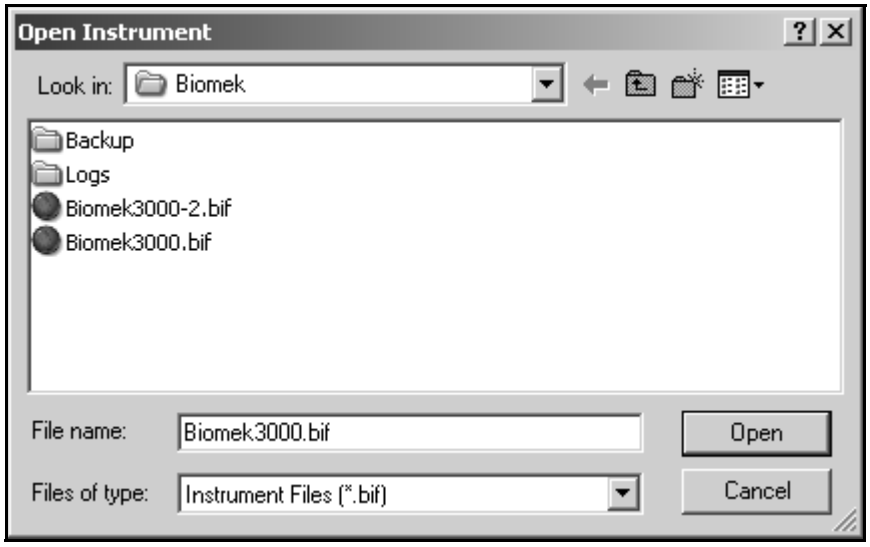


Figure 3-3. Open Instrument

2. In Open Instrument, browse to and select the desired instrument file (*.bif) to open.

Note: To open one of the daily, weekly, or monthly backup files, enter ***.*backup** in File name and press **Enter**. All the backup files are displayed in Open Instrument.

---

3. Choose **Open** to open the selected instrument file. The selected instrument file is opened.

3.3 Restoring Instrument Settings from Backup Files

Backup files are created daily, weekly, and monthly by Biomek Software whenever an instrument file is saved, typically when **File>Save Instrument** is selected or when Biomek Software is closed.

Note: By default, backup files for instruments are saved in the C:\Documents and Settings\All Users\Shared Documents\Biomek\ directory with the following naming convention:

<Instrument File Name>.bif.DailyBackup
<Instrument File Name>.bif.WeeklyBackup
<Instrument File Name>.bif.MonthlyBackup

To restore an instrument file from a backup file when settings are deleted or lost:

1. Close the Biomek main editor.
2. Open Windows Explorer and locate the instrument file (*.bif) in the shared application data directory. Typically, the path to this directory is: C:\Documents and Settings\All Users\Shared Documents\Biomek\.
3. If the instrument file needs to be replaced rather than recovered, rename the latest instrument file to <Instrument File Name>.old.

   Note: Rename the original only if it is available.

   OR

   If the instrument file needs to be recovered, rename the backup file to the instrument file name, such as <Instrument File Name>.bif.DailyBackup to <Instrument File Name>.bif.
4. Open the Biomek main editor. The instrument file has been restored.

3.4 Sharing Instrument Settings Using the Import/ Export Utility

Specific segments of a current instrument file, called instrument file settings, can be restored using the Import/Export Utility (Figure 3-4). Exporting settings allows settings to be shared with another system, while importing settings allows settings developed on another system to be used. Settings are imported from and exported to import files (.imp).

To share a method between two computers, any instrument settings different from the default installed with the software must be exported from the original computer and imported to the new computer using the Import/Export Utility.

Figure 3-4 shows how the Import/Export Utility works. The Instrument side of the utility displays the list of settings in the current instrument file. The Import File side of the utility displays the list of settings in the currently opened import file.

To restore settings of a current instrument file, settings from Instrument are dragged (exported) to the Import File. From Import File, these import settings can be dragged (imported) to the current Instrument.

Note: Settings may also be imported or exported by choosing **Import** or **Export** on the toolbar.

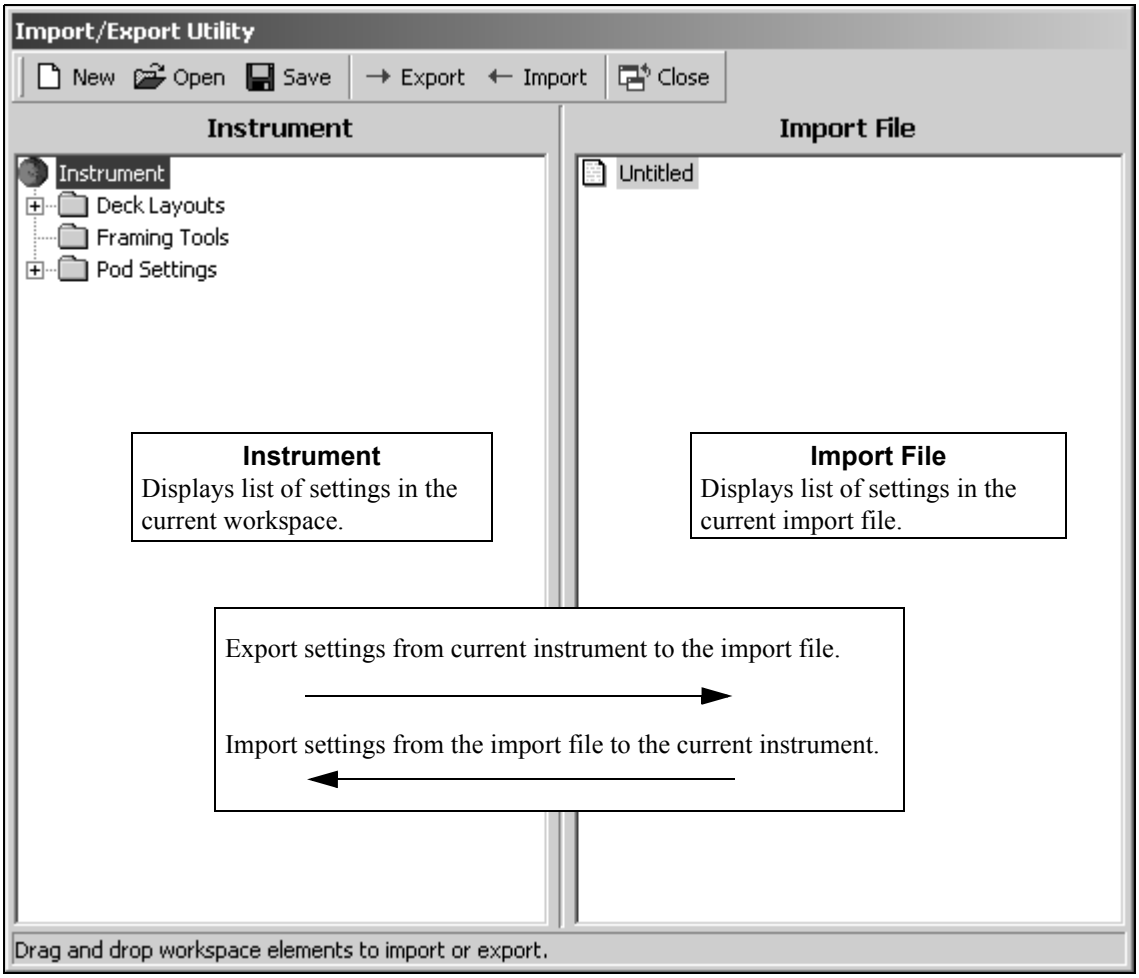


Figure 3-4. Import/Export Utility

3.4.1 Exporting Settings to an Import File

To export settings to an import file:

1. From the Instrument menu, choose **Import/Export Utility**. Import/Export Utility appears (Figure 3-5).

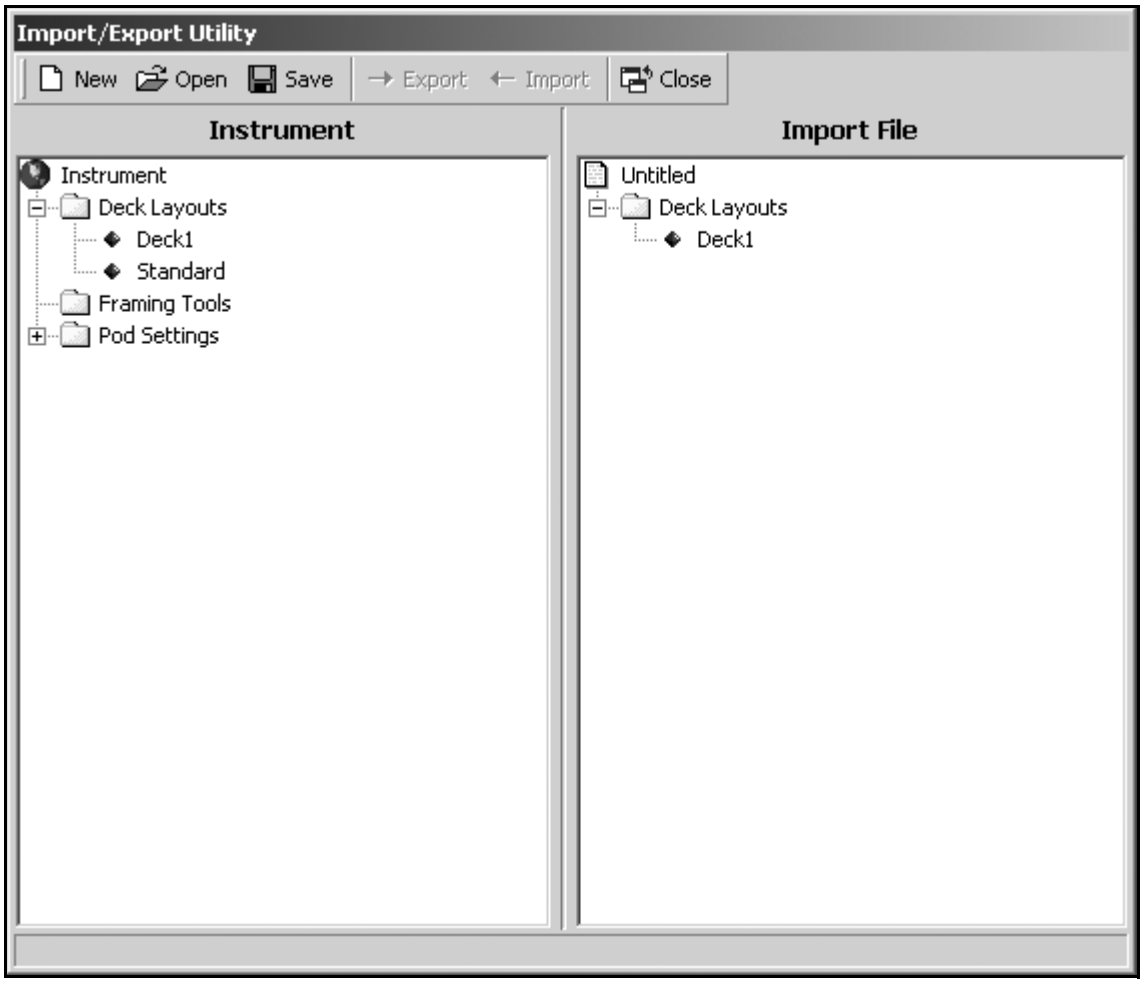


Figure 3-5. Exporting deck layout Deck1 to an import file

2. Drag and drop the desired settings from Instrument to Import File.

   OR

   Highlight the desired settings from Instrument and choose **Export**. The folder containing the desired setting and the setting itself appear in the Import File (Figure 3-5).

   Note: Dragging a folder copies all of the settings in that folder

3. Continue to export settings using step 2 until all desired settings are exported.

4. Choose **Save** to save the Biomek Import File. Save As (Figure 3-6) appears.

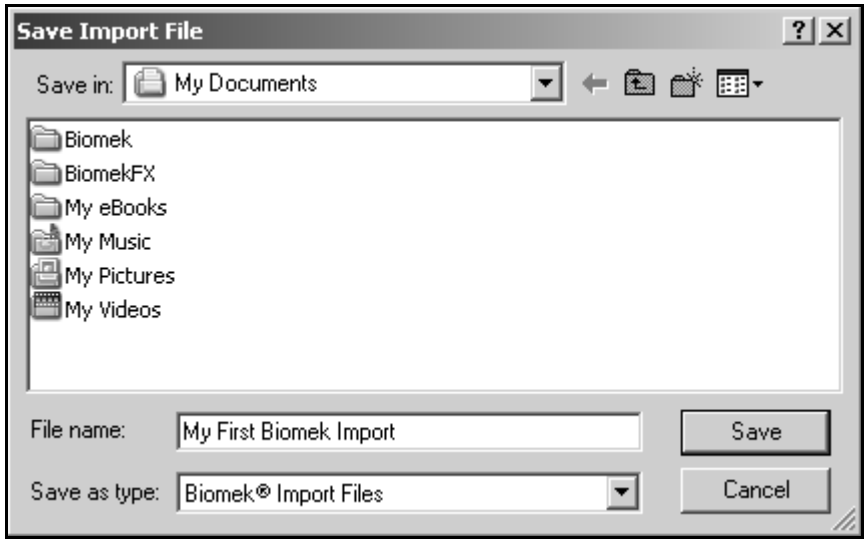


Figure 3-6. Save Import File

5. Browse to the desired file location to save the import file.
6. In File name, enter a name for the import file.
7. Choose **Save**. The import file is created and Save As closes.

Note: Note that the name of the new import file is now displayed on the top of the Import File window.

8. Choose **Close**. Import/Export Utility closes.

Note: When exporting a Deck with a stationary labware type, such as a Wash Station, the Wash Station must be present in the destination workspace or exported to the Import File.

3.4.2 Importing Settings from an Import File

To import settings from an import file:

1. From the Instrument menu, choose **Import/Export Utility**. Import/Export Utility appears (Figure 3-5).
2. Choose **Open** and open the .imp file.
3. Open the desired folder by clicking the **+** containing the desired settings from the import file.

   Note: If a setting with the same name is used in the import file and in the current instrument, it can be overwritten.

4. Drag and drop the setting from Import File to Instrument to overwrite the setting in the current workspace with the one from the import file.

   OR

   Rename the setting in the Import side, then drag and drop the setting from Import File to Instrument to not overwrite the setting.

   Note: Rename a setting by highlighting the setting, single-clicking, pausing until the name becomes editable, typing a new name, and pressing return.

   Note: Dragging an entire folder copies all of the settings in that folder.

   Note: If a setting being imported exists in the instrument file and, therefore, can be overwritten, a Confirm similar to Figure 3-7 appears. Answer Yes to overwrite the setting in the instrument file. Answer No to cancel the import of that setting. Yes to All and No to All allow multiple imported settings to overwrite the contents of the instrument file or be cancelled at the same time.

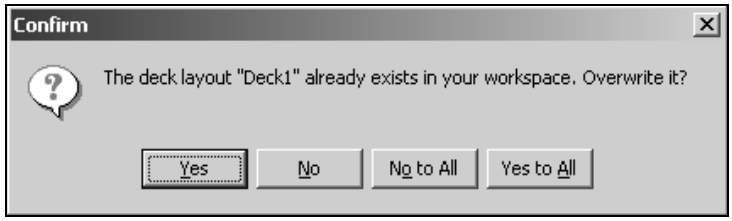


Figure 3-7. Confirmation to address to overwrite an imported setting

5. Continue to import settings using step 4 until all desired settings are imported.
6. Choose **Close** to exit the Import/Export Utility.
7. Select **Instrument>Save Instrument** to save any changes made to the workspace.

Note: When Biomek Software is updated, a backup of the instrument file is made to save previous settings. The backup instrument file is located in C:\Documents and Settings\All Users\Shared Documents\Biomek\Backup\.

3.4.3 Restoring Instrument Settings from Backup Files

To restore instrument file settings from a backup file, such as when settings are deleted or incorrectly changed:

1. From Instrument, choose **Open** to open the backup file for the instrument file. Open Instrument appears (Figure 3-8).

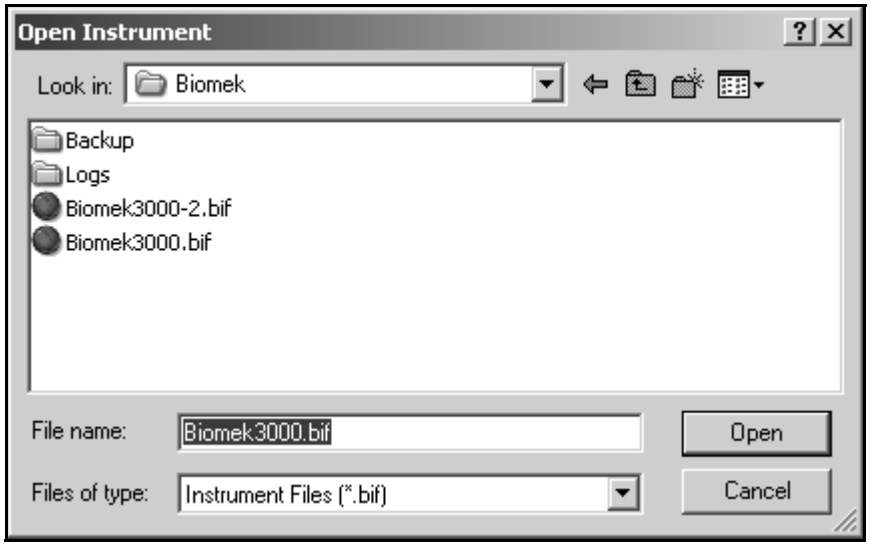


Figure 3-8. Open Instrument file

2. In File name, enter ***.*backup** and press **Enter** to show all daily, weekly, and monthly backup files in Open Instrument (Figure 3-9).

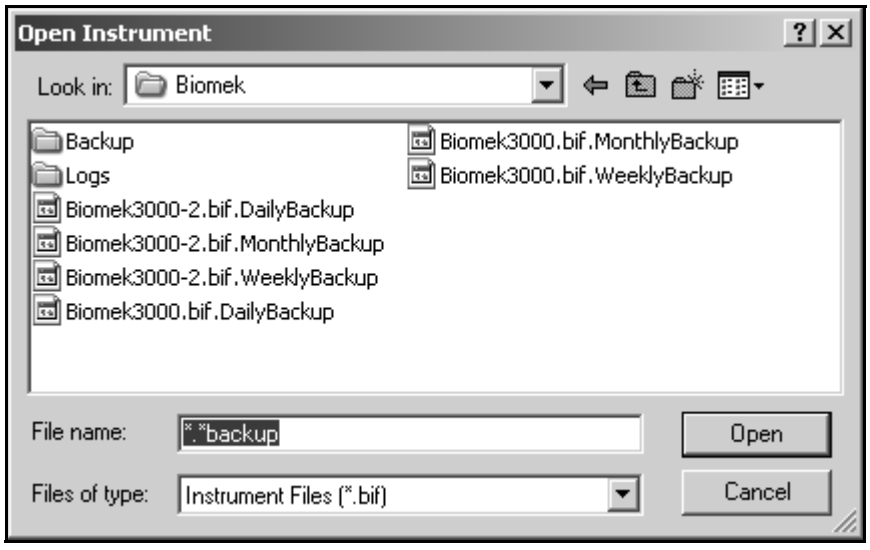


Figure 3-9. Open Instrument showing backup files

3. Select the desired backup file.
4. Choose **Open**. The selected backup file is opened as the current instrument.

5. Use the Import/Export Utility to create an import file with the desired settings from the backup instrument file (refer to Section 3.4.1, *Exporting Settings to an Import File*).
6. From the Instrument menu, choose **Open Instrument**.
7. Select the original instrument file, named **<Instrument File>.bif**.
8. Choose **Open**.
9. Use the Import/Export Utility to import settings from the import file created in step 5 (refer to Section 3.4.2, *Importing Settings from an Import File*).

Note: When Biomek Software is updated, a backup of the instrument file is made to save previous settings. The backup instrument file is located in C:\Documents and Settings\All Users\Shared Documents\Biomek\Backup\.

4 Configuring Hardware Setup

4.1 Overview

Hardware Setup is used to configure Biomek Software with the appropriate Biomek instrument information, including the instrument type and which heads and devices are available for use. The Biomek Simulator, which shows a 3-D animation of the instrument performing methods, is also configured in Hardware Setup.

After a Beckman Coulter Service Engineer has physically installed a device, the device is detected on the Biomek instrument and must be properly installed and configured in Hardware Setup. While the Service Engineer normally installs and configures new devices, it may be necessary to install, configure, and remove other devices using Hardware Setup.

For specific information on configuring Biomek instruments in Hardware Setup, refer to the appropriate hardware user's manual:

- ***FX*** — *Biomek® FX Laboratory Automation Workstation User's Manual*.
- ***3000*** — *Biomek® 3000 Laboratory Automation Workstation User's Manual*.
- ***NX-MC*** — *Biomek® NX Multichannel Laboratory Automation Workstation User's Manual*.
- ***NX-S8*** — *Biomek® NX Span-8 Laboratory Automation Workstation User's Manual*.

Refer to *ALPs User's Manual* or the appropriate integration manual for information on configuring specific ALPs and devices.

The sections in this chapter include:

4.2 Accessing Hardware Setup

Hardware Setup is accessed from within Biomek Software.

To access Hardware Setup:

From the Instrument menu, choose **Hardware Setup**. Hardware Setup appears (Figure 4-1).

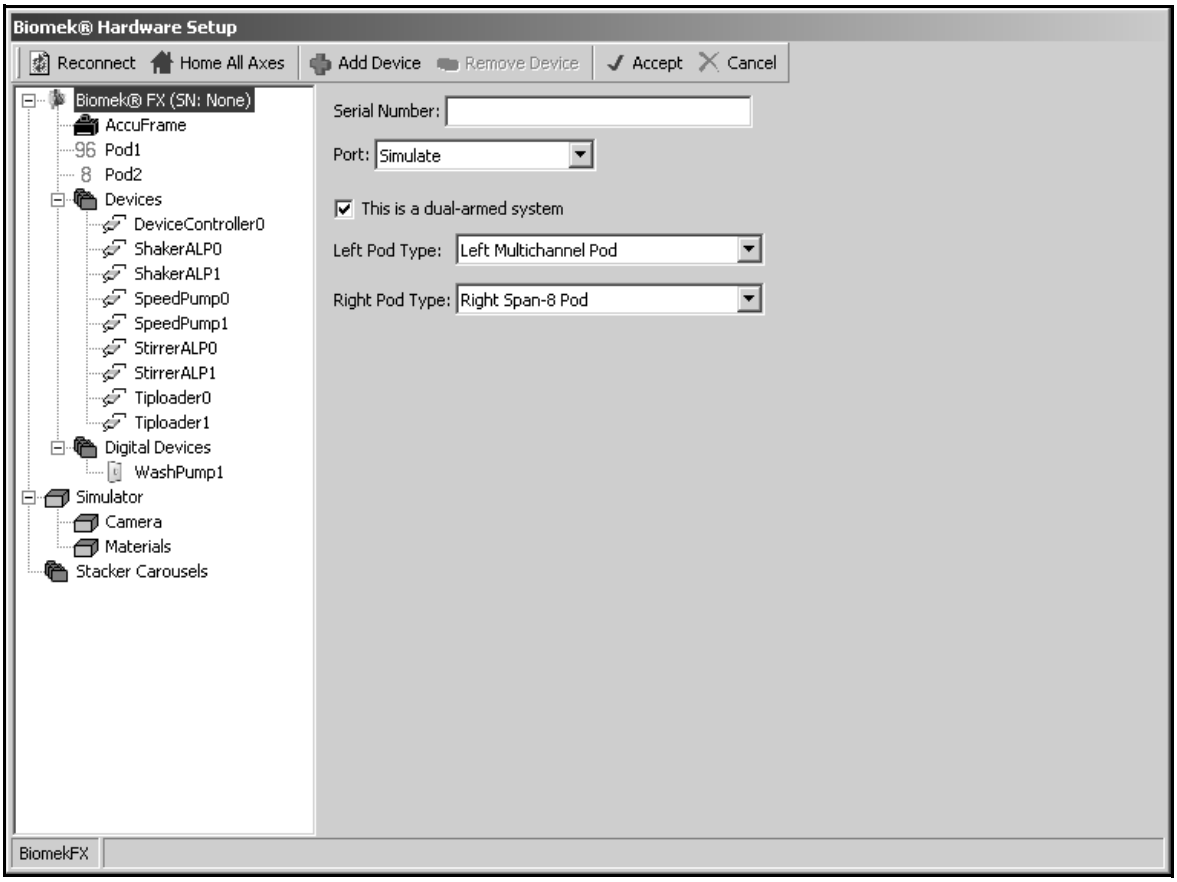


Figure 4-1. Hardware Setup for a Biomek FX instrument with a Multichannel Pod and Span-8 Pod

Note: The devices displayed in Hardware Setup are dependent on instrument type and configuration.

4.3 Understanding the Options in Hardware Setup

An understanding of the options on the toolbar in Hardware Setup is necessary to properly install, configure, and remove devices.

Table 4-1 lists and describes the toolbar options in Hardware Setup:

Table 4-1. Hardware Setup Options

Option	Description
Reconnect	Allows Hardware Setup to reexamine the devices present. Choose this option to determine what devices are present rather than closing and reopening Hardware Setup.
Home All Axes	Gives the instrument a point of reference from which to make subsequent moves. For a single-pod system, home position is left, back. For a dual-pod system, home position for the first (left) pod is left, back and for the second (right) pod is right, back. **Note:** Pods should be homed each time the instrument is powered on. Depending on the type of pods on the system, a Warning appears. After confirming that the actions have been addressed properly, choose **OK**.
Add Device	Installs a device.
Remove Device	Removes a device.
Accept	Saves all changes to the instrument and closes Hardware Setup. Choose this option after the device has been installed and configured.
Cancel	Closes Hardware Setup without saving the modifications to the instrument.

4.4 Configuring the Biomek Simulator

When a method is run in Simulate mode, the Biomek Simulator appears, showing an animated 3-D model of the instrument performing the method. Simulator settings can be configured in Hardware Setup.

Note: Modifying simulator settings is optional. The default settings are appropriate for most computers.

Configuring the simulator includes:

- *Configuring Simulator Settings* (Section 4.4.1).
- *Configuring Camera Controls* (Section 4.4.2).
- *Configuring Materials* (Section 4.4.3).

4.4.1 Configuring Simulator Settings

Simulator configures view settings, including animation speed, simulator display size, and image quality. Many of the view settings increase or decrease the image quality of the 3-D model shown in simulations. In general, increasing image quality, such as enabling blending, requires a faster computer to run the animated simulation smoothly. Conversely, decreasing image quality requires less computing power, and will run simulations more smoothly on slower computers.

The default settings in Simulator provide a good balance between image quality and smooth animation playback on most computers. Change the settings only if higher image quality or smoother playback is desired.

To configure simulator settings:

1. From the left pane of Hardware Setup, choose **Simulator**. The Biomek Simulator settings appear (Figure 4.2).

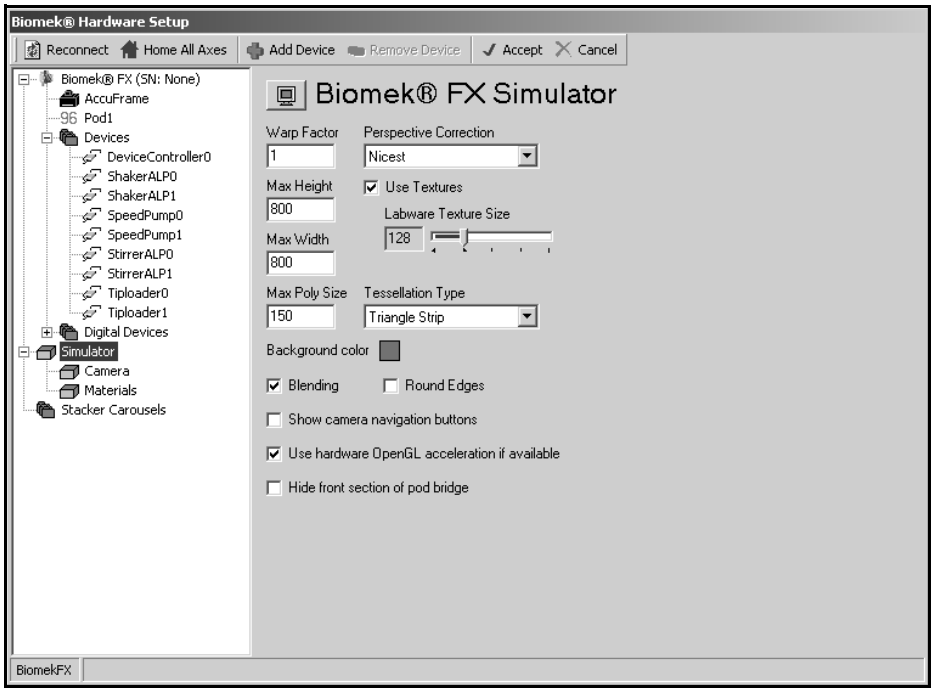


Figure 4-2. Hardware Setup — configuring the simulator settings

2. In Warp Factor, change the playback speed for simulated methods. Warp Factor 1 runs simulated methods in real time.
3. Enter the **Max Height** in pixels for the simulator display.
4. Enter the **Max Width** in pixels for the simulator display.
5. In Max Poly Size, enter the maximum size of the polygons that make up the model of the instrument shown in the simulator. Decreasing the polygon size creates a more detailed simulator view, but requires more computing power. Increasing the polygon size creates a less detailed simulator view, but requires less computing power.
6. Choose the method of Perspective Correction:
   - **Nicest** — performs more accurate perspective correction; better for faster computers.
   - **Fastest** — performs less accurate correction; better for slower computers.
   - **Don't Care** — Biomek Software automatically chooses the most appropriate correction method.
7. Choose **Use Textures** to include textures, such as microplate wells, on the instrument and labware surfaces displayed in the simulator.
8. If Use Textures is chosen, choose a **Labware Texture Size**, if desired. Dragging the slider to the right increases texture detail; dragging to the left reduces texture detail.
9. Change Tesselation Type to **Triangle Fan** or **Quad Strip** if a slight enhancement in image quality is desired. The default setting, Triangle Strip, is adequate for most computers.
10. Choose the colored box to the right of Background Color to change the background color in the simulator display. Color appears (Figure 4-3).

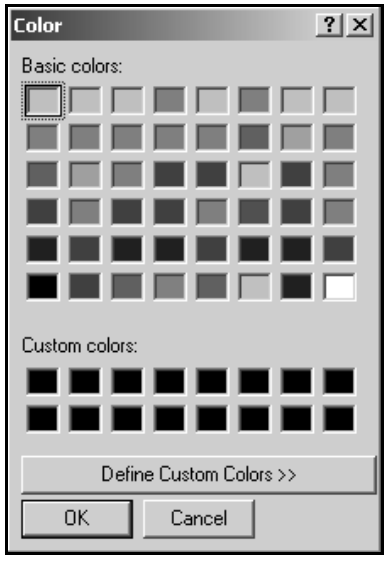


Figure 4-3. Selecting a background color

11. Select a new color, or define a custom color for the simulator background.

12. Choose **OK** to set the new background color.

    OR

    Choose **Cancel** to retain the original background color.

13. Select **Blending** to render semi-transparent objects, such as tips, correctly.

    Note: When Blending is disabled, semi-transparent objects appear opaque; for example, liquid is not visible inside tips. Leaving Blending disabled is recommended for slower computers.

14. Select **Round Edges** to smooth out and round the edges of the instrument in the simulator display.

15. Select **Show camera navigation buttons** to display camera navigation controls by default during simulated method runs and in Simulator Preview.

    Note: The camera is the position from where the 3-D model is being viewed. The camera navigation controls are used to move or rotate the camera, which changes the viewing angle of the model in the simulator.

    Note: Camera navigation controls may also be toggled on and off during simulated method runs by pressing the tilde (~) key to enable the simulator controls (refer to Section 12.18.1.1.1, *Using the Simulator Controls*).

16. Select **Use hardware OpenGL acceleration if available** to provide smoother rendering of the model and animation on supported computers.

17. Hide the bridge or canopy of the instrument to provide an unobstructed view of the pod(s) performing the steps in the method.

    - ***FX***, ***3000*** — Select **Hide front section of pod bridge**.
    - ***NX-MC***, ***NX-S8*** — Select **Hide Canopy**.

18. Choose **Preview** to access Simulator Preview at any time during simulator configuration (refer to Section 4.4.1.1, *Viewing the Simulator Preview*).

4.4.1.1 Viewing the Simulator Preview

Simulator Preview shows the 3-D model of the instrument, including current configuration changes, as it appears in animated simulations. Simulator Preview is accessible from Simulator, Camera, or Materials at any time.

To view the Simulator Preview:

1. Choose **Preview** to view changes made to the settings, if desired. Simulator Preview appears (Figure 4-4).

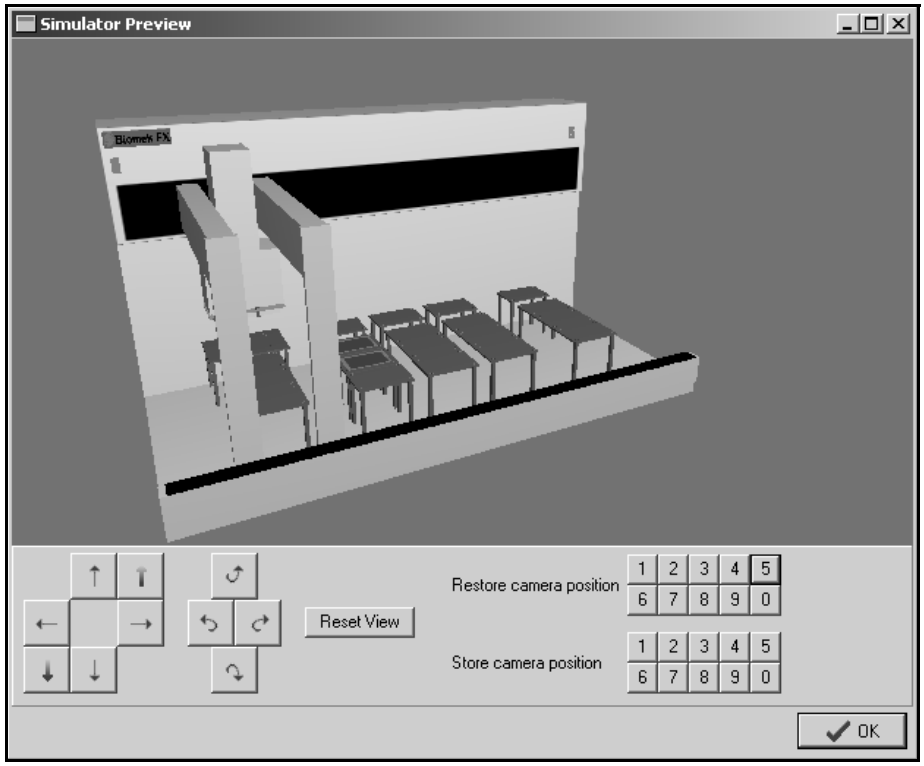


Figure 4-4. Simulator Preview with camera navigation buttons enabled

2. Change the view by placing the cursor in the simulator display, then clicking and dragging the mouse in the desired direction of rotation.

   OR

   Change the view by clicking the cursor in the simulator display and using the keyboard control keys defined in Camera (refer to Section 4.4.2, *Configuring Camera Controls*).

   OR

   Use the camera navigation buttons to change, save, and reset the view (Figure 4-5). The camera navigation buttons are displayed only when enabled in Simulator (refer to Section 4.4.1, *Configuring Simulator Settings*).

Note: The camera is the position from where the 3-D model is being viewed. The camera navigation buttons move or rotate the camera, which changes the angle at which the model is being viewed in the simulator.

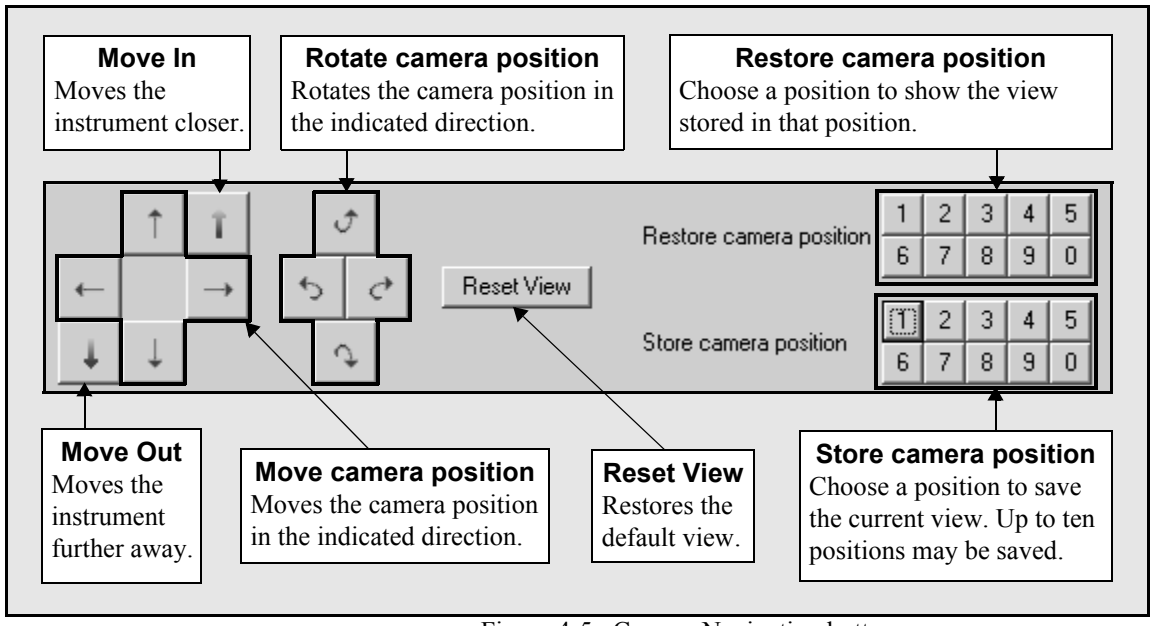


Figure 4-5. Camera Navigation buttons

3. Choose **OK** to close Simulator Preview and return to the simulator configuration in Hardware Setup.

4.4.2 Configuring Camera Controls

The camera is the position from where the 3-D model of the instrument is being viewed. To change the view of the model, the camera can be moved using the keyboard, mouse, or optional camera navigation buttons. In Camera, movements are called Actions. Keyboard and mouse controls are called Bindings. Keyboard and mouse controls can be created, edited, or deleted in Camera.

Note: Camera navigation buttons are enabled and disabled in Simulator (refer to Section 4.4.1, *Configuring Simulator Settings*).

To add or modify a camera control:

1. From the left pane of Hardware Setup, expand the **Simulator** tree, if necessary, and choose **Camera**. Camera appears (Figure 4-6).

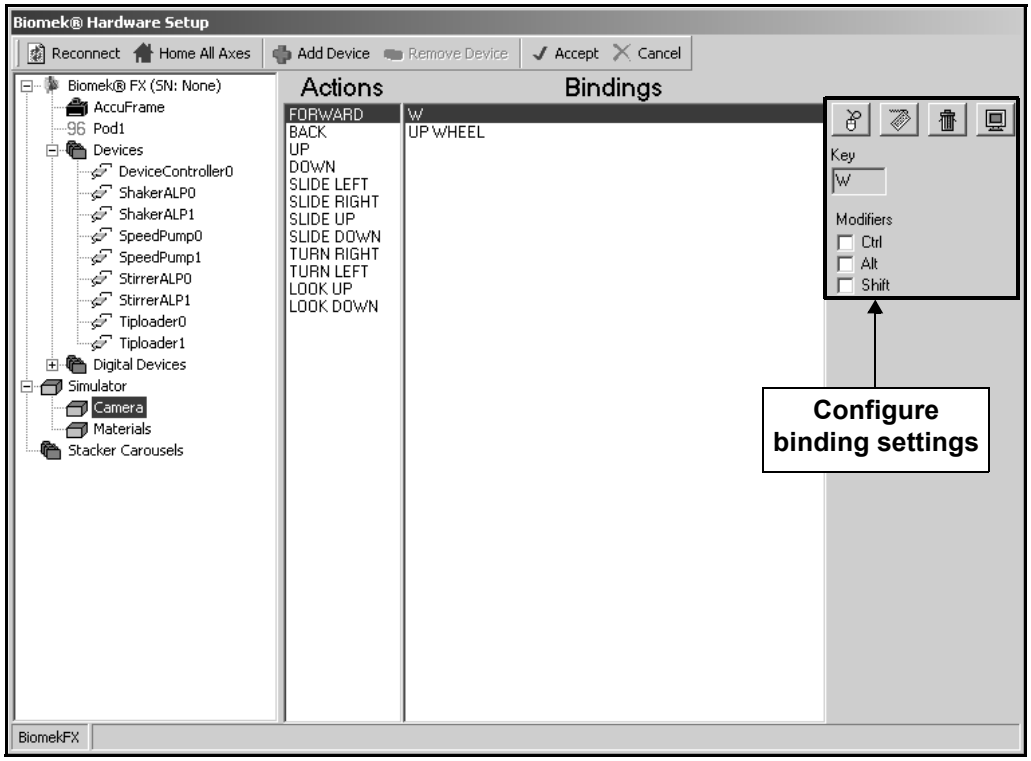


Figure 4-6. Hardware Setup — configuring camera controls

2. In the Actions pane, select the camera control to modify. The current keyboard and mouse control settings appear in Bindings.
3. In Bindings, select the binding to delete or modify.
4. Choose **Delete Bind** to delete the selected binding.

   OR

   Modify the binding. Modifications include:

   - *Creating or Editing a Mouse Binding* (Section 4.4.2.1).
   - *Recording or Editing a Key Binding* (Section 4.4.2.2).

4.4.2.1 Creating or Editing a Mouse Binding

Mouse bindings control camera actions using mouse controls. They may be configured to use a single mouse control, a combination of mouse controls, or a combination of mouse controls and modifier keys on the keyboard.

Note: The mouse buttons, wheel, and directional movement are all considered mouse controls.

To create or edit a mouse binding:

1. To create a new mouse binding, choose **Add Mouse Bind**.

   OR

   To edit an existing mouse binding, select the desired binding.

2. In Mouse Command, choose the desired command.
3. In Modifiers, select any desired keyboard modifiers and/or mouse commands.

   Note: The Ctrl, Alt, and Shift keys are keyboard modifiers. Mouse command modifiers are Right, Left, and Middle, which represent mouse buttons and Double, which represents double-clicking.

4. If creating a new mouse binding, choose **Add Mouse Bind** to add the new binding to the selected Action.

5. To test the mouse binding, choose **Preview** to access Simulator Preview at any time during simulator configuration (refer to Section 4.4.1.1, *Viewing the Simulator Preview*).

4.4.2.2 Recording or Editing a Key Binding

Key bindings control camera actions with keys on the keyboard. They may be configured to require a single key, such as "**T**", or a combination of a key and modifier.

To record or edit a key binding:

1. To create a new key binding, choose **Record Key Bind**.

   OR

   To edit an existing key binding, select the desired binding.

2. If creating a new binding, press the desired key.
3. In Modifiers, select a modifier key, if desired.

4. To test the key binding, choose **Preview** to access Simulator Preview at any time during simulator configuration (refer to Section 4.4.1.1, *Viewing the Simulator Preview*).

4.4.3 Configuring Materials

Each component of the 3-D instrument model is made of a material which has visual properties, such as color and reflectivity, specified. Properties can be edited in Materials. However, configuring the properties of materials is not necessary or recommended.

Materials can also be created and deleted using the buttons in Materials. Materials *should never* be deleted, because the deleted material will no longer be visible in the simulator. Likewise, materials created by users will not appear in the simulator either.

Note: Always preview changes in Simulator Preview before saving the new configuration. Refer to Section 4.4.1.1, *Viewing the Simulator Preview*, for more information.

To configure Materials:

1. From the left pane of Hardware Setup, expand the **Simulator** tree, if necessary, and choose **Materials**. Materials appears (Figure 4.4).

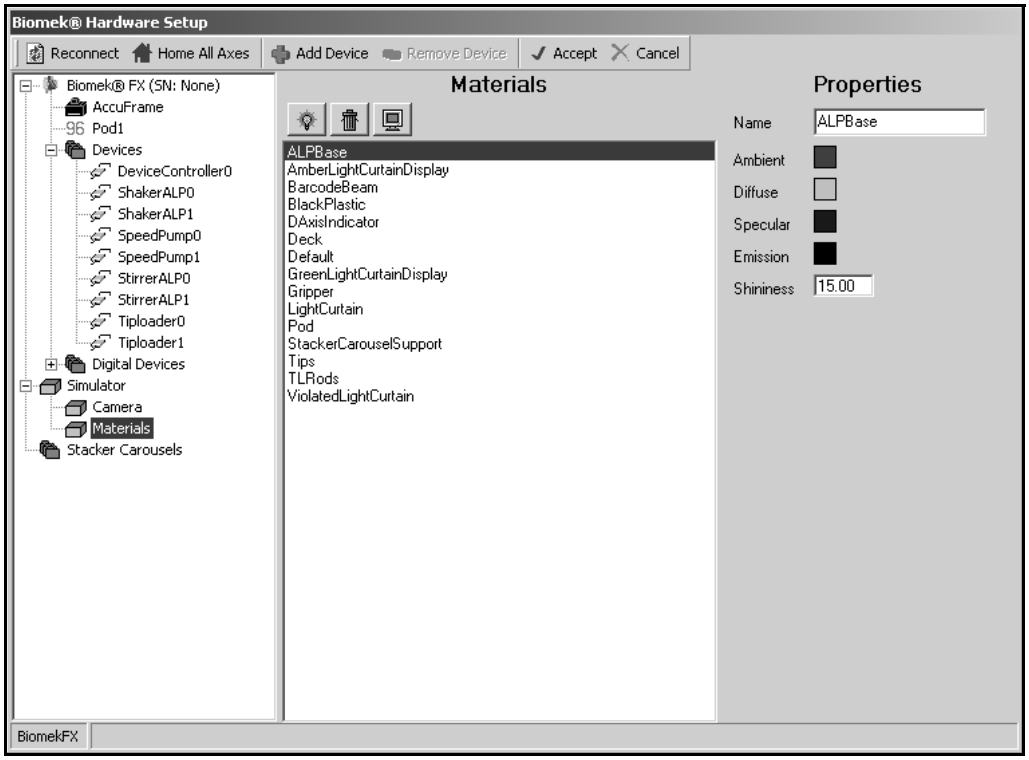


Figure 4-7. Hardware Setup — configuring materials

Note: In Materials, select the material to edit. The properties of the material appear. Table 4-2 provides descriptions of each material

2. In Properties, *do not* change the Name. Changing the name of a material causes it to no longer be visible in the simulator.

3. Choose the colored box to the right of a color parameter to change the color of the material. Color appears.

   Note: Ambient and Diffuse define the color of the material when light is present. Specular defines the color of specular highlights (glare). Emission defines the color of the material in the absence of light.

4. In Color, select a new color, or define a custom color for the color parameter.
5. Enter a new value for Shininess, if desired.

   Note: Shininess defines the reflectivity of the material on a scale of 0 – 100, with 100 being the most reflective.

6. To view changes made to materials, choose **Preview**. to access Simulator Preview at any time during simulator configuration (refer to Section 4.4.1.1, *Viewing the Simulator Preview*).

Table 4-2. Materials

Material	Description
ALPBase	Base or stand of an ALP.
AmberLightCurtainDisplay	Color of the front panel indicator light during a method run.
BarcodeBeam	Laser beam emitted by a barcode reader.
BlackPlastic	Biomek 3000 tool bodies.
DAxisIndicator	Color band that encircles the head to show upward and downward movement.
Deck	Instrument deck.
Default	Default color of a material when deleted from the simulator.
GreenLightCurtainDisplay	The color of the front panel indicator light when the instrument is not running a method.
Gripper	Gripper.
LightCurtain	Color of light curtain during a method run.
Pod	Instrument pod.
StackerCarouselSupport	Brackets that support a Stacker Carousel.
Tips	Tips.
TLRods	Tip Loader locking rods.
ViolatedLightCurtain	Color of light curtain after a violation has occurred.

5 Preparing and Managing the Deck

5.1 Overview

The Deck Editor is used to define and change the deck configurations stored in the current instrument file. A deck is a software representation of the Biomek instrument deck (Figure 5-1) and can be stored and used for multiple methods; however, the software deck must always match the physical deck of the instrument used in the method.

A deck is created and modified in the Deck Editor, configured for the method in the Instrument Setup step, and used extensively by the software. A deck also stores framing information and device associations for each position on the deck.

The Deck Editor can be used to:

- Create new decks.
- Delete unused decks.
- Define the types and locations of ALPs, labware positioners, and devices positioned on a Biomek instrument deck.
- Control device associations.
- Frame (teach) the physical positions of ALPs, labware positioners, and devices.

The sections in this chapter include:

The Deck Editor displays decks to be used during the method-building process. A deck is set as the default deck in the Deck Editor. The default deck appears when the Deck Editor is opened and is selected automatically when the Instrument Setup step is inserted into a method. The Instrument Setup step allows selection of any previously defined deck (Figure 5-1).

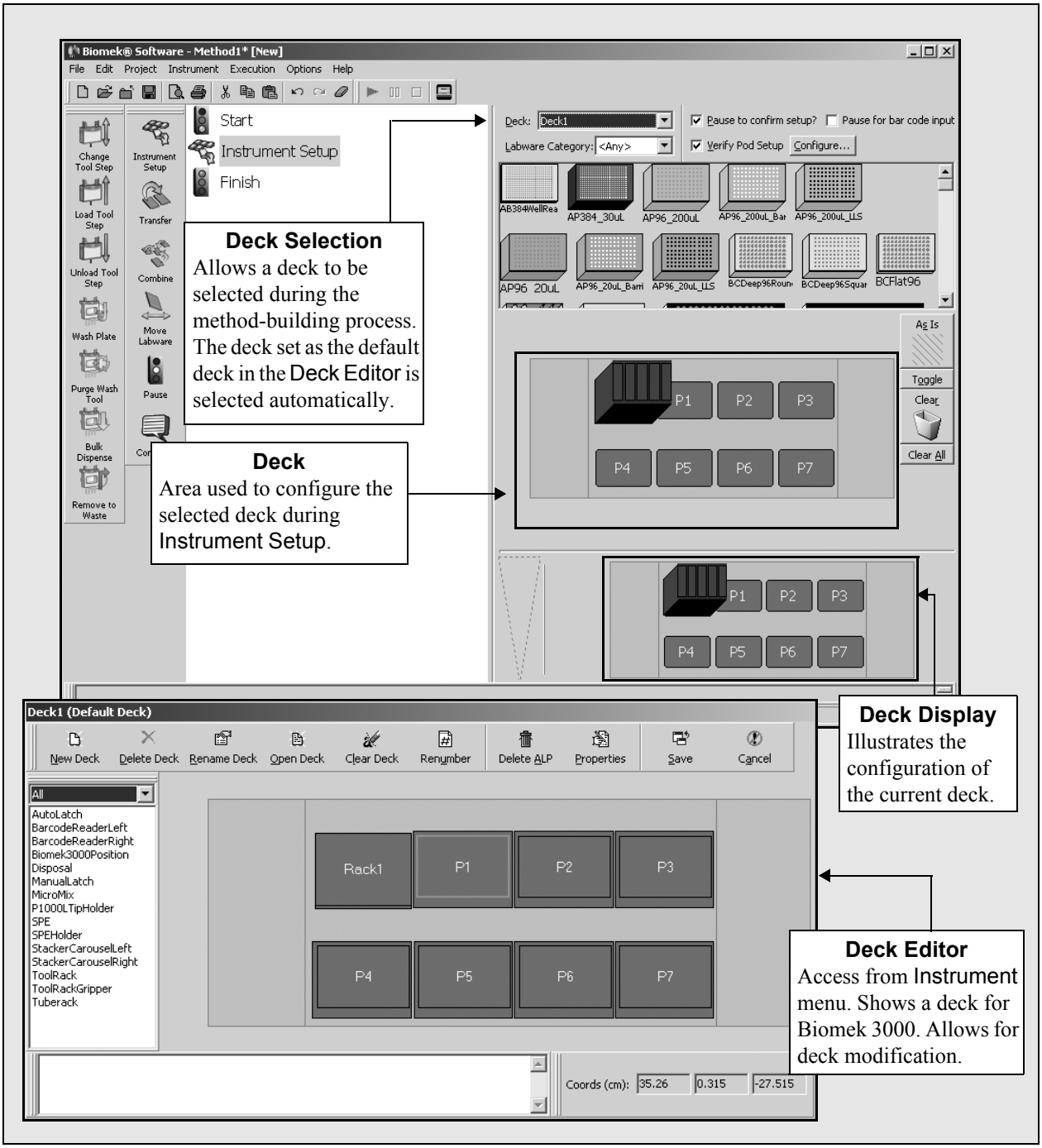


Figure 5-1. Deck relationship in Biomek 3000

5.1.1 Framing the Deck

Framing the deck allows the Biomek Software to remember each deck position for each Biomek pod, and the Deck Editor is used to set the properties of each ALP and position. Several properties, such as Position Span and Labware Offset, are preprogrammed into Biomek Software; however, other properties, such as Position, must be set by teaching.

The position offsets are taught using the framing tools with the Biomek instrument. However, different framing tools are used according to the type of instrument, type of pod, or the specific deck position. Refer to the appropriate hardware user's manual for information on framing the specific Biomek instrument.

5.2 Understanding the Deck Editor

The Deck Editor allows for creation and modification of decks. While the instructions for opening, creating, renaming, and deleting decks are the same, decks for the specific Biomek instrument have different positions since decks in the Deck Editor are based on the physical decks of the instruments.

To access the Deck Editor:

Select **Instrument>Deck Editor**. The Deck Editor appears (Figure 5-2).

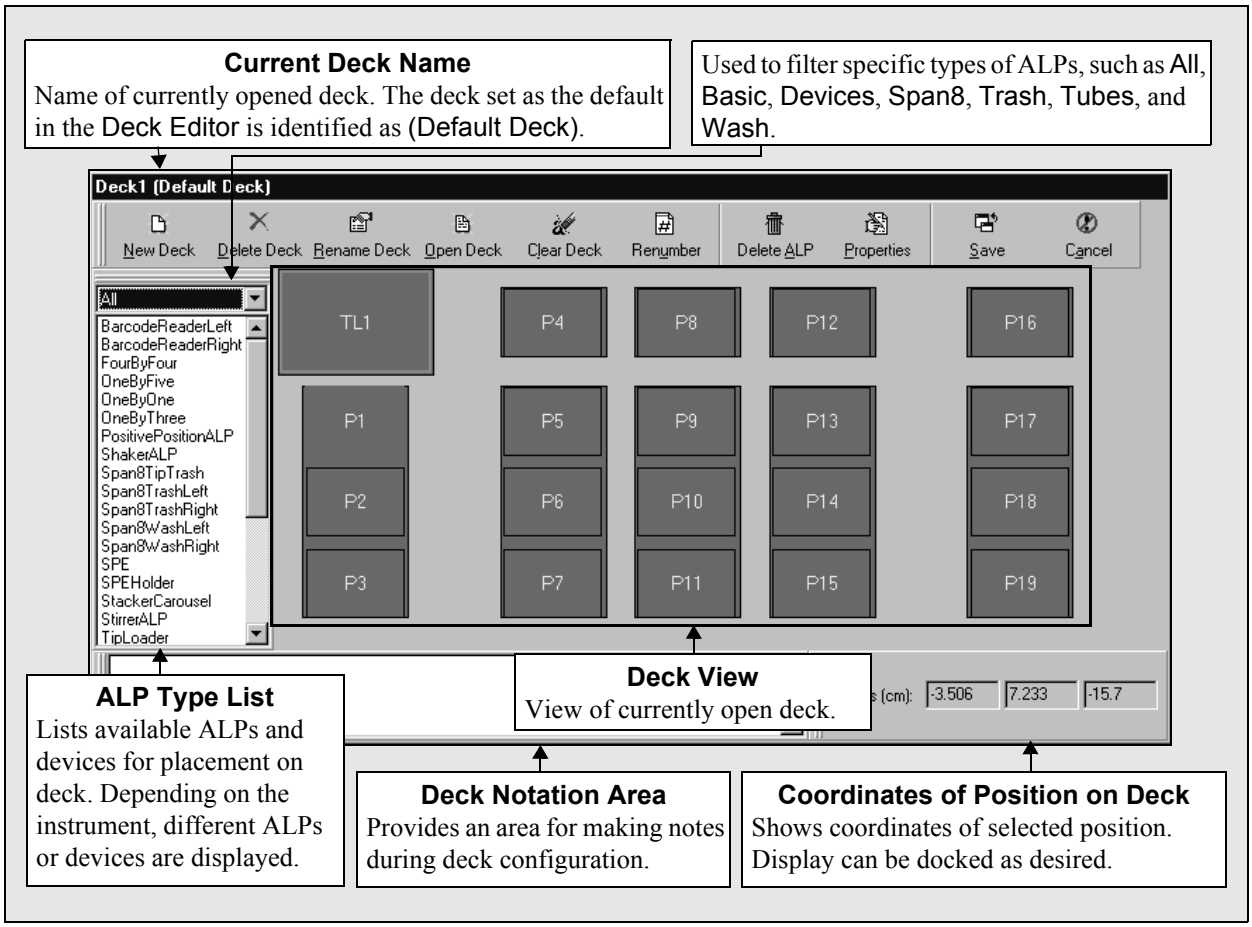


Figure 5-2. Deck Editor showing Deck1 for a Biomek FX

The Deck Editor has several options on the toolbar used to modify decks (Table 5-1).

Table 5-1. Deck Editor Options

Options	Description
New Deck	Creates a new deck based upon the current deck.
Delete Deck	Permanently removes the current deck.
Rename Deck	Changes the current deck name.
Open Deck	Opens an existing deck and sets it as the current deck.
Clear Deck	Removes all ALPs and devices from the deck.
Renumber	Renames all of the deck items based on position starting in the upper left corner.
Delete ALP	Removes an ALP or device from the deck.
Properties	Opens the properties for the selected deck position or ALP.
Save	Saves the deck and closes the Deck Editor.
Cancel	Cancels the changes made to the opened deck and closes the Deck Editor.

5.2.1 Viewing the ALP Types List

The ALP Types List (Figure 5-2) shows all standard ALPs, labware positioners, and devices available to place on the deck. Only the ALPs, labware positioners, and devices that can be placed on the deck for the current instrument type are displayed. Use the filter to list only specific types of ALPs.

CAUTION: Make sure the correct ALP is chosen when configuring the deck setup in the Deck Editor. ALPs vary in height and failure to choose the correct ALP in the Deck Editor may result in collisions between pod(s) and ALPs during operation.

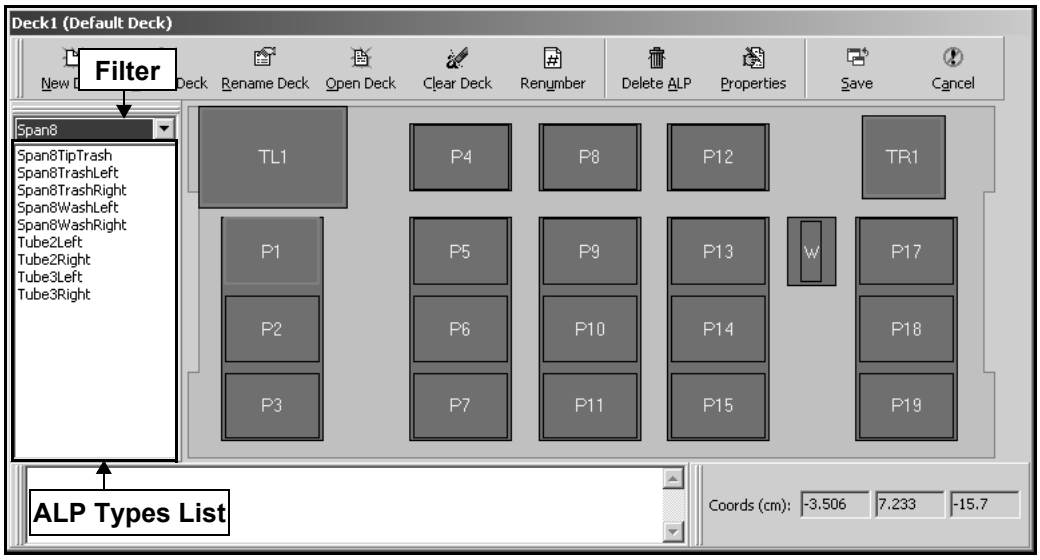


Figure 5-3. Deck Editor for a Biomek FX

Note: Refer to Section 5.4.2, *Adding ALPs and Deck Positions*, for more information on adding ALPs to a deck. Refer to the *ALPs User's Manual* for more information about specific ALPs.

5.2.2 Biomek FX Deck

Each initial Biomek FX deck (Figure 5-2) contains 1 Tip Loader ALP (TipLoader) and 19 deck positions (areas where ALPs may be placed). The 19 deck positions are made of five 1 x 3 Passive ALPs and four 1 x 1 Passive ALPs.

- Deck1 — initially has 1 Tip Loader ALP position and 19 deck positions; no tip loader device is associated with the tip loader position; can be modified to include other ALPs and other external hardware devices (Figure 5-2).
- Standard — has 1 Tip Loader ALP position and 19 deck positions; no tip loader device is associated with the tip loader position; cannot be modified; can be copied to create new decks.

Note: Do not use the Standard deck in a method; it cannot be modified and is used only to create new decks by using the New Deck option.

5.2.3 Biomek 3000 Deck

Each initial Biomek 3000 deck (Figure 5-4) contains 1 tool rack position (ToolRack) and 7 deck positions (areas where tool racks and devices may be placed).

- Deck1 — initially has 1 tool rack position and 7 deck positions; can be modified to include other tool racks and devices (Figure 5-4).
- Standard — has 1 tool rack position and 7 deck positions; cannot be modified; can be copied to create new decks

Note: Do not use the Standard deck in a method; it cannot be modified and is used only to create new decks by using the New Deck option.

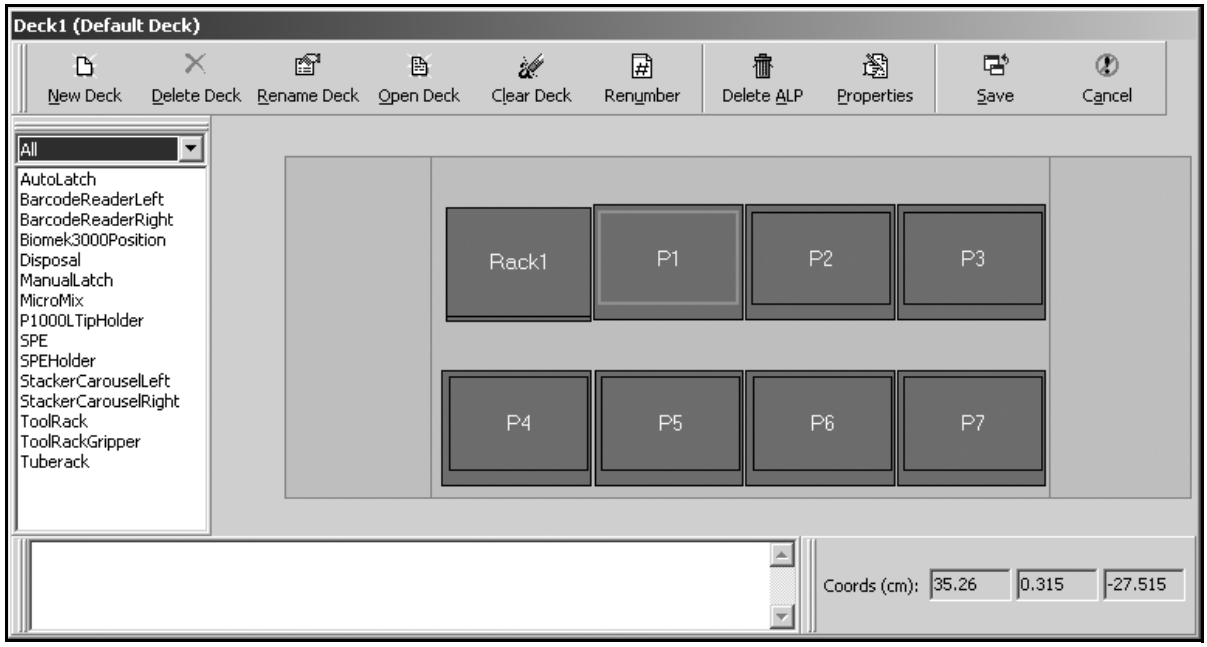


Figure 5-4. Deck Editor for a Biomek 3000

5.2.4 Biomek NX-MC Deck

Each initial Biomek NX-MC deck (Figure 5-5) contains one Tip Loader ALP (TipLoader) position and 12 labware positions. One 4 by 3 High Density ALP position provides the 12 labware positions. Two more ALPs may be placed in the back row to allow a total of 15 positions.

- Deck1 — initially has one Tip Loader ALP position and 12 labware positions; no tip loader device is associated with the tip loader position; can be modified to include other ALPs and other external hardware devices (Figure 5-5).
- Standard — one Tip Loader ALP position and 12 labware positions; no tip loader device is associated with the tip loader position; cannot be modified; can be copied to create new decks.

Note: Do not use the Standard deck in a method; it cannot be modified and is used only to create new decks by using the New Deck option.

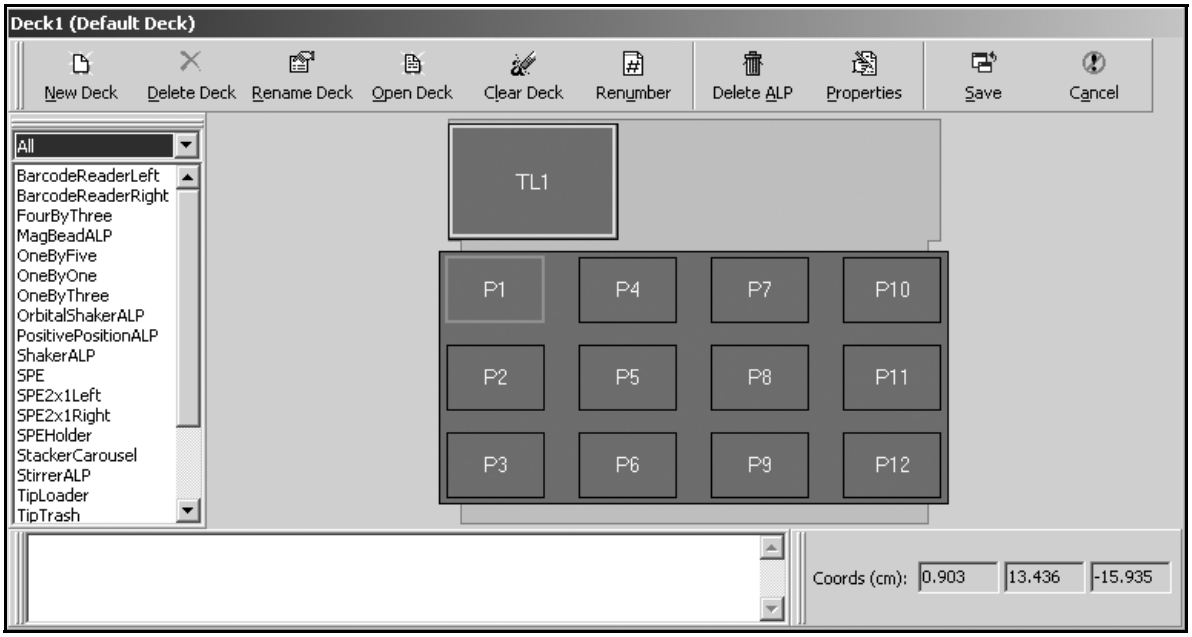


Figure 5-5. Deck Editor for a Biomek NX-MC

5.2.5 Biomek NX-S8 Deck

Each initial Biomek NX-S8 deck (Figure 5-6) contains one Span-8 Disposal ALP (Span8TipTrash) position, one Span-8 Tip Wash position (Span8WashLeft), and 12 labware positions. One 4 by 3 High Density ALP position provides the 12 labware positions. One more ALP may be placed in the back row to allow a total of 15 positions.

- Deck1 — initially has one Span-8 Disposal ALP position, one Span-8 Tip Wash position, and 12 labware positions; can be modified to include other ALPs and other external hardware devices (Figure 5-6).
- Standard — has one Span-8 Disposal ALP position, one Span-8 Tip Wash position, and 12 labware positions; cannot be modified; can be copied to create new decks.

Note: Do not use the Standard deck in a method; it cannot be modified and is used only to create new decks by using the New Deck option.

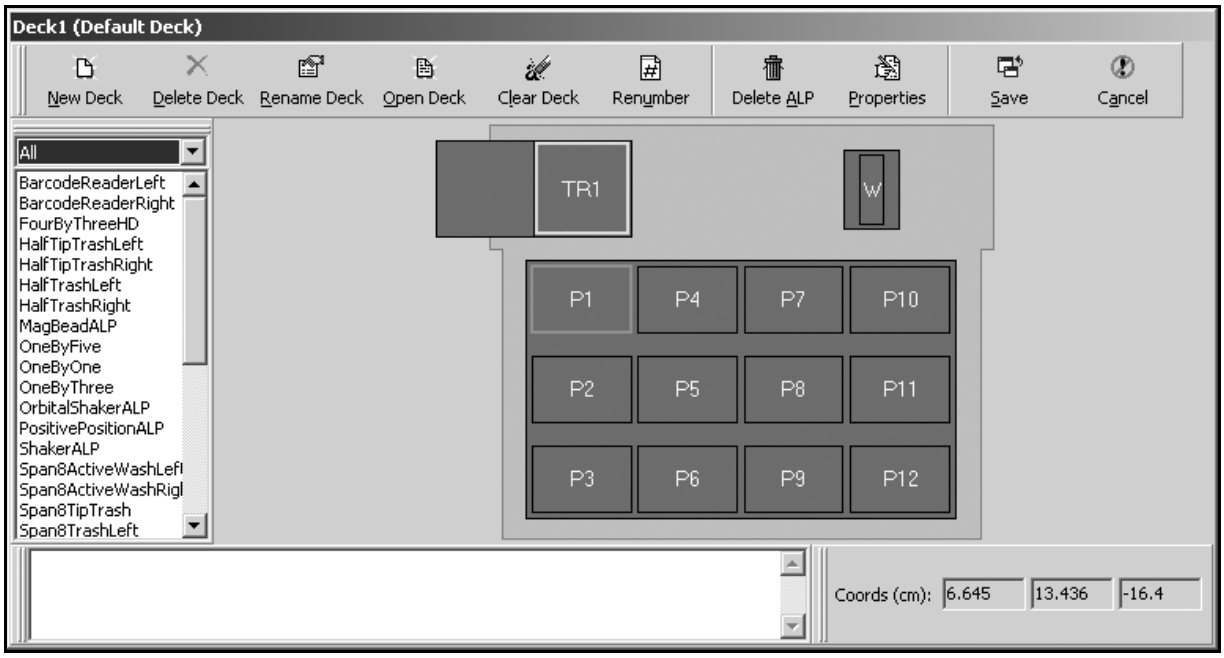


Figure 5-6. Deck Editor for a Biomek NX-S8

5.3 Opening, Selecting, Creating, Deleting, or Renaming a Deck

The Deck Editor is used to open, select, create, delete, or rename a deck in the Biomek Software.

5.3.1 Opening and Selecting a Deck

A deck is selected in Deck Editor as the default deck. Each time an Instrument Setup step is inserted into a method, the default deck appears.

To select a deck:

1. In the Deck Editor, choose **Open Deck**. Select a Deck appears (Figure 5-7).

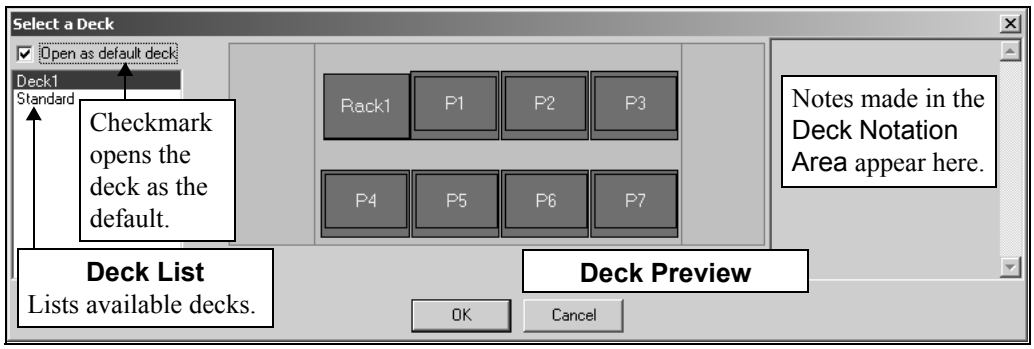


Figure 5-7. Previews deck selected

2. Select the desired deck from the Deck List.
3. Choose **OK**. The deck appears as the current deck.
4. Choose **Save** to save the deck and exit Deck Editor.

5.3.2 Creating a New Deck

When a new deck is created, it is initially a copy of the currently open deck. A new deck may be created for many reasons, including:

- To maintain the previous deck configuration when switching between different deck layouts.
- When similar deck configurations exist, but with differences between one or two positions.
- When devices replace deck positions.

To create a new deck:

1. In the Deck Editor, open the deck to copy as a basis for the new deck (refer to Section 5.3.1, *Opening and Selecting a Deck*).

2. Select **New Deck**. Choose a name for this deck: appears (Figure 5-8).

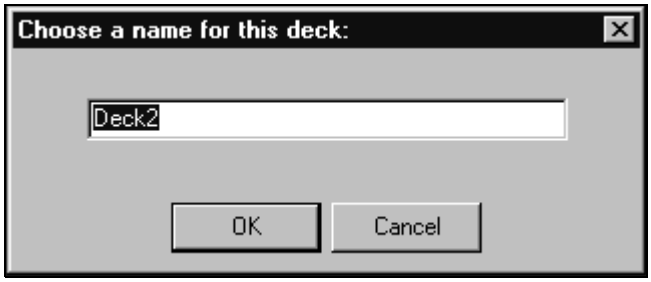


Figure 5-8. Enter a new name for the deck

3. Enter a name for the new deck.
4. Choose **OK** to save the deck name and return to the Deck Editor. A copy of the selected deck appears, using the new name and is ready for modification.
5. If desired, make modifications to the new deck.
6. Choose **Save** to save the new deck and exit Deck Editor.

Note: Choose Cancel to cancel the modifications made to the deck. A Confirm appears to confirm cancellation of the changes (Figure 5-9).

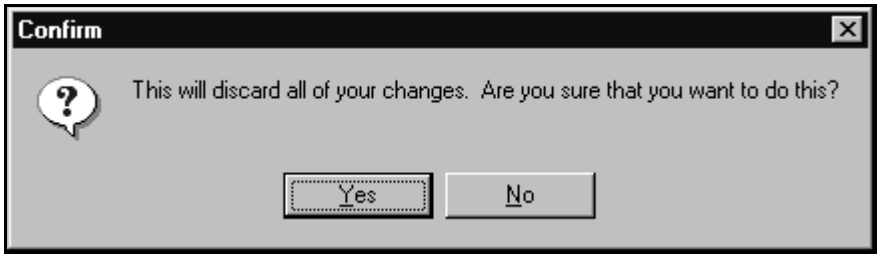


Figure 5-9. Confirmation to cancel changes

5.3.3 Deleting a Deck

If a deck is no longer needed, it may be deleted.

Note: Once a deck is deleted in the Deck Editor, it cannot be retrieved via the Deck Editor. It can be retrieved, however, using the Import/Export Utility (refer to Chapter 3, *Using Instrument Files and Settings*).

To delete a deck:

1. Open the deck to delete (refer to Section 5.3.1, *Opening and Selecting a Deck*).
2. Select **Delete Deck**. A Warning appears (Figure 5-10).

Figure 5-10. Delete Deck confirmation

3. Choose **Yes** to delete the deck. The deck is deleted.
4. Choose **Save** to exit the Deck Editor.

Note: Choose Cancel to cancel the deletion of the deck.

5.3.4 Renaming a Deck

Rename a deck to easily identify it.

To rename a deck:

1. Open the deck to rename (refer to Section 5.3.1, *Opening and Selecting a Deck*).

2. Choose **Rename Deck**. Choose a name for this deck: appears(Figure 5-11).

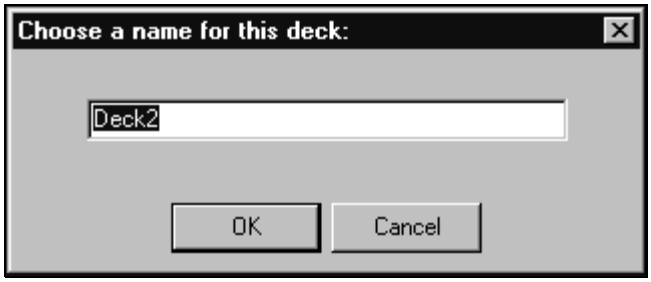


Figure 5-11. Change deck name

3. Enter the desired deck name.

Note: Names for deck positions must be alphanumeric with no spaces; the only non-alphanumeric character allowed is "_" (underscore). The first character must be a letter.

4. Choose **OK** to save the deck under the new name.

Note: An Error similar to Figure 5-12 appears if the new name already exists. Choose another name.

Figure 5-12. Error in renaming

5. Choose **Save** to exit the Deck Editor.

Note: Choose Cancel to cancel the renaming of the deck.

5.4 Modifying a Deck

➢ ***3000*** — Labware positioners and devices on a Biomek 3000 are referred to as ALPs in Deck Editor.

Modifying a deck includes:

- Opening the deck to modify or create a new deck (refer to Section 5.3.2, *Creating a New Deck*).
- Deleting ALPs and deck positions from the open deck as necessary.
- Adding ALPs and deck positions as necessary.
- Setting ALP and deck position properties.

5.4.1 Deleting ALPs and Deck Positions from a Deck

When a deck is copied or a new deck is created, it is necessary to remove ALPs no longer needed. Remove these ALPs so that other ALPs can be added.

To remove ALPs:

1. Click on the ALP to delete in the Deck View (Figure 5-2).

   Note: Notice that the ALP is highlighted with a pink border, and deck positions are highlighted with a yellow border. If a single position within a multiposition ALP is selected, it is highlighted pink.

2. Select **Delete ALP** from the toolbar.

   OR

   Press the **Delete** key on the keyboard.

   OR

   Right-click on the deck position and select **Delete** from the menu that appears. A Warning prompt appears (Figure 5-13).

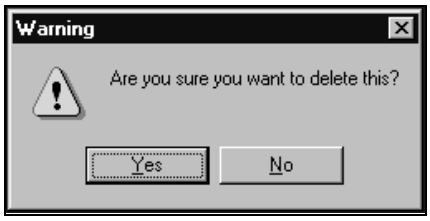


Figure 5-13. Confirmation to delete ALP

3. Choose **Yes** to delete the ALP. The modified deck appears in Deck View (Figure 5-2).

5.4.2 Adding ALPs and Deck Positions

New ALPs can be added to the deck in the appropriate locations. Deck positions are part of ALPs and are named automatically when added to a deck.

To add ALPs to the deck:

1. Click and hold the mouse button on the desired ALP in the ALP Types List (Figure 5-14). Notice that the locations capable of supporting the ALP are indicated by dashed boxes.

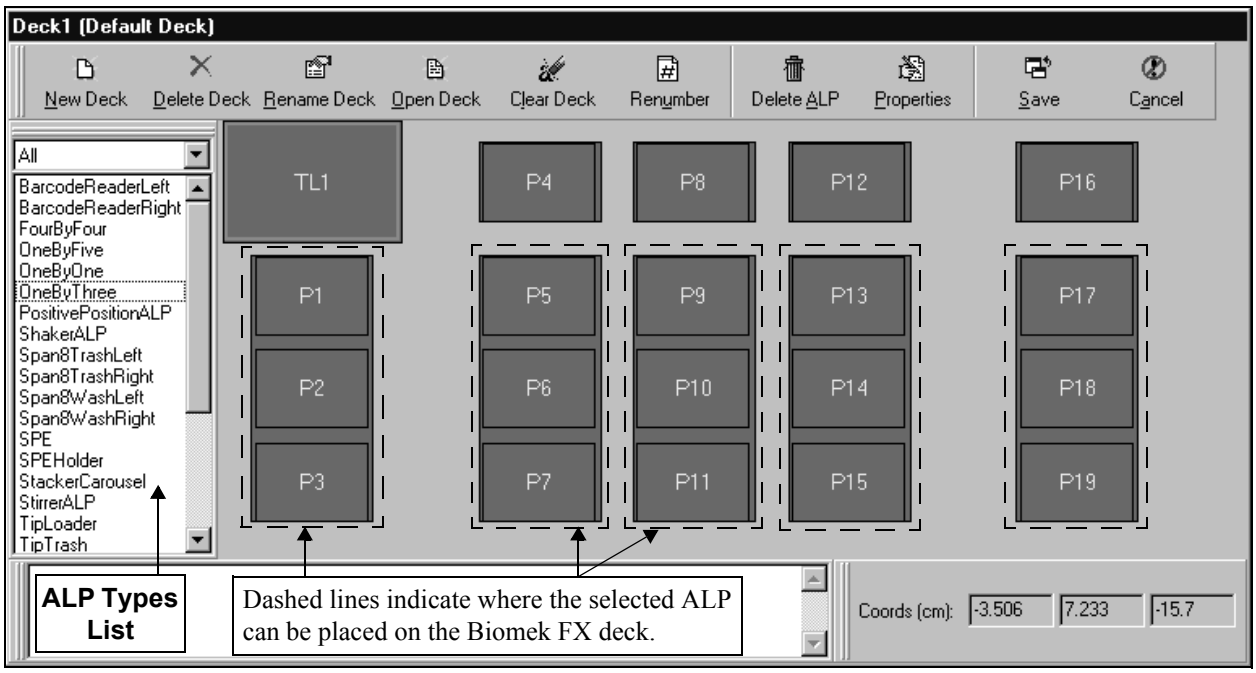


Figure 5-14. Possible OneByThree deck positions highlighted on a Biomek FX deck

2. **Drag and drop the ALP** from the ALP Types list to the desired location. The ALP appears and deck positions are named automatically.

Note: The positions may be renamed (refer to Section 5.4.3, *Setting ALP Properties and Deck Positions*).

Note: If the desired ALP is about to be placed where another ALP is currently placed on the deck, the following warning appears (Figure 5-15). Delete the currently-placed ALP before placing the desired ALP on the deck (refer to Section 5.4.1, *Deleting ALPs and Deck Positions from a Deck*).

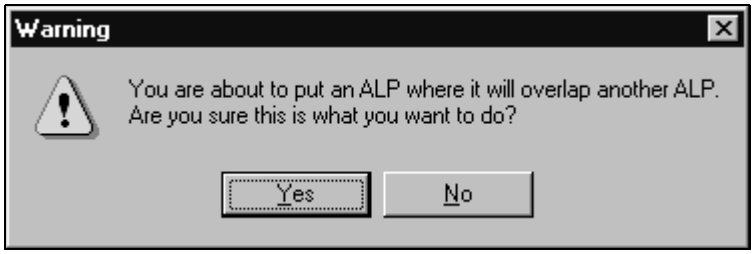


Figure 5-15. Warning appears because an ALP is about to be placed where it will overlap another ALP

5.4.3 Setting ALP Properties and Deck Positions

After a new ALP is placed on the deck, set the properties of the ALP and related deck positions (Table 5-2).

The following properties may be configured for ALPs or deck positions:

Table 5-2. ALP and Position Properties.

Property	Description	Applies To
Name	The name of the deck position as shown in the Instrument Setup step. ALPs have related names that do not appear in the Instrument Setup.	Position and ALP
Pod1 and Pod2 Coordinates	The coordinate location of the back left corner of the position on the instrument platform for each pod (Figure 5-16).	Position and ALP
Device	Instrument, such as a Stacker Carousel or Tip Loader, associated with a deck position (refer to Section 5.4.3.1, *Setting ALP Properties*). Displayed only when More>> is selected.	Position
Device Index	Location of labware in the device associated with a deck position (refer to Section 5.4.3.1, *Setting ALP Properties*). Displayed only when More>> is selected.	Position
Sensor Device	Associates the position with the Source/Waste Sensor which is used with an off deck source or waste container.	Position
Labware Offset	The coordinate difference from the Position to the back left corner of the labware (Figure 5-16). Refer to Section 5.4.3.1, *Setting ALP Properties*. Displayed only when More>> is selected.	Position
Position Span	Area of the Biomek platform the ALP or position covers. (The span for an ALP may be different from the span of a position.) Displayed only when More>> is selected.	Position and ALP
Min Safe Height	Reserved height above position needed to avoid collisions. Displayed only when More>> is selected.	Position
Per-Labware Offsets	Coordinate difference between the set Labware Offset to where specific types of labware sit on the deck position (Figure 5-16). Useful for tip loading and when using the SPE Manifold (refer to Section 5.4.3.1, *Setting ALP Properties*). Displayed only when More>> is selected.	Position

Note: Not all properties listed in Table 5-2 may be present. Properties vary according to the instrument and configuration.

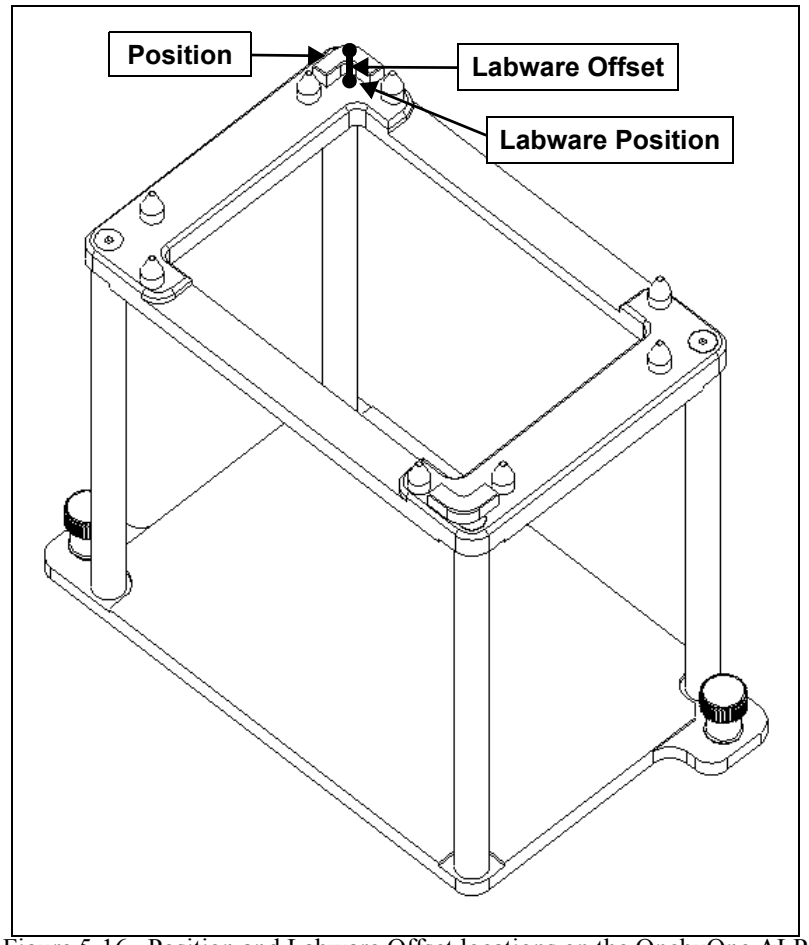


Figure 5-16. Position and Labware Offset locations on the OnebyOne ALP

5.4.3.1 Setting ALP Properties

To set properties of the ALP:

1. From the Deck View, select the ALP to modify.

   Note: The ALP is selected when the outer edges of the ALP are highlighted pink, and the associated deck positions are highlighted in yellow within the Deck View. Deck positions with green highlights are associated with devices.

2. Choose **Properties**.

   OR

   Right-click on the ALP in the Deck Editor or any of its positions and select **ALP Properties**.

   OR

   Double-click on the ALP on the deck layout. ALP Properties appears (Figure 5-17).

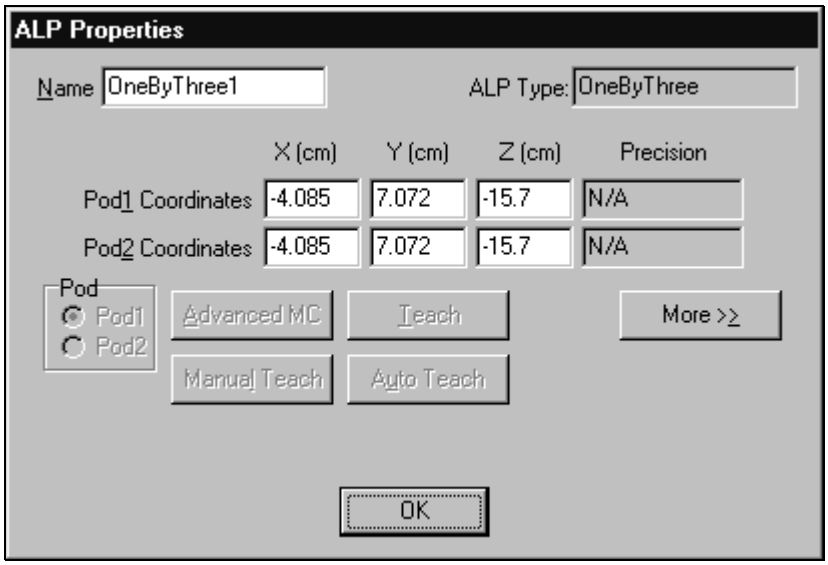


Figure 5-17. ALP Properties of a OneByThree ALP

Note: Not all properties listed on Figure 5-17 may be present. Properties vary according to the instrument and configuration.

3. Change the **Name** of the ALP, if desired.
4. Choose **OK** to save the ALP properties. Current Deck appears.
5. Choose **Save** to close the Deck Editor

5.4.3.2 Setting Deck Position Properties

Deck position properties are similar to ALP properties; however, deck positions include Labware Offsets that place the labware in the appropriate place for pipetting operations. Because some deck positions are associated with devices, such as a Stacker Carousel, the Device property must be set for these deck positions.

To set deck position properties:

1. Select the position to modify.

2. Select **Properties**.

   OR

   Double-click on the deck position.

   OR

   Right-click on the desired position and select **Properties** from the menu that appears. Position Properties appears (Figure 5-18).

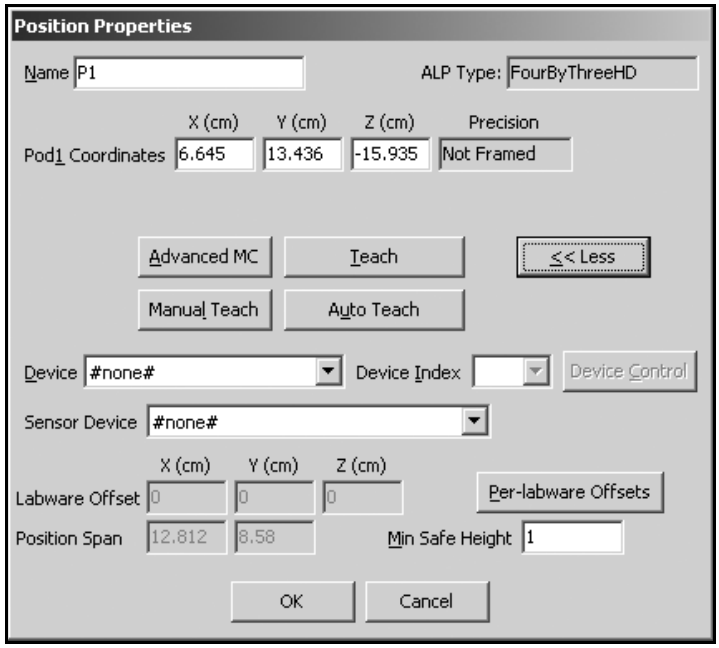


Figure 5-18. Position Properties for Deck Positions

Note: Not all properties listed on Figure 5-18 may be present. Properties vary according to the instrument and configuration.

Note: The deck position is highlighted with a pink line inside the ALP.

3. Rename the deck position, if desired.

Note: Names for deck positions must be alphanumeric with no spaces; the only non-alphanumeric character allowed is "_" (underscore). The first character must be a letter.

4. Enter the **X**, **Y**, and **Z Coordinates** of the appropriate pod by framing the ALP:
   - ***FX*** — refer to the *Biomek® FX Laboratory Automation Workstation User's Manual,* Chapter 5, *Framing the Biomek® FX*.
   - **3000** — refer to the *Biomek® 3000 Laboratory Automation Workstation User's Manual,* Chapter 13, *Framing the Biomek® 3000*.
   - ***NX-MC*** — refer to the *Biomek® NX Multichannel Laboratory Automation Workstation User's Manual,* Chapter 4, *Framing Instructions*.
   - ***NX-S8*** — refer to the *Biomek Software User's Manual,* Chapter 5, *Preparing and Managing the Deck*.
5. Select **More>>**, if necessary.
6. Choose the **Device** name to associate with the position, if required.

   Note: For devices controlled through SILAS, the SILAS module for the device must be installed prior to associating the device with a deck position.

7. If appropriate, select the **Device Index**.

   Note: The Device Index works with software modules operating instruments that have more than one position, such as the MicroMix 5 Shaker.

8. If appropriate, choose the desired **Sensor Device** to associate the Waste/Sensor with the position.
9. Choose **Per-labware Offsets** to customize the offsets for specific types of labware (refer to Section 5.4.3.3, *Changing Per-Labware Offsets*).
10. Set the **Min Safe Height**.

    Note: The Labware Offsets and Position Span are predefined in the software. Do not modify these properties.

11. Choose **OK** to save the deck position properties. Current Deck appears.
12. Choose **Save** to close the Deck Editor.

5.4.3.3 Changing Per-Labware Offsets

Modify the per-labware offsets when specialized needs arise. The X, Y, and Z coordinates for the deck position may be modified based upon the labware type. For example, the Z offsets can be changed for a plasmid filter when performing a filtration-based DNA plasmid purification.

To modify the per-labware offsets:

1. Select **Instrument>Deck Editor**.
2. Open the desired deck (refer to Section 5.3.1, *Opening and Selecting a Deck*).
3. Select the position to modify.
4. Select **Properties**

   OR

   Double-click on the deck position

   OR

   Right-click on the desired position and select **Properties**. Position Properties appears (Figure 5-18).
5. Choose **More>>**, if necessary.
6. Choose **Per-labware Offsets**.
7. In Per-Labware Offsets, select the labware to modify (Figure 5-19).

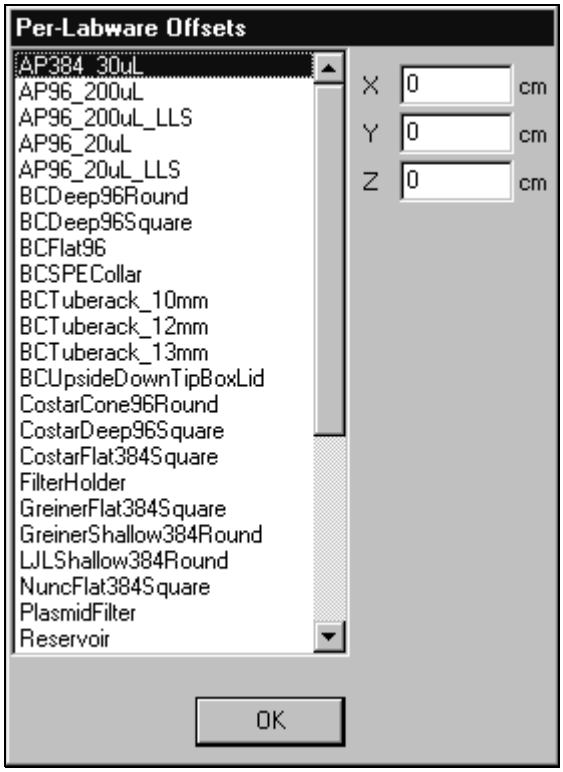


Figure 5-19. Per-Labware Offsets

Note: Per-Labware Offsets includes labware that is specific to the instrument.

8. Enter the desired **X**, **Y**, and **Z** offsets.

   Note: While the offset values may be calculated using calipers, a more precise measurement should be obtained from the manufacturer's drawings.

9. Choose **OK** to save the offset values. Position Properties appears (Figure 5-18).
10. Choose **OK**.
11. Choose **Save** to close Deck Editor.

6 Understanding and Using Project Files

6.1 Overview

A project file stores information about liquid types; labware and tip types; well patterns; and pipetting templates and techniques as revisions that are used by a method file to configure the actions of the instrument. Project files store a history of all changes, additions, and deletions of items from the project file.

When a project file is checked in, all items become revisions that are permanently saved. If an item is deleted, that item is no longer available in method building; however, the revision remains in the project file and is used for older validated methods that utilize that revision. If an item is modified, the new definition is stored as a separate revision. Older revisions remain as part of the project file and are used by older validated methods that utilize that record. However, only the newest revision, or working revision, is available in method building. In this way, a validated method can always be run with the exact same revisions, even if those revisions have since been modified or deleted (refer to Section 12.11, *Validating a Method*).

Note: If Beckman Coulter Accounts & Permissions is used with Biomek Software, project files also maintain a history of who makes changes to any revisions in the project file.

The active project file and instrument file are displayed in the status bar of the Biomek method editor (Figure 6-1). Any project file can be used with any instrument file. Validated methods, however, are validated for a specific instrument and are no longer validated when used with a different instrument file, even if the instrument file is equivalent to the one on which the method is validated.

Note: Validating a method for a specific instrument is not the same as validating a method before a run to internally test the method for errors before it is run. To validate a method to test for errors before it is run, check **Validate the current method before running it** in Preferences (refer to Section 29.2, *Changing Display Preferences*).

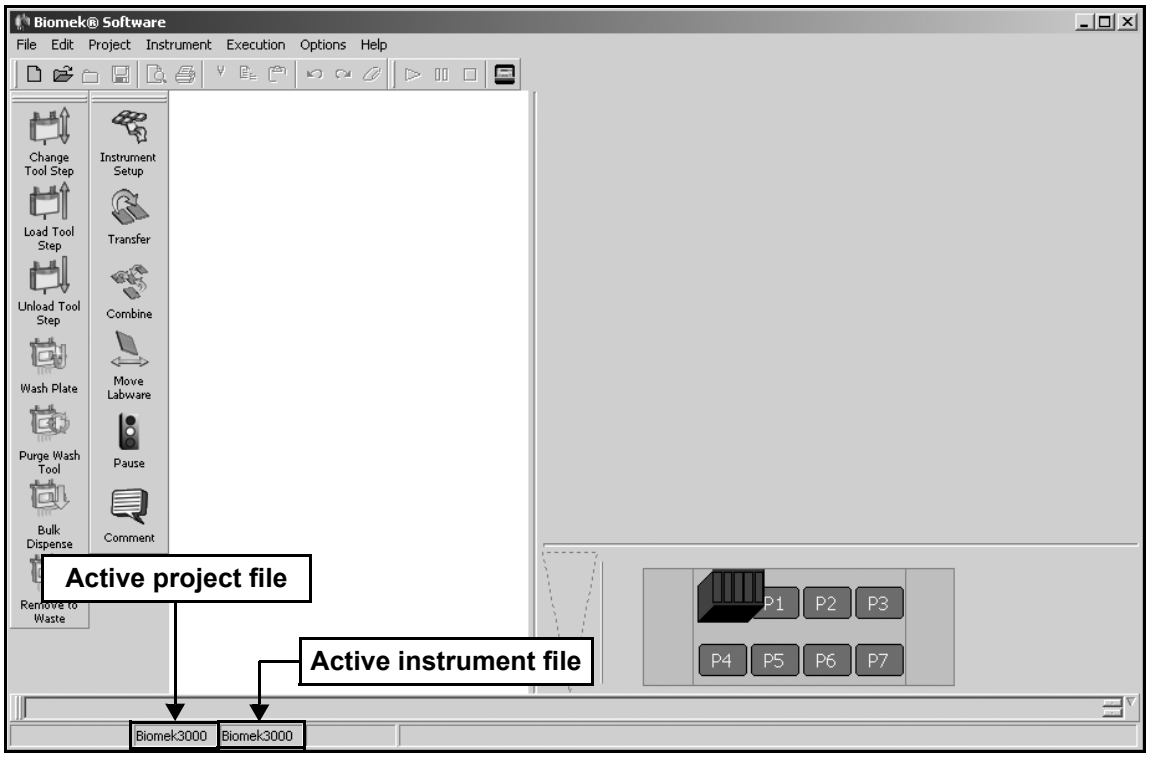


Figure 6-1. Biomek method editor

The Project menu contains options to access, create, view contents, and check in projects, as well as provide access to the editors to create, modify, and delete project items.

The sections in this chapter include:

- *Creating a New Project File* (Section 6.2).
- *Opening a Project File* (Section 6.3).
- *Deleting and Restoring Project Files* (Section 6.4).
- *Renaming a Project File* (Section 6.5).
- *Creating a Copy of a Project File* (Section 6.6).
- *Checking In a Project File* (Section 6.7).
- *Viewing Project Contents* (Section 6.8).
- *Reverting Projects* (Section 6.9).
- *Importing and Exporting Project Files* (Section 6.10).

6.1.1 Contents of a Project File

A project file contains all:

- Labware Classes — definitions for microplates, reservoirs, tip boxes, and other labware used in a method, as specified in the Labware Type Editor (refer to Section 7.3, *Defining Labware Types*).
- Labware Patterns — definitions of patterns of wells to aspirate or dispense from, as specified in the Well Pattern Editor (refer to Chapter 11, *Creating Well Patterns*).
- Liquid Types — definitions for reagents used in a method, as specified in the Liquid Type Editor (refer to Chapter 8, *Understanding and Creating Liquid Types*).
- Pipetting Templates — templates of how pipetting operations are performed, as specified in the Pipetting Template Editor (refer to Chapter 10, *Using the Pipetting Template Editor*).
- Techniques — configuration of properties and parameters for all pipetting operations, as specified in the Technique Browser and Technique Editor (refer to Chapter 9, *Understanding and Creating Techniques*).
- Tip Classes — definitions for tips used in a method, as specified in the Tip Type Editor (refer to Section 7.2, *Defining Tips*).

In addition, methods are associated with a project file. To open a method, the project file that was used to create the method must be the active project.

Note: If a method is open when a project file is closed to open a new project, a prompt appears to check in, save, or discard the current method.

6.2 Creating a New Project File

Any number of project files may exist on any system. This allows separate project files to be created for different applications or different users. Project files customize the instrument performance to the needs of users. For example, users could create their own project files. In this way, users can guarantee that the definitions used are not changed without their knowledge, and keep labware and liquid type catalogs limited to only the ones they use.

Create Project is used to create a new, blank project file. A new project file has no existing revisions for labware types, liquid types, tip types, pipetting templates or techniques, or well patterns.

Note: A default project file is automatically created during installation of Biomek Software. The contents of the default project file depend on the options selected during the installation wizard.

To create a new blank project file:

1. From the Project menu, choose **New Project**. Create Project appears (Figure 6-2).

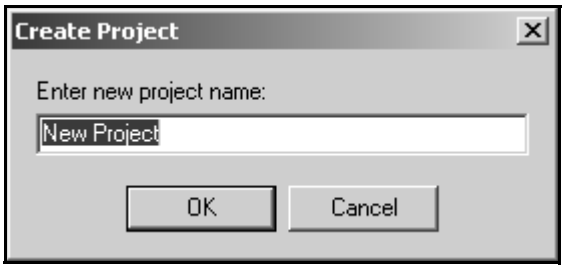


Figure 6-2. Create new project

2. Enter a name for the new project file.

   Note: The project file name must be different from all other project files.

3. Choose **OK** to create a new project with the specified name. Create Project closes and the new project becomes the active project file.

   OR

   Choose **Cancel** to close Create Project without creating a new project file.

6.3 Opening a Project File

A project file can be opened at any time. Opening a project file closes the current active project and any methods that may be open, and opens the selected project.

To open a project file:

1. From the Project menu, choose **Open Project**. Open Project appears (Figure 6-3).

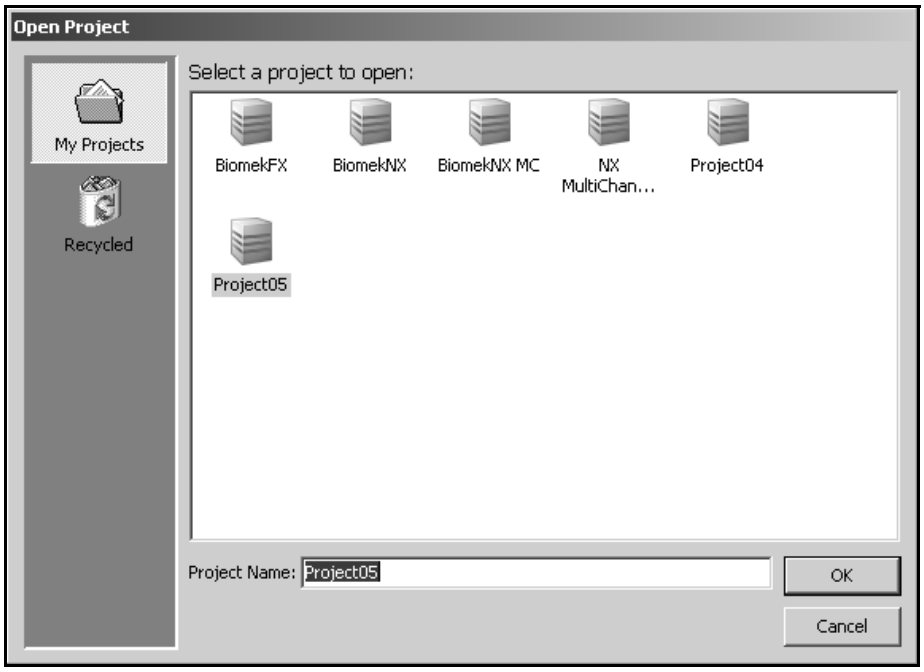


Figure 6-3. Opening a project file

2. Select the desired project file to open.
3. Choose **OK** to open the selected (highlighted) project file. Open Project closes and the selected project file becomes the active project.

   OR

   Choose **Cancel** to close Open Project without opening a new project file. The current project remains active.

6.4 Deleting and Restoring Project Files

Projects may be deleted, but are never permanently removed from the system, and may be restored at any time.

Note: When multiple instances of the Biomek Software are running simultaneously, such as when controlling multiple Biomek instruments, project files are locked. Locked project files may be opened, but not deleted, renamed, or saved.

6.4.1 Deleting Projects

To delete a project:

1. From the Project menu, choose **Open Project**. Open Project appears (Figure 6-4).

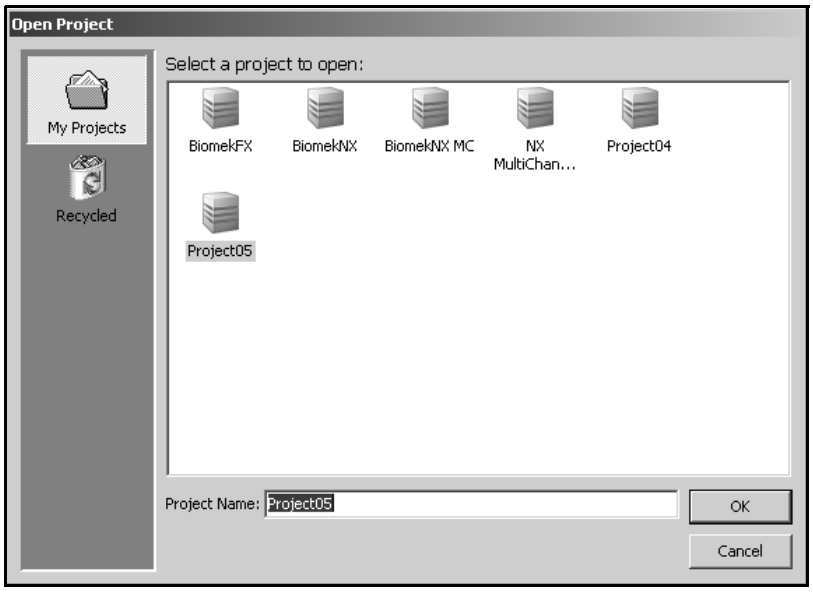


Figure 6-4. Open Project

2. Right-click the desired project to delete and choose **Delete**. A confirmation appears (Figure 6-5).

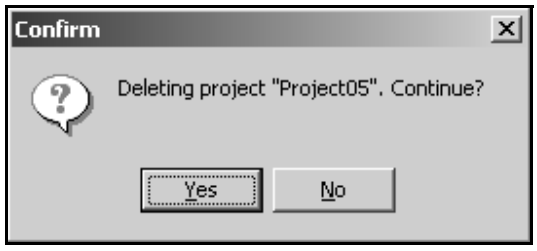


Figure 6-5. Confirm deletion of selected project

3. Choose **Yes** to confirm deletion of the selected project. The project is removed from My Projects and placed in Recycled.

   OR

   Choose **No** to keep the selected project.

6.4.2 Restoring Projects

To restore a deleted project:

1. From the Project menu, choose **Open Project**. Open Project appears (Figure 6-4).
2. In the left panel of Open Method, choose **Recycled** to view all the projects that have previously been deleted.

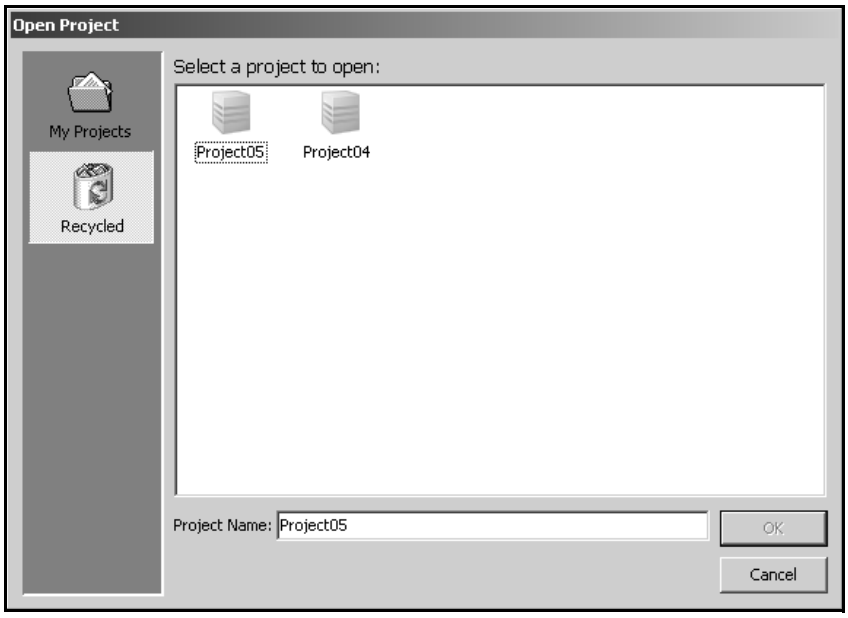


Figure 6-6. Recycled projects

3. Right-click the desired project to restore and choose **Restore**. The project is moved from Recycled to My Projects.

Note: A project may be opened directly from the Recycled folder by selecting the project and choosing **OK**. A confirmation appears stating that the project will be restored prior to opening the project. Choose **OK** to restore and open the project.

6.5 Renaming a Project File

A project file may be renamed at any time, regardless of whether it is open or closed. Renaming a project file does not create a copy of the file with the new name.

Note: To save a copy of a project file with a new name, use the Save Project As command (refer to Section 6.6, *Creating a Copy of a Project File*).

Note: When multiple instances of the Biomek Software are running simultaneously, such as when controlling multiple Biomek instruments, project files are locked. Locked project files may be opened, but not deleted, renamed, or saved.

6.5.1 Renaming the Active Project File

To rename the project file currently open in the Biomek Software:

1. From the Project menu, choose **Rename Project**. Rename Project appears (Figure 6-7).

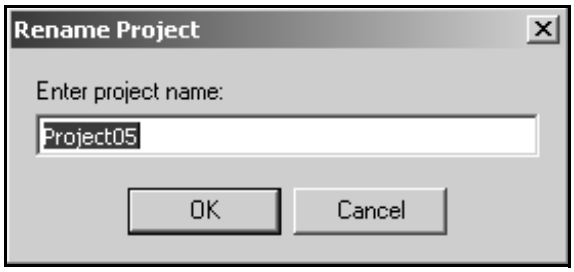


Figure 6-7. Renaming the open project

2. Enter a new name for the project file.
3. Choose **OK** to rename the project file.

   OR

   Choose **Cancel** to retain the original name.

6.5.2 Renaming a Saved Project File

To rename a saved project file:

1. From the Project menu, choose **Open Project**. Open Project appears (Figure 6.8).

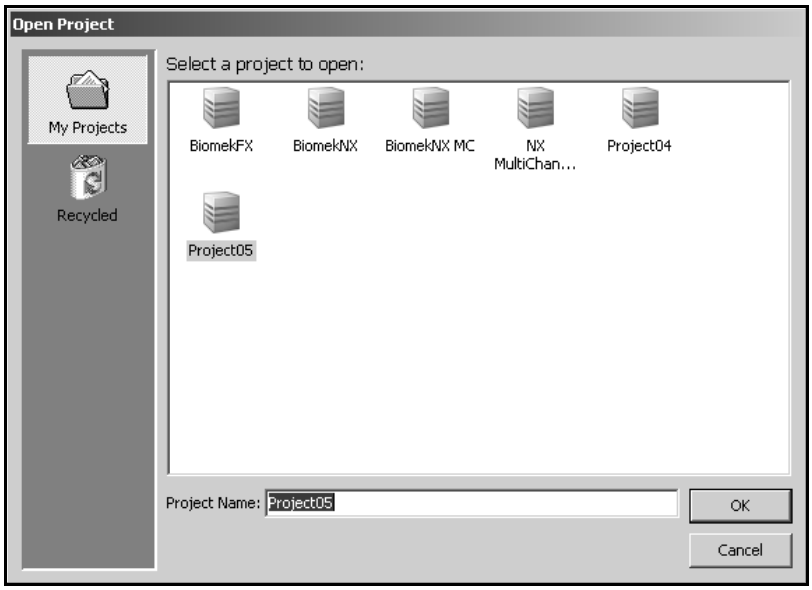


Figure 6-8. Open Project

2. Right-click the desired project to rename and choose **Rename**. The project file name is highlighted.
3. Enter a new name, and press **Enter**.
4. Choose **OK** to close Open Project, save the project file with the new name, and open the new project file.

   OR

   Choose **Cancel** to close Open Project and save the project with the new name only.

6.6 Creating a Copy of a Project File

A project file can be copied to create a new project file based on the original using the Save Project As command. A new project created using Save Project As maintains all the records from the original project in a new project file.

Note: Using Save Project As copies only the working revision of each project item and does not include prior revisions of project items or any method files in the project. Methods must be imported separately using the import and export options in the File menu. Refer to Section 12.16, *Importing and Exporting Methods*, Section 12.16.1, *Exporting a Method*, and Section 12.16.2, *Exporting All Methods Associated With a Project File*, for more information.

To create a copy of a project file:

1. If the project file to copy is not the active file, open the desired project file (refer to Section 6.3, *Opening a Project File*).
2. From the Project menu, choose **Save Project As**. Save Project As appears (Figure 6-9).

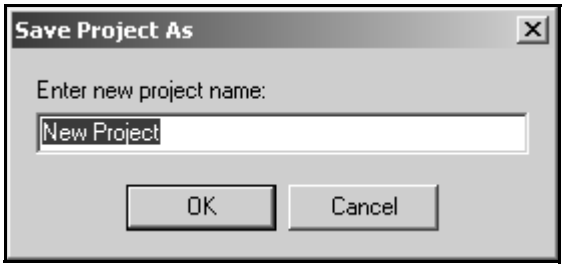


Figure 6-9. Saving project as to create a copy

3. Enter a name for the new project file.

   Note: The project file name must be different from all other project files.

4. Choose **OK** to create a new project with the specified name. Save Project As closes and the new project becomes the active project file.

   OR

   Choose **Cancel** to close Save Project As without creating a new project file.

6.7 Checking In a Project File

Changes made to any item in a project file are saved but do not become revisions until checked in. Once checked in, a new revision is created for the project items. Revisions can never be lost. If a project item is later modified or deleted, any revision of the project item may be restored.

Note: If Beckman Coulter Accounts & Permissions is enabled, methods may be validated. A validated method is a revision of a method that is checked in, approved with a reason or electronic signature, and protected from further modification (refer to Section 12.15, *Checking Out a Method*). Before a method can be validated, all items used in the method must be checked in as revisions in the project file.

To check in a project file to create new revisions:

1. From the Project menu, choose **Check In Project**. Check In Project displays a list of all project items that differ from the working revision in the project (Figure 6-10).

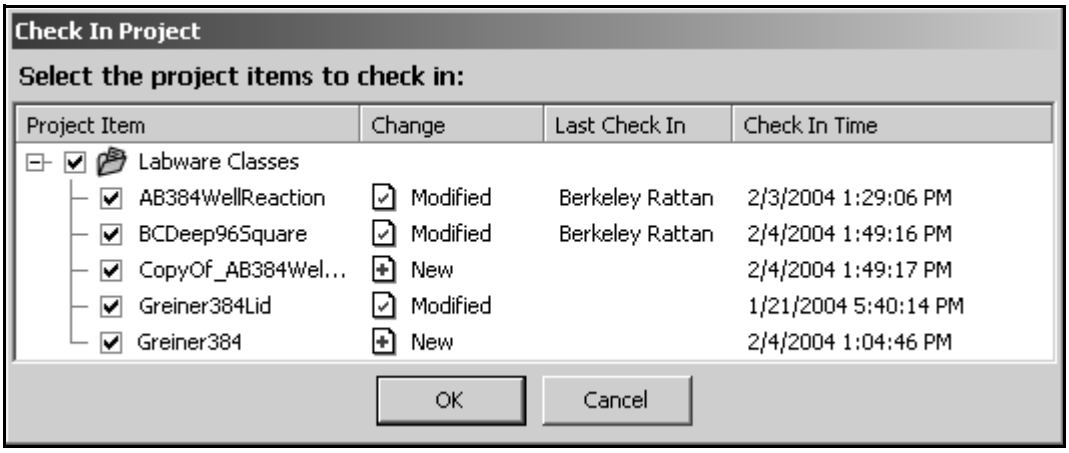


Figure 6-10. Checking in project items as official records

2. Select all project items to check in as revisions in the project file by selecting the checkbox to the left of each project item. By default, all project items are selected.

   Note: Project items are listed in a tree structure that lists items by type. Branches may be expanded or collapsed using the + and - buttons to the left.

   Note: Right-click on a type of project item and choose **Select All** from the menu to select all project items of that type, or choose **Select None** to deselect all project items of that type. Right-click on whitespace and choose **Select All** or **Select None** to select or deselect all project items for all types.

3. Choose **OK**.

   Note: If Beckman Coulter Accounts & Permissions is not in use, check in is complete. All selected project items are checked in as revisions in the project file.

   OR

   Choose **Cancel** to close Check In Project without checking any project items in as revisions.

4. If Accounts & Permissions is enabled, Check-In appears (Figure 6-11). Enter a **Reason** for checking in the project.

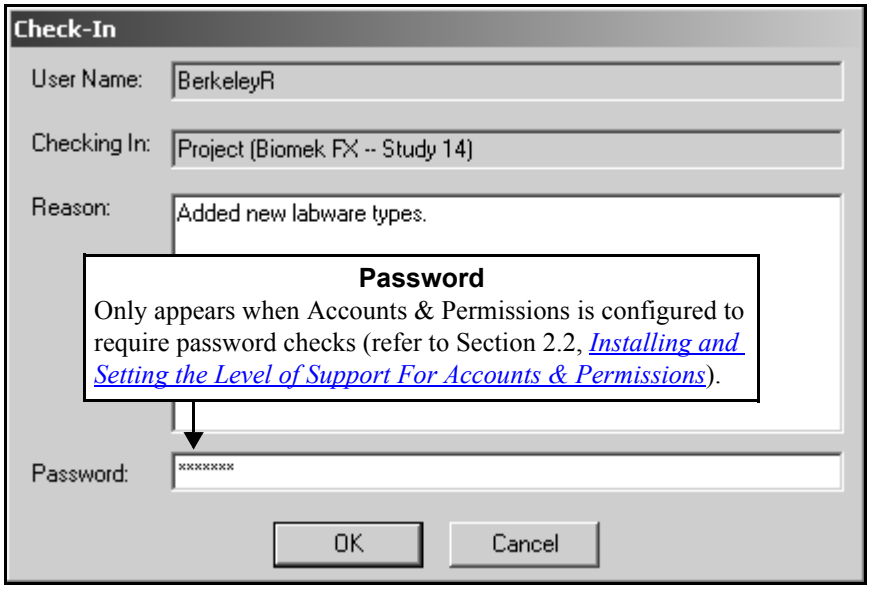


Figure 6-11. Check-In (Accounts & Permissions enabled)

5. If Accounts & Permissions is configured to require password checks for signing and check-in, enter the user **Password**.
6. Choose **OK** to check in all selected project items as revisions in the project file and close Check In.

   OR

   Choose **Cancel** to close Check-In without checking in the project.

6.8 Viewing Project Contents

The contents of a project file and status of each project item can be viewed at any time.

To view the contents of a project file:

1. From the Project menu, choose **Project Contents**. Project Contents displays a list of all project items and their status (Figure 6-12). There are six possible states that may be listed for the status:

   - Current — the project item matches the working revision.
   - New — there are no existing revisions of the project item that have been checked in.
   - Removed — the project item has been deleted and is not available for method editing.

     Note: To view Removed items, right-click in Project Contents and select **Show Deleted Items**. All project items that have been deleted are listed in Project Contents with a status of Removed.

   - Modified — the project item has changed since it was last checked in.
   - Renamed — the project item has been renamed since it was last checked in as a revision, but is otherwise unchanged.
   - Reverted — the project item has been reverted to a previous revision.

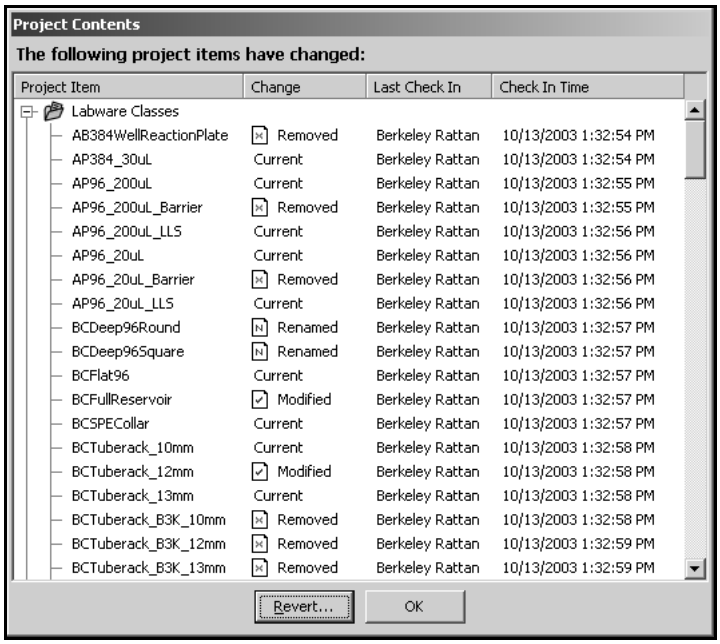


Figure 6-12. Viewing project contents (Accounts & Permissions enabled)

Note: When Accounts & Permissions is not enabled, Last Check In does not appear and Check In Time is named Modified Time.

2. Right-click on any project item and choose **History** from the menu to view the history for that record (Figure 6-13). History displays the history of changes, who made the changes, the time changes were made, and any comments that may have been entered.

Note: Changed By and Comment are blank unless Beckman Coulter Accounts & Permissions is enabled.

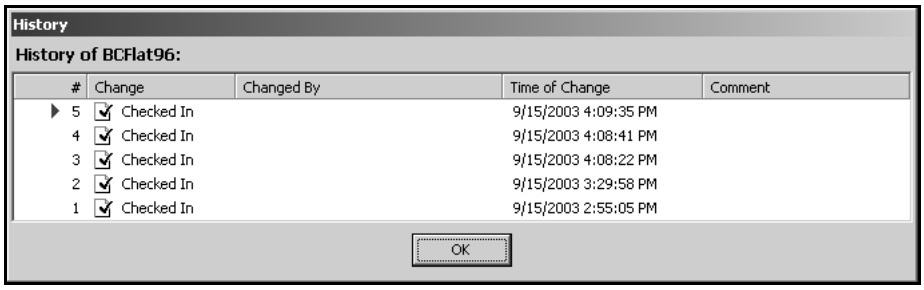


Figure 6-13. History of a project record

3. When finished viewing the history for the record, choose **OK** to close History.
4. Repeat steps 2 and 3 to view the history for additional records, if desired.
5. Choose **OK** to close Project Contents.

6.8.1 Restoring Deleted Project Items

A deleted project item may be restored at any time and made available again for method building. Restoring a project item makes available the last revision of the project item that was checked in before it was deleted.

To restore a deleted project item:

1. From the Project menu, choose **Project Contents**. Project Contents displays a list of all project items and their status.
2. Right-click in Project Contents and select **Show Deleted Items**. All project items that have been deleted are listed in Project Contents with a status of Removed.
3. Right-click on the desired deleted item to restore and select **Restore** from the menu. The status of the project item changes to Current and the project item may now be used in method building.

6.9 Reverting Projects

A project file can be reverted back to a previous revision state, if desired.

Note: A revision is created each time a project is checked in.

Options for reverting project files are:

- *Reverting Project Contents to a Certain Date and Time* (Section 6.9.1).
- *Discarding All Changes Since Last Check In* (Section 6.9.2).
- *Reverting Individual Project Items to a Specific Revision* (Section 6.9.3).

6.9.1 Reverting Project Contents to a Certain Date and Time

All items in a project file may be reverted to the working revision at a previous date and time. When reverting project contents to a date and time, the latest revision checked in prior to the specified date and time is restored as the active working revision. Revisions checked in after the specified date and time remain in the project file, but are not active.

To revert project contents to a specific date and time:

1. From the Project menu, choose **Project Contents** . Project Contents displays a list of all project items and their status (Figure 6-14).

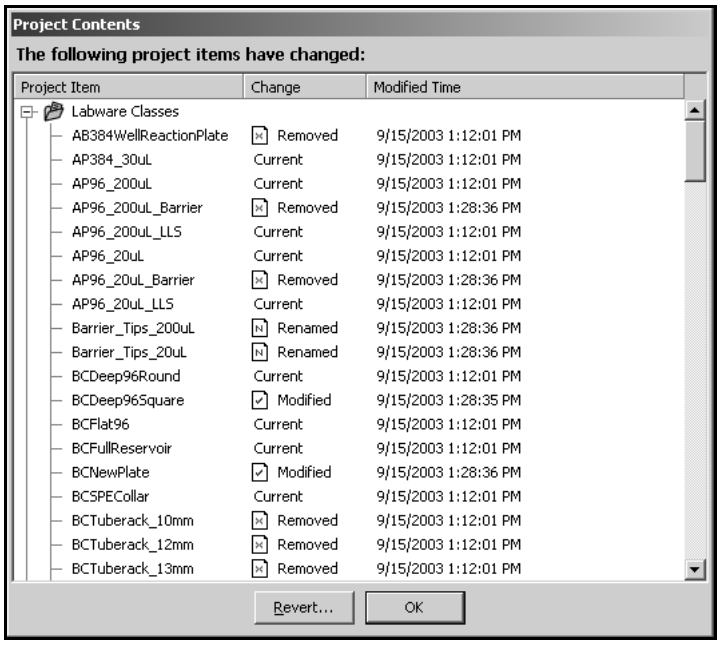


Figure 6-14. Viewing project contents

2. Choose **Revert**. Revert Project appears (Figure 6-15).

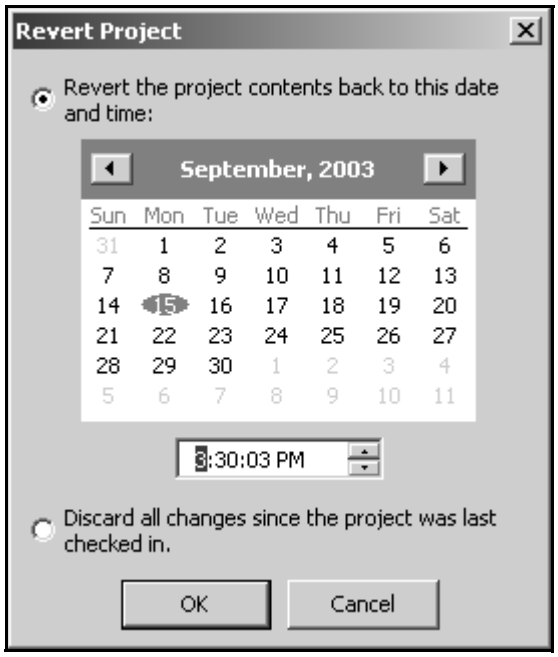


Figure 6-15. Reverting a project file to a specific date and time

3. Select **Revert the project contents back to this date and time**.
4. On the calendar, browse to and select the desired date.
5. Beneath the calendar, enter the desired time.
6. Choose **OK**. Revert Project closes and the project contents are reverted to the latest revision checked in prior to the specified date and time.

   OR

   Choose **Cancel** to close Revert Project without reverting the project contents.

6.9.2 Discarding All Changes Since Last Check In

All the changes that have been made to any project contents since the project was last checked in may be discarded. Any changes made to a project item since the last time that project item was checked in are discarded.

To discard changes since last check in:

1. From the Project menu, choose **Project Contents**. Project Contents displays a list of all project items and their status (Figure 6-16).

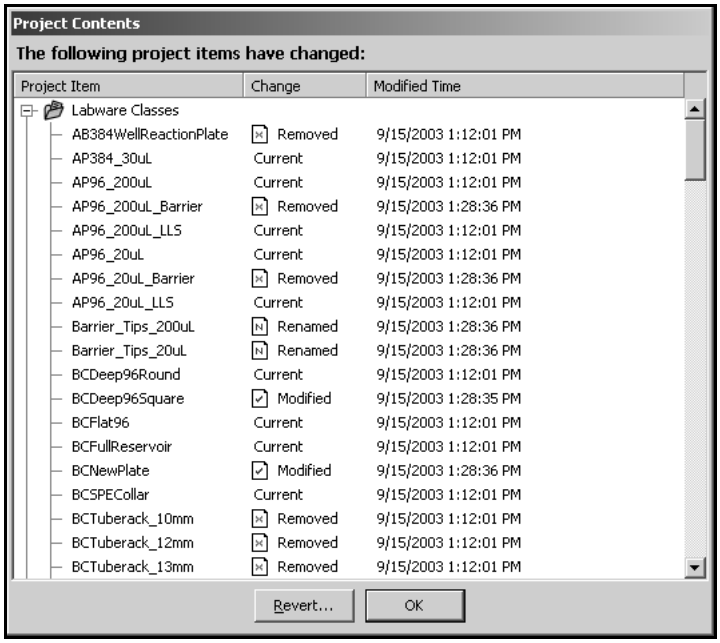


Figure 6-16. Viewing project contents

2. Choose **Revert**. Revert Project appears (Figure 6-17).

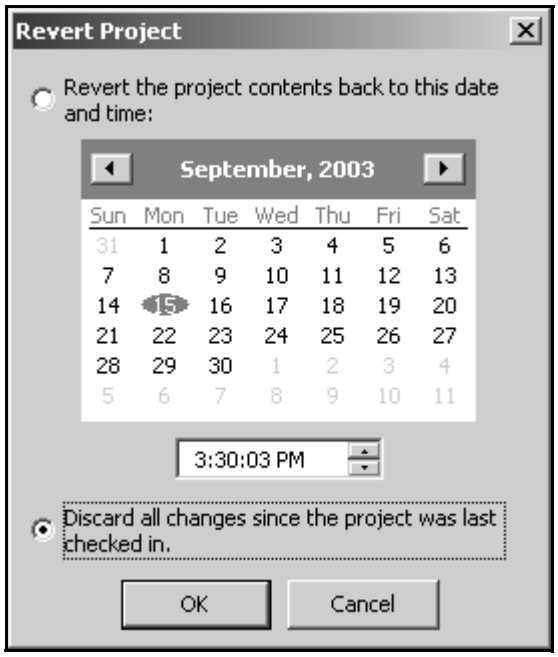


Figure 6-17. Discarding changes to a project file after a specific date and time

3. Select **Discard all changes since the project was last checked in**.
4. Choose **OK**. Revert Project closes and the all changes made to each project item since that item was last checked in are discarded.

   OR

   Choose **Cancel** to close Revert Project without discarding changes.

6.9.3 Reverting Individual Project Items to a Specific Revision

An individual project item may also be reverted back to a specific revision, if desired.

To restore an individual project item to a specific revision:

1. From the Project menu, choose **Project Contents**. Project Contents displays a list of all project items and their status (Figure 6-18).

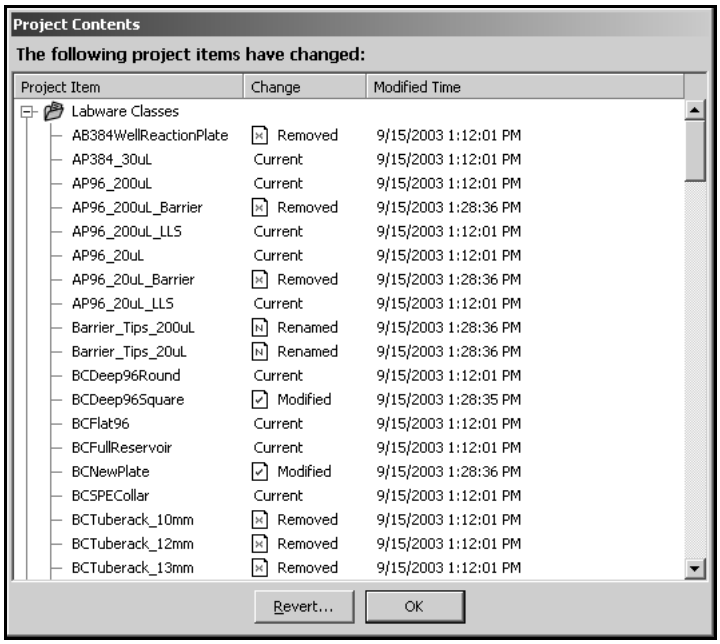


Figure 6-18. Viewing project contents

2. Right-click the desired project item to revert. History appears and displays a list of all the revisions of the project item that have been checked in. A blue arrow points to the active working revision for the project item (Figure 6-19).

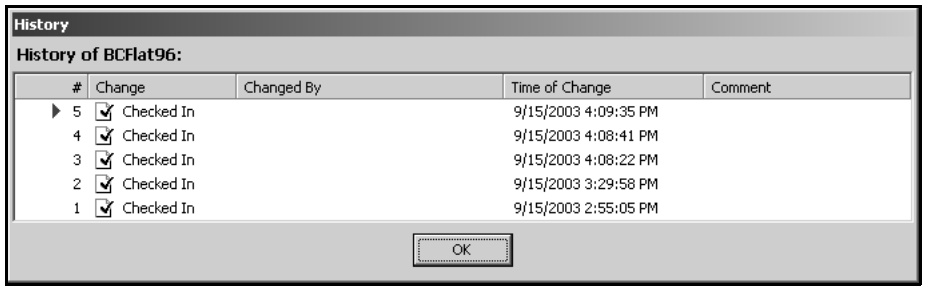


Figure 6-19. History of a project item

3. Double-click on the desired revision number of the project item to revert.

   OR

   Right-click the desired revision number and choose **Revert Changes** from the menu. The blue arrow moves to the revision to use as the working revision.

4. Choose **OK**. History closes and the selected revision is set as the working revision for the project item.

6.10 Importing and Exporting Project Files

Project files and individual records can be freely shared among projects or transferred from one computer to another using Import Project and Export Project.

Note: When Beckman Coulter Accounts & Permissions is enabled, users with the Run Validated Methods or Develop Methods permission may export methods, but only those with the Develop Methods permission may import methods into a project (refer to Chapter 2, *Using Accounts & Permissions*).

Note: Methods may also be imported and exported. Refer to Section 12.16, *Importing and Exporting Methods*, for more information.

This section covers:

- *Exporting a Project File to a Biomek Import File* (Section 6.10.1).
- *Importing a Project File from a Biomek Import File* (Section 6.10.2).

6.10.1 Exporting a Project File to a Biomek Import File

A project file or individual records from a project file can be exported to a Biomek import file, which may be imported into a different project file. Exporting a project file always exports the working revisions from the current active project file. The specific items to export from the project file are then selected from all available project items.

To export a project file:

1. From the Project menu, choose **Export Project**. Export Project appears, displaying a list of all records in the project file (Figure 6-20).

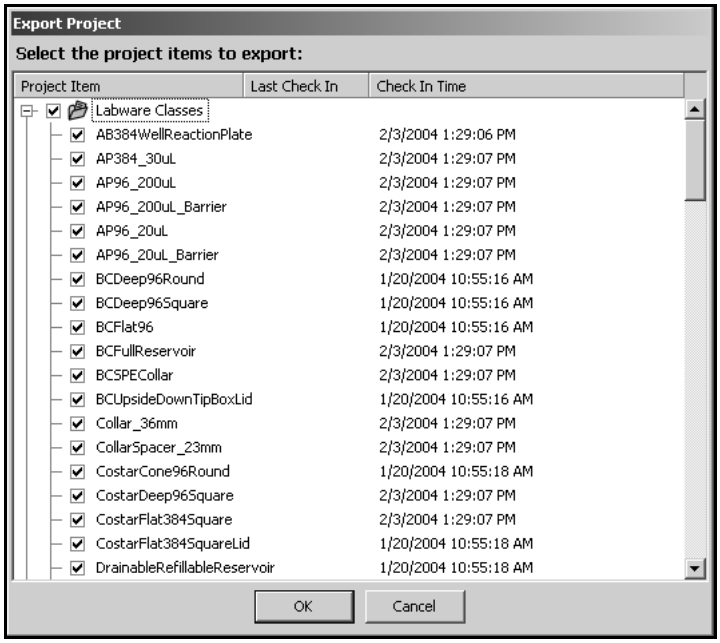


Figure 6-20. Selecting project contents to export

2. Select all project items to include in the Biomek import file by selecting the checkbox to the left of each project item. By default, all project items are selected.

   Note: Project items are listed in a tree structure that lists items by type. Branches may be expanded or collapsed using the + and - buttons to the left of the project item name.

   To select or deselect all project items of a specific type, select the checkbox to the left of folder representing the desired type of project item. Alternately, right-click on a type of project item and choose **Select All** from the menu to select all project items of that type, or choose **Select None** to deselect all project items of that type. Right-click on whitespace and choose **Select All** or **Select None** to select or deselect all project items for all types.

3. Choose **OK** to include all selected project items in the Biomek import file and close Export Project. Save As appears (Figure 6-21).

   OR

   Choose **Cancel** to close Export Project without exporting the project to a Biomek import file.

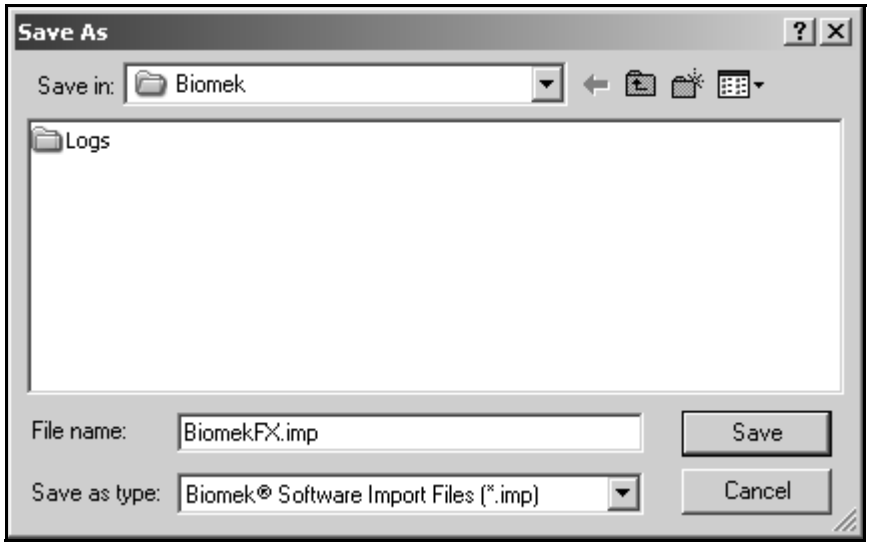


Figure 6-21. Save Import File

4. In Save As, browse to and select the location to save the Biomek import file.
5. In File Name, enter a name for the import file.
6. Choose **Save** to create the new import file.

6.10.2 Importing a Project File from a Biomek Import File

A Biomek import file previously exported from a project file can be imported into the current active project file. The records to import are selected from all available records in the import file. Biomek Software compares the selected project items in the import file to the current project and only imports those items that are different.

To import a project file from a Biomek import file:

1. If necessary, open the project file in which to import the Biomek import file.
2. From the Project menu, choose **Import Project**. Open Import File appears (Figure 6-22).

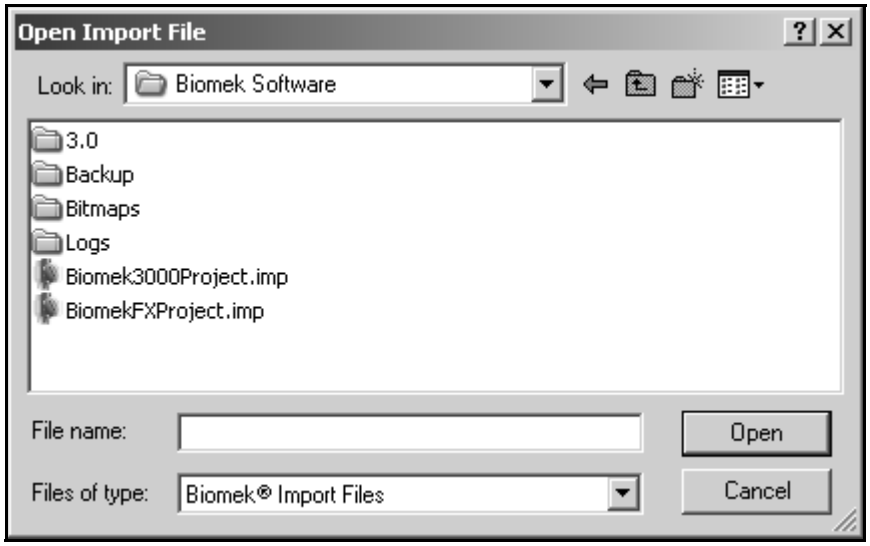


Figure 6-22. Open Import File

3. In Open Import File, browse to and select the Biomek import file to import.

Note: Workspace settings from Biomek FX software versions 2.5 or later may also be imported into a project file. To import a Biomek FX 2.5 software workspace file, from Files of type, select **Biomek® FX Workspace Files** to show all workspace files (*.wld).

4. Choose **Open**. Check In Project appears, displaying a list of all project items in the project file to import (Figure 6-23). Only the project items that do not match any of the revisions in the current project file are listed.

   Note: Biomek Software compares the project items in the import file to the current project. If the item in the import file matches any revision in the current project, that item is not displayed in Check In Project; if all items from the import file match the current project, Information (Figure 6-24) appears instead of Check In Project.

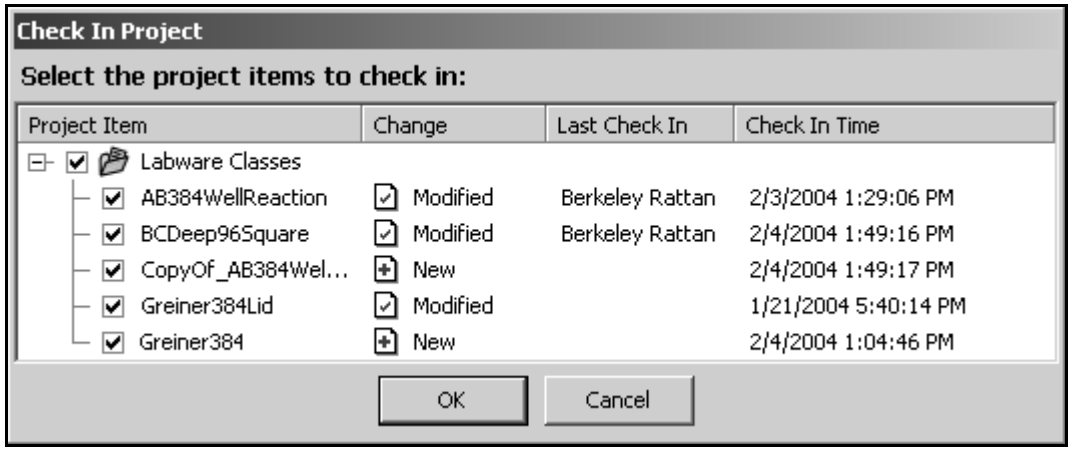


Figure 6-23. Checking in project items as official records

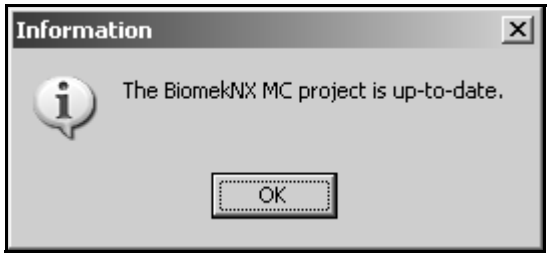


Figure 6-24. Information that appears when no project items are imported

5. Select all project items from the Biomek import file to import by selecting the checkbox to the left of each project item. By default, all project items are selected.

   Note: Project items are listed in a tree structure that lists items by type. Branches may be expanded or collapsed using the + and - buttons to the left of the project item name.

   Right-click on a type of project item and choose **Select All** from the menu to select all project items of that type, or choose **Select None** to deselect all project items of that type.

6. Choose **OK** to import all selected project items from the Biomek import file into the project file and close Check In Project.

   Note: If Beckman Coulter Accounts & Permissions is not in use, check in is complete.

   OR

   Choose **Cancel** to close Check In Project without including any project items in the Biomek import file.

7. If Accounts & Permissions is enabled, Check-In appears (Figure 6-25). Enter a **Reason** for checking in the project.

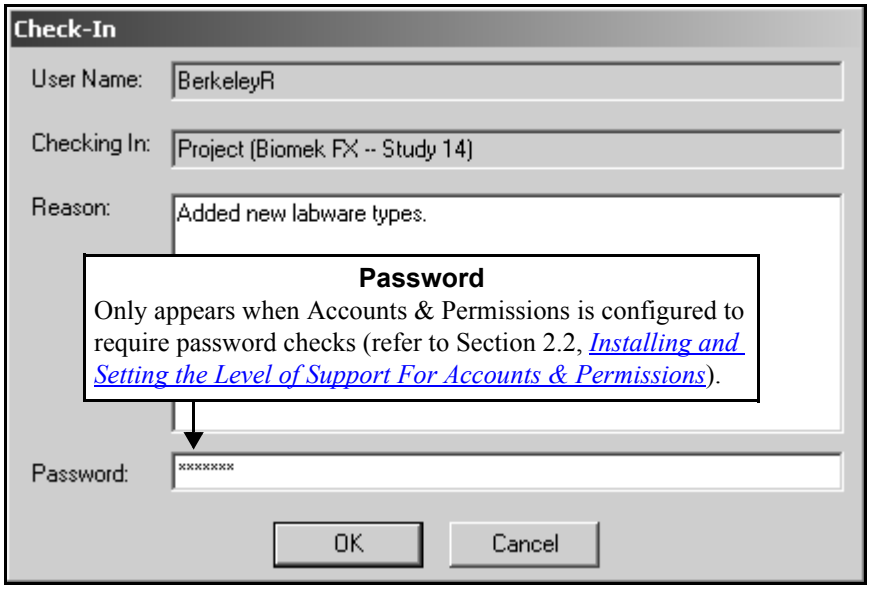


Figure 6-25. Check-In (Accounts & Permissions enabled)

8. If Accounts & Permissions is configured to require password checks for signing and check-in, enter the user **Password**.

9. Choose **OK** to close Check-In. The project items from the import file are imported to the project file.

7 Creating and Modifying Tip and Labware Types

7.1 Overview

Biomek Software must know the properties of the tips and labware used with the instrument to correctly perform liquid handling and gripper movement operations. A set of predefined tip and labware types commonly used in automated laboratories is preloaded with the software.

However, there may be instances when a tip or labware type used in the laboratory is not predefined in Biomek Software, or specifications of a predefined tip or labware type change. When this occurs, tip modifications are made in the Tip Type Editor and labware type modifications are made in the Labware Type Editor.

Note: Tips must be associated with a labware type in order to be used in a method.

All labware types have a graphic associated with them in Biomek Software. Any new labware type created in the Labware Type Editor will have a corresponding graphic generated, based upon the labware type properties. The graphic then appears in the Labware Category Graphical Display of the Instrument Setup step for use in methods (Figure 7-1).

Tip and labware types, along with information about liquid types; well patterns; and pipetting templates and techniques, are stored as part of a project file. Project files store a history of all changes, additions, and deletions of items from the project file. Refer to Chapter 6, *Understanding and Using Project Files*, for more information on project files.

Note: When Beckman Coulter Accounts & Permissions is enabled, only users with the Develop Projects permission assigned may open, edit, create, and delete tip and labware types (refer to Chapter 2, *Using Accounts & Permissions*).

The sections in this chapter include:

- *Defining Tips* (Section 7.2)
- *Defining Labware Types* (Section 7.3)

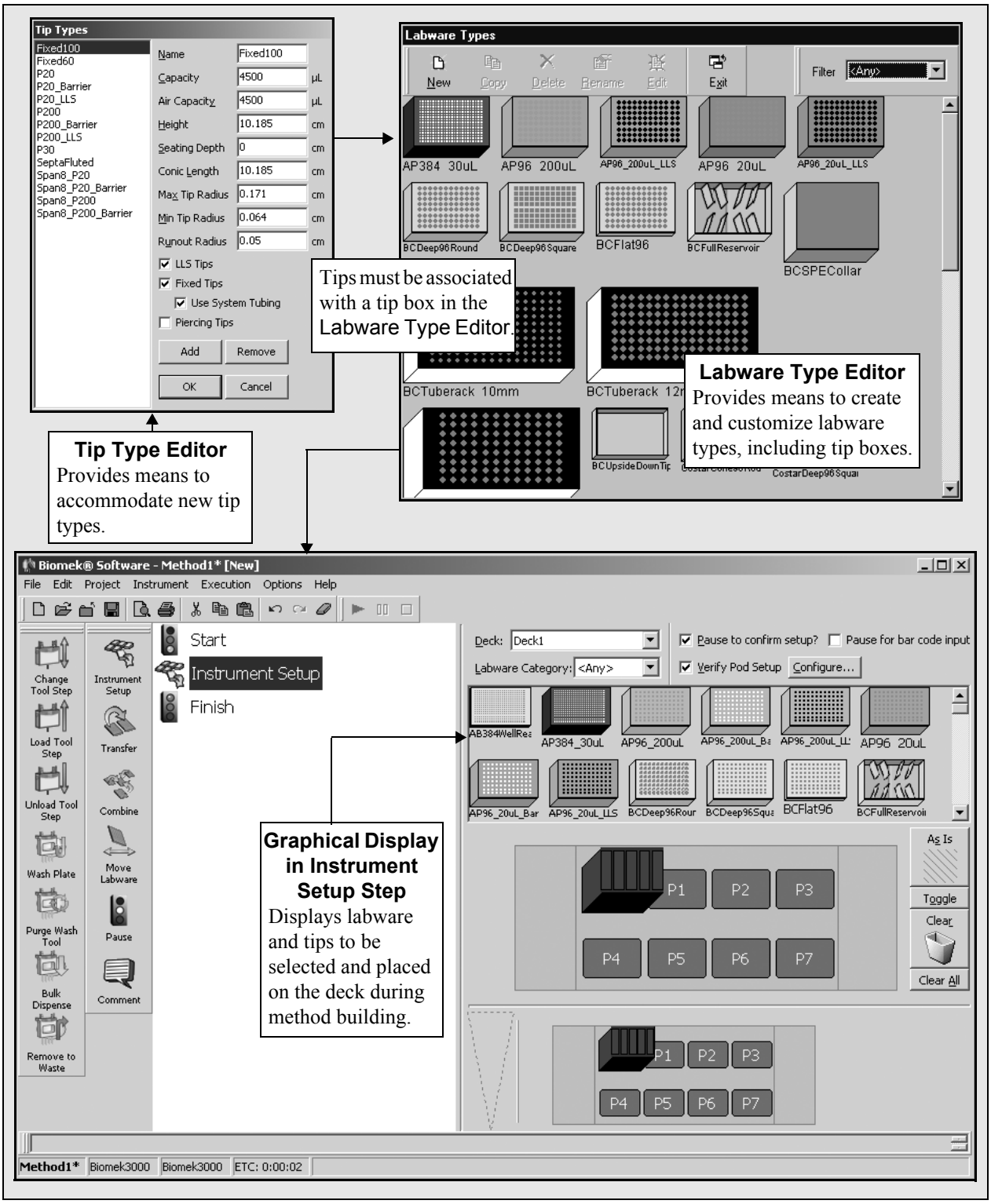


Figure 7-1. Relationships for labware and tips in Biomek Software

7.2 Defining Tips

All Beckman Coulter tip types may be used with Biomek instruments with some exceptions:

- ***FX*** — Fixed tips can only be used on the Span-8 Pod. LLS tips should only be used on the Span-8 Pod since a Multichannel Pod cannot sense the liquid level of wells.
- ***FX*** — Fixed60 and Fixed100 tips predefined in the Tip Type Editor for a Biomek FX project have a maximum capacity that is different from those in a Biomek NX project. Use caution when importing and exporting methods to and from instruments.

  Note: The Span-8 Pod is capable of accessing all types of labware supported by the Biomek FX instrument; however, specific types of tips are recommended to access specific types of labware (refer to the *Biomek® FX Laboratory Automation Workstation User's Manual,* Section 3.3.2.1, *Labware and Tip Compatibility with the Span-8 Pod*).

- ***3000*** — WashTips are only used internally with Biomek Software on the wash tool.

  Note: The Biomek 3000 head is capable of accessing all types of labware supported by the Biomek 3000 instrument; however, some tools cannot access specific types of labware. For example, multi-channel pipette tools cannot access test tubes (refer to the *Biomek® 3000 Laboratory Automation Workstation User's Manual,* Section 2.3.1, *Labware and Tip Compatibility with the Pipette Tools*).

- ***NX-S8*** — LLS tips are conductive and also used for clot detection which is available only on this instrument.
- ***NX-S8*** — SeptaFluted tips are conductive and used for clot detection and for piercing septa which is available only on this instrument.
- ***FX, NX-S8*** — Fixed60 and Fixed100 tips predefined in the Tip Type Editor for a Biomek NX project have a maximum capacity that is different from those in a Biomek FX project. Use caution when importing and exporting methods to and from instruments.

  Note: The pod is capable of accessing all types of labware supported by the Biomek NX instrument; however, specific types of tips are recommended to access specific types of labware (refer to the *Biomek® NX Span-8 Laboratory Automation Workstation User's Manual,* Section 2.3.3.1, *Labware and Tip Compatibility with the Span-8 Pod*).

Note: Refer to the specific hardware manual for a Biomek instrument for more information on tips and tip properties.

In order to use tips that are not predefined, use the Tip Type Editor to:

- Add new tips.
- Change tip properties, such as capacity and size.
- Remove tips.

7.2.1 Accessing the Tip Type Editor

To access the Tip Type Editor, choose **Project>Tip Type Editor**. Tip Types appears (Figure 7-2).

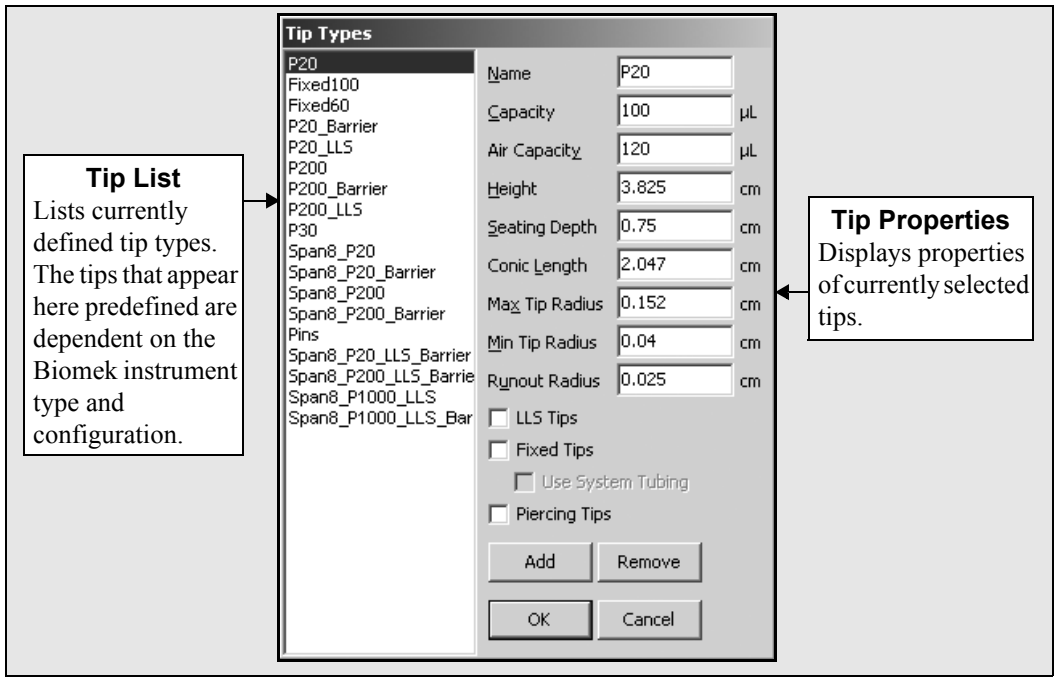


Figure 7-2. Tip Types

7.2.2 Adding New Tips

Add tips that are not previously defined to ensure that liquid transfers are performed accurately.

To add tips:

1. In the Tip Type Editor, highlight the tip type that most closely resembles the new tip type.

   Note: Adding tips copies the selected tip type, including its properties.

2. Choose **Add**. The tip type appears in the Tip List as "Tip" followed by a number. For example, the first tips created are named "Tip1".

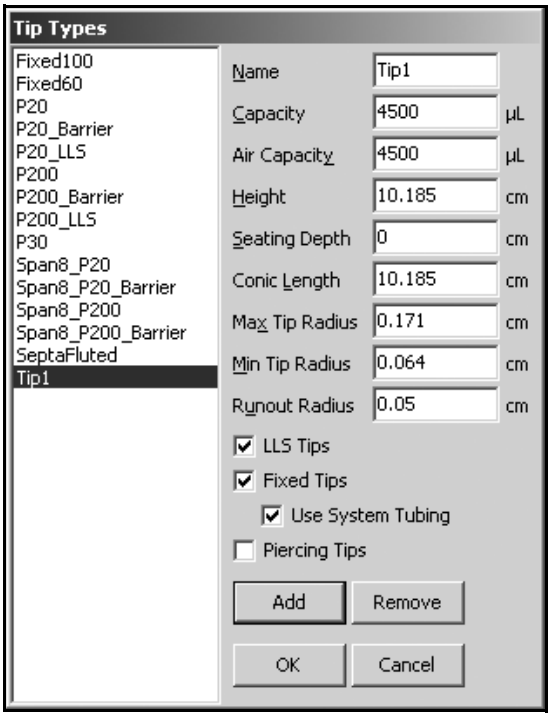


Figure 7-3. Adding a new tip type

CAUTION: After new tips are added, the correct properties must be defined in the Tip Type Editor according to the manufacturer's specifications. Inaccurate specifications may lead to hardware crashes.

3. Modify the tip properties according to the manufacturer's specifications (refer to Section 7.2.3, *Changing Tip Properties*).

4. Choose **OK**.

Note: Choose Cancel to cancel the addition of the tip type. A Warning appears to confirm the cancellation of changes (Figure 7-4).

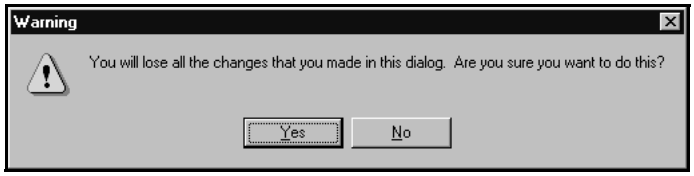


Figure 7-4. Warning to confirm cancellation of changes

7.2.3 Changing Tip Properties

Change tip properties in the Tip Type Editor when defining new tips or changing the existing tip properties.

Tip properties include the following (Table 7-1):

Table 7-1. Tip Properties

	Description
Name	Names the tips for easy identification. **Note:** Tip names must begin with a letter, and only letters, numbers, and underscores (_)can be used.
Capacity	The maximum liquid volume the tip holds.
Air Capacity	The total amount of leading air gap, plus liquid that can be aspirated. Trailing air gaps are counted against liquid capacity since they displace liquid further into the tips (Figure 7-5).
Height	The total height of the tip (Figure 7-6).
Seating Depth	The depth at which the tip seats properly on the mandrels (Figure 7-6).
Conic Length	The lowest triangular section of a tip (Figure 7-6).
Max Tip Radius	Radius of the tip at the top of the conic length (Figure 7-6).
Min Tip Radius	Radius of the tip at its narrowest point (Figure 7-6).
Runout Radius	Defined area around a tip to account for manufacturing tolerances and tip bending.
LLS Tips	Indicates the tips are conductive and capable of Liquid Level Sensing and clot detection. ➢ ***FX*** — Liquid Level Sensing is available on a Span-8 Pod only. Clot detection is not available. ➢ ***NX-S8*** — Liquid Level Sensing and clot detection are available.
Fixed Tips	Indicates the tips are not disposable. ➢ ***FX, NX-S8*** — Used on Span-8 Pods only.
Use System Tubing	Indicates the sample aspiration is allowed to enter the system tubing. ➢ ***FX, NX-S8*** — Used on Span-8 Pods only. ➢ ***3000*** — Used for WashTips.
Piercing Tips	Indicates the tips are capable of piercing septa. ➢ ***NX-S8*** — Septa piercing is available on this instrument only.

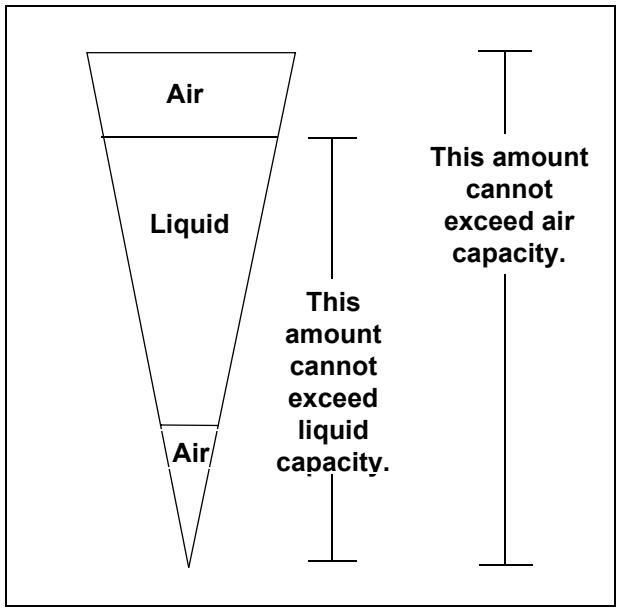


Figure 7-5. Tip capacity and air capacity

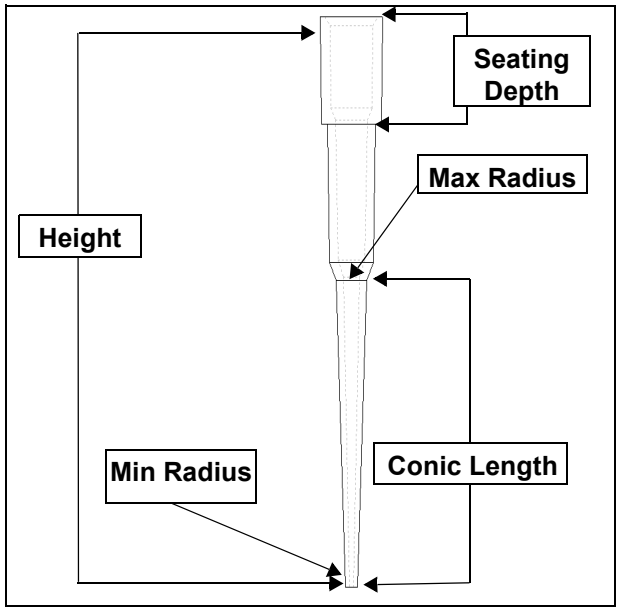


Figure 7-6. Tip dimensions

To change tip properties:

1. In the Tip Type Editor, select the desired tips from the Tip List (Figure 7-2). The current properties of the tips display in Tip Properties.
2. Change the desired properties (Table 7-1) according to the manufacturer's specifications.
3. Choose **OK**.

Note: Choose Cancel to cancel the changes made to the properties. A Warning appears to confirm the cancellation of changes (Figure 7-4).

7.2.4 Removing Tips

Remove obsolete tips from the Tip List.

Note: The Tip Type Editor does not allow tips to be deleted that are used by any labware class or that are on the pod. To delete a tip type, delete the labware type in the Labware Type Editor first (refer to Section 7.3.6, *Editing Labware Type Properties*).

To remove tips:

1. In the Tip Type Editor, select the desired tips from the Tip List.
2. Choose **Remove**. A Warning appears (Figure 7-7).

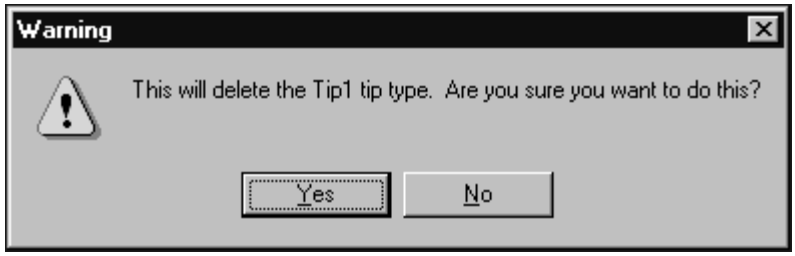


Figure 7-7. Remove tips warning

3. Choose **Yes** to confirm the removal. The tips are removed from the Tip List.
4. Choose **OK**.

Note: Choose Cancel to cancel the removal of the tip type. A Warning appears to confirm the cancellation of changes (Figure 7-4).

7.3 Defining Labware Types

Labware types are divided into categories, such as titerplates, reservoirs, tube racks, lids, and tip boxes. In Biomek Software, each labware category contains specific predefined labware, such as BCDeep96Square, BCUpsideDownTip, BoxLid, and BCTuberack_10mm.

Edit labware type properties. Use the Labware Type Editor for:

- *Adding a New Labware Type* (Section 7.3.2).
- *Copying a Labware Type* (Section 7.3.3)
- *Deleting a Labware Type* (Section 7.3.4)
- *Renaming a Labware Type* (Section 7.3.5)
- *Editing Labware Type Properties* (Section 7.3.6)

7.3.1 Accessing the Labware Type Editor

To access the Labware Type Editor, choose **Project>Labware Type Editor**. Labware Types appears (Figure 7-8).

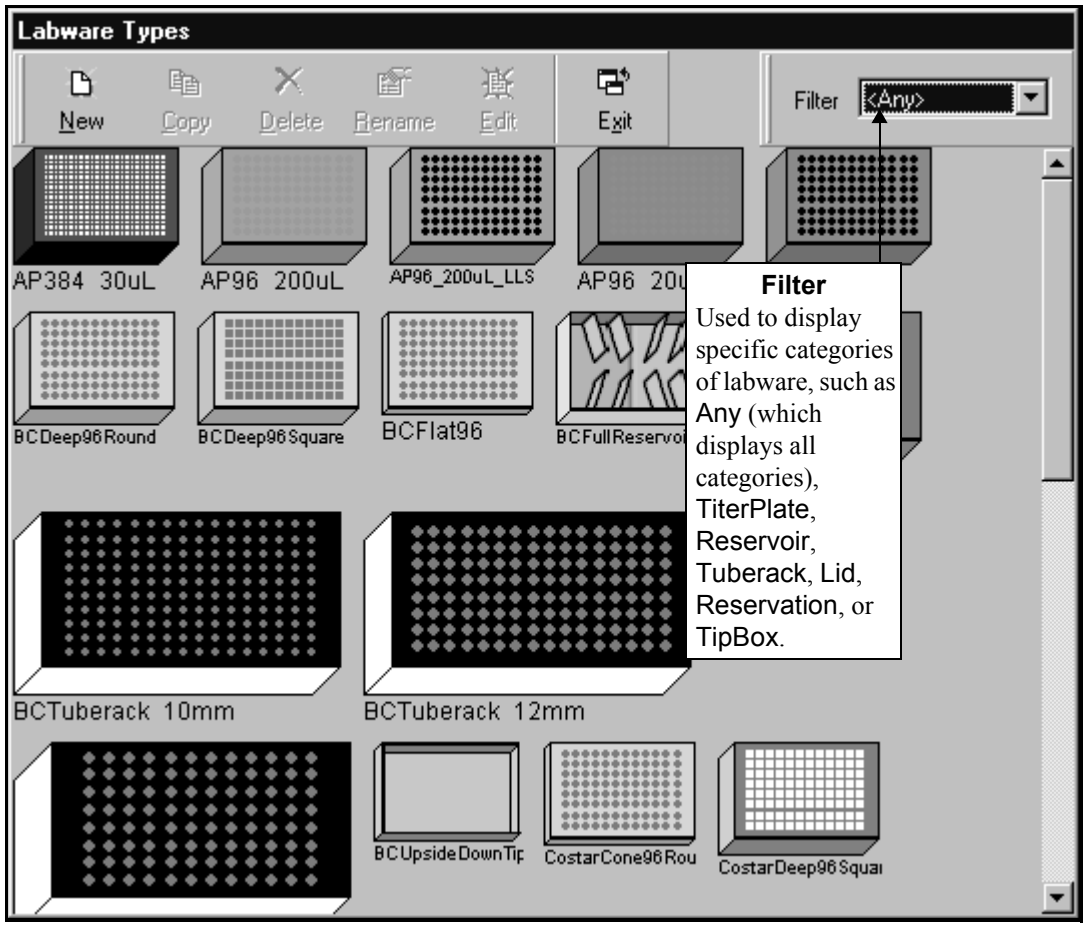


Figure 7-8. Labware Types

Note: The labware that is displayed in the Labware Type Editor is dependent on the current project file.

7.3.2 Adding a New Labware Type

Add a new labware type when the desired type is not predefined in Biomek Software. When a new labware type is added, default properties are inserted into the appropriate fields. The default properties may need to be changed to meet the manufacturer's specifications of the new labware type.

To add a new labware type:

1. From Labware Types, select **New** from the toolbar at the top. New Labware appears (Figure 7-9).

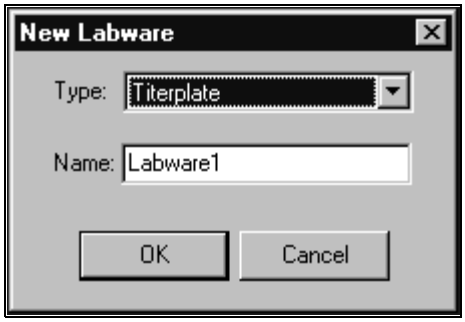


Figure 7-9. New Labware

2. Choose the labware type from the pull-down list.
3. Enter a name for the labware or use the default name.

Note: The new labware is assigned the default name of Labware plus a number representing the order in which the labware was created. For example, the first labware created is given the default name Labware1 and the second is given the default name Labware2.

4. Choose **OK**. The new labware appears graphically in Labware Types. (Figure 7-8).

Note: Use Filter or scroll down Labware Types to locate the new labware type (Figure 7-8).

7.3.3 Copying a Labware Type

Copying a labware type creates an exact copy of it, including current properties. The properties of the copied labware type can be modified to create a new labware type.

To copy a labware type:

1. From Labware Types, highlight the graphic representing the labware and select **Copy** from the toolbar at the top.

   OR

   Right-click the graphic for the labware type and choose **Copy**. Copy Labware Type appears (Figure 7-10).

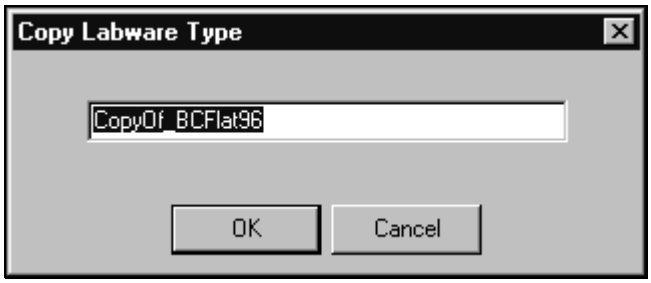


Figure 7-10. Copy Labware Type

2. Enter a name for the labware or use the default name.

   Note: Labware names must begin with a letter, and can contain only letters, numbers, and underscores (_) or an error message appears. The default name assigned to a labware type consists of the name of the labware type preceded by CopyOf_. For example, a copy of BCFlat96 is CopyOf_BCFlat96.

3. Choose **OK**. The copied labware appears graphically in Labware Types. (Figure 7-8).

7.3.4 Deleting a Labware Type

Delete any labware type from Labware Types that is no longer used.

To delete a labware type:

1. From Labware Types, highlight the graphic representing the labware and select **Delete** from the toolbar at the top.

   OR

   Right-click the graphic for the labware type and choose **Delete**. Information appears (Figure 7-11).

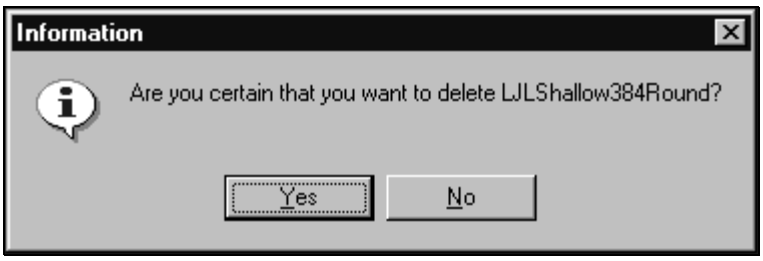


Figure 7-11. Information

2. Choose **Yes** to confirm the removal. The labware is deleted from Labware Types (Figure 7-8).

7.3.5 Renaming a Labware Type

Renaming a labware type provides the opportunity to assign a descriptive name to a labware type for easy identification.

Note: If labware types are renamed, any methods with labware under the old name will generate an error when the method is validated. The name must be changed to reflect the new name in the Instrument Setup step and any step that refers to the old name, such as in the Transfer step.

Note: The labware type names appear on the Instrument Setup Configuration. Refer to Chapter 15.2, *Instrument Setup Step*, for more information about Instrument Setup.

To rename a labware type:

1. From Labware Types, highlight the graphic representing the labware and select **Rename** from the toolbar at the top

   OR

   Right-click the graphic for the labware type and choose **Rename**. Rename Labware Type appears (Figure 7-12).

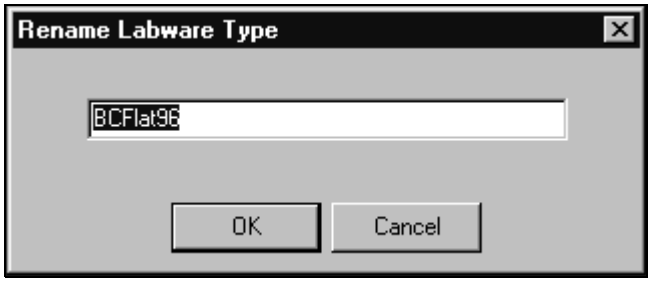


Figure 7-12. Rename Labware Type

2. Enter a new name.

   Note: Labware type names must begin with a letter, and only letters, numbers, and underscores (_)can be used.

3. Choose **OK** to save the new labware name. The new labware name appears in Labware Types (Figure 7-8).

7.3.6 Editing Labware Type Properties

The applicable properties for a labware type are arranged in the Labware Type Editor according to the following categories (Table 7-2):

Table 7-2. Labware Type Properties

Category	Properties
Basic Information	span, height, and description of the labware; bitmap graphic; and an option to edit the color of the labware (refer to Section 7.3.6.1, *Changing Labware Colors*)
Magbead	allows properties to be set for labware used on the Magnetic Bead ALP, such as magnet type; height; and options to clamp during pipetting or engaging magnet, move arms to maximum height when clamping; and sense labware before pipetting or gripping (refer to the *ALPs User's Manual,* Section 10.4.3, *Configuring LabwareTypes for Use on the Magnetic Bead ALP*).
Miscellaneous	name of the default lid, sensitivity, and clamp force, an option to hide the labware so it is not visible in the Biomek editor, and an option to require piercing tips when the labware is accessed ➢ ***NX-S8*** — Septum piercing is available on this instrument only.
Movement Information	gripper offset, gripper squeeze, gripper unsqueeze, speed limit, and an option to use the gripper sensor when available
Orbital Shaker	allows the maximum speed to be set for labware used on the Orbital Shaker ALP (refer to the *ALPs User's Manual,* Section 14.4.2, *Configuring a New Labware Type for Use on the Orbital Shaker ALP*).
Ordering Information	manufacturer and part number
Sections	an option to configure sections used in a reservoir (refer to Section 7.3.6.2, *Configuring a Reservoir with Sections*)

Table 7-2. Labware Type Properties

Category	Properties
Stacking	stack offsets and options to edit the stack offsets (refer to Section 7.3.6.3, *Specifying Stackable Items*) and to edit on which labware types or ALP types the labware can be securely stacked on top (refer to Section 7.3.6.4, *Using Secure Stacking*)
Reservation Information	"Caption" field that identifies the label that appears on the reservation and a "Reserve For" field that identifies the reason the space is reserved
Wells_1	well offset, count, spacing, maximum volume, format, column 2 offset, default volume, known default volume, and an option to configure well dimensions (refer to Section 7.3.6.5, *Configuring Well Properties*)
Tips	tip offset, count, spacing, tip load Z offset, tip unload Z offset, and tip type

To edit labware properties:

1. From Labware Types, highlight the graphic representing the labware and choose **Edit** from the toolbar.

   OR

   Right-click the graphic and choose **Edit**.

   OR

   Double-click the graphic.

2. Choose the appropriate labware category and make the desired changes to the labware properties that appear.

   Note: All distances are in centimeters unless otherwise specified.

3. Choose **Save**.

Note: Three sections of hints are offered at the bottom of the edit option. The first section displays a graphic of the labware, the second section explains the selected field, and the third section explains any errors resulting from editing the labware properties. Place the cursor over the desired labware properties field and click to access these hints.

7.3.6.1 Changing Labware Colors

Make labware stand out in the Instrument Setup step by changing the colors of the labware as desired. For example, each titerplate could be a different color. Changing labware colors also helps to make labware distinguishable in the Biomek main editor.

Note: The color fuchsia (RGB 255, 0, 255) is the system transparency color and causes odd visual behavior.

To change labware colors:

1. From Labware Types, highlight the graphic representing the labware and choose **Edit** from the toolbar at the top.

   OR

   Right-click the graphic and choose **Edit**.

   OR

   Double-click the graphic.

2. Choose **Basic Information** (Figure 7-13).

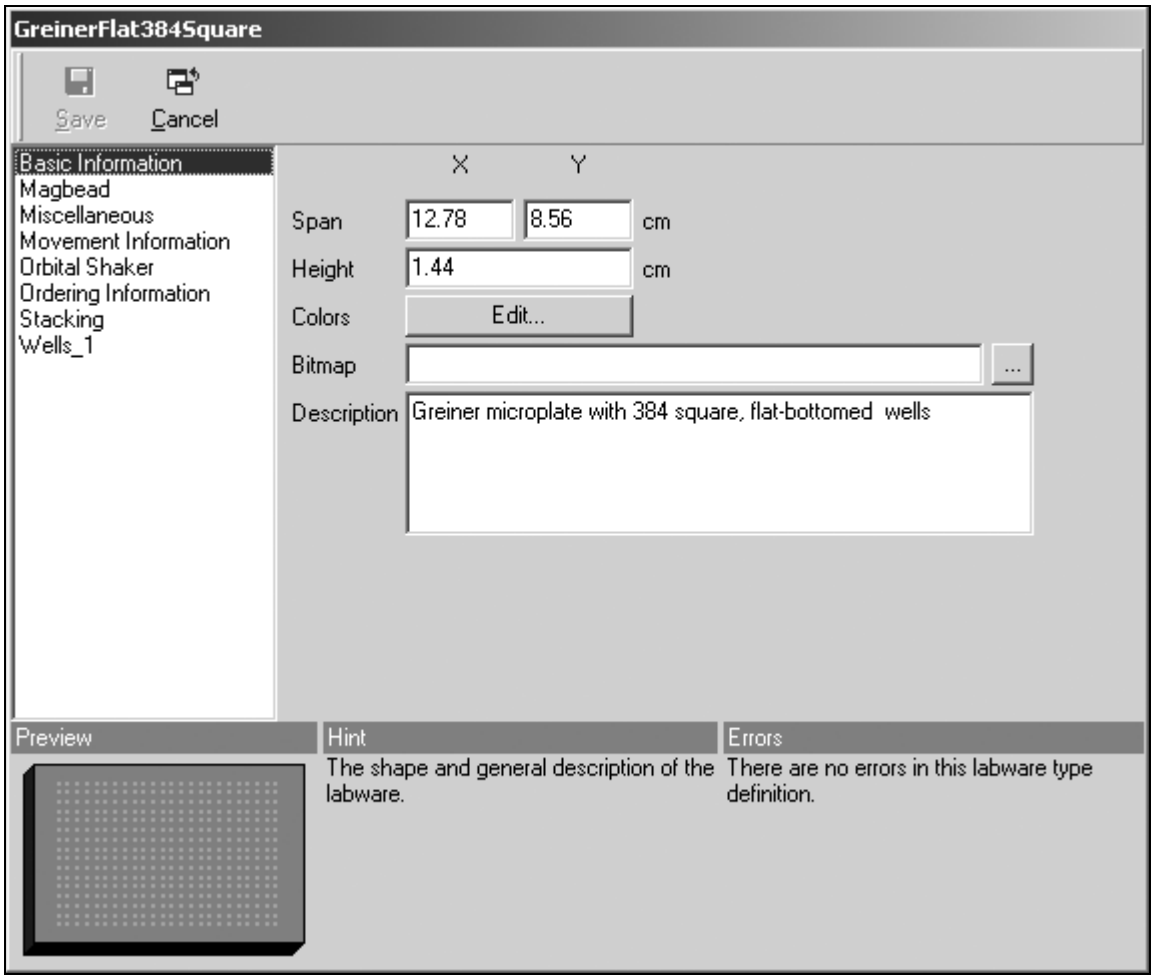


Figure 7-13. Basic Information chosen

3. Choose **Edit** next to Colors. Labware Colors appears (Figure 7-14).

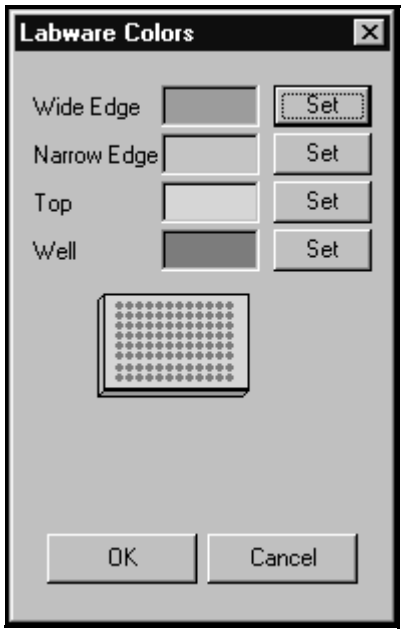


Figure 7-14. Labware Colors

4. Choose **Set** to configure the color for the following sections of the labware:
   - Wide Edge
   - Narrow Edge
   - Top
   - Well

   Color appears (Figure 7-15).

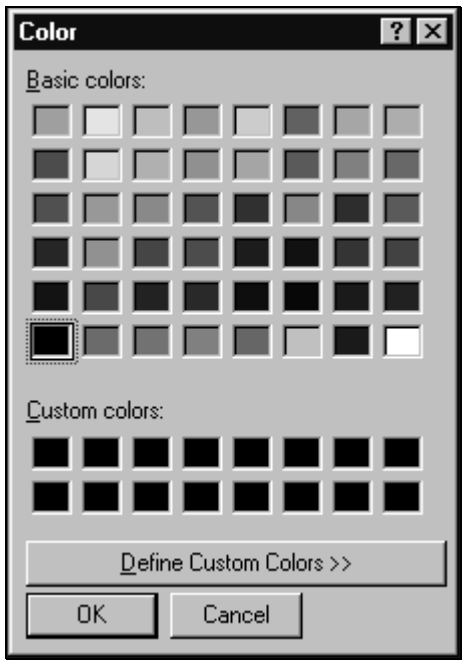


Figure 7-15. Color

5. Select the desired color or define a custom color for the labware section.
6. Choose **OK**.

Note: Choose Cancel to cancel the color selections.

7. Repeat the process for each section of the labware, if desired.
8. Choose **OK** in Labware Colors when complete.

Note: Choose Cancel to cancel the color selections.

9. Choose **Save**. Labware Types appears (Figure 7-8).

Note: Choose Cancel to cancel the changes made to the labware type. A Warning appears to confirm the cancellation of unsaved changes to the labware (Figure 7-16).

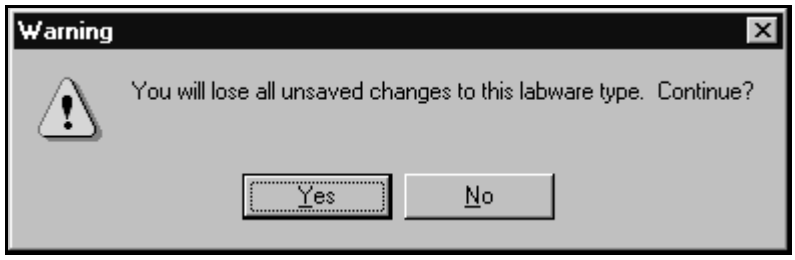


Figure 7-16. Warning to confirm cancellation of changes made

10. Choose **Exit**.

7.3.6.2 Configuring a Reservoir with Sections

Some methods require the use of a reservoir with sections. Use Sections to configure a reservoir with sections. This allows the pod to accurately aspirate, dispense, and transfer liquid using a reservoir with sections.

To configure a reservoir with sections:

1. Open Labware Types (refer to Section 7.3.1, *Accessing the Labware Type Editor*).
2. Copy an existing reservoir (refer to Section 7.3.3, *Copying a Labware Type*) or create a new one (refer to Section 7.3.2, *Adding a New Labware Type*). The new labware appears in Labware Types.
3. Highlight the graphic representing the new reservoir and choose **Edit** at the top of Labware Types.

   OR

   Right-click the graphic and choose **Edit**.

   OR

   Double-click the graphic.

4. Choose **Sections** (Figure 7-17).

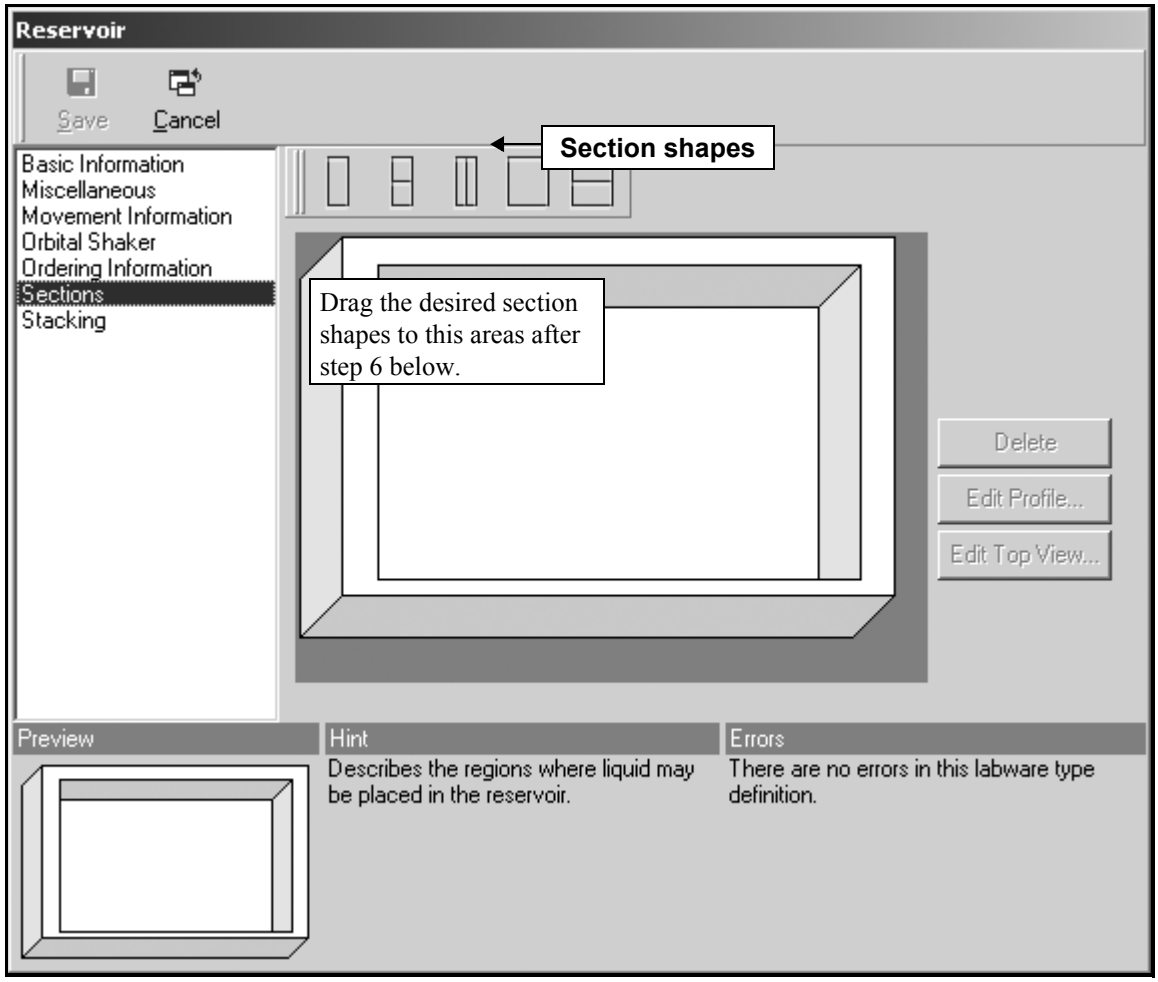


Figure 7-17. Sections chosen

5. Click in the reservoir. A green rectangle appears.
6. Choose **Delete**. Error appears as a reminder that sections are deleted and new sections must be added (Figure 7-18).

Figure 7-18. Error reminder that sections are deleted

7. Choose **OK**.
8. Drag the shape of the section(s) to the reservoir.
9. Click the area around a specific section. A green rectangle appears.

10. Choose **Edit Profile**. Edit Section Profile appears (Figure 7-19).

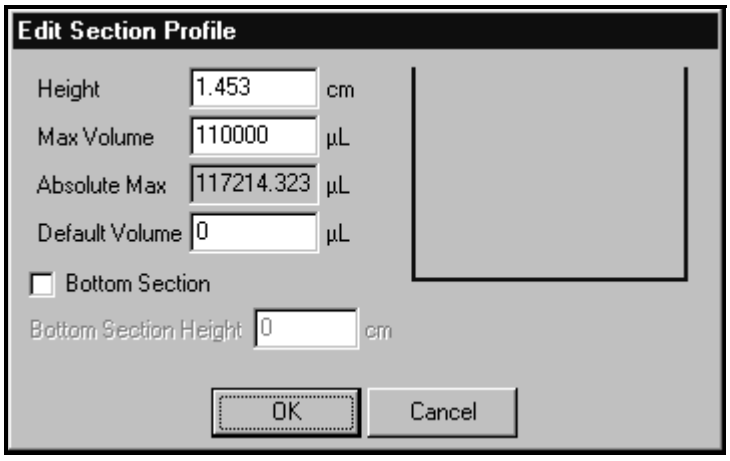


Figure 7-19. Edit Section Profile

11. If necessary, change the values in **Height**, **Max Volume**, and **Default Volume** according to the manufacturer's specifications.
12. Check **Bottom Section** if the section includes a triangular bottom.

Note: If Bottom Section is checked, enter the value in **Bottom Section Height**.

13. Choose **OK**.
14. Choose **Edit Top View**. Edit Section Top appears (Figure 7-20).

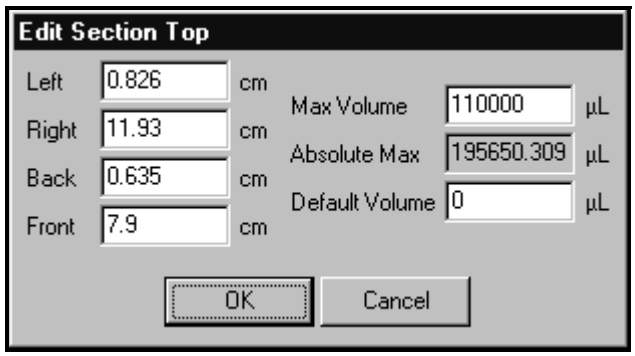


Figure 7-20. Edit Section Top

15. If necessary, change the values in **Left**, **Right**, **Back**, **Front**, **Max Volume**, and **Default Volume** according to the manufacturer's specifications.
16. Choose **OK**.

17. Repeat steps 8 through 16 for each section in the reservoir.
18. When all sections have been configured, choose **Save** (Figure 7-17). A graphic representing the reservoir with the sections appears in Labware Types.

Note: An Error (Figure 7-21) appears if the sections are not configured properly. Choose **OK** and reconfigure the sections.

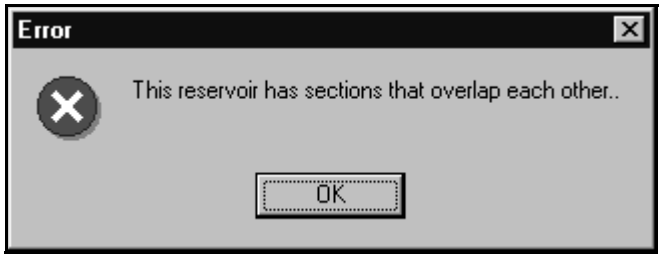


Figure 7-21. Error for an improperly configured reservoir

Note: Choose Cancel to cancel the changes made to the labware type. A Warning appears to confirm the cancellation of unsaved changes to the labware (Figure 7-16).

7.3.6.3 Specifying Stackable Items

Many common microplates are stackable up to six centimeters in height; however, items such as reservoirs, tube racks, and tip boxes are not.

Specifying stackable items is necessary to allow the software to effectively move labware stacks during liquid-handling operations. For items that are stackable, use Stackable Items to specify the distance from one piece of labware to the labware above it (stack offset). A stack offset is the distance between stacked plates, measured from the bottom, back-left corner on a microplate to the bottom back-left corner on the microplate above it. The distance is measured using X, Y, and Z coordinates.

Note: If it is desired to place more than two pieces of labware in a stack, they must stack securely to each other (refer to Section 7.3.6.4, *Using Secure Stacking*).

Stackable Items:

- specifies with a checkmark which labware types can be stacked on the labware being edited.
- may be configured to allows checkmarks to be entered when it is necessary to stack a specific type of labware on labware being edited for a specific method.

The information entered in Stackable Items is used by the software when moving labware, for example, in the Move Labware step.

To specify stacking offset:

1. From Labware Types, highlight the graphic representing the labware and choose **Edit** from the toolbar at the top.

   OR

   Right-click the graphic and choose **Edit**.

   OR

   Double-click the graphic.

2. Choose **Stacking** (Figure 7-22).

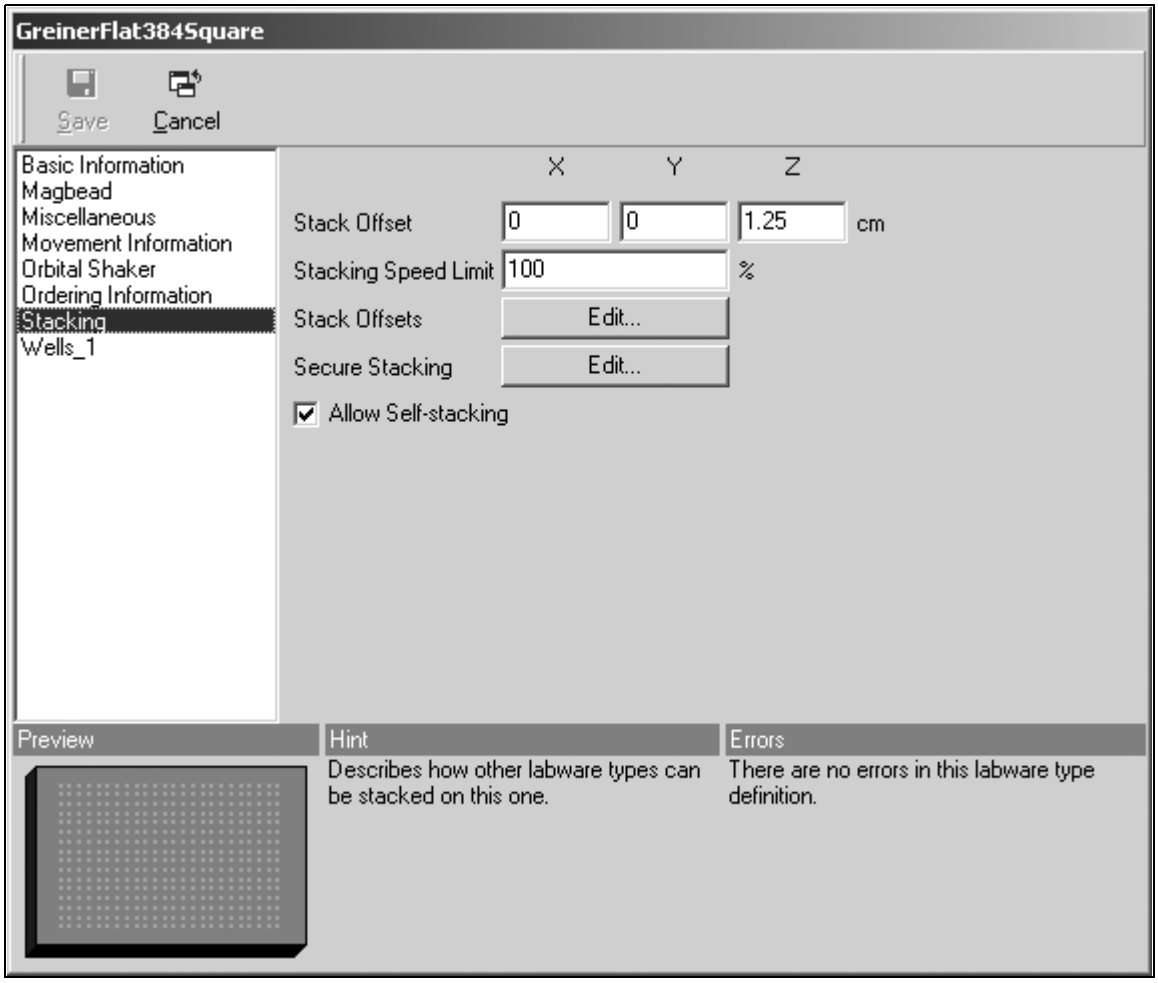


Figure 7-22. Stacking chosen

3. Choose **Edit** next to Stack Offsets. Stackable Items appears (Figure 7-23).

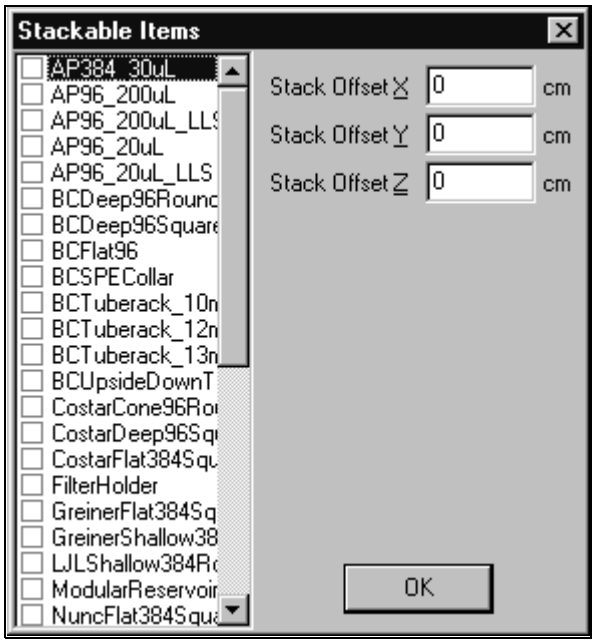


Figure 7-23. Stackable Items

4. Choose the desired labware types that can be stacked on top of the labware type being edited.

Note: If an item does not have a checkmark next to it, that type of labware cannot be stacked on the labware type being edited (selected in Labware Types); however, if Allow Self-stacking is checked in Stacking, it is not necessary to check it in Stackable Items.

5. If applicable, type the desired value for **Stack Offset X**, **Stack Offset Y**, and **Stack Offset Z**.

Note: While the offset values may be calculated using calipers, a more precise measurement should be obtained from the manufacturer's specifications.

6. Choose **OK** to save the stackable items settings.
7. Choose **Save**. Labware Types appears.

Note: Choose Cancel to cancel the changes made to the labware type. A Warning appears to confirm the cancellation of unsaved changes to the labware (Figure 7-16).

8. Choose **Exit**.

7.3.6.4 Using Secure Stacking

Use Secure Stacking when it is necessary to securely stack more than two plates. The notations made in Secure Stacking are used by the software to allow the creation of stacks for a Solid Phase Extraction (SPE) assembly or tall stacks. It is necessary to use Secure Stacking with Stackable Items to ensure that specific labware can be stacked on top of other specific labware.

Like Stackable Items, Secure Stacking allows checkmarks to be entered when it is necessary to stack a specific type of labware on another specific type of labware for certain methods. The information entered in Secure Stacking will be used by the software when moving labware, for example, in the Move Labware step.

To effectively use Secure Stacking, an understanding of the Biomek stacking rules is necessary. The Biomek stacking rules apply to stacks on all Biomek instrument decks.

7.3.6.4.1 Biomek Stacking Rules

When stacking or unstacking labware, Biomek Software works from the bottom up. If there is a stack of four microplates on deck, the top three are moved by the gripper, then the top two, and finally the top piece of labware.

The maximum height of stacks of microplates allowed on the Biomek instrument decks is as follows:

- ***FX, NX-MC*** — 5.5 cm (2.17 in.)
- ***3000*** — 6.0 cm (2.36 in.)
- ***NX-S8*** — 6.5 cm (2.56 in.)

Note: A stack of four standard 96-well plates is approximately 5.2 cm (2.05 in.) tall.

A plate (or stack of plates) can be removed from the source position if one of the following conditions is true:

- The stack at the source position has fewer than three plates.
- The entire stack is being moved.
- The selected plate to be moved is the plate immediately above the bottom plate.
- All of the plates below the selected plate to be moved securely stack to each other.
- The selected plate to be moved securely stacks to the source position.
- The plate immediately below the selected plate to be moved securely stacks to the source position.

A plate (or stack of plates) can be moved to a destination position if one of the following conditions is true:

- The destination position has fewer than two plates (one or none).
- All of the plates that are currently stacked at the destination position securely stack to each other.
- The top plate of the destination stack securely stacks to the destination position.
- The selected plate to be moved securely stacks to the destination position.

7.3.6.4.2 Configuring Secure Stacking

To use Secure Stacking:

1. From Labware Type Editor, highlight the graphic representing the labware and choose **Edit**.

   OR

   Right-click the graphic and choose **Edit**.

   OR

   Double-click on the graphic.

2. Choose **Stacking** (Figure 7-22).
3. Choose **Edit** next to Secure Stacking. Secure Stacking appears (Figure 7-24).

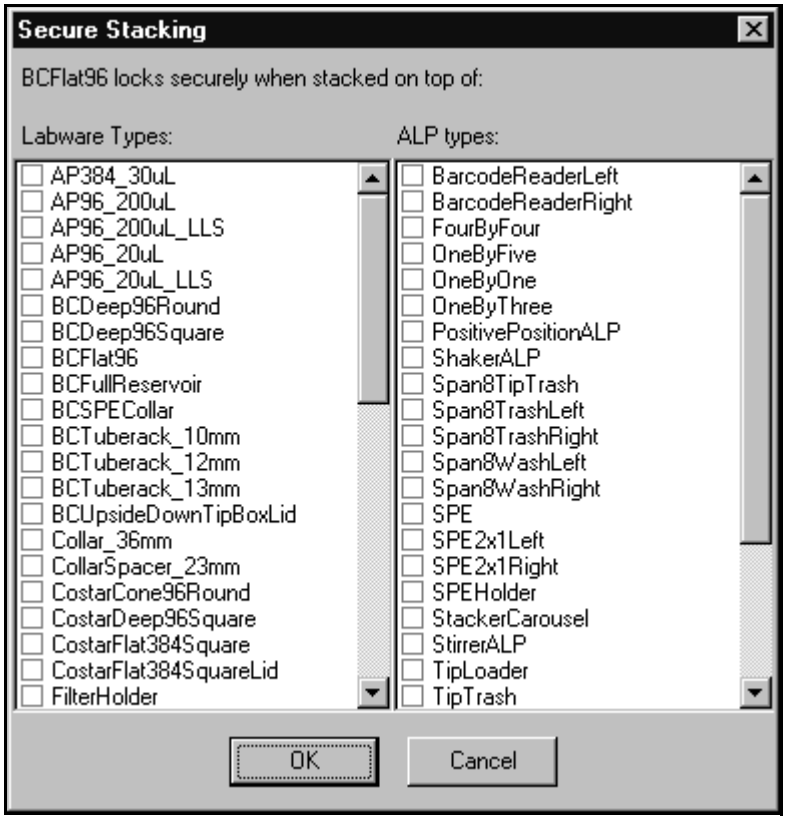


Figure 7-24. Secure Stacking

4. Check the labware types and/or ALP types which lock securely to the labware type being edited.
5. Choose **OK** to save the settings.
6. Choose **Save**. Labware Types appears.

   Note: Choose Cancel to cancel the changes made to the labware type. A Warning appears to confirm the cancellation of unsaved changes to the labware (Figure 7-16).

7. Choose **Exit**.

7.3.6.5 Configuring Well Properties

Well properties must be configured when new labware is added to the deck.

CAUTION: The correct well properties must be defined in Labware Types according to the manufacturer's specifications. Inaccurate specifications may lead to inaccurate pipetting.

To configure well properties:

1. From Labware Types, highlight the graphic representing the labware and choose **Edit**.

   OR

   Right-click the graphic and choose **Edit**.

   OR

   Double-click the graphic.

2. Choose **Wells_1** (Figure 7-25).

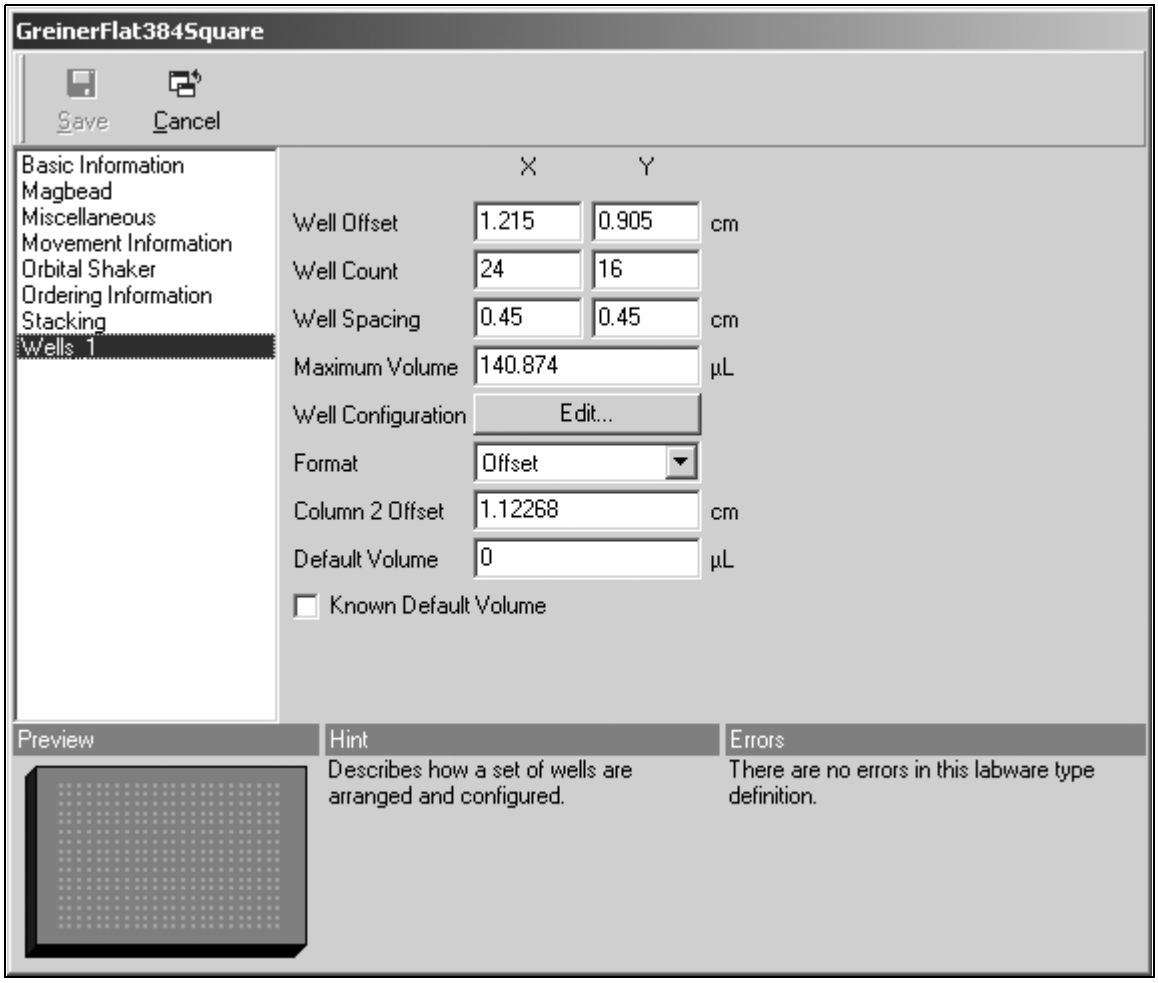


Figure 7-25. Wells_1 chosen

3. Choose **Edit** next to Well Configuration. Well Configuration Dialog appears (Figure 7-26).

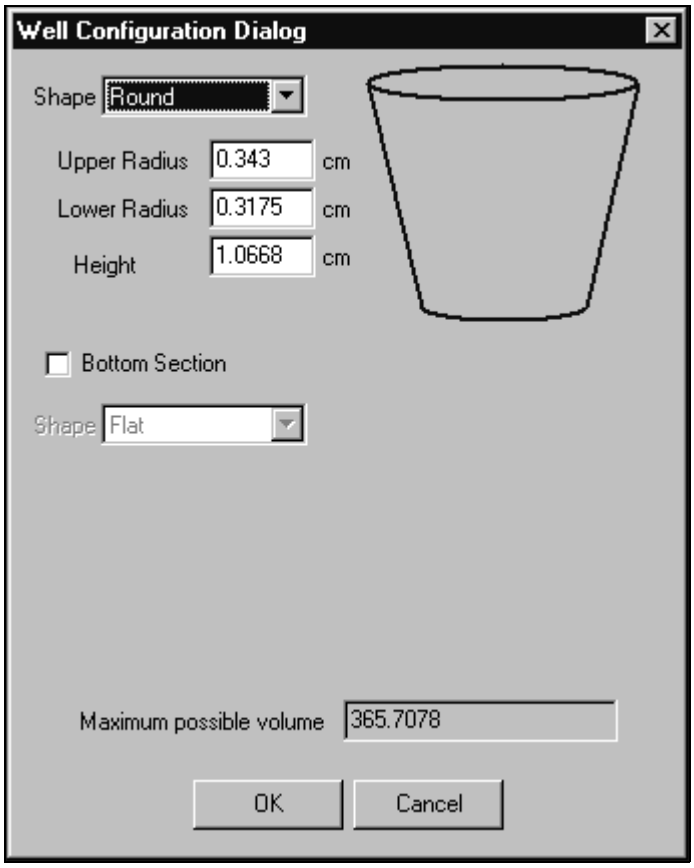


Figure 7-26. Well Configuration Dialog

4. Choose the Shape from the drop down menu.

5. Configure the specifications according to the manufacturer's specifications.

Note: Placing the cursor in the specification fields identifies the measurement area on the graphic shape. Placing a check in the Bottom Section field identifies the measurement area on the graphic shape that represents the bottom section of the well (Figure 7-27).

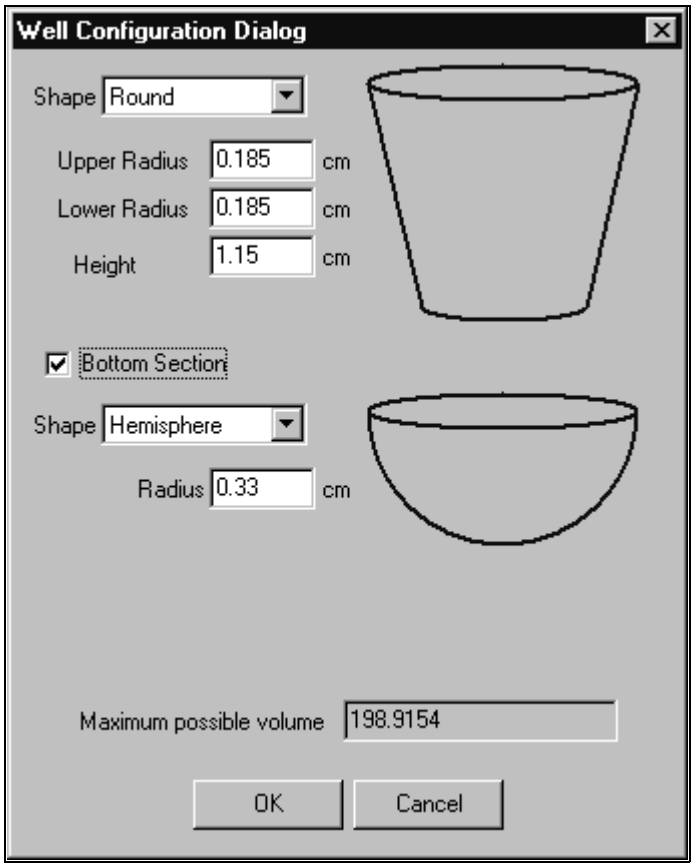


Figure 7-27. Well Configuration Dialog with Bottom Section checked

6. Choose **OK** in Well Configuration Dialog when complete.
7. Choose **Save**. Labware Types appears.

Note: Choose Cancel to cancel the changes made to the labware type. A Warning appears to confirm the cancellation of unsaved changes to the labware (Figure 7-16).

8. Choose **Exit**.

8 Understanding and Creating Liquid Types

8.1 Overview

The Liquid Type Editor (Figure 8-1) is used to create new liquid types or to modify existing liquid types for methods. Each time a new liquid type is created, it becomes available for all new and existing methods created in a Biomek Software project file. Any liquid type may be set as the default liquid type. In a method, the default liquid type is used when a piece of labware is not configured with a specific liquid.

Note: When Beckman Coulter Accounts & Permissions is enabled, only users with Develop Projects permission may open, edit, create, and delete liquid types (refer to Chapter 2, *Using Accounts & Permissions*).

The following is configured in the Liquid Type Editor:

- Aspirate — configures the delay, speed, and trailing air gap applicable to the liquid.

  Note: A trailing air gap draws air into the tips after aspirate to help prevent drips during a method run.

- Blowout — configures the amount of air used in the blowout, and the delay after the air has been dispensed.
- Prewet — configures the amount of additional liquid to aspirate, and the amount of time to pause before dispensing.
- Wash — configures the amount of liquid used to clean a tip and the default number of aspirate and dispense cycles used during the wash.
  - ***3000*** — Wash is *not* applicable for liquid types.
- Dispense — configures the delay and speed of the dispense operation during a method run and the cutoff velocity.
  - ***FX***, ***NX-S8*** — Cutoff velocity is applicable when the liquid is handled by a Span-8 Pod *only*.
- Tip Touch — configures the position and amount of time to pause while the tip is in contact with the side of the well and the speed at which the pod should move during the operation.

- Liquid Level Sensing Sensitivity — configures the sensitivity of the liquid level sensing for the liquid type.
  - ***FX***, ***NX-S8*** — Liquid Level Sensing Sensitivity is applicable when the liquid is handled by a Span-8 Pod *only*.
- Clot Detection Sensitivity — configures the sensitivity of the clot detection for the liquid type.
  - ***NX-S8***— Clot Detection is applicable on this instrument *only*.

Note: When Override Liquid Type Settings is selected in the technique, the liquid type settings created in Liquid Type Editor are not used (overridden). Refer to Chapter 9, *Understanding and Creating Techniques* for more information about creating and editing techniques.

Liquid types, along with information about tip and labware types; well patterns; and pipetting templates and techniques, are stored as part of a project file. Project files store a history of all changes, additions, and deletions of items from the project file. Refer to Chapter 6, *Understanding and Using Project Files*, for more information on project files.

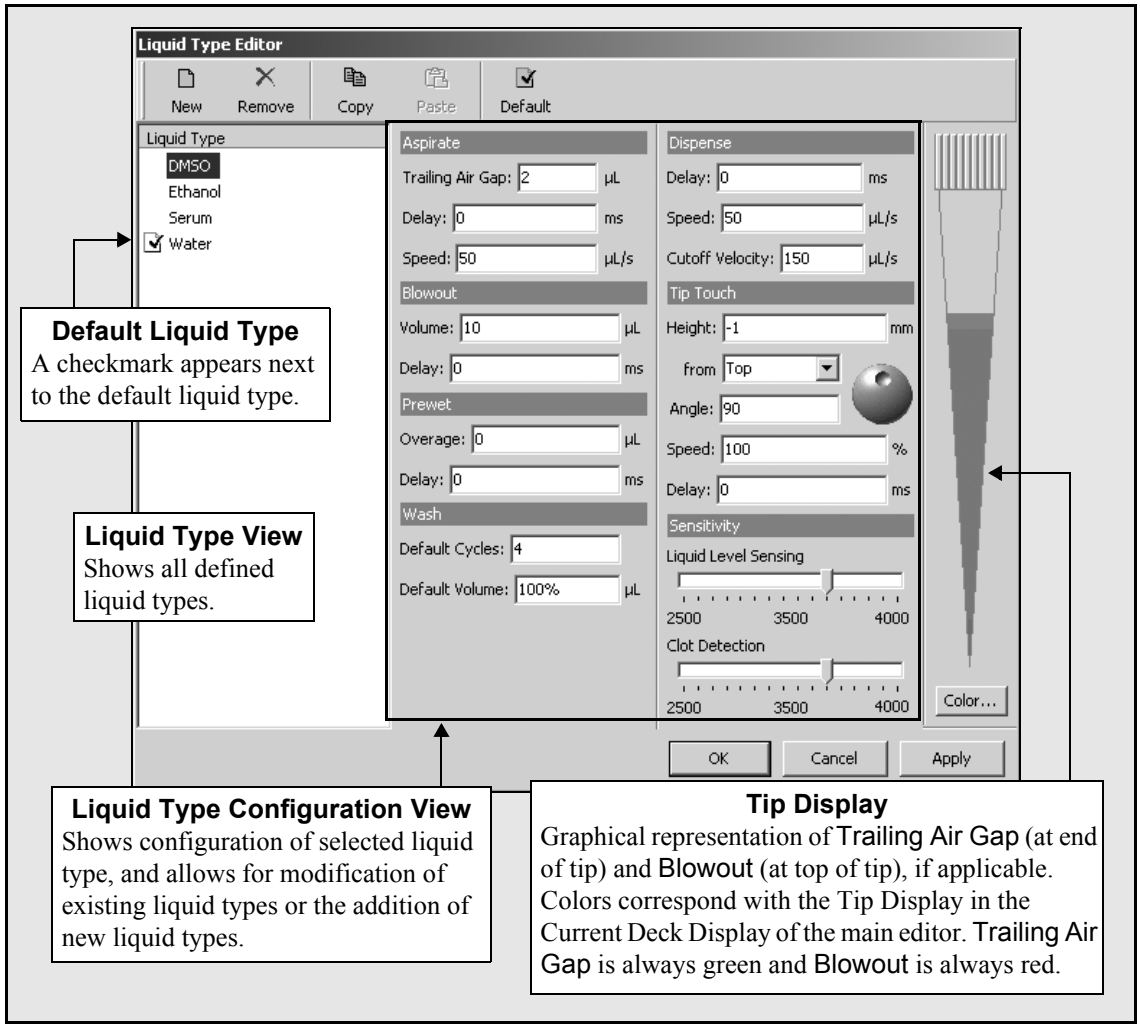


Figure 8-1. Liquid Type Editor

8.1.1 Understanding Liquid Types

Liquid type information is used by techniques to help control the aspirate and dispense operations of a method. Due to liquid characteristics such as viscosity or volatility, each type of liquid may need to be pipetted in a different way. By defining liquid types in the Liquid Type Editor, the liquids will pipette consistently among methods. Liquid types containing properties such as Prewet Delay, Tip Touch, or Blowout Volume may be configured within the Liquid Type Editor. Any configured liquid type may be set as the default and used when labware is not configured for any particular liquid type.

8.2 Creating New Liquid Types

New liquid types are created by setting information in the Liquid Type Editor. Liquid type settings are used by Biomek Software in the steps of a method to determine how pipetting operations occur.

To create a new liquid type:

1. Choose **Project>Liquid Type Editor**. Liquid Type Editor appears (Figure 8-1).

2. Choose **New**. The new liquid type appears in the Liquid Type with the name "NewLiquid" (Figure 8-2).

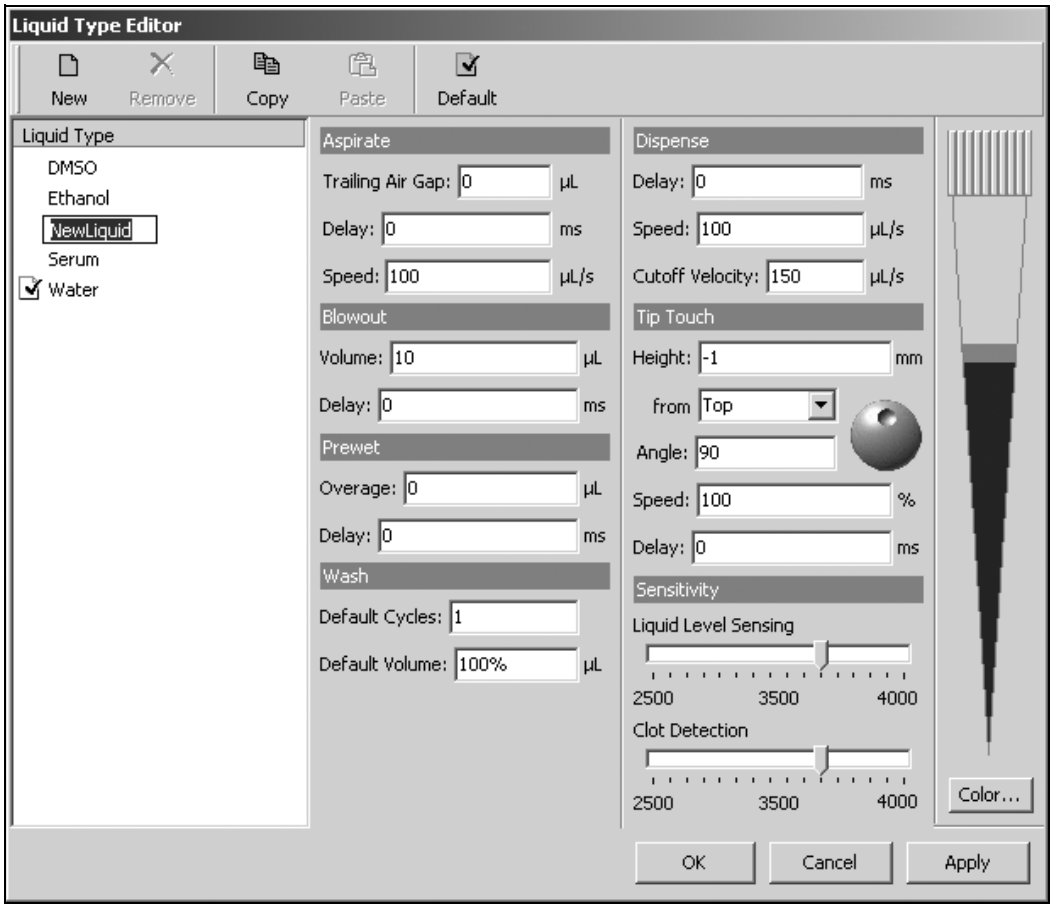


Figure 8-2. Liquid Type Editor with a new liquid

3. Click on **NewLiquid**, pause briefly, and click on **NewLiquid** again to select the liquid name as text.
4. Enter the name of the new liquid and press **Enter** to save it.

Note: Liquid type names may contain only alphanumeric characters and the underscore (_).

5. In Aspirate, enter the volume of the **Trailing Air Gap** in microliters (µL). After aspirating the liquid, a Trailing Air Gap is aspirated to prevent dripping.

6. In Aspirate, enter the desired **Delay** in milliseconds (ms). Delay specifies the amount of time after an aspirate operation before continuing.
7. In Aspirate, enter the desired **Speed** in microliters per second (µL/s). This indicates the speed along the D-axis during aspirate.
8. In Blowout, enter the desired **Volume** of the leading air gap to blow out after dispensing the liquid.
9. In Blowout, enter the desired **Delay** in milliseconds (ms). Delay specifies the amount of time after a blowout before continuing.
10. In Prewet, enter the desired **Overage** in microliters. Overage is the amount of liquid to be aspirated over the amount specified in the step configuration.
11. In Prewet, enter the desired **Delay** in milliseconds (ms). Delay specifies the amount of time from when the Prewet volume is completely aspirated until it begins to dispense.
12. In Wash, enter the **Default Cycles**. Default Cycles is the number of aspirate and dispense cycles to use when washing.
13. In Wash, enter the **Default Volume** as a percentage of the maximum used volume followed by the percent sign (%) or as an absolute amount in microliters. The Default Volume is the amount of liquid to aspirate and dispense in each cycle.
14. In Dispense, enter the desired **Delay** in milliseconds (ms). Delay specifies the amount of time after a dispense operation before continuing.
15. In Dispense, enter the desired **Speed** in microliters per second (µL/s). This indicates the speed along the D-axis during dispense.
16. In Dispense, enter the desired **Cutoff Velocity** in microliters per second (µL/s).
    - ***FX***, ***NX-S8*** — Cutoff velocity is applicable when the liquid is handled by a Span-8 Pod *only*.

Note: Cutoff Velocity is the dispense speed of the syringe before it abruptly stops, allowing droplets to break off from the tip of a Span-8 Pod. This is particularly useful for low-volume dispensing.

Note: The minimum and maximum cutoff velocities vary with the syringe type. The value entered must fall within the acceptable range for the syringe type. Refer to Table 8-2 for the minimum, maximum, and recommended cutoff velocities for each syringe type.

17. In Tip Touch, enter the desired **Height**.

Note: Height, along with from and Angle, specify where along the well the Tip Touch occurs.

18. In Tip Touch, select the desired **from**: Top, Bottom, or Liquid. This indicates the location the Height is measured from.

Note: Top measures from the top of the well, Bottom from the bottom of the well, and Liquid from the top of the liquid.

19. In Tip Touch, enter the desired **Angle**.

    OR

    Select the position along the edge on the graphic by positioning the smaller circle at the desired location. The Angle adjusts to the current location.

    Note: The Angle specifies the location along the well wall where the Tip Touch occurs at the specified Height and from location.

20. In Tip Touch, enter the desired **Delay.**
21. In Tip Touch, enter the desired **Speed** as a percentage of the total speed.
22. In Liquid Level Sensing, select the desired **Sensitivity**. Sensitivity is the magnitude of change required for LLS to detect the liquid. A larger Sensitivity detects smaller changes.

    - ***FX***, ***NX-S8*** — Liquid Level Sensing Sensitivity is applicable when the liquid is handled by a Span-8 Pod *only*.

    Note: The Sensitivity value is only used if the selected technique has Inherit From Liquid Type selected for the technique sensitivity. Refer to Section 9.4.5, *Setting Liquid Level Sensing Values (FX, 3000, and NX-S8 only)*.

23. In Clot Detection, select the desired **Sensitivity**. Sensitivity is the magnitude of change required for clots to be detected during an aspiration. A larger Sensitivity detects smaller changes.

    - ***NX-S8*** — Clot Detection is applicable on this instrument *only*.

    Note: The Sensitivity value is only used if the selected technique has Inherit From Liquid Type selected for the technique sensitivity.

24. Choose **Color...** to designate a new display color for the liquid, if desired.

    Note: The color affects only the display of aspirated liquid. The Trailing Air Gap is always green and Blowout is always red.

25. Choose **OK** to enter the new liquid type and close the Liquid Type Editor.

    OR

    Choose **Apply** to save the new liquid type without closing Liquid Type Editor.

    OR

    Choose **Cancel** to close the Liquid Type Editor without saving changes.

8.2.1 Changing the Aspirate and Dispense Speeds in the Liquid Type Editor

The aspirate and dispense speed is expressed in units of microliters per second. This represents the speed of the plunger in the D-axis on the Biomek instrument during pipetting operations. Each head or tool has a minimum and maximum allowable speed, as shown in Table 8-1.

Note: Earlier versions in Biomek Software expressed this speed as a percentage of the maximum speed.

Table 8-1. Minimum and Maximum Pipetting Speeds in D-Axis

Pod and Head or Tool		Minimum Speed (µL/s)	Maximum Speed (µL/s)
Biomek FX — Multichannel Pod	AP96 96-channel pod: P20 Head	0.3715	37.15
	P200 Head	1.486	148.6
	AP384 384-channel pod P30 Head	0.3715	37.15
Biomek FX — Span-8 Pod	250 µL syringe	2.083	241.67
	500 µL syringe	4.167	483.33
	1000 µL syringe	8.333	966.67
Biomek 3000	P20 Single-Tip Pipette Tool	0.039	39.4
	MP20 Multi-Tip Pipette Tool	0.039	39.4
	P200 Single-Tip Pipette Tool	0.304	304
	MP200 Multi-Tip Pipette Tool	0.304	304
	P1000 Single-Tip Pipette Tool	1.779	1780
Biomek NX Multichannel	AP96 96-channel pod: P20 Head	0.3715	37.15
	P200 Head	1.486	148.6
	AP384 384-channel pod P30 Head	0.3715	37.15
Biomek NX Span-8	100 µL syringe	0.833	96.667
	250 µL syringe	2..083	241.667
	500 µL syringe	4.167	483.33
	1000 µL syringe	8.333	966.667
	2.5 mL	20.833	2416.667
	5 mL	41.667	4833.333

8.2.2 Changing the Cutoff Velocity for Span-8 Pods in Liquid Type Editor (FX, NX-S8 only)

The minimum and maximum Cutoff Velocity and the instruments on which they are supported are listed in Table 8-2. When changes to Cutoff Velocity are required, they must be made to the technique governing the pipetting operation in the Technique Editor, and to the parameters of the fluid used during the pipetting operation in the Liquid Type Editor.

Note: The minimum Cutoff Velocity for each syringe is established using the equation: 50 x <Syringe size in µL>/6000. The maximum Cutoff Velocity for each syringe is established using the equation: 2700 x <Syringe size in µL>/6000.

The cutoff velocity should be adjusted in all Span-8 techniques for better pipetting accuracy every time syringes are changed from one type to another. The Cutoff Velocities displayed in Table 8-2 are intended as a starting point. The values provided should be experimented with to determine the most accurate Cutoff Velocity for a specific liquid handling operation.

Table 8-2. Span-8 Cutoff Velocities for Syringes for Span-8 Pods

Syringe Size	Minimum Cutoff Velocity	Maximum Cutoff Velocity	Instruments
100 µL	0.833 µL/second	45.0 µL/second	***NX-S8***
250 µL *	2.08 µL/second	112.5 µL/second	***FX, NX-S8***
500 µL**	4.17 µL/ second	225 µL/second	***FX, NX-S8***
1 mL ***	8.33 µL/ second	450 µL/second	***FX, NX-S8***
2.5 mL	20.8 µL/second	1125 µL/second	***NX-S8***
5 mL	41.7 µL/second	2250 µL/second	***NX-S8***

* Recommended cutoff velocity is 100 µL/second.
** Recommended cutoff velocity is 150 µL/second.
*** Recommended cutoff velocity is 150 µL/second.

To change the parameters of a fluid to conform to the Cutoff Velocity supported by 250 µL and 500 µL syringes:

1. With Biomek Software open, choose **Project>Liquid Type Editor**. The Liquid Type Editor appears (Figure 8-3).

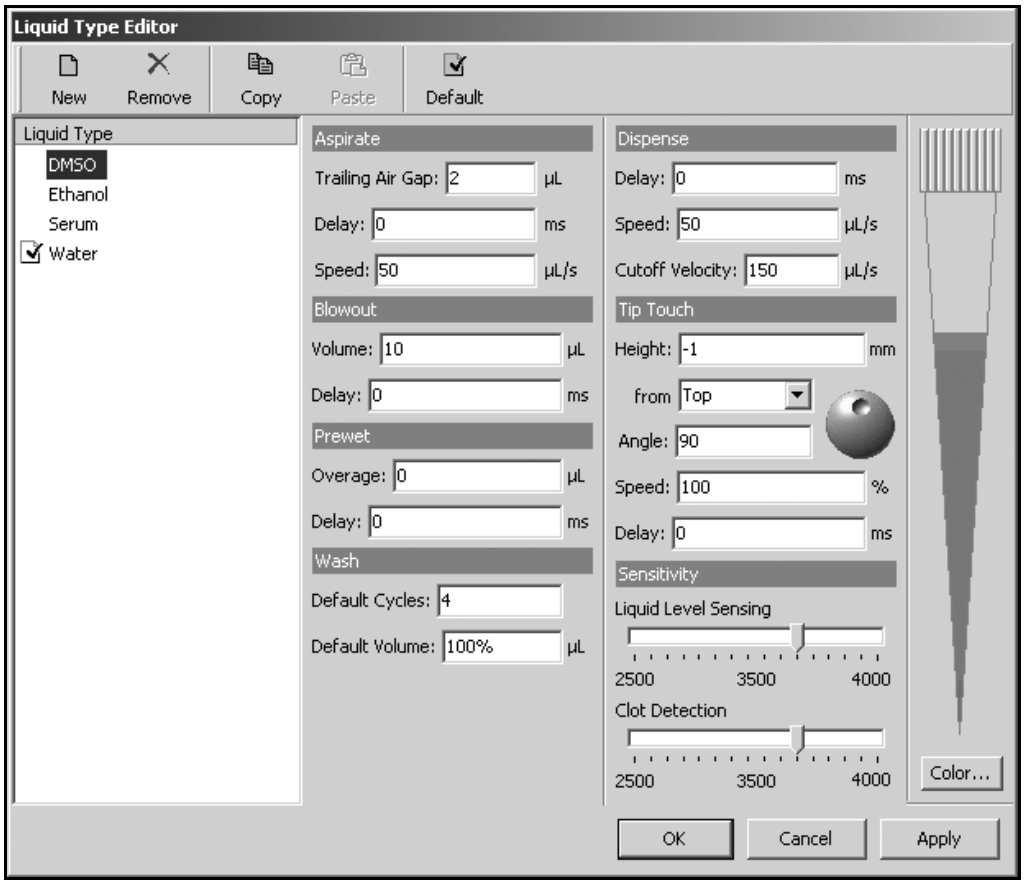


Figure 8-3. Liquid Type Editor

2. Select the liquid used during the pipetting operation.
3. In Dispense, enter the desired **Cutoff Velocity**, in microliters per second (µL/s) (refer to Table 8-2 for the correct Cutoff Velocity).
4. Choose **OK** to save the liquid type and exit the Liquid Type Editor.

8.3 Removing Liquid Types

If a liquid type is no longer needed, it can be removed from the project.

Note: When a liquid type is removed, previous revisions of the liquid type will remain available for validated methods, but will not be available for future method editing tasks.

To remove a liquid type:

1. In the Liquid Type Editor, select the liquid type to remove.

2. Select **Remove**.
3. Choose **OK**. The liquid type is removed.

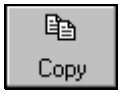
8.4 Copying and Pasting Liquid Types Within a Project File

To use the same liquid type with different parameters within a project, copy and paste the liquid type within the Liquid Type Editor.

Note: Liquid types can be exported to and imported from other projects. Refer to Section 6.10, *Importing and Exporting Project Files* for information about importing and exporting liquid types.

To copy and paste liquid types:

1. In the Liquid Type Editor, select the liquid type to copy.



2. Choose **Copy**.

3. Choose **Paste**. The new liquid appears with the name "Copy_of_(Liquid Type)".
4. Rename the liquid type as desired.

   Note: Liquid type names may contain only alphanumeric characters and the underscore (_).

5. Make any desired changes to the liquid type (refer to Section 8.2, *Creating New Liquid Types*).
6. Choose **OK**.

8.5 Specifying the Default Liquid Type

Any defined liquid type can be the default. Any labware on the deck not configured with a specific liquid type uses the default liquid type for pipetting operations.

To set the default liquid type:

1. In the Liquid Type Editor, select the liquid type to set as default.
2. Choose **Default**.

Note: The default liquid type appears with a check mark in the Liquid Type list. When the default liquid type is highlighted in the Liquid Type list, the Default button is toggled on.

9 Understanding and Creating Techniques

9.1 Overview

A technique stores a set of values and properties that instruct the Biomek instrument in performing pipetting operations, such as aspirate, dispense, mix, pod height, pod speed, and tip touch. The Biomek Software also stores a set of properties related to each technique, such as labware type and liquid type. Based upon these values and properties, the appropriate technique is selected automatically for the pipetting operation.

Techniques, along with information about tip and labware types; liquid types; well patterns; and pipetting templates, are stored as part of a project file. Project files store a history of all changes, additions, and deletions of items from the project file. Refer to Chapter 6, *Understanding and Using Project Files*, for more information on project files.

Note: When Beckman Coulter Accounts & Permissions is enabled, only users with the Develop Projects permission assigned may open, edit, create, and delete techniques (refer to Chapter 2, *Using Accounts & Permissions*).

9.1.1 How Techniques Work

Biomek Software is preprogrammed with a variety of techniques. The properties input during method building are matched with technique properties to select the most appropriate technique for use in the pipetting operation. Techniques are selected automatically based upon the number of properties that match the method. For example, a technique that matches five properties in a method is selected over a technique with four matching properties.

In most instances, one technique will have the closest match with the properties of the current pipetting operation; however, if more than one technique matches the same number of properties, Biomek Software selects the technique with the highest rank.

Because Biomek Software selects techniques automatically, any change within a method may result in a new technique selection. When a single value or property is changed in the method, Biomek Software makes sure the technique is still the most appropriate technique to use.

9.1.2 Why Techniques are Valuable

Techniques are a flexible way to make the pipetting process easier. Techniques allow the pipetting settings to be saved globally and used in multiple methods. Each time a method is created, the technique most appropriate for the pipetting operation is selected with no additional configuration required. When multiple sources and liquids are used in a method, each pipetting operation may use a different technique. This allows for appropriate pipetting throughout the entire method.

Customized techniques may also be created. Once additional techniques are created, they appear and function like predefined techniques.

9.2 Accessing the Technique Browser

To access the Technique Browser:

From the Project menu, choose **Technique Browser**.

The Technique Browser appears (Figure 9-1). The Technique Browser contains two main views:

- Groups — displays all user-created groups that contain a subset of techniques in the project; refer to Section 9.7, *Creating Technique Groups*, for more information.
- Techniques View — lists all techniques defined in the selected group with their technique properties.

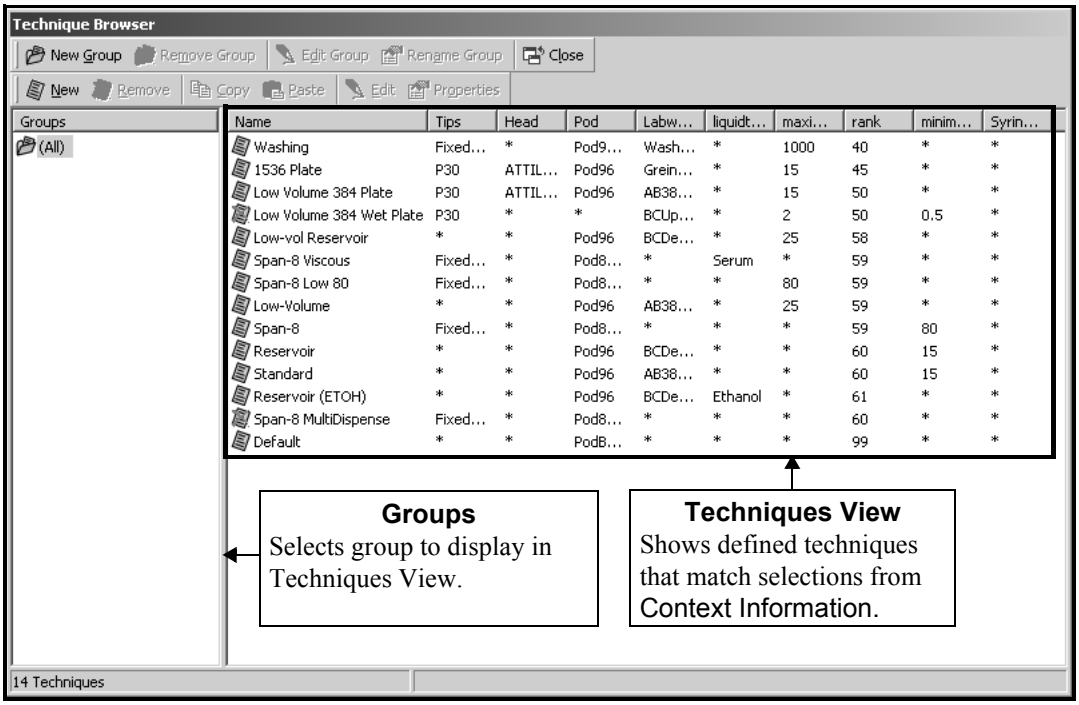


Figure 9-1. Technique Browser

9.2.1 Identifying Techniques

Techniques are identified by name in the Technique Browser (Figure 9-2). The name of the technique is a control name (identifier) which is related to and identifies the values used during a method run. When a technique is selected, the name appears in the Technique field (Figure 9-25).

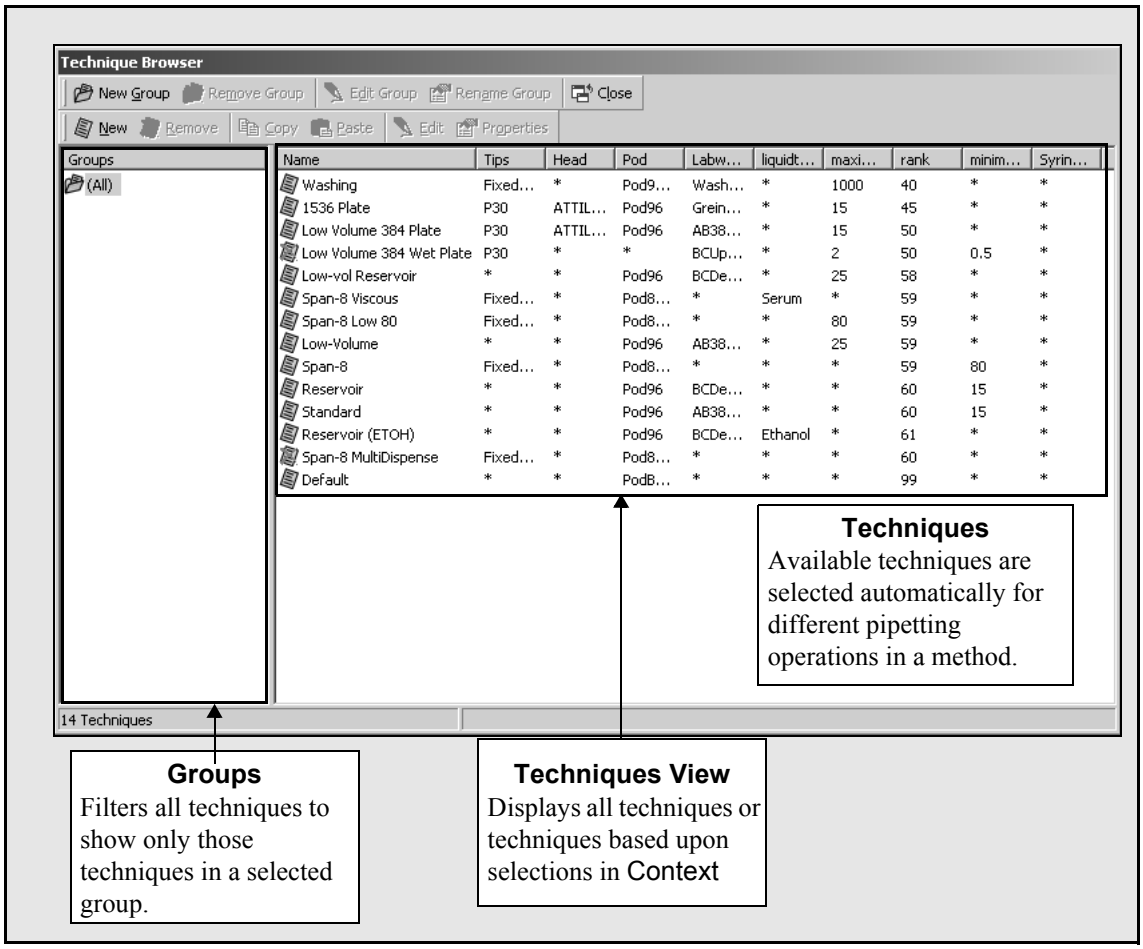


Figure 9-2. Technique Browser where technique parameters are displayed

9.3 Creating New Techniques

The default techniques are sufficient for some pipetting operations and are meant as a starting point; there are instances when additional techniques may be required. For example, a method may call for a technique for a 384-well titerplate that transfers a volume between 5 µL and 10 µL of DMSO. When creating a new technique, the properties of the technique must be configured. For best results, all techniques should be evaluated and fine-tuned for the specific application through experimentation.

Techniques are automatically selected using properties. Properties identify certain aspects of the pipetting operation which might affect how the pipetting operation is performed. For a technique to be available for selection for a specific pipetting operation, all properties for the operation must match the properties in the technique.

The following properties are used to determine the optimal technique to use:

- Head — identifies the tool types for which the technique is applicable; for example, a technique could be created which is only to be used with a specific tool or tools, such as single-channel tools, eight-channel tools, or wash tools. The technique is only used when the tool used for the pipetting operation matches this selection.
- Labware — identifies labware types for which the technique is applicable; for example, a technique could be created which is only to be used when pipetting from a certain type of labware, such as reservoirs, deepwell microplates, or test tube racks. The technique is only used when the labware type used in the pipetting operation matches this selection.
- Liquid type — identifies the liquid types for which the technique is applicable; for example, a technique could be created which is only to be used when pipetting a certain liquid type, such as DMSO or water. This can be useful to create special techniques when aspirating or dispensing viscous liquids. The technique is only used when the liquid type used in the pipetting operation matches this selection.
- Pod — identifies the pod performing the pipetting operation; for example, separate techniques could be created for use with each pod type. The technique is only used when the pod type used in the pipetting operation matches this selection.
- Syringe Type — identifies the syringe sizes for probes on a Span-8 Pod for which the technique is applicable. The technique is only used when the syringe type for the probes used in the pipetting operation matches this selection.
  - ***FX***, ***NX-S8*** — Applicable for Span-8 Pods only.
- Tips — identifies the tip types for which the technique is applicable; for example, a technique could be created which is only to be used with a certain type of tips, such as barrier tips or fixed tips. The technique is only used when the tip type used in the pipetting operation matches this selection.

- Volume — identifies the volume range for which a technique is applicable; for example, a technique could be created that is only to be used when pipetting low volumes, such as 0-10 µL. The technique is only used when the volume entered in the step configuration falls within the specified range.
- Group — if groups have been created (refer to Section 9.7, *Creating Technique Groups*), an additional property is listed to allow the new group to be added to an existing group, if desired. Group is for organizing techniques only and is not used for selecting the technique to use.

Create additional techniques using the Technique Browser (Figure 9-1).

Note: Automatic selection of techniques may be turned off and new techniques created within a step configuration (refer to Section 9.10, *Selecting and Modifying Techniques Manually in a Method*).

To create a new technique and set its properties:

1. From the Project menu, choose **Technique Browser.** Technique Browser appears (Figure 9-1).

2. In the Technique Browser, choose **New**. **Technique Properties** appears (Figure 9-3).

   OR

   Right-click in the Techniques View and choose **New** from the menu.

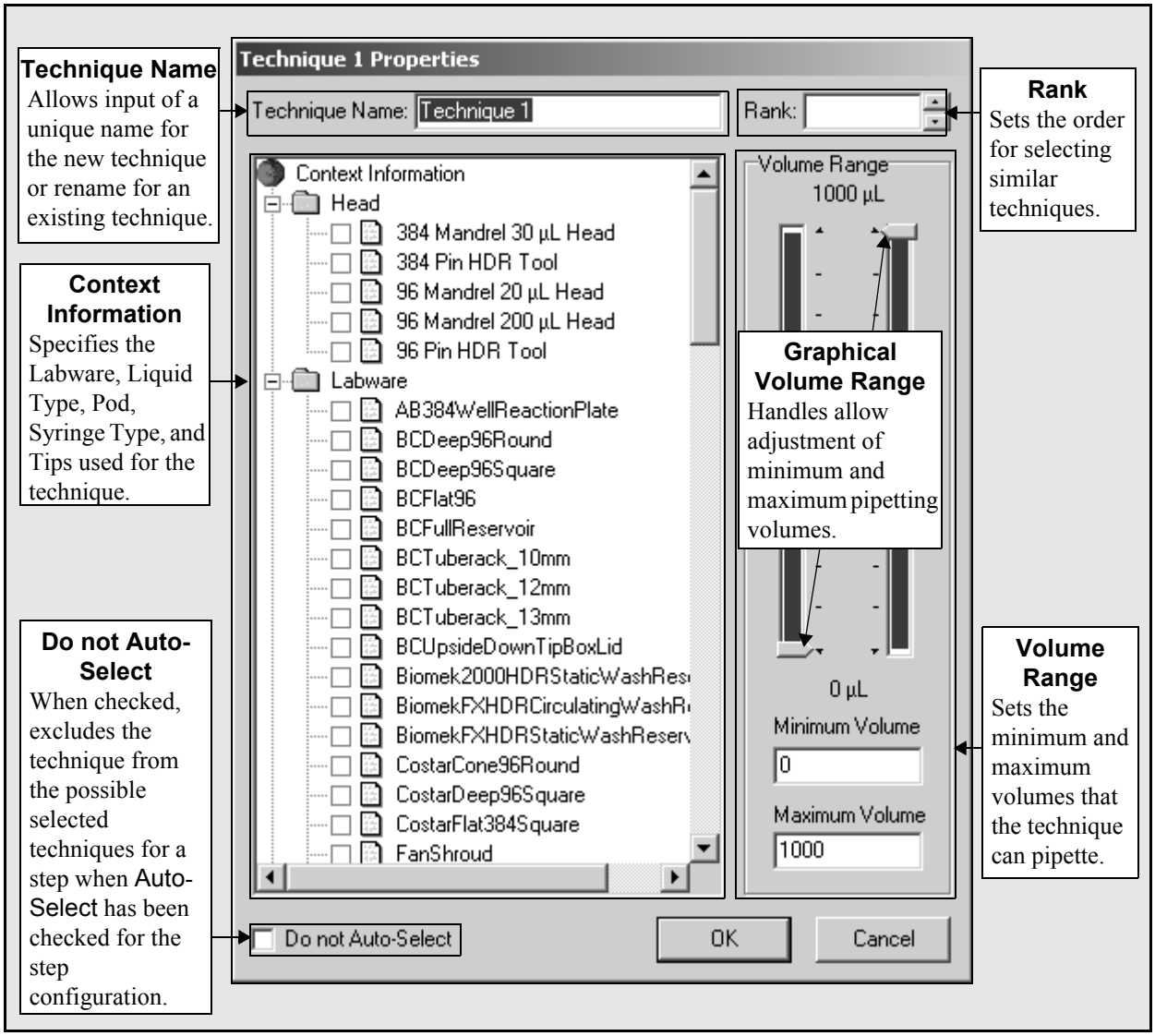


Figure 9-3. Setting Technique Properties for a Biomek FX technique

3. In Technique Name, enter a name to identify the technique.

4. In Rank, enter a value to set the relative preference of the technique to other techniques with similar properties.

   Note: Rank allows Biomek Software to give techniques preference over others. For example, if two techniques use a 384-well titerplate and P20 tips, with the difference between techniques being the Mix Before Aspirate values, one technique may have a higher priority (Rank of 1) over the other (Rank of 2) for automatic selection, depending upon properties input during method building.

5. In Context Information, select the desired **Head, Labware, Liquid Type, Pod, Syringe Type,** and **Tips** to use for the technique.

   Note: If no selection is made for a category, the technique is applicable for all items within that category. For example, if no labware types are selected under Labware, the technique is available for use with all labware types.

   Note: To remove all current selections from the Technique Properties, right-click in Context Information and select **Clear Selections**. Clear Selections removes all selections from all categories.

6. In Volume Range, enter the **Minimum Volume** and **Maximum Volume** for the technique to aspirate or dispense.

   OR

   Change the minimum and maximum volumes graphically using the handles on the graphical Volume Range (Figure 9-3).

   Note: The left gauge is for Minimum Volume and the right gauge is for Maximum Volume.

7. Select **Do not Auto-Select** to exclude the new technique from the possible selected techniques for a step, such as Transfer or Combine, when the Auto-Select has been checked for the step configuration. The technique will not be automatically selected by Biomek Software for any pipetting operations, but is still available when manually selecting a technique if the properties match (refer to Section 9.10, *Selecting and Modifying Techniques Manually in a Method*).

   Note: A technique that has Do not Auto-Select selected is displayed in the Technique Browser with a red **x** in the icon next to a technique.

8. Choose **OK**. The technique is created and added to the list in Technique Browser.

To access the properties of an existing technique to view or modify them:

Choose the **Properties** button on the Technique Browser toolbar.

OR

Right-click on the technique entry in the browser and select **Properties**.

Note: Check **Do not Auto-Select** to exclude the existing technique from the possible selected techniques for a step, such as Transfer or Combine, when the Auto-Select has been checked for the step configuration.

9.4 Setting Technique Values

After creating a technique and setting the related properties, set the technique values, such as Tip Touch or Mix After Dispense, in Technique Editor before performing a method.

Note: The Technique Browser lists all available techniques. The Technique Editor allows for configuration of the technique values for a specific technique.

In the Techniques Editor, a drop-down list is used to select the Pipetting Template (refer to Chapter 10, *Using the Pipetting Template Editor*). When the Pipetting Template is selected, the following nine tabs appear depending on instrument type and configuration.

The nine tabs are:

- General — *Viewing Technique Description* (Section 9.4.1).
- Aspirate — *Setting Aspirate Values* (Section 9.4.2).
- Dispense — *Setting Dispense Values* (Section 9.4.3).
- Mix — *Setting Mix Values* (Section 9.4.4).
- Calibration — *Calibrating Techniques* (Section 9.5).
- Liquid Level Sensing — *Setting Liquid Level Sensing Values (FX, 3000, and NX-S8 only)* (Section 9.4.5).
  - ***FX***, ***NX-S8*** — Available with a Span-8 Pod.
  - ***3000*** — Available with P200L or P1000L Single-Tip Pipette Tool
- Clot Detection — *Setting Clot Detection Values (NX-S8 only)* (Section 9.4.6).
  - ***NX-S8*** — Available on this instrument only.
- Piercing — *Setting Piercing Values (NX-S8 only)* (Section 9.4.7).
  - ***NX-S8*** — Available on this instrument only.
- Liquid Type — *Overriding Liquid Type Values* (Section 9.4.8).

9.4.1 Viewing Technique Description

The General tab (Figure 9-4) summarizes the technique configuration on the Aspirate, Dispense, and Mix tabs in sentence form. The icons below each heading identify some of the operations the technique performs (Table 9-1).

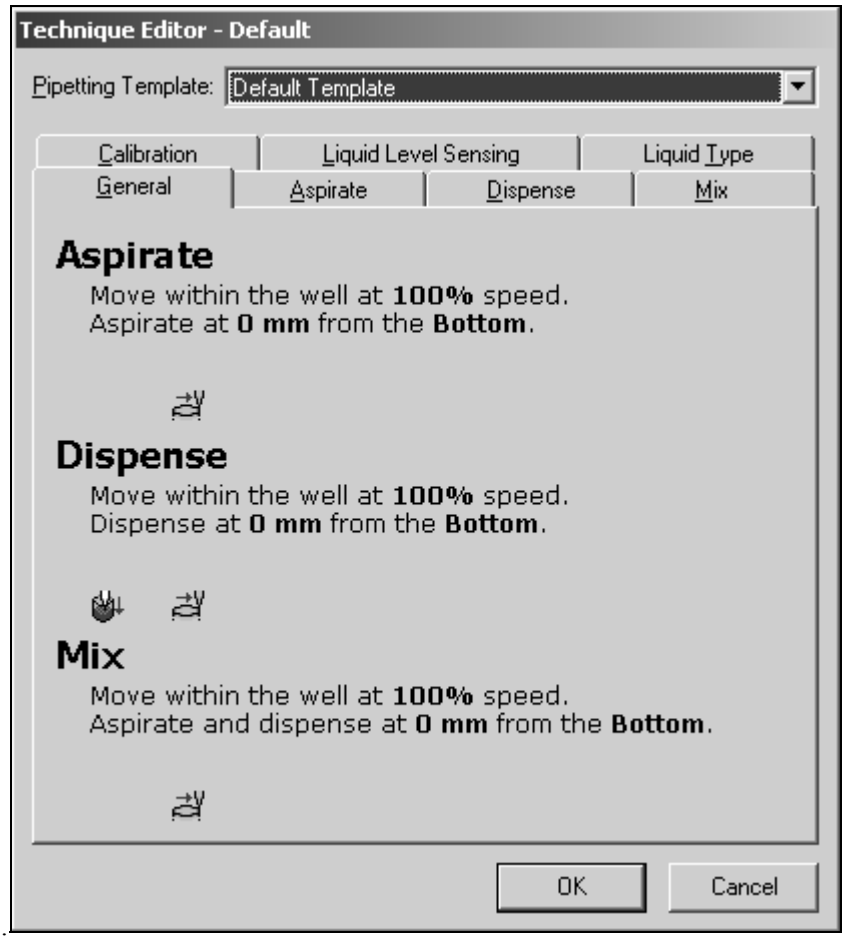


Figure 9-4. Technique Editor — General tab

The icons are:

Table 9-1. Technique Icons

Icon	Associated Operation
	Tip Touch — touches the tip on the side of the well.
	Blowout (used in Dispense operations only) — aspirates an air gap before the liquid aspirates, and dispenses the air gap after the liquid has been dispensed.
	Follow Liquid — tip follows liquid level during pipetting operations.
	Prewet (Aspirate operations only) — quickly aspirates and dispenses liquid before the main aspirate operation occurs.
	Mix — mixes liquid in wells before aspirate or after dispense.
	Trailing Air Gap (Aspirate operations only) — aspirates air after liquid is aspirated to help prevent drips.

To view technique values in the General tab:

1. From the Project menu, choose **Technique Browser.** Technique Browser appears.
2. In Technique Browser, select the technique to modify.
3. Choose **Edit**.

OR

Double-click on the technique.

OR

Right-click in the Techniques View and choose **Edit** from the menu. The **General** tab is displayed by default (Figure 9-4).

Note: Access the Technique Editor (Figure 9-4) through the step configuration by choosing **Customize...** in the step configuration. This overrides the current technique in the pipetting operation only.

9.4.2 Setting Aspirate Values

Setting aspirate values allows for the technique to perform specific aspirate operations by changing related values, such as Aspirate Height, Pod Speed, and Mix Before Aspirate.

Note: When setting aspirate values from the Customize button in a step configuration, the Technique Editor is specific to the operation (Figure 9-5).

To configure Aspirate options:

1. From the Project menu, choose **Technique Browser.** Technique Browser appears.
2. In Technique Browser, select the technique to modify.
3. Choose **Edit**.

   OR

   Double-click on the technique.

   OR

   Right-click in the Techniques View and choose **Edit** from the menu. The **General** tab is displayed by default (Figure 9-4).
4. In Technique Editor, select the **Aspirate** tab (Figure 9-5).

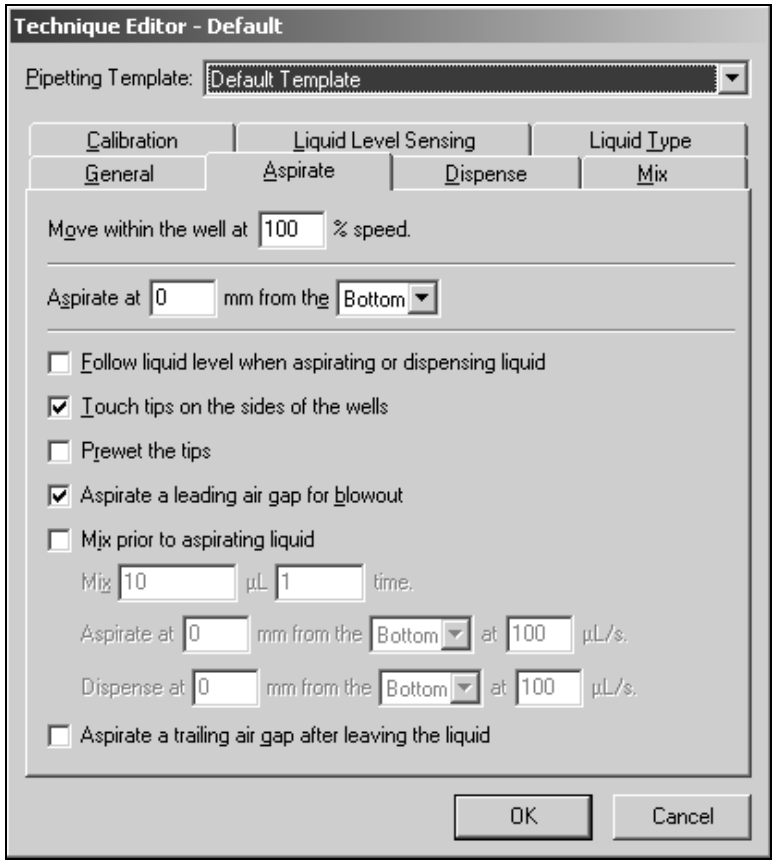


Figure 9-5. Technique Editor — Aspirate tab

5. In Move within the well at, enter the speed as a percentage of the maximum speed of the pod. This value must be between 0 and 100.

   Note: This controls the speed of the X-, Y-, and Z-axes. This will affect the speed at which the pod moves to the aspirate and dispense heights. The actual aspirate and dispense speeds and the speed for tip touch are controlled by settings in the Liquid Type Editor (refer to Section 8.2, *Creating New Liquid Types*).

6. In Aspirate at, enter the distance in millimeters (mm) to measure from the selected position for the aspirate.

7. Select from where to measure the aspirate height: **Top, Bottom,** or **Liquid**.

   Note: Top measures the aspirate height from the top of the well, Bottom from the bottom of the well, and Liquid from the top of the liquid. The only time a liquid level is required is when Aspirate is set to Liquid. It is not necessary to define the liquid level to use Follow Liquid.

   When a specific height is entered in Aspirate at, the aspirate operation occurs at that distance relative to the aspirate position.

   Note: A positive value is measured above the selected location; a negative value is measured below the selected location. For example, to aspirate a liquid 1.0 mm below the liquid level, a value of **-1.0** is entered in Aspirate at and **Liquid** is chosen as the aspirate position.

8. Choose **Follow liquid level when aspirating or dispensing liquid** to allow the tip to follow the liquid level during the aspirate operation.

9. Choose **Touch tips on the sides of the wells** to allow tips to rest against the sides of the wells for a specific amount of time after aspirating (refer to Section 8.2, *Creating New Liquid Types*).

10. Choose **Prewet the tips** to perform an aspirate and dispense cycle before performing the actual aspirate operations (refer to Section 8.2, *Creating New Liquid Types*).

11. Choose **Aspirate a leading air gap for blowout** to dispense an air gap on the Dispense operation.

    Note: Blowout all leading air gaps must also be chosen on the Dispense tab to perform a complete blowout; just choosing Aspirate a leading air gap for blowout on the Aspirate tab will not perform a complete blowout.

12. Choose **Mix prior to aspirating liquid** to mix liquid before the aspirate occurs, if desired. Refer to Section 9.4.2.1, *Setting Mix Before Aspirate Values*, for instructions on configuring mix properties.

    Note: Mix aspirates and dispenses a specified number of times within a piece of labware.

13. Choose **Aspirate a trailing air gap after leaving liquid** to use the defined Trailing Air Gap from the Liquid Type Editor or from the Liquid Type tab (refer to Section 8.2, *Creating New Liquid Types*).

9.4.2.1 Setting Mix Before Aspirate Values

Set the Mix prior to aspirating liquid values when a mix occurs before the liquid aspirates.

To set the Mix prior to aspirating liquid values:

1. In Mix, enter the amount of liquid to mix, and the number of times to mix.
2. Enter the **Aspirate at** height in millimeters (mm) at which to perform the Aspirate.
3. Choose the desired aspirate position: **Top, Bottom,** or **Liquid**.
4. Enter the speed at which to aspirate in µL/s.
5. Enter the **Dispense at** height in millimeters (mm) at which to perform the Dispense.
6. Choose the Dispense location: **Top, Bottom,** or **Liquid**.
7. Enter the speed at which to dispense in µL/s.

9.4.3 Setting Dispense Values

Setting the dispense values allows for specific dispense operations to occur by changing related values, such as Dispense Height, Pod Speed, and Mix After Dispense.

Note: When setting dispense values from the Customize button in a step configuration, the Technique Editor is specific to the operation (Figure 9-6).

To set Dispense values, complete the following:

1. From the Project menu, choose **Technique Browser.** Technique Browser appears.
2. In Technique Browser, select the technique to modify.
3. Choose **Edit**.

OR

Double-click on the technique.

OR

Right-click in the Techniques View and choose **Edit** from the menu. The **General** tab is displayed by default (Figure 9-4).

4. In Technique Editor, select the **Dispense** tab (Figure 9-6).

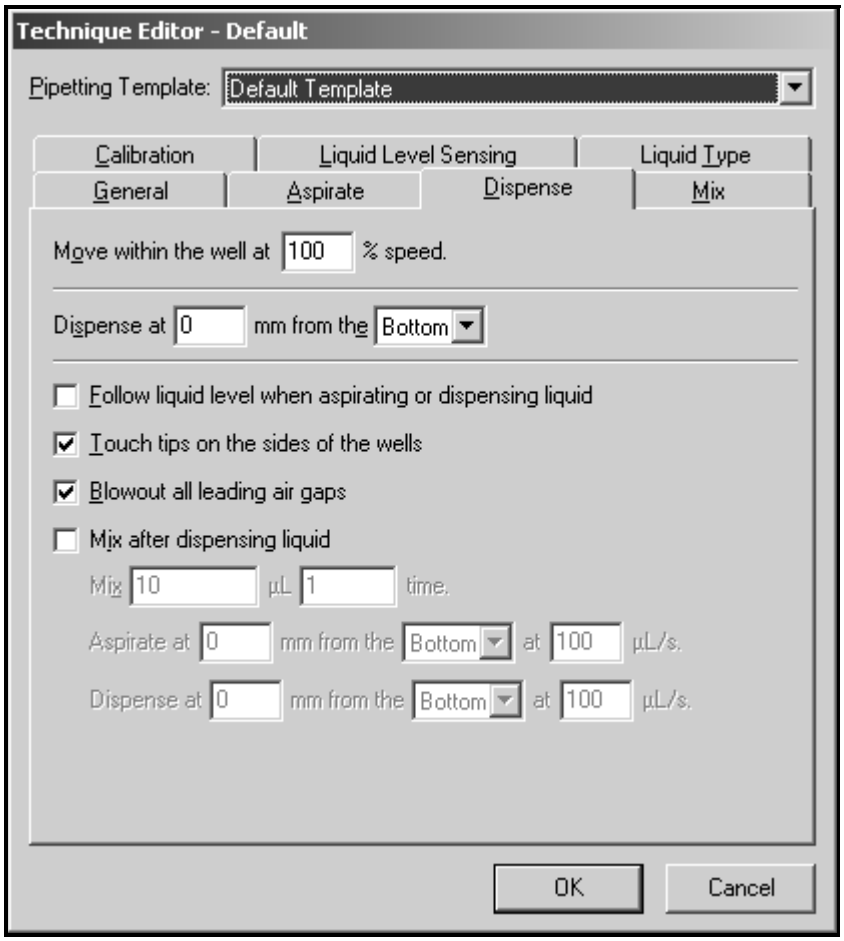


Figure 9-6. Technique Editor — Dispense tab

5. In Move within the well at, enter the speed as a percentage of the maximum speed of the pod. This value must be between 0 and 100.

Note: This controls the speed of the X-, Y-, and Z-axes. This will affect the speed at which the pod moves to the aspirate and dispense heights. The actual aspirate and dispense speeds and the speed for tip touch are controlled by settings in the Liquid Type Editor (refer to Section 8.2, *Creating New Liquid Types*).

6. In Dispense at, enter the distance in millimeters (mm) to measure from the selected position for the dispense.

7. Select from where to measure the dispense height: **Top, Bottom,** or **Liquid**.

   Note: Top measures the dispense height from the top of the well, Bottom from the bottom of the well, and Liquid from the top of the liquid. The only time a liquid level is required is when Dispense is set to Liquid. It is not necessary to define the liquid level to use Follow Liquid.

   When a specific height is entered in Dispense at, the dispense operation occurs at that distance relative to the dispense position.

   Note: A positive value is measured above the selected location; a negative value is measured below the selected location. For example, to dispense liquid 1.0 mm below the liquid level, a value of **-1.0** is entered in Dispense at and **Liquid** is chosen as the dispense position.

8. Choose **Follow liquid level when aspirating or dispensing liquid** to allow the tip to follow the liquid level during the dispense cycle.
9. Choose **Touch tips on the sides of the wells** to allow tips to rest against the sides of the wells for a specific amount of time after dispensing.
10. Choose **Blowout all leading air gaps** to dispense an air gap, if necessary (refer to Section 8.2, *Creating New Liquid Types*).

    Note: Aspirate a leading air gap for blowout must also be chosen on the Aspirate tab to perform a complete blowout; just choosing Blowout all leading air gaps on the Dispense tab will not perform a complete blowout.

11. Choose **Mix after dispensing liquid** to mix liquid after the dispense occurs. Refer to Section 9.4.3.1, *Setting Mix After Dispense Values*, for instructions on configuring mix properties.

9.4.3.1 Setting Mix After Dispense Values

Set the Mix after dispensing liquid values when a mix occurs after the liquid dispenses.

To set the Mix after dispensing liquid values:

1. In Mix, enter the amount of liquid to mix, and the number of times to mix.
2. Enter the **Aspirate** height in millimeters (mm) at which to perform the Aspirate.
3. Choose the desired aspirate position: **Top, Bottom,** or **Liquid**.
4. Enter the speed at which to aspirate liquid in µL/s.
5. Enter the **Dispense** height in millimeters (mm) at which to perform the Dispense.
6. Choose the Dispense location: **Top, Bottom,** or **Liquid**.
7. Enter the speed at which to dispense liquid in µL/s.

9.4.4 Setting Mix Values

Set Mix values to create a custom mix. Mix step aspirates and dispenses liquid a specified number of times during a method.

Note: The number of cycles is configured in the Mix step configuration.

To configure Mix:

1. From the Project menu, choose **Technique Browser.** Technique Browser appears.
2. In Technique Browser, select the technique to modify.

3. Choose **Edit**.

   OR

   Double-click on the technique.

   OR

   Right-click in the Techniques View and choose **Edit** from the menu. The **General** tab is displayed by default (Figure 9-4).

4. In Technique Editor, select the **Mix** tab (Figure 9-7).

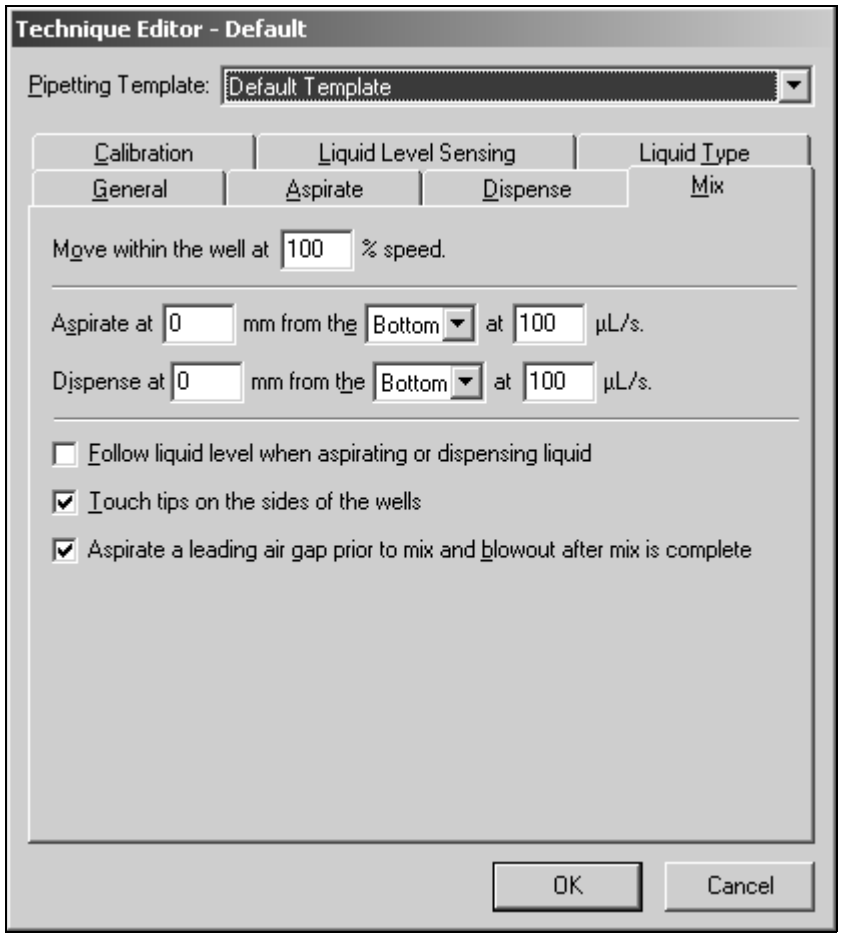


Figure 9-7. Technique Editor — Mix tab

5. In Move within the well at, enter the speed as a percentage of the maximum speed of the pod. This value must be between 0 and 100.

   Note: This controls the speed of the X, Y, and Z axes. This will affect the speed at which the pod moves to the aspirate and dispense heights. The actual aspirate and dispense speeds and the speed for tip touch are controlled by settings in the Liquid Type Editor (refer to Section 8.2, *Creating New Liquid Types*).

6. Enter the **Aspirate at** height in millimeters (mm) at which to perform the Aspirate.
7. Choose the desired aspirate position: **Top, Bottom,** or **Liquid**.
8. Enter the speed at which to aspirate liquid in µL/s.
9. Enter the **Dispense at** height in millimeters (mm) at which to perform the Dispense.
10. Choose the Dispense location: **Top, Bottom,** or **Liquid**.
11. Enter the speed at which to dispense liquid in µL/s.
12. Choose **Follow liquid level when aspirating or dispensing liquid** to allow the tip to follow the liquid level during the aspirate and dispense cycles.
13. Choose **Touch tips on the sides of the wells** to allow tips to rest against the sides of the wells for a specific amount of time after mixing.
14. Choose **Aspirate a leading air gap prior to mix and blowout after mix is complete** to dispense an air gap, if necessary (refer to Chapter 8, *Understanding and Creating Liquid Types*).

9.4.5 Setting Liquid Level Sensing Values (FX, 3000, and NX-S8 only)

- ***FX*** — Available with a Span-8 Pod only.
- ***3000*** — Available on P200L or P1000L Single-Tip Pipette Tool only. Some options are not available with this instrument and do not appear.

Set Liquid Level Sensing values to utilize liquid level sensing to determine the liquid level. Liquid level detection is necessary only if the Aspirate, Dispense, or Mix height is measured from the liquid and the liquid level is unknown. The pod, head, and tips must all be compatible with liquid level sensing to detect the liquid level.

The Liquid Level Sensing tab consists of four collapsible sections to configure various aspects of using LLS. Each section is expanded by clicking the down arrow or sentence summary for that section and may then be configured. Only one section may be expanded at a time. When collapsed, each sections displays a sentence summary describing the configuration for that section.

The four sections are:

- General Settings — specify the start height and sense speed.
- Repetition Settings — specify the number of times to perform LLS
  - ***FX, NX-S8*** — Available on these instruments only.
- Sensitivity Settings — select to inherit sensitivity from labware type, liquid type, or define a custom setting
  - ***FX, NX-S8*** — Available on these instruments only.
- Error Handling Settings — specify the action to take if LLS fails

To configure Liquid Level Sensing:

1. From the Project menu, choose **Technique Browser.** Technique Browser appears.
2. In Technique Browser, select the technique to modify.

3. Choose **Edit**.

   OR

   Double-click on the technique.

   OR

   Right-click in the Techniques View and choose **Edit** from the menu. The **General** tab is displayed by default (Figure 9-4).

4. In Technique Editor, select the **Liquid Level Sensing** tab (Figure 9-8).

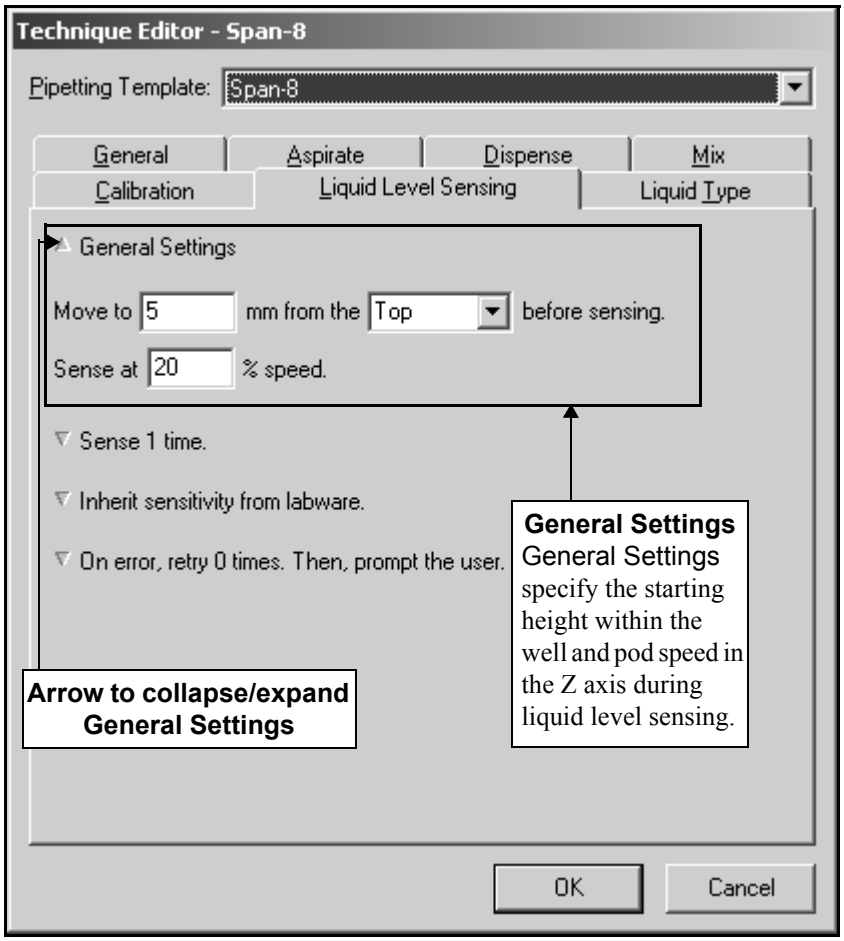


Figure 9-8. Technique Editor — General Settings on Liquid Level Sensing tab

9.4.5.1 Configuring General Settings

General Settings is used to configure the starting height of the probe within the well and the pod speed in the Z axis during liquid level sense operations.

1. If General Settings is not displayed, click on the topmost sentence summary to expand the General Settings configuration (Figure 9-8).
2. Enter the height in millimeters (mm) to **Move to** and start sensing from.
3. Select the from the start location: Top or Bottom. The probe moves to the specified height measured from the top or bottom of the well before sensing.
4. Enter the **Sense at** speed as a percentage of the maximum speed of the pod.

Note: The speed affects the Z-axis speed only. The default sense speed is 20 percent.

9.4.5.2 Configuring Repetition Settings (FX, NX-S8 only)

Repetition Settings is used to configure the number of times to sense and conditions to accept results early or fail.

1. If Repetition Settings is not displayed, click on the sentence summary second from the top to expand the Repetition Settings configuration (Figure 9-9).

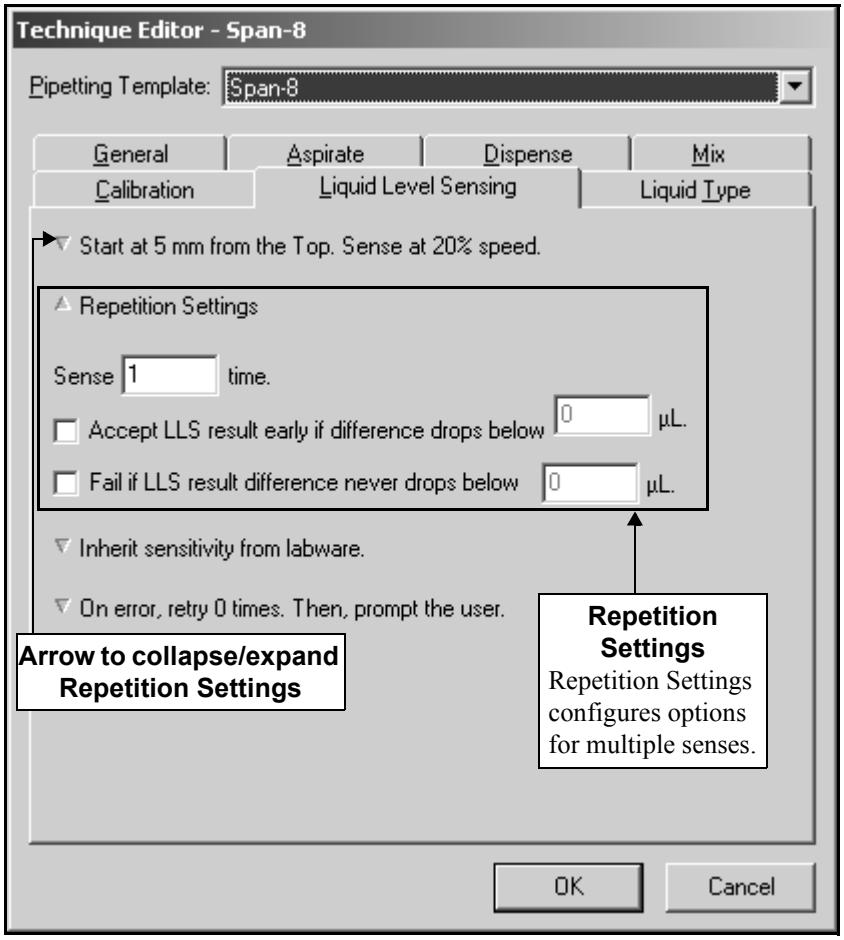


Figure 9-9. Technique Editor — Repetition Settings on Liquid Level Sensing tab

2. In **Sense**, enter the number of times to sense. Specifying a Sense of zero (0) disables liquid level sensing for the technique.

   Note: Sensing multiple times helps to pop air bubbles in the wells and increases the accuracy in the liquid level detection.

3. Select **Accept LLS result early** to halt liquid level sensing if consecutive readings are within a specified tolerance, if desired.
4. In **drops below**, enter the desired tolerance for Accept LLS result early. When a reading falls within the entered tolerance of the previous reading, the result is accepted as the liquid level.
5. Select **Fail if LLS result** to fail liquid level sensing if consecutive readings never fall within a specified tolerance, if desired.
6. In **never drops below**, enter the desired tolerance for Fail if LLS result. If after completing all the desired Sense readings consecutive values never fall within the entered tolerance, the liquid level sensing fails and an error displays.

9.4.5.3 Configuring Sensitivity Settings (FX, NX-S8 only)

Liquid level is determined using specially designed liquid level sensing (LLS) tips that detect a shift in the capacitance of the probe. The tip moves to a specified height within the well and then slowly moves down into the well. When the tip contacts liquid, there is a large change in capacitance detected. The liquid level is sensed by determining the height at which this change in capacitance occurs.

Sensitivity Settings is used to configure how sensitive the probes are to changes in capacitance. A larger sensitivity value detects smaller capacitance changes more easily.

1. If Sensitivity Settings is not displayed, click on the sentence summary second from the bottom to expand the Sensitivity Settings configuration (Figure 9-10).

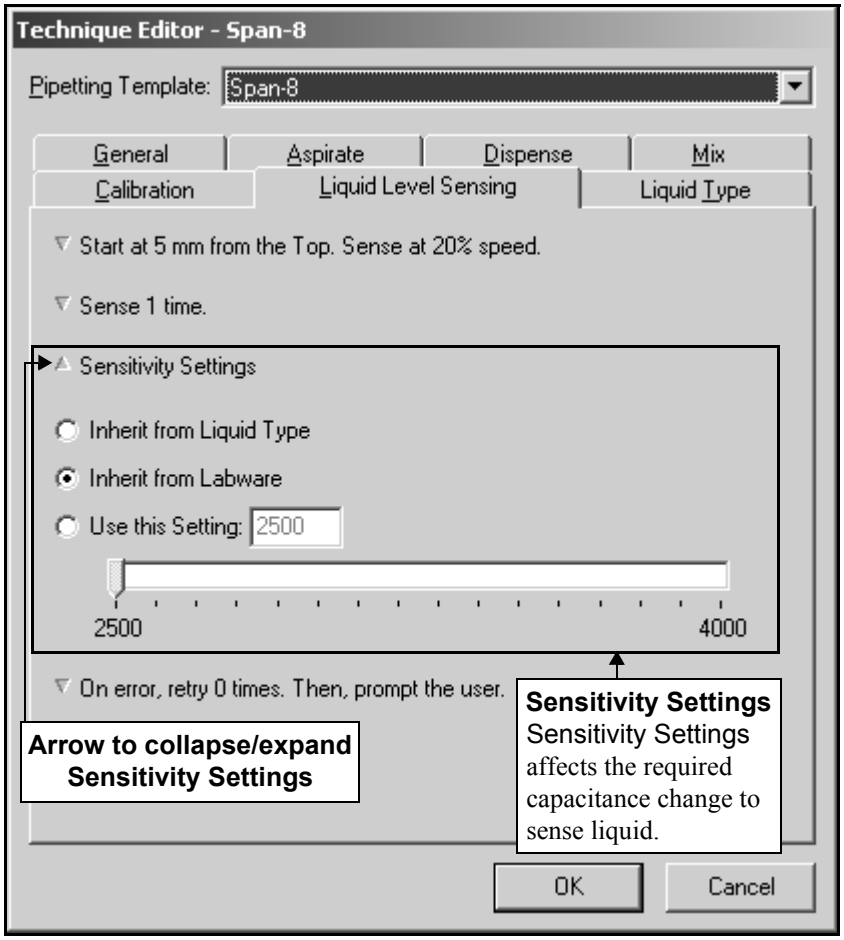


Figure 9-10. Technique Editor — Sensitivity Settings on Liquid Level Sensing tab

2. Select the **Sensitivity** of the liquid detection. Sensitivity is the magnitude of change required for LLS to detect the liquid. A larger sensitivity value detects smaller capacitance changes more easily. Options include:

   - Inherit from Liquid Type — uses sensitivity specified for the liquid in Liquid Type Editor; refer to Chapter 8, *Understanding and Creating Liquid Types*.
   - Inherit from Labware — uses sensitivity specified for the labware in Labware Type Editor; refer to Section 7.3, *Defining Labware Types*.
   - Use this Setting — uses the setting specified in the Technique Editor; specify the **Sensitivity** by entering the value or dragging the bar to the desired values.

Note: The default sensitivity setting is Inherit from Labware.

9.4.5.4 Configuring Error Handling Settings

Error Handling Settings specify the action to take if liquid level sensing fails.

1. If Error Handling Settings is not displayed, click on the last sentence summary to expand the Error Handling Settings configuration (Figure 9-11).

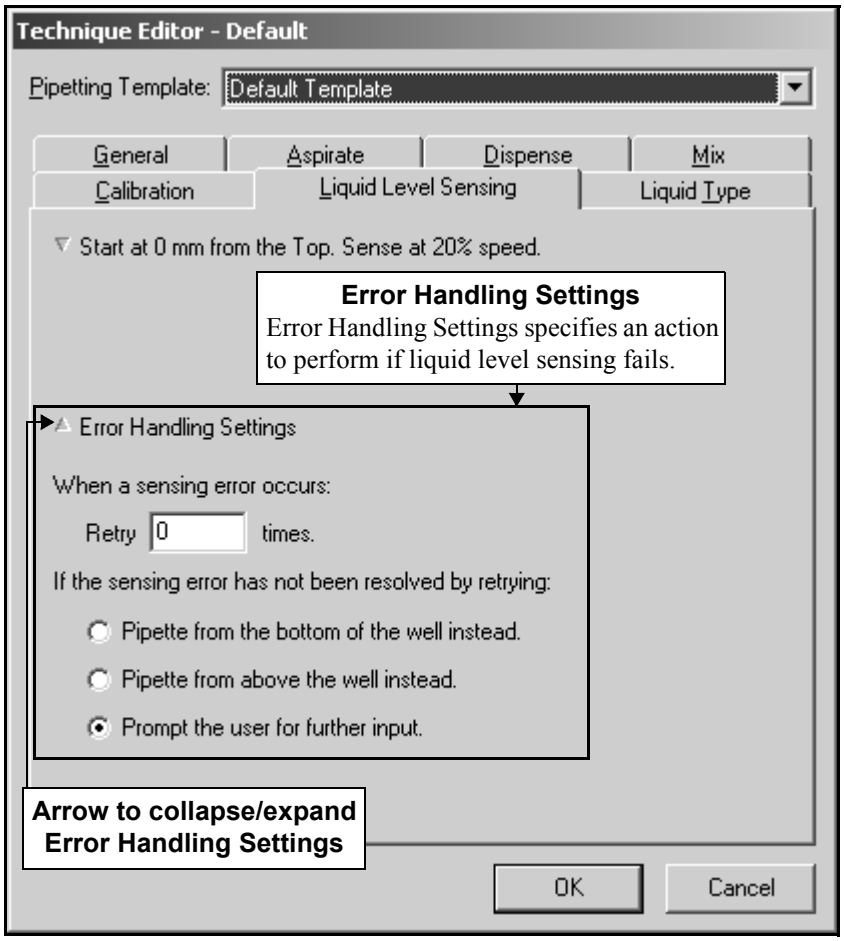


Figure 9-11. Technique Editor — Error Handling Settings on Liquid Level Sensing tab

2. In Retry, enter the number of times to try to detect the liquid level when a sensing error occurs.

   ➢ ***FX, NX-S8*** — Retry only applies to these instruments.

3. In If the sensing error has not been resolved by retrying, select the action to perform:

   - Pipette from the bottom of the well instead — measures the pipetting height from the bottom of the well instead of from liquid level

     Note: When pipetting from the bottom of the well, the minimum pipetting height as defined on the Calibration tab for the technique (refer to Section 9.5, *Calibrating Techniques*) is used.

   - Pipette from the top of the well instead — measures the pipetting height from the top of the well instead of from liquid level

     Note: When pipetting from the top of the well, the operation is performed at a height 1.0 millimeters (mm) above the top of the well.

   - Prompt the user for further input — prompts the user for further instruction (Figure 9-12) and provides options to pipette from the top of the well (Pipette Air), pipette from the bottom of the well (Pipette from Bottom), retry (Seek Again), snap a continuation (Snap), or stop the method (Abort).

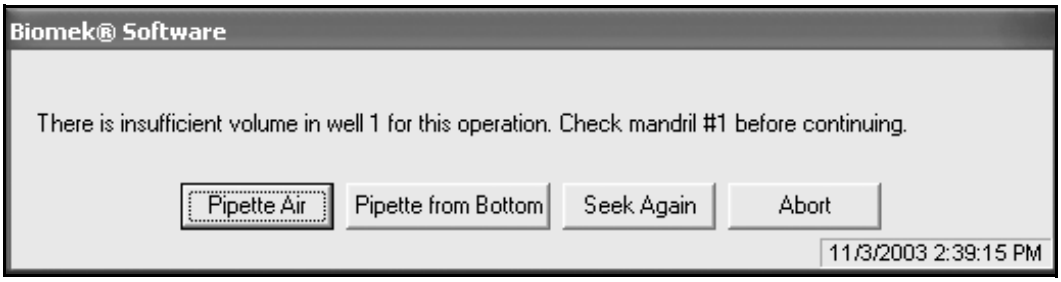


Figure 9-12. Liquid Level Sensing Error Handling prompt for Biomek 3000

9.4.6 Setting Clot Detection Values (NX-S8 only)

The settings for clot detection allow the technique to perform clot detection during an aspirate. Refer to the *Biomek® NX Span-8 Laboratory Automation Workstation User's Manual,* Chapter 2.3.2, *Clot Detection*, for information on how clot detection works with the Biomek NX Span-8 instrument and Biomek Software.

The Clot Detection tab consists of three collapsible sections to configure various aspects of using clot detection. Each section is expanded by clicking the down arrow or sentence summary for that section and may then be configured. Only one section may be expanded at a time. When collapsed, each sections displays a sentence summary describing the configuration for that section.

The three sections are:

- General Settings — specify the detection height and speed.
- Sensitivity Settings — select to inherit sensitivity from labware type, liquid type, or define a custom setting
- Error Handling Settings — specify the action to take if a clot is detected.

To configure Clot Detection:

1. From the Project menu, choose **Technique Browser.** Technique Browser appears.
2. In Technique Browser, select the technique to modify.

3. Choose **Edit**.

   OR

   Double-click on the technique.

   OR

   Right-click in the Techniques View and choose **Edit** from the menu. The **General** tab is displayed by default (Figure 9-4).

4. In Technique Editor, select the **Clot Detection** tab (Figure 9-13)

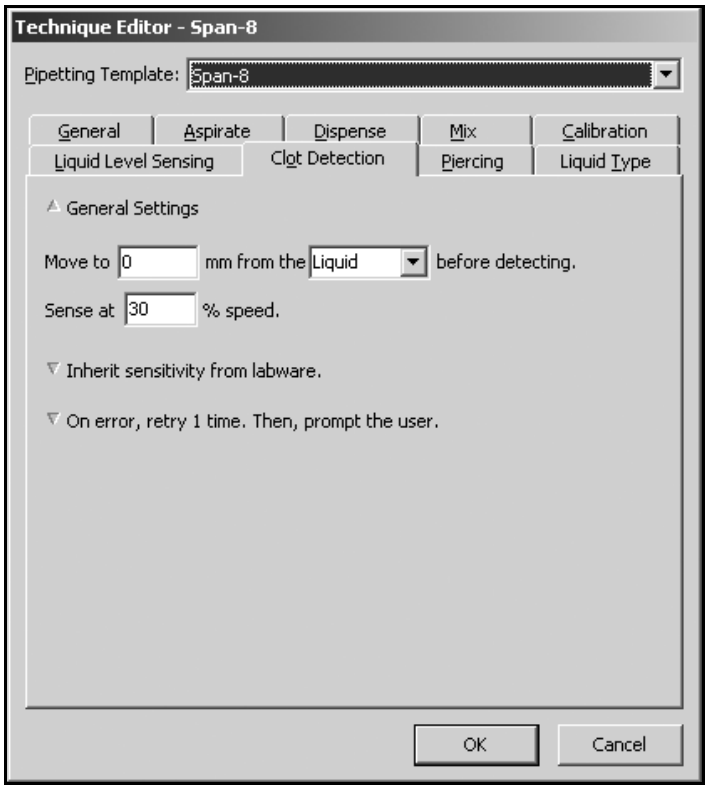


Figure 9-13. Technique Editor — General Settings on Clot Detection tab

9.4.6.1 Configuring General Settings

General Settings is used to configure the height of the probe within the well and the pod speed in the Z axis during clot detection operations.

1. If General Settings is not displayed, click on the topmost sentence summary to expand the General Settings configuration (Figure 9-13).
2. Enter the height in millimeters (mm) to **Move to** and detect from.

   Note: The suggested starting height for Move to should be between 3.175 and 4.7625 mm. The height may be adjusted, but starting with these heights is suggested.

3. Select the from the start location: **Liquid**, **Top,** or **Bottom**. The probe moves to the specified height measured from the liquid, top, or bottom of the well before detecting.
4. Enter the **Sense at** speed as a percentage of the maximum speed of the pod.

   Note: The speed affects the Z-axis speed only.

9.4.6.2 Configuring Sensitivity Settings

Sensitivity Settings is used to configure how sensitive the probes are to changes in capacitance. A clot is detected by determining the change in capacitance as the tip moves up after aspiration. Clot detection is determined using conductive tips (identified as LLS tips in the Tip Type Editor), fixed tips, or SeptaFluted tips that detect a shift in the capacitance of the probe.

The tip moves to a specified height within the well and then slowly moves down into the well. When the tip aspirates and rises from the liquid and if there is a large change in capacitance, no clot is detected. If there is no change or a small change in capacitance, a clot is detected.

To configure Sensitivity Settings:

1. If Sensitivity Settings is not displayed, click on the sentence summary second from the bottom to expand the Sensitivity Settings configuration (Figure 9-14).

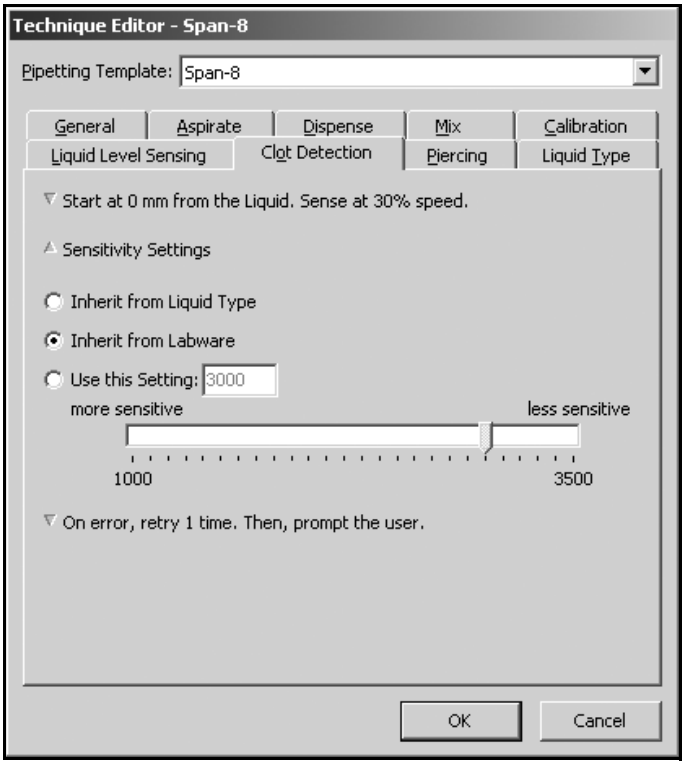


Figure 9-14. Technique Editor - Sensitivity Settings on Clot Detection tab

2. Select the **Sensitivity** of the clot detection. Sensitivity is the magnitude of change required for the conductive tips to detect a clot. A smaller sensitivity value detects smaller capacitance changes more easily. Options include:

   - Inherit from Liquid Type — (default sensitivity setting) uses sensitivity specified for the liquid in Liquid Type Editor; refer to Chapter 8, *Understanding and Creating Liquid Types*.
   - Inherit from Labware — uses sensitivity specified for the labware in Labware Type Editor; refer to Section 7.3, *Defining Labware Types*.
   - Use this Setting — uses the setting specified in the Technique Editor; specify the **Sensitivity** by entering the value or dragging the bar to the desired values.

9.4.6.3 Error Handling Settings

Error Handling Settings specify the action to take if a clot has been detected.

1. If Error Handling Settings is not displayed, click on the last sentence summary to expand the Error Handling Settings configuration (Figure 9-11).

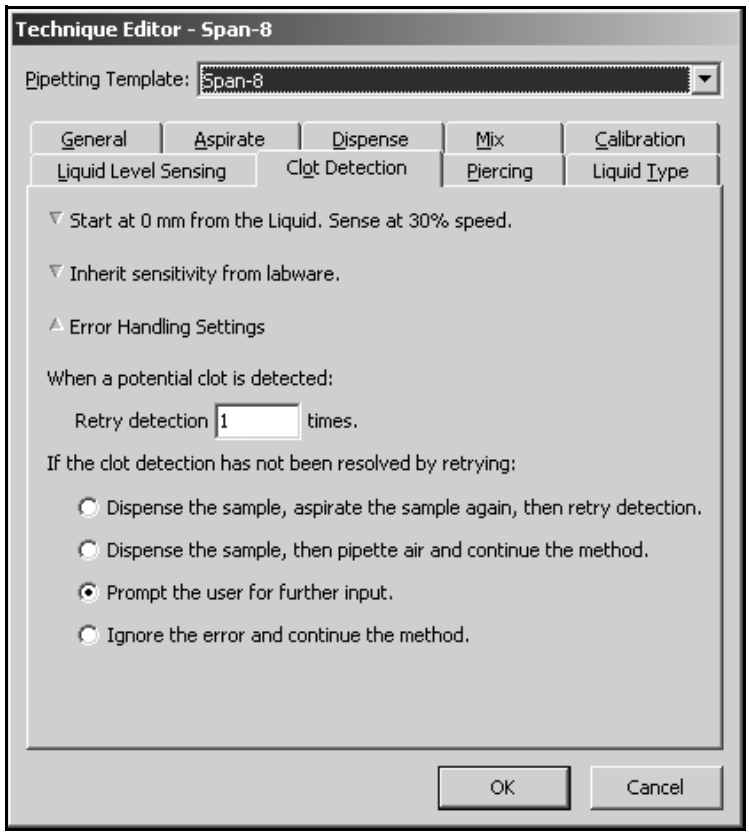


Figure 9-15. Technique Editor - Error Handling Settings on Clot Detection tab

2. In Retry detection, enter the number of times to retry the detection of a clot.
3. In If the clot detection has not been resolved by retrying, select the action to perform:
    - Dispense the sample, aspirate the same again, then retry detection.
    - Dispense the sample, then pipette air and continue the method.
    - Prompt the user for further input. — Requests further instruction and provides the options Dispense, Aspirate Again, then Retry Detection; Ignore and Continue; Snap [a Continuation]; or Abort.
    - Ignore the error and continue the method. — Ignores the error and continues the method.

Note: Ignoring the error and continuing the method when a clot exists may contaminate the deck.

9.4.7 Setting Piercing Values (NX-S8 only)

Setting the piercing values allows the technique to pierce septum within specified parameters during an aspirate.

To configure Piercing:

1. From the Project menu, choose **Technique Browser.** Technique Browser appears.
2. In Technique Browser, select the technique to modify.
3. Choose **Edit**.

   OR

   Double-click on the technique.

   OR

   Right-click in the Techniques View and choose **Edit** from the menu. The **General** tab is displayed by default (Figure 9-4).
4. In Technique Editor, select the **Piercing** tab (Figure 9-13)

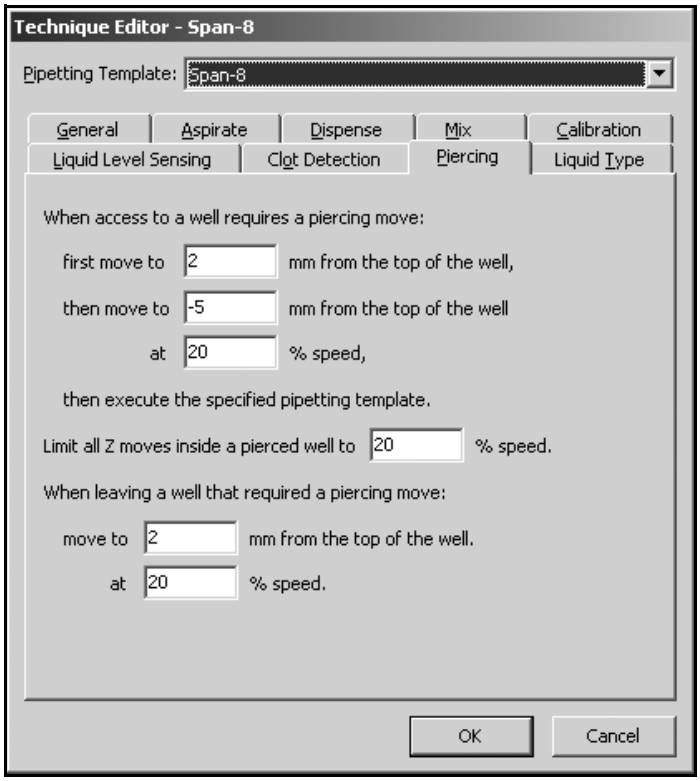


Figure 9-16. Technique Editor - Piercing tab

5. In When access to a well requires a piercing move: first move to, enter the distance in millimeters (mm) from the top of the well to move to before piercing.
6. In then move to, enter the distance in millimeters (mm) to then move to from the top of the well to pierce.
7. In at, enter the speed as a percentage of the maximum speed of the pod while accessing the well. The value must be between 0 and 100.

8. In Limit all Z moves inside a pierced well to, enter the speed of all Z-axis moves as a percentage of the maximum speed of the pod.
9. In When leaving a well that required a piercing move: move to, enter the distance in millimeters (mm) to move away from the top of the well that was pierced.
10. In at, enter the speed as a percentage of the maximum speed of the pod while leaving the well. The value must be between 0 and 100.

9.4.8 Overriding Liquid Type Values

The settings configured on the Liquid Type tab override values set in the Liquid Type Editor (refer to Section 8.2, *Creating New Liquid Types*). Configure the liquid type override values so specific pipetting characteristics will result, such as the amount of air to use as a blowout, or speeds for aspirate and dispense.

Configuring the Liquid Type tab is optional. When overriding liquid type values, the settings entered in the Liquid Type tab are used instead of the settings from the particular liquid type. To use the settings from the liquid type, do not select Override Liquid Type Settings.

Note: Use the Liquid Type tab only when overriding the liquid type. Create additional liquid types when using common liquid type settings.

To set liquid type override values for this technique:

1. From the Project menu, choose **Technique Browser.** Technique Browser appears.
2. In Technique Browser, select the technique to modify.
3. Choose **Edit**.

OR

Double-click on the technique.

OR

Right-click in the Techniques View and choose **Edit** from the menu. The **General** tab is displayed by default (Figure 9-4).

4. In Technique Editor, choose the **Liquid Type** tab (Figure 9-17).

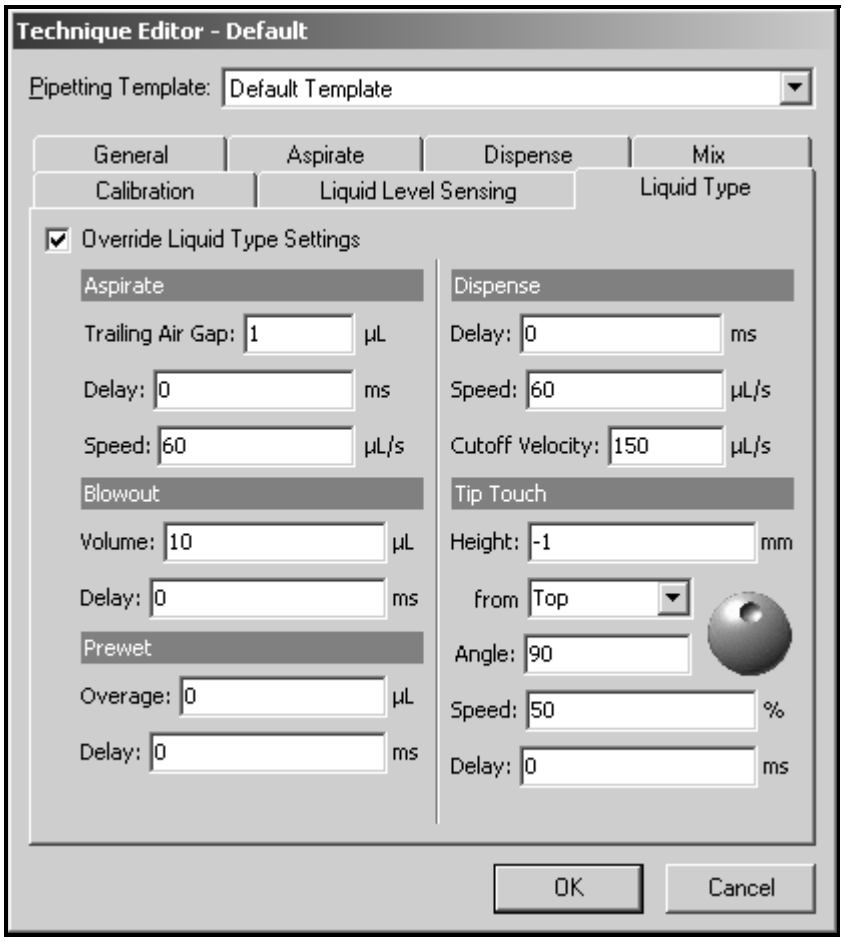


Figure 9-17. Technique Editor — Liquid Type tab

5. Select **Override Liquid Type Setting** to activate the Liquid Type tab configuration.

Note: When overriding liquid type values, the settings entered in the Liquid Type tab are used instead of the settings from the particular liquid type. To use the settings from the liquid type, do not select Override Liquid Type Settings.

6. In Aspirate, enter the volume of the **Trailing Air Gap** in microliters (µL). After aspirating the liquid, a Trailing Air Gap is aspirated to prevent dripping.
7. In Aspirate, enter the desired **Delay** in milliseconds (ms). Delay specifies the amount of time after an aspirate operation before continuing.
8. In Aspirate, enter the desired **Speed** in microliters per second (µL/s). This indicates the speed along the D axis during aspirate.
9. In Blowout, enter the desired **Volume** of the leading air gap to blow out after dispensing the liquid.
10. In Blowout, enter the desired **Delay** in milliseconds (ms). Delay specifies the amount of time after a blowout before continuing.

11. In Prewet, enter the desired **Overage** in microliters. Overage is the amount of liquid to be aspirated over the amount specified in the step configuration.
12. In Prewet, enter the desired **Delay** in milliseconds (ms). Delay specifies the amount of time from when the Prewet volume is completely aspirated until it begins to dispense.
13. In Dispense, enter the desired **Delay** in milliseconds (ms). Delay specifies the amount of time after a dispense operation before continuing.
14. In Dispense, enter the desired **Speed** in microliters per second (µL/s). This indicates the speed along the D axis during dispense.
15. In Dispense, enter the desired **Cutoff Velocity**, in microliters per second (µL/s).
    - ***FX, NX-S8*** — Cutoff Velocity applies to a Span-8 Pod only.

    Note: The minimum and maximum cutoff velocity varies with the syringe type. The value entered must fall within the acceptable range for the syringe type. Refer to Section 9.4.8.1, *Syringe Cutoff Velocities (FX, NX-S8 only)*, for more information on the cutoff velocity.
16. In Tip Touch, enter the desired **Height**.

    Note: Height, along with from and Angle, specify where along the well the Tip Touch occurs.
17. In Tip Touch, select the desired **from**: Top, Bottom, or Liquid. This indicates the location the Height is measured from.
18. In Tip Touch, enter the desired **Angle**

    OR

    Select the position along the edge on the graphic by positioning the smaller circle at the desired location. The Angle adjusts to the current location.

    Note: The Angle specifies the location along the well wall where the Tip Touch occurs at the specified Height and from location.
19. In Tip Touch, enter the desired **Delay.**
20. In Tip Touch, enter the desired Speed as a percentage of the total pod speed. This indicates the pod speed along the X-, Y-, and Z-axes as the pod moves to the tip touch position.

9.4.8.1 Syringe Cutoff Velocities (FX, NX-S8 only)

The speed per second at which fluid is dispensed prior to the dispense action stopping abruptly is called the Cutoff Velocity. If the Cutoff Velocity in the technique or liquid type governing the pipetting operation is too slow, droplets can be left at the end of tips after a dispense pipetting operation. Accurately setting the Cutoff Velocity causes the liquid to be ejected at a speed sufficient to prevent droplets from forming on the end of a tip.

The minimum and maximum Cutoff Velocity and the instruments on which they are supported are listed in Table 9-2. When changes to Cutoff Velocity are required, they must be made to the technique governing the pipetting operation in the Technique Editor, and to the parameters of the fluid used during the pipetting operation in the Liquid Type Editor.

The cutoff velocity should be adjusted in all Span-8 techniques for better pipetting accuracy every time syringes are changed from one type to another. The Cutoff Velocities displayed in Table 9-2 are intended as a starting point. The values provided should be experimented with to determine the most accurate Cutoff Velocity for a specific liquid handling operation.

Table 9-2. Span-8 Cutoff Velocities for Syringes for Span-8 Pods

Syringe Size	Minimum Cutoff Velocity	Maximum Cutoff Velocity	Instruments
100 µL	0.833 µL/second	45.0 µL/second	***NX-S8***
250 µL *	2.08 µL/second	112.5 µL/second	***FX, NX-S8***
500 µL**	4.17 µL/ second	225 µL/second	***FX, NX-S8***
1 mL ***	8.33 µL/ second	450 µL/second	***FX, NX-S8***
2.5 mL	20.8 µL/second	1125 µL/second	***NX-S8***
5 mL	41.7 µL/second	2250 µL/second	***NX-S8***
* Recommended cutoff velocity is 100 µL/second. ** Recommended cutoff velocity is 150 µL/second. *** Recommended cutoff velocity is 150 µL/second.			

Note: The minimum Cutoff Velocity for each syringe is established using the equation: 50 x <Syringe size in µL>/6000. The maximum Cutoff Velocity for each syringe is established using the equation: 2700 x <Syringe size in µL>/6000.

To change techniques to conform to the Cutoff Velocity supported by the syringe size:

1. From the Project menu, choose **Technique Browser.** Technique Browser appears.
2. In Technique Browser, select the technique to modify.
3. Choose **Edit**.

   OR

   Double-click on the technique.

   OR

   Right-click in the Techniques View and choose **Edit** from the menu. The **General** tab is displayed by default (Figure 9-4).
4. In Technique Editor, choose the **Liquid Type** tab (Figure 9-17).
5. In Dispense, enter the desired **Cutoff Velocity**, in microliters per second (µL/s).
6. Choose **OK** to save the technique and exit the Technique Editor.
7. Choose **Close** to exit the Technique Browser.

Note: If the size of syringes installed in the Biomek instrument changes frequently, or if two different sizes of syringes are installed at the same time, create a duplicate set of the Span-8 techniques for each syringe size (refer to Section 9.9, *Modifying Saved Techniques*) and edit the Cutoff Velocity on the Liquid Type tab to support the syringes.

9.5 Calibrating Techniques

Calibrating techniques improves the accuracy of pipetting operations. All method steps involving aspirating, dispensing, and mixing volumes of liquids use calibration to make sure an accurate volume is aspirated and dispensed. Calibration is also necessary to adjust for liquid properties, such as viscosity.

During a method run, the Biomek instrument aspirates and dispenses liquid based on the results of the following equation:

Displaced Volume = Desired Volume * Scaling Factor + Offset Volume

The properties in the equation are:

- Displaced Volume — the amount physically aspirated and dispensed.
- Desired Volume — the amount that is expected to be aspirated and dispensed.
- Scaling Factor — the amount to multiply a given volume by to achieve the desired calibration.
- Offset Volume — the amount of overage by a specific amount, such as 2 µL.

The results of the equation are displayed in sentence form in the middle section of the Calibration tab (Figure 9-18). The displaced volume changes as adjustments are made to the Scaling Factor and Offset to indicate the result of the equation.

To calibrate techniques:

1. From the Project menu, choose **Technique Browser.** Technique Browser appears.
2. In Technique Browser, select the technique to modify.

3. Choose **Edit**.

   OR

   Double-click on the technique.

   OR

   Right-click in the Techniques View and choose **Edit** from the menu. The **General** tab is displayed by default (Figure 9-4).
4. In Technique Editor, select the **Calibration** tab.

5. If the Volume Calibration configuration is not displayed, click on **Volume Calibration** to expand the Volume Calibration configuration.

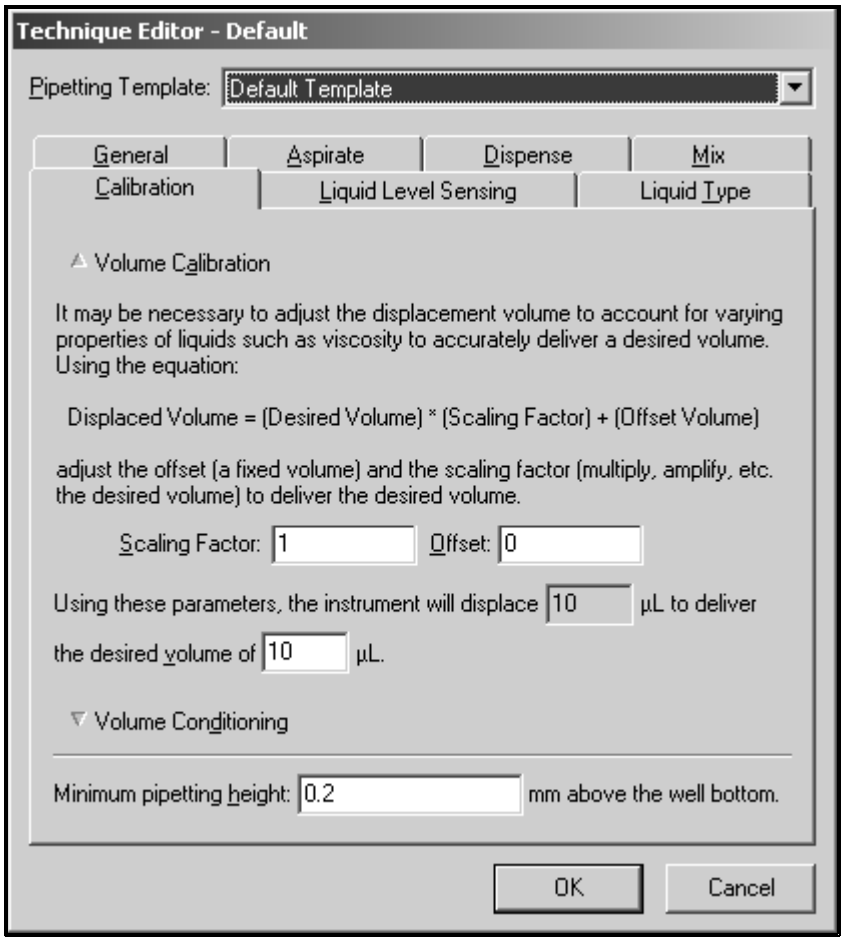


Figure 9-18. Technique Editor — Volume Calibration on Calibration Tab

6. Enter the **Scaling Factor** at which to calibrate. The sentence display adjusts accordingly.

   Note: Scaling Factor should be greater than 0. A Scaling Factor of 1 and an Offset of 0 does not alter the volume manipulated during a pipetting operation.

7. Enter the desired **Offset**. The sentence display adjusts accordingly.
8. Verify the calibration equation by reading the sentence display. Adjust the Scaling Factor and Offset as necessary.
9. In Minimum pipetting height, enter the number of millimeters from the bottom of the labware that the tip is not allowed to go below.
10. Choose **OK**.
11. Choose **Close** to close Technique Browser.

Note: It is recommended that techniques be tested after calibrating to verify the desired results are achieved.

9.6 Conditioning Techniques for Multiple Dispense (FX, NX-S8 only)

Conditioning is a specified volume of liquid to dispense when performing multiple dispense operations from a single aspirate operation, and is used to enhance precision when switching from aspirate mode to dispense mode. If a multiple dispense technique is not properly conditioned, the first dispense may be greater than the volume specified in the step.

When using a technique that utilizes volume conditioning, the Biomek instrument aspirates and dispenses liquid according to Figure 9-19:

Note: Volume conditioning is used by a technique only if the associated pipetting template is designed to use volume conditioning. Refer to Chapter 10, *Using the Pipetting Template Editor*, for more information on pipetting templates and the Pipetting Template Editor. The Span-8 MultiDispense pipetting template is the only standard template designed to use volume conditioning.

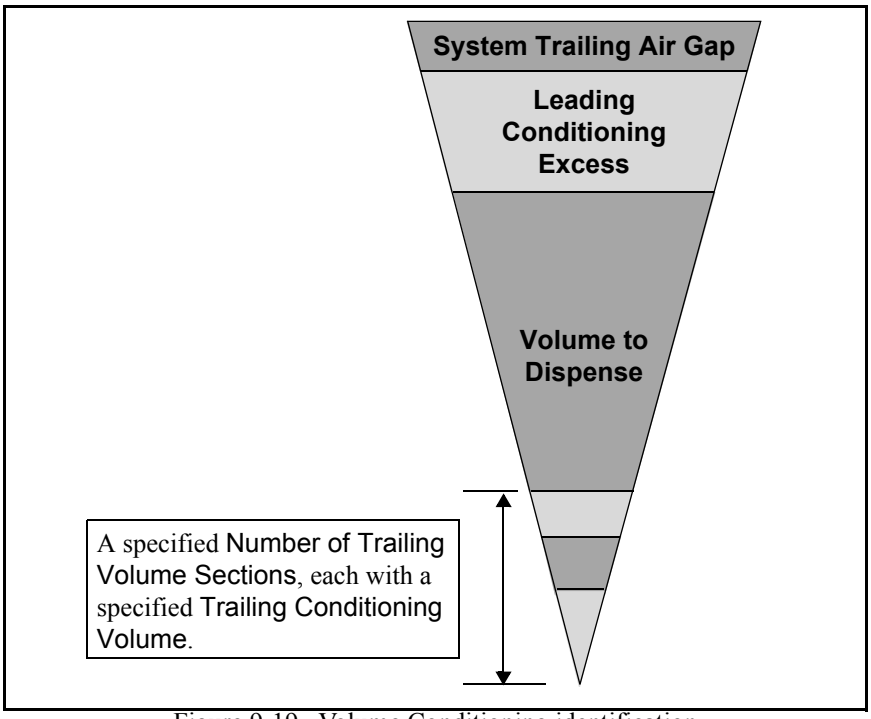


Figure 9-19. Volume Conditioning identification

The volumes displayed in Figure 9-19 are:

- System Trailing Air Gap — air gap between the system fluid and volume aspirated. The system trailing air gap is configured in Hardware Setup.
  - ***FX*** — refer to the *Biomek® FX Laboratory Automation Workstation User's Manual,* Chapter 4.4.6, *Setting Span-8 Pod Properties* or
  - ***NX-S8*** — refer to the *Biomek® NX Span-8 Laboratory Automation Workstation User's Manual,* Chapter 3.3.6, *Setting Span-8 Pod Properties*

  Note: The System Trailing Air Gap is initially configured by a Beckman Coulter Service Engineer and should not be modified without specific instructions from a Beckman Coulter Service Engineer or Technical Support.

- Leading Conditioning Excess — volume of source aspirated in excess of the sample Volume to Dispense that serves as a buffer between the system fluid and the liquid dispensed to protect from sample dilution. The Leading Conditioning Excess is purged to waste after completing all dispense operations.

  Note: The Span-8 MultiDispense pipetting template automatically includes an excess of 15 percent of the volume aspirated.

- Volume to Dispense — the total volume of source aspirated for all dispense operations. For example, if dispensing 10 µL across 12 wells of a microplate, the volume aspirated is 120 µL.
- Trailing Conditioning Volume — an extra volume of source is aspirated a specified Number of Trailing Volume Sections times following the Volume Aspirated. Each trailing volume section is dispensed back into the source well separately prior to leaving the well to condition the dispense operation for more precise pipetting. For example, in Figure 9-19, each of the three bottom sections is dispensed back into the source well with three separate dispense actions.

To condition techniques:

1. From the Project menu, choose **Technique Browser.** Technique Browser appears.
2. In Technique Browser, select the technique to modify.

3. Choose **Edit**.

   OR

   Double-click on the technique.

   OR

   Right-click in the Techniques View and choose **Edit** from the menu. The **General** tab is displayed by default (Figure 9-4).
4. In Technique Editor, select the **Calibration** tab.

5. If the Volume Conditioning configuration is not displayed, click on **Volume Conditioning** to expand the Volume Conditioning configuration (Figure 9-18).

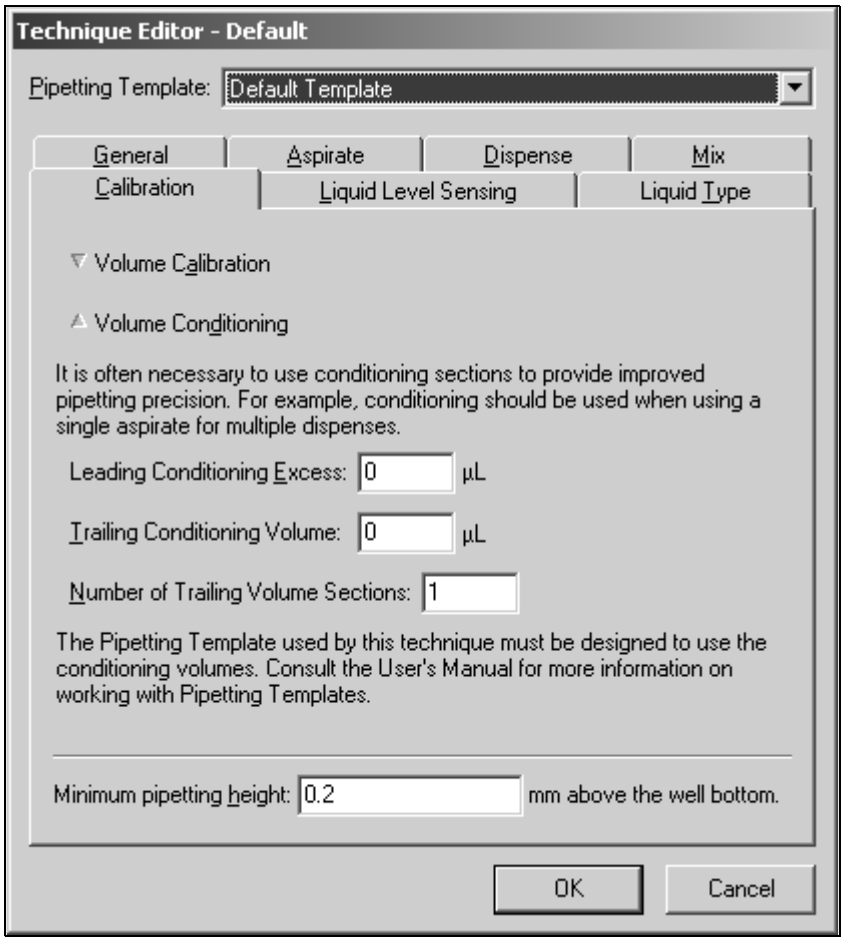


Figure 9-20. Technique Editor — Volume Conditioning on Calibration Tab

6. Enter the volume of **Leading Conditioning Excess** to aspirate as an additional buffer in excess of that aspirated automatically as part of the pipetting template between the system fluid and the source liquid.

Note: The Span-8 MultiDispense pipetting template automatically includes an excess of 15 percent of the volume aspirated. The Leading Conditioning Excess is the volume to aspirate in addition to the 15 percent specified in the pipetting template for the buffer between the system fluid and source.

7. Enter the **Trailing Conditioning Volume** to aspirate for each trailing volume section.

8. Enter the **Number of Trailing Volume Sections** to aspirate.

Note: After aspirating the volume of source to dispense, an additional volume of source equal to the Number of Trailing Volume Sections times the Trailing Conditioning Volume is aspirated. Prior to leaving the well, each trailing volume section of Trailing Conditioning Volume is dispensed back into the source well in separate dispense actions equal to the specified Number of Trailing Volume Sections.

9.7 Creating Technique Groups

A Group is a user-created subset of techniques and can be used to organize techniques by their properties via the Technique Editor using Groups. For examples, all techniques for use with a Span-8 Pod on a Biomek FX instrument could be placed in a group called Span-8.

Techniques may be in more than one group, if desired. For example, another group could have all techniques for use with the Multichannel Pod on a Biomek FX instrument. Any techniques that can use both the Span-8 Pod and the Multichannel Pod would appear in both groups.

To create a new group:

1. From the Project menu, choose **Technique Browser.** Technique Browser appears.

2. Choose **New Group**.

   OR

   Right-click under Groups and select **New Group** from the menu that appears. A new group is added under Groups and a checkbox appears to the left of each technique (Figure 9-21).

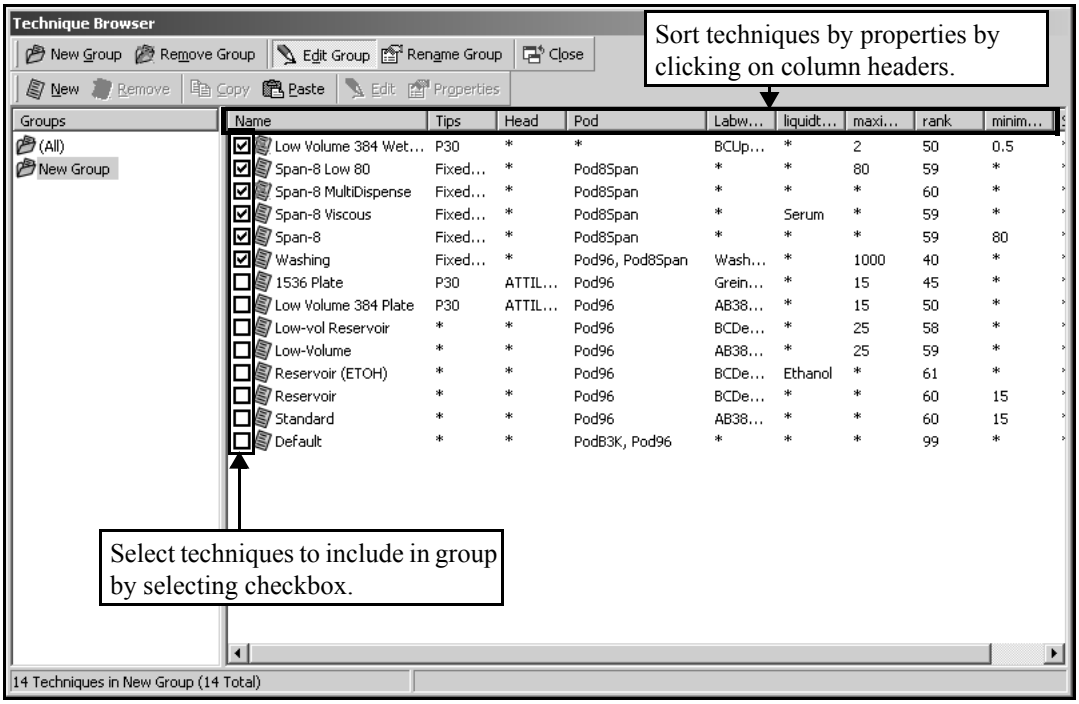


Figure 9-21. Creating a new group in the Technique Browser

3. Enter a name for the new group.

4. In the list of techniques, select the checkbox to the left of each technique to include that technique in the new group.

Note: Techniques can be sorted by any of the properties by clicking on the column headings. Selecting a heading once sorts the column in ascending order; clicking on the same heading a second time sorts that column in descending order.

5. Choose **Edit** to exit group editing mode. The checkboxes disappear and only the methods that were selected remain in the group.

Note: The status bar in the Technique Browser displays how many techniques are in the selected group and how many techniques there are in the project.

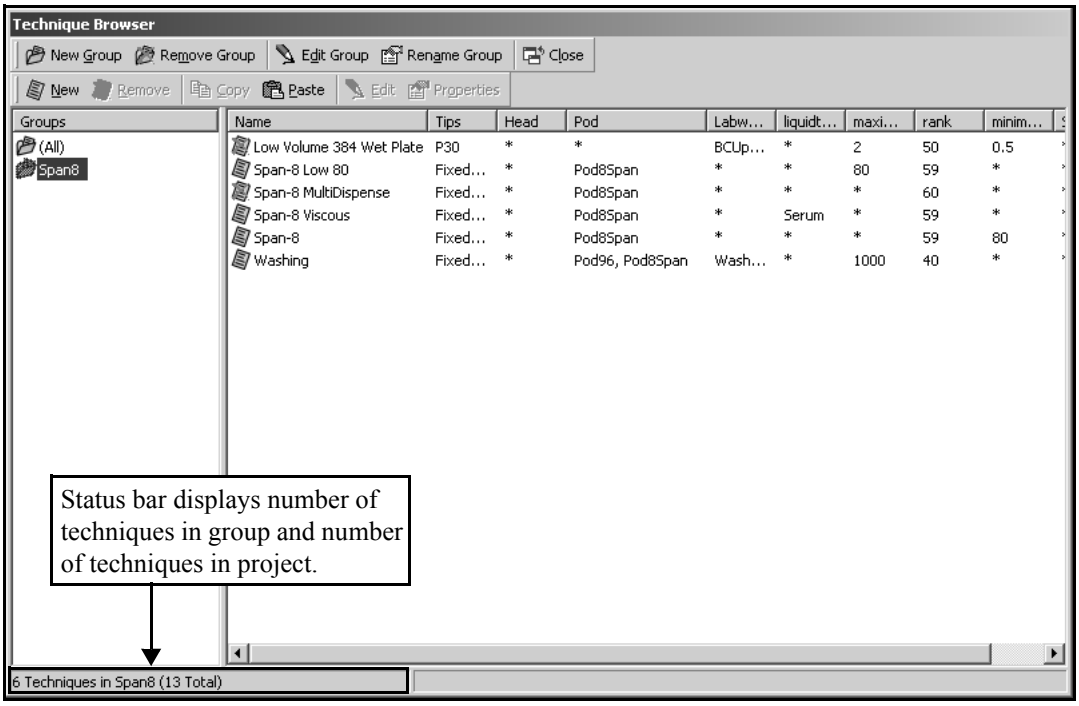


Figure 9-22. New group created in the Technique Browser

9.7.1 Renaming Groups

Groups may be renamed at any time, if desired.

To rename a group:

1. From the Project menu, choose **Technique Browser.** Technique Browser appears.

2. Choose **Rename Group**.

   OR

   Right-click under Groups and select **Rename Group** from the menu that appears.

3. Enter the desired new name for the group and press **Enter**. The group is renamed.

9.7.2 Adding and Removing Techniques from Groups

Techniques may be added to or removed from a group at any time using the Edit Group command.

Note: Techniques may also be added to a group when they are created by selecting the groups to which the technique is to be added when configuring technique properties (refer to Section 9.3, *Creating New Techniques*).

To edit a group:

1. From the Project menu, choose **Technique Browser.** Technique Browser appears.

2. Choose **Edit Group**.

   OR

   Right-click under Groups and select **Edit Group** from the menu that appears. A checkbox appears to the left of each technique (Figure 9-21).

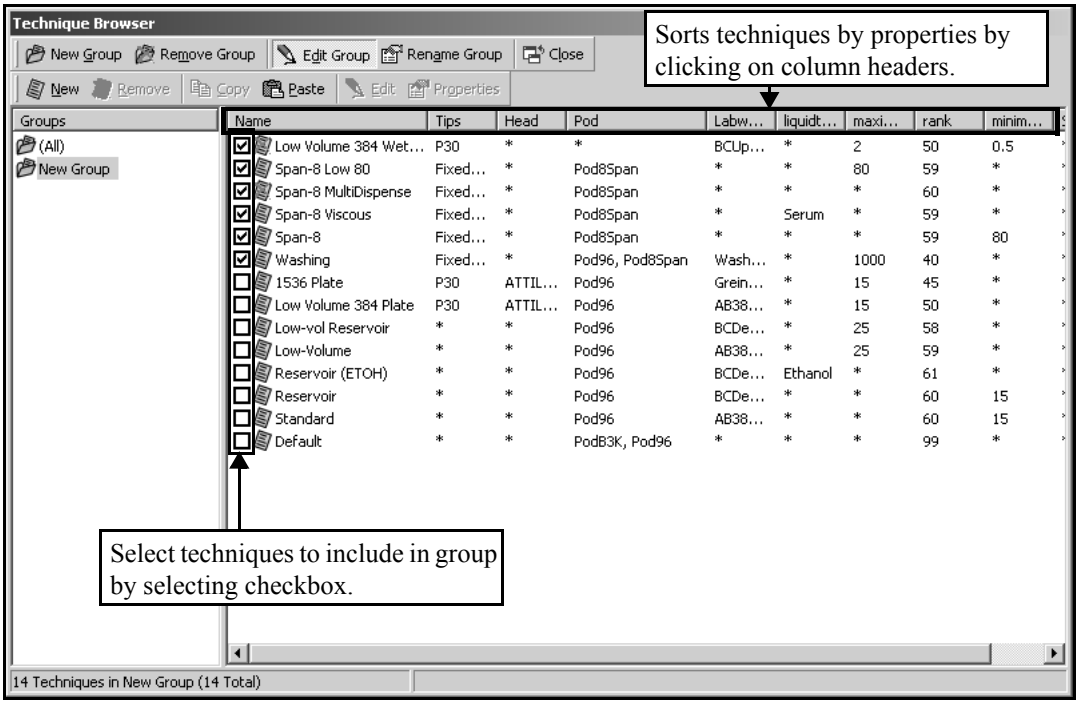


Figure 9-23. Creating a new group in the Technique Browser

3. In the list of techniques, select the checkbox to the left of each technique to include in the new group, or deselect the checkbox to the left of each technique to remove that technique from the group.

Note: Techniques can be sorted by any of the properties by clicking on the column headings. Selecting a heading once sorts the column in ascending order; clicking on the same heading a second time sorts that column in descending order.

Note: Right-clicking on the technique in the techniques list and selecting **Remove** removes the technique from the project, not the group.

4. Choose **Edit Group** to exit group editing mode. The checkboxes disappear and only the methods that were selected remain in the group.

Note: The status bar in the Technique Browser displays how many techniques are in the selected group and how many techniques there are in the project.

9.7.3 Removing Groups

When a group is no longer needed, it can be removed from the Technique Browser.

To remove a group:

1. From the Project menu, choose **Technique Browser.** Technique Browser appears.
2. Under Groups, select the desired group to remove.

3. Choose **Remove Group**.

   OR

   Right-click under Groups and select **Remove Group** from the menu that appears. The group is removed from the list under Groups.

9.8 Removing Techniques

To prevent Biomek Software from choosing techniques during a method run that may have become obsolete, remove the techniques from the Technique Editor.

When a technique is removed, it is no longer available in method building. However, the latest checked-in revision of the technique remains in the project file and may be restored at any time (refer to Section 6.8.1, *Restoring Deleted Project Items*).

To remove techniques:

1. In Technique Browser, select the technique.

2. Choose **Remove**.

   OR

   Right-click and choose **Remove** from the menu. A Confirm prompt appears (Figure 9-24).

Figure 9-24. Remove technique confirmation prompt

3. Choose **Yes** to remove the technique.

9.9 Modifying Saved Techniques

When a method uses pipetting requirements that are slightly different from the requirements of previously created techniques, modify the technique that most closely resembles the new pipetting requirements by copying and pasting.

To copy and paste techniques:

1. In Technique Browser, select the technique to copy.
2. Choose **Copy**.

   OR

   Right-click and choose **Copy** from the menu.
3. Choose **Paste**. The copy appears with the name "Copy of (Technique)".

   OR

   Right-click and choose **Paste** from the menu.
4. Select the copied technique.
5. Choose **Properties**.

   OR

   Right-click and choose **Properties** from the menu.
6. Enter a new name for the technique, if desired.
7. Make any changes to the technique (refer to Section 9.4, *Setting Technique Values*).
8. Choose **OK**.

9.10 Selecting and Modifying Techniques Manually in a Method

Automatic selection of techniques is turned on by default; however, there may be instances when manual selection of techniques is desired. When Auto-Select is unchecked, manual selection of techniques is possible in the source and destination configuration of a pipetting step, such as Transfer or Combine. Biomek Software shows all techniques that match the properties of the step configuration (pod, tips, labware type, liquid type, volume) in a drop-down list in the Technique field (Figure 9-25).

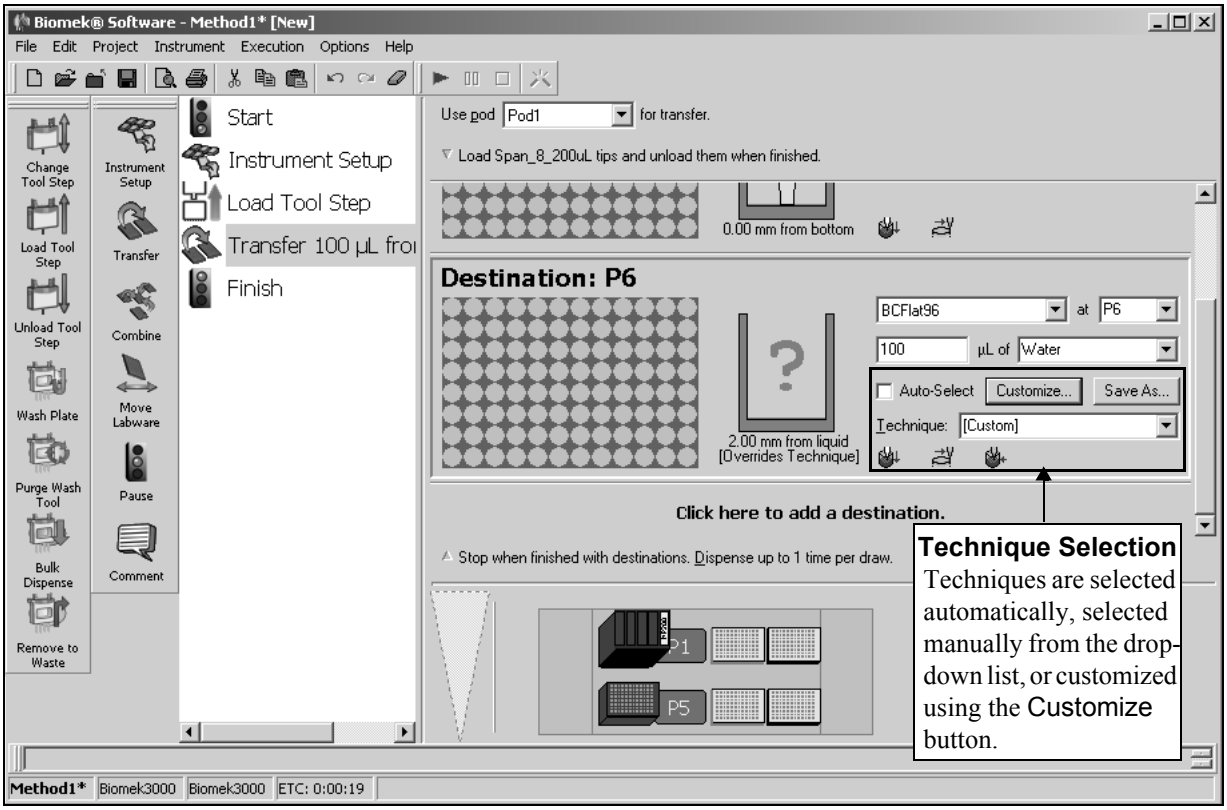


Figure 9-25. Customize techniques or manually select techniques from a list in source or destination configurations of a pipetting step

Techniques used in methods are normally auto-selected by Biomek Software; however, circumstances may require modifications to techniques due to the current setup or liquid type. Many pipetting steps provide access to the Technique Editor during method development.

9.10.1 Modifying a Technique Through a Method Step

Custom techniques created within a method are saved within the current method only and are accessible only in the pipetting operation for which the technique was created. The technique can be saved for global use after configuration, if desired.

When modifying techniques or creating new techniques within a method, only the parameters for the specific operation, along with Liquid Type, Liquid Level Detection, and Calibration settings, may be modified.

To modify a technique within a step or method:

1. Select the desired step in the method.
2. Select the desired source or destination.
3. Choose **Customize** (Figure 9-26). Technique Editor - [Custom] appears (Figure 9-27).

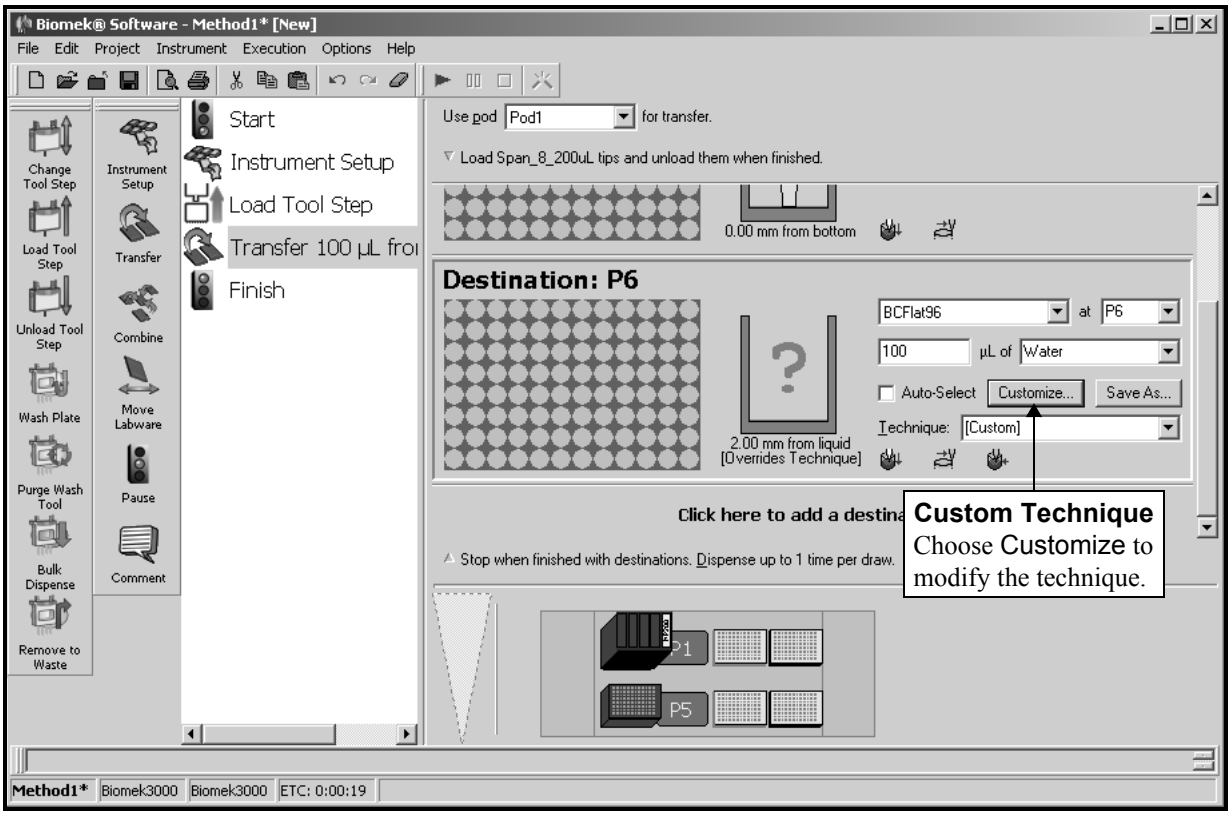


Figure 9-26. Technique selection within a method

4. Customize the technique as needed (refer to Section 9.4, *Setting Technique Values*).

   Note: Technique Properties, such as Labware Type, Liquid Type, and Tips, cannot be configured for the custom technique when creating the technique within a method. The technique uses the known properties of the specific operation being customized. Technique Properties are configured upon saving the technique for global use (refer to Section 9.10.2, *Saving Custom Techniques*).

5. Choose **OK**. [Custom] replaces the technique name.

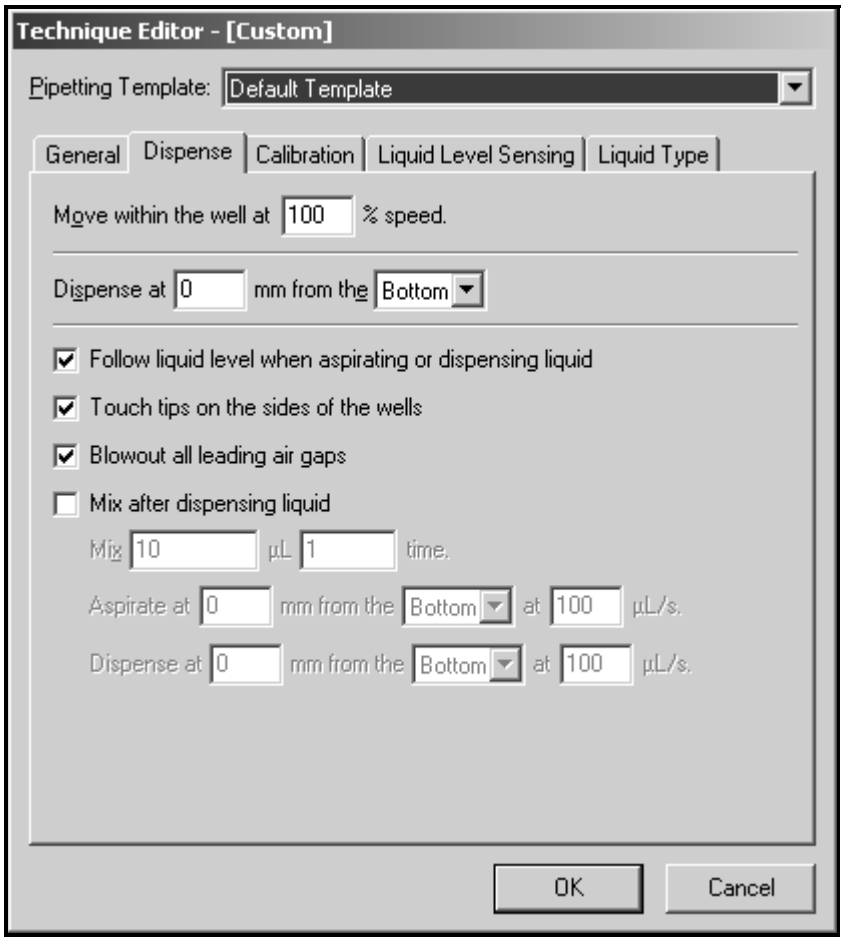


Figure 9-27. Dispense Tab appears when Customize is selected from destination

9.10.2 Saving Custom Techniques

A custom technique is saved within the method in which it was created; however, any custom technique can be saved for global use.

To save a custom technique for global use:

1. Choose **Save As** in the step configuration (Figure 9-28). Technique Properties appears.

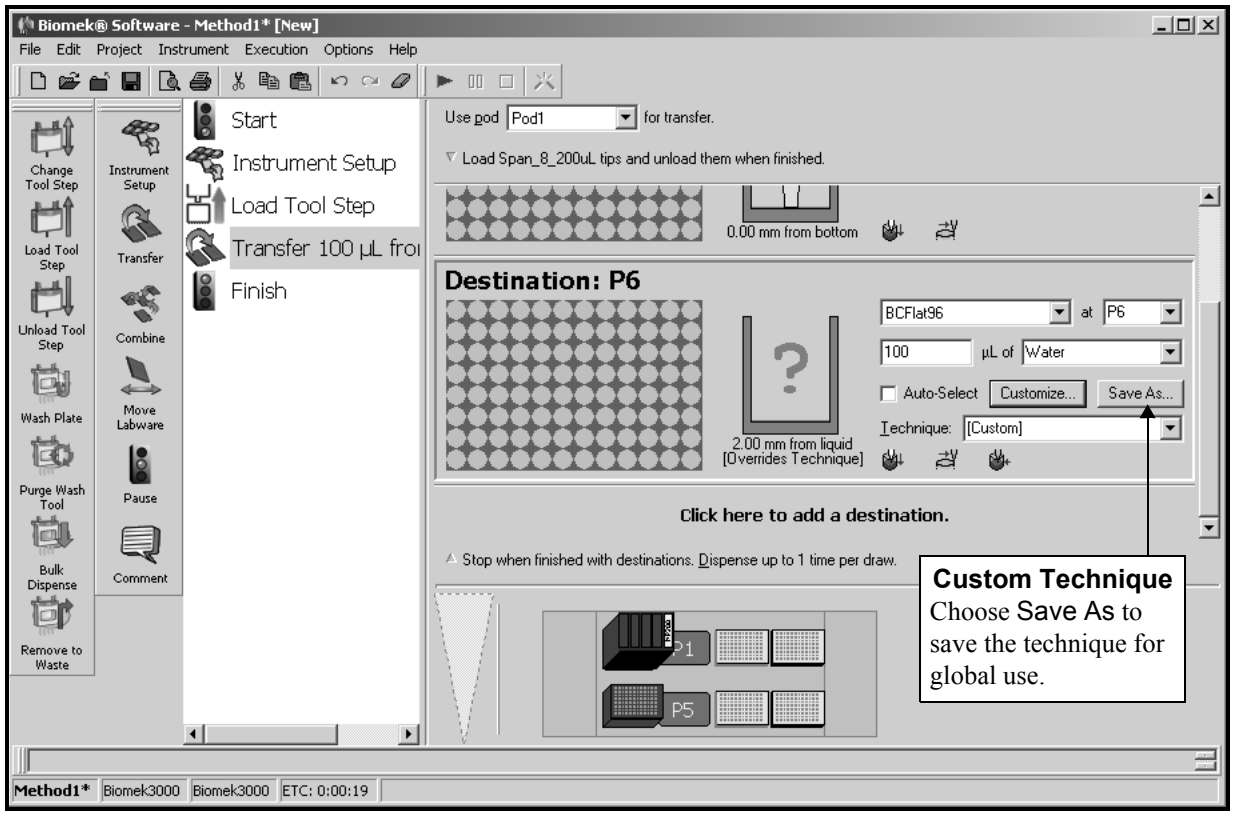


Figure 9-28. Save a custom technique within a step

2. Enter the **Technique Name,** then select the properties desired for the technique (refer to Section 9.3, *Creating New Techniques*).
3. Choose **OK**. The new technique name appears in Technique.

10 Using the Pipetting Template Editor

10.1 Overview

Pipetting operations within steps of a method are configured using techniques. Techniques are associated with a pipetting template that controls how the instrument performs pipetting operations for aspirating, dispensing, and mixing liquids. While using the Pipetting Template Editor is not necessary to successfully operate the instrument, it does present the opportunity for finer control over pipetting operations in order to optimize performance for specific applications.

A pipetting template is not used unless it is associated with a technique. Likewise, a technique is useless without the pipetting template that controls it. Biomek Software contains several default pipetting templates by which all predefined techniques are controlled.

Pipetting templates can be modified, or new templates created, using the Pipetting Template Editor. Templates are created by configuring a series of steps that dictate the actions the instrument makes, similar to building a method in the Main Editor. Template steps are configured using context variables; however, only the template steps that are applicable to the instrument and configuration appear. A context variable retrieves values from the technique or liquid type used in the pipetting operation.

Pipetting templates, along with information about liquid types; labware and tip types; well patterns; and pipetting techniques, are stored as part of a project file. Project files store a history of all changes, additions, and deletions of items from the project file. Refer to Chapter 6, *Understanding and Using Project Files*, for more information on project files.

Note: When Beckman Coulter Accounts & Permissions is enabled, only users with the Develop Projects permission assigned may open, edit, create, and delete pipetting templates (refer to Chapter 2, *Using Accounts & Permissions*).

10.2 Creating and Modifying Pipetting Templates

Creating and modifying pipetting templates is achieved with the Pipetting Template Editor.

To open the Pipetting Template Editor:

Choose **Project>Pipetting Template Editor**. The Pipetting Template Editor appears (Figure 10-1).

- ***FX***, ***NX-S8*** — Bulk Dispense appears *only* with these instruments.
- ***NX-S8*** — Clot Detection appears *only* with this instrument.

Pipetting templates are created in one of the following ways:

- Create a blank template and insert template steps
- Copy and paste an existing template and modify as needed

Note: The most expedient way to create pipetting templates is to copy and paste the template that resembles the desired operations most closely (refer to Section 10.2.3, *Modifying Existing Pipetting Templates*).

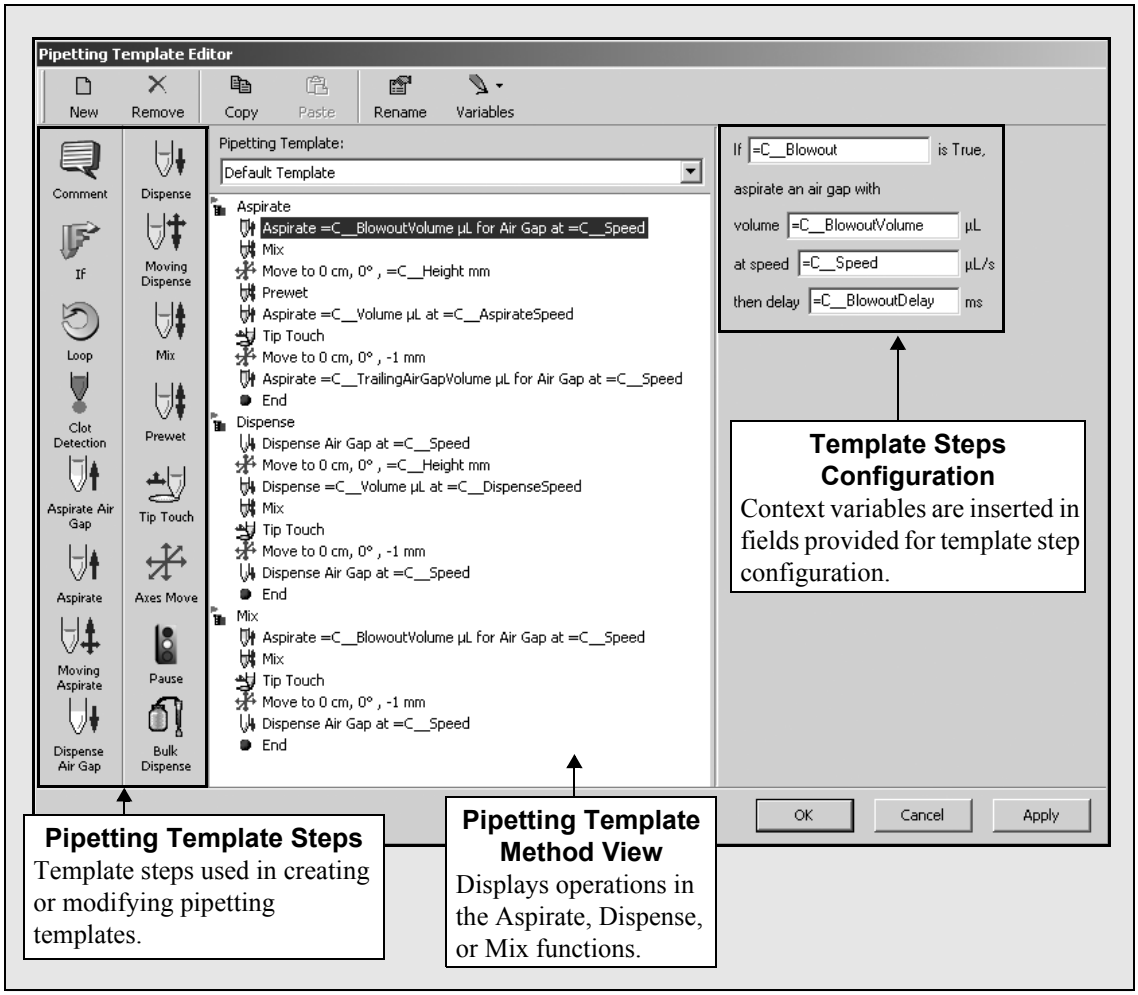


Figure 10-1. Pipetting Template Editor

10.2.1 Viewing Existing Pipetting Templates

Several default pipetting templates are included with Biomek Software. These templates have specific operations which they perform, and are associated with each technique to control liquid-handling operations. In order to understand the operations the pipetting template performs, view a pipetting template.

Note: Refer to Section 10.5, *Configuring Pipetting Template Steps*, for more information regarding each template step within the technique.

To view the pipetting template and related operations:

1. Choose **Project>Pipetting Template Editor**. The Pipetting Template Editor opens (Figure 10-1).
2. Select the desired **Pipetting Template**.
3. Click on the appropriate step to view the settings for the step.

10.2.2 Creating a New Pipetting Template

New pipetting templates are created using template steps that make up a pipetting procedure (refer to Section 10.5, *Configuring Pipetting Template Steps*). The template steps control the order of operations in aspirate, dispense, and mix operations.

Note: Before creating or customizing templates, be sure to understand where each of the context variables finds and retrieves the values used in the configured pipetting operations (refer to Section 10.3, *Understanding Context Variables*).

To create a new pipetting template:

1. Choose **Project>Pipetting Template Editor**. The Pipetting Template Editor opens (Figure 10-1).
2. Choose **New**. A blank template with Aspirate, Dispense and Mix steps appears (Figure 10-2).

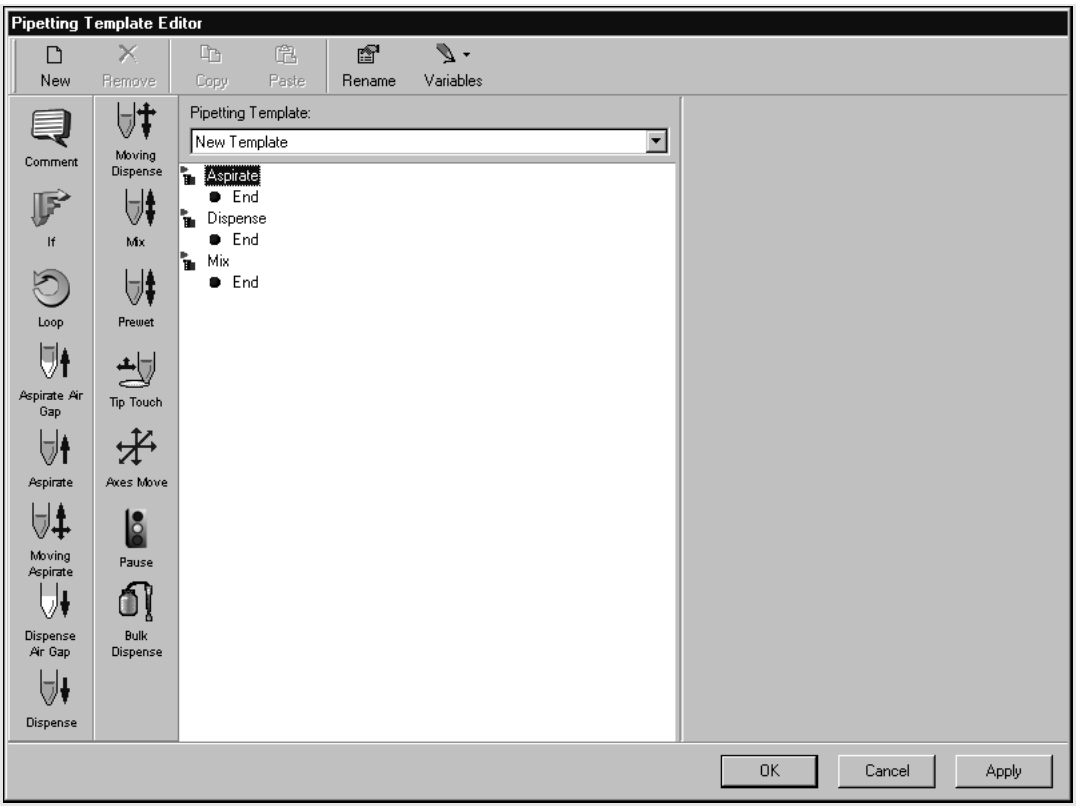


Figure 10-2. New pipetting template

3. Insert and configure the desired template steps (refer to Section 10.5, *Configuring Pipetting Template Steps*).

4. Choose **Rename** to change the template name. Rename Pipetting Template appears (Figure 10-3).

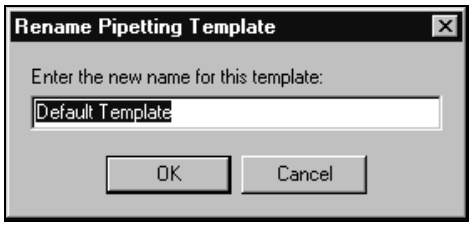


Figure 10-3. Rename pipetting template

5. Enter the name of the new pipetting template and choose **OK**.
6. Choose **OK**. The template is saved and the Pipetting Template Editor closes.

   OR

   Choose **Apply**. The template is saved and the Pipetting Template Editor remains open.

   OR

   Choose **Cancel**. The template is not saved and the Pipetting Template Editor closes.

10.2.2.1 Associating a Pipetting Template with a Technique

A pipetting template is not used by the instrument unless it has been associated with a technique. Every time a pipetting operation occurs in a method that uses a technique with the template assigned, the operations are executed as configured in the pipetting template.

To associate a pipetting template with a technique:

1. Select **Project>Technique Browser**. The Technique Browser appears (Figure 10-4).

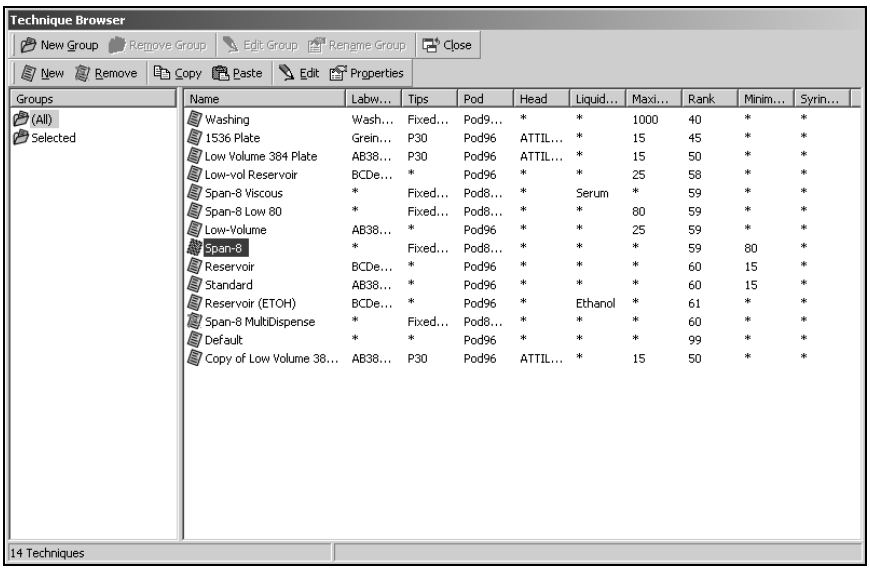


Figure 10-4. Technique Browser

2. Select the desired technique and choose **Edit** from the toolbar.

   OR

   Double-click the desired technique on the right side of the Technique Browser.

   OR

   Right-click the desired technique and select **Edit** from the menu. The Technique Editor appears (Figure 10-5).

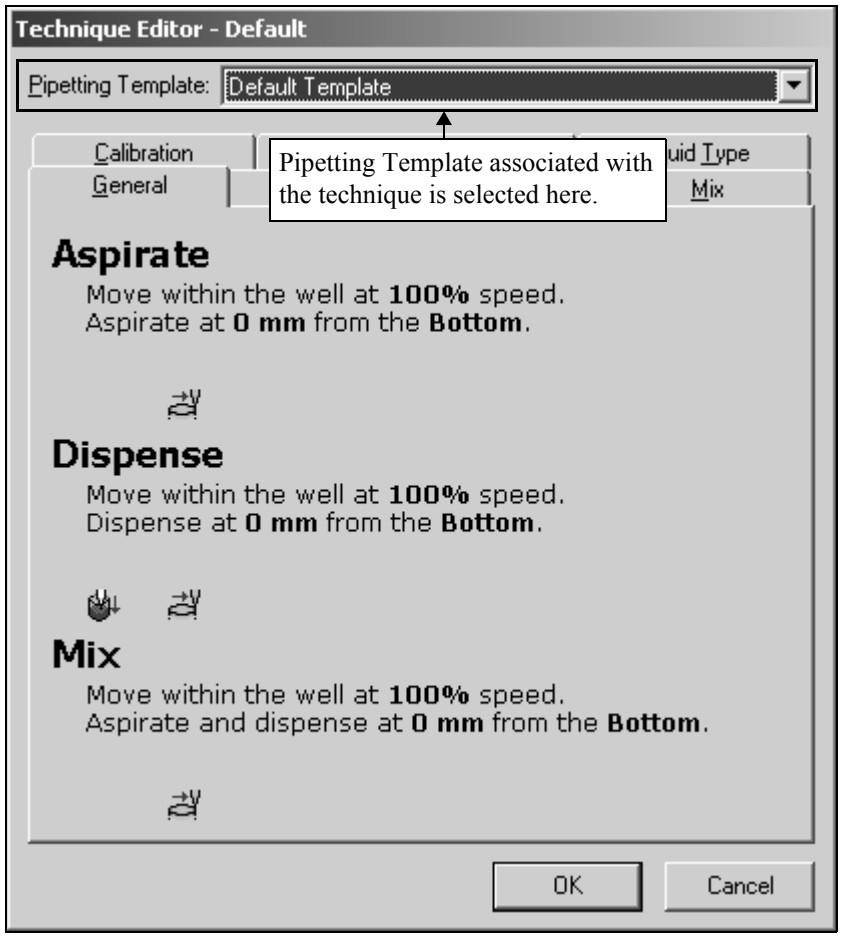


Figure 10-5. Technique Editor

3. Select the appropriate **Pipetting Template** from the list.
4. Choose **OK**. The changes to the technique are saved and the Technique Editor closes.

10.2.3 Modifying Existing Pipetting Templates

Copy and paste pipetting templates when making modifications to an existing template. Once the template is copied and pasted as a new template, any changes made do not affect the original.

Note: Pipetting templates can be exported to and imported from other projects. Refer to Section 6.10, *Importing and Exporting Project Files* for information about importing and exporting pipetting templates.

To copy and paste a pipetting template:

1. Choose **Project>Pipetting Template Editor** to open the Pipetting Template Editor.
2. In Pipetting Template, select the template to copy.
3. Choose **Copy**.
4. Choose **Paste** to insert the copied template as a new template. The new template appears with the name "Copy of (Original Template's Name)".
5. Choose **Rename** to change the template name. Rename Pipetting Template appears.
6. Enter the name of the new pipetting template and choose **OK**.
7. Make changes to the pipetting template by inserting and configuring steps (refer to Section 10.5, *Configuring Pipetting Template Steps*).
8. Choose **OK**. The template is saved and the Pipetting Template Editor closes.

   OR

   Choose **Apply**. The template is saved and the Pipetting Template Editor remains open.

   OR

   Choose **Cancel**. The template is not saved and the Pipetting Template Editor closes.

10.3 Understanding Context Variables

Pipetting templates make use of context variables to configure pipetting operations. Context variables are inserted into the template steps configuration and are used to retrieve values from the appropriate technique or liquid type in the Technique Editor or Liquid Type Editor. For example, C__DispenseDelay retrieves the value from Dispense Delay of the appropriate liquid type in the Liquid Type Editor.

Using context variables gives pipetting templates greater versatility, as the values for context variables are determined by the liquid type or technique used for the specific pipetting operation.

Note: Variables configured within Start, Let, and Worklist can be placed into a pipetting template, but doing so may limit the usefulness of the pipetting template. When variables defined in Start, Let, and Worklist are used in a pipetting template, the template may only be used in methods with the same variable names defined. Be sure that these variables are defined in the method, or an error may occur during method execution.

10.3.1 Inserting Variables and Expressions

Insert variables the appropriate fields of a pipetting template step, or by using the Variables button on the Pipetting Template Editor.

Expressions using a combination of variables, numerical constants, and mathematical operators, may also be entered in the fields of the appropriate template steps. For example, an expression could be entered for adding a volume or delay to a variable.

To insert variables in a template step:

1. Insert a template step from the Pipetting Template Step Palette into the desired operation: Aspirate, Dispense, or Mix.

   OR

   Select a template step already configured in the current template.

2. Choose the field in which to insert a variable.
3. Enter the variable name (Table 10-1).

   Note: When entering context variables into a field, always use a double-underscore (__) between C and the variable name.

   OR

   Choose **Variables**. Preprogrammed variables arranged by groups appear.

4. Choose the desired variable group. The group variables appear.

5. Choose the desired variable (Figure 10-6). The variables listed depend on the variable group selected.

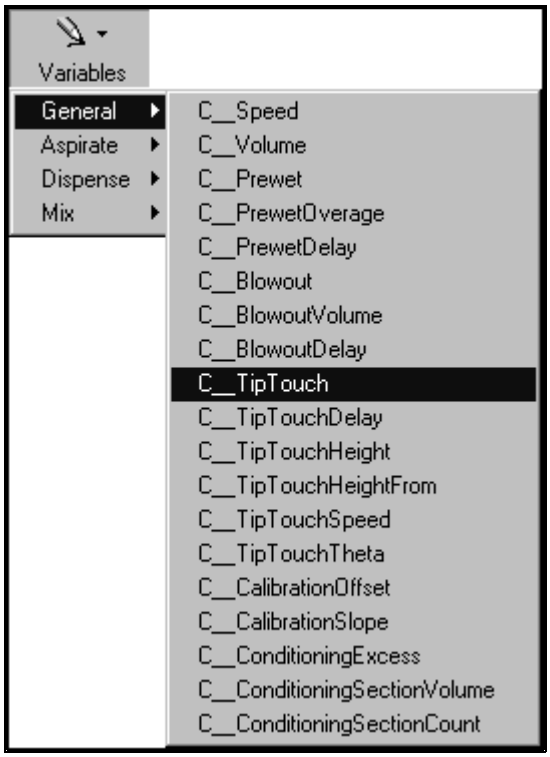


Figure 10-6. Selecting variable from selected group

6. Repeat steps 2 to 5 until the template step is configured.

Note: Refer to Section 10.5, *Configuring Pipetting Template Steps*, for more information about inserting and configuring variables in template steps.

10.3.2 Defining Context Variables

To retrieve values, context variables reference fields in the Technique Editor and Liquid Type Editor. Table 10-1 describes context variables that can be used when creating or modifying a pipetting template. Figure 10-7 and Figure 10-8 identify the fields in the Technique Editor and Liquid Type Editor from which the context variables defined in Table 10-1 reference and retrieve values.

Note: Template steps default to the most appropriate variable; however, any variable may be used in any field.

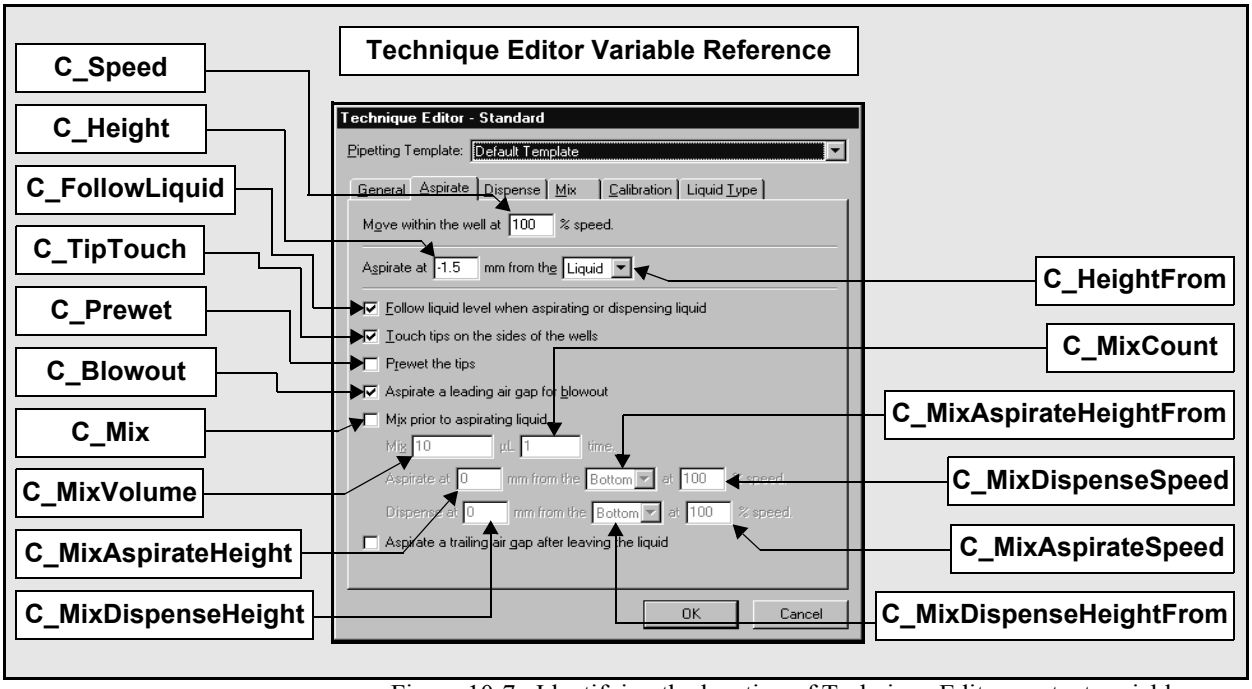


Figure 10-7. Identifying the location of Technique Editor context variables

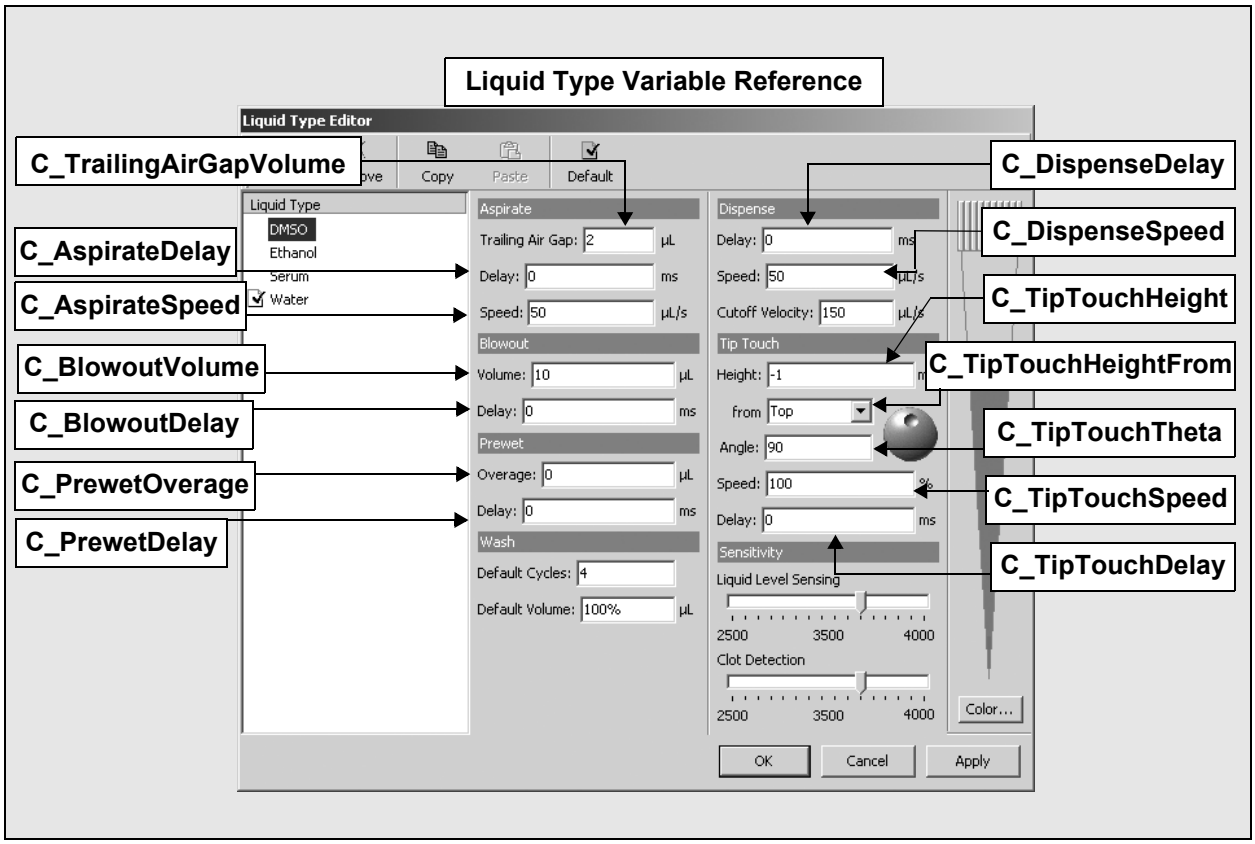


Figure 10-8. Identifying the location of Liquid Type Editor context variables

Table 10-1. Context Variables

Variable Group	Variable	Description	Associates with:
General	C__Blowout	Tells Biomek instrument to perform a blowout.	Blowout in technique
	C__BlowoutDelay	The delay in milliseconds after a blowout.	Blowout Delay in liquid type
	C__BlowoutVolume	The volume of the air gap to blow out.	Blowout Volume in liquid type or technique
	C__CalibrationOffset	Additional volume aspirated or dispensed to accurately deliver the desired volume.	Offset in technique calibration
	C__CalibrationSlope	Scaling factor used to accurately deliver the desired volume	Scaling Factor in technique calibration
	C__ConditioningExcess	Excess volume aspirated as a buffer between the system fluid and source.	Leading Conditioning Excess in technique calibration
	C__ConditioningSectionCount	Number of conditioning sections aspirated following the source.	Number of Trailing Volume Sections in technique calibration
	C__ConditioningSectionVolume	Volume of each conditioning section following the source	Trailing Conditioning Volume in technique calibration
	C__Prewet	Tells Biomek instrument to perform a prewet cycle.	Prewet in technique
	C__PrewetDelay	The delay in milliseconds from the time the Prewet volume is completely aspirated to the time it begins to dispense.	Prewet Delay in liquid type or technique
	C__PrewetOverage	The volume to add for a prewet cycle.	Prewet Overage in liquid type
	C__Speed	The speed of the pod movement (X, Y, Z axes).	Pod Speed % in technique
	C__TipTouch	Tells Biomek instrument to perform a tip touch operation.	Tip Touch in technique
	C__TipTouchDelay	The delay in milliseconds at the side of wells.	Tip Touch Delay in liquid type or technique
	C__TipTouchHeight	The height of the tip touch.	Tip Touch Height in liquid type or technique
	C__TipTouchHeightFrom	Level — top, bottom, or liquid — from which C__TipTouchHeight is measured.	Tip Touch Height, from in liquid type or technique

Table 10-1. Context Variables (Continued)

Variable Group	Variable	Description	Associates with:
General (Continued)	C__TipTouchTheta	Position along well edge tip touch occurs	Tip Touch Angle in liquid type or technique
	C__TipTouchSpeed	The speed of the pod movement.	Tip Touch Speed in technique
	C__Volume	The volume given in the pipetting operation (such as Transfer or Combine).	Volume in step configuration
	C__CDHeight	The height of the clot detection.	Clot Detection in technique.
	C__CDHeightFrom	Level—liquid, bottom, or top—from which C__CDHeight is measured	Clot Detection in technique.
	C__CDSpeed	The speed of the pod movement.	Clot Detection in technique.
Aspirate	C__AspirateDelay	The delay in milliseconds after an aspirate cycle.	Aspirate Delay in liquid type
	C__AspirateSpeed	The speed in µl/sec along the D axis for an aspirate cycle.	Aspirate Speed in liquid type
	C__TrailingAirGapVolume	The volume of the post-aspirate air gap.	Aspirate Trailing Air Gap in liquid type or technique
	C__TrailingAirGap	Tells Biomek instrument to aspirate a trailing air gap.	Trailing Air Gap in technique
Dispense	C__DispenseDelay	The delay in milliseconds after a dispense operation.	Dispense Delay in liquid type or technique
	C__DispenseSpeed	The speed in µl/sec of the D axis for a dispense operation.	Dispense Speed in liquid type or technique
Aspirate/ Dispense	C__Height	The height of the aspirate or dispense.	Aspirate at x mm in technique
	C__HeightFrom	Level—top, bottom, or liquid—from which C__Height is measured.	Aspirate x mm from (Top, Bottom, Liquid) in technique
Mix	C__Mix	Tells Biomek instrument to perform a mix operation in labware.	Mix Before Aspirate or Mix after Dispense in technique
	C__MixAspirateHeight	The height of the mix operation from the relative well location.	Aspirate at x mm in technique
	C__MixAspirateFrom	The location for the mix aspirate to occur.	In Mix Before Aspirate or Mix After Dispense and Mix, from (Top, Bottom, Liquid) in technique
	C__MixAspirateSpeed	The speed at which to aspirate for the mix cycle.	Aspirate...at x% in technique

Table 10-1. Context Variables (Continued)

Variable Group	Variable	Description	Associates with:
Mix (Continued)	C__MixCount	The number of cycles in a mix.	Number of times to Mix Before Aspirate or Mix After Dispense in technique
	C__MixDispenseHeight	The height of the mix dispense.	In Mix Before Aspirate or Mix After Dispense and Mix, from (Top, Bottom, Liquid) in technique
	C__MixDispenseFrom	The height of the mix operation from the relative well location.	In Mix, from (Top, Bottom, Liquid) in technique
	C__MixDispenseSpeed	The speed at which to dispense in a mix cycle.	Dispense...at x% in technique
	C__MixVolume	The volume of the mix.	In Mix before Aspirate and Mix After Dispense, cycles to mix at specific volume in technique

10.4 Using Volume Conditioning in Pipetting Templates (FX, NX-S8 only)

Some techniques, such as the Span-8 MultiDispense technique, use volume conditioning to achieve more precise pipetting for multiple dispenses from a single aspirate. To use volume conditioning, the pipetting template associated with that technique must be designed to use volume conditioning.

- ***FX*** — Volume conditioning is available only for a Span-8 pod.

Note: The Span-8 MultiDispense pipetting template is the only standard template that is designed to use volume conditioning. To associate the Span-8 MultiDispense pipetting template to a technique, refer to Section 10.2.2.1, *Associating a Pipetting Template with a Technique*.

There are three context variables that are important when using conditioning volumes:

- C__ConditioningExcess — the Leading Conditioning Excess from the Calibration tab of the Technique Editor
- C__ConditioningSectionVolume — the Trailing Conditioning Volume from the Calibration tab of the Technique Editor
- C__ConditioningSectionCount — the Number of Trailing Volume Sections from the Calibration tab of the Technique Editor

Note: Refer to the *Biomek Software User's Manual,* Section 9.6, *Conditioning Techniques for Multiple Dispense (FX, NX-S8 only)* for more information on conditioning volumes.

10.4.1 About ListMath

Since a Span-8 Pod is capable of aspirating and dispensing up to eight separate volumes, the pipetting template must accommodate this ability. ListMath is a special set of commands that can be entered in a pipetting template step configuration used to perform mathematical operations uniformly through a list.

ListMath takes two parameters and returns a list of values after performing the specified operation. A parameter may be a variable, a constant, or an array of constants or variables.

In the Span-8 MultiDispense pipetting template, ListMath is used to calculate the volume to aspirate by adding:

- The total volume needed to perform all the desired dispense operations, as entered in the step configuration.
- The Leading Conditioning Excess volume, plus 15 percent of the total volume needed to perform all the desired dispense operations.
- The Trailing Conditioning Volume times the Number of Trailing Volume Sections.

The result of the above operations is a volume for each probe.

Use ListMath like a variable when configuring a template step. Always start with an equal sign (=).

- To add two parameters, enter **=ListMath.Add(Parameter1, Parameter2)**. Parameter2 is added to Parameter1.
- To subtract two parameters, enter **=ListMath.Sub(Parameter1, Parameter2)**. Parameter2 is subtracted from Parameter1.
- To multiply two parameters, enter **=ListMath.Mult(Parameter1, Parameter2)**. Parameter1 is multiplied by Parameter2.
- To divide two parameters, enter **=ListMath.Div(Parameter1, Parameter2)**. Parameter1 is divided by Parameter2.

10.5 Configuring Pipetting Template Steps

A pipetting template contains template steps that create the pipetting procedure. Steps are configured using context variables (Table 10-1) that retrieve information from the Technique Editor or Liquid Type Editor, or variables configured in a Start, Let, or Worklist configuration. The following conventions apply:

- All template steps, excluding Prewet, may be placed in any part of the pipetting process. Prewet is applicable only to Aspirate operations and is limited to the Aspirate process.
- Any variable defined in the system or method, including those defined in the Start, Let, or Worklist configurations, may be used to configure template steps.
- When using variables defined in Start, Let, and Worklist in a pipetting template, the template is useful only to those methods with the same variable names defined.
- The template steps are available for use in the Pipetting Template Editor only.
- When a step is inserted into the pipetting template, each field is configured with the most appropriate context variable by default. These default values may be changed to any desired value, variable, or expression.
- Hovering the mouse pointer over a template step button displays a tool tip with the name of the template step. Some steps also display information about the default configuration for that step.

10.5.1 If, Comment, and Loop

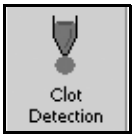
The If, Comment, and Loop steps are available for use in both methods and pipetting templates. When creating a pipetting template using these steps, configure the steps in the same manner as when configuring the step in the Method View.

Note: For more information, refer to Section 17.7, *If Step*; refer to Section 15.6, *Comment Step*; and refer to Section 16.9.1, *Configuring a Loop Step and Creating a New Variable*.

10.5.2 Clot Detection (NX-S8 only)

Clot Detection allows heights for clot detection to be configured. The template step sets the Move to height after aspiration; height measured from the liquid, bottom, or top of the well; and speed for clot detection. The heights are used to determine the difference in capacitance which indicates a clot exists.

Note: Clot Detection is usually used immediately after an Aspirate steplet.



To configure Clot Detection:

1. Insert **Clot Detection** in the desired pipetting operation of the template. The template step configuration appears (Figure 10-9)

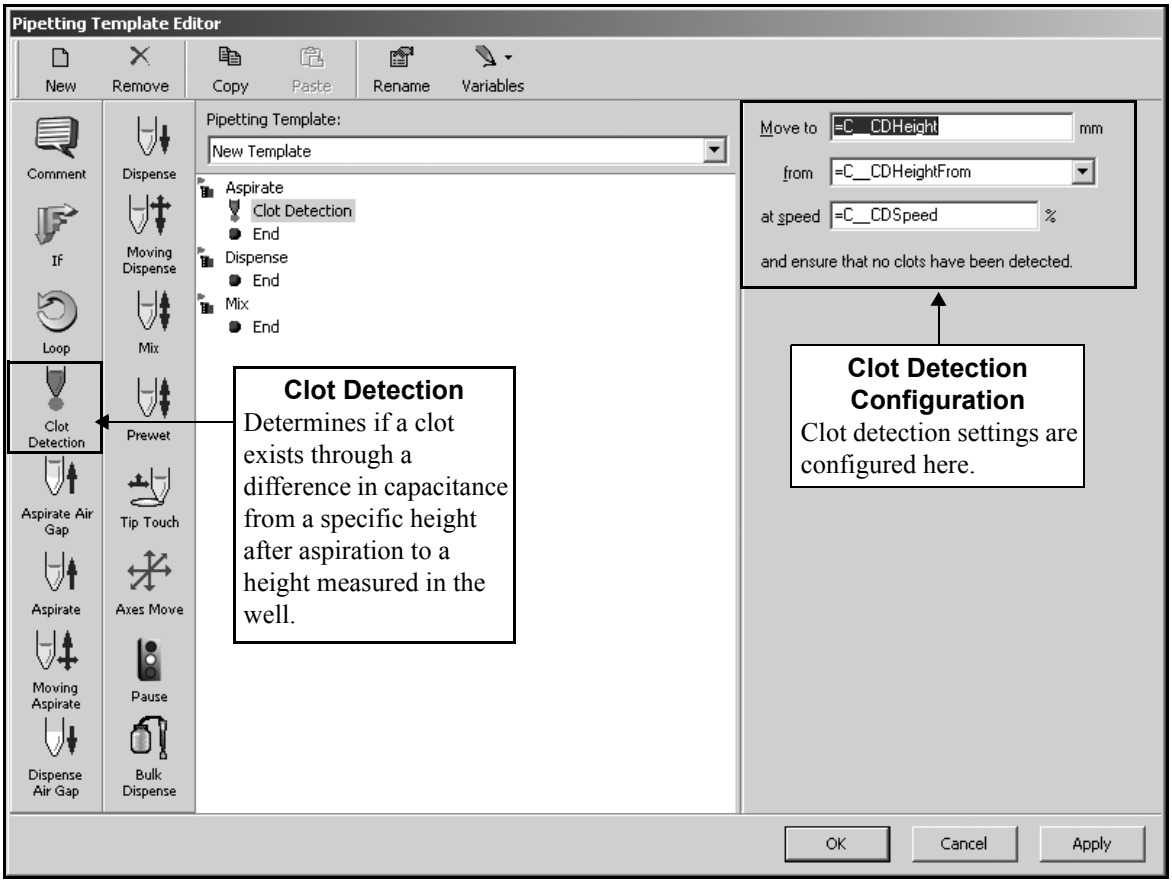


Figure 10-9. Clot Detection step configuration

2. In **Move to**, enter the variable or value to specify the desired height, in millimeters (mm), after aspiration. The default value for this field is the context variable **C_CDHeight**. (Refer to Table 10-1 for a definition of this context variable.)

3. In from, select from where to measure the height in the well: **Liquid**, **Bottom**, or **Top**. The default value for this field is the context variable **C_CDHeightFrom**. (Refer to Table 10-1 for a definition of this variable.)

   Note: Liquid measures from the top of the liquid, Bottom measures from the bottom of the well and Top measures from the top of the well.

   Note: If Liquid is selected in C_CDHeightFrom, the liquid level of the well must be known by the time clot detection is executed, either marked as known in Labware Properties or successfully liquid level sensed.

4. In **at speed**, enter the variable or value to specify the speed of the pod during clot detection as a percentage of the maximum speed of the pod. The default value for this field is the context variable **C_CDSpeed**. (Refer to Table 10-1 for a definition of this variable.)

10.5.3 Aspirate Air Gap

Aspirate Air Gap aspirates an air gap at a specific volume and speed before liquid is aspirated. If a delay between the air gap aspirate and subsequent steps is desired, configure a delay into the template step.

Aspirate Air Gap can be used to aspirate a leading air gap before aspirating liquid, or a trailing air gap after aspirating liquid, depending on where it is inserted in the template.

To configure Aspirate Air Gap:

1. Insert **Aspirate Air Gap** in the desired pipetting operation of the template. The template step configuration appears (Figure 10-10).

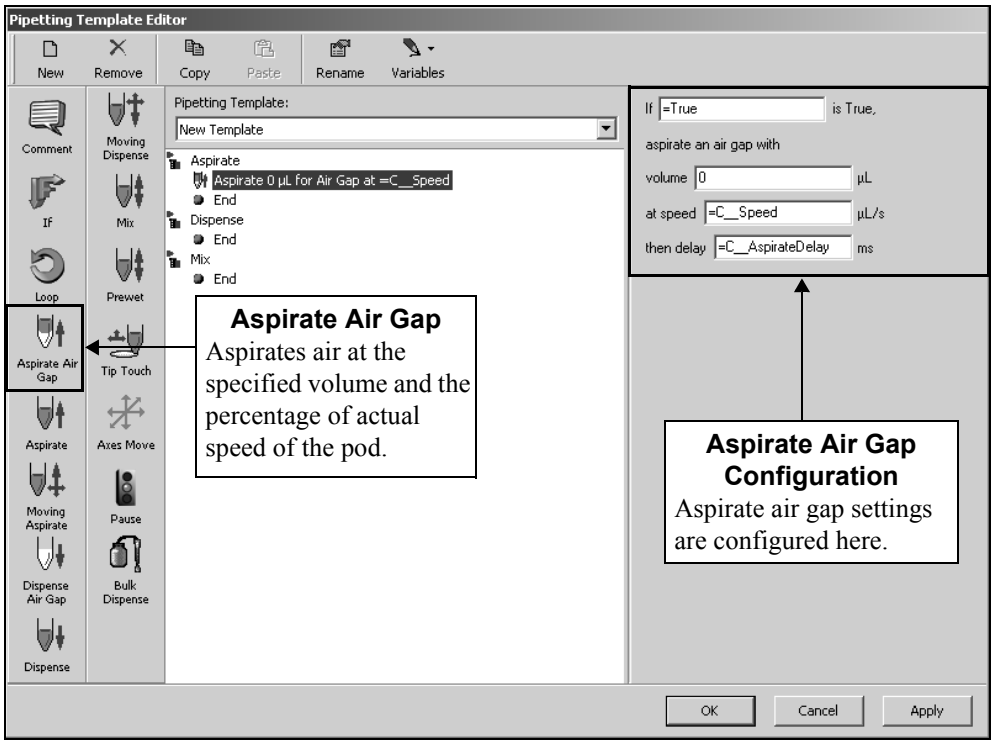


Figure 10-10. Aspirate Air Gap step configuration

2. Enter the variable to configure the **If** condition. When the variable entered is True, an air gap is aspirated. The default value, **=True**, always aspirates an air gap.
3. In **volume**, enter the variable or value to specify the amount of air to aspirate for the air gap in microliters (µL). The default value is **0** µL.

4. In **speed**, enter the variable or value to specify the speed of the pod in the D-axis in microliters per second (µl/sec) during the aspirate operation. The default value is the context variable **C__Speed**. (Refer to Table 10-1 for a definition of this variable.)

5. In **delay**, enter the variable or value to specify the length of the delay in milliseconds (ms) after aspirating an air gap. The pod pauses for the specified duration before continuing with the next operation. The default value for this field is the context variable **C__AspirateDelay**. (Refer to Table 10-1 for a definition of this variable.)

10.5.4 Aspirate

Aspirate aspirates a specific volume at a speed specified in microliters per second (µl/sec). To pause for a specific amount of time after aspirating, add a delay to the Aspirate template step.

To configure Aspirate:

1. Insert **Aspirate** at the desired position. The template step configuration appears (Figure 10-11).

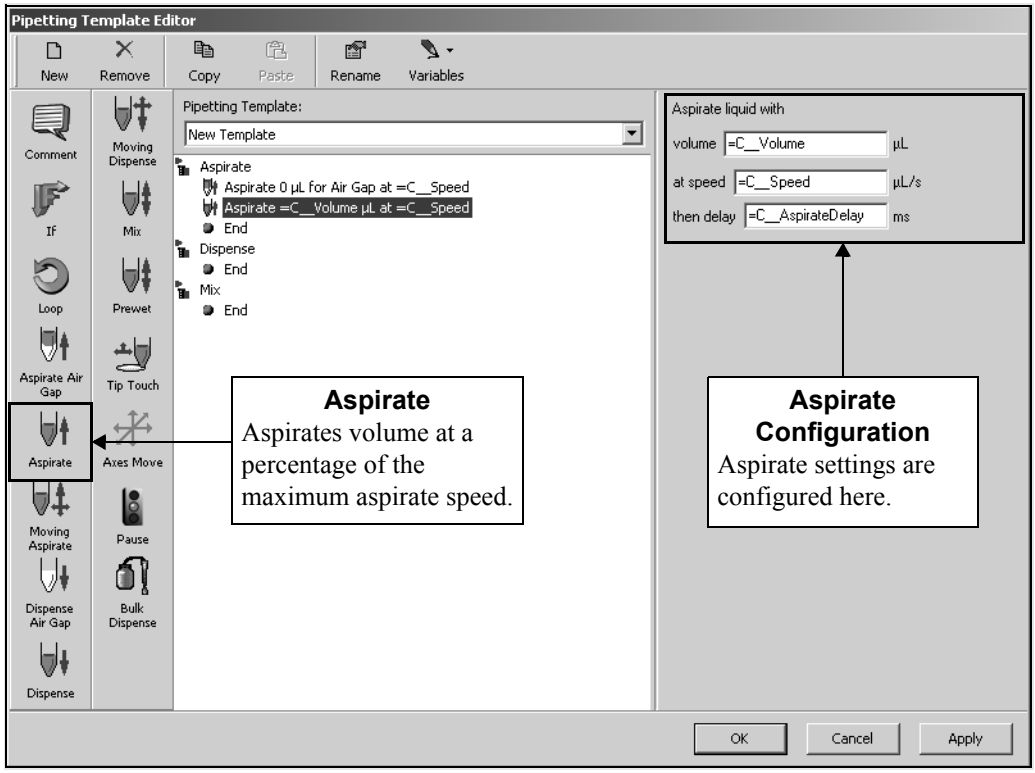


Figure 10-11. Aspirate step configuration

2. In **volume**, enter the variable or value to specify the volume of liquid to aspirate in microliters (µL). The default value for this field is the context variable **C__Volume**. (Refer to Table 10-1 for a definition of this variable.)

3. In **speed**, enter the variable or value to specify the speed of the pod in the D-axis in microliters per second (µl/sec) during the aspirate operation. The default value for this field is the context variable **C__Speed**. (Refer to Table 10-1 for a definition of this variable.)
4. In **delay**, enter the variable or value to specify the length of the delay in milliseconds (ms) after the aspirate operation. The pod pauses for the specified duration before continuing with the next operation. The default value for this field is the context variable **C__AspirateDelay**. (Refer to Table 10-1 for a definition of this variable.)

10.5.5 Moving Aspirate

Moving Aspirate aspirates while tips are moving within a well. The template step sets the initial position, final position, and a specific volume for the aspiration.

To configure Moving Aspirate:

1. Insert **Moving Aspirate** into the pipetting method. The template step configuration appears (Figure 10-12).

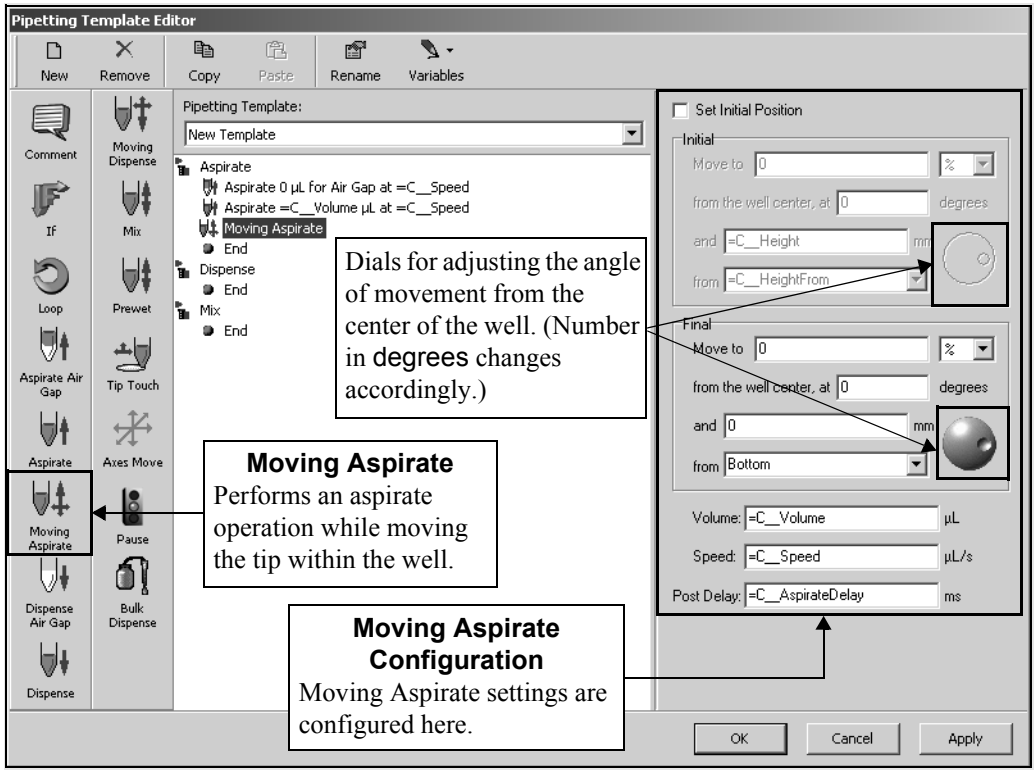


Figure 10-12. Moving Aspirate step configuration

2. Check **Set Initial Position** to set the start position for aspirate, if desired.

Note: Set Initial Position is used if an aspirate must begin at a specific well location on the labware. If this is not set, the pod moves from its current location. Set Initial Position is not selected by default.

If Set Initial Position is checked, complete the following steps to configure Initial position parameters:

1. In **Move to**, enter the variable or value to specify where within the well the aspirate operation begins, either as a percentage of the distance from the center of the well to the well edge or in centimeters (cm). The default for this field is **0**.
2. Select the units for the variable or value entered in **Move to**: % (percentage) or cm (centimeters). The default value for this field is **%**.
3. In **from the well center, at**, enter the variable or value to specify the angle at which the Move to measurement is performed.

   OR

   In the graphic representing the well, position the dial at the desired angle at which the Move to measurement is performed. The value in from the well center, at displays the current angle, in degrees. The default value for the angle is **0** degrees.
4. In **and**, enter the variable or value to specify the height of the tip, in millimeters (mm). The default value for this field is the context variable **C__Height**. (Refer to Table 10-1 for a definition of this variable.)
5. In **from**, enter the variable or value to specify from where the height in and is measured. The default value for this field is the context variable **C__HeightFrom**. (Refer to Table 10-1 for a definition of this variable.)

To configure the Final position parameters:

1. In **Move to**, enter the variable or value to specify where within the well the aspirate operation moves, either as a percentage of the distance from the center of the well to the well edge or in centimeters (cm). The default for this field is **0**.
2. Select the units for the variable or value entered in **Move to**: % (percentage) or cm (centimeters). The default value for this field is **%**.
3. In **from the well center, at**, enter the variable or value to specify the angle at which the Move to measurement is performed. The default value for the angle is **0** degrees.

   OR

   In the graphic representing the well, position the dial at the desired angle at which the Move to measurement is performed. The value in from the well center, at displays the current angle, in degrees.
4. In **and**, enter the variable or value to specify the height of the tip, in millimeters (mm). The default for this field is **0** mm.
5. In **from**, enter the variable or value to specify from where the height in and is measured. The default for this field is **Bottom**.

To complete the Moving Aspirate configuration:

1. In Volume, enter the variable or value to specify the volume of liquid to aspirate, in microliters (µL). The default value for this field is the context variable **C__Volume**. (Refer to Table 10-1 for a definition of this variable.)
2. In **Speed**, enter the variable or value to specify the speed of the pod in the D-axis in the D-axis in microliters per second (µl/sec) during the moving aspirate operation. The default value for this field is the context variable **C__Speed**. (Refer to Table 10-1 for a definition of this variable.)
3. In **Post Delay**, enter the variable or value to specify the length of the delay in milliseconds (ms) after the aspirate operation. The pod pauses for the specified duration before continuing with the next operation. The default value for this field is the context variable **C__AspirateDelay**. (Refer to Table 10-1 for a definition of this variable.)

10.5.6 Dispense Air Gap

Dispense Air Gap dispenses an air gap at a specified speed and allows a delay before further operations occur. Dispensing an air gap is sometimes called a *blowout* because it blows out the leading air gap.

Dispense Air Gap can be used to dispense a trailing or leading air gap, depending on where within the pipetting template it is inserted.

To configure Dispense Air Gap:

1. Insert **Dispense Air Gap** into the pipetting method. The template step configuration appears (Figure 10-13).

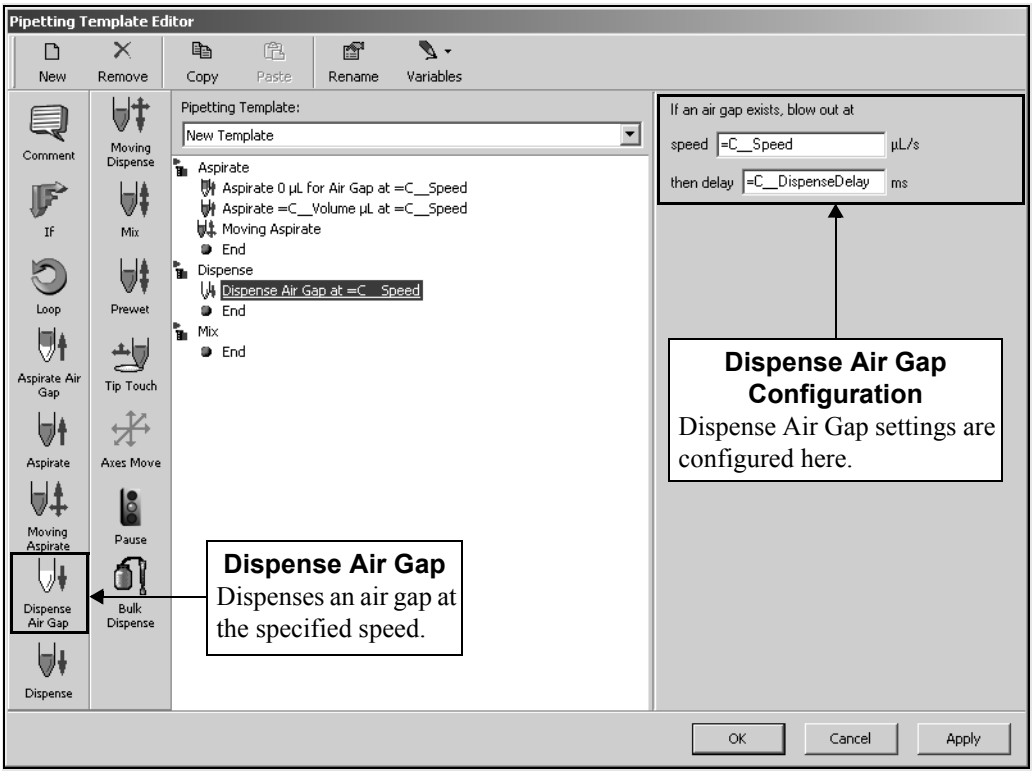


Figure 10-13. Dispense Air Gap step configuration

2. In **speed**, enter the variable or value to specify the speed of the pod in the D-axis in microliters per second (µl/sec) during the blowout. The default value for this field is the context variable **C__Speed**. (Refer to Table 10-1 for a definition of this variable.)
3. In **delay**, enter the variable or value to specify the length of the delay in milliseconds (ms) after the blowout. The pod pauses for the specified duration before continuing with the next operation. The default value for this field is the context variable **C__DispenseDelay**. (Refer to Table 10-1 for a definition of this variable.)

10.5.7 Dispense

Dispense dispenses a specific volume at a speed specified in microliters per second (µl/sec). To pause for a specific amount of time after dispensing, add a delay to the Dispense template step.

To configure Dispense:

1. Insert **Dispense** into the pipetting method. The template steps configuration appears (Figure 10-14).

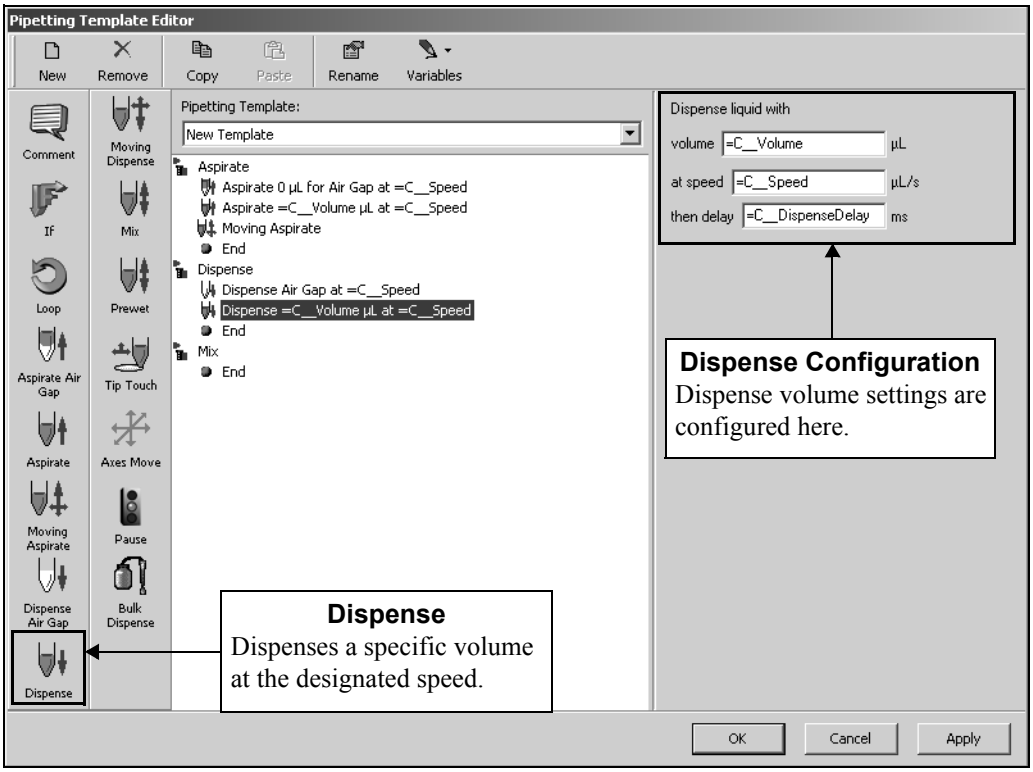


Figure 10-14. Dispense step configuration

2. In **volume**, enter the variable or value to specify the volume of liquid to dispense in microliters (µL). The default value for this field is the context variable **C__Volume**. (Refer to Table 10-1 for a definition of this variable.)

3. In **speed**, enter the variable or value to specify the speed of the pod during the dispense operation as a percentage of the maximum speed of the pod. The default value for this field is the context variable **C__Speed**. (Refer to Table 10-1 for a definition of this variable.)
4. In **delay**, enter the variable or value to specify the length of the delay in milliseconds (ms) after the dispense operation. The pod pauses for the specified duration before continuing. The default value for this field is the context variable **C__DispenseDelay**. (Refer to Table 10-1 for a definition of this variable.)

10.5.8 Moving Dispense

Moving Dispense dispenses a specific volume of liquid while moving between positions relative to the center of the well.

To configure Moving Dispense:

1. Insert **Moving Dispense** into the pipetting method. The template step configuration appears (Figure 10-15).

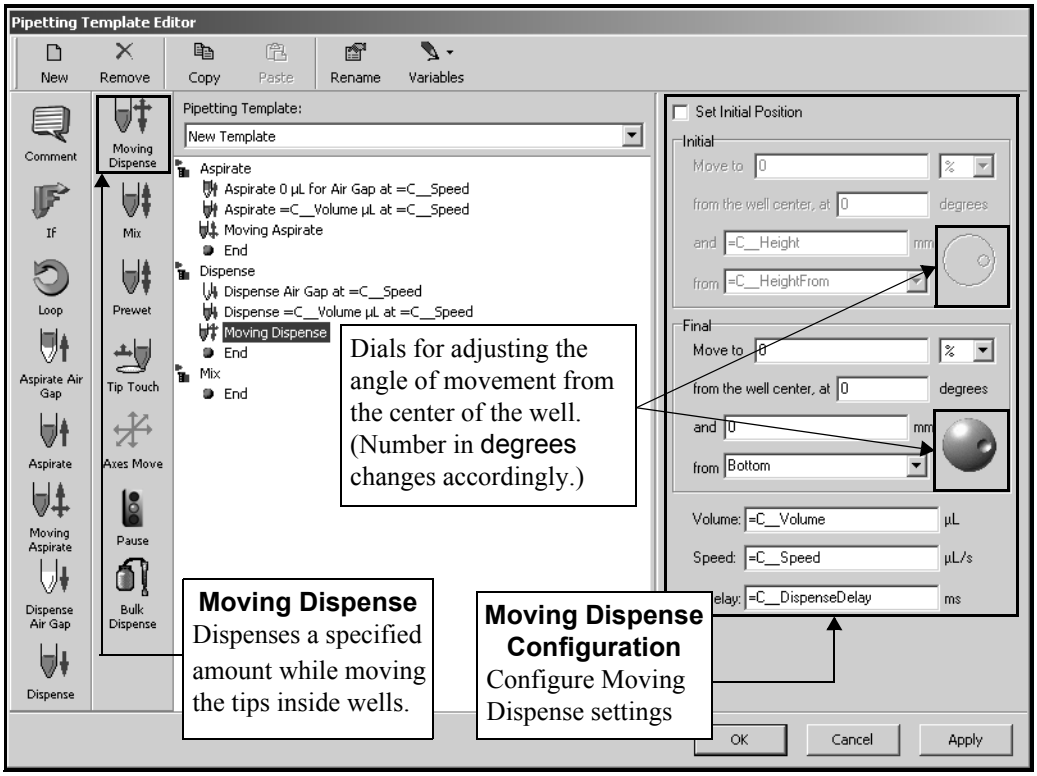


Figure 10-15. Moving Dispense step configuration

2. Check **Set Initial Position** to set the start position for dispense, if desired.

Note: Set Initial Position is used if a dispense must begin at a specific well location on the labware. If this is not set, the pod moves from its current location. Set Initial Position is not selected by default.

If Set Initial Position is checked, complete the following steps to configure Initial position parameters:

1. In **Move to**, enter the variable or value to specify where within the well the dispense operation begins, either as a percentage of the distance from the center of the well to the well edge or in centimeters (cm). The default for this field is **0**.
2. Select the units for the variable or value entered in **Move to**: % (percentage) or cm (centimeters). The default value for this field is **%**.
3. In **from the well center, at**, enter the variable or value to specify the angle at which the Move to measurement is performed. The default value for the angle is **0** degrees.

   OR

   In the graphic representing the well, position the dial at the desired angle at which the Move to measurement is performed. The value in from the well center, at displays the current angle, in degrees.
4. In **and**, enter the variable or value to specify the height of the tip, in millimeters (mm). The default value for this field is the context variable **C__Height**. (Refer to Table 10-1 for a definition of this variable.)
5. In **from**, enter the variable or value to specify from where the height in and is measured. The default value for this field is the context variable **C__HeightFrom**. (Refer to Table 10-1 for a definition of this variable.)

To configure the Final position parameters:

1. In **Move to**, enter the variable or value to specify where within the well the dispense operation moves, either as a percentage of the distance from the center of the well to the well edge or in centimeters (cm). The default for this field is **0**.
2. Select the units for the variable or value entered in **Move to**: % (percentage) or cm (centimeters). The default value for this field is **%**.
3. In **from the well center, at**, enter the variable or value to specify the angle at which the Move to measurement is performed. The default value for the angle is **0** degrees.

   OR

   In the graphic representing the well, position the dial at the desired angle at which the Move to measurement is performed. The value in from the well center, at displays the current angle, in degrees.
4. In **and**, enter the variable or value to specify the height of the tip, in millimeters (mm). The default for this field is **0** mm.
5. In **from**, enter the variable or value to specify from where the height in and is measured. The default for this field is **Bottom**.

To complete the Moving Dispense configuration:

1. In **Volume**, enter the variable or value to specify the volume of liquid to dispense, in microliters (µL). The default value for this field is the context variable **C__Volume**. (Refer to Table 10-1 for a definition of this variable.)
2. In **Speed**, enter the variable or value to specify the speed of the pod in the D-axis in microliters per second (µl/sec) during the moving dispense operation.The default value for this field is the context variable **C__Speed**. (Refer to Table 10-1 for a definition of this variable.)
3. In **Post Delay**, enter the variable or value to specify the length of the delay in milliseconds (ms) after the dispense operation. The pod pauses for the specified duration before continuing. The default value for this field is the context variable **C__DispenseDelay**. (Refer to Table 10-1 for a definition of this variable.)

10.5.9 Mix

Mix aspirates and dispenses liquid in wells of labware as a mixing operation.

Note: This template step performs operations only when Mix is selected in the Technique Editor for the technique being used during method run.

To configure Mix:

1. Insert **Mix** into the pipetting method. The template steps configuration appears (Figure 10-16).

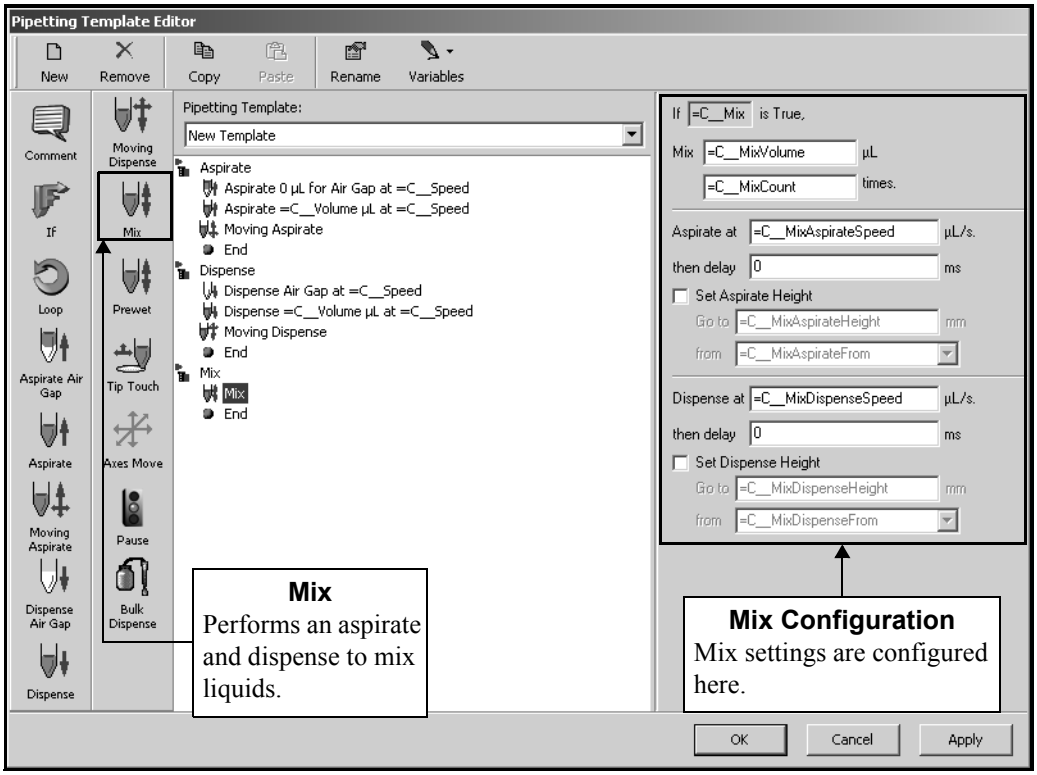


Figure 10-16. Mix step configuration

2. In **Mix**, enter the variable or value to specify the volume of liquid to mix, in microliters (µL). The default value for this field is the context variable **C__MixVolume**. (Refer to Table 10-1 for a definition of this variable.)
3. In **times**, enter the variable or value to specify the number of times to mix the liquid. The default value for this field is the context variable **C__MixCount**. (Refer to Table 10-1 for a definition of this variable.)
4. In **Aspirate at**, enter the variable or value to specify the speed of the pod in the D-axis in microliters per second (µl/sec) for the aspirate operation. The default value for this field is the context variable **C__MixAspirateSpeed**. (Refer to Table 10-1 for a definition of this variable.)
5. In **then delay**, enter the variable or value to specify the length of the delay in milliseconds (ms) after the mix operation. The pod pauses for the specified duration before continuing with the next operation. The default value for this field is **0** ms.
6. Check **Set Aspirate Height** to enter the variable or expression for the height of the tips during aspiration.

   Note: If Set Aspirate Height is not selected, the mix operation occurs at the current height and the tips do not move vertically before aspirating.

7. In **Go to**, enter the variable or value to specify the height of the tip for the aspirate operations, in millimeters (mm). The default value for this field is the context variable **C__MixAspirateHeight**. (Refer to Table 10-1 for a definition of this variable.)
8. In **from**, enter the variable or value to specify from where the height in Go to is measured. The default value for this field is the context variable **C__MixAspirateFrom**. (Refer to Table 10-1 for a definition of this variable.)
9. In **Dispense at**, enter the variable or value to specify the speed of the pod in the D-axis in microliters per second (µl/sec) for the dispense operation. The default value for this field is the context variable **C__MixDispenseSpeed**. (Refer to Table 10-1 for a definition of this variable.)
10. In **then delay**, enter the variable or value to specify the length of the delay in milliseconds (ms) after the mix operation. The pod pauses for the specified duration before continuing with the next operation. The default value for this field is **0** ms.
11. Check **Set Dispense Height** to enter the variable or expression for the height of the tips during dispense.

    Note: If Set Dispense Height is not selected, the mix operation occurs at the current height and the tips do not move vertically before dispensing.

12. In **Go to**, enter the variable or value to specify the height of the tip for the dispense operations, in millimeters (mm). The default value for this field is the context variable **C__MixDispenseHeight**. (Refer to Table 10-1 for a definition of this variable.)
13. In **from**, enter the variable or value to specify from where the height in Go to is measured. The default value for this field is the context variable **C__MixDispenseFrom**. (Refer to Table 10-1 for a definition of this variable.)

10.5.10 Prewet

Prewet aspirates, then dispenses the liquid to prepare tips for the main aspiration. Prewet should only be used in the Aspirate operation of a pipetting template. The delay occurs between the aspirate and dispense of the Prewet.

Note: This template step performs operations only when Prewet is selected in the Technique Editor for the technique being used during method run.

To configure Prewet:

1. Insert **Prewet** into the pipetting method. The template steps configuration appears (Figure 10-17).

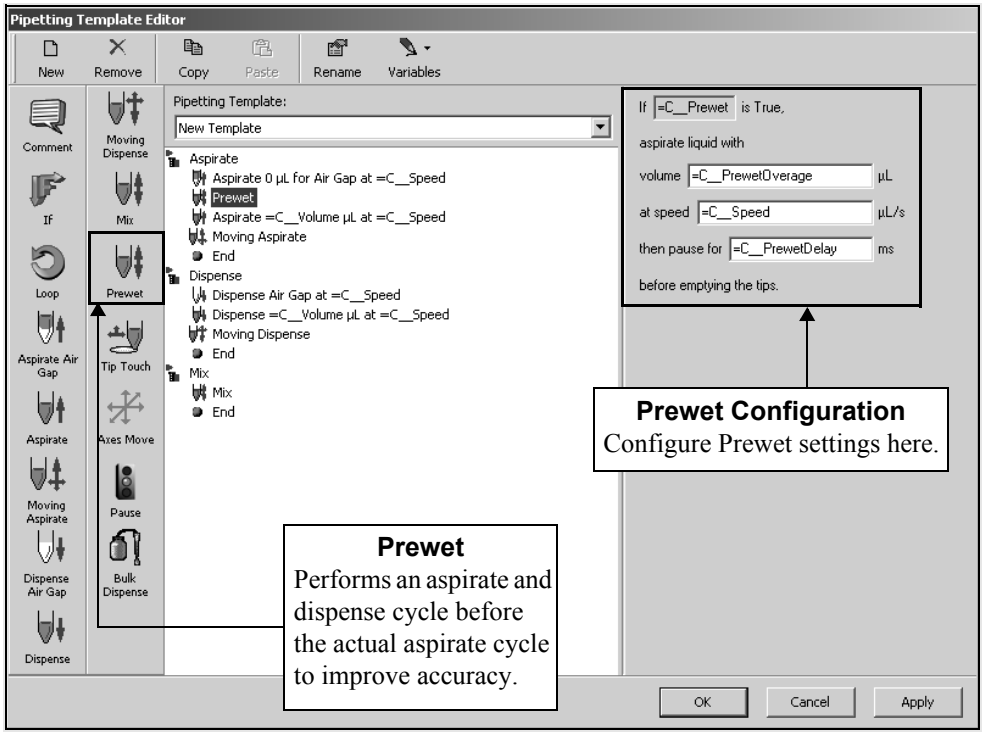


Figure 10-17. Prewet step configuration

2. In **volume**, enter the variable or value to specify the volume of liquid used to prewet the tips. The default value for this field is the context variable **C__PrewetOverage**. (Refer to Table 10-1 for a definition of this variable.)
3. In **speed**, enter the variable or value to specify the speed of the pod in the D-axis in microliters per second (µl/sec) during the prewet operation. The default value for this field is the context variable **C__Speed**. (Refer to Table 10-1 for a definition of this variable.)
4. In pause, enter the length of time to delay between aspirating and dispensing the prewet liquid. The pod pauses for the specified duration after aspirating the prewet liquid and before dispensing the prewet liquid. The default value for this field is the context variable **C__PrewetDelay**. (Refer to Table 10-1 for a definition of this variable.)

10.5.11 Tip Touch

If Tip Touch is selected in the technique, the tip touches the side of the well and performs any specified delays. The tip then moves back to the center of the well.

Note: This template step performs operations only when Tip Touch is selected in the Technique Editor for the technique being used during method run.

To configure Tip Touch:

1. Insert **Tip Touch** into the pipetting method. The template step configuration appears (Figure 10-18).

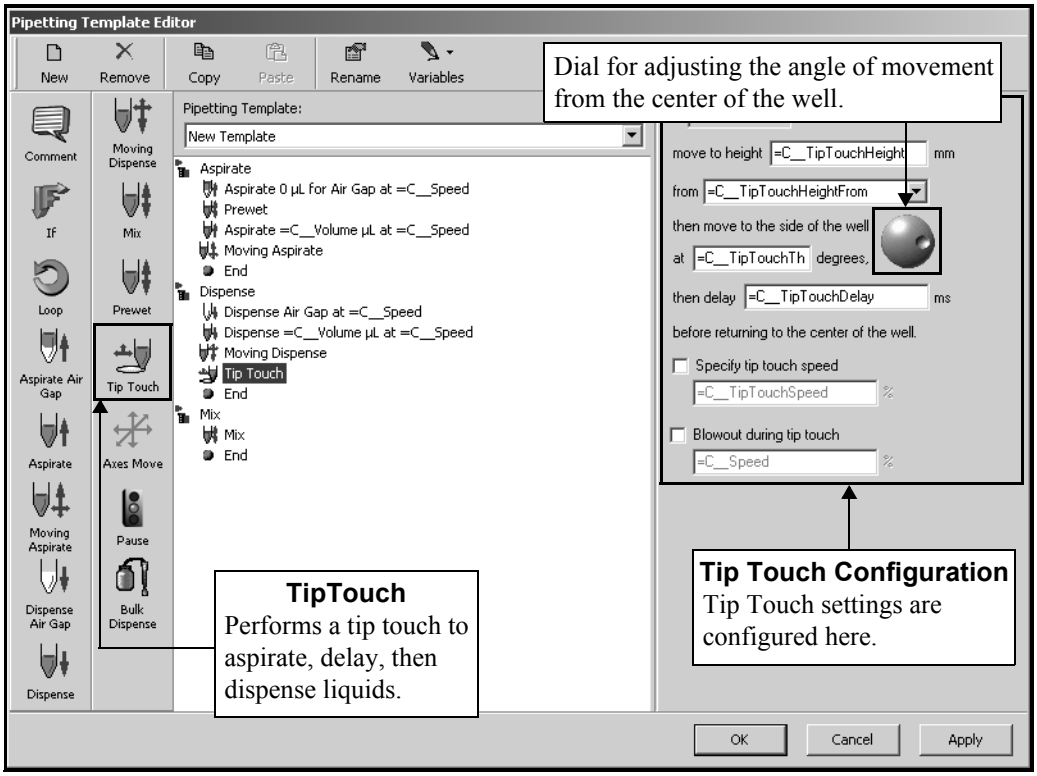


Figure 10-18. Tip Touch step configuration

2. In **move to height**, enter the variable or value to specify the desired height, in millimeters (mm), at which to touch the well edge. The default value for this field is the context variable **C__TipTouchHeight**. (Refer to Table 10-1 for a definition of this variable.)
3. In **from**, enter the variable or value to specify from where the move to height is measured for the tip touch location. The default value for this field is the context variable **C__TipTouchHeightFrom**. (Refer to Table 10-1 for a definition of this variable.)

4. In **at**, enter the desired variable or value to specify the angle along the well edge at which to touch. The default value for the angle is the context variable **C__TipTouchTheta**. (Refer to Table 10-1 for a definition of this variable.)

   OR

   In the graphic representing the well, position the dial at the desired angle at which the Move to measurement is performed. The value in from the well center, at displays the current angle, in degrees.

5. In **then delay**, enter the variable or value to specify the length of the delay before returning to the center of the well. The default value for this field is **0** milliseconds (ms).

6. To control the tip touch speed, check **Specify tip touch speed**.

   Note: If Specify tip touch speed is not selected, the tip touch operation occurs at the operation speed as defined in the technique.

7. In the text box below Specify tip touch speed, enter the variable or value to specify the speed of the pod during the tip touch operation as a percentage of the maximum speed of the pod. The default value for this field is the context variable **C__TipTouchSpeed**. (Refer to Table 10-1 for a definition of this variable.)

8. To add a blowout, check **Blowout during tip touch**.

   Note: The blowout occurs during the vertical move configured at the beginning of the tip touch.

9. In the text box below Blowout during tip touch, enter the variable or value to specify the speed of the pod during the blowout operation as a percentage of the maximum speed of the pod. The default value for this field is the context variable **C__Speed**. (Refer to Table 10-1 for a definition of this variable.)

10.5.12 Axes Move

Axes Move moves the tips to a defined place within a well. For example, the template steps may move the tips 10% from the well center and 90 degrees around the edge of the well.

To configure Axes Move:

1. Insert **Axes Move** into the pipetting method. The template step configuration appears (Figure 10-19).

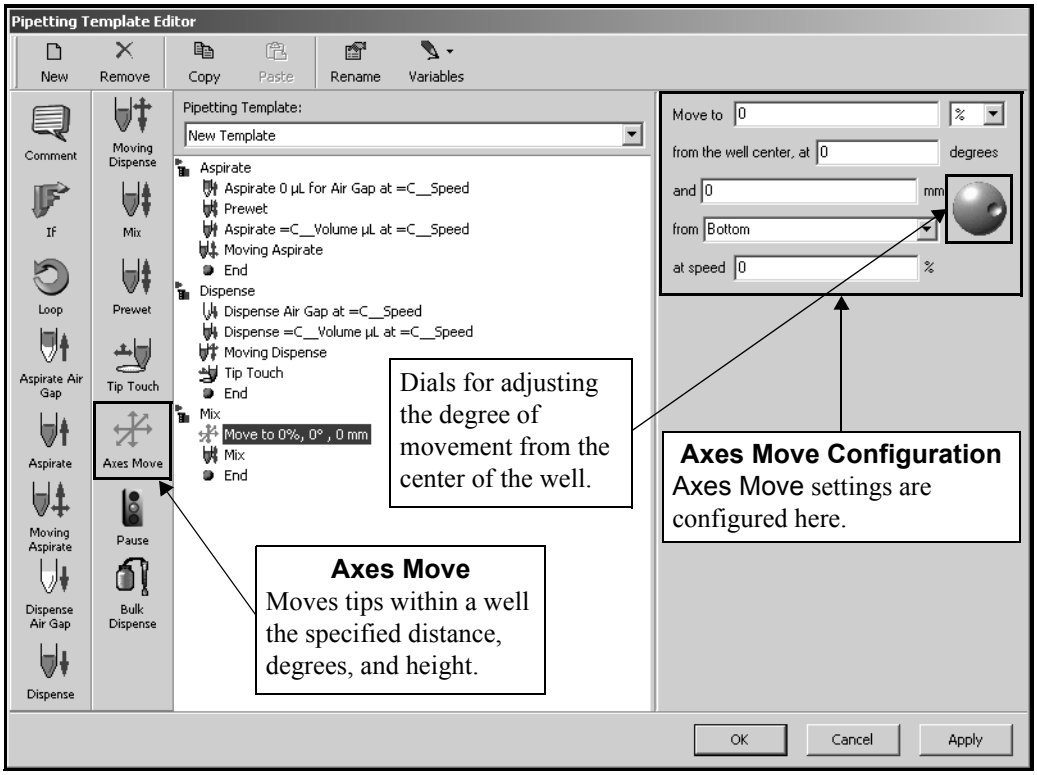


Figure 10-19. Axes Move step configuration

2. In **Move to**, enter the variable or value to specify where within the well to move the tip, either as a percentage of the distance from the center of the well to the well edge or in centimeters (cm). The default for this field is **0**.
3. Select the units for the variable or value entered in **Move to**: % (percentage) or cm (centimeters). The default value for this field is **%**.
4. In **from the well center, at**, enter the variable or value to specify the angle at which the Move to measurement is performed. The default value for the angle is **0** degrees.

   OR

   In the graphic representing the well, position the dial at the desired angle at which the Move to measurement is performed. The value in from the well center, at displays the current angle, in degrees.

5. In **and**, enter the variable or value to specify the height of the tip, in millimeters (mm). The default value for this field is **0** mm.
6. In **from**, enter the variable or value to specify from where the height in and is measured. The default value for this field is **Bottom**.
7. In **at speed**, enter the variable or value to specify the speed of the pod during the axes move as a percentage of the maximum speed of the pod. The default value for this field is **0**%.

10.5.13 Pause

Pause allows the template to stop operations temporarily. Pause is configured in milliseconds only.

To configure Pause:

1. Insert the **Pause** template steps into the pipetting method. The template steps configuration appears (Figure 10-20).

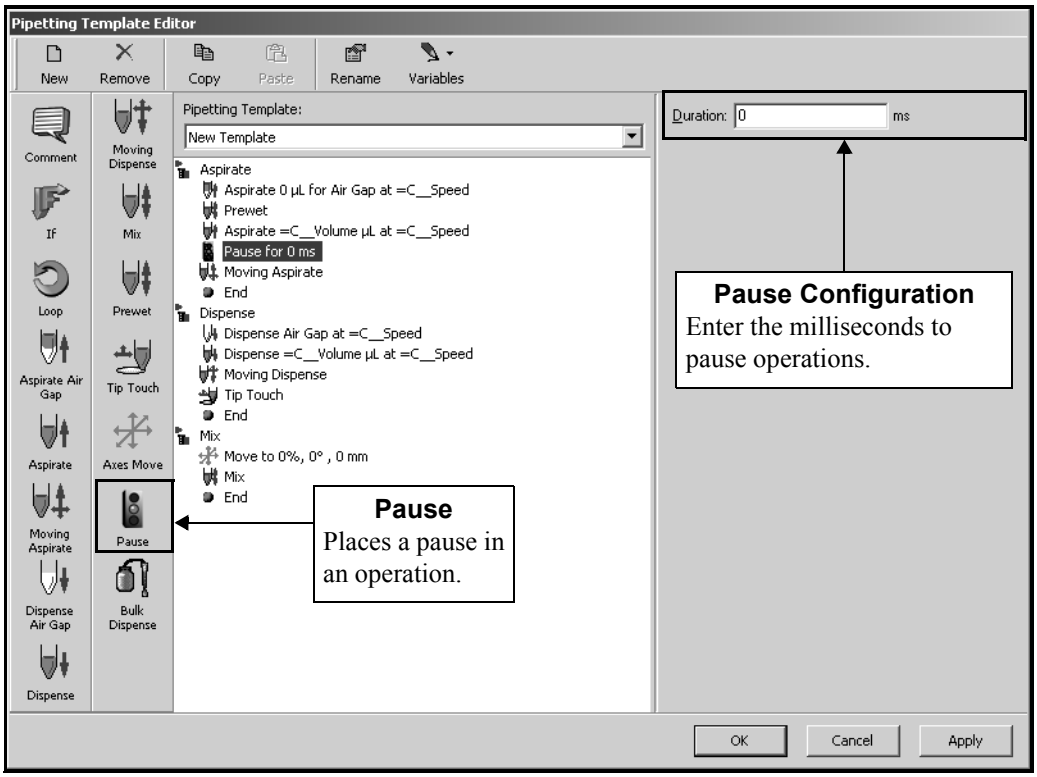


Figure 10-20. Pause step configuration

2. In **Duration**, enter the variable or value for the length of the pause, in milliseconds (ms). The default value for this field is **0** ms.

10.5.14 Bulk Dispense (FX and NX-S8 only)

Bulk Dispense dispenses system fluid through the system tubing using the tips and syringes of the Span-8 Pod.

To configure Bulk Dispense:

1. Insert **Bulk Dispense** into the pipetting method. The template step configuration appears (Figure 10-21).

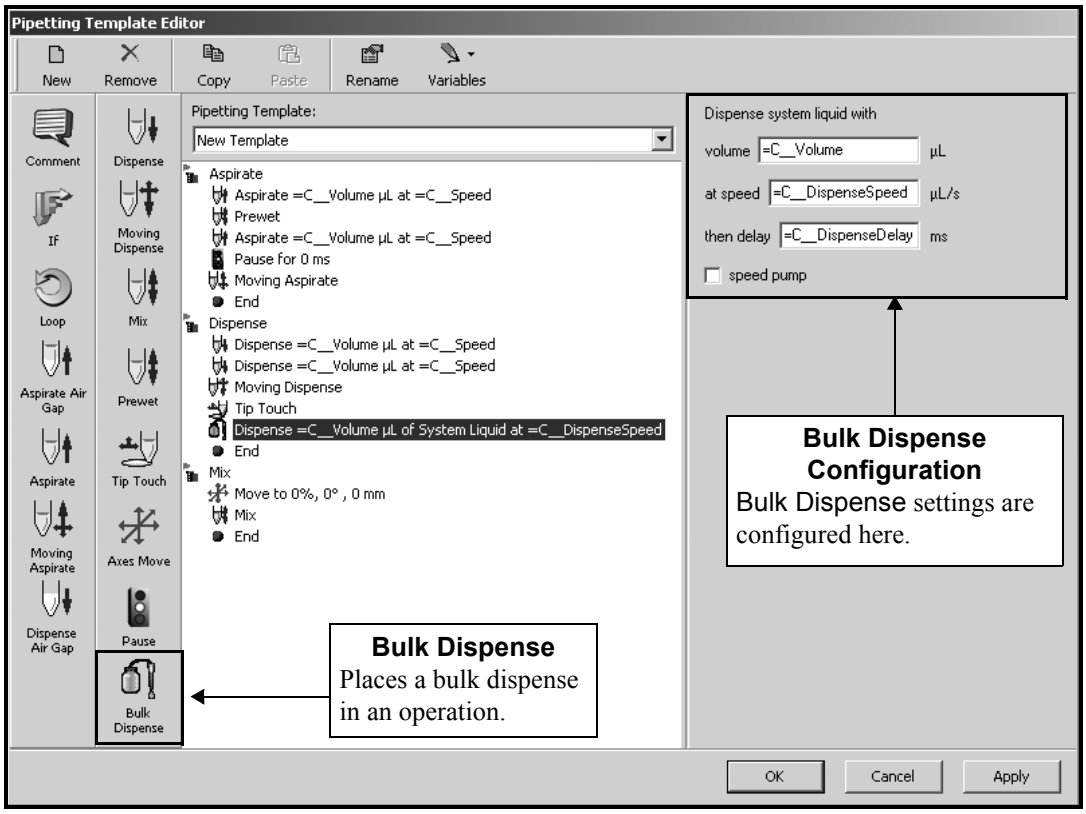


Figure 10-21. Bulk Dispense step configuration

2. In **volume**, enter the variable or value to specify the amount of system fluid to dispense, in microliters (µL). The default value for this field is the context variable **C__Volume**. (Refer to Table 10-1 for a definition of this variable.)

3. In **speed**, enter the variable or value to specify the speed of the pod in microliters per second (µl/sec) during the bulk dispense operation. The default value for this field is the context variable **C__Speed**. (Refer to Table 10-1 for a definition of this variable.)
4. In **delay**, enter the variable or value to specify the length of the delay in milliseconds (ms) after the bulk dispense operation. The pod pauses for the specified duration before continuing with the next operation. The default value for this field is the context variable **C__DispenseDelay**. (Refer to Table 10-1 for a definition of this variable.)
5. Depending on instrument configuration, speed pump or purge pump appears.
   - ***FX*** — Choose **speed pump** to use this optional device.
   - ***NX-S8*** — Choose **purge pump** to use it.

11 Creating Well Patterns

11.1 Overview

- ***FX***, ***NX-S8*** — Only the Span-8 Pod can be used to create well patterns.
- ***3000*** — Only a Single-Tip Pipette Tool can be used to create well patterns.

Creating certain methods requires the probes to access specific wells in labware. Well Patterns (Figure 11-1) is an editor which allows patterns for accessing specific wells to be created and stored. There are also well patterns already created in the editor which may be used, copied, or revised to create new patterns. Any well pattern stored in Well Patterns may be renamed or deleted.

The patterns created and stored in Well Patterns are accessible in the Transfer and Combine steps (refer to Section 15.3, *Configuring Transfer and Combine Steps*). Well patterns may also be created in the Transfer and Combine steps and then stored in Well Patterns.

Well patterns, along with information about tip and labware types; liquid types; and pipetting templates and techniques, are stored as part of a project file. Project files store a history of all changes, additions, and deletions of items from the project file. Refer to Chapter 6, *Understanding and Using Project Files*, for more information on project files.

Note: When Beckman Coulter Accounts & Permissions is enabled, only users with the Develop Projects permission assigned may open, edit, create, and delete well patterns (refer to Chapter 2, *Using Accounts & Permissions*).

To access the Well Pattern Editor, choose **Project>Well Pattern Editor**. Well Patterns appears (Figure 11-1).

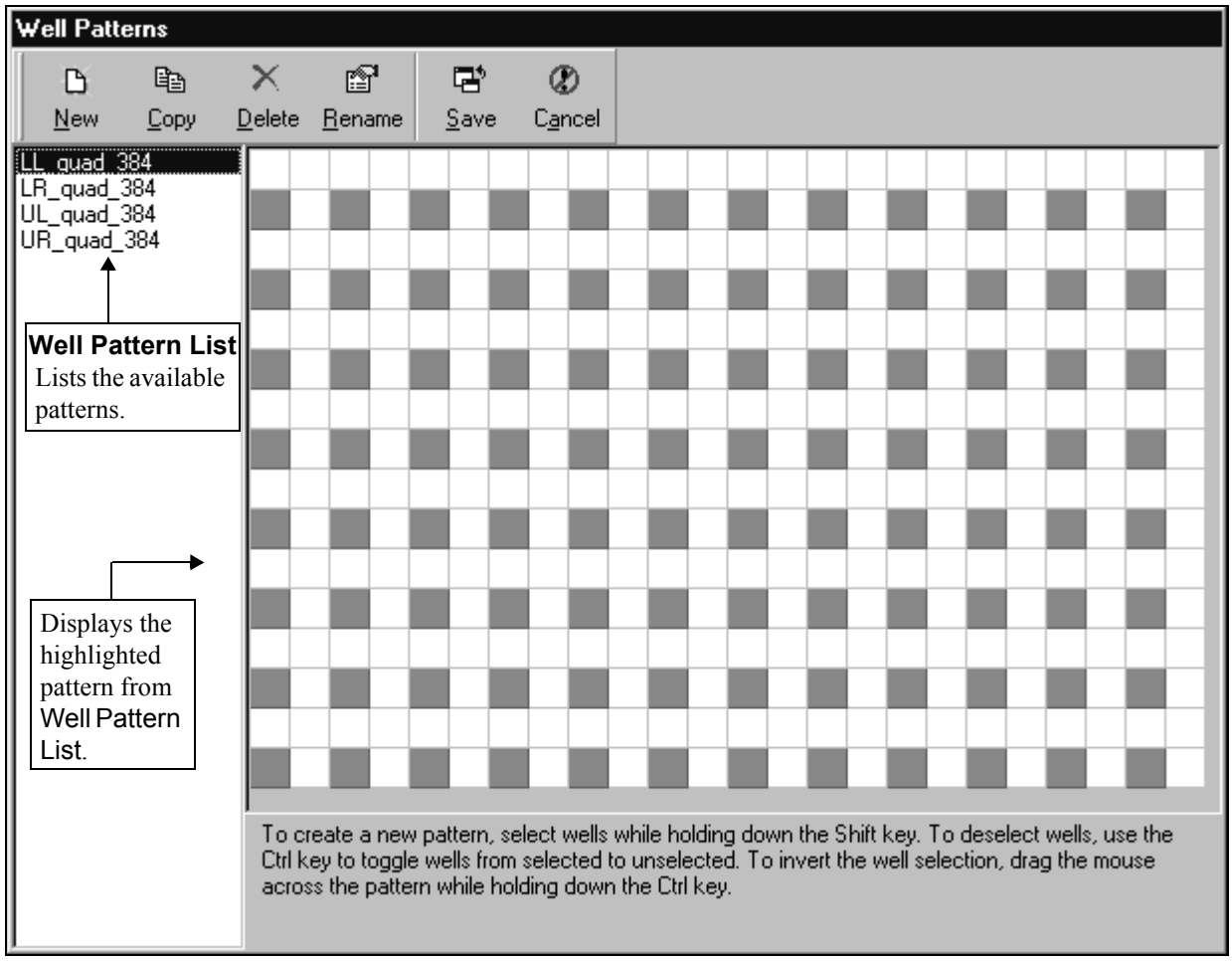


Figure 11-1. Well Patterns

Use the Well Pattern Editor for:

- *Creating a New Well Pattern* (Section 11.2)
- *Copying a Well Pattern* (Section 11.3)
- *Deleting a Well Pattern* (Section 11.4)
- *Renaming a Well Pattern* (Section 11.5)

11.2 Creating a New Well Pattern

New well patterns are created based on the type of labware accessed by the specific probes.

Note: To make sure the desired pattern is not already created, view the patterns in Well Patterns by highlighting the well pattern in the list displayed in Well Patterns (Figure 11-1).

To create a new well pattern:

1. From Well Patterns (Figure 11-1), choose **New**. New Pattern appears (Figure 11-2).

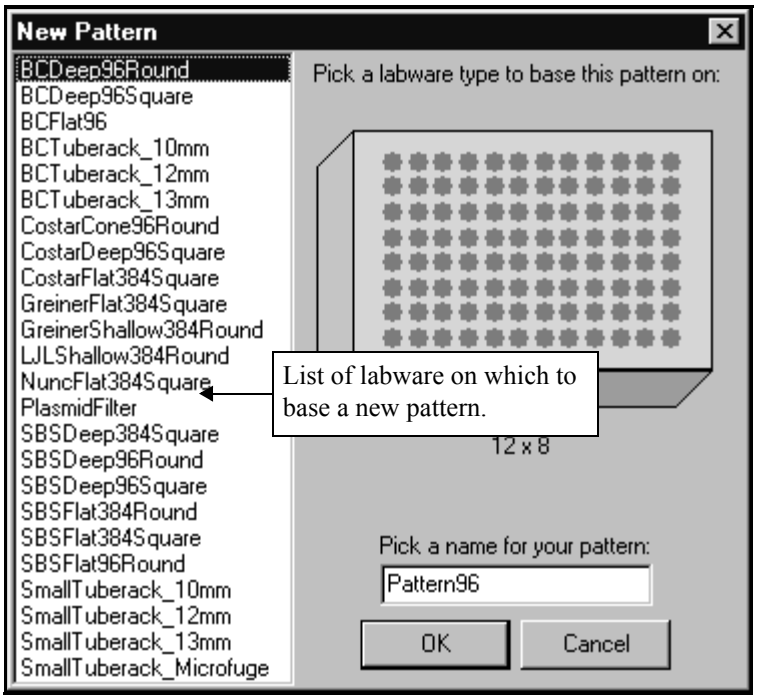


Figure 11-2. New Pattern

2. From the list of labware, choose a labware type on which to base the new pattern.
3. In Pick a name for your pattern:, rename the new pattern, if desired.

   Note: By default, the first new pattern is named after the number of wells on the labware type. Subsequent patterns using the same labware type are named after the number of wells plus a number. For example, the first new pattern created for a 96 well would be Pattern96, the second new pattern would be Pattern96_1, and the third new pattern would be Pattern96_2.

4. Choose **OK**. The labware grid based on the labware type appears in Well Patterns.

5. Create the new pattern from the labware grid by dragging the mouse and using Ctrl and Shift on the keyboard.

   Note: To create a new pattern, select wells while holding down the Shift key. To deselect wells, use the Ctrl key to toggle the wells from select to deselect. To invert the well selection, drag the mouse across the pattern while holding down the Ctrl key.

   Note: If Shift is not held down when dragging and selecting, the previous selection will be deleted when subsequent selections are made.

6. Choose **Save** to save the changes. Well Patterns closes and all the changes made in the dialog are saved.

   OR

   Choose **Cancel** to cancel the changes. A Warning (Figure 11-3) appears. Choose **Yes**. Well Patterns closes and all the changes made in the dialog are cancelled.

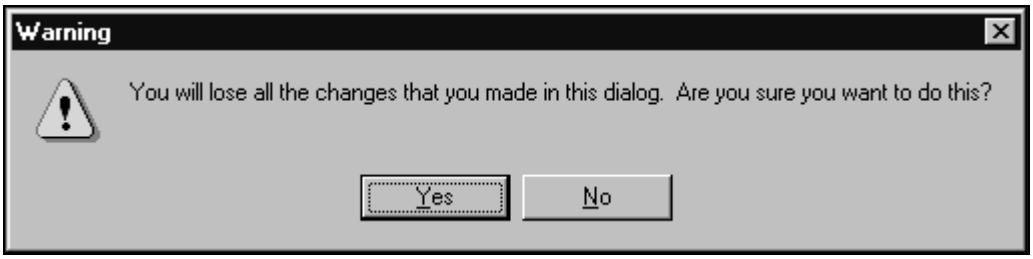


Figure 11-3. Warning when Cancel is chosen

11.3 Copying a Well Pattern

Copying a well pattern creates an exact copy of it. The copied well pattern can be modified to create a new well pattern.

To copy a well pattern:

1. From Well Patterns (Figure 11-1), highlight the desired pattern from the Well Pattern List.
2. Choose **Copy**. Copy Pattern (Figure 11-4) appears.

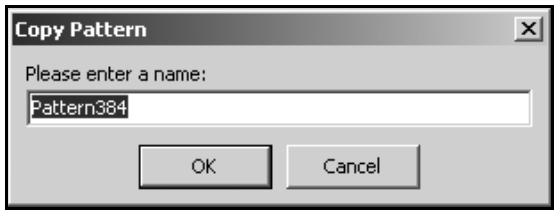


Figure 11-4. Copy Pattern

3. Rename the pattern, if desired.

   Note: By default, the first new pattern is named after the number of wells on the labware type. Subsequent patterns using the same labware type are named after the number of wells plus a number. For example, the first new pattern created for a 96 well would be Pattern96, the second new pattern would be Pattern96_1, and the third new pattern would be Pattern96_2.

4. Choose **OK**. The copied pattern appears in Well Patterns.

   Note: If desired, modify the well pattern.

5. Choose **Save** to save the changes. Well Patterns closes and all the changes made in the dialog are saved.

   OR

   Choose **Cancel** to cancel the changes. A Warning (Figure 11-3) appears. Choose **Yes**. Well Patterns closes and all the changes made in the dialog are cancelled.

11.4 Deleting a Well Pattern

To delete a well pattern stored in Well Patterns:

1. From Well Patterns (Figure 11-1), highlight the desired pattern from the Well Pattern List.
2. Choose **Delete**. A Warning (Figure 11-5) appears, confirming the deletion.

Figure 11-5. Warning confirming deletion of a pattern

3. Choose **OK**. The pattern is deleted from the list of patterns in Well Patterns.
4. Choose **Save** to save the changes. Well Patterns closes and all the changes made in the dialog are saved.

   OR

   Choose **Cancel** to cancel the changes. A Warning (Figure 11-3) appears. Choose **Yes**. Well Patterns closes and all the changes made in the dialog are cancelled.

11.5 Renaming a Well Pattern

Renaming a labware type provides the opportunity to assign a descriptive name to a well pattern for easy identification.

To rename a well pattern in Well Patterns:

1. From Well Patterns (Figure 11-1), highlight the desired pattern from the Well Pattern List.
2. Choose **Rename**. Rename Pattern (Figure 11-6) appears.

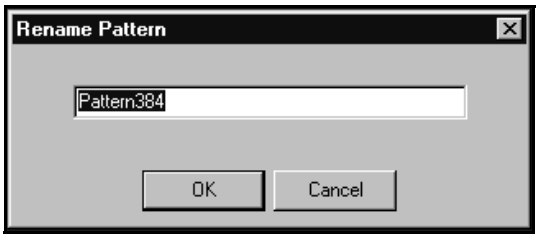


Figure 11-6. Rename Pattern

3. Rename the pattern.
4. Choose **OK**. The pattern is renamed in the list of patterns in Well Patterns.
5. Choose **Save** to save the changes. Well Patterns closes and all the changes made in the dialog are saved.

   OR

   Choose **Cancel** to cancel the changes. A Warning (Figure 11-3) appears. Choose **Yes**. Well Patterns closes and all the changes made in the dialog are cancelled.

12 Creating and Using Methods

12.1 Overview

A method is a series of steps controlling the operations of the Biomek instrument. When steps are inserted into a method, they represent operations performed during the method run. The steps available for insertion into a method are located on the left of the Biomek main editor in the Step Palettes (Figure 12-1).

Note: When Beckman Coulter Accounts & Permissions is enabled, only users with Develop Methods permission may develop, open, and edit methods (refer to Chapter 2, *Using Accounts & Permissions*).

Biomek Software does a substantial amount of the method-building work while at the same time allowing direct and precise control over the building of methods.

Methods are saved as part of a project file, and may also have revisions created by checking in the method. A revision of a method is connected to the current revision for all project items. When a specific revision of a method is opened, it uses the revision of all project items that was current at the time the method was checked in.

Note: The appearance of the main editor (Figure 12-1), such as the Current Deck Display and step palettes, varies based on the current instrument file and project file. The current instrument and project file names are displayed in the status bar of the main editor.

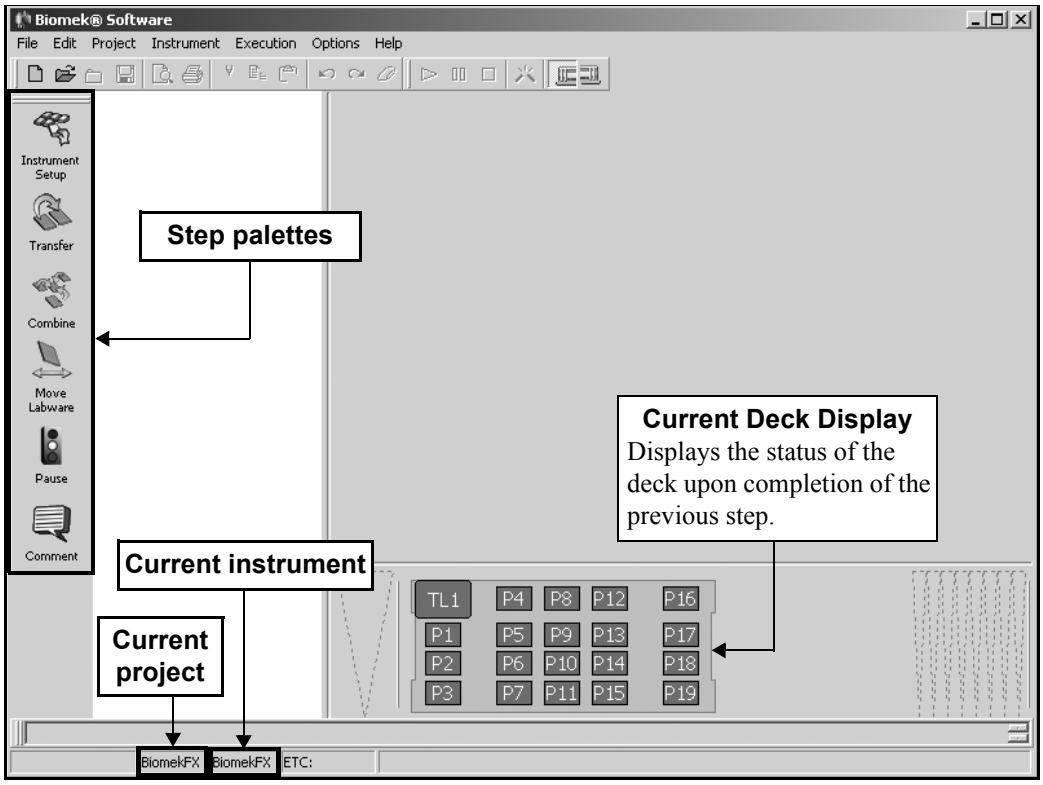


Figure 12-1. Biomek Software main editor for method creation

Using methods to control the operations of the Biomek instrument includes:

- *Creating a New Method* (Section 12.2).
- *Inserting Steps in a Method* (Section 12.3).
- *Using Additional Step Palettes* (Section 12.4).
- *Copying, Cutting, and Pasting Steps in a Method* (Section 12.5).
- *Deleting Steps in a Method* (Section 12.6).
- *Using Undo and Redo in Method Building* (Section 12.7).
- *Entering and Viewing Method Properties* (Section 12.8).
- *Saving a Method* (Section 12.9)
- *Checking In a Method* (Section 12.10).
- *Validating a Method* (Section 12.11)
- *Signing a Method* (Section 12.12).
- *Viewing Method History* (Section 12.13).
- *Opening a Saved Method* (Section 12.14).
- *Checking Out a Method* (Section 12.15).
- *Importing and Exporting Methods* (Section 12.16).
- *Running, Pausing, and Stopping a Method* (Section 12.18).
- *Printing a Method* (Section 12.19).
- *Improving a Method* (Section 12.20).

12.2 Creating a New Method

The main editor (Figure 12-1) is the starting point for creating a liquid-handling method using the Biomek instrument. Method steps from the step palette are inserted into the Method View in a linear fashion.

When steps are inserted into a method, the configuration associated with that step appears on the right side of the Biomek main editor (Figure 12-2).

Note: Steps not configured appropriately generate errors when the method is validated or run.

To create a new method:

1. Launch **Biomek Software**. The main editor appears (Figure 12-1).
2. From the toolbar, select the **New Method** icon.

   OR

   From the File menu, choose **New**.

   OR

   Drag and drop a step, such as Instrument Setup, into the Method View. A new method is created and assigned the default name Method# [New] (Figure 12-2).

   Note: The Start and Finish steps appear automatically in a new method.

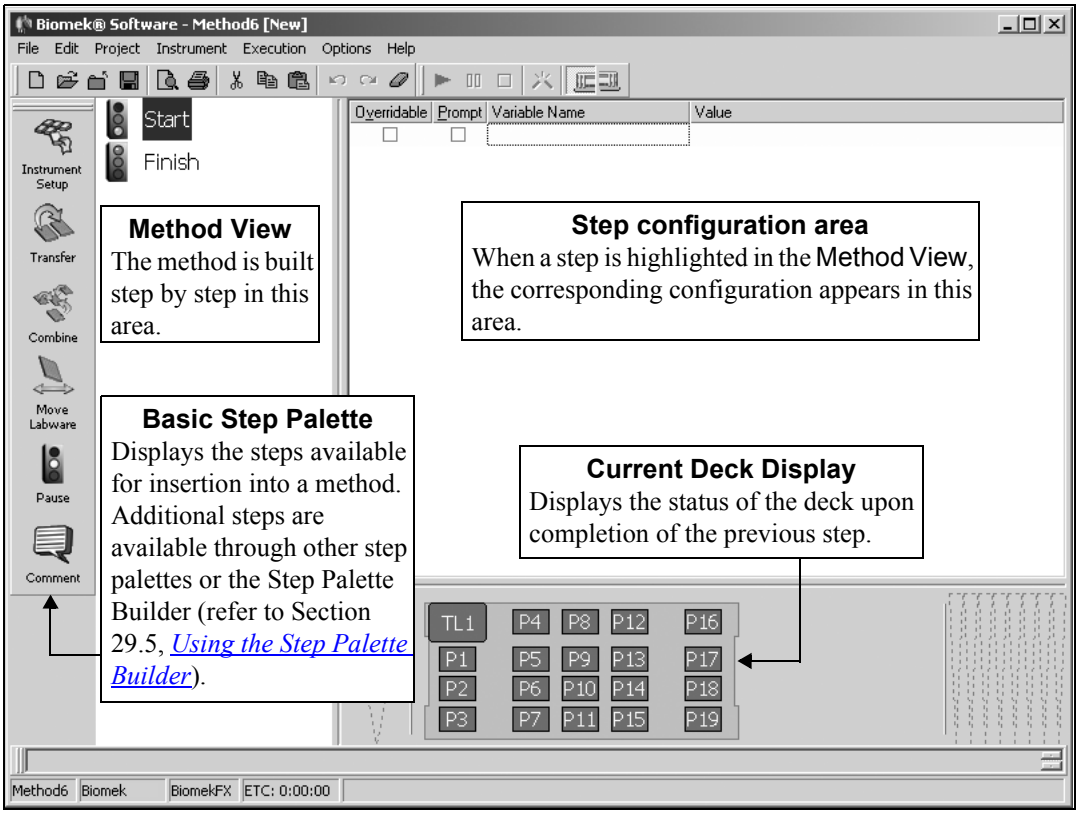


Figure 12-2. Biomek Software main editor for dual-pod Biomek FX instrument

There are two steps automatically present in every method created and executed by Biomek Software:

- Start — the first step in a method; allows creation of global variables that are applicable to the entire method, as opposed to a variable applicable only to one step within the method.

- Finish — the final step in a method; provides options to clear the Biomek instrument deck, clear the devices on the deck, unload tips from the pod, clear all global variables, and generate a report on data sets.

12.2.1 Configuring the Start Step

Use the Start step to define variables used throughout the entire method, as opposed to variables defined within individual steps. A variable is a value that has been assigned a name (Figure 12-3).

Note: Variables defined in individual steps, such as the Let step, are applicable only to that step and any nested substeps. Refer to Section 17.6, *Let Step*, for more information about the Let step.

To use a variable created in the Start step, that variable name is entered into the configuration of the step using the variable. In the example, the variable AspValue, created in the Start configuration (Figure 12-4), is entered in the µL (volume) field of the Transfer step.

The Biomek Software internally substitutes the name with its value, but the name remains in the field. In the example (Figure 12-4), AspValue is substituted internally by the value '10'. The value of '10' is never displayed, only the variable name AspValue. The method can be run subsequently with a different value for AspValue, and the software automatically replaces AspValue with the new value.

Variables created in the Start step can also give a prompt at the start of a method run allowing new values to be entered for each variable at runtime.

Note: Refer to Chapter 13, *Using Variables and Expressions in a Method*, for more information on using variables in a method.

To configure a variable in the Start step:

1. Select **Start** in the Method View. The Start step configuration appears (Figure 12-3).

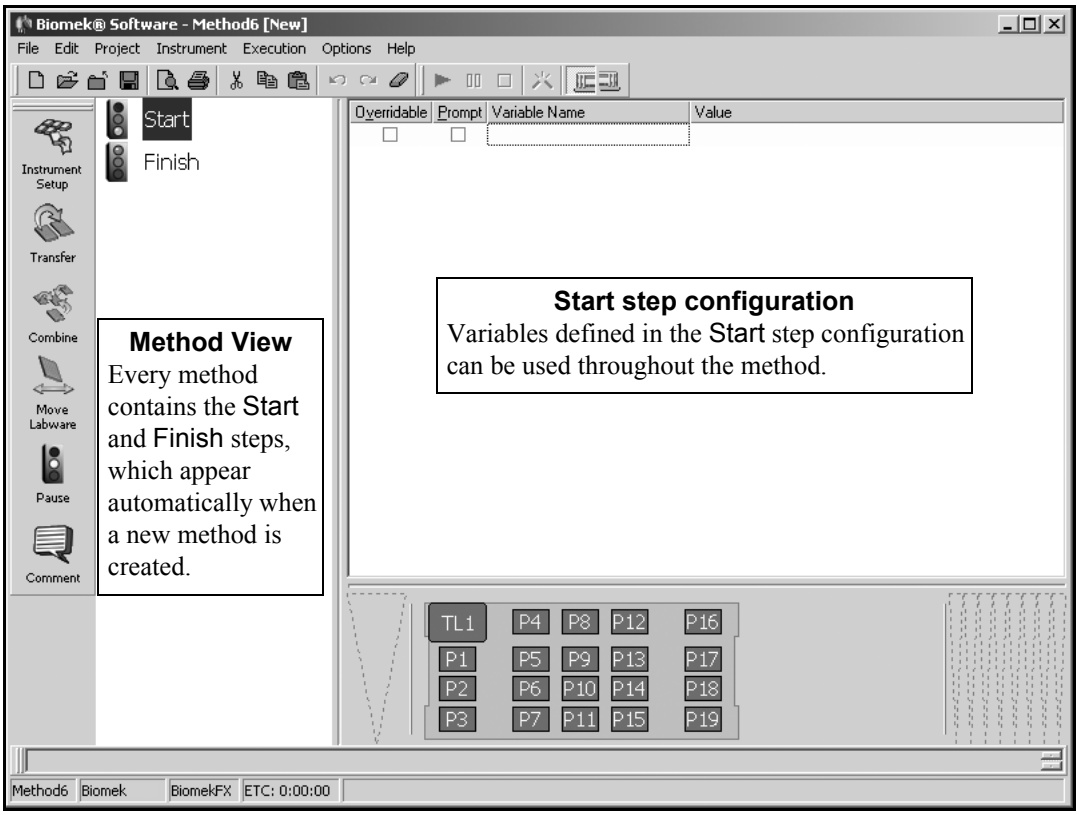


Figure 12-3. Start step and configuration

2. Click under **Variable Name** (Figure 12-4) to position the cursor in the Variable Name field.

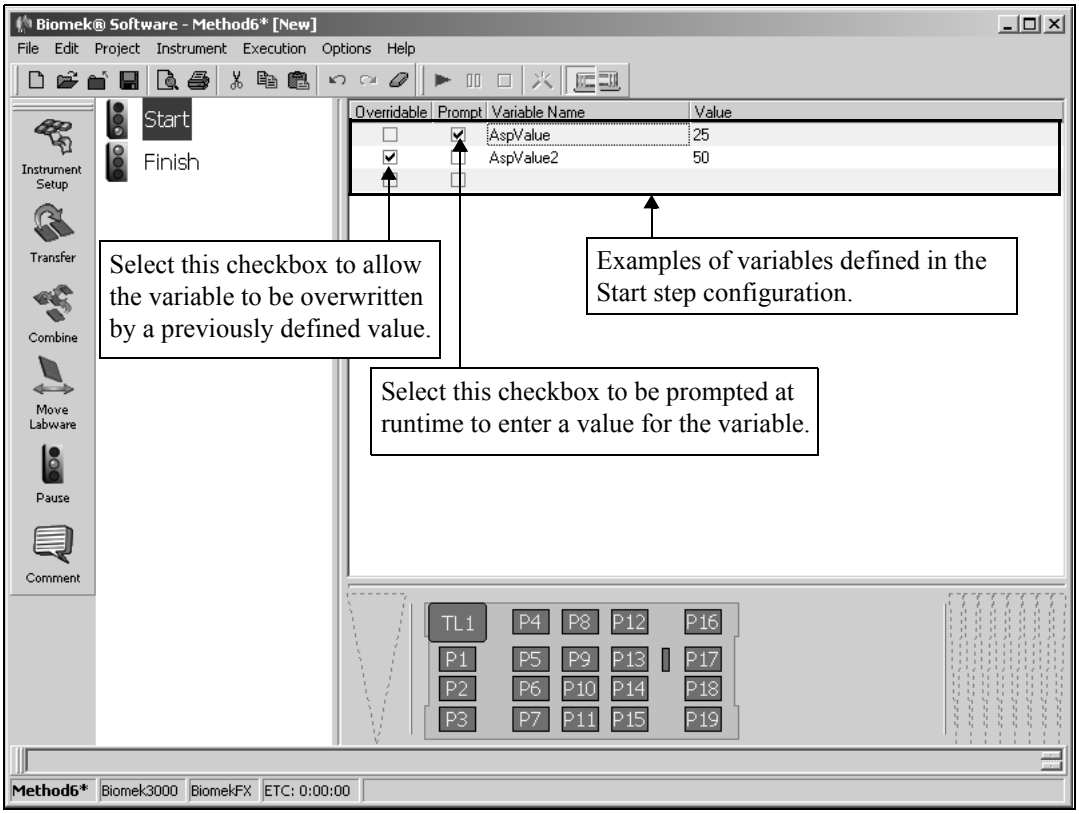


Figure 12-4. Start step with variables configured

3. Enter a **Variable Name**.

Note: Variable names must begin with a letter, may only use alphanumeric characters (0-9, A-Z) and the underscore (_), and may not exceed 255 characters. Variable names are not case sensitive.

4. Enter the desired default **Value** for the variable.

5. Check the box under **Overridable** (Figure 12-4) if the variable can be overridden by a previously defined value. For example, a variable Test is created in the Start step with a value of 10. A Let step later in the method assigns a value of 15 to the Test variable. If Overridable is selected in the Let step, the previously existing value from the Start step of 10 overrides the value in the Let step. If Overridable is not selected, however, the variable is assigned the value of 15 defined in the Let step.

6. Check the box under **Prompt** (Figure 12-4) to activate a prompt for the variable at run time. Each time the method is run, a prompt similar to the one shown in Figure 12-5 asks for verification of the variables and their values. Verification of the variables provides an opportunity to change the default values associated with the variables each time the method is run, if desired.

Note: A separate prompt appears for each variable that has Prompt selected.

Figure 12-5. Prompt to enter value for variable at runtime

7. Repeat steps 2-6 for each variable.

Note: To get a new line for another variable, press **Enter** with the cursor in the Value field of the last defined variable.

12.2.2 Configuring the Finish Step

The Finish step is the last step in every Biomek method. The Finish step indicates the end of a method and provides opportunities to control pod, deck, and device status upon completion of a method.

When highlighted in the Method View:

- The Finish step configuration is displayed on the right side of the Biomek main editor.
- The software runs an internal validation to check for errors in the method.
- An Estimated Time to Completion (ETC) of the method is displayed in the status bar at the bottom of the Biomek main editor.

Note: When the Finish step is highlighted in the Method View, the software estimates the real time required to complete the entire method. When any other step is highlighted in the Method View, the length of time displayed in the ETC field represents the time required to complete the method up to the selected step. If an error is found in validation, ETC is displayed as Failed.

Use the Finish step to re-initialize the software state of the deck and external hardware devices, and to physically remove tips from the pod when a method is completed.

The default configuration for the Finish step is all options selected (Figure 12-6). If the options are not selected, errors may occur due to conflicts between the labware in a new method and the labware from the previous method. The error occurs because software and hardware remain in their final state after a method is run, unless told otherwise.

Note: Each of the Finish step options is independent of the others, so any combination of the options may be selected.

Note: If the Finish step configuration options are not used, steps must be added to the new method to reset the software and hardware.

The options of the Finish step reset the hardware and software so a new method can populate the deck as required, without encountering labware errors. The Finish step also allows for reports to be generated on labware data from data sets (refer to Chapter 14, *Using Sample Tracking and Data Sets in a Method*).

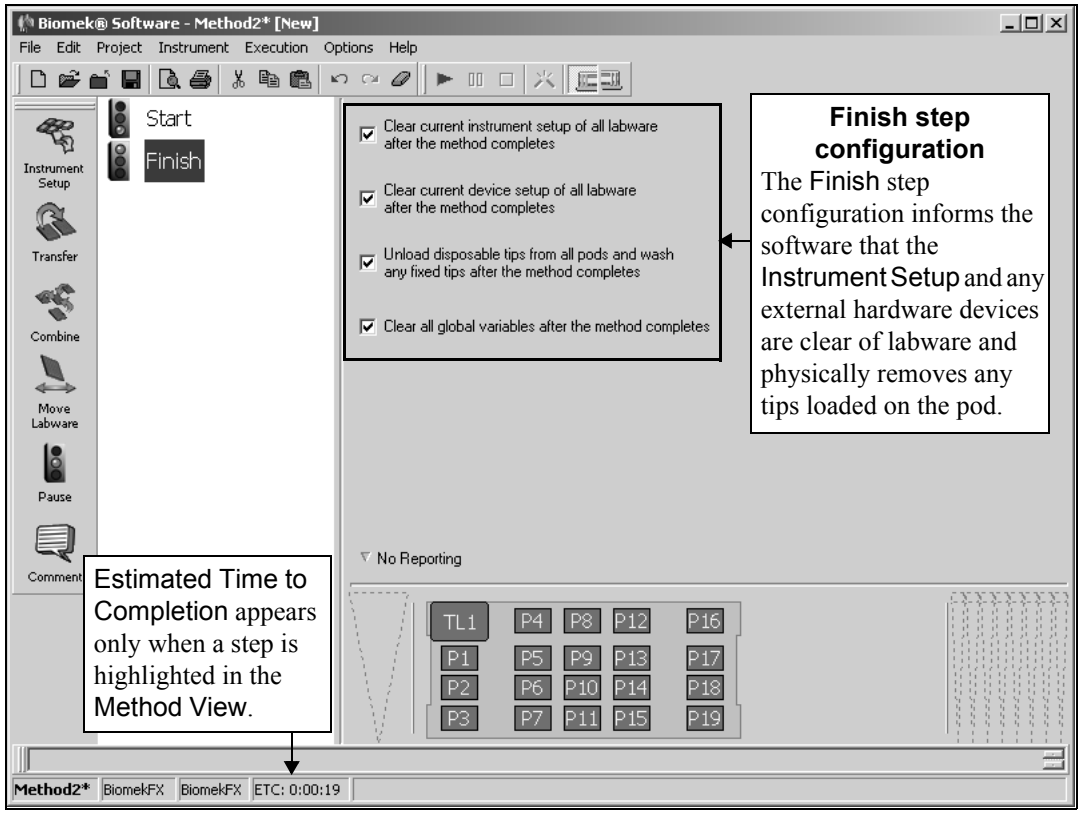


Figure 12-6. The Finish step configuration for a Biomek FX instrument

12.2.2.1 Clear Current Instrument Setup of All Labware After the Method Completes

The Current Deck Display represents the status of the labware on the deck upon completion of a method run (Figure 12-6). Typically, a clear deck is needed at the start of a method.

To clear the deck in the software after a method, select **Clear current instrument setup of all labware after method completes** in the Finish step configuration. This ensures a clear deck for the next method.

Note: To use the same deck setup for a subsequent method, do not select **Clear current instrument setup of all labware after method completes** in the Finish step configuration. The labware positions, volumes, and marks carry over to the next method. Use the **As Is** option in the Instrument Setup step in the subsequent method to leave those positions in their current state.

12.2.2.2 Clear Current Device Setup of All Labware After the Method Completes

The Device Setup remembers the contents of the devices on the deck at completion of a method run (Figure 12-6). Typically, devices are clear of labware at the start of a method.

To clear all devices of labware, select **Clear current device setup of all labware after method completes** in the Finish step configuration. This ensures clear devices for the next method.

Note: Insert an Instrument Setup step at the beginning of the next method to specify where labware is located on the deck (refer to Section 15.2, *Instrument Setup Step*). Use the Deck Editor to specify the location of devices on the deck (refer to Chapter 5, *Preparing and Managing the Deck*), and use the Device Setup step to configure the contents of the external devices. Refer to Section 22.4, *Using External Devices with Biomek Laboratory Automation Workstations*, and Section 22.5, *Device Setup Step*, for more information about configuring external devices.

12.2.2.3 Unload Disposable Tips from All Pods and Wash Any Fixed Tips After the Method Completes

Tips remain on the pod(s) or tools unless they are removed during a step or in the Finish step (Figure 12-6). Typically, the pod or tool needs to be clear of tips at the start of a method.

- ***FX***, ***NX-MC***, ***NX-S8*** — Disposable tips can be removed from any Multichannel Pod and any probes on a Span-8 Pod. If any probes on a Span-8 Pod are equipped with fixed tips, they can be washed at the conclusion of the method.

  Note: To wash any fixed tips on a Span-8 Pod, the deck must have a Span-8 Wash ALP accessible by the Span-8 Pod (refer to the *ALPs User's Manual,* Chapter 18, *Span-8 Tip Wash ALP*) and configured in the Deck Editor (refer to Chapter 5, *Preparing and Managing the Deck*).

- ***3000*** — Disposable tips can be removed from any pipetting tool.

To clear all pods of disposable tips and wash any fixed tips, select **Unload disposable tips from all pods and wash any fixed tips after method completes** in the Finish step configuration.

12.2.2.4 Clear All Global Variables After the Method Completes

Global variables are set in the Start or Set Global steps. A variable is a value that has been assigned a name and can be referenced repeatedly during a method. Global variables are carried over into subsequent methods unless they are cleared in the Finish step.

To clear all global variables, select **Clear all global variables after the method completes** in the Finish step configuration.

12.2.2.5 Unload the Current Tool After the Method Completes (3000 Only)

When using Biomek Software to create methods for the Biomek 3000 instrument, an additional option to unload whatever tool is installed on the Biomek 3000 head assembly at the end of the method is available (Figure 12-7). Selecting this option instructs the instrument to unload any tool installed on the Biomek 3000 head assembly upon completion of the method to ensure no tool is installed at the start of the next method.

If Unload the current tool after method completes is not selected, it may be necessary to add additional steps to the start of any subsequent methods to unload or change the tool on the head assembly.

To unload the tool at the end of the method, select **Unload the current tool after the method completes** in the Finish step configuration. Any tool loaded onto the Biomek 3000 head assembly is removed and placed back onto the tool rack at the conclusion of the method.

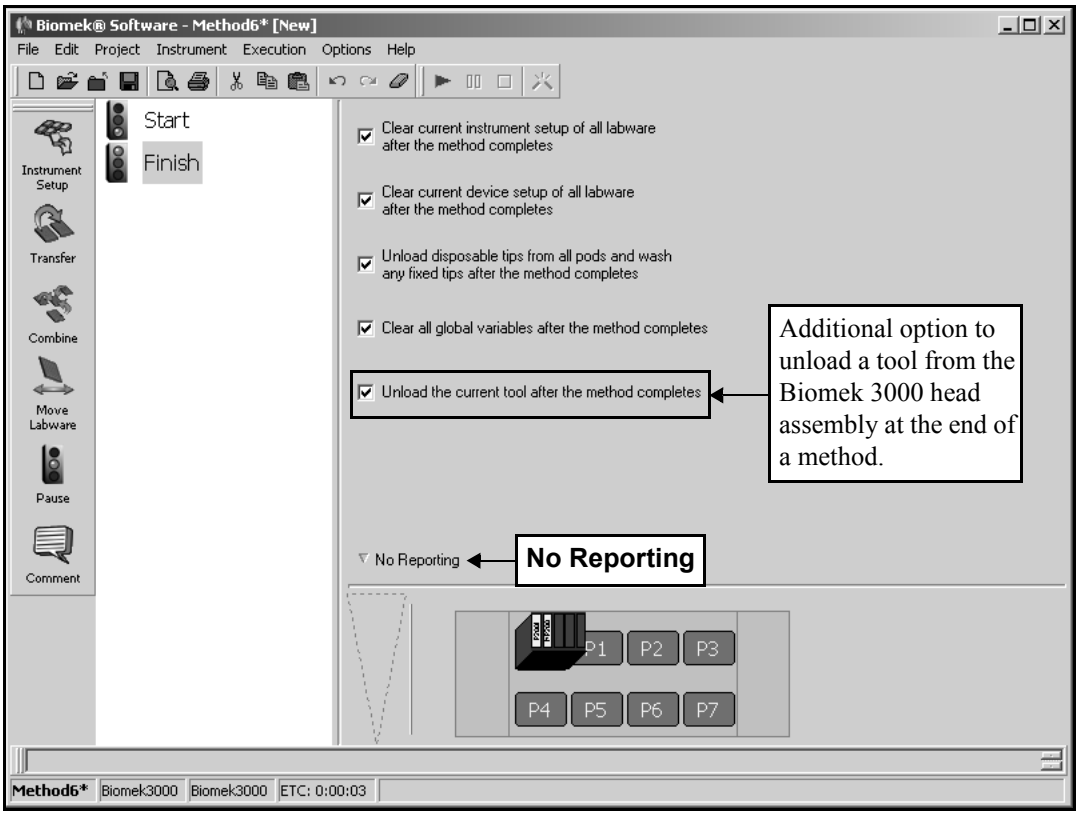


Figure 12-7. Finish step options for a Biomek 3000 instrument

12.2.2.6 Configuring a Report in the Finish Step

The Finish step may be configured to create a report on data sets at the end of the method. Refer to Chapter 14, *Using Sample Tracking and Data Sets in a Method*, for more information on using data sets in a method.

Note: To create a report on data sets after any transfer or pipetting operation, a Reporting step may be inserted into a method at any time (refer to Section 24.6, *Configuring the Reporting Step*)

To choose the report style and location of a report at the end of a method:

1. From the Finish step, check **No Reporting** (Figure 12-7) to open the Reporting configuration (Figure 12-8).

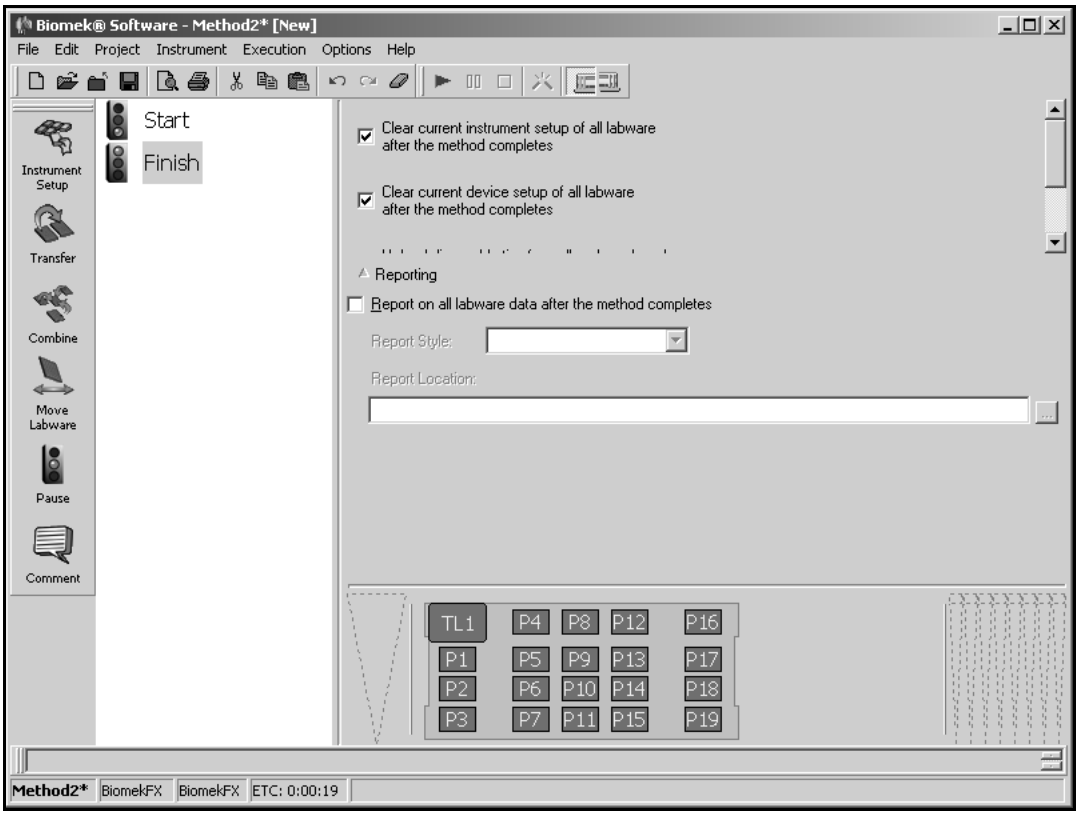


Figure 12-8. Reporting enabled on Finish step

2. Select **Report on all labware data after the method completes** to enable reporting.

3. From **Report Style**, choose one of the following:
    - Text File
    - Per-Plate HTML Files
    - Per-Plate Text Files
    - SQL Server (refer to Section 24.6.2, *Configuring a SQL Server Report Style*)

    Note: Refer to Section 24.6.1, *Report Styles*, for examples and information on the types of reports that may be generated.

4. In **Report Location**, browse to find the location where the file is saved. Reporting on the Finish step is configured.

12.2.2.6.1 Generating a Report When a Method Stops

When a method is stopped or aborted and reporting is configured in the Finish step, a prompt appears asking if a report should be generated as configured in the Finish step (Figure 12-9) (refer to Section 12.2.2.6, *Configuring a Report in the Finish Step*).

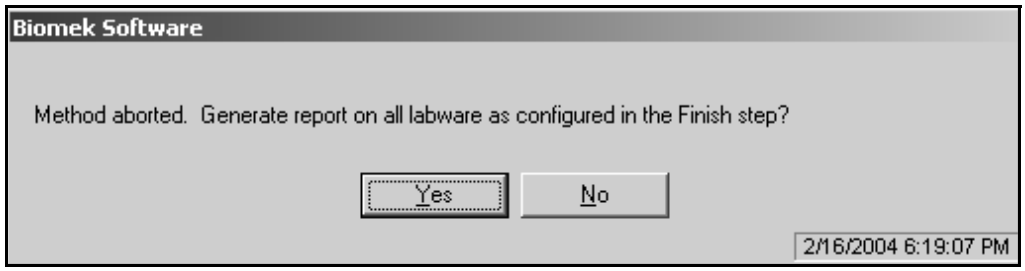


Figure 12-9. Prompt when method is aborted

To generate a report when a method stops:

From Figure 12-9, choose **Yes**. The report is generated as configured in the Finish step.

12.2.2.7 Completing Finish Step Configuration

Once all the desired options on the Finish step have been selected, the method can be run. When the method is completed, any actions selected in the Finish step are performed.

12.3 Inserting Steps in a Method

Steps can be added to a method in a sequential order or inserted at any location in the Method View during the method building process; however, steps must represent the desired order of execution when the method is run.

To insert a step in a method, choose one of the following procedures:

1. Select the step above the desired insertion point (Figure 12-10).
2. Click the desired step on the step palette. The step is inserted below the selected step.

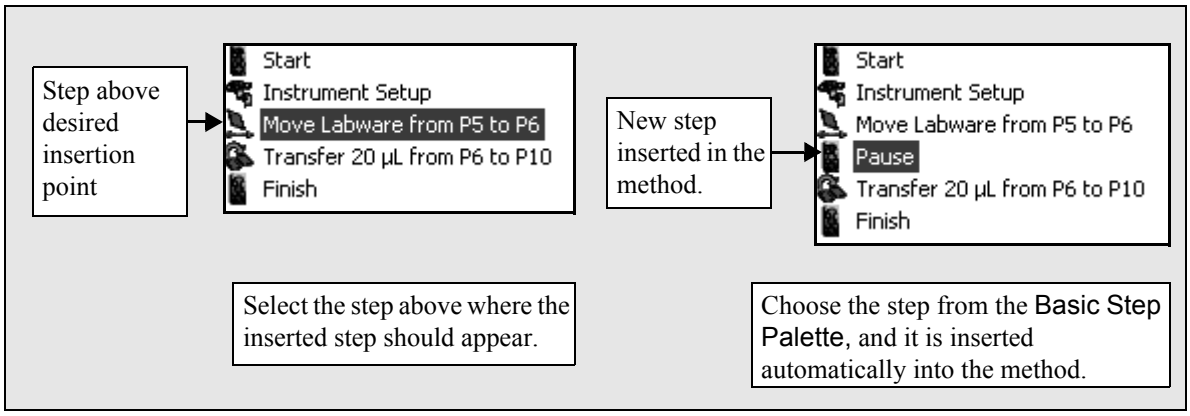


Figure 12-10. Inserting a step into a method

OR

Drag and drop the desired step from the step palette to the desired location in the Method View. A black bar appears at the insertion point (Figure 12-11).

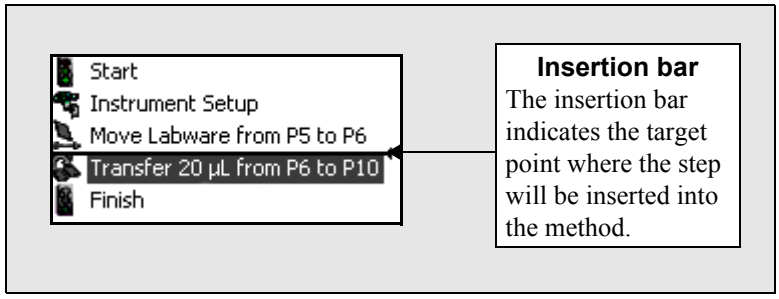


Figure 12-11. Inserting a step by drag and drop

12.3.1 Understanding Techniques

All pipetting operations in a method are controlled using techniques. A technique instructs the Biomek instrument in performing pipetting operations, such as aspirate, dispense, and mix. Technique selections are made anytime liquid needs to be aspirated or dispensed during a method.

A technique stores a set of values, such as aspirate and dispense height, pod speed, and tip touch, used in pipetting operation. Biomek Software also stores a set of properties, such as labware type and liquid type, related to each technique. Based upon these values and properties, the appropriate technique is selected automatically for the pipetting operation. This auto-selection can be overridden and a technique selected manually for each operation, if desired.

Pipetting options used in the selected technique are represented visually under the Auto-Select field in the step configuration. These pipetting options may include:

- Prewet the tips — aspirates and dispenses a specified volume of liquid before pipetting to prewet the tips.

- Tip Touch — allows tips to touch a designated location briefly in a well after aspirating or dispensing.

  Note: Movement of a tip touch first centers the tip in the well, performs the pipetting operation, moves to the side of the well, performs a specified delay, and returns to the center of the well for dispensing.

- Mix prior to aspirating liquid or Mix after dispensing liquid — mixes the liquid before aspirating or after dispensing.

- Follow liquid level when aspirating or dispensing — is accomplished with calculations that determine the difference in height of a liquid level after an aspirate or dispense operation is completed. The Z and D axis are coordinated according to that liquid level.

- Aspirate a trailing air gap after leaving the liquid — draws air into tips after aspirating liquid, and blows out that air before dispensing.

- Blowout all leading air gaps — draws air into tips before aspirating liquid, and blows out that air after dispensing to ensure all liquid has been dispensed.

Note: Refer to Chapter 9, *Understanding and Creating Techniques*, for more information on pipetting techniques.

12.4 Using Additional Step Palettes

Additional steps, other than those displayed on the Basic Step Palette, may be added to a method by displaying one of the existing step palettes or creating a new step palette using the Step Palette Builder (refer to Chapter 29.5, *Using the Step Palette Builder*).

To display an existing step palette:

- From the Options menu, select **Toolbars** and then select the desired step palette to display.

Note: The step palettes available depend on instrument type and configuration.

OR

Right-click any empty palette space, and select the desired step palette to display from the step palette menu (Figure 12-12).

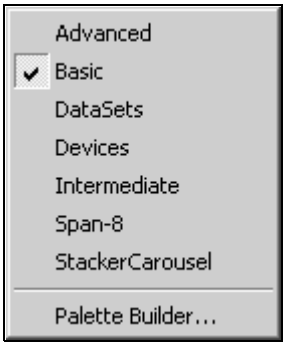


Figure 12-12. Step palette menu

Note: To create a custom step palette or add steps to existing step palettes, select **Palette Builder** to open the Step Palette Builder.

12.5 Copying, Cutting, and Pasting Steps in a Method

One or more steps can be copied, cut, and pasted within a method or between methods in a sequential order. Steps can be inserted at any location in the Method View during the method building process; however, they must represent the desired order of execution when the method is run.

The originating method and the destination method must use the same deck and instrument setups when copying, cutting, and pasting steps between methods. Verifying that the deck and instrument setups are the same in both methods ensures that Biomek Software knows where labware is physically located on the deck. If the decks do not match, steps copied from another method may need to be modified to work in the new method.

To copy, cut, and paste one or more steps in a method:

1. Highlight a step in the Method View for copy (or cut).
2. To select multiple steps to copy (or cut):
   - While holding down **Shift**, select the final step in the series to copy (or cut). All the steps between the first and second steps selected are now highlighted.
   - While holding down **Ctrl**, select additional steps to copy (or cut). All the selected steps are highlighted.
3. From the Edit menu, select **Copy** (or **Cut**).

   OR

   Right-click on any of the selected steps and select **Copy** (or **Cut**) from the menu that appears.

   Note: If Cut is selected, the highlighted step(s) are removed from the Method View. If any other step is Copied or Cut prior to Pasting the first step in the Method View, the first copied or cut step is lost or overwritten.

4. If the step is to be pasted in a different method, open the desired method (refer to Section 12.14, *Opening a Saved Method*).
5. Highlight the step below where the copied or cut step(s) are to be pasted.
6. From the Edit menu, select **Paste**.

   OR

   Right-click the step below where the copied or cut step(s) are to be pasted and select **Paste** from the menu that appears. The step(s) are inserted above the highlighted step.

12.6 Deleting Steps in a Method

Steps can be deleted from a method during the method-building process if they are no longer desired.

To delete a step from a method:

1. Highlight the step in the Method View.
2. To select multiple steps to delete:
   - While holding down **Shift**, select the final step in the series to delete. All the steps between the first and second steps selected are now highlighted.
   - While holding down **Ctrl**, select additional steps to delete. All the selected steps are highlighted.
3. Press **Delete** on the keyboard.

   OR

   From the Edit menu, select **Clear**. The highlighted step(s) are deleted.

   OR

   Right-click on any of the selected steps and select **Clear** from the menu that appears.
4. If Ask for confirmation before removing a step from a method is selected in Preferences, a prompt appears asking for confirmation each time a step is deleted from a method (Figure 12-13).
5. Choose **Yes** to delete the step from the method.

   OR

   Choose **No** to cancel the deletion.

Figure 12-13. Confirmation to delete steps in a method

12.7 Using Undo and Redo in Method Building

The Biomek Software maintains a history of actions performed during method building. By using the Undo and Redo features located on the toolbar, this history can be accessed and the actions undone or redone while building a method. Hovering the mouse over the Undo or Redo button on the toolbar displays a tool tip indicating what action will be undone or redone.

The following actions are stored in the history and may be undone and redone while building a method:

- Adding a step.
- Removing a step.
- Moving a step.
- Configuring a step.
- Changing active selection.

Note: The active selection is the currently selected (highlighted) step within the method. Selecting another step in the method changes the active selection.

12.7.1 Using Undo

Undo is used to undo the most recent method-building action. Multiple actions may be undone by performing consecutive Undo actions; there is no limit to how many actions can be undone.

To undo an action:

- Select **Undo** from the Edit menu

  OR

- Click **Undo** on the toolbar

Note: When Undo is used while configuring a step, it undoes all actions made to the configuration. For example, while configuring Instrument Setup step and placing labware on deck positions, choosing Undo will undo the entire Instrument Setup step and not just the last deck position that was configured.

12.7.2 Using Redo

Redo is used to redo an action that has been undone using the Undo feature. By performing consecutive Redo actions, multiple actions can be redone if multiple actions were undone.

Note: If another action is performed after undoing an action, Redo is disabled and the previously undone action cannot be redone.

To redo an undone action:

- Select **Redo** from the Edit menu

  OR

- Click **Redo** on the toolbar

12.8 Entering and Viewing Method Properties

Method Properties allows for entry of a description of the method that can be viewed or modified.

Note: Method properties can be viewed, but not modified when running a method in validated mode (refer to Section 12.14, *Opening a Saved Method*). Validated mode is available only when Beckman Coulter Accounts & Permissions is enabled (refer to Chapter 2, *Using Accounts & Permissions*).

To enter or view Method Properties:

1. From the File menu, select **Properties**. Method Properties appears (Figure 12-14).

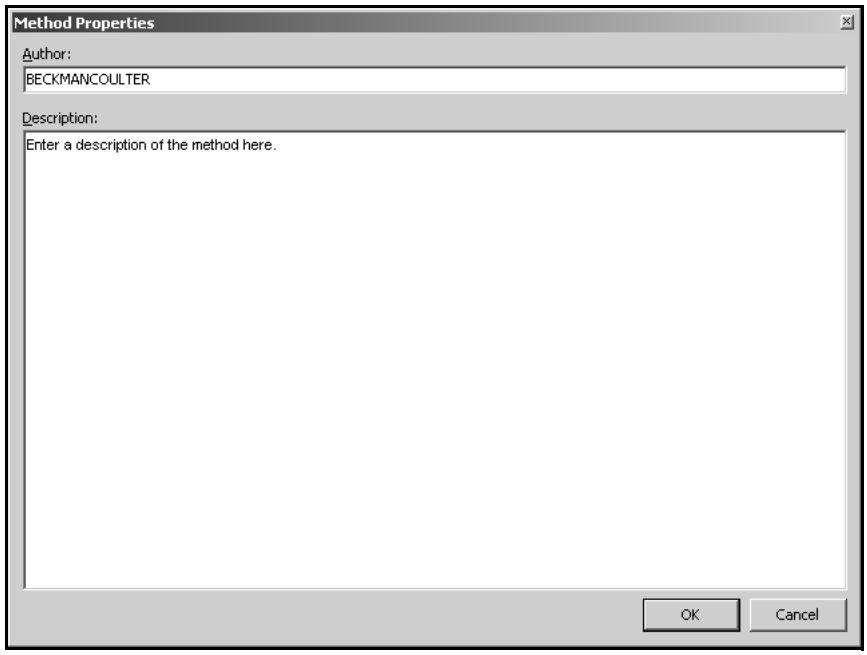


Figure 12-14. Method Properties

2. In Author, enter the name or user name of the method designer.
3. In Description, enter a description of the method.
4. Choose **OK** to save changes and close Method Properties.

   OR

   Choose **Cancel** to close Method Properties without saving changes.

12.9 Saving a Method

Methods may be saved at any time during their development. Saving a method only saves the current status of the method and does not create a revision or check in project items as revisions. If any of the project items, such as labware class definitions or techniques, changes after the method is saved, when the method is opened next, it uses the latest definitions.

Methods are saved as elements of the project file, not as separate files. To use a method in another project file or on another system, it must be exported to a Biomek method file (*.bmf) and imported into the desired project (refer to Section 12.16, *Importing and Exporting Methods*).

To save a method:

1. Choose the **Save Method** icon on the toolbar.

   OR

   From the File menu, choose **Save**. Save Method appears (Figure 12-15).

Note: Save Method appears only the first time the method is saved; subsequent saves to the method do not prompt for a new file name. To save an existing method with a different file name, choose **Save As** from the File menu.

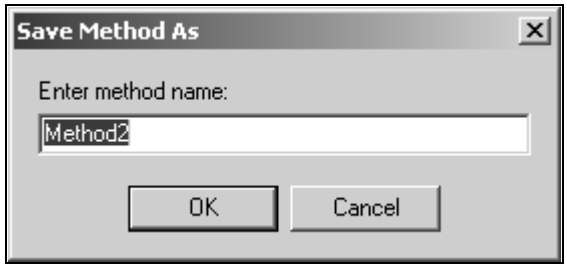


Figure 12-15. Save method

2. In Enter method name, enter the name under which the method is saved.
3. Choose **OK**. The method is saved with the specified method name and Save Method closes. The title bar of the Biomek Software main editor displays the method name as MethodName [Development] (Figure 12-16).

   OR

   Choose **Cancel**. Save Method closes without saving the method.

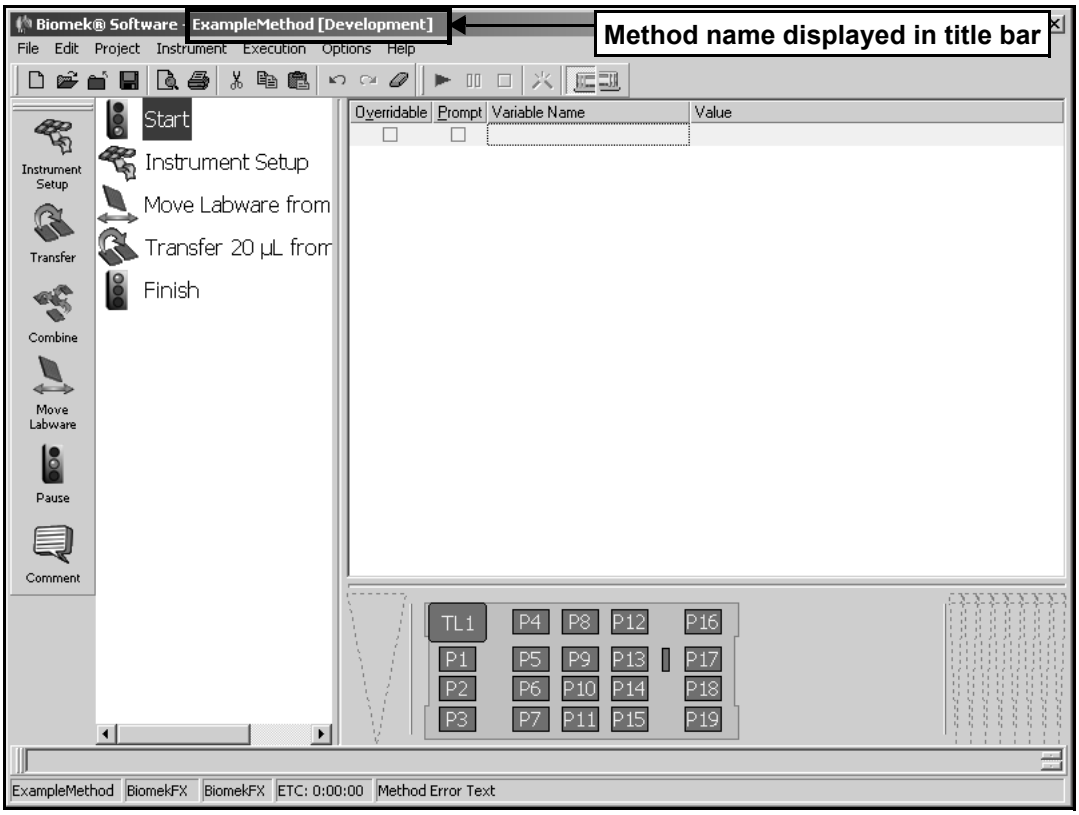


Figure 12-16. Biomek Software main editor after saving method ExampleMethod

12.10 Checking In a Method

Checking in a method is similar to saving a method, but in addition creates a new revision of the method, checks in all project items of the project file, and creates new revisions for any items that have changed. A relational link is created between the method and all items in the project file.

Note: Methods must be saved once before being checked in. A prompt to save appears automatically if the method has not been saved before.

To check in a method:

1. From the File menu, choose **Check In**. If any project items have changed since the last revision, Check In appears, listing all project items that have changed (Figure 12-17).

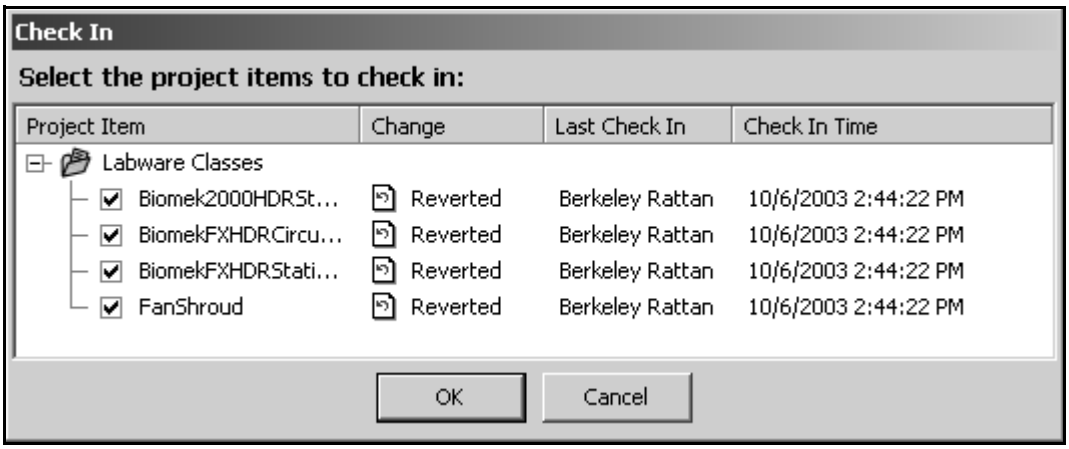


Figure 12-17. Check In

2. Select the project items to check in as new revisions. By default, all project items in Check In are selected.

   Note: When a method is checked in, the title bar updates the method title to show the current revision of the method and that it is in Development mode. Methods can only be validated or opened in validated mode when Beckman Coulter Accounts & Permissions is enabled (refer to Section 12.11, *Validating a Method*).

3. Choose **OK** to check in the new revisions of project items.

   Note: If Accounts & Permissions is not enabled, check in is complete.

   OR

   Choose **Cancel** to close Check In without checking in the method.

4. If Accounts & Permissions is enabled, Check-In appears (Figure 12-18). In Reason, enter information or notes about the method or project revision being checked in. Text entered in Reason is date and time stamped, and stored in the audit log of all user activity.

5. If Accounts & Permissions is configured to require password checks for signing and check-in, enter the user **Password**.

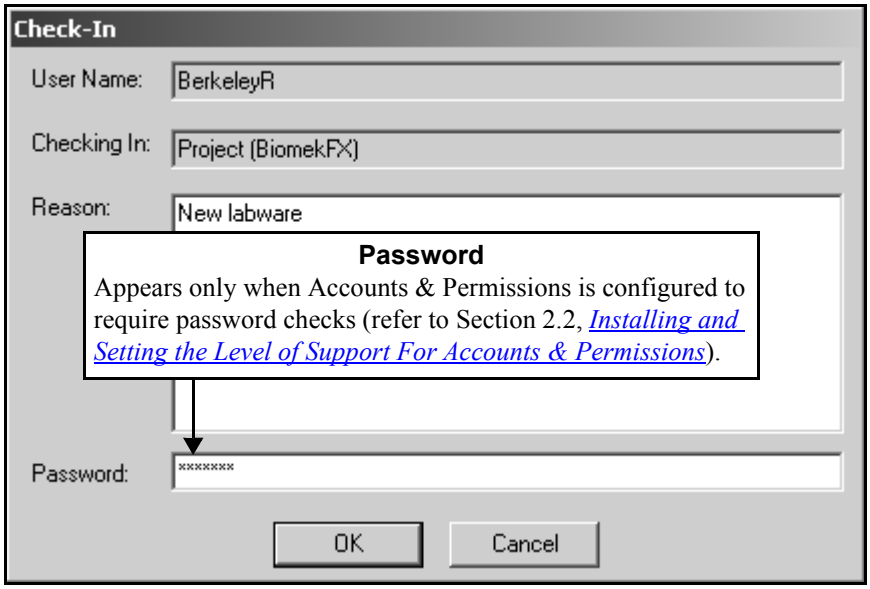


Figure 12-18. Check-In

6. Choose **OK** to check in the method or project. If project items were modified, only the project was checked in. Check-In appears a second time to check in the method.

   OR

7. Choose **Cancel** to close Check-In without checking in the method or project.
8. Repeat steps 4 – 6 to check in the method, if necessary.

12.11 Validating a Method

When Beckman Coulter Accounts & Permissions is enabled, methods may be validated. A validated method is a revision of a method that is checked in, approved with an electronic signature, and protected from further modification. Revisions of project items required to run the validated method are also checked in and protected from further modification. This ensures that validated method runs are reproducible.

Validating a revision of a method is not the same as validating a method before a run to internally test for errors before the method is actually run. To validate a method to test for errors before it is run, check **Validate the current method before running it** in Preferences (refer to Section 29.2, *Changing Display Preferences*).

Note: Only users with Validate Methods permission can validate methods. Refer to Chapter 2, *Using Accounts & Permissions* for more information about Beckman Coulter Accounts & Permissions. Permissions can be configured so that a user may be permitted to run only validated methods (refer to Section 12.14, *Opening a Saved Method*).

To validate a method:

1. From the File menu, choose **Validate**. If any project items have changed since the last revision, Check In appears, listing all project items that have changed (Figure 12-17).

   Note: Methods must be saved at least once before being checked in. A prompt to save appears automatically if the method has not yet been saved.

2. Select the project items to check in as new revisions. By default, all project items in Check In are selected.

   Note: All project items used in the method must be checked in order for the correct revision of each item to be used in a validated method run.

3. Choose **OK** to check in the new revisions of project items. Check-In appears (Figure 12-18).

   OR

   Choose **Cancel** to close Check In without checking in and validating the method.

4. In Reason, enter information or notes about the method or project revision being checked in. Text entered in Reason is date and time stamped, and stored in the audit log of all user activity.

5. If Accounts & Permissions is configured to require password checks for signing and check-in, enter the user **Password** (refer to Section 2.2, *Installing and Setting the Level of Support For Accounts & Permissions*).

6. Choose **OK** to check in the method or project. If project items were modified, only the project was checked in. Check-In appears a second time to check in the method. Repeat steps 4 – 6.

   OR

   Choose **Cancel** to close Check-In without checking in or validating the method.

7. After the project and method are checked in, Signature appears (Figure 12-19). In Reason, enter information or notes about the method being validated. Text entered in Reason is date and time stamped, and stored in the audit log of all user activity.

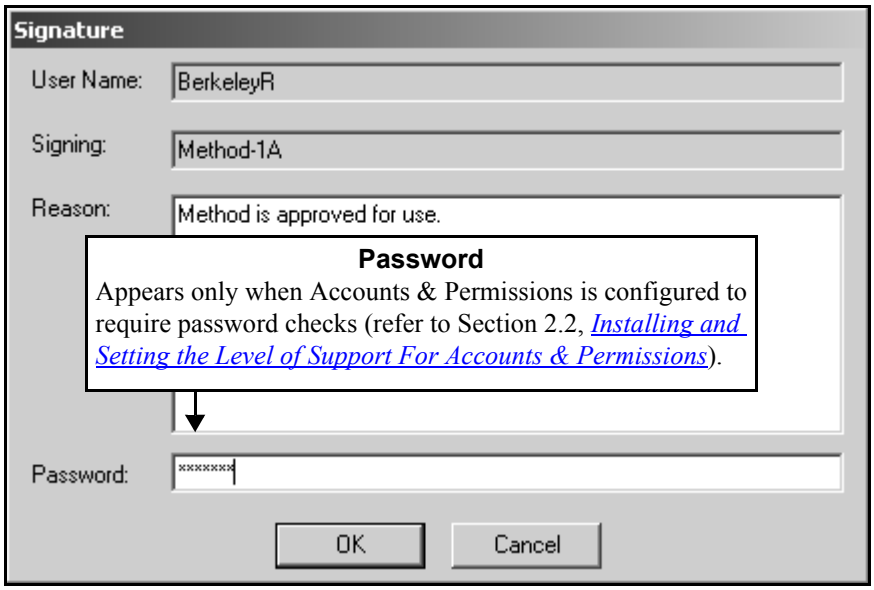


Figure 12-19. Signature

8. If Accounts & Permissions is configured to require password checks for signing and check-in, enter the user **Password** (refer to Section 2.2, *Installing and Setting the Level of Support For Accounts & Permissions*).
9. Choose **OK** to validate the method.

   OR

10. Choose **Cancel** to close Signature without validating the method.

Note: After validating a method, it remains in development mode. To use the method in validated mode, it must be closed and then opened in validated mode. Refer to Section 12.14, *Opening a Saved Method* for more information about opening methods in validated mode.

12.12 Signing a Method

When Beckman Coulter Accounts & Permissions is enabled, methods that are checked in or validated may be signed. Signing allows users to add comments with an electronic signature to the audit trail for the method open in the editor. Signing is useful when laboratory policies require personnel to review and sign off on procedures; for example, a supervisor could approve a new validated method via the electronic signature generated by signing the method in Biomek Software.

Note: Refer to Chapter 2, *Using Accounts & Permissions* for more information about Beckman Coulter Accounts & Permissions.

To sign a method:

1. Ensure the method has been checked in (refer to Section 12.10, *Checking In a Method*).
2. From the File menu, choose **Sign**. Signature appears (Figure 12-20).

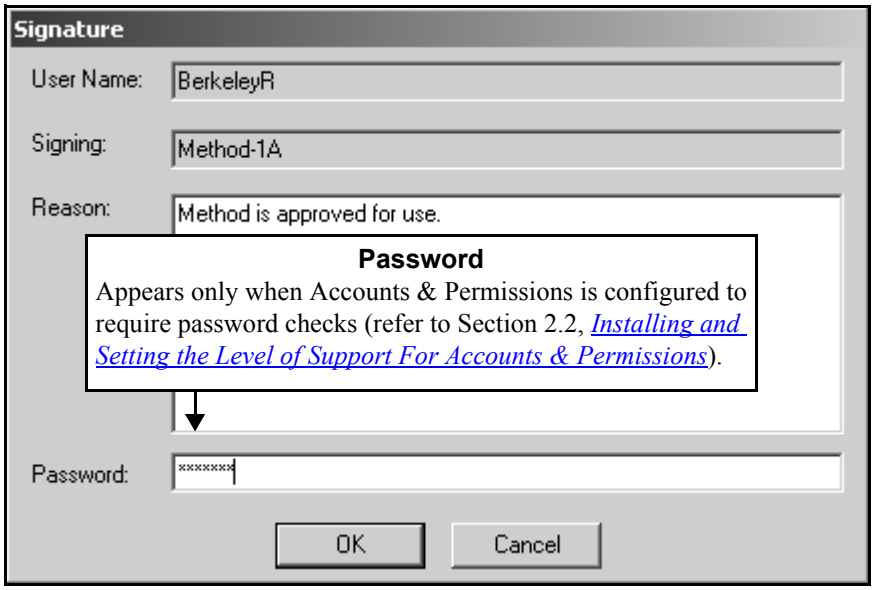


Figure 12-20. Signature

3. In Reason, enter information or notes about the method being signed. Text entered in Reason is date and time stamped, and stored in the audit log of all user activity.
4. If Accounts & Permissions is configured to require password checks for signing and check-in, enter the user **Password** (refer to Section 2.2, *Installing and Setting the Level of Support For Accounts & Permissions*).
5. Choose **OK** to sign the method.

   OR

6. Choose **Cancel** to close Signature without signing the method.

12.13 Viewing Method History

Revision and run history for the current method can be viewed at any time. Method history is viewed in two windows:

- History — view all checked in and validated revisions of the current method (refer to Section 12.13.1, *Viewing Revision History*).
- Validated Run History — view information about each validated run of the current method (refer to Section 12.13.2, *Viewing Validated Run History*).

Note: Validated methods and Validated Run History are available only when Beckman Coulter Accounts & Permissions is enabled (refer to Chapter 2, *Using Accounts & Permissions*).

12.13.1 Viewing Revision History

A revision history that tracks each time the current method has been checked in or validated can be viewed when the method is open.

Note: Methods can be validated only when Beckman Coulter Accounts & Permissions is enabled (refer to Chapter 2, *Using Accounts & Permissions*).

To view the history for a method:

1. From the File menu, choose **History**. History appears (Figure 12-21).

   Note: Revision history details are listed in a tree structure that lists information by run and type. Branches may be expanded or collapsed using the + and - buttons to the left.

   The Changed By and Comment columns appear only when Accounts & Permissions is enabled.

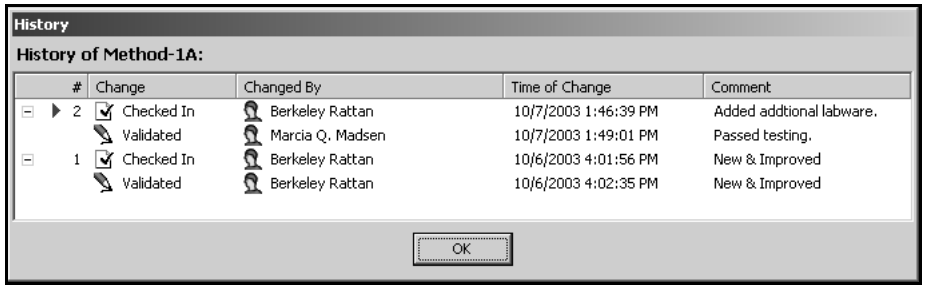


Figure 12-21. Method history

2. When finished viewing the history, choose **OK** to close History.

12.13.2 Viewing Validated Run History

Validated methods run in validated mode generate a run history that can be viewed when the method is open. A run history includes access to all dialog alerts, log reports, worklists, and other files associated with or generated by the method during the run.

Many of the files listed in the run history can be viewed, saved, and printed (refer to Section 12.13.2.1, *Viewing, Saving, and Printing Run History Details*).

Note: Validated methods and their run history are available only when Beckman Coulter Accounts & Permissions is enabled. Refer to Section 2, *Using Accounts & Permissions* and Section 12.15, *Checking Out a Method*.

Note: Text files, such as *.csv files used by the Worklist, Define Pattern, and Transfer From File steps, appear in the run history and may be opened directly from the window. However, when a project or validated method is exported, they are excluded from the Biomek import (*.imp) or method (*.bmf) file. To use a *.csv file in a method exported to another system, it must be copied to the system along with the Biomek import or method file.

To view the validated run history for a method:

1. From the File menu, choose **Run History**. Validated Run History appears (Figure 12-22).

   Note: Run history details are listed in a tree structure that lists information by run and type. Branches may be expanded or collapsed using the + and - buttons to the left.

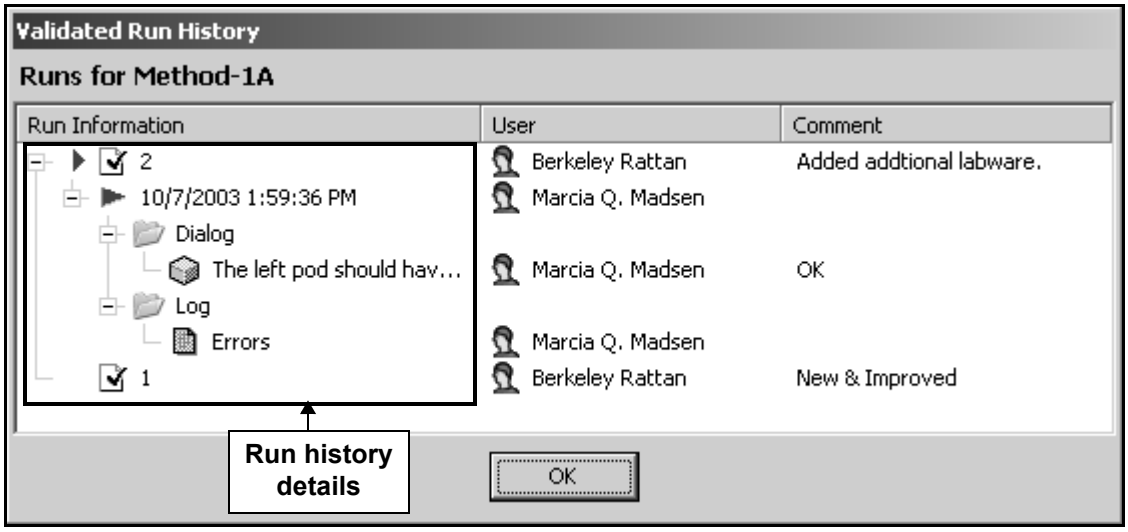


Figure 12-22. Validated Run History displayed in validated mode

2. When finished viewing the history, choose **OK** to close History.

12.13.2.1 Viewing, Saving, and Printing Run History Details

Many of the files listed in the run history details can be viewed, saved, and printed.

To view and print log and other text files:

Right click on the desired file and choose **Open** from the menu. The file opens in Print Preview with printing and viewing options (Figure 12-23).

To save a file listed in the run history:

Note: Dialog details cannot be viewed or saved.

1. Right click on a file and choose **Save** from the menu that appears.
2. Save files in text format by appending **.txt** to the end of the filename for best file compatibility.

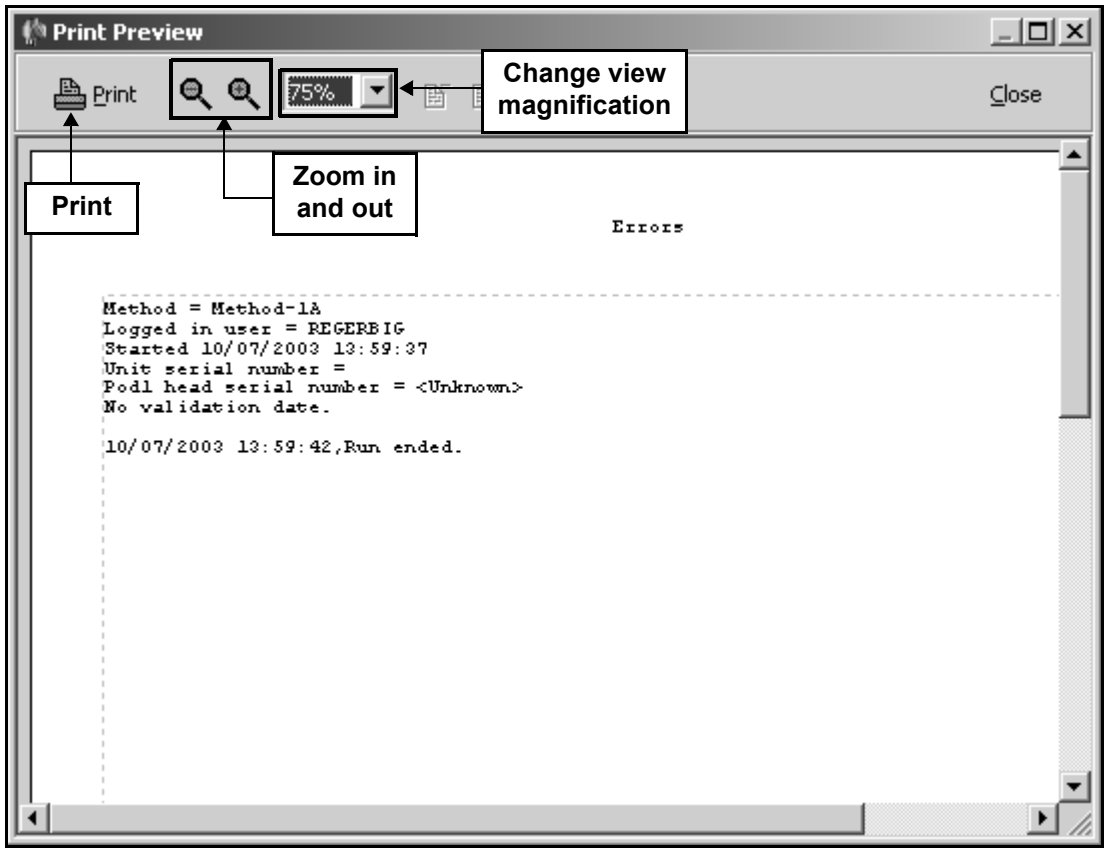


Figure 12-23. Print Preview

12.14 Opening a Saved Method

Methods saved in a project file can be opened only in that project file. Opening a method using the Open command opens it in development mode using the current revision for all project items. A revision of a method can be opened in read-only mode using the Check Out command (refer to Section 12.15, *Checking Out a Method*).

Note: Methods may also be opened from Recent Methods on the **File** menu. A deleted method may be opened from the Recycled folder. Opening a deleted method automatically restores it.

To open a saved method:

1. Choose **Open Method** on the toolbar

   OR

   From the **File** menu, choose **Open**. Open Method appears, listing all methods saved in the project file (Figure 12-24).

2. Right-click on a method and select **History** to view the history for the selected method.

3. Use Check Out (refer to Section 12.15, *Checking Out a Method*) to open a specific revision of a method in read-only mode.

4. Choose **View** and select the desired option, Icon, List, or Details, to change how methods are displayed in Open Method. Icon is the default view selection.

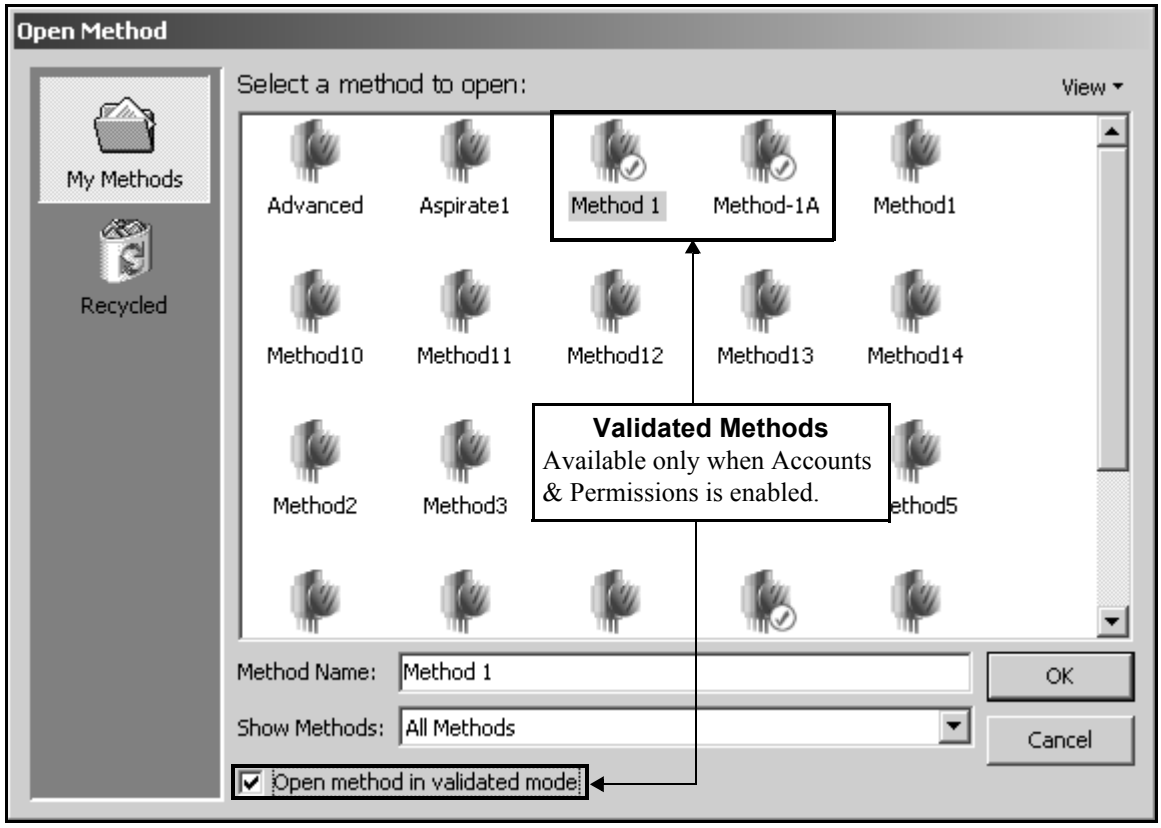


Figure 12-24. Open saved methods

5. Select the desired method to open.

   Note: When Accounts & Permissions is enabled, validated methods are denoted by a circled check (Figure 12-24). Only validated methods appear in Open Method for users that only have Run Validated Methods permission.

   Users with Develop Methods permission have the option to Open method in validated mode. Only previously validated methods can be opened in validated mode. Methods opened in validated mode are locked and cannot be modified.

6. Choose **OK**. The selected method is opened in the main editor.

   OR

   Choose **Cancel** to close Open Method without opening a method.

12.15 Checking Out a Method

Methods that have been checked in may be checked out. Checking out a method allows any revision of the method to be opened in read-only mode. The links created when the method was checked in allows Biomek Software to open the method with the same project items as when it was checked in. A method revision that is checked out may also be exported to a Biomek method file for use in another project or on a different system (refer to Section 12.16.1, *Exporting a Method*).

Note: Validated methods may be checked out in validated mode when Accounts & Permissions is enabled.

To check out a method:

1. From the File menu, choose **Check Out**. Check Out Method appears (Figure 12-25).

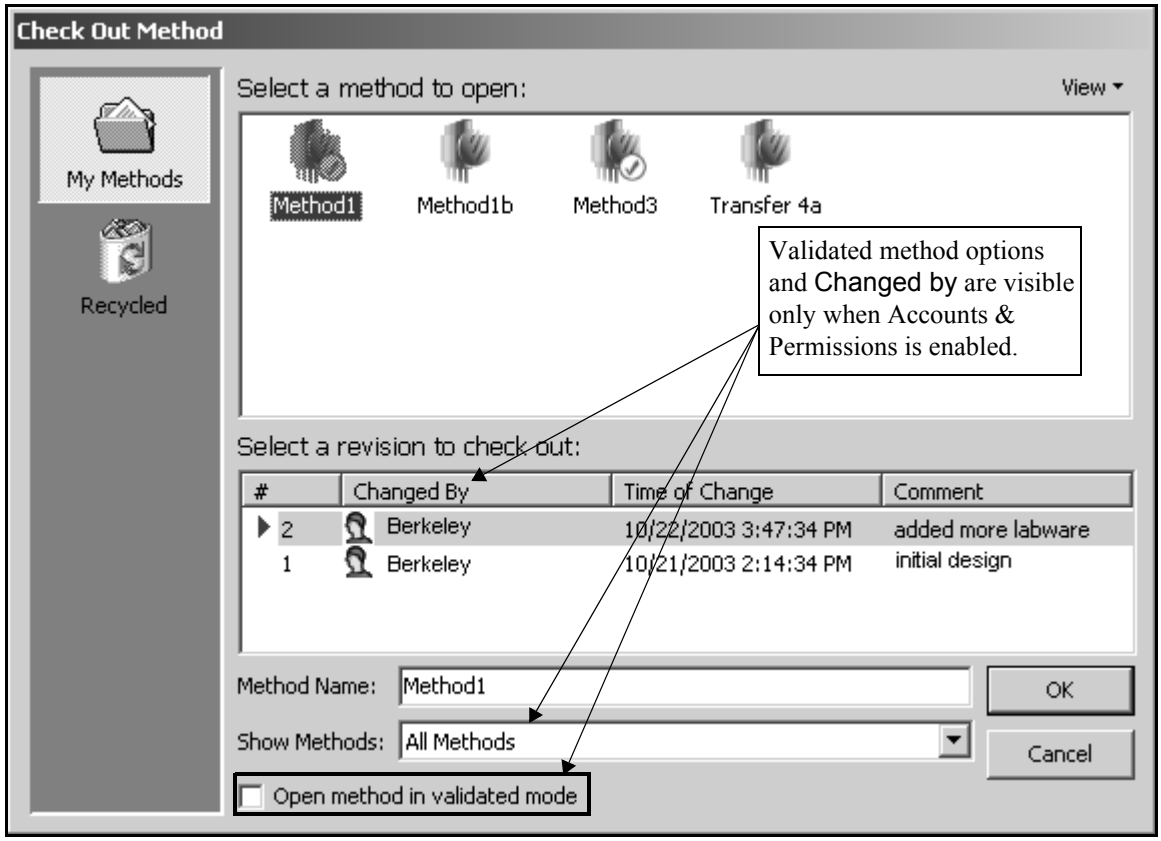


Figure 12-25. Check Out Method (Accounts & Permissions enabled)

2. In Select a method to open, select the desired method. All revisions of the selected method appear in Select a revision to check out.

   Note: When Accounts & Permissions is enabled, validated methods are denoted by a circled check (Figure 12-25). Only validated methods appear in Check Out Method for users that only have Run Validated Methods permission.

   Users with Develop Methods permission also have the option to Open method in validated mode. Only previously validated methods can be checked out in validated mode. When methods are checked out in validated mode, Accounts & Permissions generates the audit log during method runs.

3. In Select a revision to check out, select the desired revision.
4. Choose **OK** to check out the selected revision of the method.

   OR

   Choose **Cancel** to close Check Out Method.

12.16 Importing and Exporting Methods

Methods can be freely shared between projects or transferred between computers by exporting and importing Biomek method files. A method file is created by exporting a method from the active project file, and contains the method and all records required to execute the method. This allows the method to execute correctly when the method file is imported into a different project.

Note: When Beckman Coulter Accounts & Permissions is enabled, users with the Run Validated Methods or Develop Methods permission may export methods, but only those with the Develop Methods permission may import methods into a project (refer to Chapter 2, *Using Accounts & Permissions*).

Note: Projects may also be imported and exported. Refer to Section 6.10, *Importing and Exporting Project Files*, for more information.

This section covers:

- *Exporting a Method* (Section 12.16.1).
- *Exporting All Methods Associated With a Project File* (Section 12.16.2).
- *Importing Methods* (Section 12.16.3).

12.16.1 Exporting a Method

The method currently open in Biomek Software can be exported to a Biomek method file (*.bmf). The method file contains all records necessary to allow the method to be imported into another project file and executed.

Note: Method files exported from Biomek 3.0 or later are not compatible with earlier versions of the Biomek FX software.

Note: When Accounts & Permissions is enabled, users with Run Validated Methods or Develop Methods permission may export the currently open method. However, when validated methods are exported and later imported into different projects, they are no longer considered validated and open in development mode. After being imported, they can then be validated by users with Validate Methods permission.

Note: Text files, such as *.csv files used by the Worklist, Define Pattern, and Transfer From File steps, appear in the run history and may be opened directly from the window. However, when a project or validated method is exported, they are excluded from the Biomek import (*.imp) or method (*.bmf) file. To use a *.csv file in a method exported to another system, it must be copied to the system along with the Biomek import or method file.

To export the currently open method:

1. From the File menu, choose **Export**. Export Method appears (Figure 12-26).

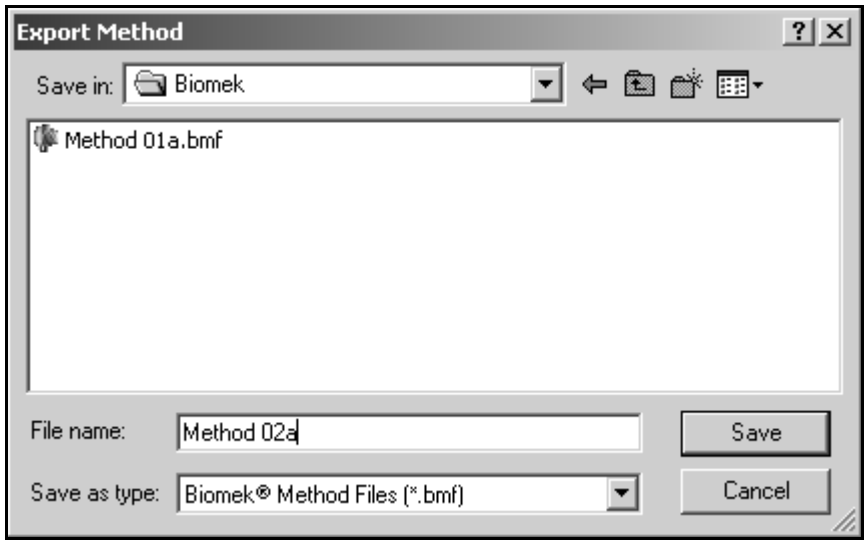


Figure 12-26. Export Method

2. In Save in, browse to the desired location to save the exported Biomek method file.
3. In File name, enter a name for the method file.
4. Choose **Save** to export and save the method file.

   OR

   Choose **Cancel** to close Export Method without exporting the method.

12.16.2 Exporting All Methods Associated With a Project File

All methods associated with the currently open project file may be exported at the same time. Method files are exported to a folder selected or created by the user.

Note: When Accounts & Permissions is enabled, users with Run Validated Methods or Develop Methods permission may export the currently open method. However, when validated methods are exported and later imported into different projects, they are no longer considered validated and open in development mode. After being imported, they can then be validated by users with Validate Methods permission.

To export all saved methods:

1. From the File menu, choose **Export All**. Browse For Folder appears (Figure 12-27).

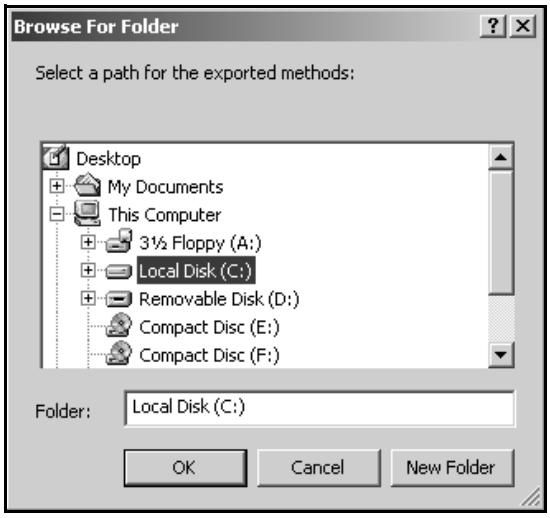


Figure 12-27. Browse For Folder

2. Use the tree view to browse to the folder where the exported method files will be saved.

   OR

   Choose **New Folder** to create a new folder for the method files. The new folder appears in the tree view with the name highlighted.

   Note: New Folder is available only when Biomek Software is run on a Windows 2000 or Windows XP system.

3. If a new folder has been created, enter a new name for it.

   OR

   To change the name of an existing folder, select the folder, click on the folder name a second time, and enter the new name.

4. Choose **OK** to export all methods to the selected folder.

   OR

   Choose **Cancel** to stop the operation without exporting any methods.

12.16.3 Importing Methods

Biomek method files previously exported from a project file can be imported into the project file currently active. Importing a method file also imports all the necessary records to execute the method.

Multiple methods can be selected and imported simultaneously.

To import methods into the project file:

1. From the File menu, choose **Import**. Import Method appears (Figure 12-28).

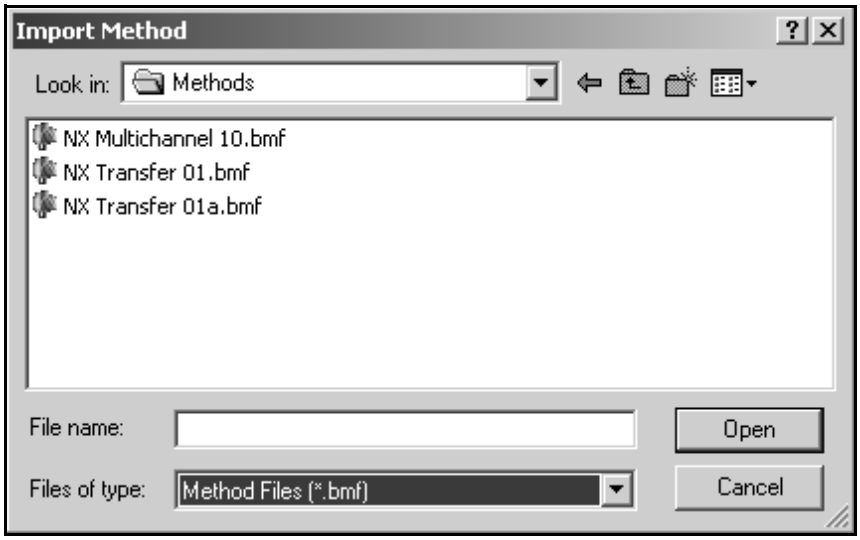


Figure 12-28. Import Method

2. In Look in, browse to the location where the desired Biomek method file(s) is saved.
3. Select the desired method file(s) to import. To import several method files, hold the **CTRL** key while selecting each method desired to import.
4. Choose **Open** to import the selected method file(s). Confirm appears (Figure 12-29).

   OR

   Choose **Cancel** to close Import Method without importing the method file.

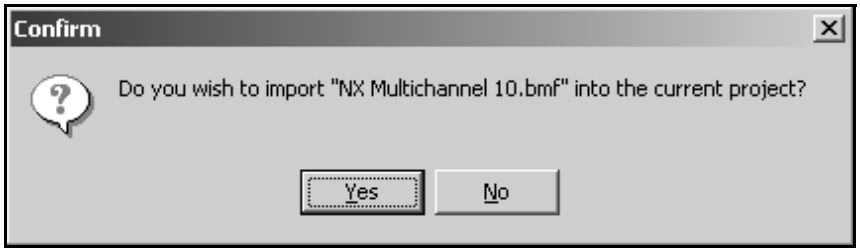


Figure 12-29. Confirming the method file(s) to import

5. Choose **Yes** to confirm the desired method file is selected. Confirm appears (Figure 12-30).

   OR

   Choose **No** to cancel the import operation without importing the method file.

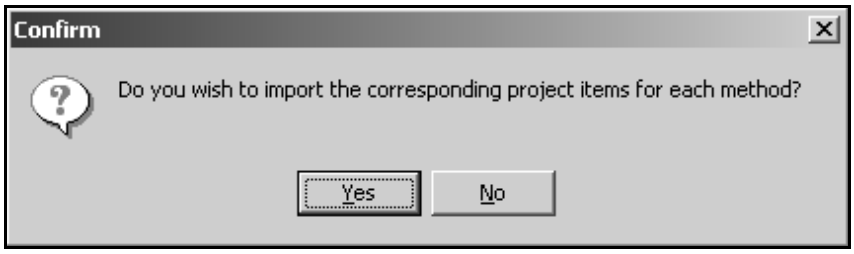


Figure 12-30. Choosing to import project items corresponding to the method

6. Choose **Yes** to import the method and project items used by the method, but not currently stored in the active project file. Check In Project appears, listing only project items used by the method that do not currently exist in the current project. These project items will be imported into the current project and linked to the method.

   Note: Check In Project may not appear if all project items in the current project file are compatible with the imported method.

   Items in the current project that are not used by the imported method are not linked to the method.

   OR

   Choose **No** to import the method but not the project items. No project items are linked to the method. The import operation is complete.

   Note: Importing project items used by the method is recommended. Choosing No may prevent the imported method from executing properly.

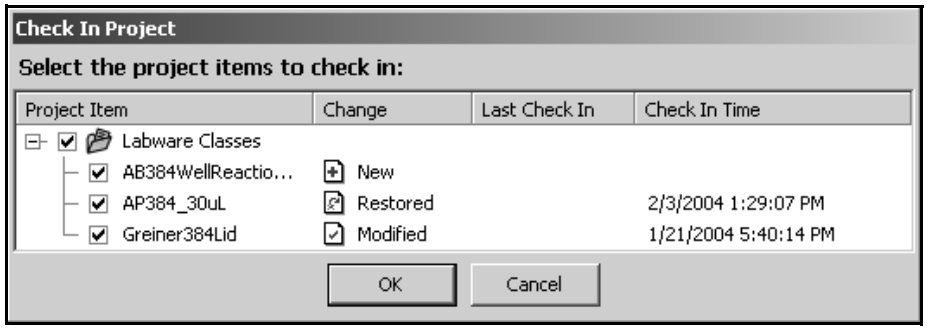


Figure 12-31. Check In Project

7. Choose **OK** to check in the revisions of project items associated with the method. If Accounts & Permissions is enabled, Check-In appears (Figure 12-32).

   Note: If Accounts & Permissions is not enabled, importing the method is complete.

   OR

   Choose **Cancel** to close Check In without checking in the project items.

8. In Reason, enter information or notes about the method or project revision being checked in. Text entered in Reason is date and time stamped, and stored in the audit log of all user activity.

9. If Accounts & Permissions is configured to require password checks for signing and check-in, enter the user **Password**.

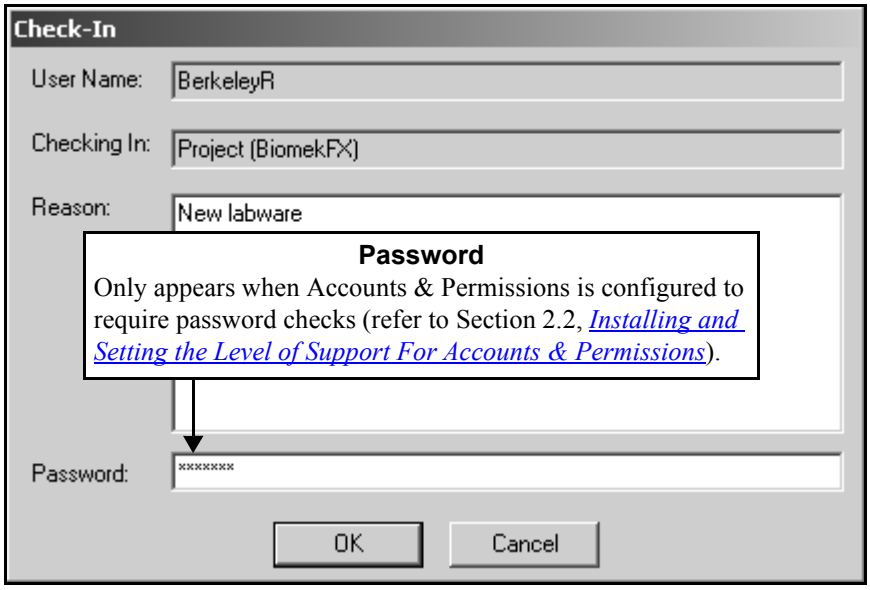


Figure 12-32. Check-In

10. Choose **OK** to check in the project items associated with the imported method(s).

    OR

    Choose **Cancel** to close Check-In without checking in project items associated with the imported method.

12.17 Deleting and Restoring Methods

Methods may be deleted from a project file, but are not removed from the project file and may be restored at any time.

12.17.1 Deleting Methods

To delete a saved method:

1. Choose **Open Method** on the toolbar.

   OR

   From the **File** menu, choose **Open**. Open Method appears, listing all methods saved in the project file (Figure 12-33).

2. Right-click on a method and select **History** to view the history for the selected method.

3. Choose **View** and select the desired option, Icon, List, or Details, to change how methods are displayed in Open Method. Icon is the default view selection.

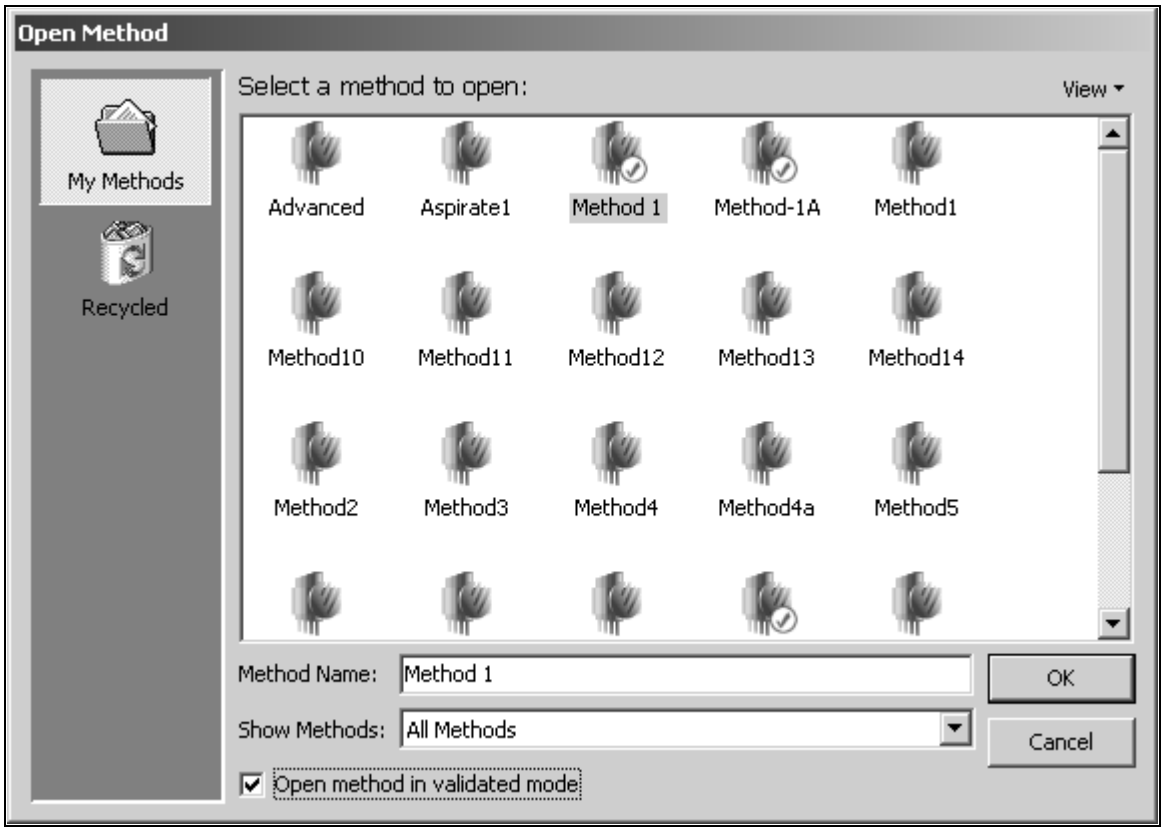


Figure 12-33. Open saved methods

4. Right-click the desired method to delete and select **Delete**. A confirmation appears (Figure 12-34).

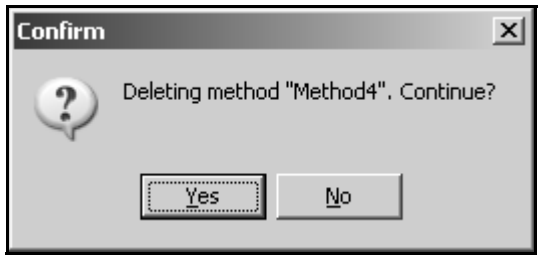


Figure 12-34. Confirm deletion of selected method

5. Choose **Yes** to confirm deletion of the selected method. The method is removed from My Methods and placed in Recycled.

   OR

   Choose **No** to keep the selected method.

12.17.2 Restoring Methods

To restore a deleted method:

1. Choose **Open Method** on the toolbar.

   OR

   From the **File** menu, choose **Open**. Open Method appears, listing all methods saved in the project file (Figure 12-33).

2. Right-click on a method and select **History** to view the history for the selected method.

3. Choose **View** and select the desired option, Icon, List, or Details, to change how methods are displayed in Open Method. Icon is the default view selection.

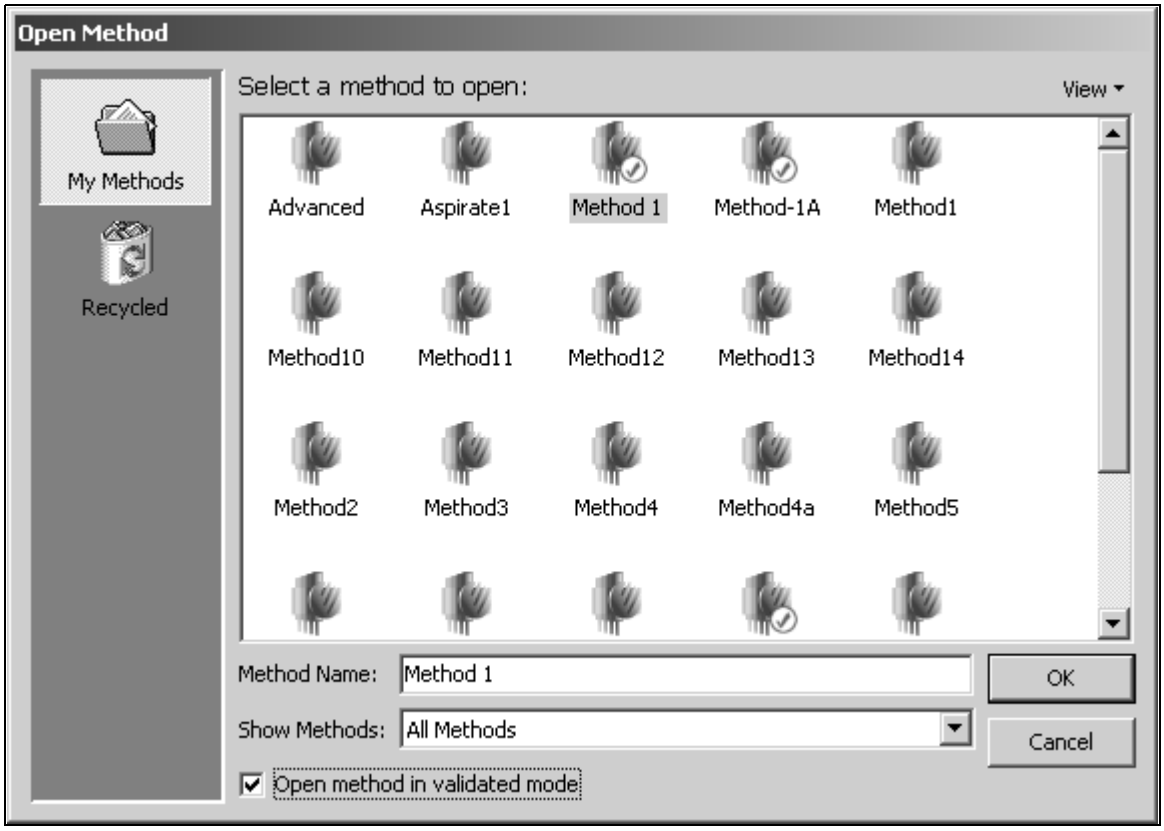


Figure 12-35. Open saved methods

4. Choose **Recycled** on the left side of Open Method to display all the methods that have previously been deleted (Figure 12-36).

5. Choose **View** and select the desired option, Icon, List, or Detail, to change how methods are displayed in Open Method. Icon is the default view selection.

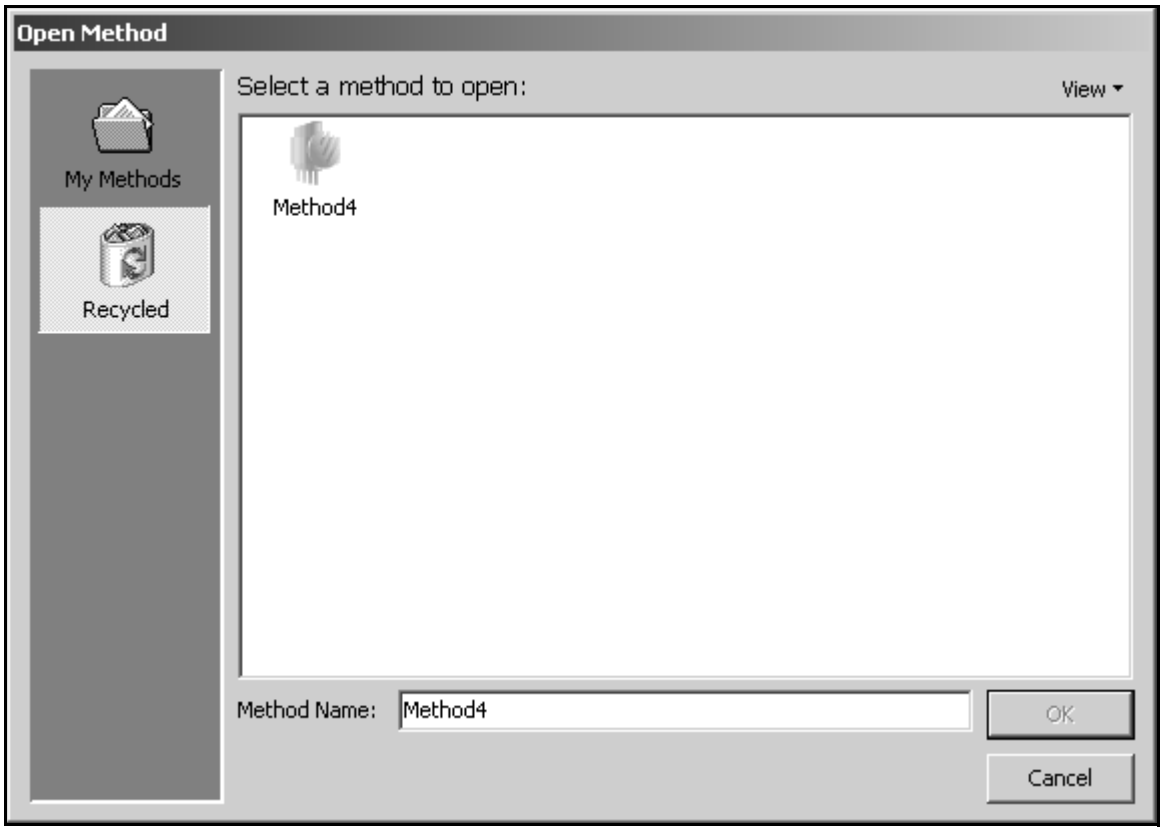


Figure 12-36. Recycled methods

6. Right-click the desired method to restore and choose **Restore**. The method is moved from Recycled to My Methods.

Note: A method may be opened directly from the Recycled folder by selecting the method and choosing **OK**. A confirmation appears stating that the method will be restored prior to opening the method. Choose **OK** to restore and open the method.

12.18 Running, Pausing, and Stopping a Method

Methods may be run on the Biomek instrument or in simulation mode immediately after they are built. If desired, methods may be configured to check for internal errors and confirm that labware on the instrument deck matches the layout specified in the method before every run.

This section covers:

12.18.1 Running a Method

After a method has been built, it may be run immediately on the Biomek instrument or in Simulate mode. In simulate mode, the software runs the method and checks for configuration errors in each step. While the method is running, the Biomek Simulator shows an animated 3-D model of the instrument performing the method.

When simulate mode is chosen, validated methods run in validated mode are recorded in Run History. Validated methods run in development mode are not logged. Validated methods are only available when Accounts & Permissions is enabled.

Note: When Beckman Coulter Accounts & Permissions is enabled, only users with Develop Methods or Run Validated Methods permission may run methods. Users with Develop Methods permission may run any method saved on the system; users with Run Validated Methods permission may only run validated methods. Refer to Section 2.3.1, *Assigning Biomek Software Permissions* for more information about the permissions available to users of Biomek Software.

To run a Biomek method:

1. From Hardware Setup in Port, choose:
   - Simulate to run the method in simulated mode.

     OR
   - Com1 to run the method on the instrument.
2. If running the method on the instrument, from the Instrument menu, choose **Home All Axes** to home the pod(s), if necessary. The pod(s) must be homed before performing methods each time the instrument is powered on.

   Note: Refer to the instrument hardware manual for more information about homing the pod(s).
3. To start the method run, on the toolbar, click the **green arrow** button.

   OR

   From the Execution menu, choose **Run**.

The method run begins. Depending on how Biomek Software is configured, two events may precede the execution of steps in the method:

- If Validate Before Run is selected in Options>Preferences, the method is validated internally to check for errors (refer to Section 29.2.1, *Configuring General Options*).

  Note: Validating the method for errors is a different process from validating a revision of a method when Accounts & Permissions is enabled. Refer to Section 12.11, *Validating a Method* for more information about validating a revision of a method.

- If Pause to confirm setup? is selected in the Instrument Setup step, a deck confirmation prompt appears (Figure 12-37).

CAUTION: Make sure the correct ALP is chosen when configuring the deck setup in the Deck Editor. ALPs vary in height and failure to choose each ALP correctly in the software may result in collisions between pod(s) and ALPs during operation.

To confirm that the deck setup is correct:

1. Visually confirm the deck setup on the instrument matches the display.

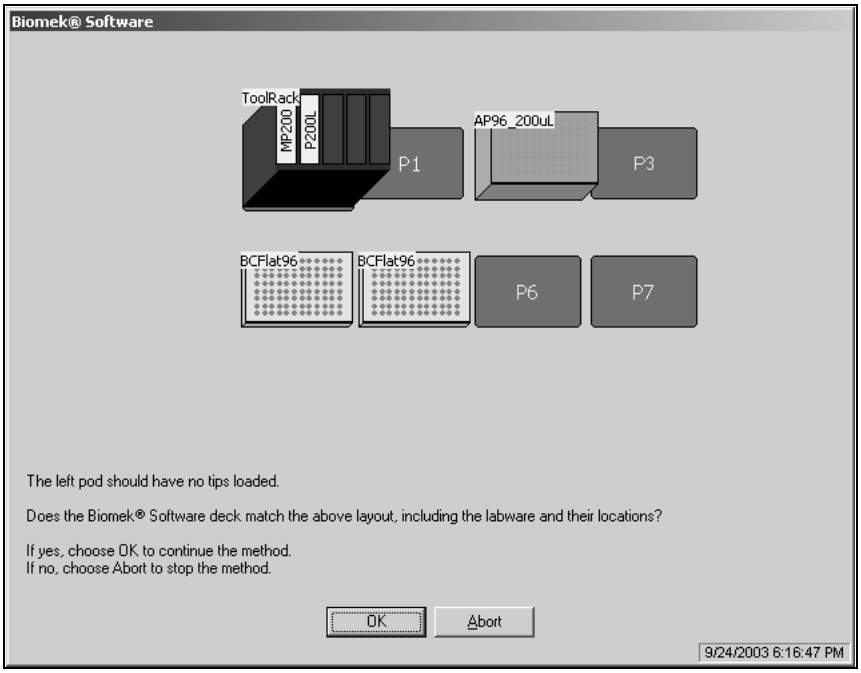


Figure 12-37. Deck layout confirmation prompt for a Biomek 3000 method

2. Choose **OK** if the setup is acceptable.

   OR

   Choose **Abort** to close the deck confirmation prompt and cancel the method run.

Note: To set up the deck correctly, either set up labware on the instrument deck to match the layout displayed in the deck confirmation prompt, or change the Deck Layout in the Instrument Setup step (refer to Section 15.2.4, *Populating the Deck with Labware*).

The method runs as soon as the deck setup is confirmed. The method run can be visually followed in the Method View; steps are highlighted in green as they are executed.

When a method runs in simulate mode, the Biomek Simulator appears and shows a 3-D animation of the method being performed (refer to Section 12.18.1.1, *Viewing the Method Run In the Biomek Simulator*).

Note: If Accounts & Permissions is configured to automatically log off users after a set period of operating system inactivity, the possibility exists that a user may be logged off automatically during a method run. When a user is logged off, the method run continues, but any prompts, such as the deck layout confirmation (Figure 12-37), are hidden from view until the same user, or another user with permission to run methods, logs on.

12.18.1.1 Viewing the Method Run In the Biomek Simulator

When a method is run in simulate mode, the Biomek Simulator appears and shows an animated 3-D model of the instrument performing the method (Figure 12-38).

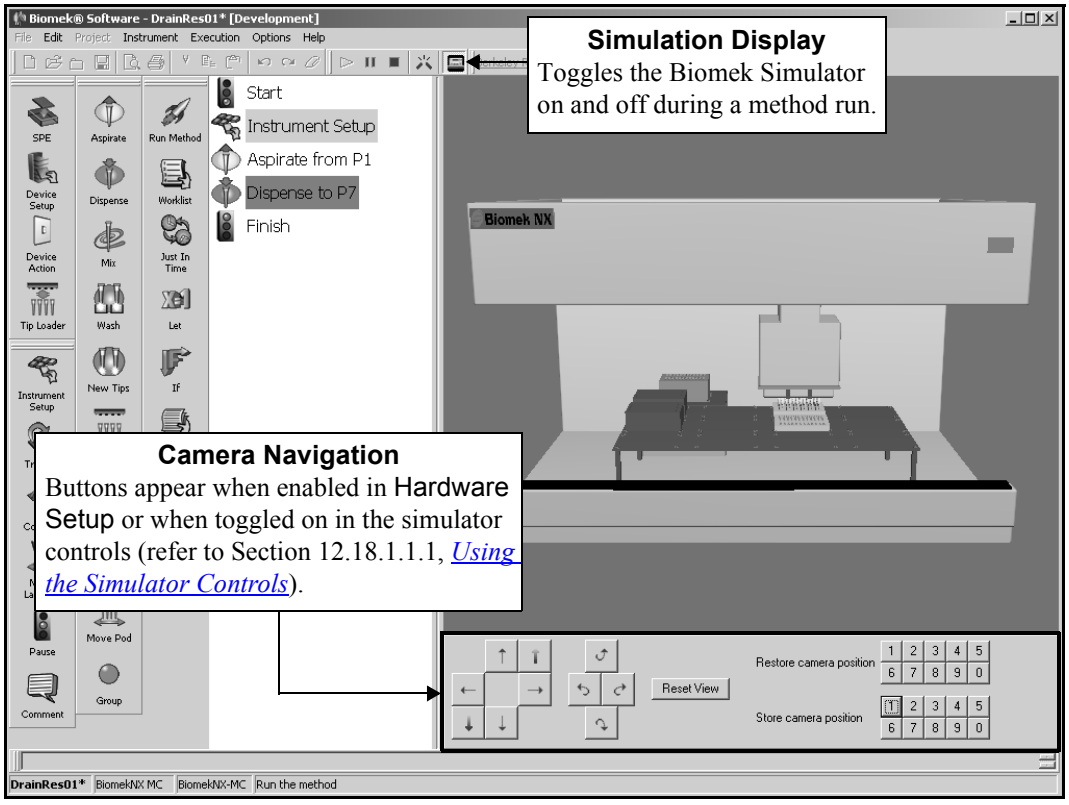


Figure 12-38. The Biomek Simulator showing a method run on an NX-MC

Five methods of controlling the simulator view are available:

- From the toolbar, choose **Simulation Display** to toggle the Biomek Simulator on and off while the method is executing.

  Note: The simulator automatically launches when the method run begins and closes when it is finished. If the animation does not run smoothly, try reducing the image quality setting in Hardware Setup (refer to Section 4.4.1, *Configuring Simulator Settings*).

- Change the view by placing the cursor in the simulator display, then clicking and dragging the mouse in the desired direction of rotation.
- Change the view by clicking the cursor in the simulator display and using the keyboard control keys defined in Camera (refer to Section 4.4.2, *Configuring Camera Controls*).
- Use the camera navigation controls to change, save, and reset the view (Figure 12-39). The navigation controls are displayed when enabled in Hardware Setup or when toggled on using the simulator controls (refer to Section 12.18.1.1.1, *Using the Simulator Controls*).

  Note: Additional simulator parameters may also be configured in Hardware Setup (refer to Section 4.4, *Configuring the Biomek Simulator*).

- Press the tilde (~) key to access the simulator controls (refer to Section 12.18.1.1.1, *Using the Simulator Controls*). The simulator controls provide the ability to change the simulation playback speed, toggle the camera navigation controls on and off, and modify the lighting that illuminates the simulated instrument.

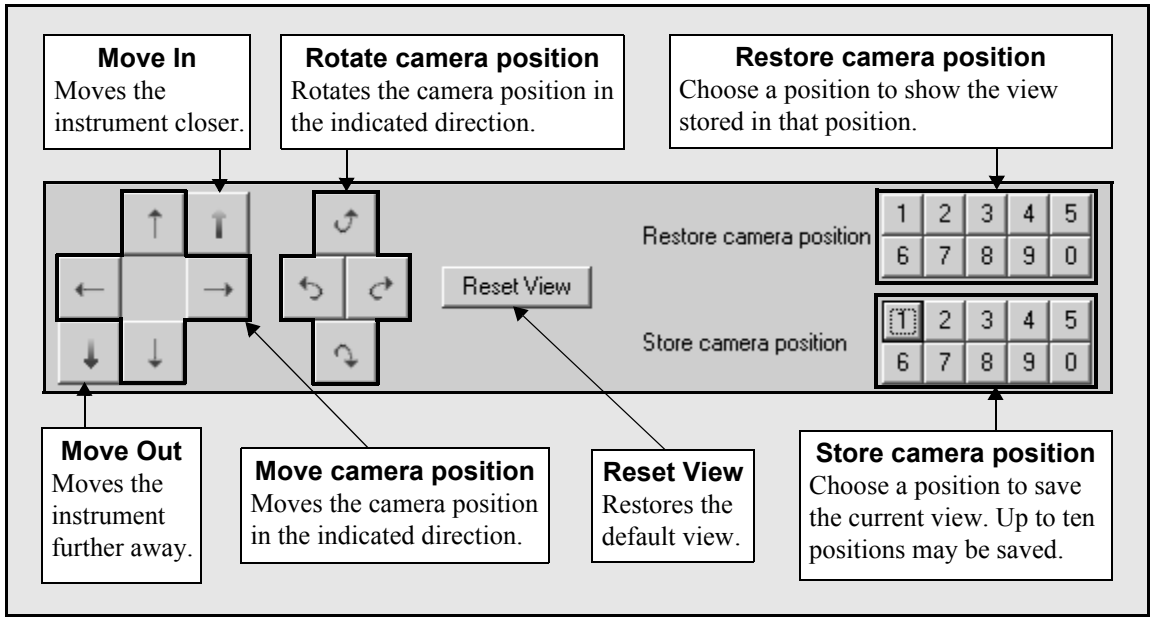


Figure 12-39. Camera navigation controls

12.18.1.1.1 Using the Simulator Controls

The simulator controls provide the ability to change the simulation playback speed, toggle the camera navigation controls on and off, and modify the lighting that illuminates the simulated instrument.

To access and use the simulator controls:

1. During a simulated method run, press the tilde (~) key to toggle the simulator controls on. The simulator controls appear (Figure 12-40).

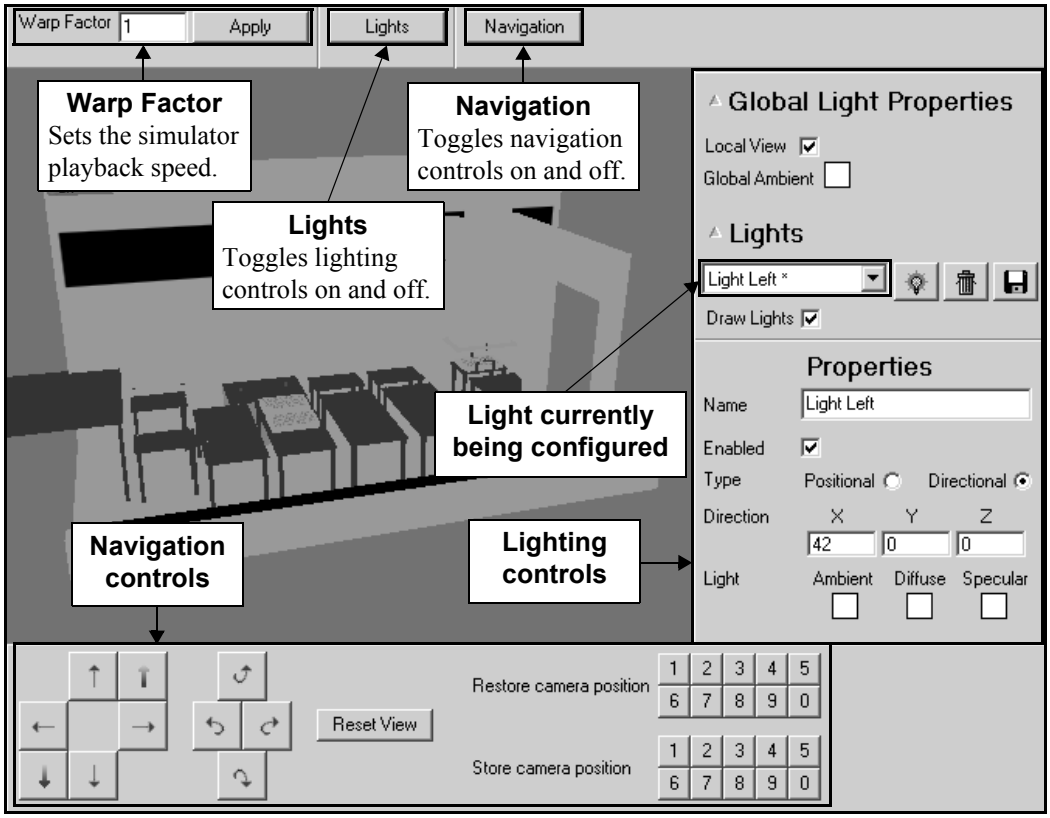


Figure 12-40. Biomek Simulator with all simulator controls enabled

2. Enter a new **Warp Factor** and choose **Apply** to change the simulator playback speed, if desired. Warp Factor 1 runs the simulation in real time, Warp Factor 2 at twice normal speed, and so on.
3. Choose **Lights** to toggle the lighting controls on, if necessary.
4. Create a new light or choose an existing light from the pull-down menu, and use the lighting controls to modify the lighting properties as desired. Table 12-1 provides a description of each lighting control.

   Note: Modifying the lighting parameters is not recommended because the default parameters cannot be restored if changed or deleted.

5. Choose **Navigation** to toggle the camera navigation controls on, if necessary. Refer to Section 12.18.1.1, *Viewing the Method Run In the Biomek Simulator*, for detailed information about using the navigation controls.
6. Press the tilde (~) key to toggle the simulator controls off, if desired.

Table 12-1. Simulator Lighting Controls

Control	Description	Additional Information
Global Light Properties		
Local View	Select to subtly change the intensity of light.	
Global Ambient	Choose the color of ambient light present in the simulator view.	
Lights		
 (new light)	Create a new light.	
 (delete light)	Delete the light currently selected in the pull-down menu.	A light that has been deleted cannot be restored.
 (save light)	Save the configuration of the light currently selected in the pull-down menu.	
Draw Lights	Select to display the light sources in the simulator view.	
Properties		
Name	Change or enter a new name for the selected light.	
Enabled	Select to enable (turn on) the selected light.	
Type	Choose the type of light: **Positional** or **Directional**.	Positional light radiates from the source in all directions; directional light radiates from the source in a single direction.
Direction	Enter X, Y, and Z coordinates for the direction from which the selected light is directed at the instrument.	
Light	Choose colors for the **Ambient**, **Diffuse**, and **Specular** properties of the light.	Ambient and Diffuse define the color of the 3-D model of the instrument when the light is enabled. Specular defines the color of specular highlights (glare).
Attenuation	Enter values in each field to define the fall off from the center of the light.	Available only when Positional is the type of light selected. Entering higher values causes the light to fall off quicker.
Spotlight	Choose to cast a tightly focused beam of light at the 3-D model of the instrument.	Available only when Positional is the type of light selected.
Spot Direction	Enter X, Y, and Z coordinates for the direction from which the spotlight is directed at the instrument.	Available only when Spotlight is the type of light selected.

Table 12-1. Simulator Lighting Controls

Control	Description	Additional Information
Spot Exponent	Enter a value to set the focus of the spotlight.	Available only when Spotlight is the type of light selected. A low value distributes the light evenly across the illuminated area; a high value concentrates more light in the center of the spotlight.
Spot Cutoff	Enter a value to set the size of the spotlight cone, which determines the total surface area covered by the spotlight.	Available only when Spotlight is the type of light selected.

12.18.2 Pausing a Method in Progress

Pause causes the method to halt after the Biomek instrument has completed the move in progress. For example, if the instrument is in the process of loading tips when Pause is selected, it finishes loading the tips before the system halts. When the method is resumed, it continues as though it were never halted.

Note: A method cannot be edited during a pause.

Use one of the following procedures to pause a method:

CAUTION: No changes to the Biomek state are permitted while a method is paused. Changes can be made to the labware contents, but not the deck or the devices.

From the Execution menu, choose **Pause**.

OR

Choose **Pause** on the toolbar. The instrument completes the move in progress and stops.

- ***FX***, ***NX-MC***, ***NX-S8*** — The instrument deactivates the light curtain when the method is paused.

To resume the method run, choose **Pause** again. The light curtain is reactivated, and the method resumes from the point where it was paused.

12.18.3 Stopping a Method in Progress

WARNING: The light curtain is a safety device. Use it to stop a method only in an emergency.

Use Stop to halt a method during its run when there is no intent to resume method execution. If the pod is in the process of a move, the operation is not completed. Since the method is halted, this option allows edits to the method or changes to the hardware and deck.

Note: Stop may not halt operations already in progress on external devices, such as Stacker Carousels.

Use one of the following procedures to stop a method during a run:

- From the Execution menu, choose **Stop**.

  OR

- Choose **Stop** on the toolbar.

  OR

- ***FX***, ***NX-MC***, ***NX-S8*** — Break (violate) the light curtain by no more than one inch, and choose Abort.
- ***3000*** — Press the STOP button on the front of the instrument

Note: Use standard procedures to rerun the method.

12.18.4 Snapping a Continuation (FX, NX only)

Another way to halt a method in progress is by snapping a Continuation. Continuations stop the current method and allow corrections in the middle of a method run. The method can be restarted from the point where the method was halted. For more information about Continuations, refer to Section 25.11, *Using Continuations (not available on a 3000)*.

To snap a continuation, choose **Snap** to create a Continuation (refer to Section 25.11, *Using Continuations (not available on a 3000)*).

12.18.5 Disabling Steps Within a Method

Individual steps within a method can be disabled for execution. When the method is run, Biomek Software ignores any disabled steps.

Disabling steps is useful for experimenting with the configuration of certain steps during method development, or when only a subset of the steps in a method need to be executed in a method run for an assay.

Note: If a method is checked out in validated mode, steps cannot be disabled or enabled.

To disable a step in a method:

1. Select the desired step to disable.
2. From the Edit menu, choose **Disable step**.

   OR

   Right-click the step and choose **Disable step** from the menu. The step icon changes to grayscale with a red X to indicate the step is disabled.

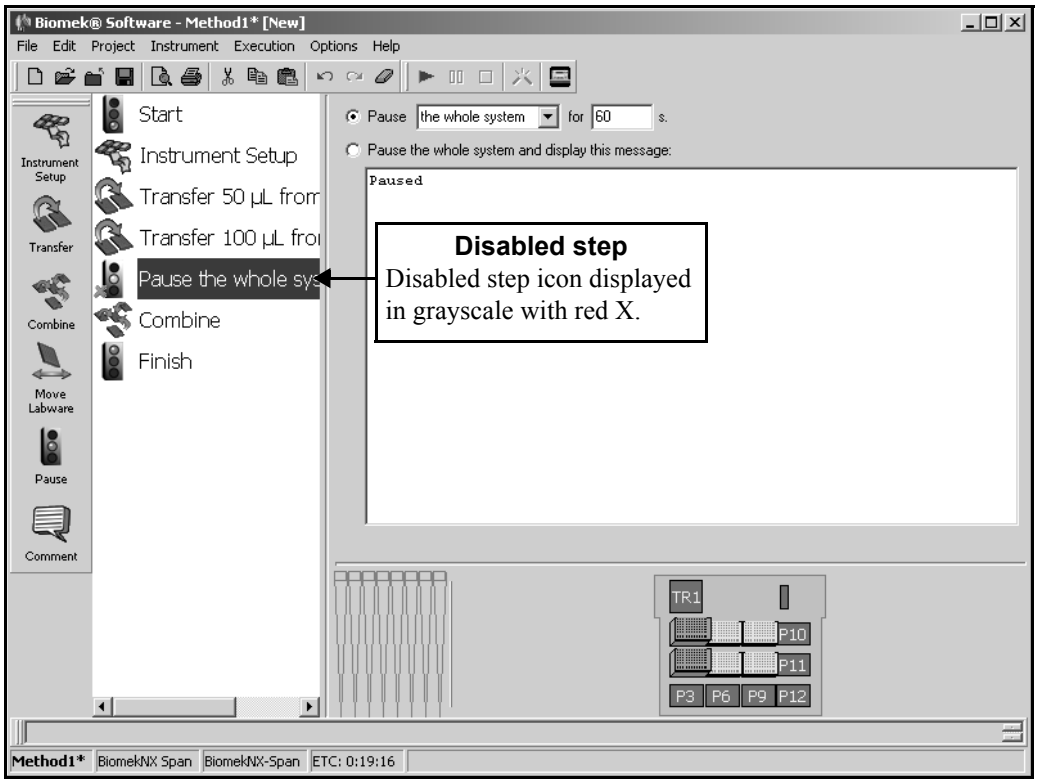


Figure 12-41. Step disabled in Method View

To enable a previously disabled step:

1. Select the disabled step to enable.
2. From the Edit menu, choose **Enable step**.

   OR

   Right-click the step and choose **Enable step** from the menu. The red X disappears and the step icon changes to color to indicate the step is enabled.

12.18.6 Purging Air From Span-8 Pod Before a Method Run (FX and NX-S8 Only)

When a Span-8 Pod is idle, air bubbles form in the tubing and syringes and interfere with pipetting accuracy. These air bubbles may form prior to beginning a method run or while the pod is sitting idle during a method run. Therefore to accurately transfer liquid, air *must* be purged from the tubing and syringes of the Span-8 Pod. The purging process draws system fluid through the tubing and syringes until all air bubbles are removed.

Purging the tubing and syringes of air is accomplished through Manual Control (refer to Section 6.5.7, *Purging Air from the Syringes and Tubing*) or by inserting a Span-8 Wash Tips step (refer to Section 18.8.1, *Configuring the Span-8 Wash Tips Step for a Passive Wash*) in a method before the Span-8 Pod moves:

- Use Manual Control immediately before running a method or insert a Span-8 Wash Tips step at the beginning of the method to purge the tubing and syringes of air.
- A Span-8 Wash Tips step using approximately 10 to 15 mL of system fluid may be inserted after the Instrument Setup step to purge the tubing and syringes of air.
- When using a dual-pod system, it may be necessary to insert another Span-8 Wash Tips step into the method immediately before a Span-8 Pod begins to move if the pod has been idle.

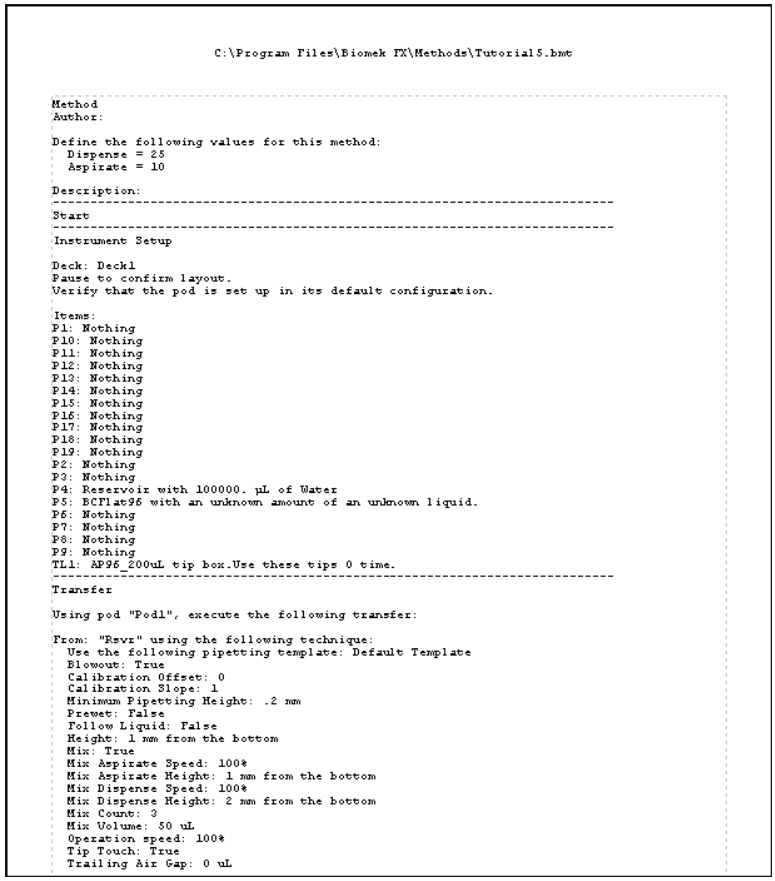
12.19 Printing a Method

Printing a hard copy of a method is useful if a computer monitor is some distance from the instrument, it is necessary to show the method steps to someone away from the lab, or a hard-copy record of the method is needed to recreate the method. All of the step configurations are listed in the hard copy.

To print a Biomek method in sequential text form:

1. Select the **File** menu.
2. Choose **Print**. A print-out similar to Figure 12-42 is produced at the default printer.

Note: Use **Print Preview** from the File menu to open a dialog which displays how the method appears when printed.



C:\Program Files\Biomek FX\Methods\Tutorial5.bmt

Method
Author:

Define the following values for this method:
  Dispense = 25
  Aspirate = 10

Description:

Start

Instrument Setup

Deck: Deck1
Pause to confirm layout.
Verify that the pod is set up in its default configuration.

Items:
P1: Nothing
P10: Nothing
P11: Nothing
P12: Nothing
P13: Nothing
P14: Nothing
P15: Nothing
P16: Nothing
P17: Nothing
P18: Nothing
P19: Nothing
P2: Nothing
P3: Nothing
P4: Reservoir with 100000. µL of Water
P5: BCPlate96 with an unknown amount of an unknown liquid.
P6: Nothing
P7: Nothing
P8: Nothing
P9: Nothing
TL1: AP96_200uL tip box.Use these tips 0 time.

Transfer

Using pod "Pod1", execute the following transfer:

From: "Rsvr" using the following technique:
  Use the following pipetting template: Default Template
  Blowout: True
  Calibration Offset: 0
  Calibration Slope: 1
  Minimum Pipetting Height: .2 mm
  Prewet: False
  Follow Liquid: False
  Height: 1 mm from the bottom
  Mix: True
  Mix Aspirate Speed: 100%
  Mix Aspirate Height: 1 mm from the bottom
  Mix Dispense Speed: 100%
  Mix Dispense Height: 2 mm from the bottom
  Mix Count: 3
  Mix Volume: 50 uL
  Operation speed: 100%
  Tip Touch: True
  Trailing Air Gap: 0 uL

Figure 12-42. Printed method

12.20 Improving a Method

Biomek provides procedures that allow a method to be observed in order to make adjustments to improve the way it runs.

Here are three procedures to improve the way a method runs:

- *Running the Method at Slow Speed* (Section 12.20.1).
- *Snapping a Continuation (FX and NX Only)* (Section 12.20.2).
- *Using Logging* (Section 12.20.3).

12.20.1 Running the Method at Slow Speed

To slow down the pod speed to provide more time to examine the method in progress:

1. From the Instrument menu, choose **Hardware Setup**. Hardware Setup appears (Figure 12-43).
2. On the left side of Hardware Setup, select the desired pod.
3. Expand the Additional Pod Settings.
4. Set the Speed Limit to **20%**. This is the recommended speed for observing a method as it runs (Figure 12-43).

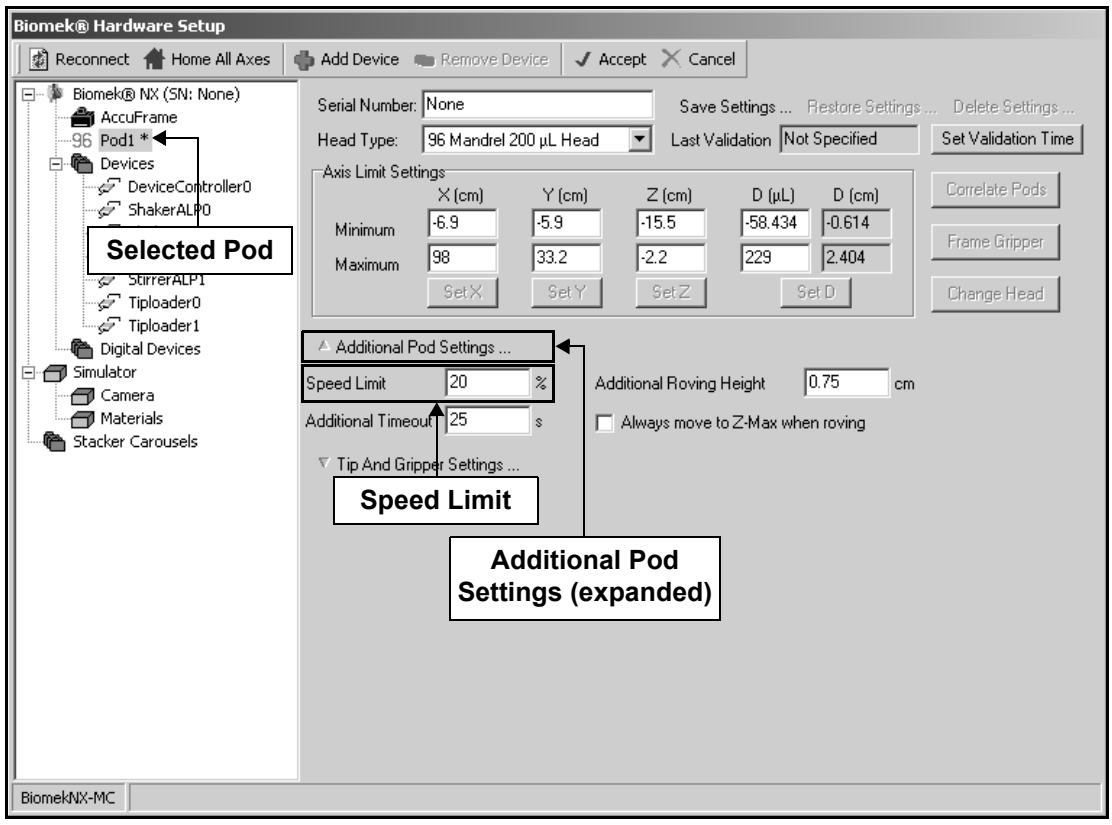


Figure 12-43. Changing the method speed in Hardware Setup

5. Choose **Accept** to save the changes and close Hardware Setup.
6. From the Execution menu, choose **Run** to start the method.

Note: Another way to run the method slowly is to use Single Step on the Execution menu. Single Step allows the unit to move one operation at a time by clicking the launch button for each move. Refer to Section 25.12, *Performing Single Operations Within Steps*, for more information about using Single Step.

12.20.2 Snapping a Continuation (FX and NX Only)

Possible changes in a method may be desired after observing a method. Snapping a Continuation stops the method in progress, allows settings to be changed, and then continues the run. Another option is to snap a Continuation after the run has been observed at slow speed to return the speed to 100%. This causes the first part of the method to run slowly to observe the execution, but the rest of the method runs at full speed.

Note: Refer to Chapter 25, *Handling and Preventing Errors*, for more information about continuations.

1. Once the method is running, choose **Snap Continuation** from the toolbar.
2. Modify the method as desired.
3. Start the continuation.

12.20.3 Using Logging

Text format logs are used for close examination of every operation that occurs during method execution in order to modify the run to improve the method. These generated logs give detailed information, including the date and time.

There are several logs available in the Biomek Software:

- Details — Provides comprehensive information on every operation the instrument performs.
- Errors — Lists errors for a method, if any.
- Pipetting — Lists aspirate and dispense operations.
- Span8Pipetting — captures only Span-8 pipetting operations that occur during a method run, including location and labware name or type.
- Span8Transfer — captures only Span-8 transfer operations that occur during a method run, including location and labware name or type.

  Note: The addition of SampleID data sets also allows the Span8Pipetting and Span8Transfer logs to include well identification information.

  - ***FX***, ***NX-S8*** — Span8Pipetting and Span8Transfer logs are available only for these instruments.
- UnifiedPipetting — Captures pipetting operations, along with Sample IDs for wells, performed by any pods, including information on where the aspirate or dispense operation occurs.
- UnifiedTransfer — Captures transfer operations, along with Sample IDs for wells, performed by any pods, including information on the source and destination labware.

To turn logging on or off:

1. From the toolbar, choose **Options**.
2. Choose **Log Configuration**.
3. Check or uncheck the desired Log(s).

Note: Refer to Chapter 26, *Generating and Using Log Data*, for more information on generating and using log data.

13 Using Variables and Expressions in a Method

13.1 Overview

A variable is a value that has been assigned a name. A value can contain text strings, arrays, expressions, objects, operators, or numerical constants. Any value assigned a name can be referenced repeatedly during a method by inserting the variable name in any applicable field in a step configuration.

An expression is a one-line combination of alphanumeric characters and/or variables combined using mathematical operations. An expression can be used anywhere a variable can be used, and it may use one or more variables.

Note: For example the variable Volume may be required in a field, but accuracy may require additional information. The variable Volume may be modified into an expression, such as Volume+ 10 or Volume/4.

.Advantages to using variables include:

- Several variables can be created in one step; for example, the Start step can be used to define multiple variables that are available to every step within a method, while the Let and Worklist steps can be used to create multiple variables that can be used by their substeps.
- Several variables can be used in one step.
- A name can be entered as a variable or expression in any step configuration field where the value associated with the variable or expression is required. Biomek Software then interprets the variable or expression and replaces it with the associated value.
- A variable can be used as many times as necessary; for example, multiple steps within Let and Loop steps can all use the same variable.

  Note: To make variables available to all steps in a method, define the variables in the Start step.

- Variables used extensively in a method need only be changed in the step they are defined to change the value in every step in the method that uses the variable.
- When a method is run more than once, the value associated with that variable can be changed in the step, and the associated values within the method automatically change accordingly.

13.2 Using Variables

A variable consists of a name and a value. To use a variable, enter an equal sign (=) followed by the variable name into the step configuration requiring the variable. For example, in Figure 13-1, the variable =AspValue, created in the Start step configuration of the method (Figure 13-2), is entered in the Volume field.

The Biomek Software internally substitutes the name with its value, but the name remains in the field. In the example, the variable AspValue is substituted internally by the value 25. The value of 25 is never displayed, only the variable name.

Variable values are not assigned a unit of measure. When a variable is identified in a step, the unit of measure is defined by the requirements of the step. For example, if a variable named Aspirate is assigned a value of 5, and **=AspValue** is entered in a field that requires microliters, the software interprets the value of 5 as 5 microliters; likewise, if **=AspValue** is entered in a field that requires seconds, the software interprets the value as 5 seconds.

Note: If a variable is used in a pipetting step with an auto-selected technique, and the value of the variable changes such that a new technique would be selected, the technique is automatically updated when the step is executed.

Note: Enter the variable name preceded by the equal (=) sign in any field where the value it represents is appropriate.

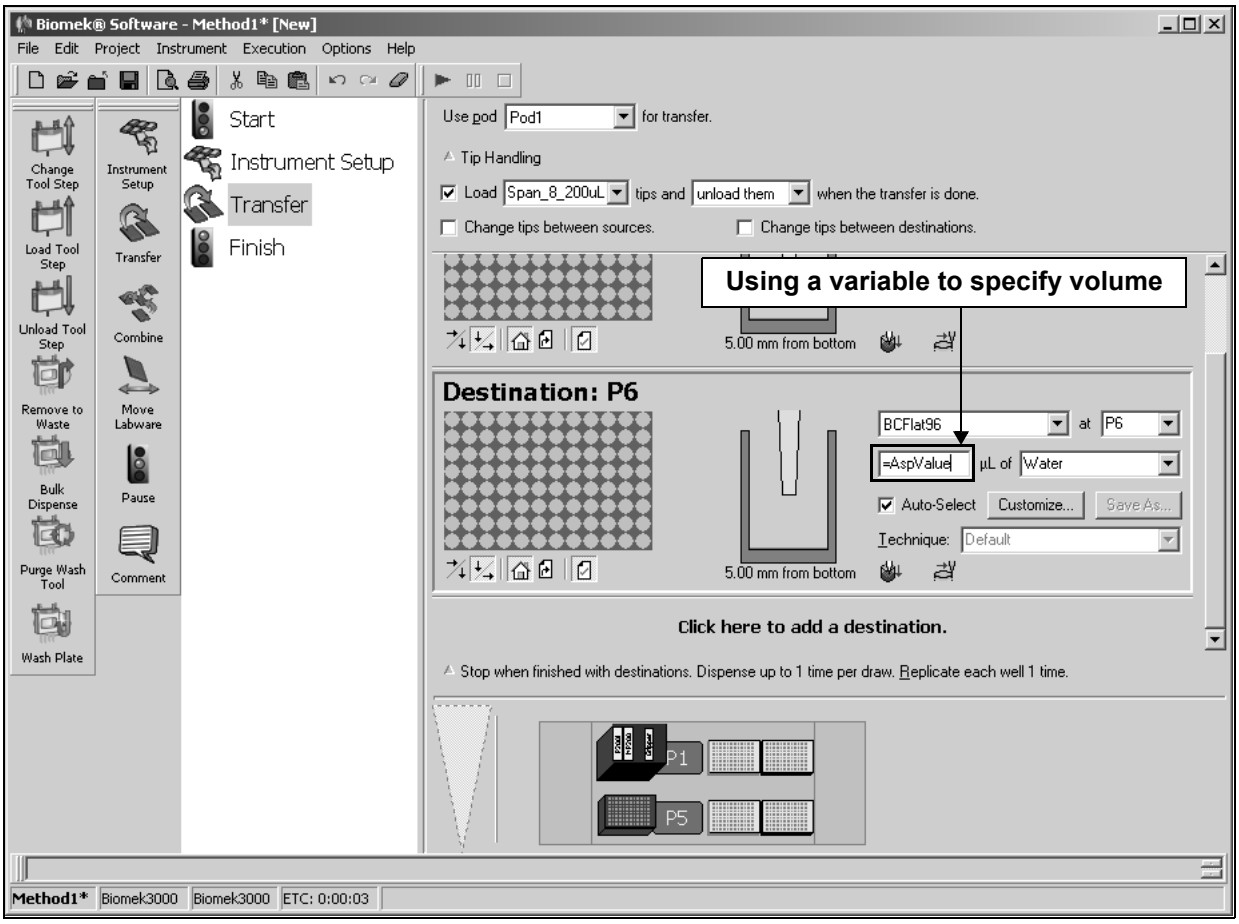


Figure 13-1. Transfer step using the AspValue variable

13.2.1 Creating Variables

Variables may be created in several steps. Refer to the section for the step for more specific information on creating variables with that step:

- *Configuring the Start Step* (Section 12.2.1).
- *Loop Step* (Section 16.9).
- *Run Method Step* (Section 17.3).
- *Worklist Step* (Section 17.4).
- *Let Step* (Section 17.6).
- *Create Group Step* (Section 21.3).
- *Set Global Step* (Section 21.7).
- *Define Procedure Step* (Section 21.8.1).
- *Run Procedure Step* (Section 21.8.2).

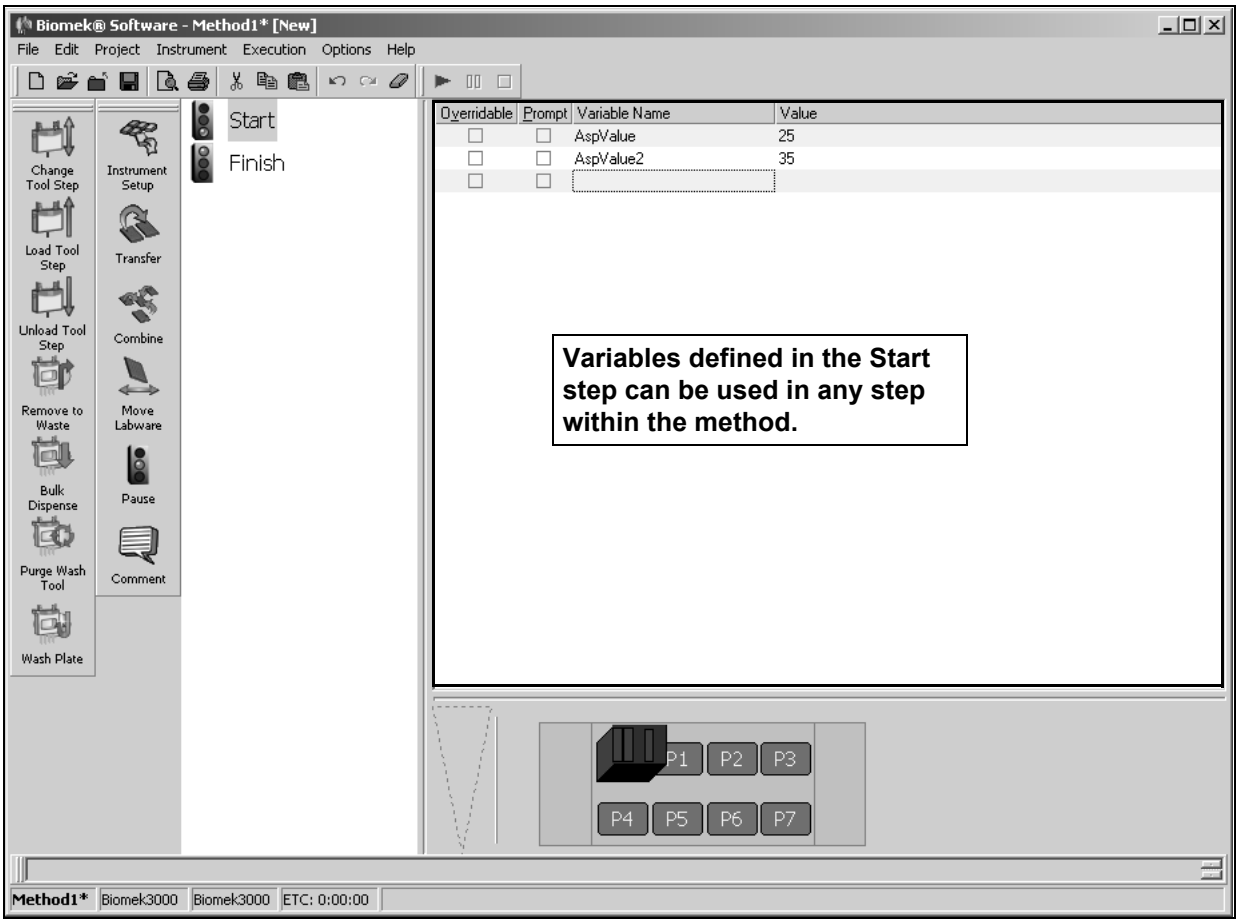


Figure 13-2. Variables configured in the Start step

13.2.2 Using Variables in a Method

To use a variable created previously in the method, the variable name is entered into the configuration of the step. In the example, the variable AspValue, created in the Start configuration (Figure 13-2), is entered in the µL (volume) field of the Transfer step (Figure 13-3).

Note: Enter the Variable Name in any field where the value it represents is appropriate.

The Biomek Software internally substitutes the name with its value, but the name remains in the field. In the example (Figure 13-2), AspValue is substituted internally by the value 25. The value of 25 is never displayed, only the variable name AspValue.

Variables previously configured in any step may be used in any field where the value of the variable is a valid value for the field. For example, a variable with a value of 50 would be appropriate in a Volume field, but not in a field asking for a deck position.

Any variables used in a method must be defined prior to the step in which they are used, or an error occurs. For example, if the variable AspValue is not defined when it is entered in the Transfer step, an error results.

Note: Keep this in mind when writing a method that will be run in another method using the Run Method step. If the Run Method step in the other method specifies any variable values, those variables must be created in the method for method validation. When the method is run through the Run Method step, it is run using the variable values specified in the Run Method step.

Note: Variables created with some steps are only applicable for that step and its substeps. For example, a variable created with a Let step may only be used for substeps of the Let step.

To use a previously created variable in a step configuration:

1. Select the appropriate field in the desired step configuration.
2. Enter the variable name, preceded by an equal sign. For example, **=AspValue** in the Volume field of the Transfer step (Figure 13-3) indicates that a volume equal to the value of the variable AspValue is dispensed in the selected destination labware.

Note: Variables may be used in any field which the value is a valid entry. For example, a variable that has a text value cannot be entered in a field that is expecting a numerical input.

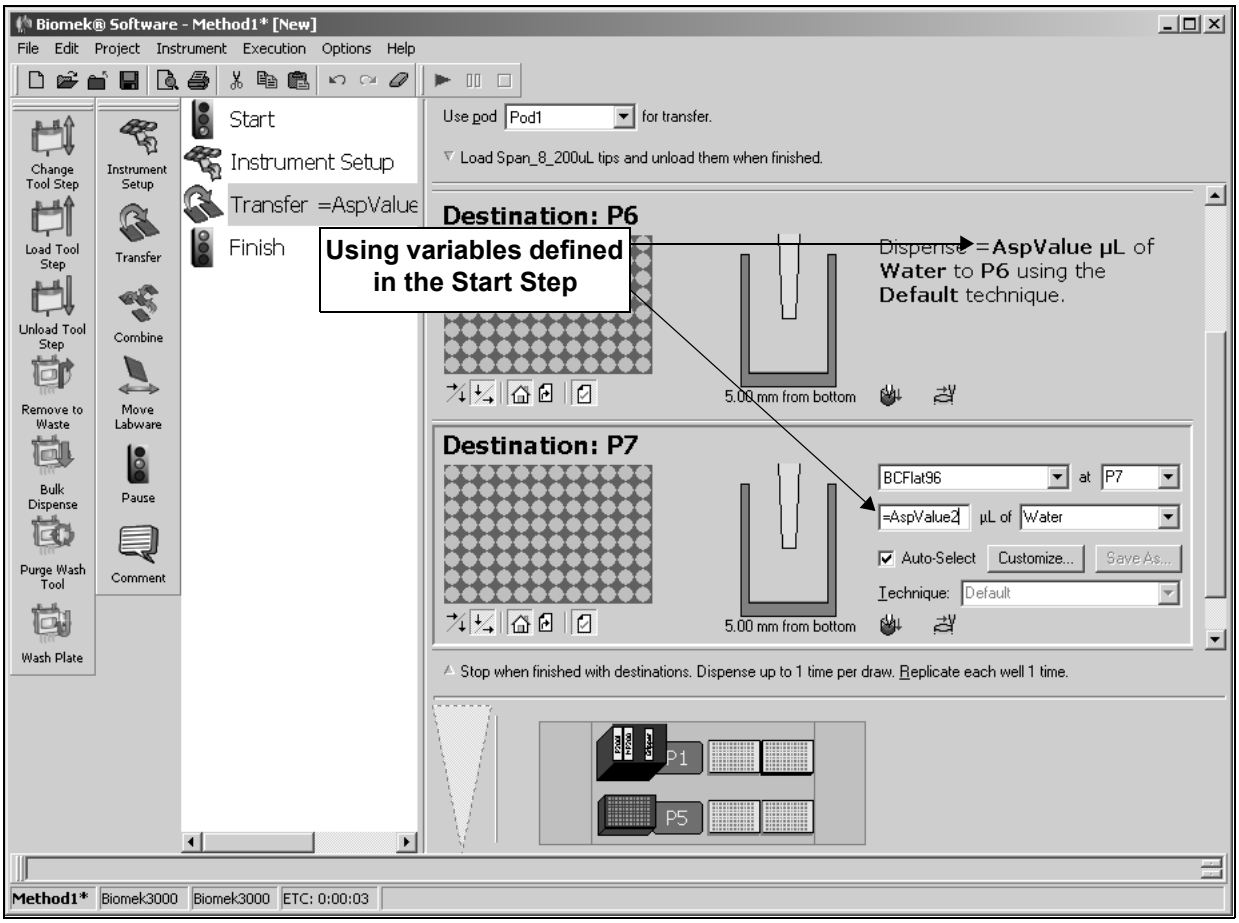


Figure 13-3. Transfer step using the AspValue and AspValue2 variables defined in the Start step

13.3 Using Expressions

An expression is a one-line combination of variables, such as Aspirate; mathematical operators, such as addition (+); string constants, such as “P4”; and numeric constants. An expression can be used anywhere a variable can be used and may contain one or more variables; for example, the variable Volume may be required in a field, but accuracy may require additional information. The variable Volume may be modified into an expression, such as Volume + 10 or Volume/4.

Like variables, expressions start with an equal sign and can contain operators allowed in VBScript programming, such as addition (+), division (/), exponentiation (^), concatenation of strings (&), and functions like random (Rnd), rounding (Round), or absolute value (Abs).

An expression can be entered in any step configuration field where the value associated with the expression is required. Biomek Software interprets the expression and replaces it with the associated value.

Three examples of expressions are:

- If a variable called my_volume is defined, transferring from a 96-well microplate to each quadrant of a 384-well microplate could be accomplished by placing =my_volume / 4 in the volume field.
- If the three variables VolumeA, VolumeB, and VolumeC are defined to represent the volumes transferred to a destination microplate from three different sources, mixing the entire contents of the destination microplate could be accomplished by configuring a Mix step using the expression = VolumeA + VolumeB + VolumeC in the volume field.
- In a Loop step, a variable called count is created and appended to the letter “P” in a step configuration as the expression = “P” & count. If the Loop is configured to start at 1 and end at 10, the Loop results would be P1, P2, ..., P10.

14 Using Sample Tracking and Data Sets in a Method

14.1 Overview

Sample tracking means the contents of the plate or tube are known at any time in the method and decisions may be made during transfer or pipetting operations based on the contents of the plate or tube.

Sample tracking is possible in Biomek Software using data sets, which store specific information about wells or tubes (refer to Section 14.1.2, *Data Set Definition*).

14.1.1 Sample Tracking

Sample tracking allows information about a sample in an individual well to be moved along with the sample when it is moved to another well. Sample tracking is enabled through the following functions of Biomek Software:

- association of a sample ID with wells or tubes through data sets.
- automatic copying of the SampleID data set (and any other data sets) during transfer and pipetting operations.
- reporting of information.

14.1.2 Data Set Definition

Data sets allow information about a sample in an individual well or tube to be tracked when the sample is moved to another well or tube. During any transfer or pipetting operation, all data sets associated with a plate are automatically copied from the source plate to the destination plate; however, only the wells in the data set affected by the transfer or pipetting operation are copied to the destination plate. The information in the data set can be used in decision-making; for example, during a Transfer or Combine step, a data set can be used to determine from which wells or tubes liquid should be aspirated or dispensed.

14.1.3 Data Set Steps in the Biomek Software

Four steps in Biomek Software allow data sets to track samples. Knowledge of these steps is necessary to understand how data sets are used in Biomek Software to track samples:

- Create Data Set — specifies data in a data set (refer to Section 24.3, *Configuring the Create Data Set Step*).
- Data Set Management — renames, removes, copies, or modifies the properties of a data set (refer to Section 24.4, *Configuring the Data Set Management Step*)
- Data Set Processing — applies a transformation expression to an existing data set to create a new data set (refer to Section 24.5, *Configuring the Data Set Processing Step*).
- Reporting — generates a report on data sets at any point during a method (refer to Section 24.6, *Configuring the Reporting Step*).

Note: Refer to Chapter 24, *Using the Data Sets Step Palette*, for complete information on displaying the Data Sets Step Palette and configuring the data sets steps.

14.1.4 Example of Sample Tracking Using Data Sets

While there are numerous ways in which sample tracking can be implemented using data sets, the following is an example of using data sets to track sample ID:

If a sample ID is associated with a tube and an amount is transferred from the tube to specified wells on a microplate, the Sample ID data set for the tube is copied to the specified wells on the microplate. The report will show the sample ID in the tube and the sample ID in the specified wells.

14.2 Understanding How Data Sets Are Created

The information contained in a data set is chosen in the Create Data Set step (refer to Section 24.3, *Configuring the Create Data Set Step*); however, some data sets may be generated in other ways through the software.

Biomek Software creates data sets in several ways:

- automatically (refer to Section 14.2.1, *Understanding the Volume Data Set*).

  Note: The Volume data set is created automatically.

- using the Instrument Setup step (refer to Section 15.2.6, *Creating the SampleID Data Set Using the Instrument Setup Step*).
- using the Create Data Set step (refer to Section 24.3, *Configuring the Create Data Set Step*).
- using the SILAS step (refer to Section 22.8.3, *Creating Data Sets from SILAS Messages*).
- using VB scripting (refer to Section 28.3, *Scripting Data Sets*).

  Note: Creating data sets using scripting requires prior knowledge of Visual Basic scripting.

Note: While Biomek Software retains information on all data sets and allows the information to be used anytime during the method, the specific information on a data set can only be viewed in a report configured in the Reporting (refer to Section 24.6, *Configuring the Reporting Step*) or Finish steps (refer to Section 12.2.2, *Configuring the Finish Step*).

14.2.1 Understanding the Volume Data Set

The volume of each well or tube is automatically tracked and stored for each piece of labware in a data set called Volume. The Volume data set is read-only and cannot be changed or manipulated, but may be used in other steps in the method to specify well patterns or volumes.

The Volume data set is reported when reports on data sets are generated and configured in the Reporting step (refer to Section 24.6, *Configuring the Reporting Step*). The Volume data set allows the volume of a well or tube to be known at any time during a method by inserting a Reporting step after any transfer or pipetting operation.

14.3 Using Data Sets in a Transfer or Combine Step

- ***FX***, ***NX-S8*** — Only the Span-8 Pod can be used to define patterns with data sets in a Transfer or Combine step.
- ***3000*** — Only a Single-Tip Pipette Tool can be used to define patterns with data sets in a Transfer or Combine step.

Not only are data sets automatically copied from the source plate to the destination plate during all transfer and pipetting operations, data sets may also be used in a Transfer or Combine step to define patterns for aspirating and dispensing liquid or to specify transfer volumes to specific wells. However, to use data sets to define well patterns for the Transfer and Combine steps, a data set must first be created for the source or destination labware in the Create Data Set step (refer to Section 24.3, *Configuring the Create Data Set Step*).

Note: The well patterns defined using data sets are for use during the transfer operation for the specific Transfer or Combine step; they cannot be saved in the Well Pattern Editor.

Data sets can be used in a Transfer or Combine step for:

- *Defining Well Patterns Using Data Sets* (Section 14.3.1).
- *Specifying Volumes Using Data Sets* (Section 14.3.2).

14.3.1 Defining Well Patterns Using Data Sets

Data sets may be used in a method to define well patterns for aspirating and dispensing liquid using the Transfer and Combine steps.

To use data sets to configure source or destination labware in a Transfer or Combine step:

1. Insert a **Transfer** or **Combine** step into the Method View anywhere after the specific data set that is used has been created (Figure 14-1).

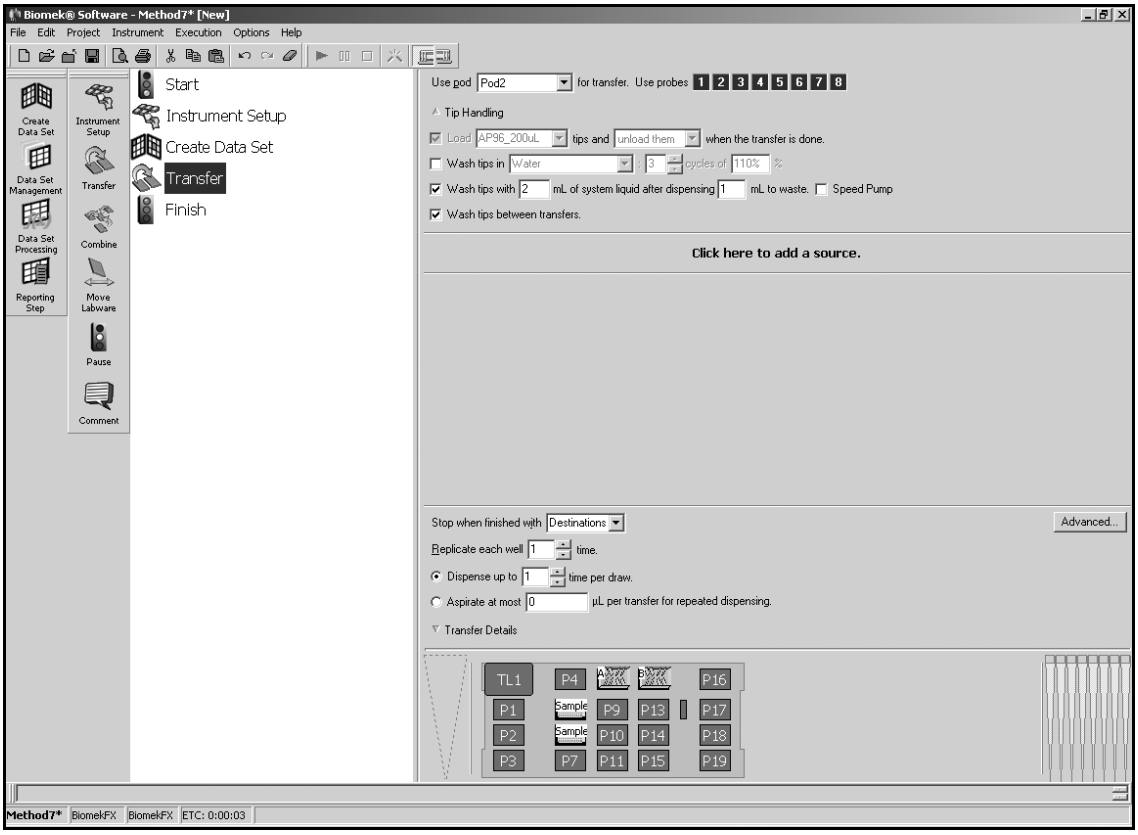


Figure 14-1. Transfer step in Method View after data set is created

2. In Use Pod, select the Span-8 Pod. Use Probes is displayed (Figure 14-1).

Note: If using a single-pod instrument, Pod1 is the only available selection.

3. In Use Probes, select the probes of the Span-8 Pod to use for the transfer.

➢ ***3000*** — Use Probes is not displayed.

4. Configure the Tip Handling as desired.

Note: Refer to Section 15.3.1, *Configuring Tip Handling*, for information on configuring Tip Handling.

5. Select the Source or Destination labware.

6. Double-click on the graphic of the labware to zoom in (Figure 14-2).

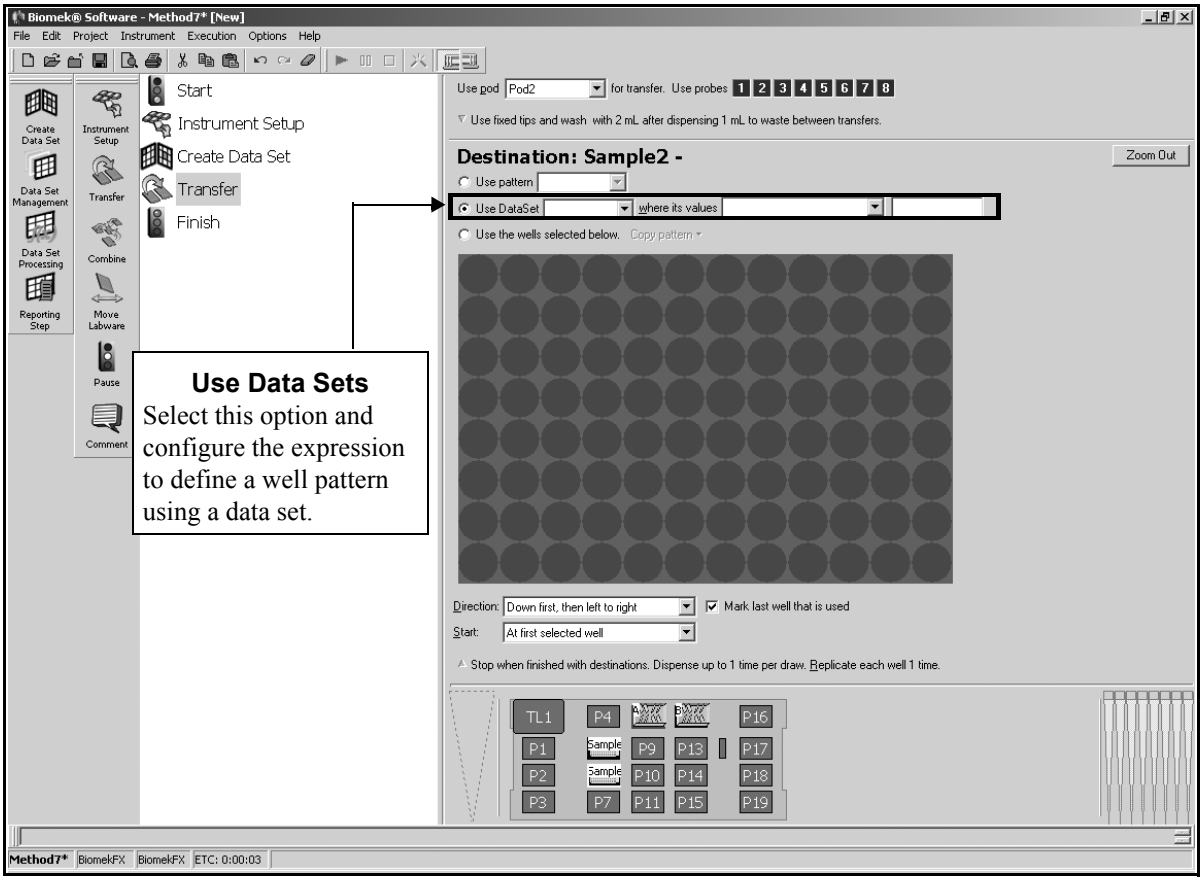


Figure 14-2. Transfer step — zoomed-in destination labware

7. Select **Use Data Set** to define a pattern using a data set.

Note: All data sets defined for the specified Source or Destination labware are available for selection.

8. In where its values, select the desired option:
    - are equal to — wells that have a value for the selected data set that are equal to a specified value or string are included in the pattern.

      Note: Strings used with are equal to must be entered as **=“string”**.
    - are greater than — wells that have a value for the selected data set that are greater than a specified value are included in the pattern.
    - are greater than or equal to — wells that have a value for the selected data set that are greater than or equal to a specified value are included in the pattern.
    - are less than — wells that have a value for the selected data set that are less than a specified value are included in the pattern.
    - are less than or equal to — wells that have a value for the selected data set that are less than or equal to a specified value are included in the pattern.
    - are not equal to — wells that have a value for the selected data set that are not equal to a specified value or string are included in the pattern.

      Note: Strings used with are not equal to must be entered as **=“string”**.
    - contains — wells that contain a specified numeric or text string within their value for the selected data set are included in the pattern.

      Note: Strings used with contains must be entered as **=“string”**.
9. Enter a value to complete the expression.
10. Double-click the graphic of the labware or choose **Zoom Out** to return to the Transfer step configuration.

14.3.2 Specifying Volumes Using Data Sets

Data sets may be used in a method to specify transfer volumes using the Transfer and Combine steps.

To use data sets to configure volumes in a Transfer or Combine step:

1. Insert a **Transfer** or **Combine** step into the Method View anywhere after the specific data set that is used has been created (Figure 14-3).

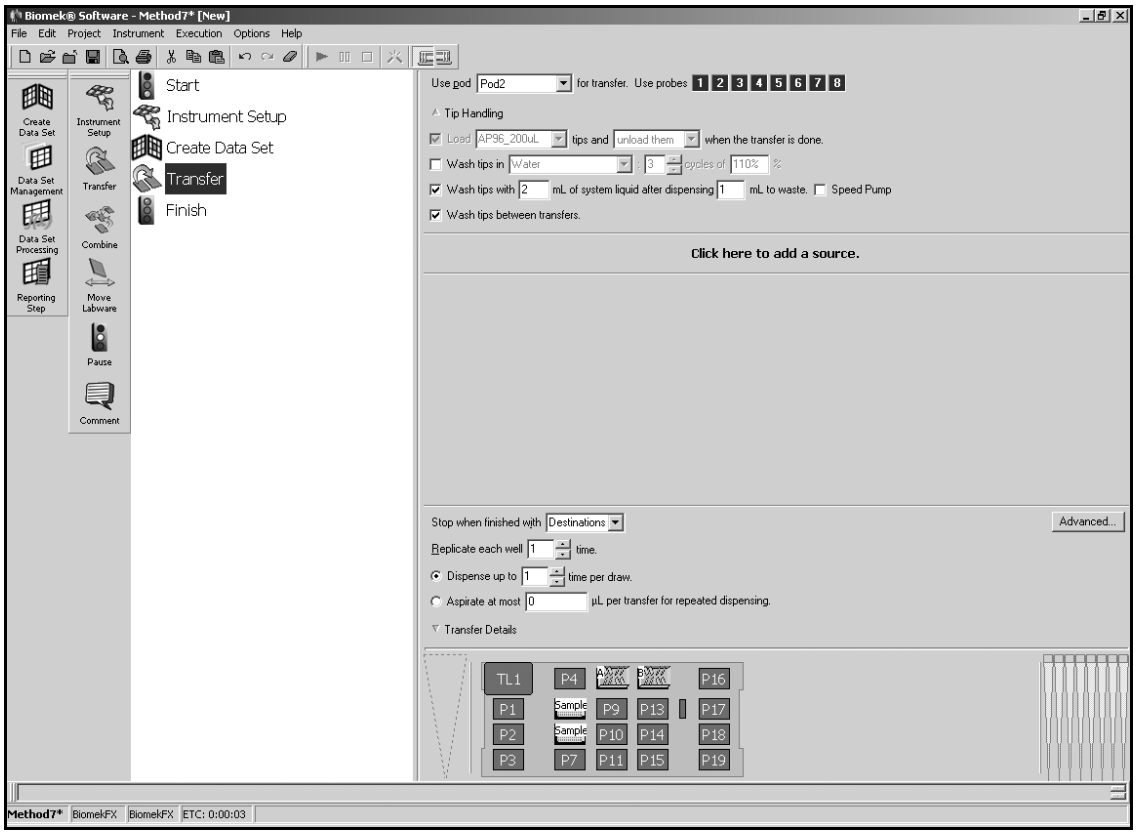


Figure 14-3. Transfer step in Method View after data set is created

2. In Use Pod, select the Span-8 Pod.

   Note: If using a single-pod instrument, Pod1 is the only available selection.

3. In Use Probes, select the probes of the Span-8 Pod to use for the transfer.

   ➢ ***3000*** — Use Probes is not displayed.

4. Configure the Tip Handling as desired.

   Note: Refer to Section 15.3.1, *Configuring Tip Handling*, for information on configuring Tip Handling.

5. Select the Source or Destination labware.

   Note: For a Transfer step, Volume is configured in the destination labware; for a Combine step, Volume is configured in the source labware.

6. In Volume, choose one of the following:

   - To retrieve all values of a data set, enter **=positions.PositionName.labware.DataSets("name").GetAll**, where PositionName is the name of the deck position assigned by the Deck Editor (for example, **p5** or **p8**) and name is the name of the data set from which to retrieve values.
   - To get a single value from the data set, enter **=positions.PositionName.labware.DataSets("name")("A1")**, where "A1" is the position in the data set of the desired value.
   - To get a subset of values from the data set, enter **=positions.PositionName.labware.DataSets("name")(array("A1", "B1, "C1"))**, where "A1", "B1", and "C1" are the positions in the data set of the desired values.

Note: Data sets can also be used in an expression using the above and the ListMath functions (refer to Section 10.4.1, *About ListMath*). For example, to normalize the volume of all wells on the plate at P5 to 250 µL, enter:
= Listmath.Sub (250, positions.p5.labware.DataSets("Volume").GetAll).

15 Using the Basic Step Palette

15.1 Overview

The Basic Step Palette incorporates the basic steps that provide essential functionality for the Biomek instruments, including general instrument setup, pipeting operations, and labware manipulation.

CAUTION: Make sure the correct ALP is chosen when configuring the deck setup in the Deck Editor. ALPs vary in height and failure to choose each ALP correctly in the software may result in collisions between pod(s) and ALPs during operation.

The steps available in the Basic Step Palette are:

- Instrument Setup — specifies the type of labware used for a liquid transfer, the position the labware occupies on the Biomek instrument deck, and some labware content configuration.

  Note: The type and position of ALPs and other hardware on the deck is specified in the Deck Editor.

- Transfer — comprises tip load, aspirate, dispense, and unload tip functions in one step to transfer liquid from a single source to one or more destinations.

- Combine— similar to a Transfer step, except Combine transfers liquids from one or more sources to a single destination.

- Move Labware — moves labware via automatic manipulation using the gripper on the Biomek instrument.
  - ***NX-S8*** — The optional gripper must be installed to move labware.

- Pause — halts instrument interaction with a lab position for a specified amount of time or the entire deck for an indefinite period of time.

- Comment — documents the method or adds instructions in the Method View.

15.2 Instrument Setup Step

CAUTION: An inaccurate Instrument Setup may result in pod and labware collisions, or in inappropriate pipetting.

When preparing the Biomek instrument for a method, it is important to understand a critical concept that applies every time the instrument is set up: obstacle avoidance. When building a method, always tell the software what labware and ALPs are on the deck, and the deck position each occupies. In the Instrument Setup step, labware is selected and positioned on the Biomek instrument deck.

As the bridge and pod move during method execution, the pod rises just enough to clear the objects sitting on the deck, and not much higher; therefore, if the software is not aware of what and where objects are on the deck, a hardware crash may occur.

Insert an Instrument Setup step to specify the labware, devices, and ALPs that are on the deck and the deck position each occupies. The Instrument Setup step can be inserted immediately after the Start step (Figure 15-1), or at any point in the method flow.

The Sample ID data set is also created in the Instrument Setup step by configuring the option Pause for bar code (refer to Section 15.2.6, *Creating the SampleID Data Set Using the Instrument Setup Step*).

Note: It is not necessary to add the Instrument Setup to a method if the current method is using the same deck setup as the previously run method, and the setup was not cleared in the Finish step of the previous method.

To insert an Instrument Setup step into a method, drag and drop **Instrument Setup** into the Method View (Figure 15-1).

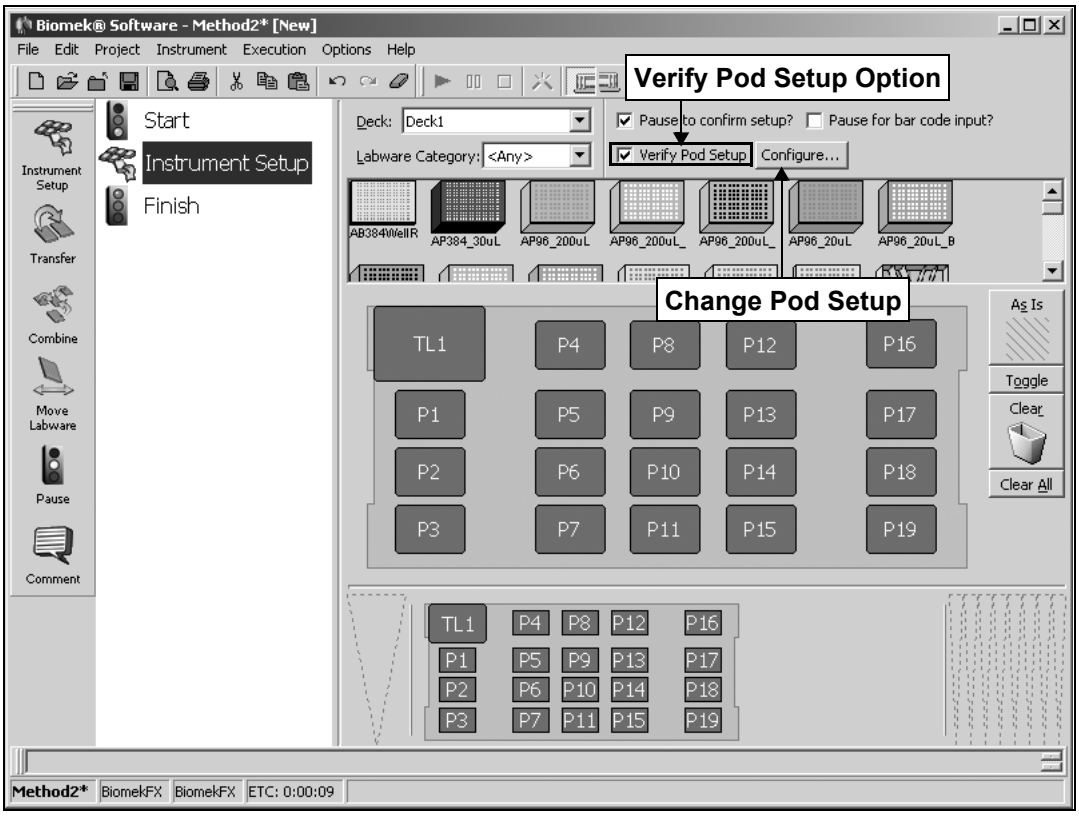


Figure 15-1. Instrument Setup step and configuration

CAUTION: To make sure the Biomek pod avoids all obstacles during its travel, always specify the labware, ALPs, and devices that are on the deck, and the deck position each occupies.

Configuring the Instrument Setup step includes:

- *Selecting a Deck Layout* (Section 15.2.1).
- *Verifying Deck Layout* (Section 15.2.2).
- *Configuring Pod Setup Options* (Section 15.2.3).
- *Populating the Deck with Labware* (Section 15.2.4).
- *Configuring Tip and Labware Properties* (Section 15.2.5).
- *Creating the SampleID Data Set Using the Instrument Setup Step* (Section 15.2.6).
- *Creating Custom Labware* (Section 15.2.7).

15.2.1 Selecting a Deck Layout

CAUTION: Make sure the correct ALP is chosen when configuring the deck setup in the Deck Editor. ALPs vary in height, and failure to choose each ALP correctly in the software may result in collisions between pod(s) and ALPs during operation.

The Instrument Setup step uses a Deck Layout as a map for the placement of labware, ALPs, and external hardware devices, such as stacker carousels.

A Deck Layout is a blueprint, or map, of the Biomek instrument deck. Biomek Software provides two predefined Deck Layout options: Deck1 and Standard. These two deck layouts represent the basic deck layout for the specific instrument with only standard deck positions.

Note: The Standard deck layout is read-only and may not be modified.

When an Instrument Setup step is inserted into a method, the default Deck Layout set in the Deck Editor is automatically selected. If another deck layout other than the default deck is desired, choose any existing Deck Layout in Deck from the drop-down list.

Note: Refer to Chapter 5, *Preparing and Managing the Deck*, for more information on creating and modifying a deck layout and setting the default deck layout.

15.2.2 Verifying Deck Layout

It is possible to verify the Deck Layout selected for a method before the method is run by selecting the Pause to Confirm Setup? option (Figure 15-2). The default selection for the Pause to Confirm Setup? option is On.

Verification of the Deck Layout is recommended when a method is run repeatedly, or when modifications have been made to a method. A prompt appears (similar to the one below) when Pause to Confirm Setup? is selected prior to running the method. The prompt displays the deck layout and the labware type and name (if assigned a name in Labware Properties) of the labware on each position.

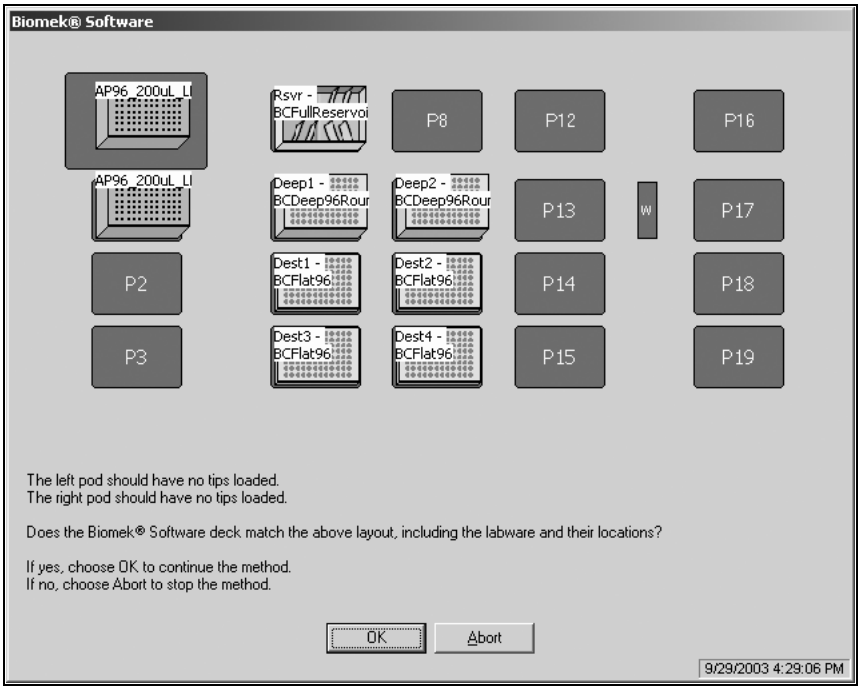


Figure 15-2. Pause to Confirm Setup? Deck Layout confirmation prompt

15.2.3 Configuring Pod Setup Options

Verify Pod Setup? is used to configure the current state of the pod or tool on the Biomek instrument at the beginning of the Instrument Setup step. However, selecting Tips Loaded or Tool Loaded informs the Biomek Software that tips or a tool are loaded on the instrument; it does not instruct the instrument to load tips or a tool.

Verify Pod Setup? is recommended when multiple methods are run one following another, when a single method is run repeatedly, or when tips are not loaded during the method.

Options for Verify Pod Setup depend on the instrument and pod type.

- ***FX*** — With a Multichannel Pod, has two options to verify the pod setup:
  - Pod must have the gripper retracted instructs the instrument to retract the gripper on the pod. The default setting is **On**.
  - Tips Loaded informs the software that tips are loaded at the time of the Instrument Setup step. The default setting for the Tips Loaded option is **Off**.
- ***FX*** — With Span-8 Pod, has only one option to verify the pod setup:
  - Tips Loaded informs the software that tips are loaded at the time of the Instrument Setup step. The default setting is **Off**.
- ***3000*** — Has two options to verify the pod setup:
  - Tool Loaded informs software that a tool is loaded on the head assembly at the time of the Instrument Setup step. The default setting is **Off**.
  - Tips Loaded informs the software that tips are loaded onto the tool at the time of the Instrument Setup step, if Tool Loaded is **On** and a pipetting tool is selected. The default setting is **Off**.
- ***NX-MC*** — Has two options to verify the pod setup:
  - Pod must have the gripper retracted instructs the instrument to retract the gripper on the pod. The default setting is **On**.
  - Tips Loaded informs the software that tips are loaded at the time of the Instrument Setup step. The default setting is **Off**.
- ***NX-S8*** — Has only one option to verify pod setup:
  - Tips Loaded informs the software that tips are loaded at the time of the Instrument Setup step. The default setting is **Off**.

To verify the pod setup prior to a method run:

1. Select **Verify Pod Setup?**.

2. Choose **Configure** to change the Pod Setup, if desired. Pod Setup appears (Figure 15-3).

Figure 15-3. Pod Setup prompt for dual-pod Biomek FX instrument

- ***FX*** — If the instrument is a dual-pod system, Pod Setup provides options for the Left Pod and the Right Pod.

3. Uncheck **Pod must have the gripper retracted**, if the gripper position is not critical.
4. Select **Tips Loaded**, if tips must be loaded at the beginning of the method. The Tips Loaded field has three states:
   - Checked — indicates tips are loaded
   - Unchecked — indicates tips are not loaded
   - Gray-checked — instructs the software to leave the tips in their current state, whether tips are loaded or not loaded
5. If Tips Loaded is selected, select the tip type loaded at the beginning of the method.
6. Choose **OK** to save the changes made to the Pod Setup.

15.2.4 Populating the Deck with Labware

The labware available for selection is displayed graphically below Labware Category (Figure 15-4). A specific type of labware can be viewed in the graphical display, or all types of labware available can be viewed simultaneously, using the Labware Category filter.

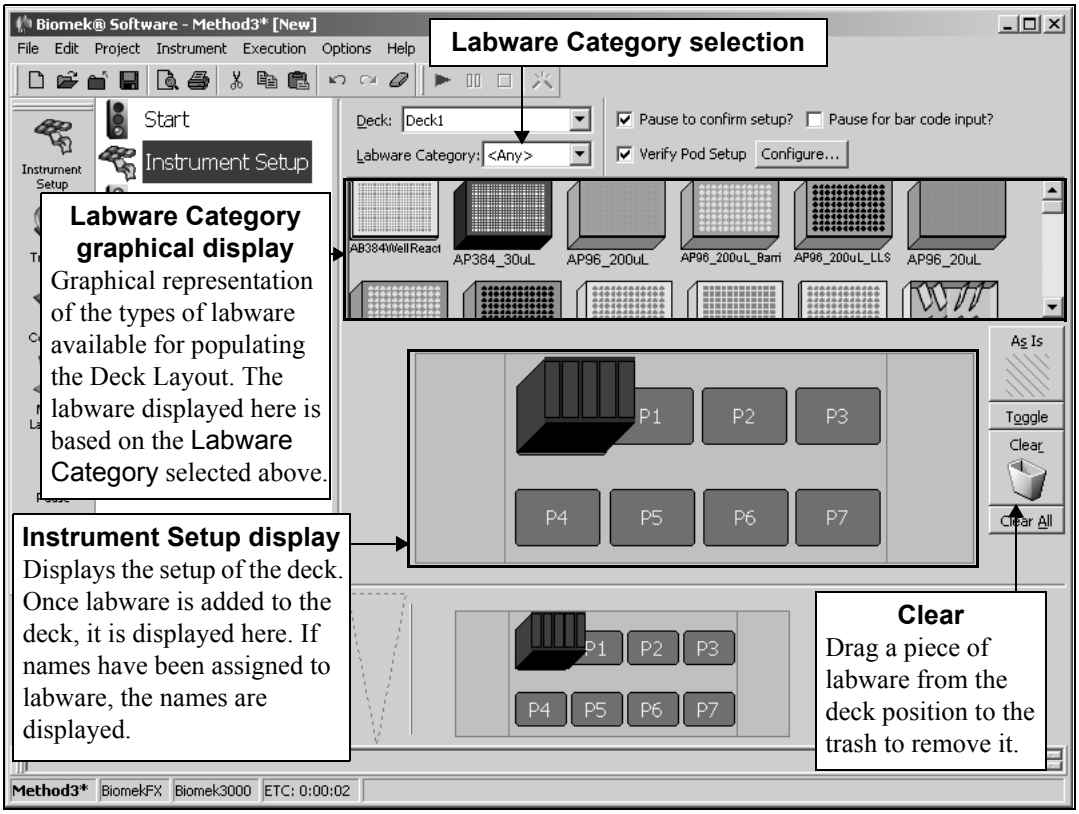


Figure 15-4. Populating the Deck Layout of a Biomek 3000 instrument

To populate the Deck Layout with labware, select from the graphical display below Labware Category and add them to the Deck Layout display.

Note: When populating the deck with labware, consider the tip to labware accessibility of the instrument pod or tool as described in the hardware manual for the specific instrument.

1. To display labware, select the type of labware desired in **Labware Category**. Labware Category choices include:
   - Any — lists all types of labware available, including lids and deck positions reserved for swapping labware.
   - Custom — lists any labware stored with defined properties (refer to Section 15.2.7, *Creating Custom Labware*).
   - Lid — lists lids associated with labware available.
   - Reservation — reserves deck positions for specific purposes; for example, to enable swapping of labware between positions or tip loading for the Span-8 Pod.
   - Reservoir — lists reservoirs available.
   - TipBox — lists types of tips available.
   - Titerplate — lists types of microplates available.
   - Tuberack — lists types of tube racks available.

   Note: Labware types and their characteristics are defined in the Labware Type Editor. Refer to Chapter 7, *Creating and Modifying Tip and Labware Types*, for information using the Labware Type Editor. If the Hide Labware option was chosen while defining a labware type, it will not be displayed in the Instrument Setup step.

CAUTION: Do not place labware other than a tip box on a tip loader position (TL#).

2. To place labware on the Deck Layout, drag and drop each desired labware graphic to the desired position on the Deck Layout display.

   OR

   Click on the labware graphic, and then on the desired position in Deck Layout display. The same type of labware can be added to as many deck positions as required by continuing to click on deck positions.

   OR

   Click on the labware graphic, and then click and drag the mouse over multiple deck positions in the Deck Layout display. This places the labware in all the highlighted positions.

   Note: To move labware to a different position, drag the desired labware to the new position in the Deck Layout.

3. To remove unwanted labware from the Deck Display during setup, drag and drop the labware to the **Clear** (trash) icon (Figure 15-4).

   OR

   Right-click the unwanted labware and select **Delete** from the menu that appears.

15.2.4.1 Changing Instrument Setup During a Method

When changing the instrument setup during a method, a second Instrument Setup step must be added. The additional Instrument Setup step reflects modifications to the current state of the deck (Figure 15-5).

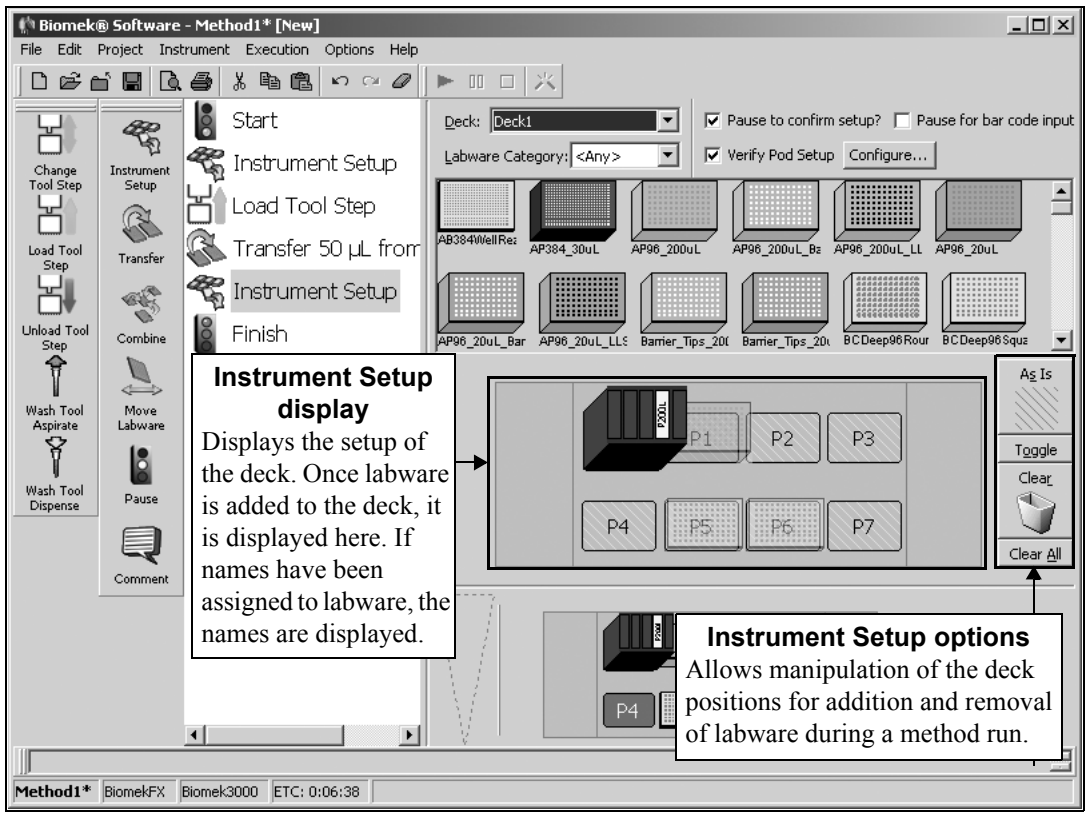


Figure 15-5. A second Instrument Setup step with deck positions specified As Is

Additional Instrument Setup steps can be inserted into a method as many times as necessary to complete a liquid-handling process, and to accommodate the addition of labware to the deck throughout a method.

The following options are available to help modify all instrument setups, either globally or by individual deck positions. These options are:

- As Is — individual deck positions retain their current state, whether empty or occupied by labware or a device.
- Toggle — toggles all empty deck positions to the As Is state and from the As Is state to their initial status, allowing those deck positions to retain their empty state.
- Clear — clears individual deck positions, whether empty or occupied by labware.
- Clear All — clears all deck positions, whether empty or occupied by labware or a device.

15.2.4.1.1 As Is and Toggle

As Is indicates that a deck position retains its current state, whether empty or occupied by labware or a device. Previously populated deck positions are indicated with the As Is option in the subsequent Instrument Setup step configuration. When As Is is applied to a deck position, the position becomes grayed out in the Deck Layout display (Figure 15-5).

As Is may also be used at the start of a method to indicate that deck positions retain their state from a previously run method that did not clear the deck of all labware in the Finish step.

To indicate that a deck position retains its current state:

1. Click **As Is**.
2. Click any deck position on the Deck Layout, and it is displayed As Is.
3. Repeat step 2 for each desired deck position.

   OR

   Click on a deck position, and then click and drag the mouse over multiple deck positions in the Deck Layout display. This toggles all the highlighted positions to the As Is state.

Toggle toggles all empty deck positions in the Instrument Setup Display between As Is, preserving the deck position's current state (Figure 15-6), and Clear, which empties a deck position. When Toggle is selected, deck positions labeled As Is revert to Clear.

Note: Adding labware to a deck position that is set to As Is removes the As Is status and replaces that position with the added labware. Any labware at that position is assumed to be removed from the deck and replaced with the new labware.

To indicate that a deck position retains its current state:

Toggle

Click **Toggle**, and any deck position not occupied by a piece of labware in the Instrument Setup display is toggled to the As Is state.

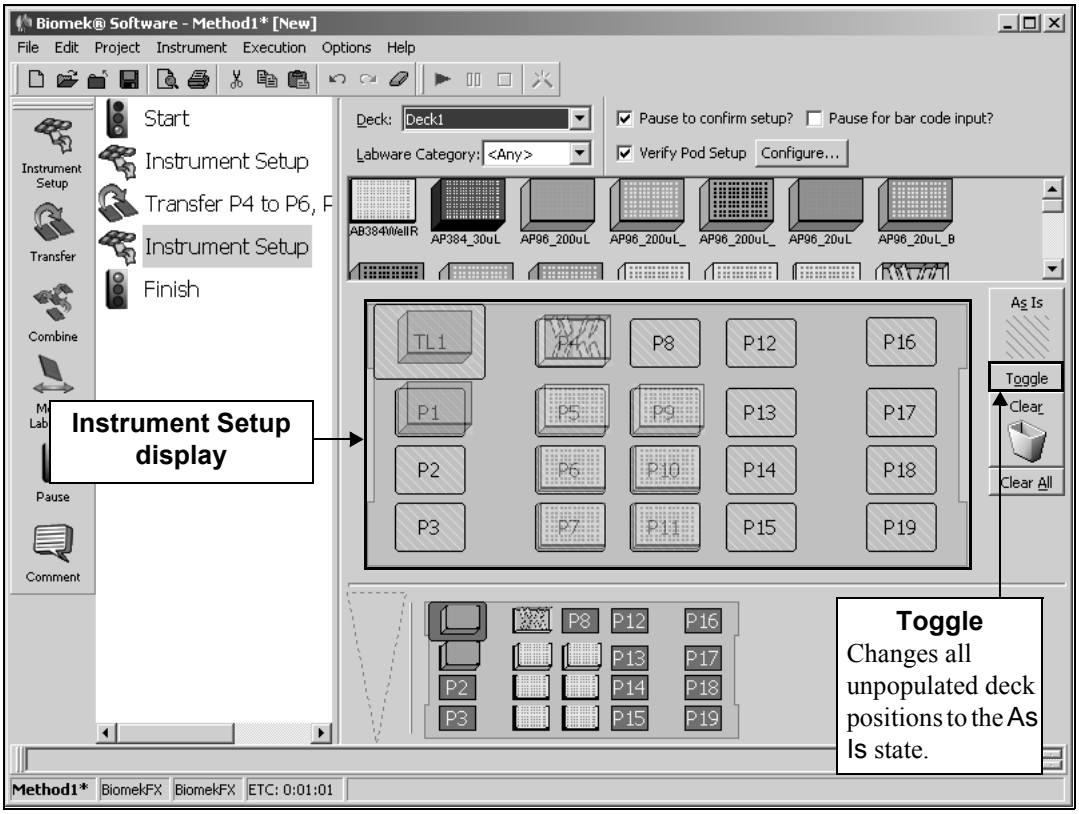


Figure 15-6. Toggle applied to the Deck Layout

15.2.4.1.2 Clear and Clear All

Clear removes labware or the As Is designation from individual deck positions. There is no confirmation for Clear, so once Clear is chosen, and a deck position is selected, the position is cleared of any labware or the As Is option (Figure 15-7).

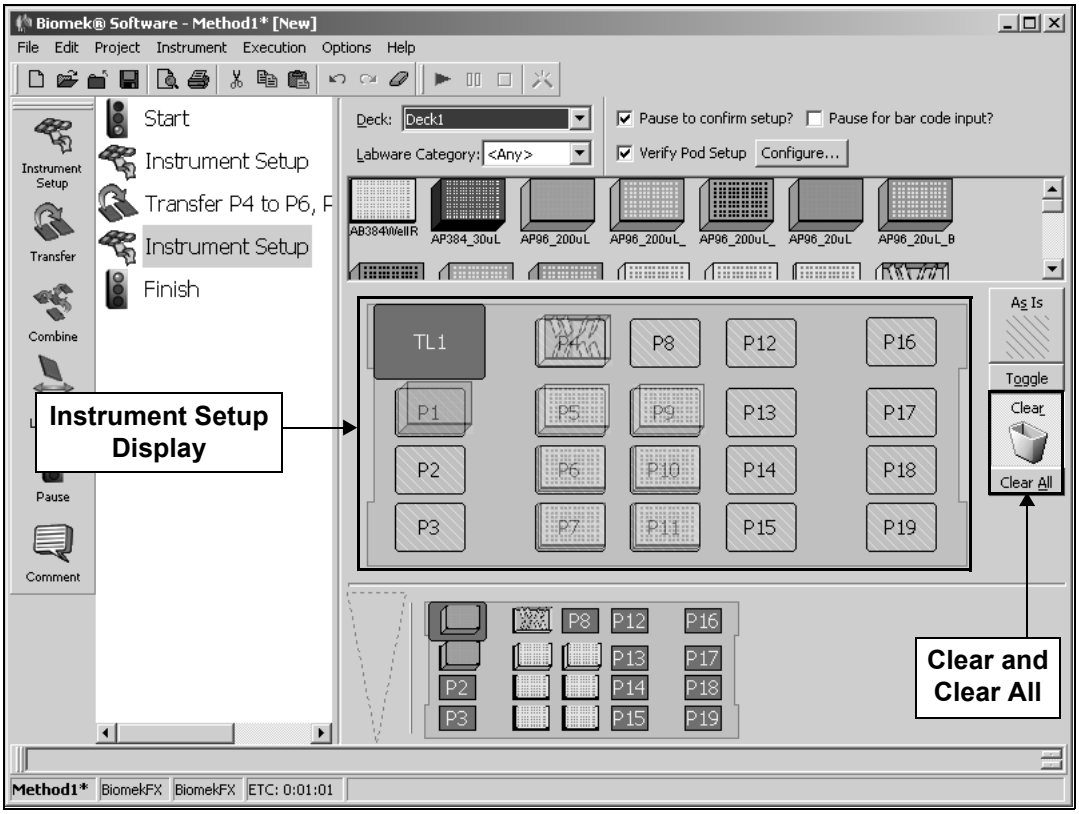


Figure 15-7. Clear Deck Layout designation applied to deck position TL1

The Clear All option removes all labware and As Is designations from the Instrument Setup. Clear All displays a prompt before the deck is cleared of all labware and As Is designations.

Note: If a deck position that contained labware from a previous Instrument Setup step is set to Clear, the labware is assumed to have been removed from the deck and that position no longer contains any labware.

To remove labware from the Instrument Setup configuration:

1. Choose **Clear** to clear a single deck position of labware or an As Is designation.
2. Click on the deck position in the Deck Layout display.
3. Continue to click on individual deck positions to empty them.

   OR

   Drag and drop labware from Deck Layout into **Clear**.

   OR

   Right-click on the labware in the Deck Layout display and select **Delete**.

Clear All

4. To clear the entire deck at one time, choose **Clear All**.
5. A confirmation prompt asking for verification appears. Choose **Yes** to remove all labware from the deck (Figure 15-8).

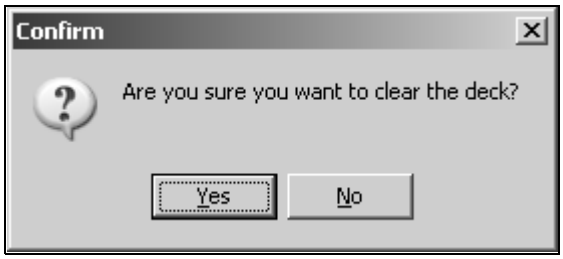


Figure 15-8. Confirmation prompt to Clear All labware from the Deck Layout

15.2.5 Configuring Tip and Labware Properties

Labware Properties is used to configure properties for each piece of labware added to the Deck Layout. The information provided in Labware Properties is used when a pipetting technique is selected, and when tips are loaded and unloaded.

To access Labware Properties:

1. Double-click on a piece of labware in the Deck Layout.

   OR

   Right-click on a piece of labware in the Deck Layout and choose **Properties** to open Labware Properties.

   Note: If there is a stack of labware at the selected position, a submenu appears from Properties listing labware from bottom to top.

The configuration options in Labware Properties provide the following information, if it applies to the type of labware selected:

- Name assigned to a piece of labware, if desired
- Labware type
- Maximum volume per well
- Bar code
- Sense liquid level options
- Volume for each well, if known The default volume for a labware type may be set in the Labware Type Editor (refer to Section 7.3.6, *Editing Labware Type Properties*).
- Liquid type
- Where to dispose of tips
- Where to dispose of tip boxes
- Maximum number of times tips may be loaded
- Available tips

Note: Variables and expressions may be entered in any field that can be configured. Refer to Section 13.2, *Using Variables*, and Section 13.3, *Using Expressions*, for more information on using variables and expressions.

15.2.5.1 Configuring Labware Properties for Tips

When the labware selected for configuration is a tip box, Labware Properties provides the ability to configure the following information:

1. Double-click the tip box to configure in the Deck Layout.

   OR

   Right-click the tip box to configure in the Deck Layout and select **Properties** from the menu. Labware Properties for tips appears (Figure 15-9).

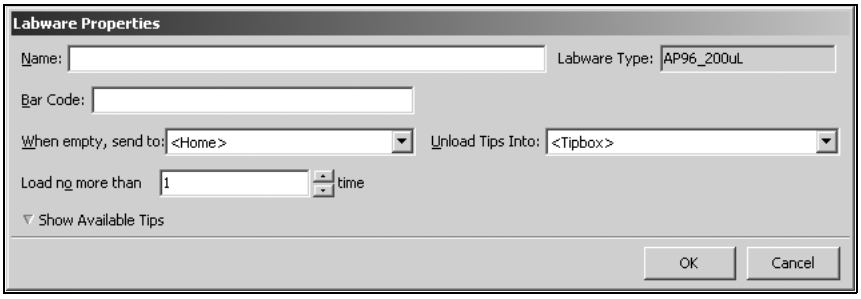


Figure 15-9. Labware Properties for tips

2. In **Name**, enter the name assigned to the tip box, if applicable. Naming a tip box forces the instrument to look for the specific box of tips, rather than any tip box on the deck that contains the specified tip type.

   Note: Multiple tip boxes can be given the same name. This is useful for creating a pool of tip boxes for a specific use.

   OR

   Leave Name blank. When Name is blank, tips are accessed by the information displayed in the Labware Type field.

3. In Labware Type, verify the tip type.
4. In Bar Code, enter the bar code. Use the bar code field to identify a specific tip box in certain methods, such as plate replication. This field may be left blank.
5. In When empty, send to, select a final destination for the tip box at the end of the method.
6. In Unload Tips Into, select the location reserved for tip disposal.
7. In Load no more than, enter the number of times tips can be loaded onto the pod during the method.

8. Choose **Show Available Tips** to display a graphic of the tip box (Figure 15-10).

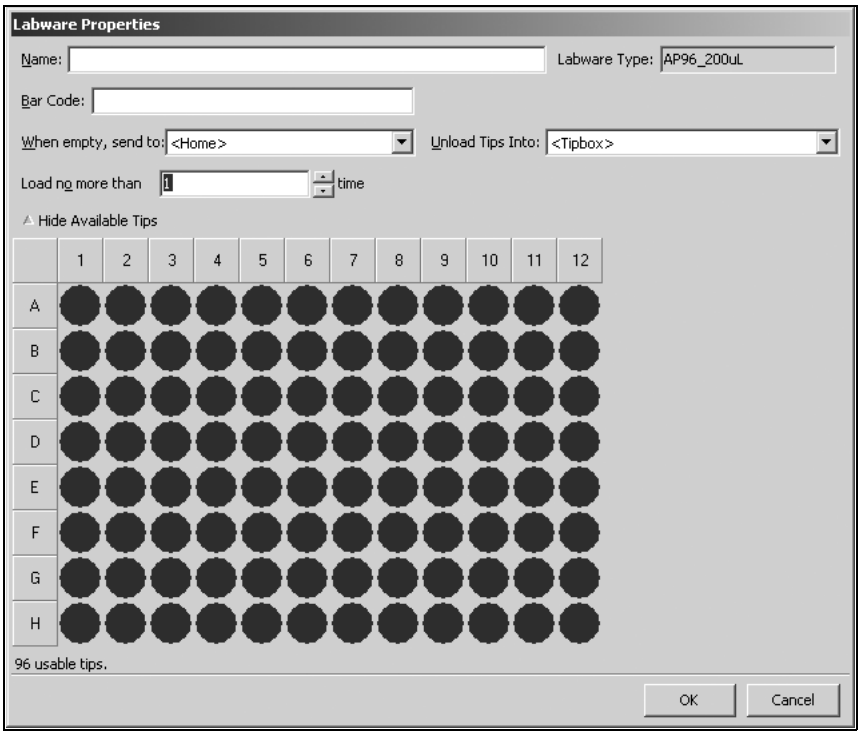


Figure 15-10. Labware Properties for tips with Available Tips shown

9. On the graphic of the tip box, select the usable tips. By default, all tips are selected. This can be used to indicate missing tips or tips that are otherwise not used in the method.
10. Choose **Hide Available Tips** to collapse the graphic of the tip box.
11. Choose **OK** to save Labware Properties and return to the Instrument Setup step configuration.

15.2.5.2 Configuring Labware Properties of Microplates, Reservoirs, and Tube Racks

When the labware selected for configuration is a microplate, reservoir, or tube rack, Labware Properties provides the opportunity for configuration (Figure 15-11).

1. Double-click the piece of labware to configure in Deck Layout.

   OR

   Right-click the piece of labware to configure in Deck Layout and select **Properties** from the menu. Labware Properties for microplates, reservoirs, and tube racks appears (Figure 15-11).

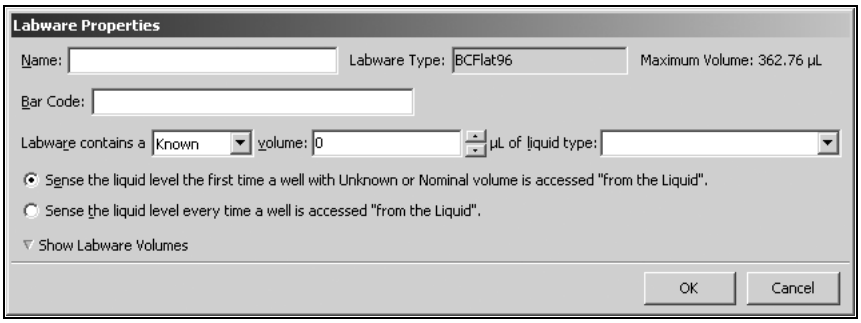


Figure 15-11. Labware Properties for microplates, reservoirs, and tube racks

2. Verify the Labware Type.
3. In **Name**, enter a name for the labware.

   Note: When a deck is populated by numerous pieces of labware, naming labware is recommended. Names should be descriptive of the contents of the labware or the work being accomplished during the method. Naming labware in a meaningful fashion may reduce confusion.

4. In **Bar Code**, enter the bar code to identify a specific plate in certain methods, such as plate replication. This field may be left blank.
5. Make a selection in **Labware contains**. This information is used by many of the techniques supplied with Biomek Software that aspirate or dispense at a certain offset from the liquid level.

   Note: Some pods or tools can detect the liquid level using liquid-level sensing technology.

   - If Known is selected, the liquid level is not detected during method run and the entered value is used during validation and method run. Known Volume should be supplied whenever possible.
   - If Unknown is selected, the liquid level is detected during method run if required by the technique, and the wells are assumed to be full when validating the method.
   - If Nominal is selected, the liquid level is detected during method run, but the volume in the wells is assumed to be the entered value when validating the method.

6. Enter the **Volume**, if Nominal or Known volume is selected. A value entered in Volume is assigned to each well on the selected labware.

7. Select the **Liquid Type** contained in the labware. Specifying liquid type is useful when Biomek Software auto-selects a pipetting technique for any aspirate and dispense operations on this piece of labware. This technique is auto-selected based on the physical factors of the liquid, as well as the physical attributes of the labware, and the pod or tool performing the operation. For more information on liquid types, refer to Chapter 8, *Understanding and Creating Liquid Types*.

8. Select **Sense the liquid level the first time a well with Unknown or Nominal volume is accessed "from the Liquid"** to use liquid level sensing to determine the liquid level only the first time it accesses a well with an Unknown or Nominal volume from the liquid. When the same well on the piece of labware is accessed, the liquid level is calculated internally based on the result of the earlier liquid level sense and the amount aspirated or dispensed to the well in previous steps.

   OR

   Select **Sense the liquid level every time a well is accessed "from the Liquid"** to use liquid level sensing to determine the liquid level every time it accesses a well with an Unknown or Nominal volume from the liquid.

Note: Liquid level sensing options apply only if the pod or tool accessing the labware is liquid level sensing capable. If not, the selected option is ignored.

---

9. If the labware does not contain uniform volumes, choose **Show Labware Volumes** to display a graphic of the labware (Figure 15-12) and assign two or more volumes to wells on the same piece of labware.

Note: If a volume for all wells is specified in step 6, proceed to step 15.

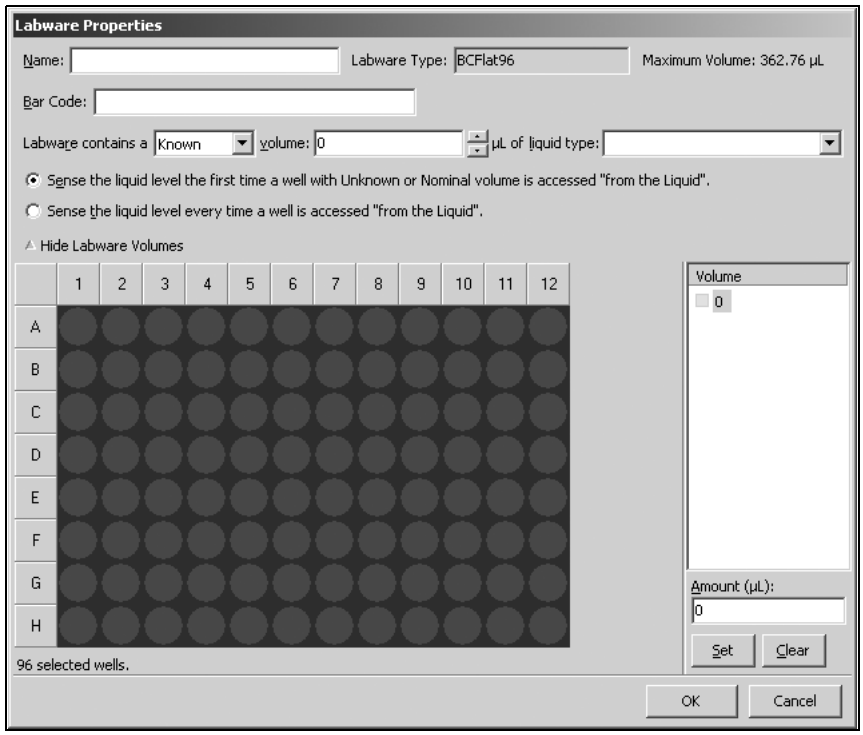


Figure 15-12. Labware Properties for a 96-well microplate with Labware Volumes shown

Note: Show Labware Volumes may appear different depending on the number of wells on the selected labware.

10. Select the desired wells on the graphic.

Note: Hold down Ctrl to toggle wells between selected and deselected without affecting the selection status of other wells. Click a column or row heading to select all wells of a column or row.

11. Enter the volume to assign to the currently selected wells in **Amount**.
12. Choose **Set** to assign the current Amount to the currently selected wells. The wells are given a color code that corresponds to the list of set volumes under Volume.
13. Repeat steps 10-12 until all desired wells have been assigned the desired volume. Clear sets the volume for all wells back to zero.
14. Choose **Hide Labware Volumes** to collapse the graphic of the labware.
15. Choose **OK** to save Labware Properties and return to the Instrument Setup step configuration.

15.2.5.3 Configuring Labware Properties for a Biomek 3000 Tool Rack

The Tool Rack on the Biomek 3000 instrument stores various interchangeable tools for head assembly on the instrument deck during a method. The Biomek 3000 can load and unload tools from the Tool Rack to give the instrument different capabilities. The tools available to the head assembly are configured from Labware Properties in an Instrument Setup step.

Since a gripper tool may be placed physically on the Gripper Tool Rack only (refer to the *Biomek® 3000 Laboratory Automation Workstation User's Manual,* Chapter 3.2, *Installing the Gripper Tool in the Tool Rack*), it must be configured in Instrument Setup using a Gripper Tool Rack.

Since the HDR tool occupies all five positions of a standard tool rack and cannot be placed on the gripper tool rack (refer to the *Biomek® 3000 Laboratory Automation Workstation User's Manual,* Chapter 5.2.2, *Installing the HDR Tool on a Tool Rack*), it must be configured in Instrument Setup occupying all five positions of a Tool Rack. However, if the tool rack is installed on the left end of the Biomek 3000 deck, and there is no disposal unit installed on the left side, the HDR tool body may be installed in slot 1 or 2 of the tool rack. Additional tools may then be installed in slots 4 and 5 of the tool rack.

To configure the tools available at a Tool Rack in Instrument Setup:

1. Double-click the piece of labware to configure in Instrument Setup

   OR

   Right-click the piece of labware to configure in Instrument Setup and select **Properties** from the menu. Labware Properties for the Biomek 3000 Tool Rack appears (Figure 15-13).

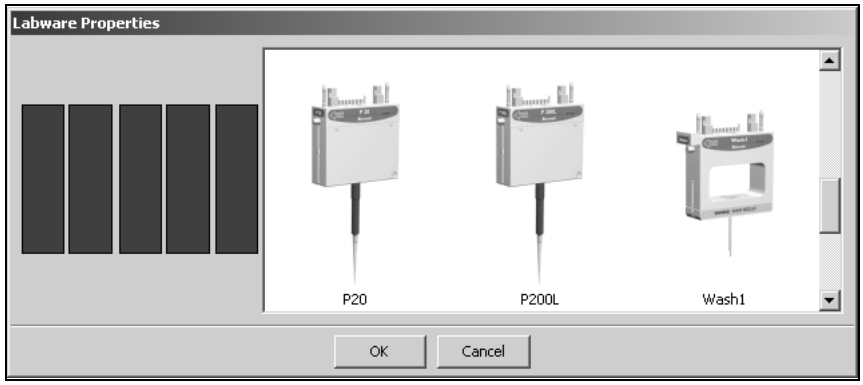


Figure 15-13. Labware Properties for a Biomek 3000 Tool Rack

2. Locate the desired tool on the right side of Labware Properties and drag it to one of the unoccupied (black) positions on the Tool Rack. The selected tool is placed in the position (Figure 15-14).

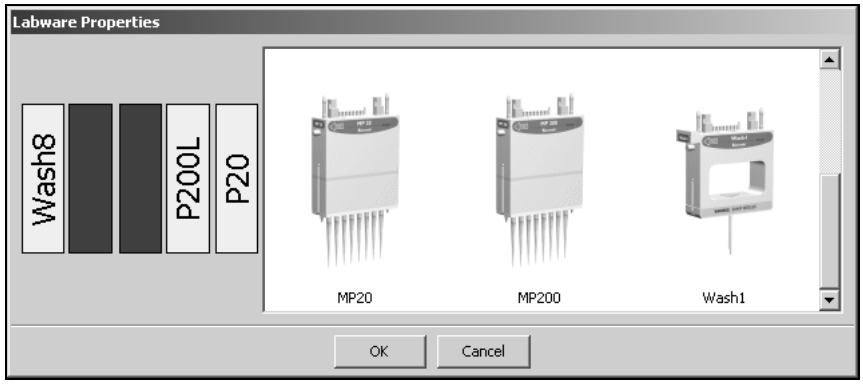


Figure 15-14. Labware Properties for a Biomek 3000 Tool Rack with tools loaded

3. Repeat step 2 until the Tool Rack is full or all desired tools have been placed on the Tool Rack.
4. Choose **OK** to save the Labware Properties for the Tool Rack.

15.2.6 Creating the SampleID Data Set Using the Instrument Setup Step

The Instrument Setup step contains an option to **Pause for bar code input?** during a method run (Figure 3-11). When this option is selected, the method pauses at the Instrument Setup step and allows for per-well or per-tube bar codes to be entered for all labware on the deck. Using the specified bar codes, a data set called SampleID is created for each piece of labware.

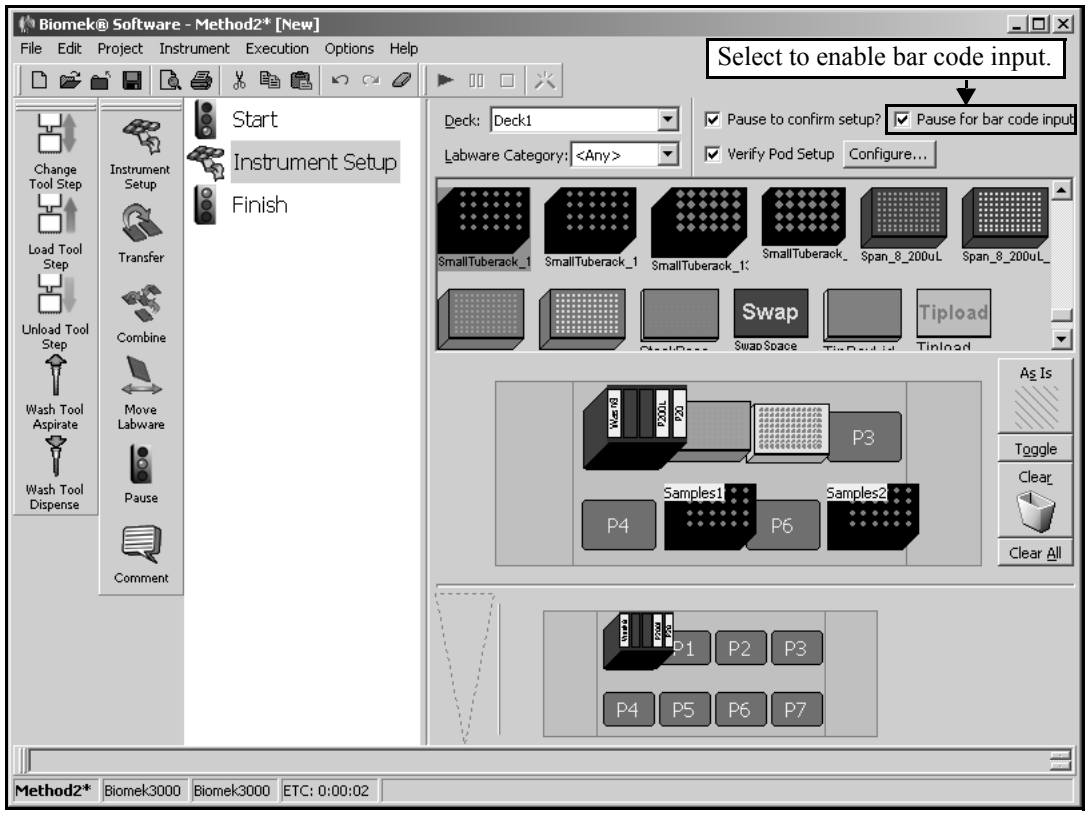


Figure 15-15. Enabling bar code input in the Instrument Setup step

When Pause for bar code input? is selected, Bar code input (Figure 15-16) appears during the method run at the Instrument Setup step.

If Pause to confirm setup? is also selected, Bar code input appears after the Deck Confirmation prompt (refer to Section 15.2.2, *Verifying Deck Layout*).

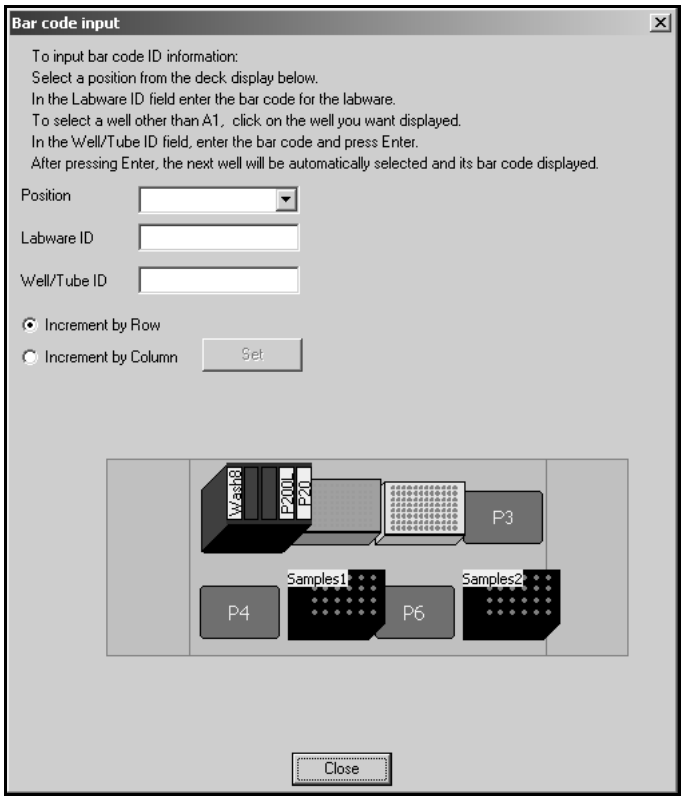


Figure 15-16. Bar code input

If desired, only labware IDs or only sample IDs may be entered in Bar code input. It is not necessary to enter both labware and sample IDs for any piece of labware.

Note: Labware must be unstacked to assign Labware ID and/or Well/Tube ID in Bar code input.

To enter labware and sample IDs:

5. In Position, select the deck position of the labware to specify labware or sample IDs.

   OR

   Click on the desired piece of labware in the Deck Display. A graphic of the selected labware type appears (Figure 15-17).

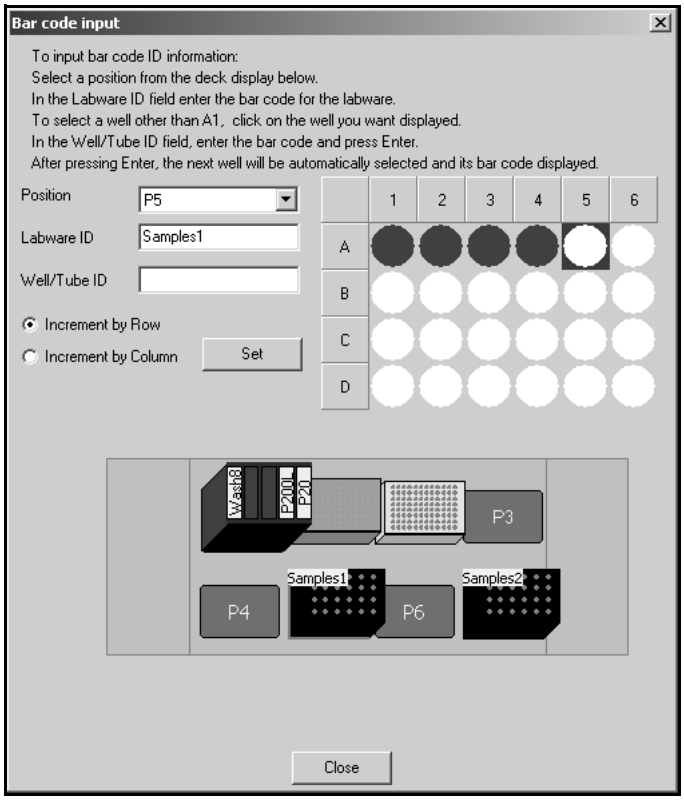


Figure 15-17. Entering sample IDs for labware in Bar code input

6. In Labware ID, enter the plate bar code or name.
7. Select **Increment by Row** to enter sample IDs by row.

   OR

   Select **Increment by Column** to enter sample IDs by column.

   Note: The Increment selection determines which well is automatically selected when a sample ID is set by choosing Set or pressing Enter.

8. Select the well or tube in the labware graphic to assign a sample ID.
9. In Well/Tube ID, enter the bar code or sample ID to assign to the selected well or tube.

10. Press **Enter** or choose **Set** to assign the Labware ID and Well/Tube ID to the selected labware and well or tube. The well or tube is assigned the sample ID and turns green to indicate a sample ID has been assigned to that well or tube. The next well or tube on the labware is automatically selected.
11. After each Well/Tube ID assignment and/or Labware ID assignment, press **Enter** or choose **Set**.

    Note: If using a handheld bar code reader, ensure the bar code on the plate or tube ends with a carriage return and line feed.

12. Repeat steps 4-6 to assign a sample ID to all desired wells or tubes of the labware.
13. Repeat steps 1-7 to assign sample IDs to each desired piece of labware.
14. After sample IDs have been entered to all desired labware, choose **Close**. The SampleID data set is created for every piece of labware on the deck.

Each Instrument Setup step with Pause for bar code input? selected allows wells or tubes to be assigned IDs. If a new ID is assigned to a well or tube that previously had a SampleID created, the new value overwrites the old value. To maintain a record of all SampleIDs for a well or tube, use the Data Set Management step to rename or create a copy of the SampleID data set before the additional Instrument Setup step assigns the new sample ID (refer to Section 24.4, *Configuring the Data Set Management Step*).

15.2.7 Creating Custom Labware

The Custom labware category offers the option to create and reuse labware with defined and stored Labware Properties. New labware stored in the Custom labware category maintains the Labware Properties defined when the labware was created or added to the deck, including the name, bar code, liquid type, and volume information.

Custom labware creates an instance of the labware type containing the attributes of the working revision of the labware type it is based on at the time the custom labware is created and the configured Labware Properties. Custom labware is saved to the instrument file.

Note: The default volume for a labware type can be specified in the labware definition stored in the Labware Type Editor (refer to Section 7.3.6, *Editing Labware Type Properties*).

To create Custom labware:

1. Highlight the **Instrument Setup** step.
2. Add the desired labware to create the custom labware from to the deck; for example, if creating a custom reservoir, add a reservoir to the deck. Refer to Section 15.2.4, *Populating the Deck with Labware*.
3. Configure the **Labware Properties** for that piece of labware. (Refer to Section 15.2.5.1, *Configuring Labware Properties for Tips* and Section 15.2.5.2, *Configuring Labware Properties of Microplates, Reservoirs, and Tube Racks* to configure Labware Properties.)

4. In Labware Category, display the **<Custom>** labware category. If no custom labware has been created, no labware is displayed.

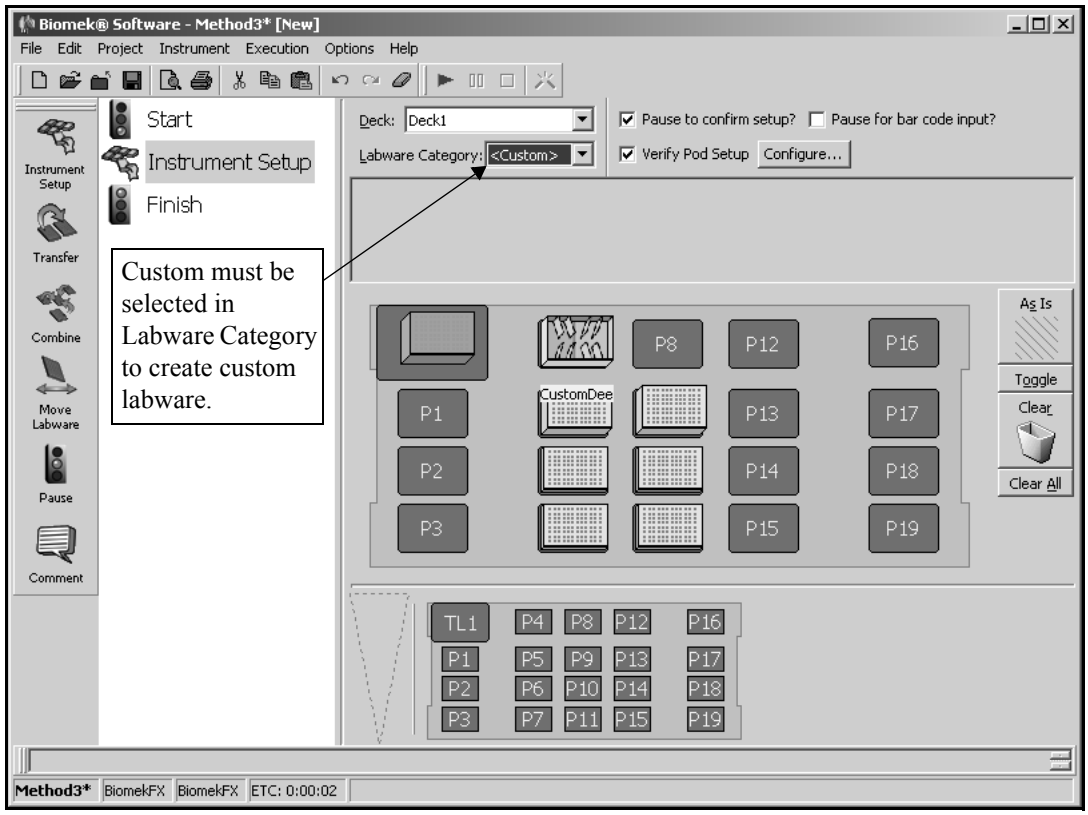


Figure 15-18. Custom labware category displayed

5. Drag and drop the labware graphic from the Deck Layout to the <Custom> Labware Category display. If the <Custom> labware category is not visible, dragging and dropping the labware has no effect.

Note: Multiple pieces of labware, or stacks of labware, cannot be added to the <Custom> labware category simultaneously; each piece of labware must be added individually.

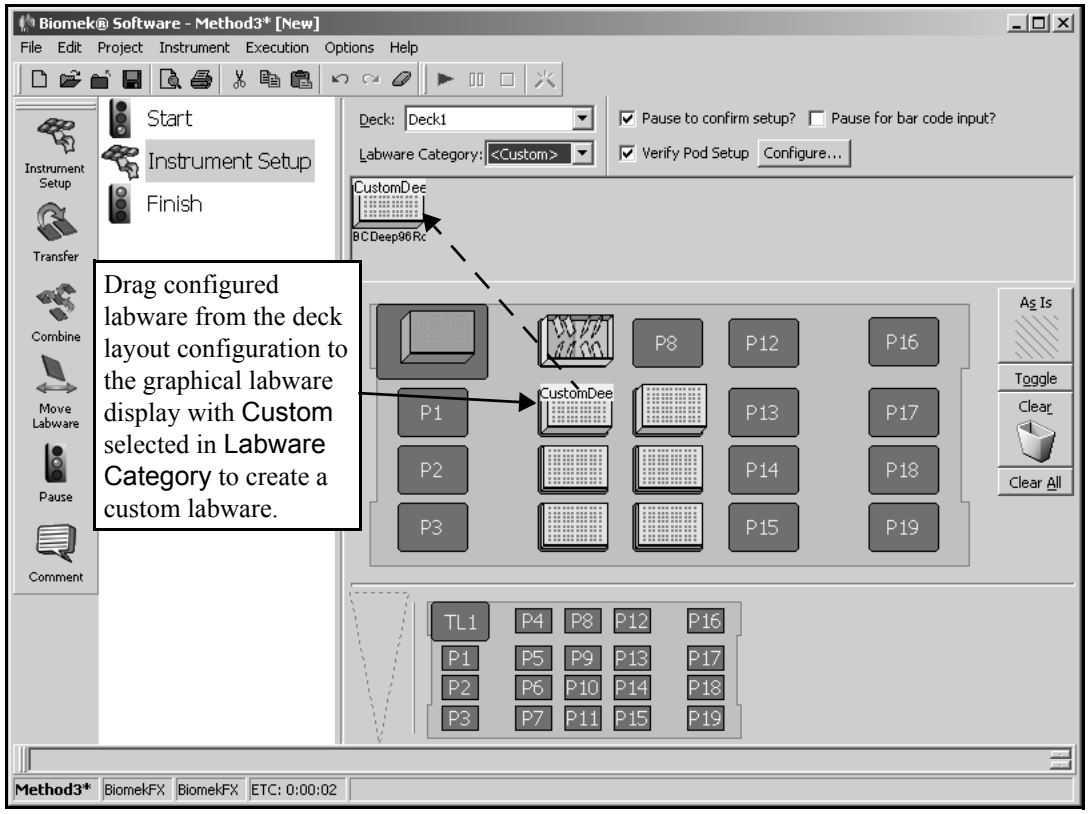


Figure 15-19. Custom labware created

6. To delete a piece of labware from the <Custom> labware category, drag the labware from the <Custom> labware category display to Clear.

Note: Custom labware added to the <Custom> labware category in the Instrument Setup step is visible in the Device Setup (refer to Section 22.5, *Device Setup Step*) and Stacker Carousel Setup (refer to Section 23.3, *Using the Stacker Setup Step*).

15.3 Configuring Transfer and Combine Steps

The Transfer and Combine steps configure multiple aspirate and dispense operations using the selected pod or tool to transfer liquid from all specified source wells to all specified destination wells. The Transfer step transfers liquid from a single source to one or more destinations, while the Combine step transfers liquid from one or more sources to a single destination.

The Transfer and Combine steps may be used with any Biomek instrument; however, the capabilities of the steps vary depending on the pod or tool configuration of the instrument:

- ***FX, NX-MC*** — Using the Multichannel Pod, the same volume is transferred from each of the 96 or 384 channels in each aspirate and dispense cycle.
- ***FX, NX-S8*** — Using the Span-8 Pod, a different volume may be aspirated from each well of a source labware and a different volume may be dispensed to each destination. The pod may also use only selected probes to aspirate from specified wells on the source labware and dispense to specified wells on the destination labware.
- ***3000*** — The pipetting tool aspirates from all channels at once (one for a single-channel tool or eight for an eight-channel tool). The tool transfers the same volume from each channel in each aspirate and dispense cycle.

Note: If there are multiple sources or destinations, each source or destination may have a different volume transferred, but all wells on any single source or destination must have the same volume transferred. To transfer different volumes to or from wells on the same piece of labware, configure multiple sources or destinations using the same labware but specify different wells and volumes.

The Transfer and Combine steps perform four liquid-handling functions through the step configuration, eliminating the need to insert multiple steps to complete the liquid transfer:

- Load tips onto pod or tool.
- Aspirate liquid from source(s).
- Dispense liquid to destination(s).
- Unload tips from pod or tool.

The Transfer and Combine step configuration includes:

- *Configuring Tip Handling* (Section 15.3.1).
- *Configuring Source Labware* (Section 15.3.2).
- *Configuring Destination Labware* (Section 15.3.3).
- *Configuring Transfer Details* (Section 15.3.4).

Insert a Transfer or Combine step into the Method View (Figure 15-20).

- ***3000*** — If a specific pipetting tool is desired, it must first be loaded using either a Change Tool (refer to Section 20.3, *Change Tool Step*) or a Load Tool step (refer to Section 20.4, *Load Tool Step*).

Note: The appearance of the Transfer or Combine step configuration varies depending on the instrument and pod selection.

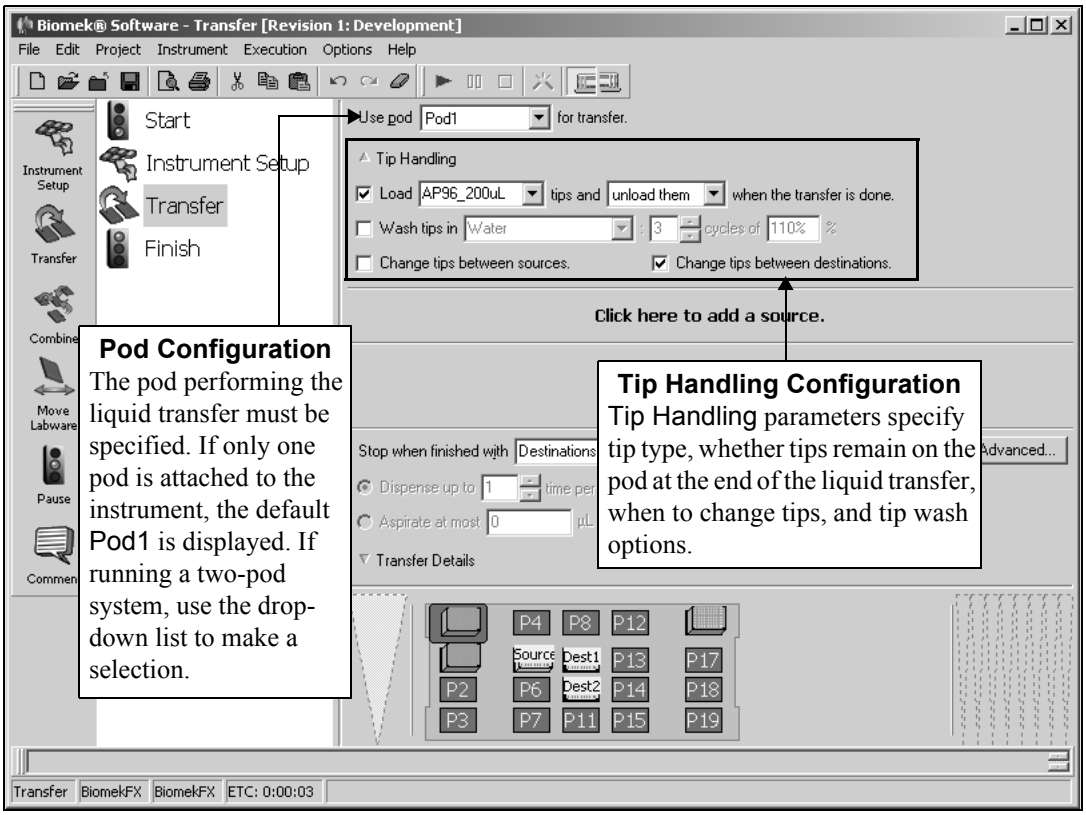


Figure 15-20. Transfer step configuration for a Multichannel Pod

15.3.1 Configuring Tip Handling

Configuring Tip Handling in the Transfer and Combine steps is not required, because the default Tip Handling configuration locates and loads clean tips automatically every time a Transfer or Combine steps is initiated and unloads them when the step is completed. It is recommended, however, that Tip Handling configuration be supplied if cross contamination or conserving consumables is a concern, or a specific tip type should be used.

Tip Handling is also used to configure washing or changing tips between transfer operations. Tips may be washed or changed between sources or between destinations. Options for washing or changing tips vary according to the instrument and configuration.

- ***3000*** — Tip wash options are not available for this instrument.

To configure Tip Handling (Figure 15-20) for the Transfer or Combine steps:

1. If using a dual-pod ***FX*** instrument, specify the **Pod** to perform the transfer operation. The pod configured as the default pod is displayed in Pod. If the other pod is desired, select the pod from the drop-down list or the Current Deck Display.
2. If using a Span-8 Pod on ***FX*** or ***NX-S8***, select the probes used in the transfer by clicking the probe numbers in **Use Probes**. Any combination of probes may be used as long as all selected probes are using the same type of tips and syringes.

   OR

   Right-click any of the probe numbers in **Use Probes** and make a selection from the menu. Options include:

   - Use Disposable Tips — selects all probes with disposable tips
   - Use Fixed Tips — selects all probes with fixed tips
   - Use Selection — allows for custom selection

   Note: If the probes selected are equipped with fixed tips, the Load and unload them/leave them on options (steps 4 to 6) are unavailable and the fixed tips are used for the transfer. Proceed to step 7.

   Note: Disposable tips are selected by default. If the pod has only fixed tips, all fixed tips are selected by default. For example, if the pod is equipped with fixed tips on probes 1-4 and disposable tips on probes 5-8, probes 5-8 are selected by default. However, if probes 5-8 are also equipped with fixed tips, all eight probes are selected by default.
3. If Tip Handling is not already displayed, click the arrow or sentence summary to expand the Tip Handling configuration (Figure 15-20).
4. Select **Load** to load new tips at the start of the Transfer or Combine step.

   Note: If Load is not selected, the Transfer or Combine step uses previously loaded tips, rather than loading new tips at the start of the step.

   If Load is selected and the tips loaded to the pod have been used, an error may occur. To increase the number of uses allowed for tips, increase the Usages count in the Labware Properties configuration in the Instrument Setup step (refer to Section 15.2.5, *Configuring Tip and Labware Properties*).
5. If Load is selected, select the type of tips to load from the drop-down list, or from the Current Deck Display.

   Note: If tips are selected from the Current Deck Display, and the tips are named, Load displays the name, not the tip type. If a name was not assigned to the tips, the tip type is displayed in Load.

   It is recommended that tips not be named in the Instrument Setup step, because this could restrict the instrument from locating available tips.

6. To return tips to the tip box after the Transfer or Combine step is completed, select **unload them**.

   OR

   To leave tips on after the Transfer or Combine steps is completed, select **leave them on**.

   Note: To conserve tips when using the Transfer or Combine steps within a Loop step, uncheck Load and select leave them on (steps 4 and 6 above). Add a New Tips step to the method prior to the Loop step, and an Unload Tips step after the Loop. This loads new tips before the Loop step, uses the same set of tips for all Transfer or Combine steps completed as part of the Loop, and unloads the tips when the Loop step is completed.

7. Choose **Wash tips in** to use a Multichannel Channel Tip Wash ALP to wash disposable or fixed tips.

   ➢ ***3000*** — Options to wash tips are not available. Proceed to step 15.

   Note: If Wash tips in is not selected, proceed to step 11.

   Note: A Multichannel Tip Wash ALP must be added to the deck and configured in the Deck Editor before washing can occur. Clicking on the ALP while the Transfer and Combine steps is being configured places a check in Wash tips in, and populates Wash tips in with the solution configured for the Multichannel Tip Wash ALP in Labware Properties on the Instrument Setup step (refer to Section 15.2.5, *Configuring Tip and Labware Properties*).

8. In **Wash tips in**, select a solution for the wash cycle if the field does not already contain a solution.

   Note: The wash solution specified in the Transfer and Combine steps must match the solution selected in the Multichannel Tip Wash ALP configuration, or an error occurs.

9. Choose the number of cycles to aspirate and dispense during wash.

10. In **%**, provide the maximum volume of fluid contained in the tips in previous steps; for example, if the maximum volume of fluid transferred is 50 µL, and the % is set for 110%, the Transfer and Combine steps washes the tips with 55 µL of solution.

    Note: If the % sign is deleted in the % field, the field label changes to µL. Any value entered is now interpreted as a specific volume, not a percentage.

11. If using a Span-8 Pod on ***FX*** or ***NX-S8,*** choose **Wash tips with** to use the passive Span-8 Tip Wash ALP to wash fixed tips.

    Note: Only fixed tips can be washed with the Span-8 Tip Wash ALP. If using disposable tips or Wash tips with is not selected, proceed to step 15.

    Note: A Span-8 Tip Wash ALP must be added to the deck and configured in the Deck Editor before washing can occur. Clicking on a Span-8 Tip Wash ALP while the Transfer step is being configured places a check in Wash tips with, and uses default values of 2 mL of system liquid after dispensing 1 mL to waste.

12. In **Wash tips with**, enter the volume of system fluid to use when washing the outside of the tips.
13. In **after dispensing**, enter the volume of system fluid to use when washing the inside of the tips.
14. If using a Span-8 Pod on ***FX***, select **Speed Pump** to use the speed pump when flushing the tips with system fluid, if desired.

    OR

    If using a Span-8 Pod on ***NX-S8***, select **purge pump** to use the purge pump when flushing tips with system fluid, if desired.

    Note: The speed pump or purge pump is an optional device that can be used to shorten the time it takes to wash tips. A speed pump or purge pump must be added as a device and configured with the Span-8 Pod in Hardware Setup to use it when washing tips.

15. If using a Multichannel Pod on ***FX*** or ***NX-MC***, or a ***3000***, select **Change/Wash tips between sources**, to change or wash tips each time a new source well is accessed.

    - ***3000*** — Tips can only be changed.

    Note: Change/Wash tips between sources changes or washes tips any time it is required to aspirate liquid from a different well or wells than the previous aspirate operation. For example, if aspirating from quadrants of a 384-well microplate with a 96-channel head, Biomek Software instructs the instrument to use new tips when aspirating from each quadrant.

16. If using a Multichannel Pod on ***FX*** or ***NX-MC***, or a ***3000***, select **Change/Wash tips between destinations**, to change or wash tips each time a new destination well is accessed.

    - ***3000*** — Tips can only be changed.

    Note: Change/Wash tips between destinations changes or washes tips after all dispense operations, except the last. Tips are removed after the last dispense operation only if unload them is selected in Tip Handling. If there is only one Destination Labware configured, Change tips between destinations does not change tips.

17. If using a Span-8 Pod on ***FX*** or ***NX-S8***, select **Change/Wash tips between transfers**, to change or wash tips between each liquid transfer.

The Tip Handling configuration can be collapsed to allow more room during Source and Destination Labware configuration. When collapsed, the tip handling configuration is displayed as a sentence summary (Figure 15-21). Use the sentence summary to verify that tip handling has been configured appropriately.

To collapse or expand the Tip Handling configuration, click the arrow to the left of Tip Handling or the textual display (Figure 15-21).

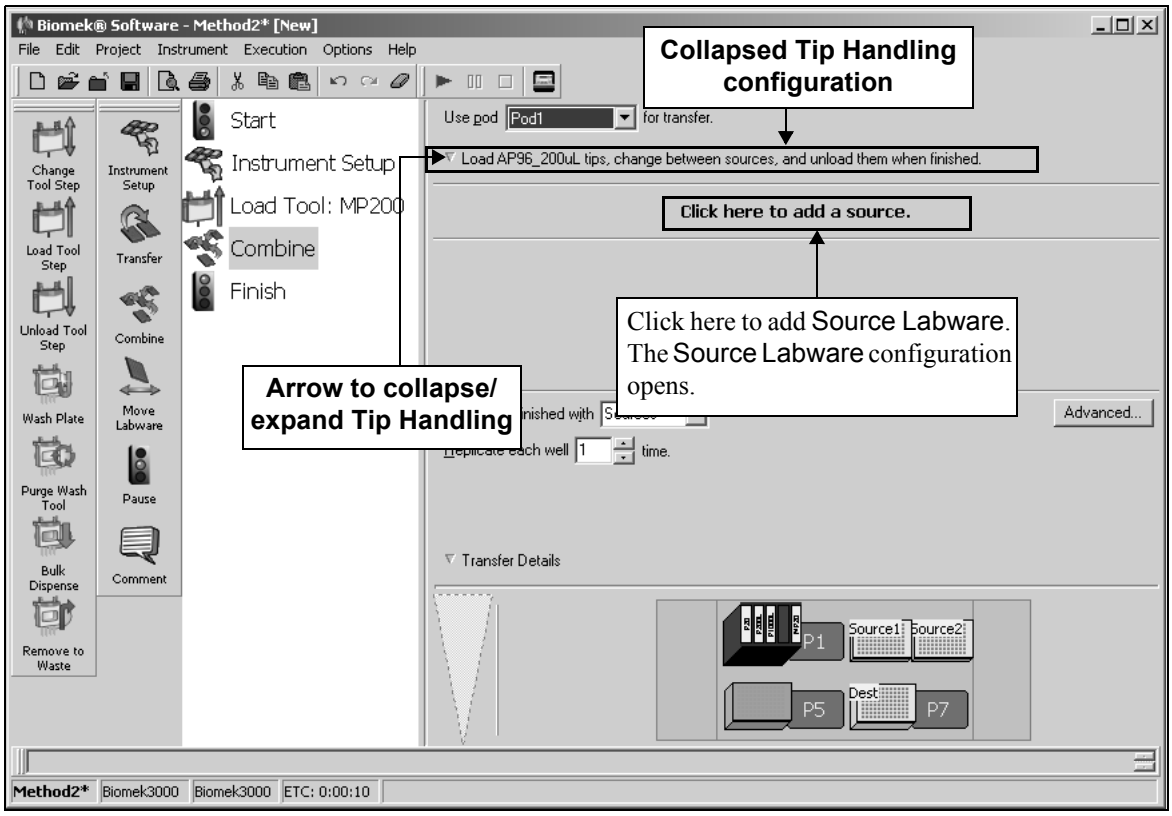


Figure 15-21. Combine step — Adding Source Labware

15.3.2 Configuring Source Labware

A ‘source’ is a group of wells accessed at one time by the Biomek instrument to aspirate liquid; for example:

- ***FX, NX-MC*** — A Multichannel Pod aspirates from either 96 or 384 wells at a time, depending on the head installed.

  Note: If configuring a 384-well microplate using a 96-channel pod or a 1536-well microplate using a 384-channel pod as source labware, any combination of quadrants may be used. For example, if it is desired to transfer liquid from the first, second, and third quadrants but not the fourth, the source labware may be configured to transfer only from those quadrants.

- ***FX, NX-S8***— A Span-8 Pod aspirates from one to eight wells at a time, depending on the selected probes.

- ***3000*** — Depending on the tool loaded onto the head assembly, aspirates from either 1 or 8 wells at a time.

Note: If there are multiple sources in a Combine step, each source may have a different volume transferred, but all wells on each source must have the same volume transferred. To transfer different volumes from wells or quadrants on the same microplate, configure multiple sources using the same source plate but specifying different well or quadrants and volumes.

The Source Labware configuration for the Transfer and Combine steps includes specifying:

- Labware type
- Labware location
- Liquid amount to transfer (for Combine step only)
- Liquid type
- Well pattern or quadrants to access

  Note: Quadrants are applicable only when accessing a 384-well microplate using a 96-channel pod or a 1536-well microplate using a 384-channel pod.

- Technique selection
- Pipetting height

Note: A single source is configured for the Transfer step, because the Transfer step moves liquid from a single source to one or more destinations. Multiple sources can be configured for the Combine step, because the Combine step moves liquid from multiple sources to a single destination.

To configure Source Labware for the Transfer and Combine steps:

1. Select **Click here to add a source** (Figure 15-21). The Source Labware configuration appears.
2. Click on the desired piece of labware in the Current Deck Display. The labware type and position for that piece of labware is entered automatically into the Source Labware configuration.

Note: If the selected labware is named, the name of the labware appears instead of the deck position.

OR

Select a **Source Labware** (Figure 15-22) type and specify the deck position.

Note: To configure additional Source Labware for a Combine step, select **Click here to add a source**, and then select another piece of labware from the Current Deck Display. A Destination labware must be configured before configuring additional source labware. If an incorrect piece of labware is selected, right-click on the labware title and select **Delete** on the menu that appears, or change the Source Labware selection by clicking anywhere in the source labware configuration area, and selecting another piece of labware.

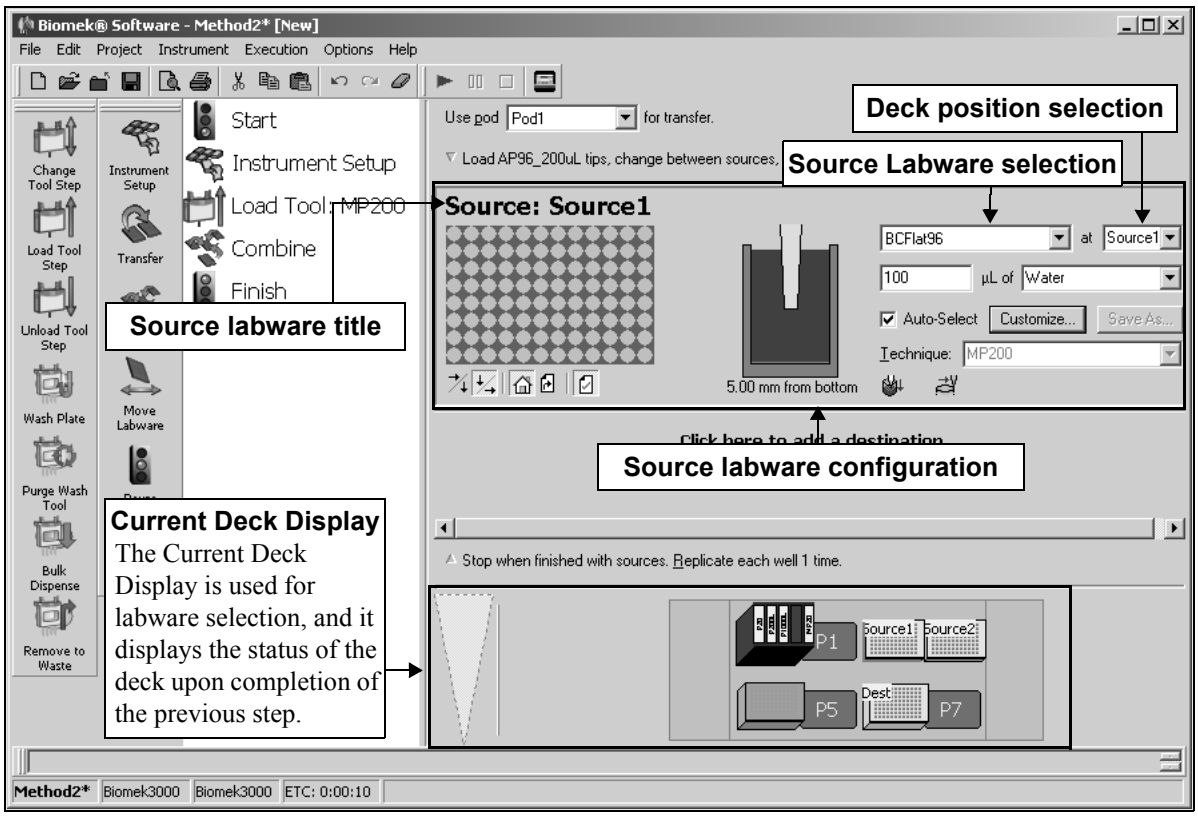


Figure 15-22. Combine step — Source Labware configuration

3. Verify the deck position of the labware.

Note: A bright blue outline appears in the Current Deck Display around the labware designated as the Source Labware.

4. To specify the wells or quadrants in a microplate to access, double-click the source labware in the step configuration to zoom in on the labware (Figure 15-23).

Note: To call up a menu for Zoom and a Specify Selection as Text option, right-click on the labware.

Specify Selection as Text allows selection of wells or quadrants as targets for aspirate and dispense operations. Specify Selection as Text may also be used to enter variables or expressions.

Note: Specify Selection as Text is not applicable for 96-well microplates, reservoirs, or 384-well microplates accessed by a 384-channel pod.

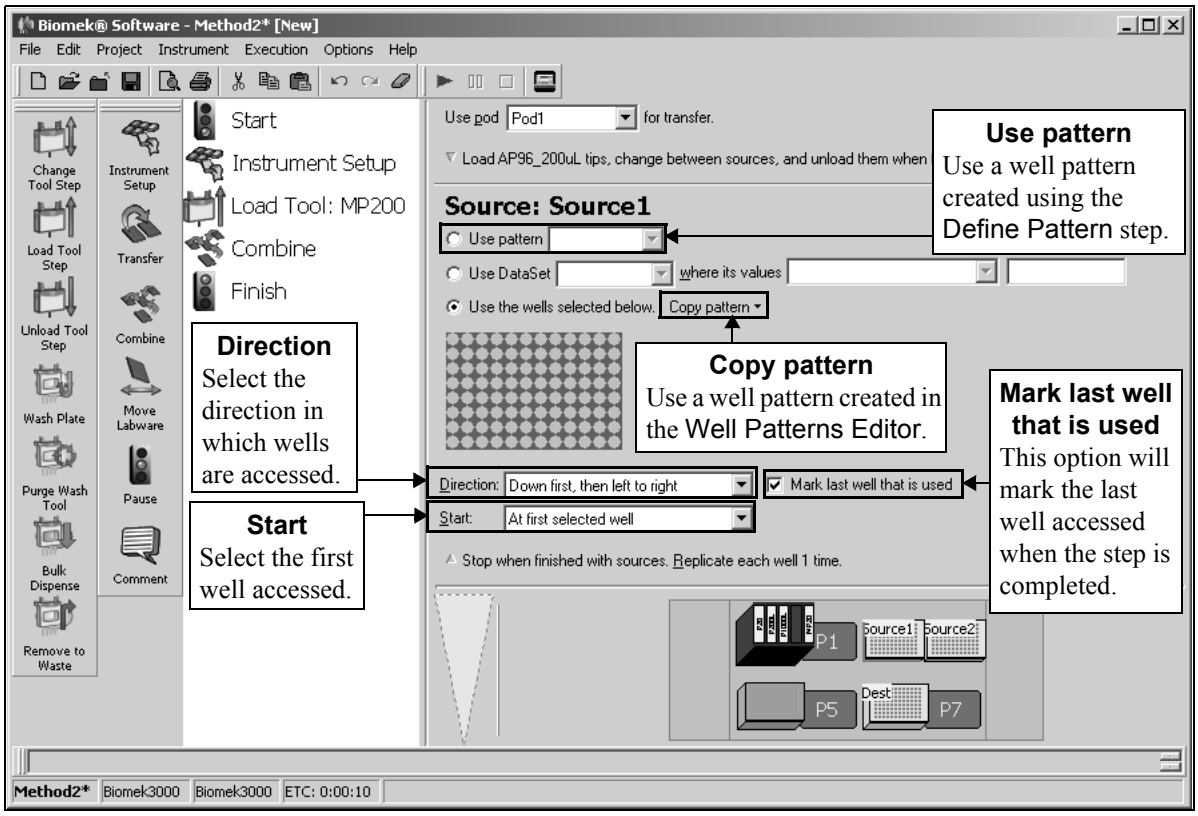


Figure 15-23. Transfer Step — Zoomed-in Source Labware configuration

- ***FX, NX-MC*** — Using a Multichannel Pod, some options are not available
- ***3000*** — Using a Multi-Tip Pipette Tool, some options are not available.

5. Select the wells from which to transfer using one of the following techniques:

   - ***FX, NX-MC*** — A Multichannel Pod can only select quadrants of a microplate.
   - ***FX, NX-S8*** — A Span-8 Pod can select individual wells.
   - ***3000*** — A multi-tip pipette tool always selects groups of wells in columns of 8 while a single-tip pipette tool can select individual wells.

     - Choose **Copy Pattern** and select the desired pattern to use a previously defined well pattern created using the Well Patterns Editor (refer to Chapter 11, *Creating Well Patterns*).

       Note: The pattern must be compatible with the head or tool installed and the labware type.

     - Select **Use pattern** and choose the previously defined pattern from the list to use a pattern created in a Well Patterns Editor or Define Pattern step.

       Note: Refer to Section 18.10, *Define Pattern Step (including 3000)*, for more information about creating patterns using the Define Pattern step.

     - Define a well pattern using data sets (refer to Section 14.3.1, *Defining Well Patterns Using Data Sets*).
     - Create a custom well pattern from the labware grid by dragging the mouse and using Ctrl and Shift on the keyboard.

       Note: Hold **Shift** and click a well to select additional wells without deselecting any wells. Hold **Ctrl** and click a well to toggle the selection status of selected wells without affecting the status of other wells. If Shift or Ctrl is not held down when selecting wells, any previous selection is deleted.

Note: To save the new pattern, right click the labware graphic and select **Save Pattern** from the menu. Enter a name for the pattern in New Pattern and choose **OK**.

6. Select the **Direction** in which source wells are mapped to destinations. Down first, then left to right is the default selection.

   ➢ ***FX, NX-S8*** — Direction options only apply when using a Span-8 Pod.

Note: Direction controls how source wells are mapped to the destination, not the physical order in which wells are transferred. The Transfer step automatically determines the most efficient way to complete the transfer.

- Down first, then left to right — goes down each column from top to bottom, then goes right to the next column (Figure 15-24)

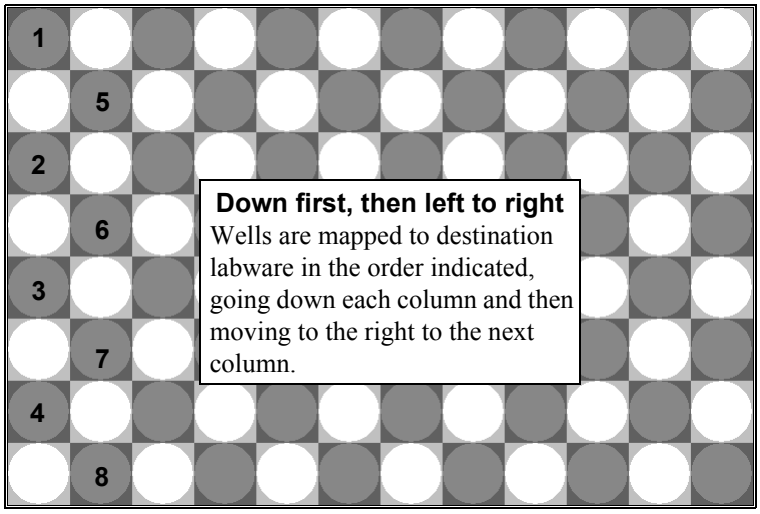


Figure 15-24. Wells accessed down first, then left to right

OR

- To the right first, then top to bottom — goes across each row from left to right, then goes down to the next row (Figure 15-25)

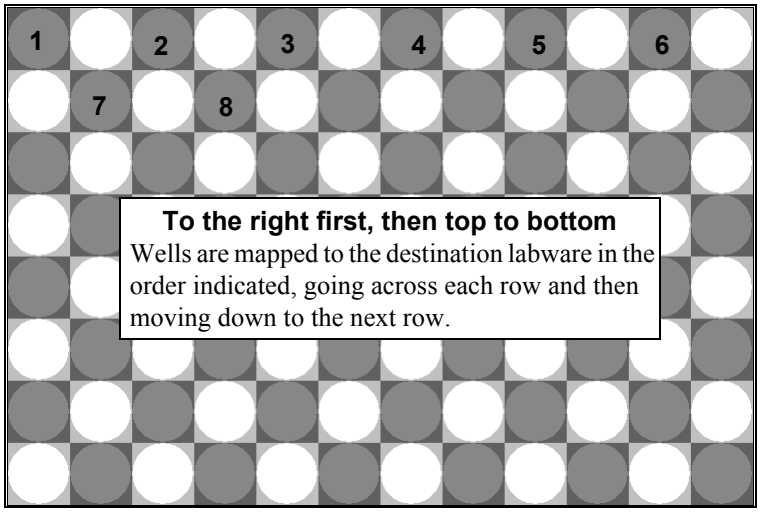


Figure 15-25. Wells accessed to the right first, then top to bottom

Note: The direction can also be selected when the labware is zoomed out by using the Down, then right or Right, then down buttons beneath the labware.

7. Select the first well accessed in **Start**. At first selected well is the default selection.

   ➢ ***FX, NX-S8*** — Start options only apply when using a Span-8 Pod.

   Note: Start controls how source wells are mapped to the destination, not the physical order in which wells are transferred. The Transfer step automatically determines the most efficient way to complete the transfer.

   - At first selected well — moves in the selected Direction starting from the first well selected on the labware

     OR

   - After last marked well — moves in the selected Direction starting from the first selected well on the labware after the marked well

     Note: The selected labware must have marks from a previous step with Mark last well that is used selected.

   Note: The start location can also be selected when the labware is zoomed out by using the Start at selection or Start at last mark buttons beneath the labware.

   Note: When transferring liquid, the first accessed source well is transferred to the first accessed destination well, the second accessed source well is transferred to the second accessed destination well, and so forth.

8. De-select **Mark last well that is used**, if it is not desired to mark wells. This option must be selected to use any options later in the method that make use of marks. For example, if Mark last well that is used is selected and the Transfer step runs out of sources before using all destinations, it marks the last well that had liquid transferred to it. Another Transfer step is transferring liquid to the same plate. By selecting **After last marked well** as the Start condition, the first source well will be transferred to the first unused destination well and continue according to the specified Direction. Mark last well that is used is selected by default.

   ➢ ***3000—*** Marks only apply when using a single-tip pipette tool.

   Note: Mark last well that is used can also be selected when the labware is zoomed out by using the Set mark button beneath the labware.

9. Choose **Zoom Out** to return to the step configuration screen.

10. For a Combine step, enter the amount of liquid (µL) to aspirate from the Source Labware. This will also be the amount of liquid dispensed into the destination labware. If using a variable or expression, enter an equal sign (=) followed by the variable name or expression; for example, =AspValue (Figure 15-26).

    Note: Refer to Section 14.3.2, *Specifying Volumes Using Data Sets*, for information on specifying volumes using a data set.

11. In **Using liquid type**, select the type of liquid in the Source Labware (Figure 15-26).

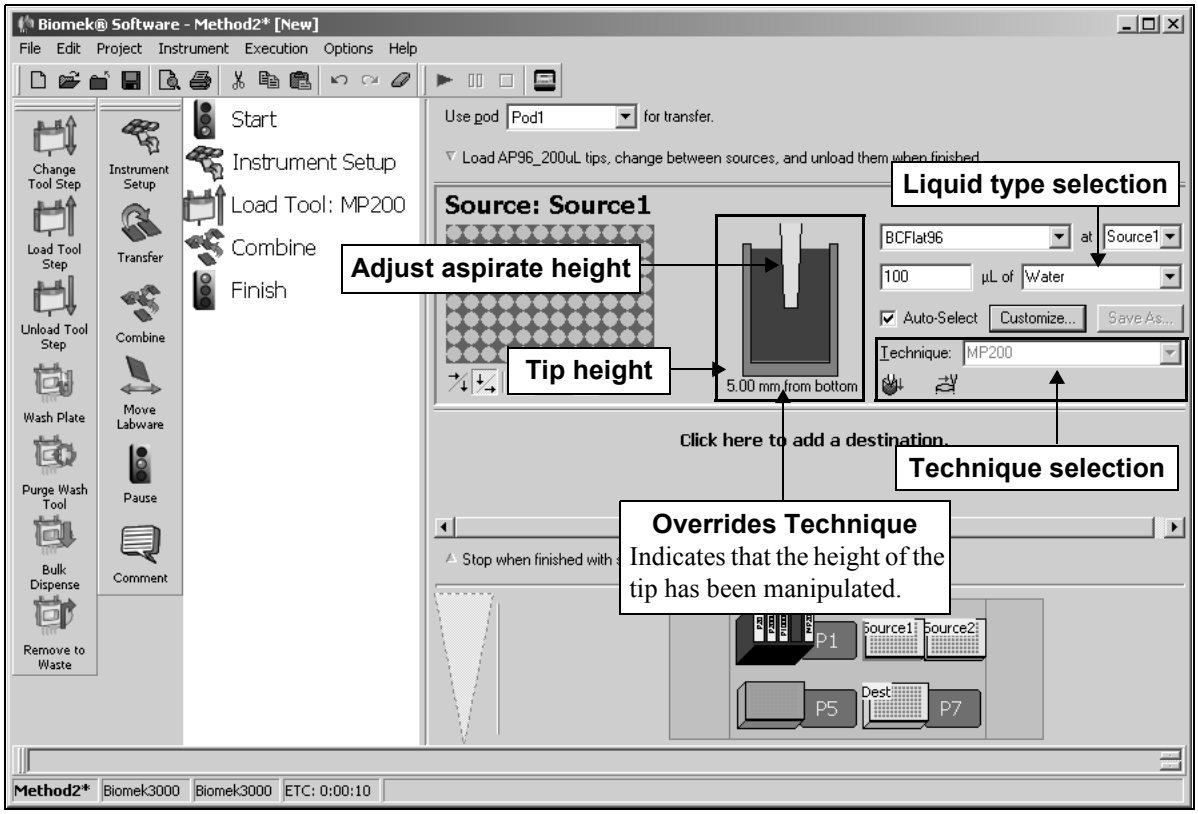


Figure 15-26. Combine step — Source Labware configuration

12. Keep the auto-selected **Technique** (refer to Section 15.3.2.1, *Auto-Selection of a Technique*).

Note: The software automatically selects a Technique based on the liquid type, labware type, tip type, and volume being aspirated.

OR

Manually select the desired **Technique**, or customize the selected Technique (refer to Section 15.3.2.2, *Customizing and Saving a Technique*).

13. Leave the height as is to use the settings specified in the pipetting technique.

    OR

    Set the aspirate height manually using one of the following techniques:

    - Set the aspirate height by positioning the cursor over the graphic of a tip inside a well (Figure 15-26). Click and drag the graphic up or down. The tip moves with the cursor, and the height displayed below the graphic is adjusted as the graphic is manipulated.

      Note: The cursor changes to a hand when positioned over the graphic.

    - Position the cursor in the graphic of a tip inside a well, and adjust the height using the ↑ and ↓ keys.
    - Right-click on the graphic of a tip inside a well, and a menu appears. Select **Custom Height**, and Custom Height appears (Figure 15-27). Insert the **Height** in millimeters (mm) and, in **from**, select a reference point from the drop-down list.

    Note: The phrase (Overrides Technique) appears below the graphic when the tip height is changed by manipulating the graphic (Figure 15-26), or when the technique is changed with the Customize option.

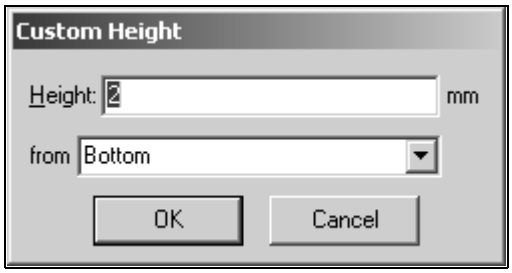


Figure 15-27. Custom Height prompt

14. For a Combine step, repeat steps 1 to 13 for each Source Labware desired.

    Note: A Destination Labware must first be selected before additional Source Labware can be configured.

15.3.2.1 Auto-Selection of a Technique

Auto-Select option is the default setting in the Transfer and Combine steps configuration. Disabling Auto-Select provides access to a list of predefined techniques, as well as allowing access to the Technique Editor so changes can be made to existing techniques.

Note: For more information on creating, editing, and saving techniques, refer to Section 15.3.2.2, *Customizing and Saving a Technique*, and Chapter 9, *Understanding and Creating Techniques*.

15.3.2.2 Customizing and Saving a Technique

Disabling Auto-Select provides access to a list of predefined techniques, as well as allowing access to the Technique Editor so changes can be made to existing techniques.

Note: For more information on creating, editing, and saving techniques, refer to Chapter 9, *Understanding and Creating Techniques*.

To select a Technique other than the technique selected automatically by Biomek Software:

1. Uncheck **Auto-Select**. The Technique: field is activated.
2. Select a **Technique:** from the list of predefined techniques.
3. Click **Customize** to modify the technique, if desired. The Technique Editor appears (Figure 15-28).

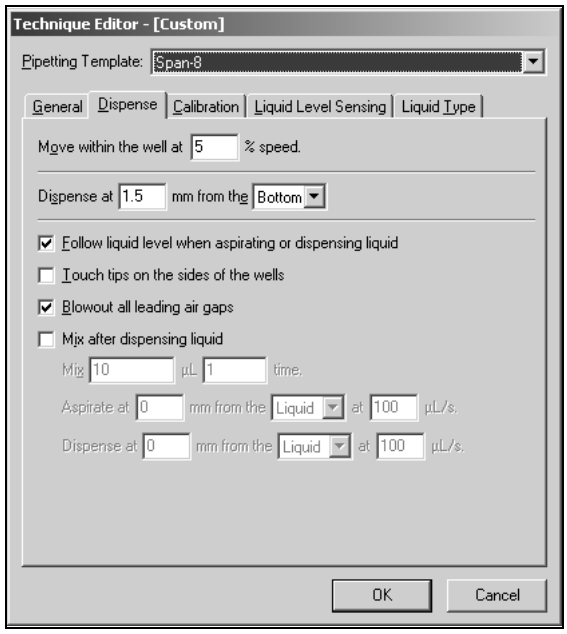


Figure 15-28. Technique Editor — Dispense options

Note: The Aspirate tab is virtually the same as the Dispense tab, with the exception of the Aspirate a trailing air gap after leaving the liquid and Prewet the tips pipetting options which appear on the Aspirate tab. When dispense operations are being configured, only the Dispense tab is displayed, while the Aspirate tab is displayed only when configuring aspirate operations. The Liquid Level Sensing tab only appears if the pod or tool supports liquid level detection.

4. Make desired changes in the applicable tabs of the Technique Editor.

5. Click **OK** to save the edited technique and return to the Transfer and Combine steps.
6. Click **Save As** to save an edited technique for use in this method and others.

Note: If Save As is not selected, the technique is saved with the current method, but it is not accessible to other methods or other steps within the current method.

15.3.3 Configuring Destination Labware

A 'destination' is a group of wells accessed at one time by the Biomek instrument to dispense liquid; for example:

- ***FX, NX-MC*** — A Multichannel Pod aspirates from either 96 or 384 wells at a time, depending on the head installed.

  Note: If configuring a 384-well microplate using a 96-channel pod or a 1536-well microplate using a 384-channel pod as source labware, any combination of quadrants may be used. For example, if it is desired to transfer liquid from the first, second, and third quadrants but not the fourth, the source labware may be configured to transfer only from those quadrants.

- ***FX, NX-S8*** — A Span-8 Pod dispenses to one to eight wells at a time, depending on the selected probes.
- ***3000*** — Depending on the tool loaded onto the head assembly, aspirates from either 1 or 8 wells at a time.

Note: If there are multiple destinations, each destination may have a different volume transferred, but all wells on each destination must have the same volume transferred. For example, to transfer different volumes to quadrants on the same 384-well plate, configure multiple destinations using the same destination plate but specifying different quadrants and volumes.

The Destination Labware configuration for the Transfer and Combine steps includes specifying:

- Labware type
- Labware location
- Liquid amount to transfer (for Transfer step only)
- Liquid type
- Well pattern or quadrants to access

  Note: Quadrants are applicable when accessing a 384-well microplate using a 96-channel pod or a 1536-well microplate using a 384-channel pod.

- Technique selection
- Pipetting height

Note: Multiple destinations can be configured for the Transfer step, because the Transfer step moves liquid from a single source to one or more destinations. A single destination is configured for the Combine step, because the Combine step moves liquid from one or more sources to a single destination.

To configure Destination Labware for the Transfer and Combine steps:

1. Select **Click here to add a destination** (Figure 15-29). The Destination Labware configuration appears.

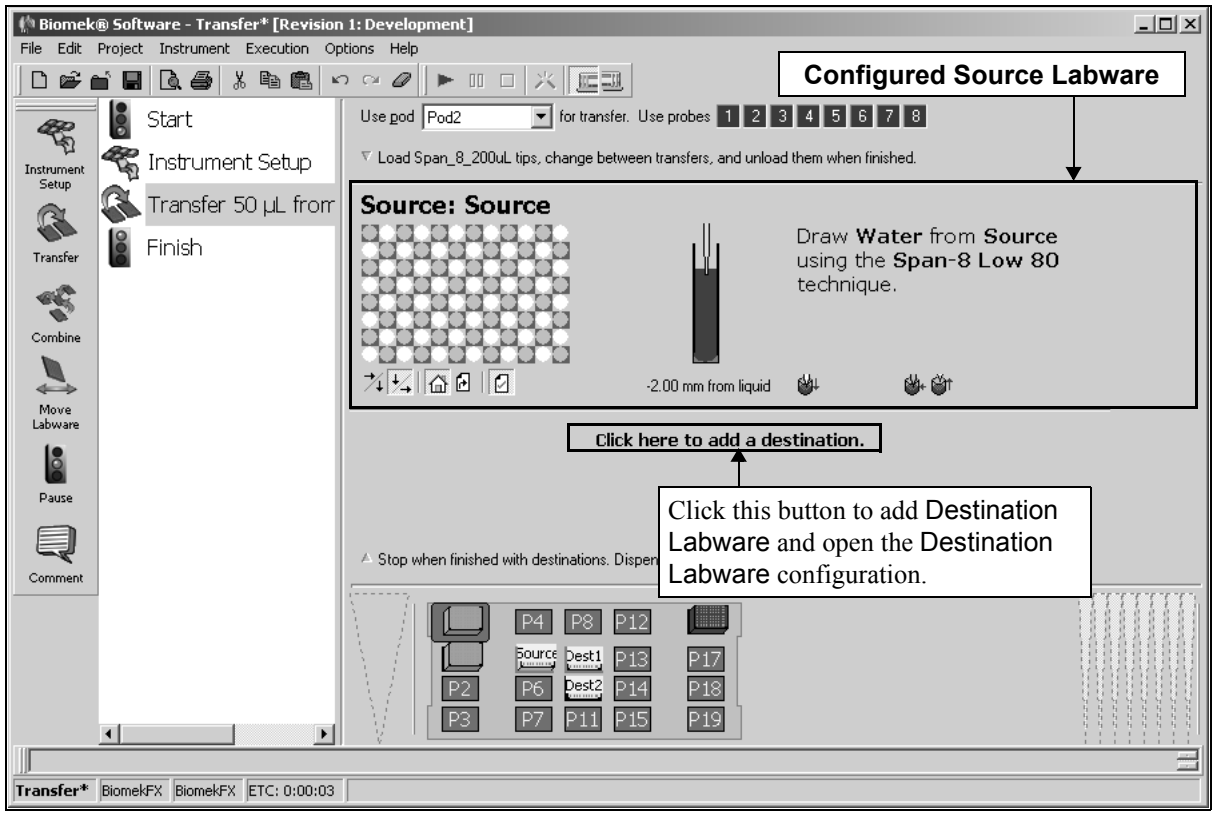


Figure 15-29. Transfer step — adding destination labware

2. Click on the desired piece of labware in the Current Deck Display. The labware type and position for that piece of labware is entered automatically into the Destination Labware configuration.

Note: If the selected labware is named, the name of the labware appears instead of the deck position.

OR

Select a **Destination Labware** (Figure 15-30) type and deck position.

Note: Once the first Destination Labware has been selected, the Source Labware parameters are collapsed to display a sentence summary. To reopen the Source labware parameters, click anywhere in the Source Labware configuration area.

Note: Subsequent labware selections modify the active Source or Destination Labware configuration. To configure additional Destination Labware, select **Click here to add a destination**, or select outside a labware configuration, and then select another piece of labware from the Current Deck Display. If an incorrect piece of labware is selected, right-click on the labware title and select **Delete** on the menu that appears.

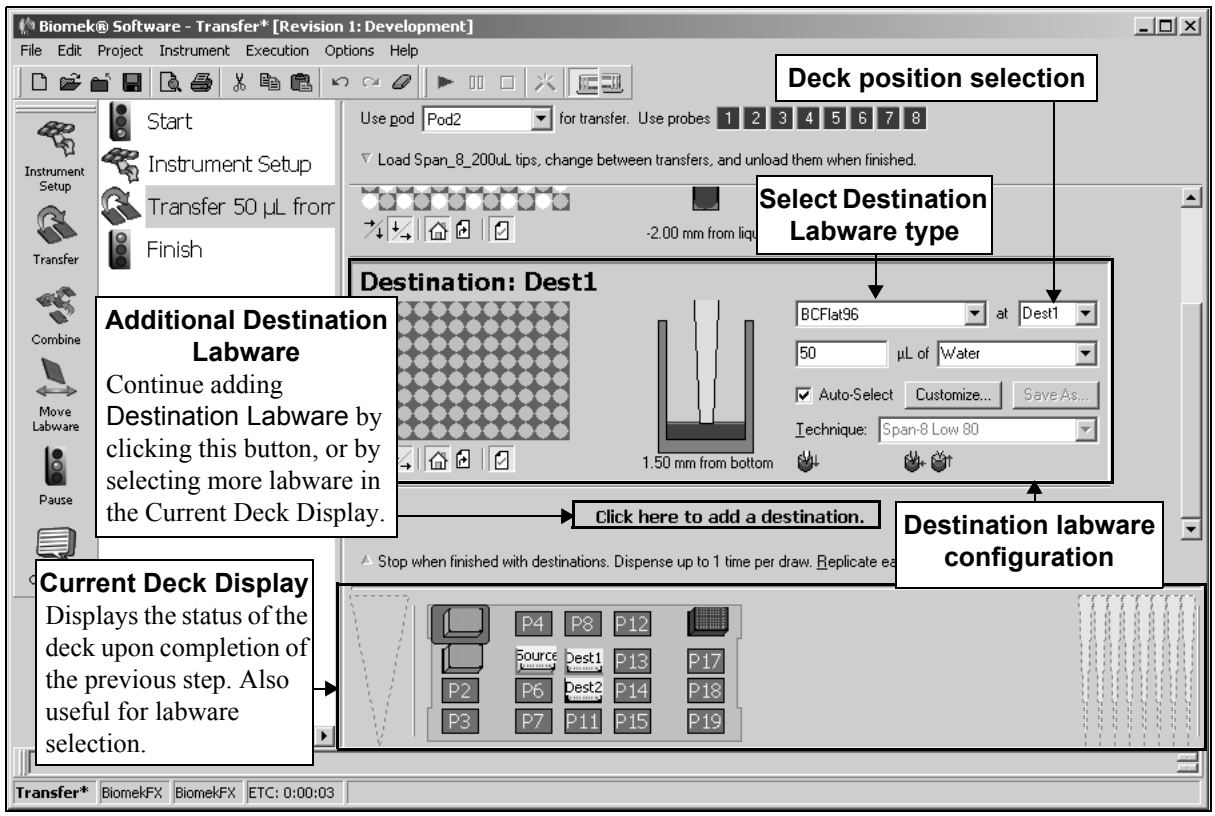


Figure 15-30. Transfer step — destination labware configuration

3. Verify the deck position of the labware.

Note: A bright yellow outline appears in the Current Deck Display around the labware designated as the Destination Labware.

4. To specify the wells or quadrants of a microplate to access, double-click the source labware in the step configuration to zoom in on the labware.

   Note: To call up a menu for Zoom and a Specify Selection as Text option, right-click on the labware.

   Specify Selection as Text allows selection of wells or quadrants as targets for aspirate and dispense operations. Specify Selection as Text may also be used to enter variables or expressions.

   Note: Specify Selection as Text is not applicable for 96-well microplates, reservoirs, or 384-well microplates accessed by a 384-channel pod.

5. Select the wells from which to transfer using one of the following techniques:

   - ***FX, NX-MC*** — A Multichannel Pod can only select quadrants of a microplate.
   - ***FX, NX-S8*** — Can select individual wells.
   - ***3000*** — A multi-tip pipette tool always selects groups of wells in columns of 8 while a single-tip pipette tool can select individual wells.
     - Choose **Copy Pattern** and select the desired pattern to use a previously defined well pattern created using the Well Patterns Editor (refer to Chapter 11, *Creating Well Patterns*).

       Note: The pattern must be compatible with the head or tool installed.

     - Select **Use pattern** and choose the previously defined pattern from the list to use a pattern created in a Well Patterns Editor or Define Pattern step.

       Note: Refer to Section 18.10, *Define Pattern Step (including 3000)*, for more information about creating patterns using the Define Pattern step.

     - Define a well pattern using data sets (refer to Section 14.3.1, *Defining Well Patterns Using Data Sets*).
     - Create a custom well pattern from the labware grid by dragging the mouse and using Ctrl and Shift on the keyboard.

       Note: Hold **Shift** and click a well to select additional wells without deselecting any wells. Hold **Ctrl** and click a well to toggle the selection status of selected wells without affecting the status of other wells. If Shift or Ctrl is not held down when selecting wells, any previous selection is deleted.

   Note: To save the new pattern, right click the labware graphic and select **Save Pattern** from the menu. Enter a name for the pattern in New Pattern and choose **OK**.

6. Select the **Direction** in which source wells are mapped to destinations. Down first, then left to right is the default selection.

   ➢ ***FX, NX-S8*** — Direction options only apply when using a Span-8 Pod.

Note: Direction controls how source wells are mapped to the destination, not the physical order in which wells are transferred. The Transfer step automatically determines the most efficient way to complete the transfer.

- Down first, then left to right — goes down each column from top to bottom, then goes right to the next column (Figure 15-31)

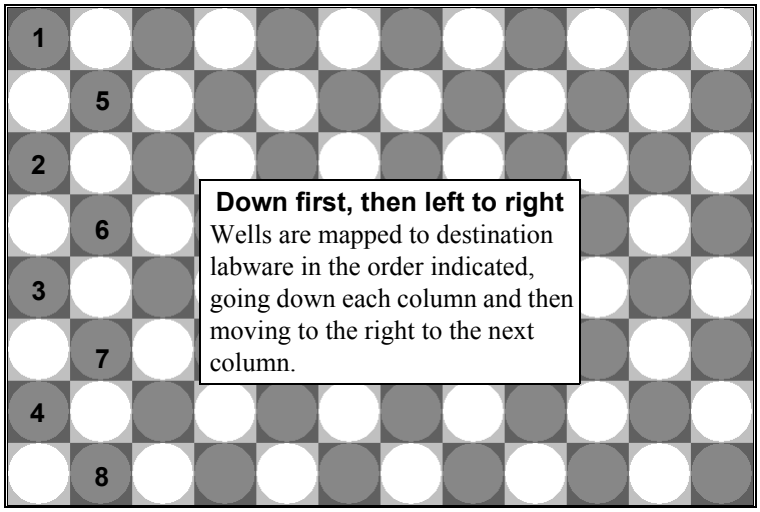


Figure 15-31. Wells accessed down first, then left to right

OR

- To the right first, then top to bottom — goes across each row from left to right, then goes down to the next row (Figure 15-32)

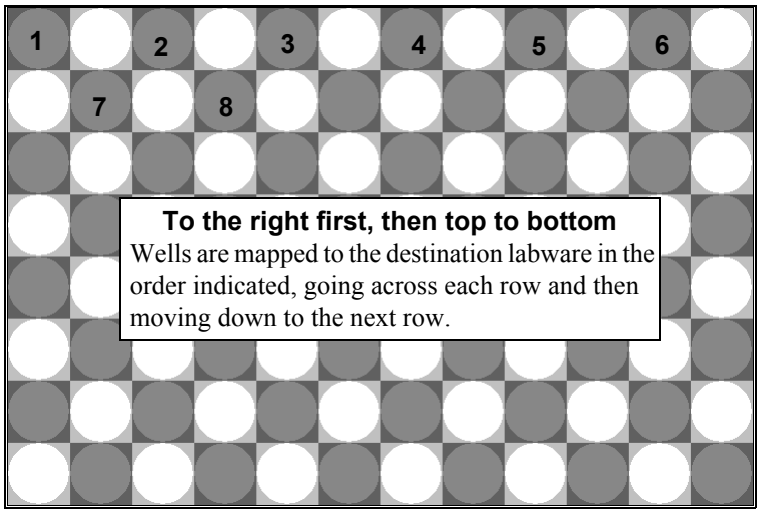


Figure 15-32. Wells accessed to the right first, then top to bottom

Note: The direction can also be selected when the labware is zoomed out by using the Down, then right or Right, then down buttons beneath the labware.

7. Select the first well accessed in **Start**. At first selected well is the default selection.

   ➢ ***FX, NX-S8*** — Start options only apply when using a Span-8 Pod.

   Note: Start controls how source wells are mapped to the destination, not the physical order in which wells are transferred. The Transfer step automatically determines the most efficient way to complete the transfer.

   - At first selected well — moves in the selected Direction starting from the first well selected on the labware

     OR

   - After last marked well — moves in the selected Direction starting from the first selected well on the labware after the marked well

     Note: The selected labware must have marks from a previous step with Mark last well that is used selected.

   Note: The start location can also be selected when the labware is zoomed out by using the Start at selection or Start at last mark buttons beneath the labware.

   Note: When transferring liquid, the first accessed source well is transferred to the first accessed destination well, the second accessed source well is transferred to the second accessed destination well, and so forth.

8. De-select **Mark last well that is used**, if it is not desired to mark wells. This option must be selected to use any options later in the method that make use of marks. For example, if Mark last well that is used is selected and the Transfer step runs out of sources before using all destinations, it marks the last well that had liquid transferred to it. Another Transfer step is transferring liquid to the same plate. By selecting **After last marked well** as the Start condition, the first source well will be transferred to the first unused destination well and continue according to the specified Direction. Mark last well that is used is selected by default.

   ➢ ***FX, NX-S8*** — Marks only apply when using a Span-8 Pod.

   Note: Mark last well that is used can also be selected when the labware is zoomed out by using the Set mark button beneath the labware.

9. Choose **Zoom Out** to return to the step configuration screen.

10. For a Transfer step, enter the amount of liquid (µL) to dispense into the Destination Labware. This will also be the amount of liquid aspirated from the source labware. If using a variable or expression, enter an equal sign (=) followed by the variable name or expression; for example, **=AspValue** (Figure 15-33).

Note: Refer to Section 14.3.2, *Specifying Volumes Using Data Sets*, for information on specifying volumes using a data set.

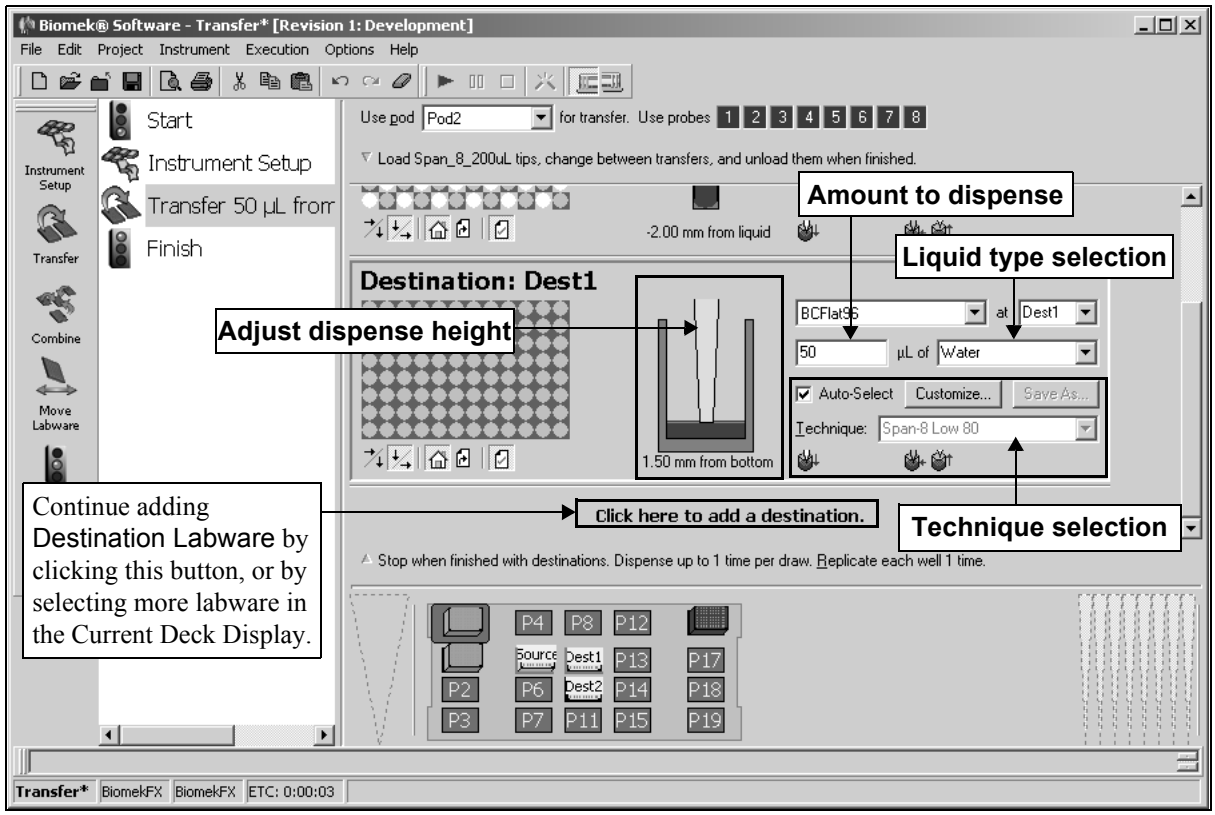


Figure 15-33. Transfer step — destination labware technique configuration

11. Verify that the liquid type indicated is correct. The liquid type dispensed to the Destination Labware should match the liquid type in the Source Labware configuration.

12. Keep the auto-selected **Technique** (refer to Section 15.3.2.1, *Auto-Selection of a Technique*).

Note: The software automatically selects a Technique based on the liquid type, labware type, tip type, and volume being aspirated.

OR

Manually select the desired **Technique**, or customize the selected Technique (refer to Section 15.3.2.2, *Customizing and Saving a Technique*).

13. Leave the height as is to use the settings specified in the pipetting technique.

    OR

    Set the dispense height manually using one of the following techniques:

    - Set the dispense height by positioning the cursor over the graphic of a tip inside a well (Figure 15-33). Click and drag the graphic up or down. The tip moves with the cursor, and the height displayed below the graphic is adjusted as the graphic is manipulated.

      Note: The cursor changes to a hand when positioned over the graphic.

    - Position the cursor in the graphic of a tip inside a well, and adjust the height using the ↑ and ↓ keys.
    - Right-click on the graphic of a tip inside a well, and a menu appears. Select **Custom Height**, and Custom Height appears (Figure 15-27). Insert the **Height** in millimeters (mm) and, in **from**, select a reference point from the drop-down list.

    Note: The phrase (Overrides Technique) appears below the graphic when the tip height is changed by manipulating the graphic, or when the technique is changed with the Customize option.

14. For a Transfer step, repeat steps 1 to 13 for each additional piece of Destination Labware.

15.3.3.1 Auto-Selection of a Technique

Auto-Select option is the default setting in the Transfer and Combine steps configuration. Disabling Auto-Select provides access to a list of predefined techniques, as well as allowing access to the Technique Editor so changes can be made to existing techniques.

Note: For more information on creating, editing, and saving techniques, refer to Section 15.3.2.2, *Customizing and Saving a Technique*, and Chapter 9, *Understanding and Creating Techniques*.

15.3.3.2 Customizing and Saving a Technique

Disabling Auto-Select provides access to a list of predefined techniques, as well as allowing access to the Technique Editor so changes can be made to existing techniques.

Note: For more information on creating, editing, and saving techniques, refer to Chapter 9, *Understanding and Creating Techniques*.

To select a Technique other than the technique selected automatically by Biomek Software:

1. Uncheck **Auto-Select**. The Technique: field is activated.
2. Select a **Technique:** from the list of predefined techniques.

3. Click **Customize** to modify the technique, if desired. The Technique Editor appears (Figure 15-34).

Note: refer to Chapter 9, *Understanding and Creating Techniques*, for more information about the Technique Editor.

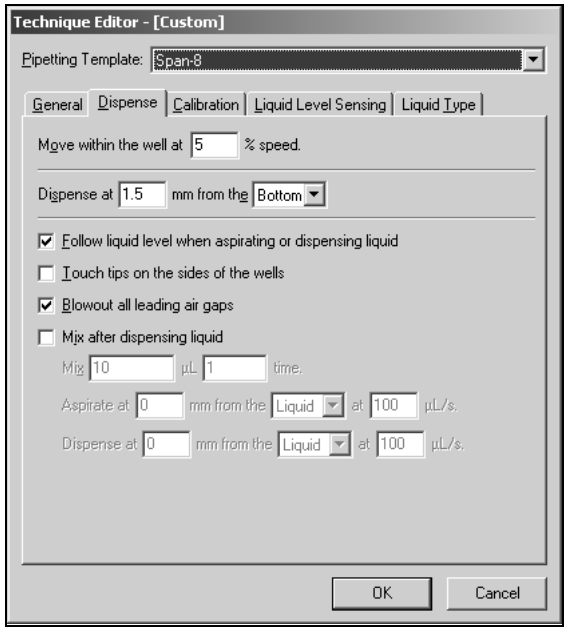


Figure 15-34. Technique Editor — Dispense options

Note: The Aspirate tab is virtually the same as the Dispense tab, with the exception of the Aspirate a trailing air gap after leaving the liquid and Prewet the tips pipetting options which appear on the Aspirate tab. When dispense operations are being configured, only the Dispense tab is displayed, while the Aspirate tab is displayed only when configuring aspirate operations.

Note: If the pod performing the pipetting operation is a Span-8 Pod, there is an additional Liquid Level Sensing tab displayed as part of the Technique Editor.

4. Make desired changes in the applicable tabs of the Technique Editor.
5. Click **OK** to save the edited technique and return to the Transfer and Combine steps.
6. Click **Save As** to save an edited technique for use in this method and others.

Note: If Save As is not selected, the technique is saved with the current method, but it is not accessible to other methods or other steps within the current method.

15.3.4 Configuring Transfer Details

Transfer Details (Figure 15-35) includes specifying:

- a stop condition for transfer operations.
- the number of replicates
  - ***FX, NX-S8*** — Replicates are available only with a Span-8 Pod.
- a repeat pipetting configuration.
- a maximum tolerance in timing between transfer operations (Figure 15-36).

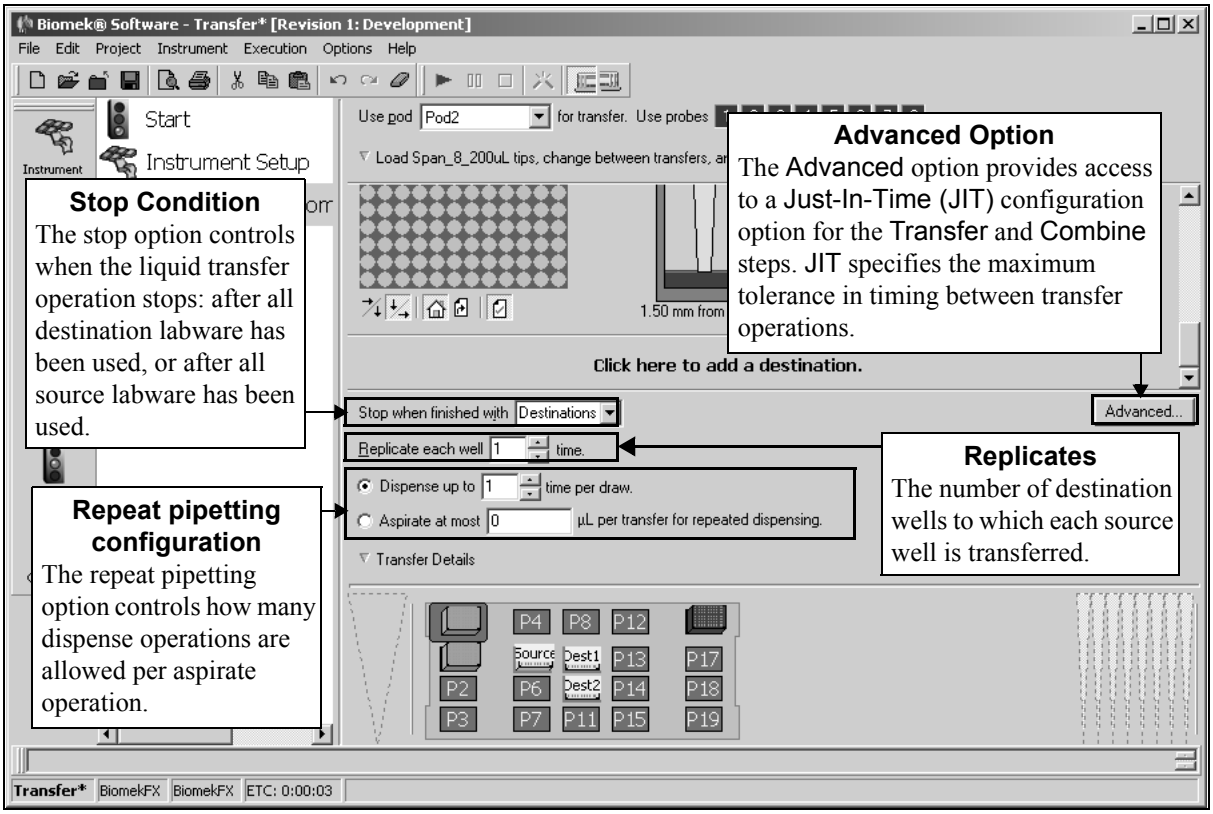


Figure 15-35. Transfer step — additional Transfer Details

To configure Transfer Details for the Transfer and Combine steps:

1. Click the arrow or sentence summary below the labware configuration section to expand Transfer Details.
2. In **Stop when finished with**, choose to determine when the liquid transfer operation stops: after Sources, Destinations, or Either.
    - **Sources** — the Transfer or Combine is complete when it runs out of sources
    - **Destinations** — the Transfer or Combine is complete when it runs out of destinations
    - **Either** — the Transfer or Combine is complete when it runs out of either sources or destinations

    Note: The default setting for Stop when finished with is Destinations to avoid cross contamination.

    Note: If there are more source wells than destination wells and Stop when finished with is set to **Sources**, after dispensing to the final destination it will go to the first selected destination and continue until it runs out of sources. If **Destinations** is selected, it will stop after dispensing to the last destination and not use the remaining sources. If **Either** is selected, it will stop after dispensing to the last destination and not use the remaining sources.

    If marks are being used, the last source and/or destination wells used will be marked. Future operations may continue from the marked wells.
3. In Replicate each well, enter the number of destination wells to transfer each source well to. Each source well is transferred to the specified number of consecutive destination wells.
    - ***FX, NX-S8*** — Replicates are available only with a Span-8 Pod.
4. Select one of the repeat pipetting configuration options: Dispense up to or Aspirate at most.

    Note: If Tip Handling is configured to Change tips between destinations, the repeat pipetting options are unavailable for selection.

    Note: Only one repeat pipetting option may be selected. Either Dispense up to or Aspirate at most may be selected, but not both.
5. In **Dispense up to**, select the number of times the instrument is allowed to dispense per draw (aspirate). For example, if dispensing 75 µL to each of six microplates, three aspirate operations of 150 µL can each dispense into two destinations. In this case, Dispense up to is set to no fewer than two.

    Note: The default setting in Dispense up to is one, which does not allow a repeat pipetting operation. Settings of two or more allow repeat pipetting.

    OR

    In **Aspirate at most**, select the maximum volume to aspirate from the source for repeat pipetting. For example, if dispensing 75 µL to each of six microplates, three aspirate operations of 150 µL can each dispense into two destinations. In this case, Aspirate at most is set to no less than 150 µL.

6. In **Replicates**, enter the number of times each source well should be transferred to the destination labware. For example, if Replicates is set at **3**, the first source well is transferred to the first three destination wells; the second source well is transferred to the next three destination wells; and so forth.
7. Select **Advanced** to change the default setting of applying a Just-In-Time (JIT) block to aspirate and dispense operations. Just In Time synchronizes the execution of the substeps within the Transfer or Combine step. The Advanced Options prompt appears (Figure 15-36).

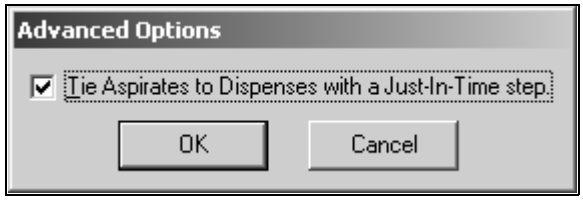


Figure 15-36. Advanced button — JIT Block

8. Uncheck **Tie Aspirate to Dispense with a JIT Block** to deactivate the JIT block.
9. Click **OK** to save any changes.

The Transfer Details configuration can be collapsed to allow more room during Source and Destination Labware configuration. When collapsed, the Transfer Details configuration is displayed as a sentence summary. Use the sentence summary to verify that Transfer Details has been configured appropriately.

To collapse or expand the Transfer Details configuration, click the arrow to the left of Transfer Details or the textual display.

15.4 Move Labware Step

- ***3000*** — The gripper tool is required to move labware.
- ***NX-S8*** — The optional gripper must be installed to move labware.

The Move Labware step moves labware from one position on the Biomek instrument deck to another position. Move Labware can also remove labware from the deck by placing it in an appropriate disposal position, or to an external hardware device without halting the Biomek instrument or the method.

15.4.1 Inserting a Move Labware Step

Insert a Move Labware step into the Method View (Figure 15-37).

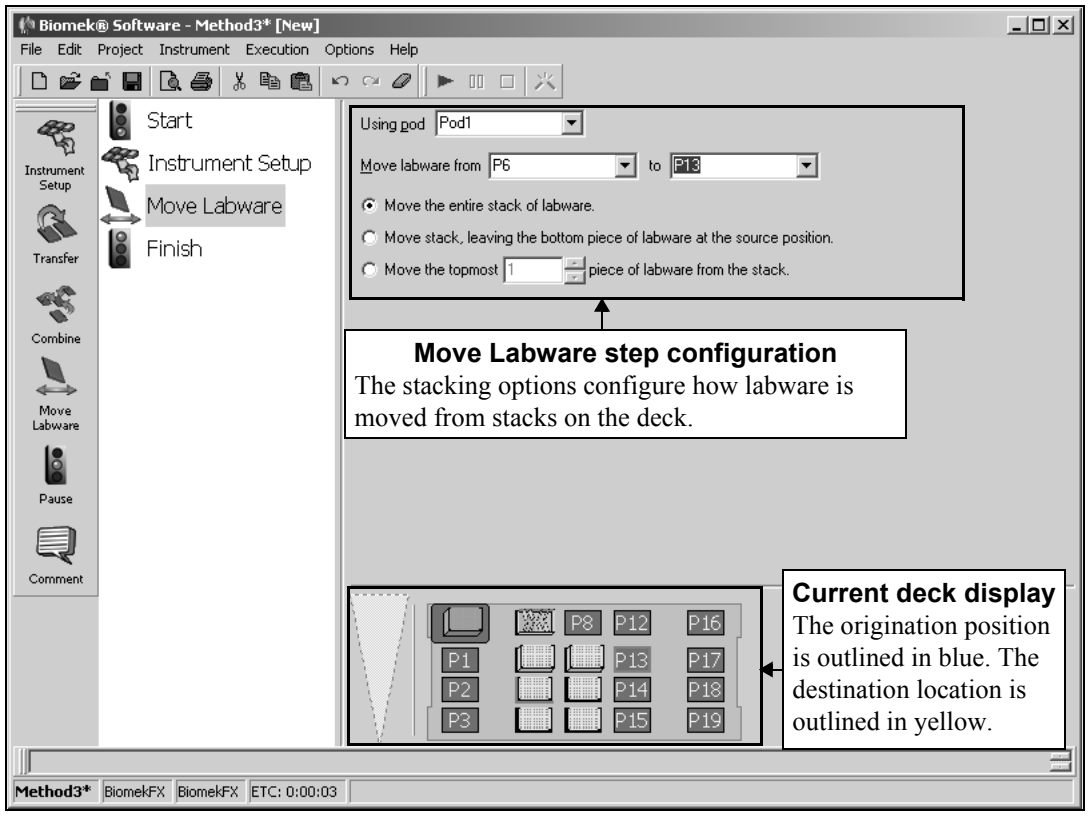


Figure 15-37. Move Labware step and configuration

15.4.2 Configuring the Move Labware Step

CAUTION: Make sure the correct ALP is chosen when configuring the deck setup in the Deck Editor. ALPs vary in height, and failure to choose each ALP correctly in the software may result in collisions between pod(s) and ALPs during operation.

To configure a Move Labware step, complete the following steps:

- ***3000*** — To use the Move Labware step with the Biomek 3000, a gripper tool must be added and configured in Hardware Setup (refer to the *Biomek® 3000 Laboratory Automation Workstation User's Manual,* Section 12.3, *Adding and Removing Tools and Devices*) and placed on a tool rack in an Instrument Setup step (refer to Section 15.2, *Instrument Setup Step*).

1. If using a dual-pod ***FX*** instrument, specify the Pod to move the labware in Using Pod. The pod configured as the default pod is automatically selected. If the other pod is desired, select the pod from the drop-down list or the Current Deck Display.
2. In Move labware from, select the original deck position for the labware from the Current Deck display. This instructs the Biomek instrument to Move labware from a specific deck position in preparation for leaving it at a final destination.
3. In to, select the final deck position for the labware from the Current Deck display. This instructs the Biomek instrument to move the labware to a final deck position.
4. Select the desired option for moving stacked labware:
   - ***FX, NX-MC*** — Gripper on the Multichannel Pod can move up to four plates at a time.
   - ***NX-S8*** — The optional gripper, if installed, can move up to four plates at a time.
   - ***3000*** — Gripper tool can move up to three microplates at a time.
     - **Move the entire stack of labware** — moves all labware in the stack; this option should be selected when moving a single unstacked piece of labware.
     - **Move stack, leaving the bottom piece of labware at the source position** — moves all labware in the stack except for the bottom piece.

       Note: Selecting Move stack, leaving the bottom piece of labware at the source position when the source deck position contains only one piece of labware results in an error.

     - **Move the topmost . . .piece(s) of labware from the stack —** moves only the specified number of labware from the top of the stack.

Note: Refer to Section 7.3.6.4.1, *Biomek Stacking Rules*, for complete information on using stacks on Biomek instruments.

15.5 Pause Step

The Pause step is used to either halt a deck position or device during a method for a specified amount of time, or pause the instrument for an indefinite period of time. During the pause, the instrument may still move and act on other deck positions. Depending on the purpose of the pause, the step can be configured in one of two ways:

- To incubate a piece of labware in a specific position for a specific amount of time, configure the desired time in seconds to hold that position idle and unavailable for interaction with the instrument (Figure 15-38). Refer to Section 15.5.1, *Configuring a Pause for a Specific Deck Position or Pod*.
- To manipulate the deck by hand during a method, configure the step to pause the instrument for an indefinite period of time (Figure 15-40). When the Pause step halts the instrument, the amber indicator lights on the front of the unit are activated, and a prompt appears. The prompt displays the text inserted in the Pause step configuration and requires acknowledgement before the method continues. Refer to Section 15.5.2, *Pausing the Whole System and Displaying a Message*.

Note: When the Pause step occurs during a method run, the Biomek pod remains in the position of the last action completed before the pause. If the purpose of the Pause step is to move labware on or off the deck, a Move Pod step must be inserted in the method prior to the Pause step so that the pod is out of the way (refer to Section 16.11, *Move Pod Step*).

Insert a Pause step into the Method View (Figure 15-38).

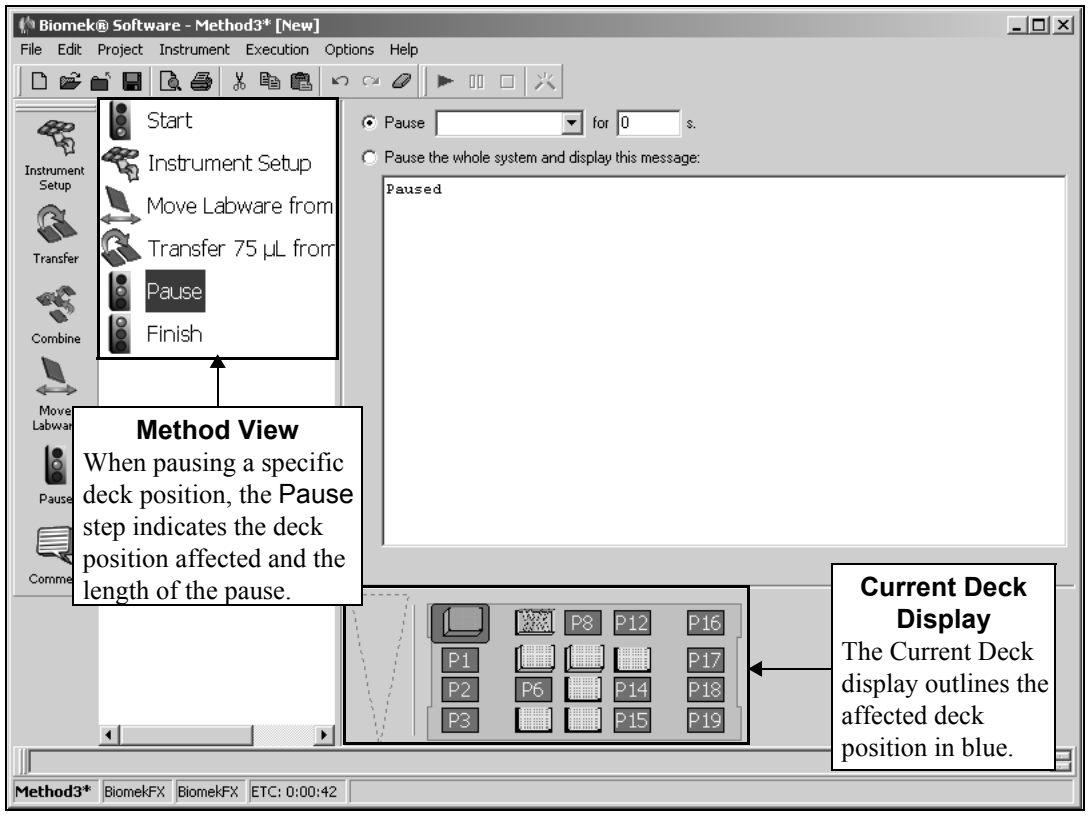


Figure 15-38. Inserting a Pause step in a method

15.5.1 Configuring a Pause for a Specific Deck Position or Pod

To configure a Pause for a specific deck position:

1. Choose **Pause** in the Pause step configuration (Figure 15-38).
2. In Pause, select the deck position or pod in the Current Deck Display or from the drop-down list (Figure 15-39).

Note: To pause the instrument for a specified length of time, select **the whole system** in Pause.

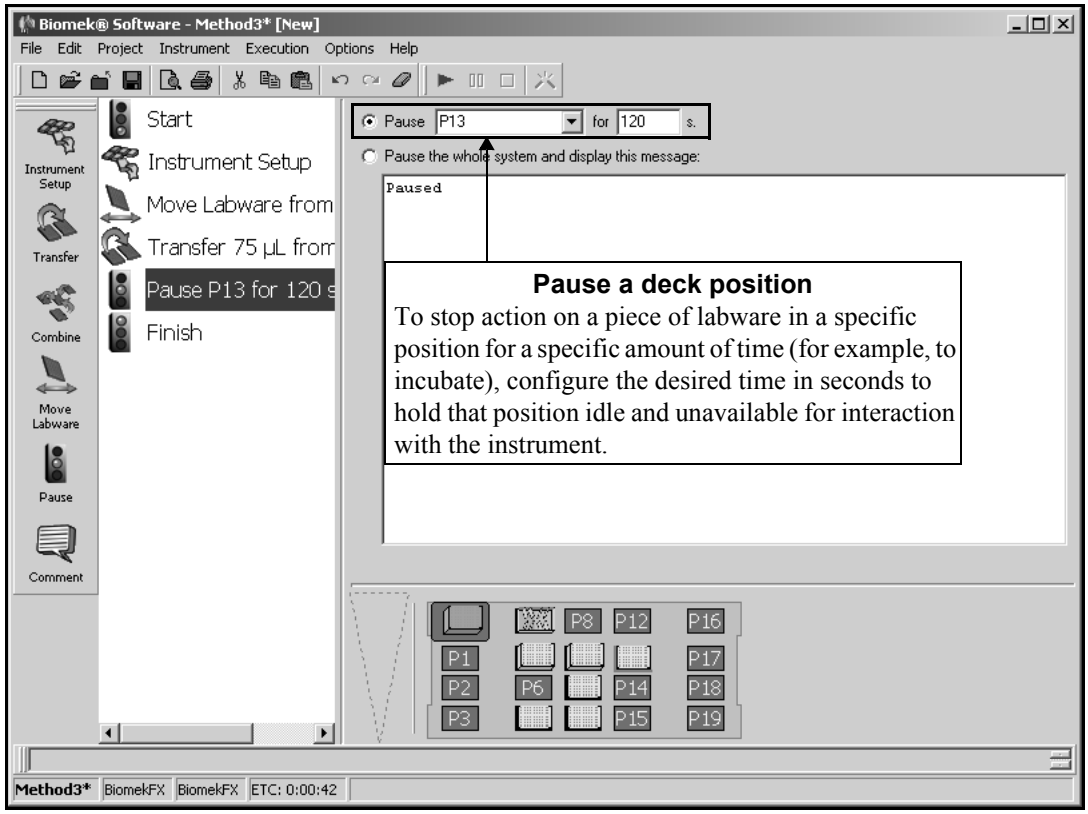


Figure 15-39. Pausing a deck position for a specified length of time

3. Choose the **length of the pause**, in seconds.

Note: The method continues with operations not affected by the Pause, when possible. If the next step is dependent upon the deck position or pod paused, the method waits until the Pause has been completed.

15.5.2 Pausing the Whole System and Displaying a Message

To configure a Pause for the entire Biomek instrument and display a message:

1. Select **Pause the whole system and display this message:** in the Pause step configuration (Figure 15-40).

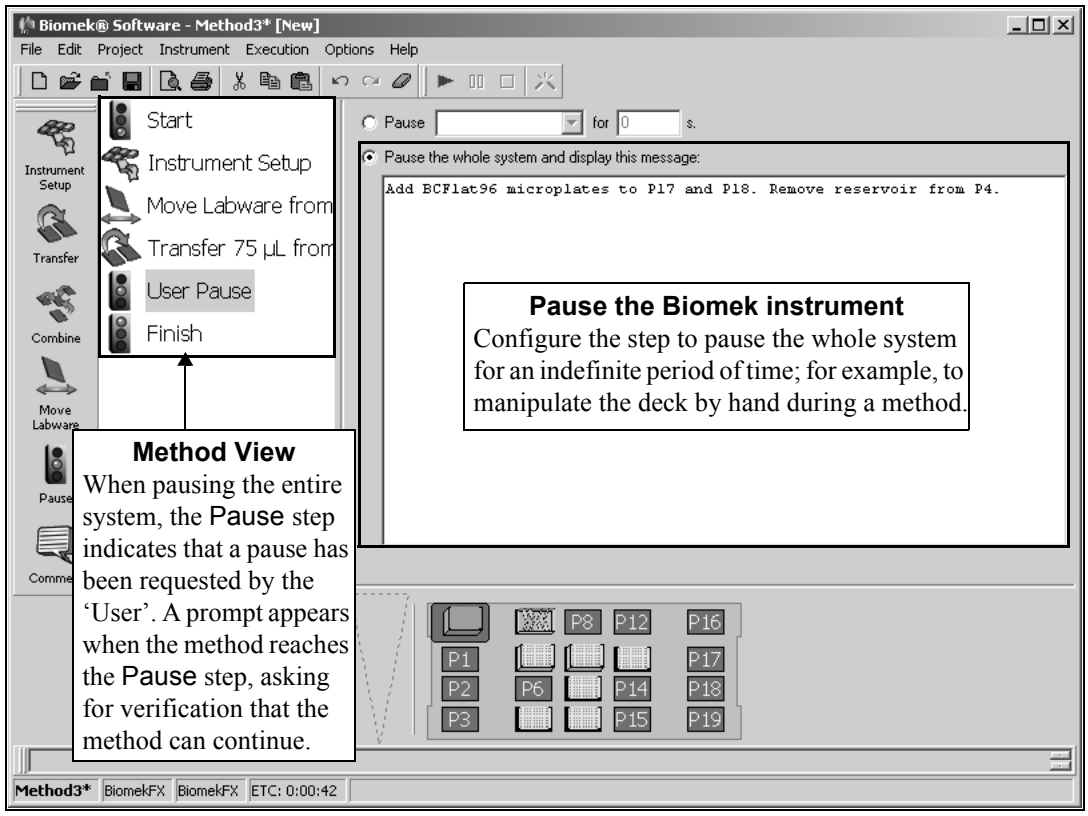


Figure 15-40. Pause step that provides instruction

2. Enter the message to display when the Pause is initiated.

Note: When Pause the whole system and display this message: is selected, a prompt (Figure 15-41) appears in the Biomek Software with the text entered in the Pause step configuration. When the action requested is completed, click **OK** to continue the method, or select Abort to halt the method without completing it.

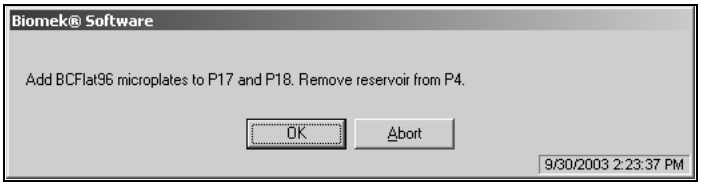


Figure 15-41. Pause message prompt

15.6 Comment Step

The Comment step documents a method and/or adds instructions in the Method View. Text inserted into the Comment step configuration may indicate the purpose of a segment of a method, prompt for an action, or convey any other desired information in the Method View. The Comment step does not initiate any actions on the Biomek instrument and is used only to provide descriptive information and notes to a method.

Note: Comments are printed when a method is printed. Choose **Print** from the File menu to print a method (refer to Section 12.19, *Printing a Method*).

Insert a Comment step into the Method View (Figure 15-42).

To configure Comment:

1. In **Description**, enter short summary of the comment. The text entered in Description is used as the step caption in the Method View.
2. In **Comment**, enter the full text for the comment.
3. Click the next step, and the Comment step in the Method View displays the text entered in Description (Figure 15-42).

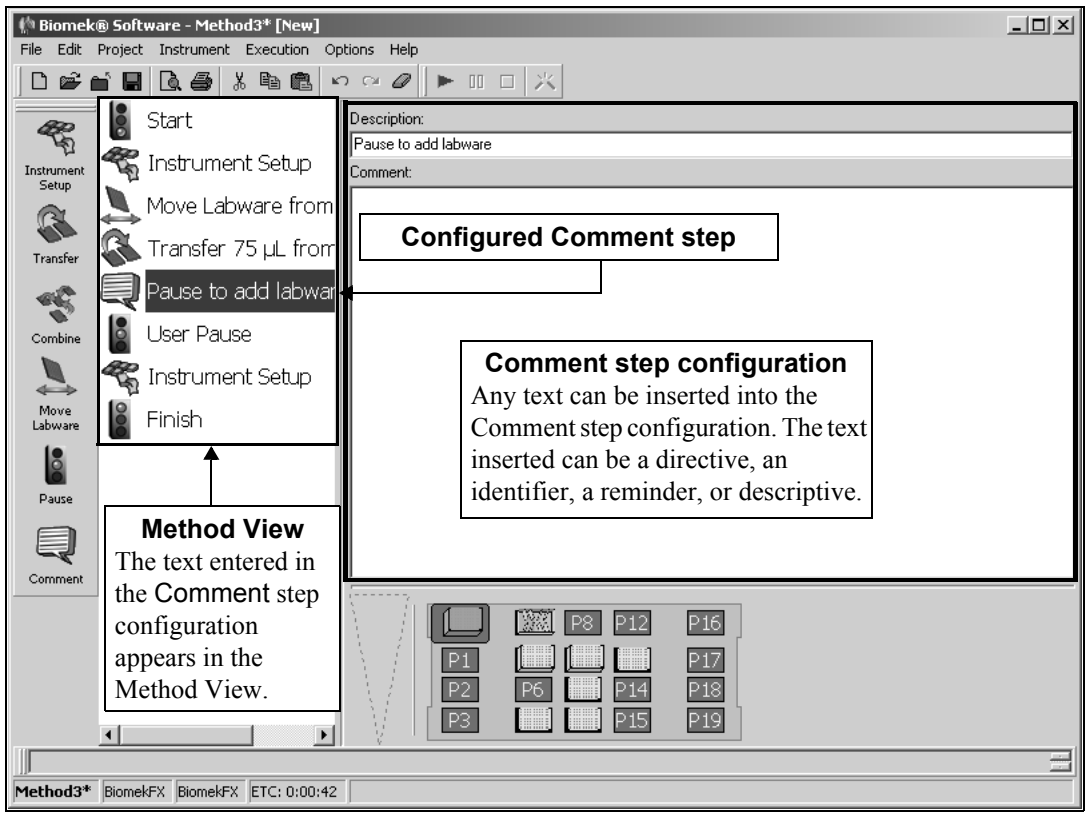


Figure 15-42. Comment step after text is inserted

16 Using the Intermediate Step Palette

16.1 Overview

Steps on the Intermediate Step Palette provide individual control over liquid-handling functions outside the Transfer and Combine steps, including tip handling operations, flow of control, tip and tip box relocation options, and pod movement.

CAUTION: Make sure the correct ALP is chosen when configuring the deck setup in the Deck Editor. ALPs vary in height and failure to choose the correct ALP in the Deck Editor may result in collisions between pod(s) and ALPs during operation.

The steps available in the Intermediate Step Palette are:

- ***FX, NX-S8*** — The pipetting and tip handling steps on the Intermediate step palette cannot be used with the Span-8 Pod; refer to Chapter 18, *Using the Span-8 Step Palette*, to perform similar functions.

- Aspirate — aspirates a specified amount of liquid from a single source in preparation for the Dispense step.

- Dispense — dispenses a specified amount of liquid into a single destination, following the Aspirate step.

- Mix — mixes the contents of a piece of labware using repeated aspirate and dispense.

- Wash — washes tips by aspirating and dispensing repeatedly at a Tip Wash ALP.
  - ***3000*** — The Wash step cannnot be used with the Biomek 3000 and does not appear on the Intermediate Step Palette.

- New Tips— loads new tips to the head.

- Unload Tips — unloads tips from the head.

- Loop — executes one or more steps a configured number of times.

- Cleanup — places tips and tip boxes at specified locations.

- Move Pod — moves the pod to a specified deck location.

- Group Step — groups a series of steps in a nested fashion under a logical name that appears in the Method View.

When one of the above steps is added to a method, the configuration associated with that step appears on the right side of the Biomek Software main editor, in step configuration (Figure 16-1).

Note: Steps not configured appropriately generate errors when the method is validated or run.

16.2 Displaying the Intermediate Step Palette

In order to add intermediate steps to a method, display the Intermediate Step Palette (Figure 16-1).

- ***FX, NX-S8*** — Only the Loop, Cleanup, Move Pod, and Group steps appear on the Intermediate step palette for Span-8 only instruments.
- ***3000*** — The Wash step does not appear on the Intermediate step palette.

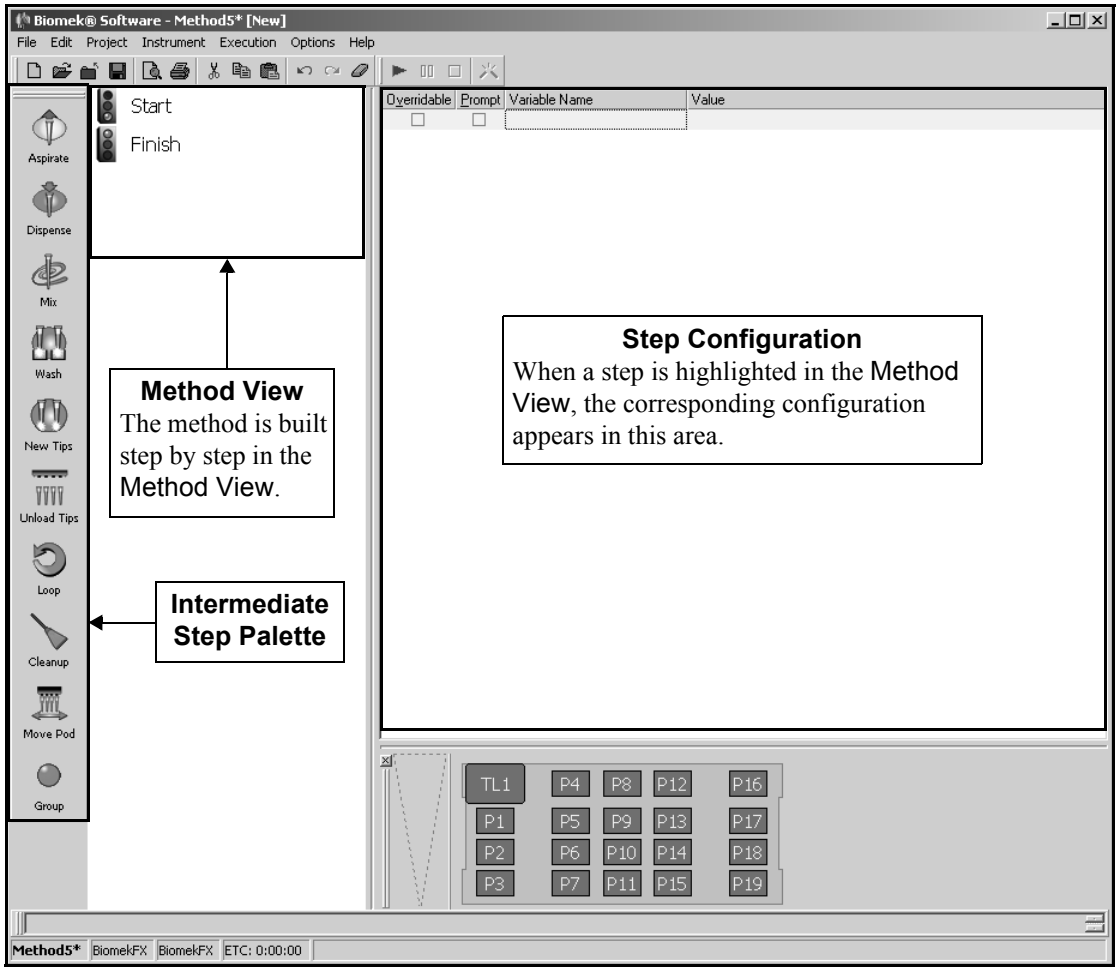


Figure 16-1. Biomek Software main editor with Intermediate Step Palette displayed

To display the Intermediate Step Palette, complete the following:

- Right-click any empty palette space, and the Step Palette menu appears. Select **Intermediate**.

  OR

- From the toolbar, select **Options>Toolbars>Intermediate**.

16.3 Aspirate Step

- ***NX-S8*** — To aspirate using a Span-8 Pod, refer to Section 18.4, *Span-8 Aspirate Step*.

The Aspirate step removes liquid from source labware in preparation for dispensing to destination labware. Each tip of the head or tool descends into the wells of the source labware and aspirates the desired volume. The Aspirate step is often used in conjunction with the Dispense, New Tips, and Unload Tips steps (Figure 16-2), but it can be used with any combination of steps. Aspirate provides more direct control over pipetting operations than the Transfer or Combine steps because any step or combination of steps can complete the liquid transfer operation started with the Aspirate step.

- ***3000*** — A Load Tool or Change Tool step must be inserted and configured to load an appropriate pipetting tool prior to an Aspirate step in the method (refer to Section 20.4, *Load Tool Step*). Depending on the tool loaded, either a single well or eight wells in a column are selected when aspirating with the Biomek 3000 instrument.

Note: A Loop step and variable can be used to aspirate to more wells on a microplate (refer to Section 16.9, *Loop Step*).

The Aspirate step configuration includes specifying:

- Labware type accessed during aspirate
- Position of the labware on the deck
- Type of liquid to aspirate
- Volume to aspirate
- Pod that performs aspirate
- Tip refresh, if desired, and the type of tips used
- Technique selection
- Quadrant or well(s) accessed, if applicable
  - ***FX, NX-MC*** — Quadrants are applicable only when accessing a 384-well microplate using a 96-channel pod or a 1536-well microplate using a 384-channel pod.
  - ***3000*** — Either a single well or eight wells in a column are selected, depending on the tool loaded.

Insert an **Aspirate** step into the method (Figure 16-2).

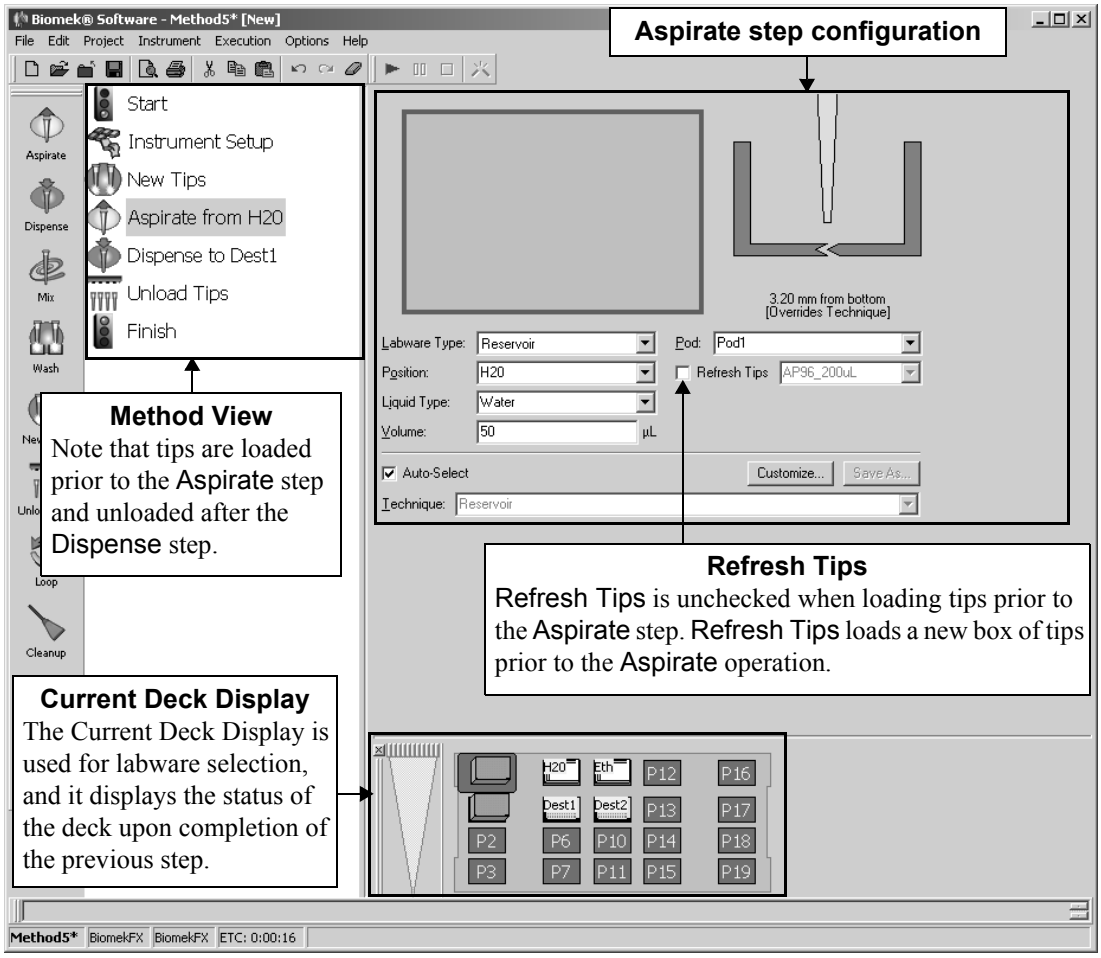


Figure 16-2. Aspirate step and configuration

16.3.1 Configuring the Aspirate Step

When an Aspirate step is added to a method, the Aspirate step configuration appears (Figure 16-2).

To configure the Aspirate step:

1. Click on the desired piece of labware in the Current Deck Display from which to aspirate. Information for that piece of labware is entered automatically into the Aspirate step configuration.

   OR

   Select a **Labware Type** (Figure 16-2).

2. Verify the **Position** of the labware.

   Note: A bright blue outline appears in the Current Deck Display around the selected labware.

3. Indicate the **Liquid Type** contained in the selected labware.

   Note: The liquid type defaults to the liquid specified for the labware in Instrument Setup.

4. Enter the **Volume** aspirated from the selected labware. If using a variable or expression, enter an equal sign (=) followed by the variable name or expression; for example, =AspValue (Figure 16-2).

5. Select the well(s) or quadrant to aspirate from by highlighting the desired quadrant on the labware graphic.

   - ***FX, NX-MC*** — Quadrants may be selected when aspirating from a 384-well plate using a 96-channel pod or a 1536-well plate using a 384-channel pod.
   - ***3000*** — Either a single well or eight wells in a column are selected, depending on the tool loaded.

   Note: To zoom in on the labware, double-click on the labware. To call up a menu for Zoom In and a Specify Selection as Text option, right-click on the labware.

   Specify Selection as Text allows the selection of a quadrant as a target for the aspirate operation. Specify Selection as Text is not applicable for 96-well microplates with a Multichannel Pod on ***FX*** or ***NX-MC***, but is applicable with pipetting tools on the ***3000***. It is never applicable with reservoirs.

6. If using a dual-pod ***FX*** instrument, specify the Multichannel **Pod** performing the aspirate operation from the drop-down list. The pod configured as the default pod is displayed in Pod. If the other pod is desired, select the pod from the drop-down list or the Current Deck Display.

7. Check **Refresh Tips**, if desired, and specify the **tip type**. Refresh Tips loads new tips to the pod whether tips are currently loaded or not.

   Note: If Biomek Software determines that tips are already loaded, the default setting for Refresh Tips is Off. If Biomek Software does not determine tips are loaded, the default setting for Refresh Tips is On.

8. The software automatically selects a Pipetting Technique based on the liquid type, labware type, tip type, and volume being transferred. To override this selection, deselect **Auto-Select** and choose the desired **Technique**

   OR

   Choose **Customize** and configure the technique as desired in the Technique Editor.

   Note: For more information on customizing, configuring, and saving a technique, refer to Section 12.3.1, *Understanding Techniques*.

9. In some cases, it may be necessary to override the aspiration height. Leave the height as is to use the settings specified in the pipetting technique.

   OR

   Set the aspirate height manually using one of the following techniques:

   - Set the aspirate height by positioning the cursor over the graphic of a tip inside a well (Figure 16-3). Click and drag the graphic up or down. The tip moves with the cursor, and the height displayed below the graphic is adjusted as the graphic is manipulated.

     Note: The cursor changes to a hand when positioned over the graphic. The phrase (Overrides Technique) appears below the graphic when the tip height is changed by manipulating the graphic (Figure 16-3) or when the technique is changed with the Customize option. For more information on selecting and editing a technique for this method, refer to Chapter 9, *Understanding and Creating Techniques*.

   - Adjust the aspirate height by selecting the graphic of a tip inside a well and using the ↑ and ↓ keys. The textual representation of the height, which is displayed below the graphic, adjusts in 0.1 millimeters (mm) increments.
   - Right-click on the graphic of a tip inside a well, and a menu appears. Select **Custom Height**, and the Custom Height prompt appears (Figure 16-4). Insert the height in mm and, in from, select a reference point from the drop-down list. Click **OK** to save the edits and return to the Aspirate step configuration.

   Note: For more information on creating, editing, and saving techniques for use with other methods, refer to Chapter 9, *Understanding and Creating Techniques*.

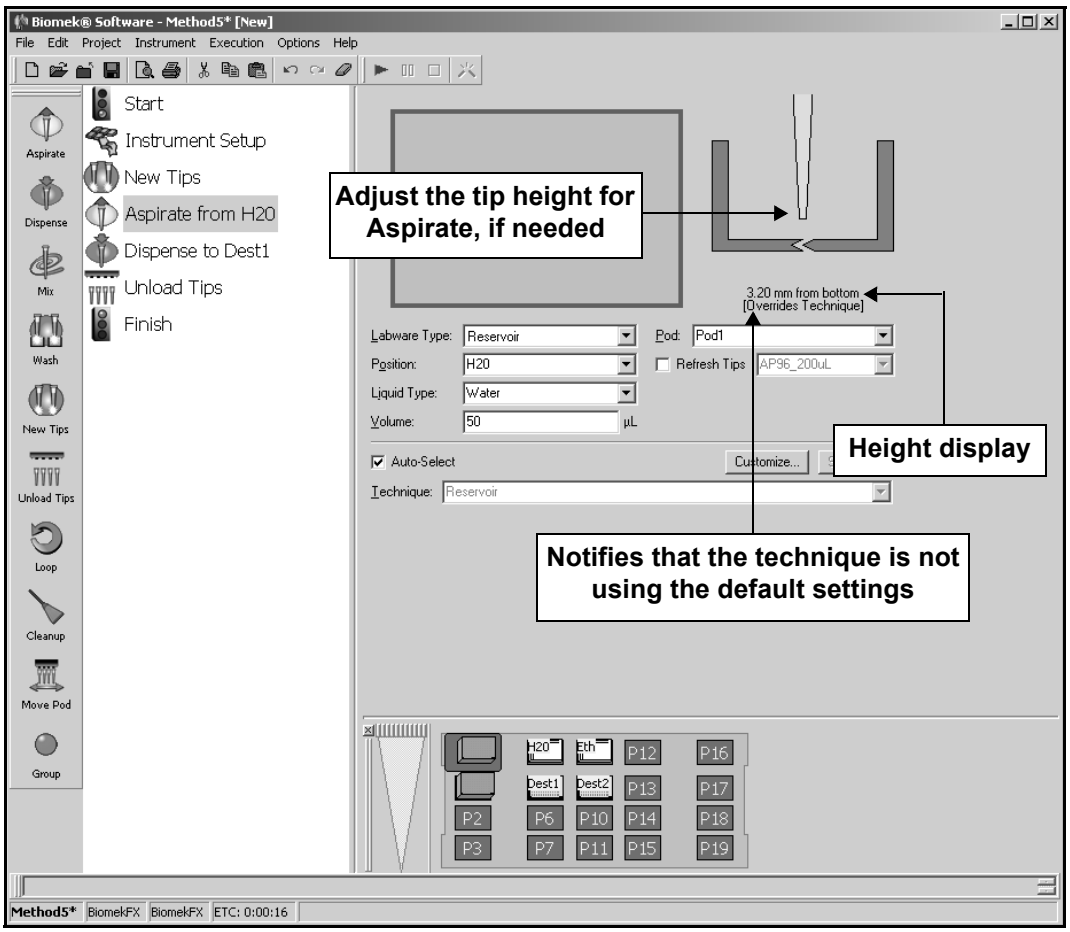


Figure 16-3. Aspirate step — Adjusting the aspirate height

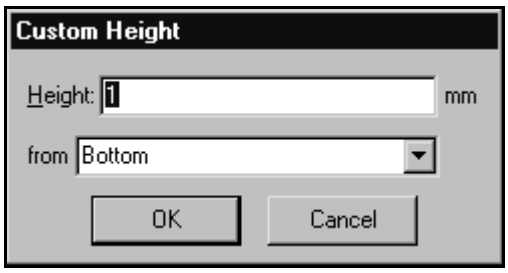


Figure 16-4. Custom Height prompt

10. Select a step that occurs after the Aspirate step or the **Finish** step to validate the step configuration.

16.4 Dispense Step

- ***FX, NX-S8*** — To dispense using a Span-8 Pod, refer to Section 18.5, *Span-8 Dispense Step*.

The Dispense step dispenses liquid into a single destination labware following aspirate. Each tip of the head or tool descends into the wells of the destination labware and dispenses the desired volume. The Dispense step is often used in conjunction with the Aspirate, New Tips, and Unload tips steps, but it can be used with any combination of steps. Dispense provides more direct control over pipetting operations than the Transfer or Combine steps because any step or combination of steps can initiate the liquid transfer operation.

Note: Tips must be loaded and have liquid in them from a previous step, such as an Aspirate step, prior to using a Dispense step.

Note: A Loop step and variable can be used to dispense from more wells on a microplate (refer to Section 16.9, *Loop Step*).

The Dispense step configuration includes specifying:

- Labware type accessed during dispense
- Position of the labware on the deck
- Type of liquid to dispense
- Volume to dispense
- Pod that performs dispense
- Empty tips, if desired
- Technique selection
- Quadrant or well(s) accessed, if applicable
  - ***FX, NX-MC*** — Quadrants are applicable only when accessing a 384-well microplate using a 96-channel pod or a 1536-well microplate using a 384-channel pod.
  - ***3000*** — Either a single well or eight wells in a column are selected, depending on the tool loaded.

Insert a **Dispense** step into the method (Figure 16-5).

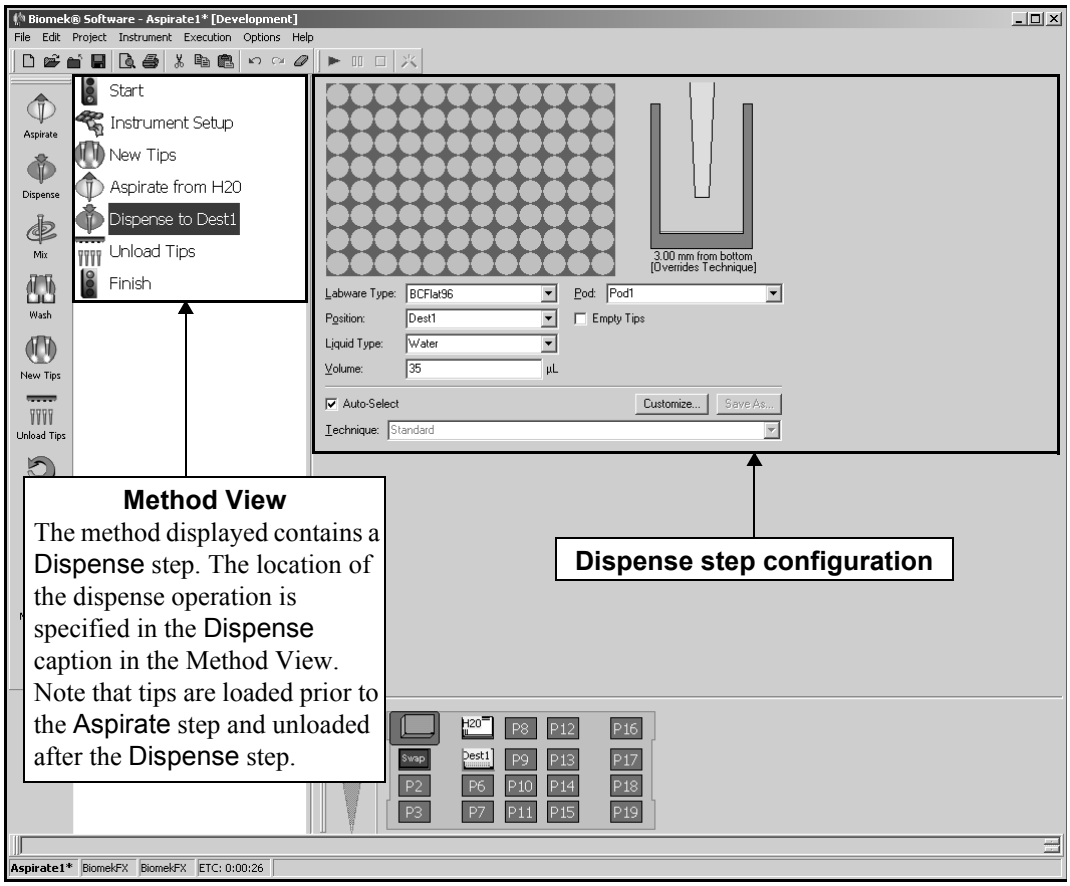


Figure 16-5. Dispense step and configuration

16.4.1 Configuring the Dispense Step

When a Dispense step is added to a method, the Dispense step configuration appears (Figure 16-5).

To configure the Dispense step:

1. Click on the desired piece of labware in the Current Deck Display. Information for that piece of labware is entered automatically into the Dispense step configuration.

   OR

   Select a **Labware Type** (Figure 16-5).

2. Verify the **Position** of the labware.

   Note: A bright yellow outline appears in the Current Deck Display around the selected labware.

3. Indicate the **Liquid Type** contained in the selected labware.

   Note: The liquid type defaults to the liquid specified for the labware in Instrument Setup.

4. Enter the **Volume** dispensed to the selected labware. If using a variable or expression, enter an equal sign (=) followed by the variable name or expression; for example, =AspValue (Figure 16-5).

5. Select the well(s) or quadrant to dispense to by highlighting the desired well(s) or quadrant on the labware graphic.

   - ***FX, NX-MC —*** Quadrants may be selected when dispensing to a 384-well plate using a 96-channel pod or a 1536-well plate using a 384-channel pod.
   - ***3000*** — Either a single well or eight wells in a column are selected when dispensing with the Biomek 3000 instrument, depending on the tool loaded.

   Note: To zoom in on the labware, double-click on the labware. To call up a menu for Zoom In and a Specify Selection as Text option, right-click on the labware.

   Specify Selection as Text allows the selection of a quadrant as a target for the aspirate operation. Specify Selection as Text is not applicable for 96-well microplates with a Multichannel Pod on ***FX*** or ***NX-MC***, but is applicable with pipetting tools on the ***3000***. It is never applicable with reservoirs.

6. If using a dual-pod ***FX*** instrument, specify the Multichannel **Pod** performing the dispense operation from the drop-down list. The pod configured as the default pod is displayed in Pod. If the other pod is desired, select the pod from the drop-down list or from the Current Deck Display.

7. Check **Empty Tips**, if desired. Empty Tips expels the Trailing Air Gap, the fluid contained in the tip, and the Blow Out all at one time, rather than as separate operations.

   Note: The default setting for Empty Tips is Off.

8. The software automatically selects a Pipetting Technique based on the liquid type, labware type, tip type, and volume being transferred. To override this selection, deselect **Auto-Select** and choose the desired **Technique**

   OR

   Choose **Customize** and configure the technique as desired in the Technique Editor.

   Note: For more information on customizing, configuring, and saving a technique, refer to Section 12.3.1, *Understanding Techniques*.

9. In some cases, it may be necessary to override the aspiration height. Leave the height as is to use the settings specified in the pipetting technique.

   OR

   Set the aspirate height manually using one of the following techniques:

   - Set the aspirate height by positioning the cursor over the graphic of a tip inside a well (Figure 16-6). Click and drag the graphic up or down. The tip moves with the cursor, and the height displayed below the graphic is adjusted as the graphic is manipulated.

     Note: The cursor changes to a hand when positioned over the graphic. The phrase (Overrides Technique) appears below the graphic when the tip height is changed by manipulating the graphic (Figure 16-6) or when the technique is changed with the Customize option. For more information on selecting and editing a technique for this method, refer to Chapter 9, *Understanding and Creating Techniques*.

   - Adjust the aspirate height by selecting the graphic of a tip inside a well and using the ↑ and ↓ keys. The textual representation of the height, which is displayed below the graphic, adjusts in 0.1 millimeters (mm) increments.
   - Right-click on the graphic of a tip inside a well, and a menu appears. Select **Custom Height**, and the Custom Height prompt appears (Figure 16-7). Insert the height in mm and, in from, select a reference point from the drop-down list. Click **OK** to save the edits and return to the Aspirate step configuration.

Note: For more information on creating, editing, and saving techniques for use with other methods, refer to Chapter 9, *Understanding and Creating Techniques*.

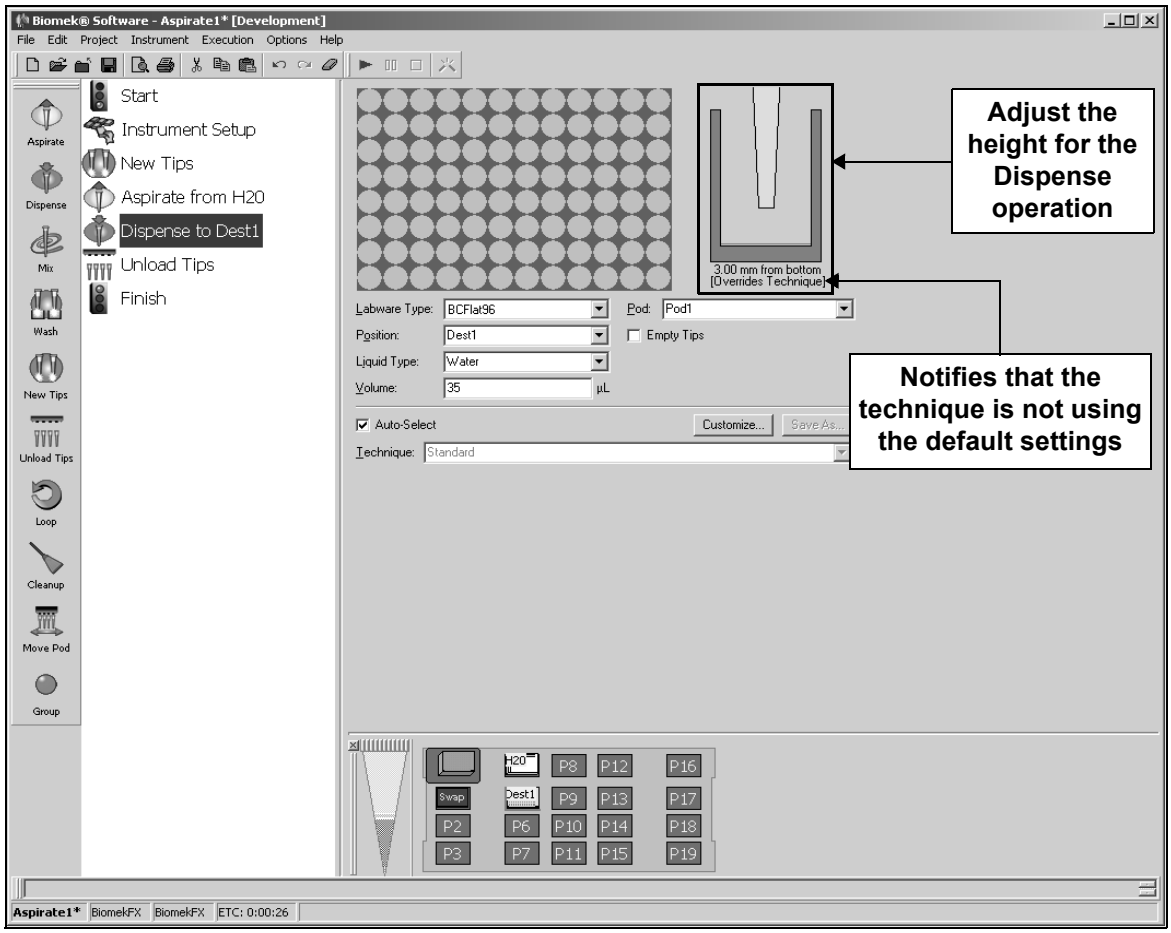


Figure 16-6. Dispense step — Adjusting the dispense height

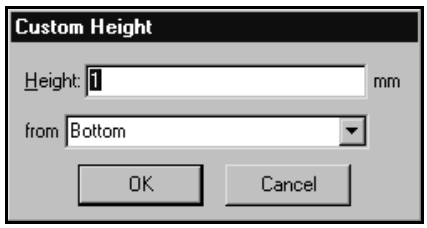


Figure 16-7. Custom Height prompt

10. Select a step that occurs after the Dispense step or the **Finish** step to validate the step configuration.

16.5 Mix Step

- ***FX, NX-S8*** — The Mix step cannot be used with a Span-8 Pod.

The Mix step provides a mixing motion for the contents of a piece of labware by performing one or more aspirate and dispense operations within a single microplate. The Mix step can be used to mix the contents of a piece of labware that has been inactive for an extended length of time, prior to aspirating.

- ***3000*** — A Load Tool or Change Tool step must be configured with an appropriate pipetting tool prior to a Mix step in the method (refer to Section 20.4, *Load Tool Step*). Depending on the tool loaded, either a single well or eight wells in a column are selected when mixing.

Note: A Loop step and variable can be used to mix more wells on a microplate (refer to Section 16.9, *Loop Step*).

The Mix step configuration includes specifying:

- Labware type accessed during mix
- Position of the labware on the deck
- Type of liquid mixed
- Volume mixed
- Pod performing the mix
- Tip refresh, if desired, and the type of tips to load
- Number of aspirate and dispense cycles to perform during the mix process
- Technique selection
- Quadrant or wells accessed, if applicable
  - ***FX, NX-MC*** — Quadrants are applicable only when accessing a 384-well microplate using a 96-channel pod or a 1536-well microplate using a 384-channel pod.
  - ***3000*** — Either a single well or eight wells in a column are selected, depending on the tool loaded.

Insert a **Mix** step into the method (Figure 16-8).

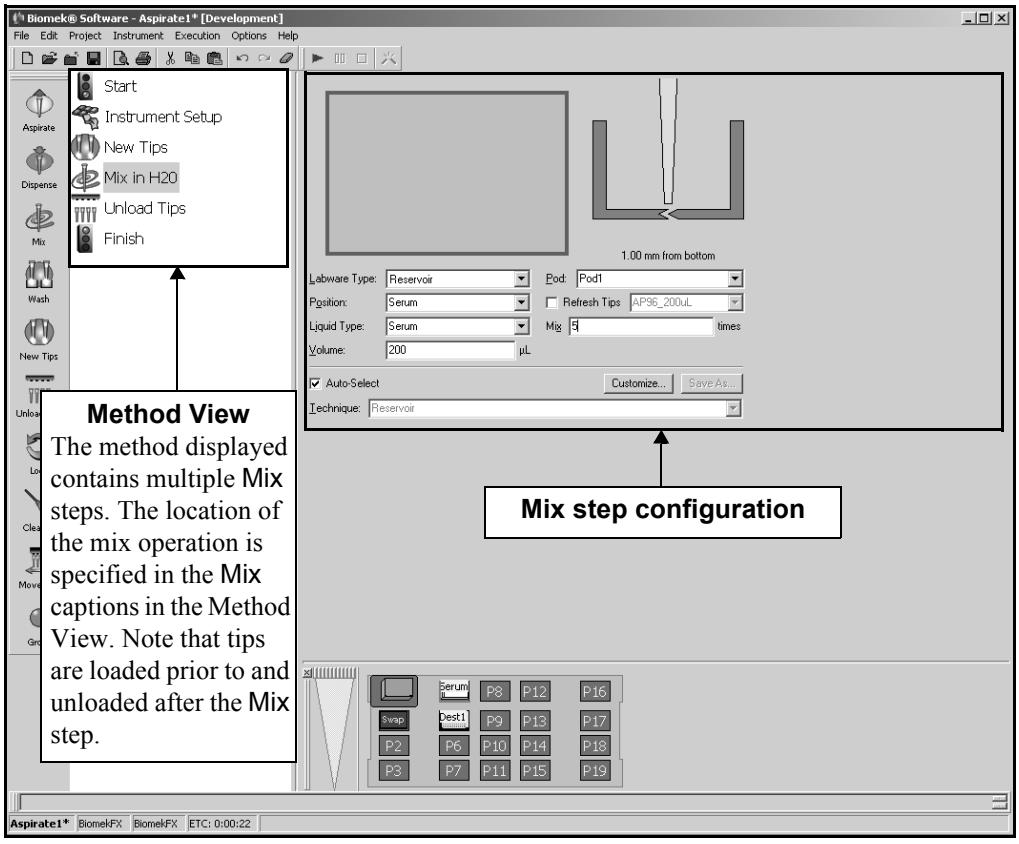


Figure 16-8. Mix step and configuration

16.5.1 Configuring the Mix Step

When a Mix step is added to a method, the Mix step configuration appears (Figure 16-8).

To configure the Mix step:

1. Click on the desired piece of labware in the Current Deck Display (Figure 16-8). Information for that piece of labware is entered automatically into the Mix step configuration.

   OR

   Select a **Labware Type** from the drop-down list.

2. Verify the **Position** of the labware.

Note: A bright blue outline appears in the Current Deck Display around the selected labware.

3. Select the well(s) or quadrant to mix by highlighting the desired well(s) or quadrant on the labware graphic.

   - ***FX, NX-MC —*** Quadrants may be selected when mixing wells in a 384-well plate using a 96-channel pod or a 1536-well plate using a 384-channel pod.
   - ***3000*** — Either a single well or eight wells in a column are selected when mixing wells, depending on the tool loaded.

   Note: To zoom in on the labware, double-click on the labware. To call up a menu for Zoom In and a Specify Selection as Text option, right-click on the labware.

   Specify Selection as Text allows the selection of a quadrant as a target for the aspirate operation. Specify Selection as Text is not applicable for 96-well microplates with a Multichannel Pod on ***FX*** or ***NX-MC***, but is applicable with pipetting tools on the ***3000***. It is never applicable with reservoirs.

4. Indicate the **Liquid Type** contained in the selected labware.
5. Enter the **Volume** mixed in the selected labware. If using a variable or expression, enter an equal sign (=) followed by the variable name or expression; for example, =AspValue.
6. If using a dual-pod ***FX*** instrument, specify the Multichannel **Pod** performing the mix operation from the drop-down list. The pod configured as the default pod is displayed in Pod. If the other pod is desired, select the pod from the drop-down list.
7. Check **Refresh Tips**, if desired, and specify the **tip type**. Refresh Tips loads new tips to the pod whether tips are currently loaded or not.

   Note: If Biomek Software detects that tips are already loaded, the default setting for Refresh Tips is Off. If Biomek Software does not detect tips, the Default setting Refresh Tips is On.

8. In **Mix**, enter the number of times the mix operation is performed.
9. The software automatically selects a Pipetting Technique based on the liquid type, labware type, tip type, and volume being transferred. To override this selection, deselect **Auto-Select** and choose the desired **Technique**

   OR

   Choose **Customize** and configure the technique as desired in the Technique Editor.

   Note: For more information on customizing, configuring, and saving a technique, refer to Section 12.3.1, *Understanding Techniques*.

10. Select a step that occurs after the Mix step or the **Finish** step to validate the step configuration.

16.6 Wash Step

- ***FX, NX-S8*** — To wash tips on a Span-8 Pod, refer to Section 18.8, *Span-8 Wash Tips Step*.
- ***3000*** — The Wash step is not for use with the Biomek 3000 and does not appear on the Intermediate Step Palette.

The Wash step combines aspirate and dispense operations into one step that cleans tips using the Multichannel Tip Wash ALP. Use the Deck Editor to add and configure the Wash Station ALP.

The Wash step configuration includes specifying:

- Pod performing the wash operation.
- Wash station accessed.
- Type of liquid contained in the wash station.
- Volume used in the wash process.
- Number of wash cycles completed.

Insert a **Wash** step into the method (Figure 16-9).

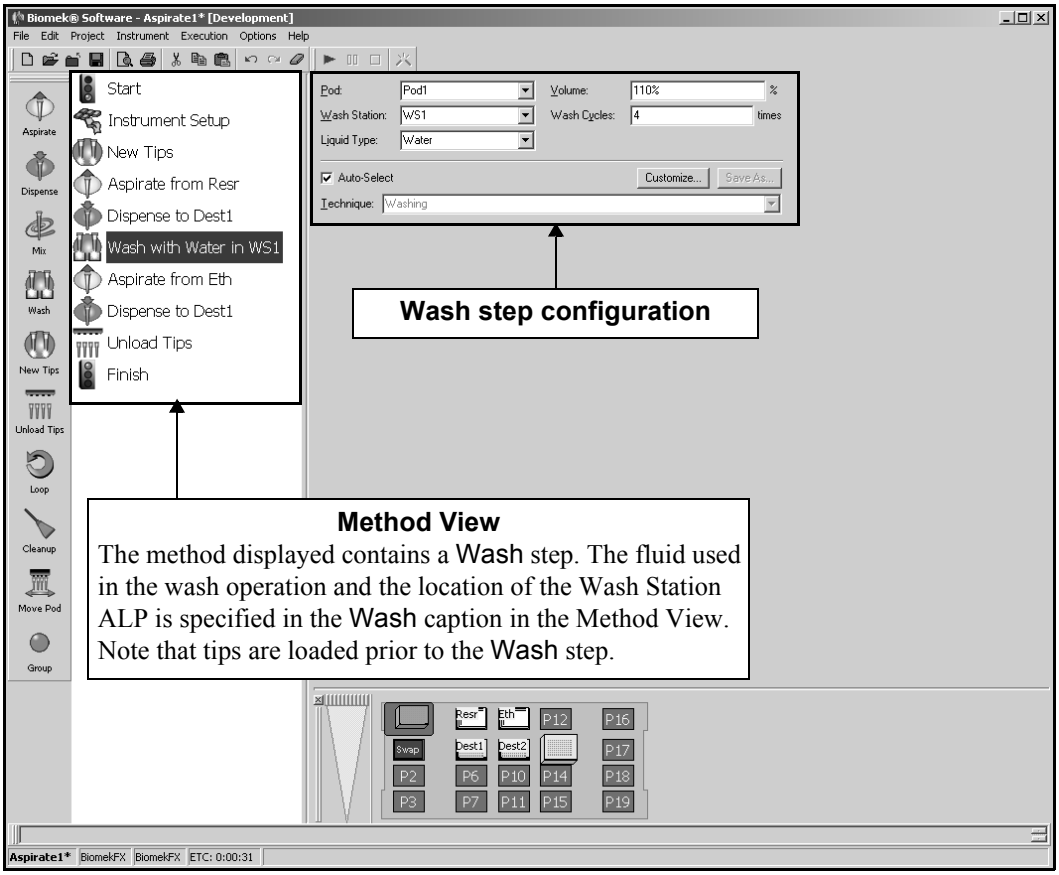


Figure 16-9. Wash step and configuration

16.6.1 Configuring the Wash Step

When a Wash step is added to a method, the Wash step configuration appears (Figure 16-9).

To configure the Wash step:

1. If using a dual-pod ***FX*** instrument, specify the Multichannel **Pod** performing the wash operation from the drop-down list. The pod configured as the default pod is displayed in Pod. If the other pod is desired, select the pod from the drop-down list or from the Current Deck Display.
2. Click on the Wash Station device in the Current Deck Display. Information for that wash station is entered automatically into the Wash step configuration.

   OR

   Select a **Wash Station** device from the drop-down list.

   Note: The Wash Station ALP can be added to the deck and configured for use with the Deck Editor.

   Note: A Wash Station does not have to be specified as long as the Liquid Type is selected. If no Wash Station is specified, the software determines the wash station with the specified Liquid Type that can be accessed by the pod.
3. Verify the **Liquid Type** contained in the selected Wash Station.

   Note: The Liquid Type contained in the Wash Station ALP is configured in the Instrument Setup step. If the Wash Station is selected from the Current Deck Display, the information is automatically inserted.
4. In Volume, provide the volume of fluid to use when washing the tips.

   Note: Enter the volume as a percent (including the percent sign, %) to specify the volume as a percent of the maximum volume of fluid contained in the tips in previous steps. For example, if the maximum volume of fluid transferred is 50 µL, and the % is set for 110%, the Wash step washes the tips with 55 µL of solution. However, if no fluid has been transferred and the volume is entered as a percent, no action is taken and tips are not washed.
5. In Wash Cycles, select the number of aspirate and dispense operations completed during the wash operation.
6. Select a step that occurs after the Wash step or the **Finish** step to validate the step configuration.

16.7 New Tips Step

- ***FX, NX-S8*** — To load new tips onto a Span-8 Pod, refer to Section 18.6, *Span-8 New Tips Step*.

The New Tips step instructs the instrument to load new tips at a specific point in a method. New Tips is used when precise tip control is required. New Tips is used in conjunction with the Unload Tips steps. Also, since tips must be loaded prior to aspirate, the New Tips step should be positioned prior to any Aspirate step if tips have not been previously loaded.

- ***3000*** — A Load Tool step must be configured with an appropriate pipetting tool prior to a New Tips step in the method (refer to Section 20.4, *Load Tool Step*).

The New Tips step is used in place of the Refresh Tips option in the Mix and Aspirate steps or the Load tips option in the Transfer and Combine steps, when more tip control is desired. New Tips is particularly useful with the Loop and Worklist steps; for example, when a Worklist step is performing a transfer that accesses the same tip box repeatedly at different points throughout the worklist, the tips can be loaded and unloaded as many times as their tip configuration allows.

Loading new tips is recommended when:

- The current tips have manipulated a caustic fluid.
- The current tips have been loaded the maximum number of times allowed in their Labware Properties.

  Note: To increase the number of uses allowed for each set of tips, increase the Load no more than count in the Labware Properties configuration in the Instrument Setup step.

- The integrity of the current tips is in question.

Insert a **New Tips** into the method (Figure 16-10).

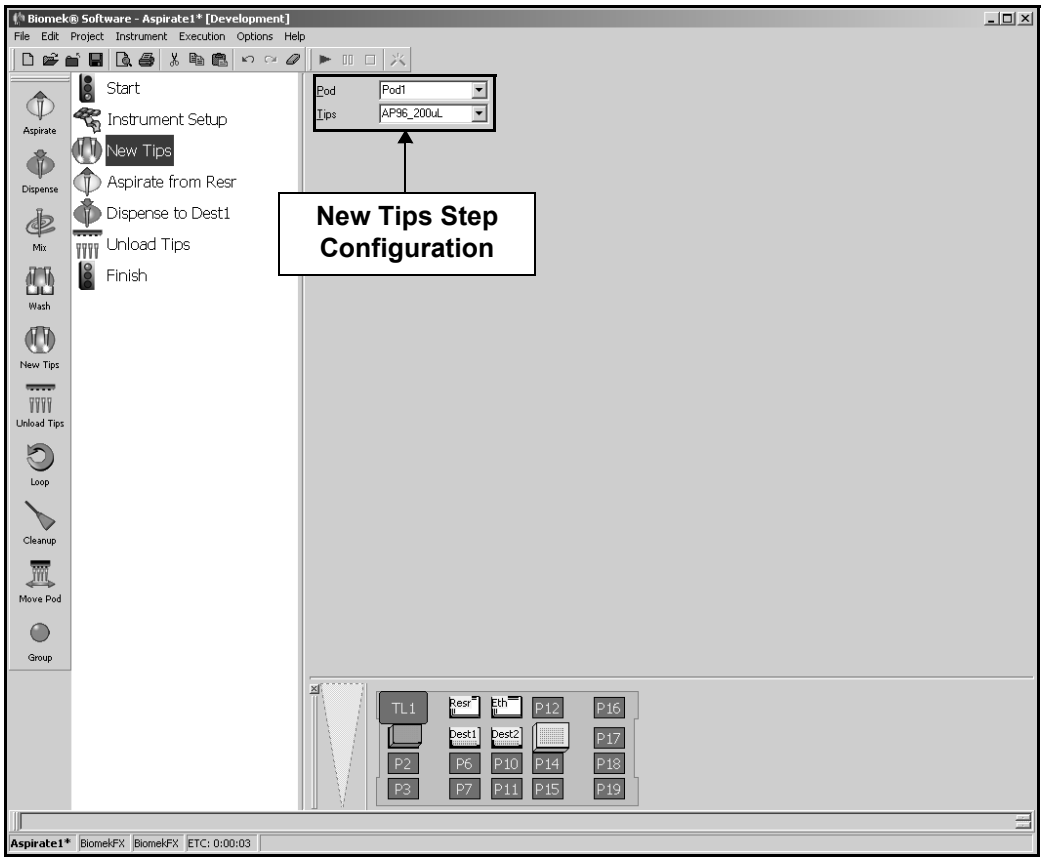


Figure 16-10. New Tips step and configuration

To configure New Tips:

1. If using a dual-pod ***FX*** instrument, specify the Multichannel **Pod** requiring new tips from the drop-down list. The pod configured as the default pod is displayed in Pod. If the other pod is desired, select the pod from the drop-down list or from the Current Deck Display.
2. Select the **Tips** loaded in the New Tips step from the drop-down list.

   OR

   Select the tip box from the Current Deck Display. Selecting tips from the Current Deck Display automatically updates Tips in the Step Configuration.

   Note: The name of a specific tip box can be entered in Tips if tip boxes were assigned names in the Instrument Setup step. If a name is specified, the New Tips step only uses tip boxes with that name. However, if the tip box type is used, New Tips uses any available tip box of that type.

3. Select a step that occurs after the New Tips step or the **Finish** step to validate the step configuration.

16.8 Unload Tips Step

- ***FX, NX-S8*** — To unload tips from a Span-8 Pod, refer to Section 18.7, *Span-8 Tip Discard Step*.

The Unload Tips step instructs the instrument to unload tips at a specific point in a method. Unload Tips is used when precise tip control is required. Unload Tips is often used in conjunction with the New Tips steps, but it can be used with any combination of steps. It is acceptable to use the Unload Tips step multiple times throughout a method.

Unload Tips is used when tip integrity is in question or when cross-contamination between labware is a concern. Unload Tips can be used in place of the Unload (Tips) option in the Transfer and Combine steps, and is particularly useful with Loop and Worklist steps; for example, when a Worklist step performs a transfer accessing the same tip box repeatedly, the tips can be loaded and unloaded as many times as the tip configuration allows with the New Tips and Unload Tips steps.

Unloading tips is recommended when:

- The current tips have manipulated a caustic fluid.
- The current tips have been loaded the maximum number of times allowed in their Labware Properties.

  Note: To increase the number of uses allowed for each set of tips, increase the Load no more than count in the Labware Properties configuration in the Instrument Setup step.

- The integrity of the current tips is in question.
- To avoid cross-contamination of samples.

Insert an **Unload Tips** step into the Method View (Figure 16-11).

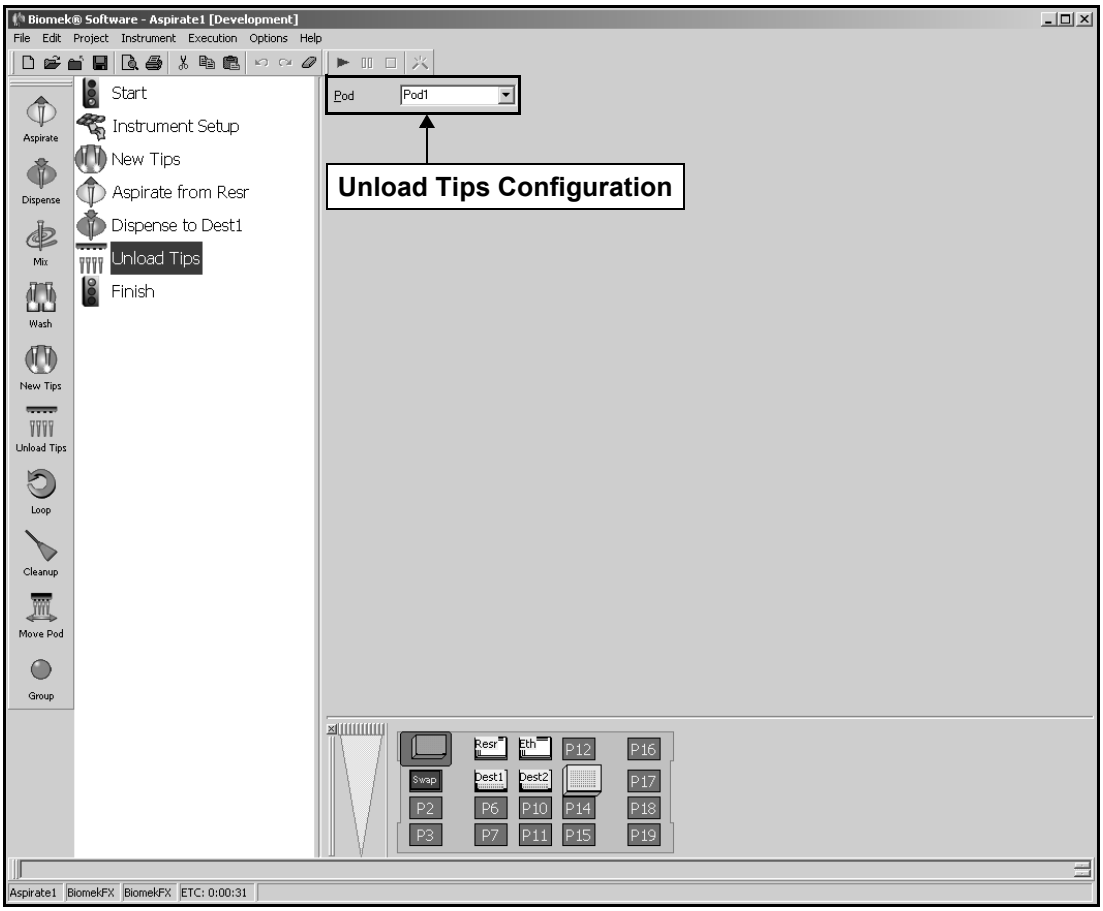


Figure 16-11. Unload Tips step and configuration

To configure Unload Tips:

1. If using a dual-pod ***FX*** instrument, specify the Multichannel **Pod** requiring tip removal from the drop-down list. The pod configured as the default pod is displayed in Pod. If the other pod is desired, select the pod from the drop-down list or Current Deck Display.
2. Select a step that occurs after the Unload Tips step or the **Finish** step to validate the step configuration.

16.9 Loop Step

The Loop step executes any steps located between the Loop and End Loop icons as many times as specified in the Loop Step Configuration; for example, if a method requires multiple repetitions of the same aspirate and dispense operations, the Loop step allows the repetition of those steps as many times as required. The steps requiring repetition, in this case the Aspirate and Dispense steps, are 'substeps' of the Loop step.

When the Loop step is added to a method, the Loop icon appears in the Method View, as well as the End Loop icon. All steps placed between the Loop and End Loop icons are contained within the Loop and are repeated as many times as indicated in the Loop Step Configuration (Figure 16-12).

Note: While the Loop step is executing, a number appears in parentheses behind each substep within the Loop step, indicating the current iteration of the loop.

Note: Variables defined in a Loop step apply only to the Loop and its substeps.

Insert a **Loop** step into the Method View (Figure 16-12).

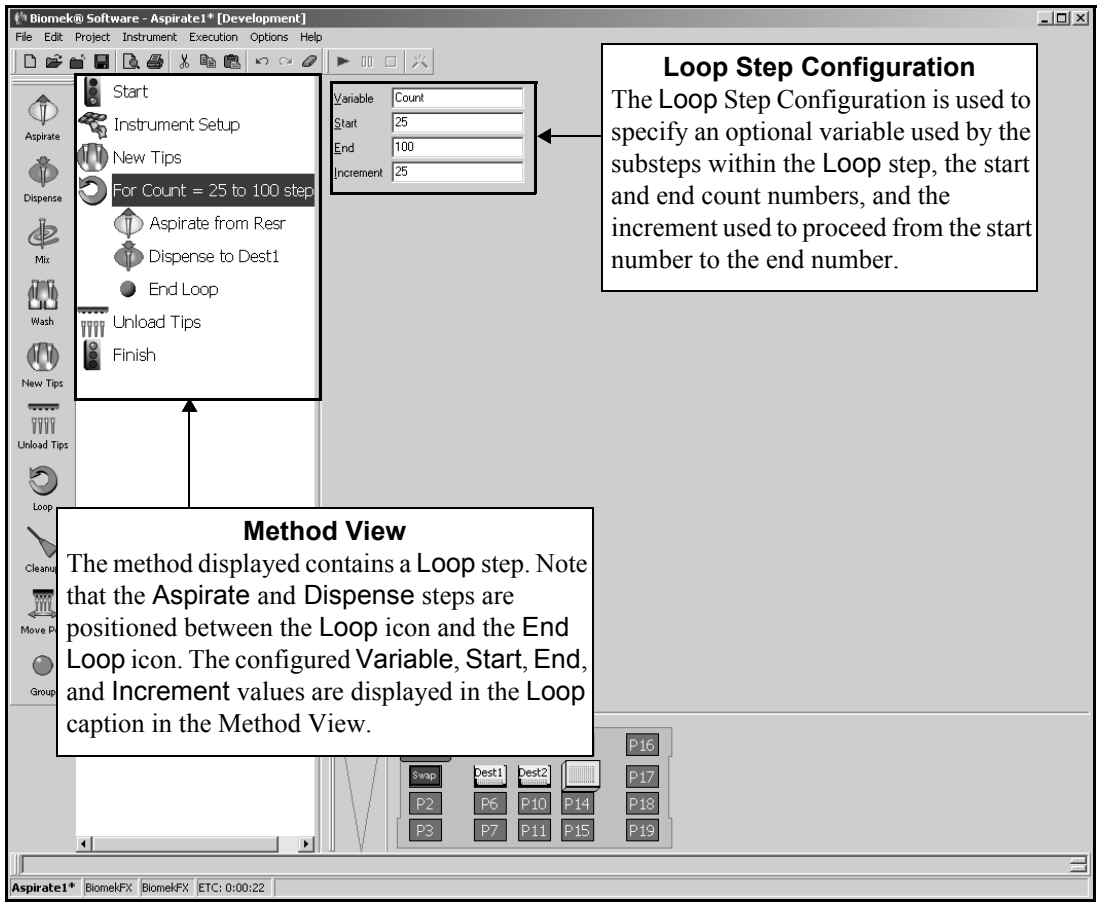


Figure 16-12. Loop step and configuration

16.9.1 Configuring a Loop Step and Creating a New Variable

To configure a Loop step and create a new variable:

1. In Variable, insert a variable for the Loop step and any substeps (Figure 16-13). Variable creates a variable that can be used in the Step Configurations for any substep of the Loop (Figure 16-14). A variable name cannot contain a space or a punctuation mark, such as a period (.), a comma (,), or an ampersand (&).

Note: An entry in Variable is optional. The Loop step can function without a Variable.

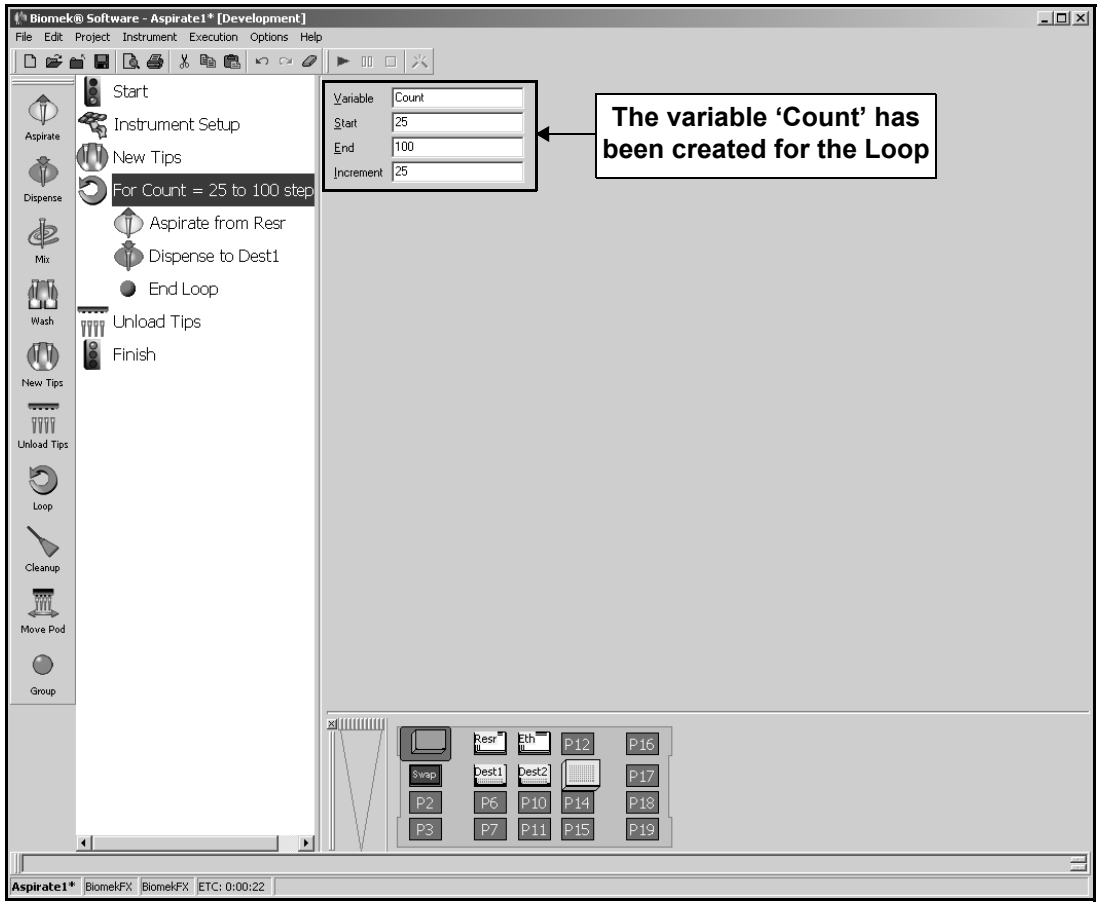


Figure 16-13. Loop step — variable created in Variable

2. Insert the **Start** value for the Loop count (Figure 16-13).

Note: A Loop usually begins counting at '1'; for example, if the Increment is '25', Start is '1', and End is '100', four passes of the loop are completed for the Increment values of 1, 26, 51, and 76. It is occasionally desirable, however, to count the passes of a loop by the Increment value; for example, if the Start value is changed from '1' to '25', four passes of the loop are completed for the Increment values of 25, 50, 75, and 100.

3. Insert the **End** value for the Loop count.

   Note: Each time the method completes a loop, its count is advanced. The method drops out of the Loop when the next pass would exceed the End number; for example, if the Increment is '25', Start is '1', and End is '100', four passes of the loop are completed for the Increment values of 1, 26, 51, and 76. The Loop stops at 76 because the value of the next pass would be 101, which exceeds the End value of 100.

4. Insert an **Increment** value for the Loop count. The Increment advances the iterations of the Loop from the Start value to the End value. Variables can be used in Increment; however, the variable must be preceded by an equal (=) sign (Figure 16-14).

   Note: When the variable is accessed in the substeps, the value of the variable is incremented until the value reaches the End value, without going over. For example, if the Increment for Count is 25, and if Start is '1', End is '100', four iterations of the loop are completed for the values 1, 26, 51, and 76. The variable 'Count' is used in the volume fields of the Aspirate and Dispense substeps of the Loop step (Figure 13-22).

5. Select **End Loop** in the Method View to add steps to the Loop.

6. Insert the desired substeps between Loop and End Loop.
7. Configure the substeps, using the variable created in Variable where applicable .

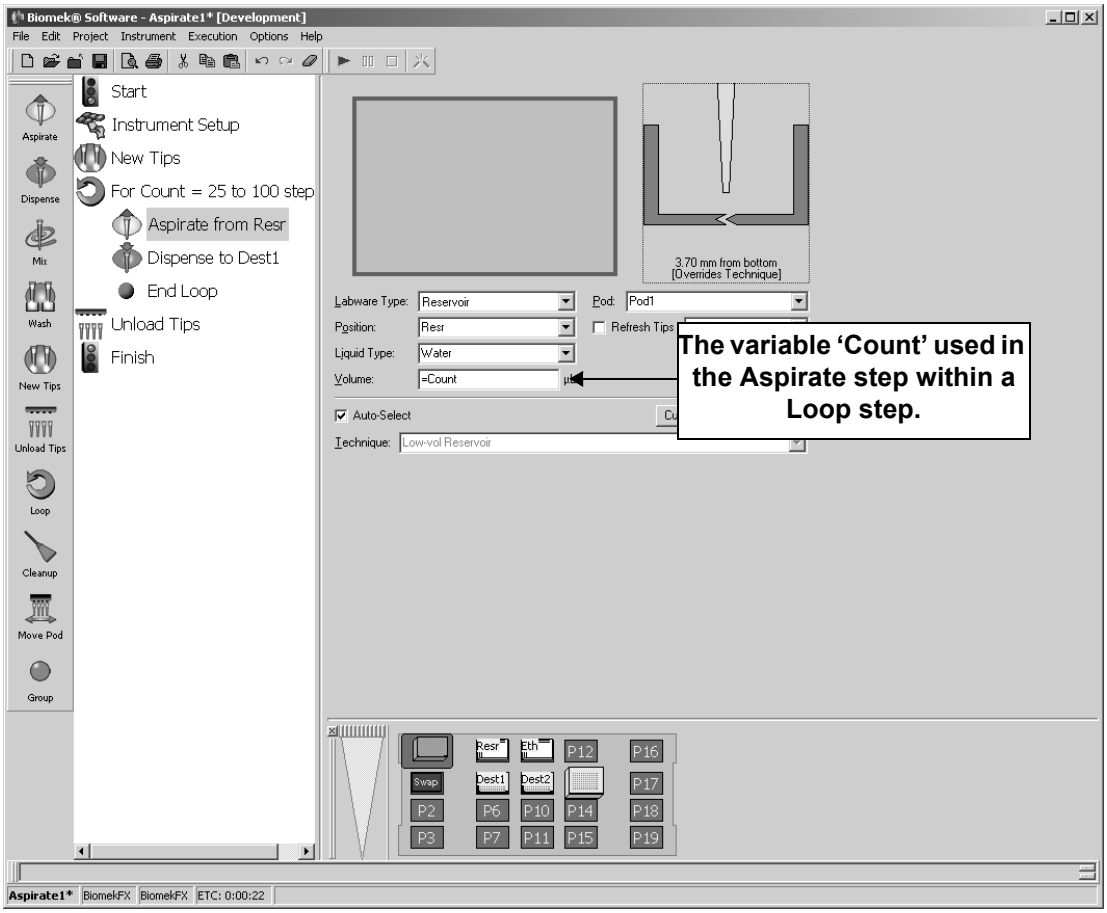


Figure 16-14. Loop step variable 'Count' used in an Aspirate substep

Note: In the example, the variable 'Count' is used in the volume fields of the Aspirate and Dispense substeps of the Loop step (Figure 16-14).

16.9.2 Configuring a Loop Step Using an Existing Variable

To configure a Loop step without creating a new variable, but using an existing variable:

1. Leave Variable blank (Figure 16-15).

Note: An entry in Variable is optional. The Loop step can function without an entry in Variable.

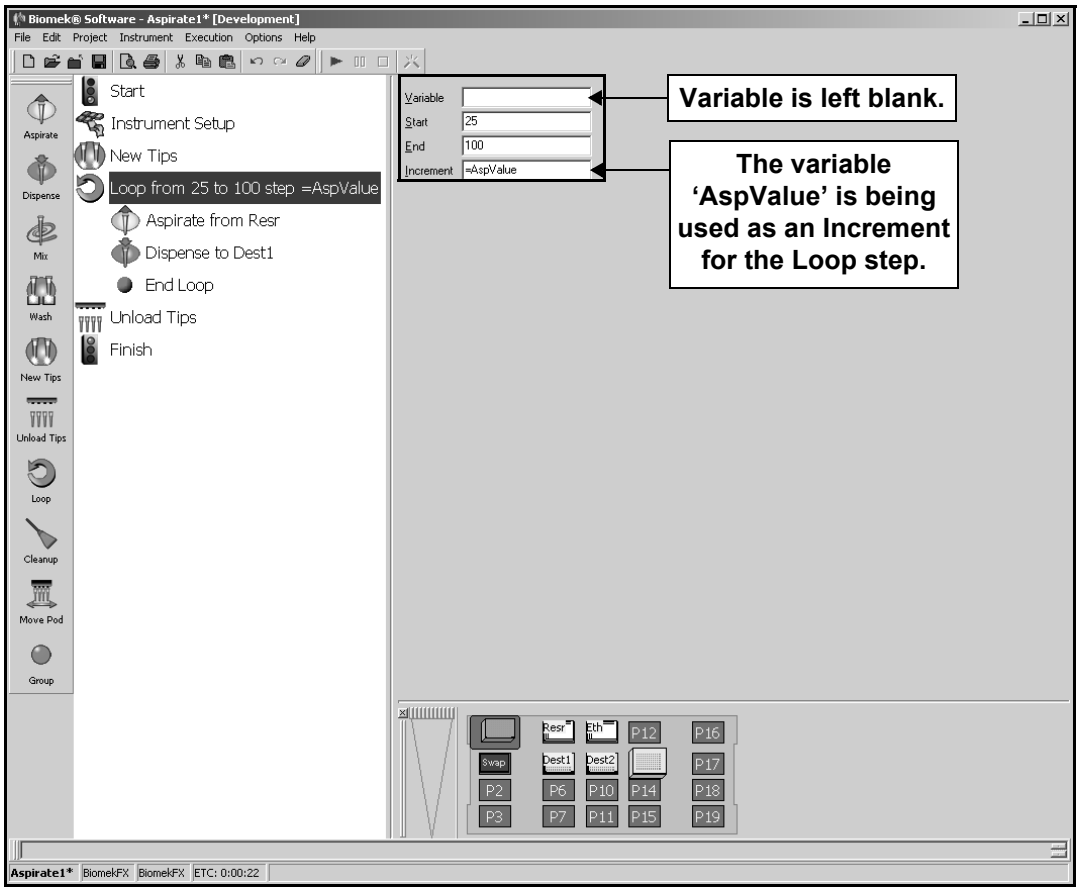


Figure 16-15. Loop step — using a previously created variable as the Increment

2. Insert the **Start** value for the Loop count.

Note: A Loop usually begins counting at '1'; for example, if Increment is '=AspValue2' and AspValue2 has an assigned value of 25, and if Start is '1' and End is '100', four iterations of the loop are completed for the values 1, 26, 51, and 76. It is occasionally desirable, however, to count the passes of a loop by the Increment value; for example, if the Start value is changed from '1' to '25', four passes of the loop are completed for the Increment values of 25, 50, 75, and 100.

3. Insert the **End** value for the Loop count.

   Note: Each time the method completes a loop, its count is advanced. The method drops out of the Loop when the next pass would exceed the End number; for example, if Increment is '=AspValue2' and AspValue2 has an assigned value of 25, and if Start is '1' and End is '100', four iterations of the loop are completed for the values 1, 26, 51, and 76. The Loop stops at 76 because the value of the next pass would be 101, which exceeds the End value of 100.

4. Insert a previously created variable in **Increment** (Figure 16-15). The value of the variable is used as the Increment to advance the iterations of the Loop from the Start value to the End value. Variables must be preceded by an equal (=) sign in the Loop step configuration, as well as in the substep configurations.

   Note: When the variable is accessed in the substeps, the value of the variable is incremented until the value reaches the End value, without going over. For example, if Increment is '=AspValue2' and AspValue2 has an assigned value of 25, and if Start is '1' and End is '100', four iterations of the loop are completed for the values 1, 26, 51, and 76.

5. Select **End Loop** in the Method View to add steps to the Loop.
6. Insert the desired substeps between Loop and End Loop.

7. Configure the substeps using the previously created variable where applicable.

Note: The variable ‘AspValue’ is used in the volume fields of the Aspirate and Dispense substeps of the Loop step (Figure 16-16).

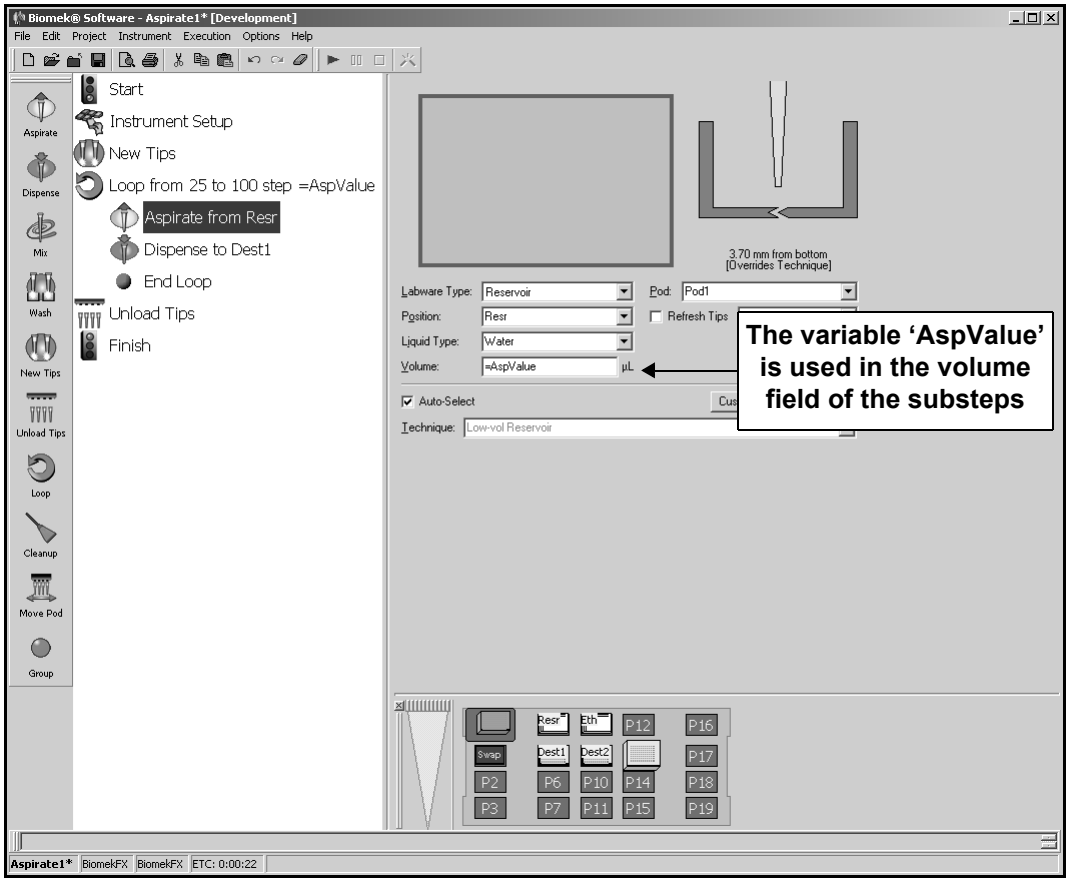


Figure 16-16. Loop step — the ‘AspValue’ variable is used as the Volume for the substeps

16.10 Cleanup Step

The Cleanup step is used to direct the instrument to dispose of tips and tip boxes. Normally, when a method is completed, tips and tip boxes are left in their final positions, regardless of their originating positions. The Cleanup step can return tips and tip boxes to their original deck position or hardware device; place them in a trash receptacle; or leave them wherever they are when the method is completed.

The Cleanup Step Configuration includes:

- With no configuration options selected, all tips are sent to their configured location at the end of the method.
- When Send tip boxes to their configured final destinations is checked, all the tip boxes that came from off deck and all those that were configured to go to trash are sent to those final destinations.
- When Send boxes that started on deck back to their original locations is checked, in addition to the operations resulting from the box checked above, any tip boxes that started on the deck are returned to their starting position. (This option is activated only when Send tip boxes to their configured final destinations is selected.)

Cleanup resets the hardware by physically returning tips and tip boxes to their original positions, while the Finish step only unloads tips and resets the software to its original state at the completion of the method. Use the Cleanup step with the Finish step to reset both the hardware and the software to the state they were in at the onset of the method, or to clear the deck of used tips and tip boxes. The Cleanup step is useful when the same method is run repeatedly, one time after another, and when trying to track which tips and tip boxes were used for which fluids and labware.

Insert a **Cleanup** step into the Method View (Figure 16-17).

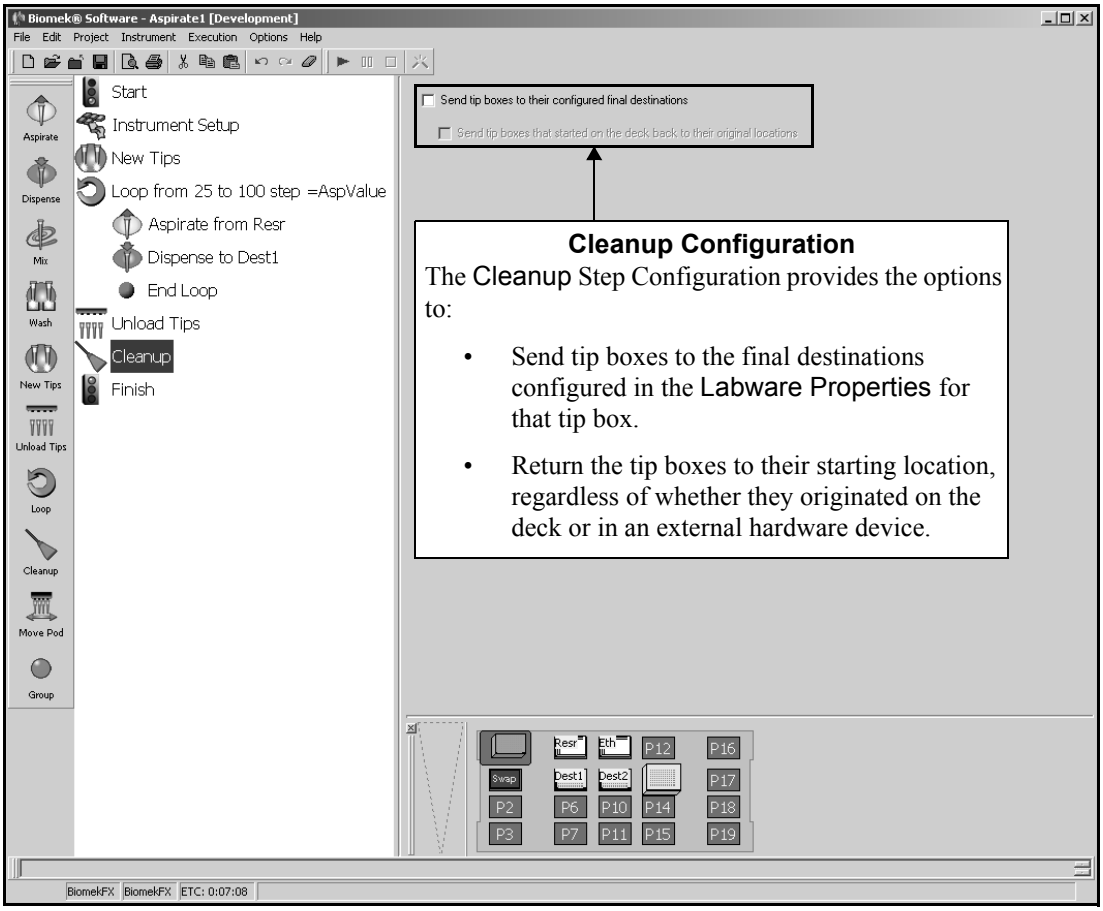


Figure 16-17. Cleanup step and configuration

To configure the Cleanup step:

1. Select **Send tip boxes to their configured final destination**, if desired. This sends the tip boxes to the final destination configured in the Labware Properties for that tip box.

Note: The default setting for the Cleanup step is both options Unchecked. Inserting the Cleanup step without selecting either option instructs the Biomek instrument to unload any tips currently on the pod to the final destination configured in Labware Properties for those tips.

---

2. Select **Send tip boxes that started on deck back to their original locations**, if desired. This returns the tip boxes to their starting location, regardless of whether they originated on the deck or in an external hardware device, such as a stacker carousel.

   Note: Send tip boxes that started on deck back to their original locations is only available when Send tip boxes to their configured final destination is selected.

3. Select a step that occurs after the Cleanup step or the **Finish** step to validate the step configuration.

16.11 Move Pod Step

The Move Pod step moves the pod to a deck position that does not hamper access to the labware, ALPs, and devices on the deck.

Use Move Pod to ensure that the pod does not interfere with activities taking place on the deck, such as the addition, removal, or relocation of labware or devices.

Insert a **Move Pod** step into the Method View (Figure 16-18).

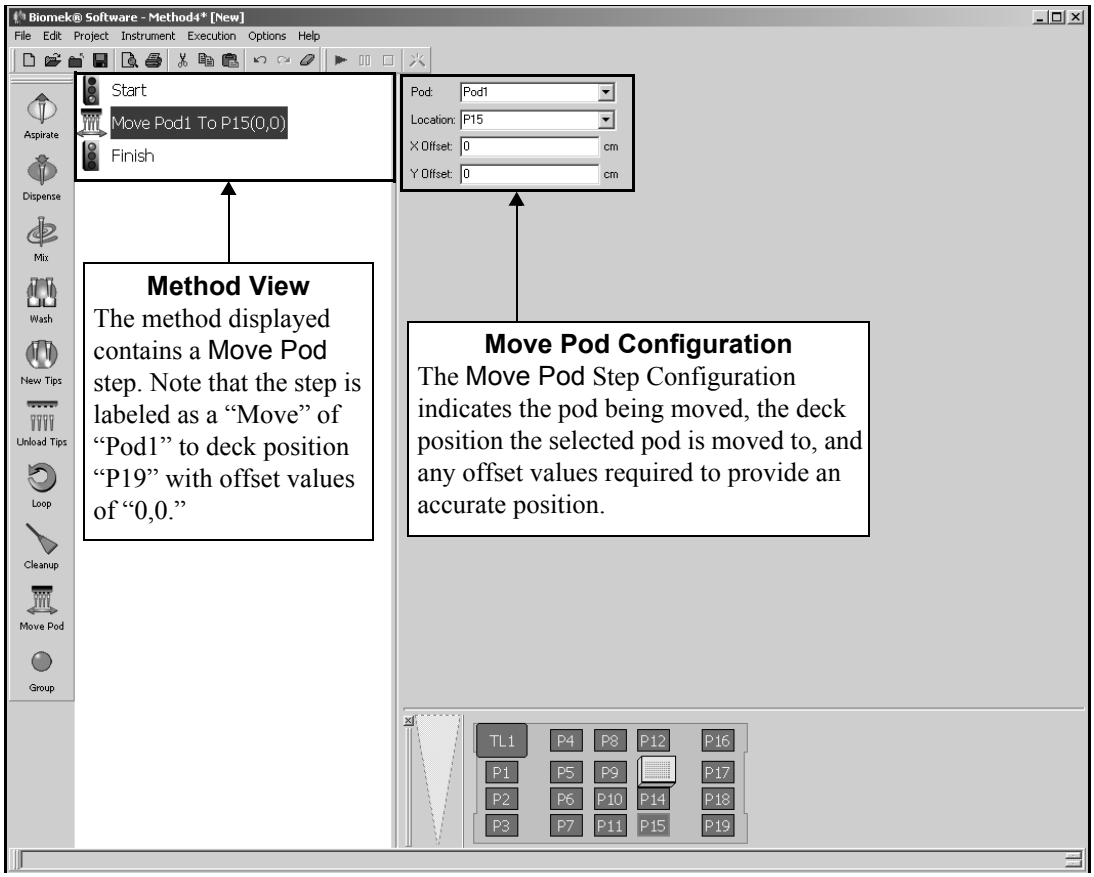


Figure 16-18. Move Pod step and configuration

To configure the Move Pod step:

1. Specify the **Pod** being moved from the drop-down list.

   OR

   Select the **Pod** from the Current Deck Display. The tip diagram on the left of the Current Deck Display represents Pod1, while the tip diagram on the right represents Pod2. Selecting a pod from the Current Deck Display automatically updates Pod in the Step Configuration.

   Note: In Pod, Pod1 is the default for a one-pod Biomek FX or Biomek 3000 system. In a two-pod Biomek FX system, the pod configured as the default pod is displayed in Pod. If the other pod is desired, select the pod from the drop-down list or the Current Deck Display.

   ---

2. In Location, select the deck position from the drop-down list.

   OR

   Select the **Location** from the Current Deck Display. Selecting a location from the Current Deck Display automatically updates Location in the Step Configuration.

   Note: A bright blue outline appears in the Current Deck Display around the selected location.

   ---

3. Insert the **X Offset** value in centimeters (cm).
4. Insert the **Y Offset** value in centimeters (cm).

   Note: Selecting the deck position without offset values is usually sufficient to relocate the pod; however, X and Y Offset values can be used to provide a more specific position.

   The final position of the pod when using X and Y Offsets is the deck position specified in Location *PLUS* the values inserted into the X and Y Offsets. For example, when framing an ALP, the labware positioned on the ALP is 'offset' from the zero (0) point, or back-left corner, of the ALP to the actual edge of the labware itself.

   ---

5. Select a step that occurs after the Move Pod step or the **Finish** step to validate the step configuration.

16.12 Group Step

The Group step gathers steps performing similar functions or steps achieving a specific result together. Group reduces the confusion that can arise when viewing large methods by consolidating and applying a single label to a number of steps. Multiple Group steps can be used within a method, and they can be placed in a Group step together to further abbreviate the steps displayed in the Method View.

Advantages to grouping steps are:

- The steps contained in the Group step are hidden from the Method View by collapsing the Group step.
- The Group step is collapsed by default when a method is opened. This means long methods appear shorter and more concise.
- Multiple steps can be identified by a single label.
- All steps related to a specific operation can be grouped together under a single label to identify the operation they perform.

Insert a **Group step** into the Method View (Figure 16-19).

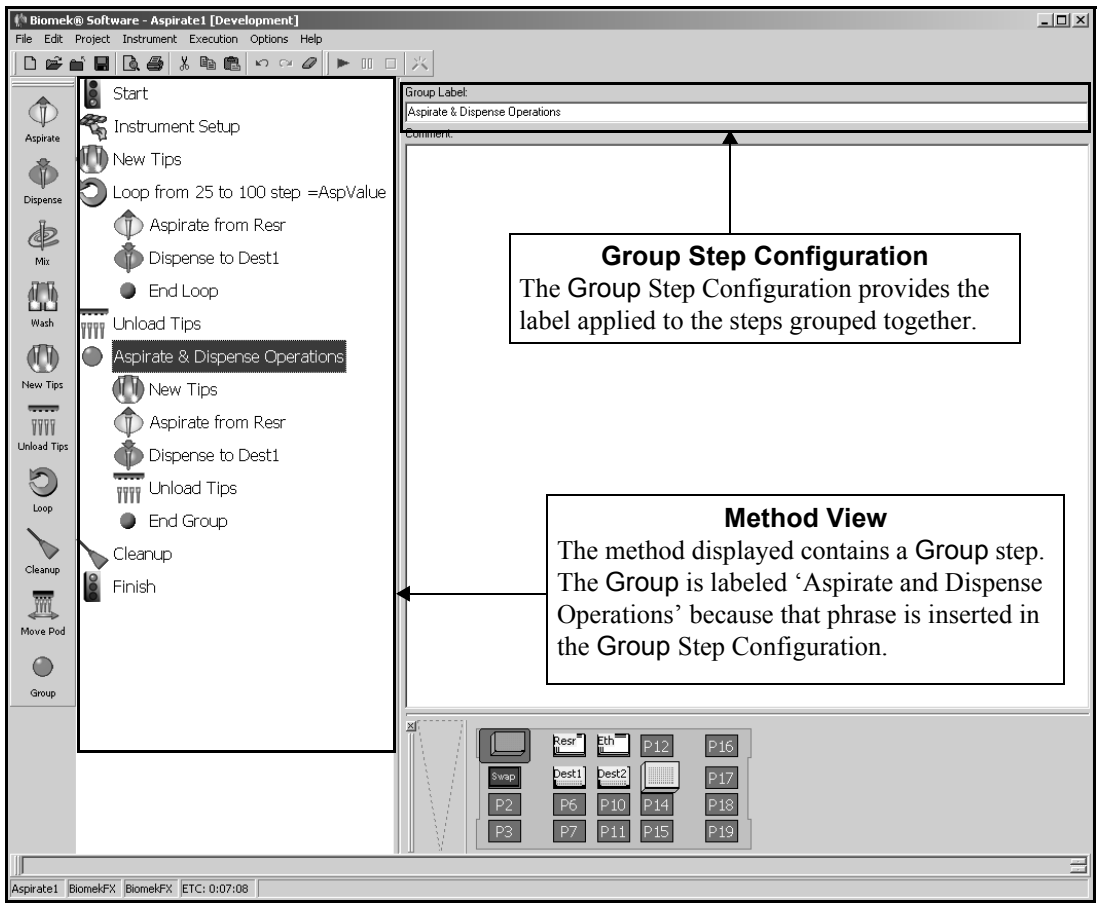
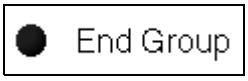


Figure 16-19. Group step and configuration

When a Group step is added to a method, the Group Step Configuration appears (Figure 16-19).

To configure the Group step:



1. Double-click on the Group step to expand it so that the End icon is visible.
2. In Group Label, enter text to identify the group.

   Note: The text inserted in Group Label appears in the Group steps caption in the Method View.

3. Insert steps between the Group and End icons.
4. Double-click on the Group step to collapse it so that the steps contained within the Group step are hidden from view.

   Note: The Group step is collapsed by default when the method opens.

17 Using the Advanced Step Palette

17.1 Overview

The steps presented in the Advanced Step Palette (Figure 17-1) provide tools for more complex management of methods. These steps are used to perform the following:

- Repeat a series of steps using a list of specified values without entering and configuring the steps repeatedly
- Access and run a method within a method
- Conditionally execute steps based on an aspect of the environment, such as the volume in a microplate

Note: The steps available in the Advanced Step Palette do not use the pod directly and may be used with any single- or dual-pod instrument.

The steps available in the Advanced Step Palette are:

- Run Method — accesses and runs a method within a method.

- Worklist — fills in variables based on a worklist file.

- Just in Time — synchronizes the execution of steps.

- Let — defines variables for its substeps.

- If — evaluates a condition within a method and runs either the “then” substeps or the “else” substeps according to the condition.

- Script — runs a list of commands providing customized control over the instrument.

- Scripted Let —similar to Script step, with the exception that it allows variables to be extended outside the script and used in the method.

When one of the above steps is inserted into a method, the configuration options associated with that step appear on the right side of the Biomek Software main editor, in Step Configuration.

Note: Steps not configured appropriately may generate errors when the method is validated or run.

17.2 Displaying the Advanced Step Palette

In order to add advanced steps to a method, display the Advanced Step Palette (Figure 17-1).

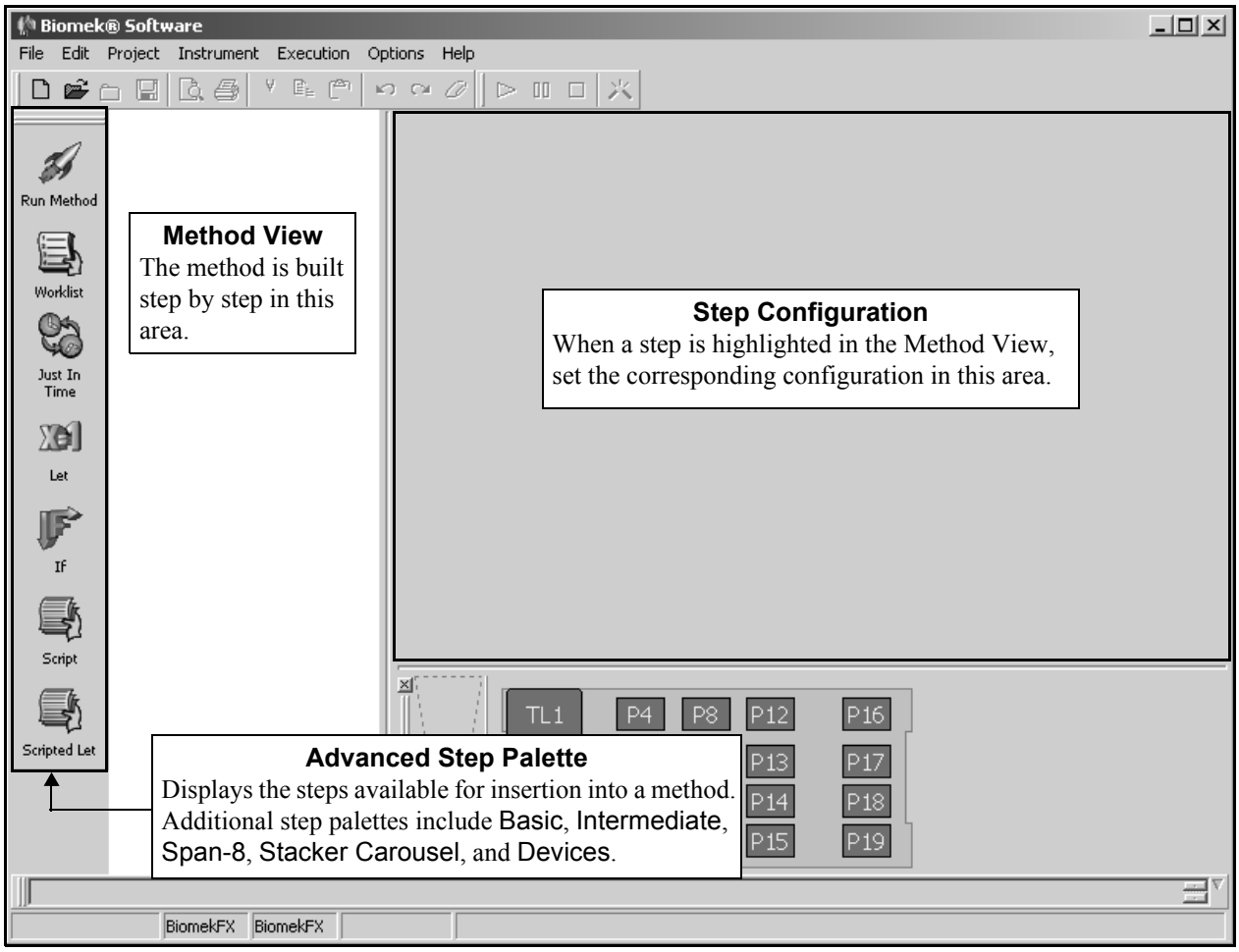


Figure 17-1. Biomek Software main editor with Advanced Step Palette displayed

To display the Advanced Step Palette:

- Right-click any empty palette space, and select **Advanced** from the menu.

  OR

- From the toolbar, select **Options>Toolbars>Advanced**.

17.3 Run Method Step

The Run Method step executes a previously created method within the method in progress. Run Method saves time by assigning variables accessible by the previously created method and by preventing unnecessary duplication of steps. If the same series of steps is used in a number of methods, a method can be created containing only those steps and accessed using a Run Method step. Multiple Run Method steps can be used within a method. Methods referenced by a Run Method step must be stored in the active project file.

Although it is not visible in the Method View, the Run Method step 'inserts' all of the steps from the referenced method into the current method at the point the Run Method step appears. All of the steps contained in the submethod are completed as a part of the current method; they are not completed as a separate method.

Note: A 'submethod' is a method run within another method. It is recommended that the submethod use the same Instrument Setup step configuration as the method in progress. If the submethod and the method in progress do not use the same Instrument Setup, an Instrument Setup step must be added to the method in progress to ensure that all labware for both methods is visible to the instrument.

The advantages of using Run Method are:

- The ability to run a method within a method
- Allows repetition of steps configured in a previously created method without recreating those steps
- Variables assigned in the Run Method step are accessible by the submethod
- Controls the size of the current method and reduces confusion by listing only the Run Method step in the Method View, not all of the steps accessed by the Run Method step

Insert **Run Method** into the Method View (Figure 17-2).

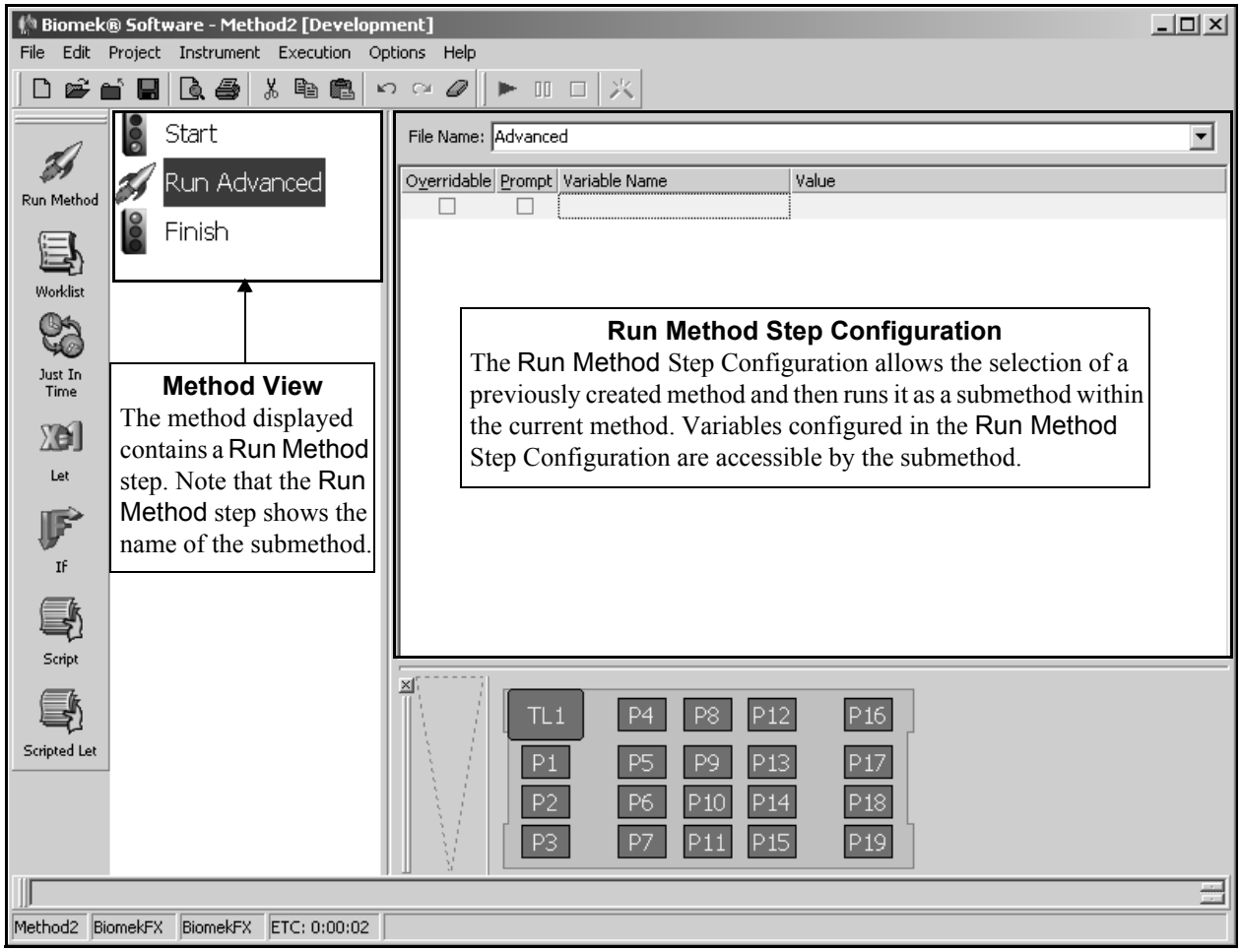


Figure 17-2. Run Method step and configuration

17.3.1 Configuring the Run Method Step

To configure the Run Method step:

1. In File Name, select a submethod to run within the method in progress. The Run Method step shows the name of the submethod.

   Note: Only submethods stored in the same project file as the method in progress are available. To access a submethod stored in another project file, import the desired submethod into the project (refer to Section 6.10, *Importing and Exporting Project Files*).

2. Configure any variables as needed (refer to Section 13.1, *Overview*).

17.4 Worklist Step

The Worklist step uses a text file to supply multiple values for one or more variables (Figure 17-3). Worklist is useful when repetition of the same step(s) is required, but a variable, or variables, needs to change each time the step(s) is executed. When a group of steps using the variable(s) defined in a text file are placed inside a Worklist step, Worklist automatically performs each step once for each line in the text file. The steps using the variable(s) defined in the text file are substeps within the Worklist step in the Method View.

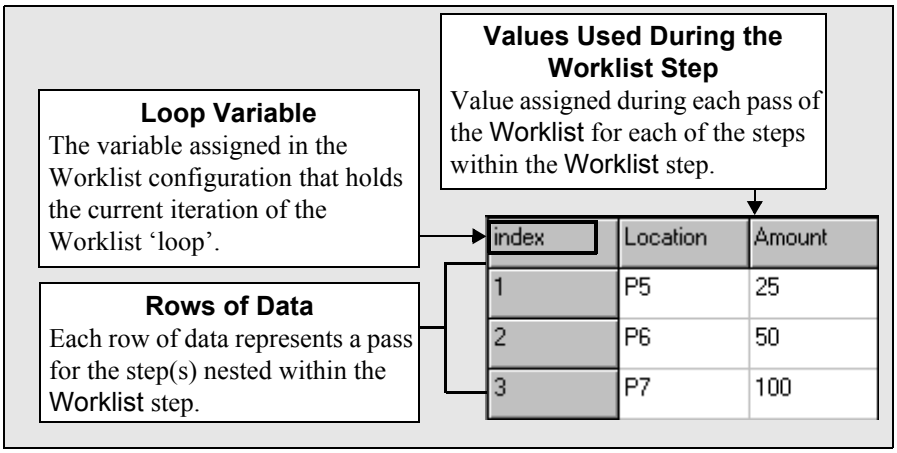


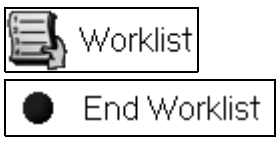
Figure 17-3. Worklist example

Note: Values read from the text file must be formatted correctly in order for Biomek Software to create the worklist with the desired row and column formatting. Each row in the text file represents a row in the worklist. In each row, columns are designated by separating individual values with commas.

Worklist text files may be created in a database, spreadsheet, or text editor. When creating a worklist in a database or spreadsheet, save the file in comma-separated values (*.csv) format. When using a text editor or word processor, manually separate values on a single line with commas and save the file in text (*.txt) format.

Note: Quotation marks may be used in the text file, but they must come in pairs. The Worklist step looks at the first set of quotation marks and interprets that everything after them is included as a row of data up to the second set of quotation marks. If quotation marks are desired in a row of data, use another set of quotation marks around the data within the quotations marks. For example, type ""this is a comment"" in the text file and "this is a comment" will appear in the row of data in the Worklist step.

The Worklist step operates like a combined Let/Loop step because it 'lets' a variable in the Worklist text file use different values for each pass of the Worklist 'loop'. Worklist 'loops' through the substeps until each step has used each line of the Worklist text file specified.



When Worklist is added to a method, the Worklist icon and an End Worklist icon appear in the Method View. Any step(s) inserted between the Worklist and End Worklist icons use the variables contained in the Worklist text file configured in the Worklist step.

Advantages of using a Worklist include:

- Data in a text file is accessible by any Biomek Software method.
- Selecting the text file in the Worklist Step Configuration copies all of the variable data from the text file into the Worklist Step Configuration without individually entering all of the variables and their values in each of the steps performed inside the Worklist step (Figure 17-4).
- A dynamic link exists between the method and the text file. The Worklist step accesses the text file each time the method is run; therefore, any updates made to the text file are included in the next method run.

Note: The text file configured in the Worklist step must maintain its original file path, or the method will not be able to find the text file. If the text file path changes, update the Worklist Step Configuration to reflect the new file path.

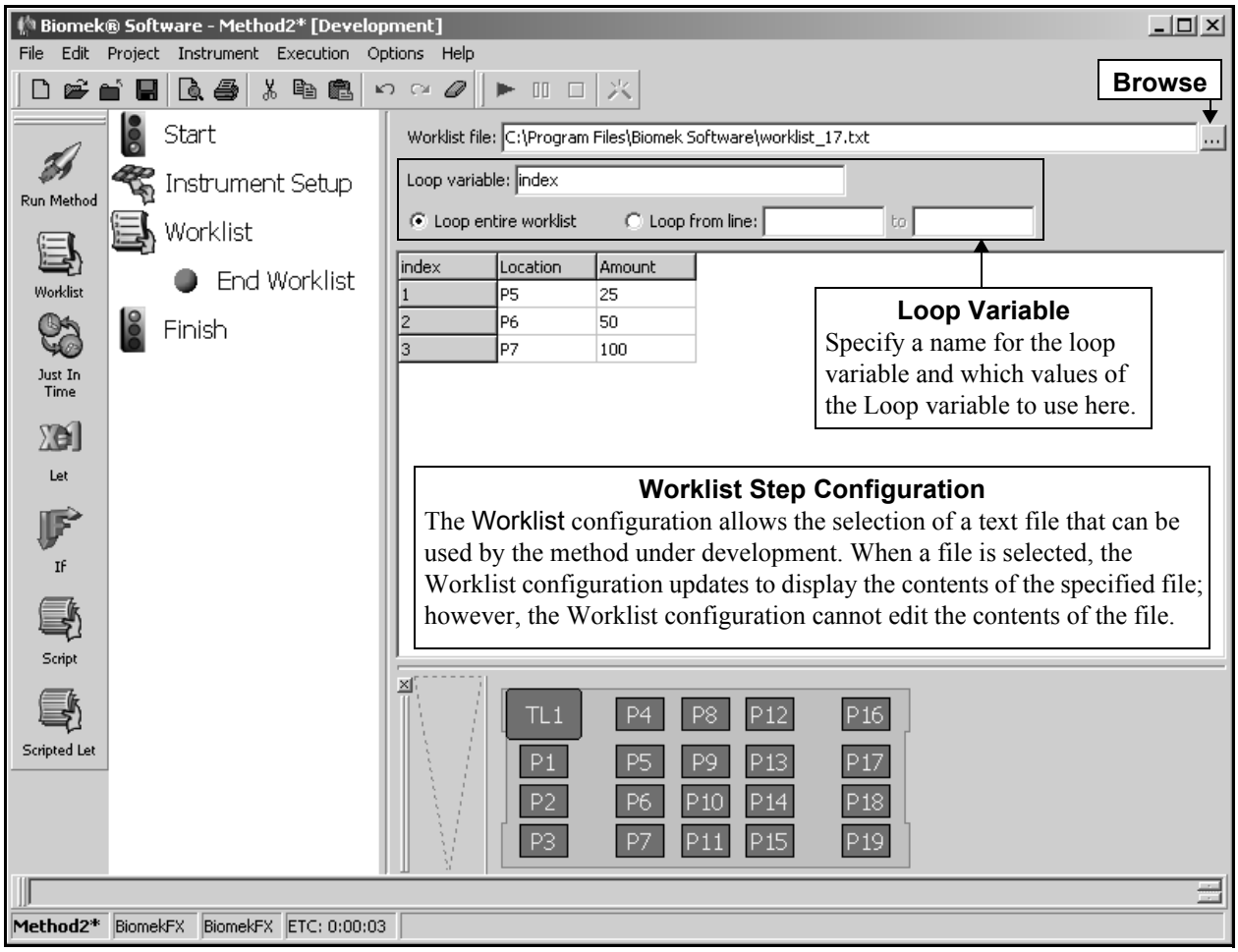


Figure 17-4. Worklist step and configuration

Insert **Worklist** into the Method View (Figure 17-4).

17.4.1 Configuring the Worklist Step

To configure Worklist, complete the following:

1. Click the Browse. . . button following File Name. Open appears (Figure 17-5).

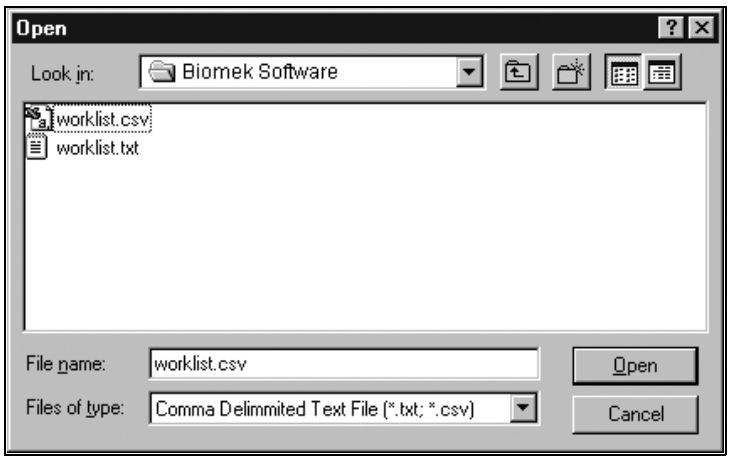


Figure 17-5. Worklist — text file selection

2. Browse to and select the text file accessed during the method run.

   Note: The file path and the file name of the text file are included in the Worklist step in the Method View.

3. Click **Open** to add the file to the Worklist configuration and return to the main Biomek Software window.
4. Enter a name for the **Loop Variable**. The loop variable holds the current iteration number of the worklist.
5. Select **Loop entire worklist** to use all rows of the worklist.

   OR

   Select **Loop from line** and enter the start and end row numbers to use a specific range of rows from the worklist.

17.5 Just in Time Step

Just In Time synchronizes the execution of the substeps within the Just In Time step (Figure 17-6).

The steps within the Just In Time step are queued in the order in which they appear in the Method View, but it is possible to execute two or more steps simultaneously. In Figure 17-6, for example, the first two substeps are completed, then deck position P8 is paused. While the pause on P8 is in process, the next four steps are completed because they do not require access to deck position P8. Finally, the last two steps are completed once the pause is finished because they require access to deck position P8.

Note: An incubation period is accomplished using the Pause step (refer to Section 15.5, *Pause Step*).

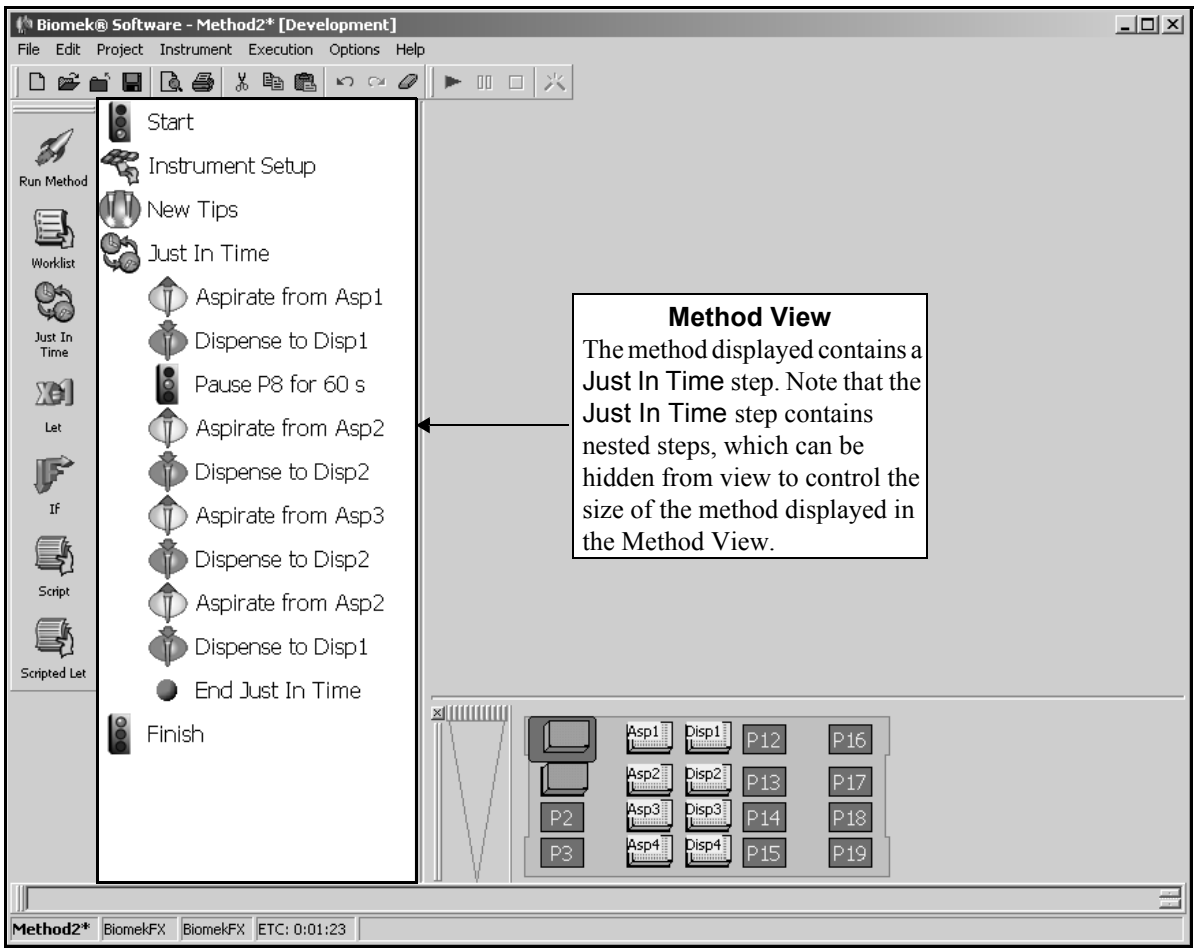
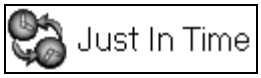


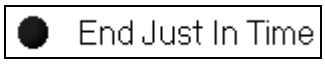
Figure 17-6. Just In Time step

Since Just In Time is a part of the Transfer, Combine, and Move Labware steps, it is not necessary to use these steps in conjunction with the Just In Time step.

Use Just In Time when an Aspirate operation and its subsequent Dispense operation must occur immediately following an incubation period (Figure 17-6) or when a method requires that a preparatory operation should not occur too early with respect to another related operation.

Note: Any steps placed between the Just In Time and End Just In Time icons are configured in their individual Step Configurations, but they are completed when appropriate within the Just In Time step.





Insert **Just In Time** into the Method View. The Just In Time icon appears in the method, as well as an End Just In Time icon (Figure 17-6).

To configure Just In Time, enter the steps requiring synchronized timing between the Just In Time and End Just In Time icons.

Note: The Just In Time step does not affect the Estimated Time to Completion for the method when its substeps are already synchronized steps, such as the Transfer, Combine, or Move Labware steps.

17.6 Let Step

The Let step is used to create variables accessible only to the sub-steps of the Let step (Figure 17-7). The variables can be used by multiple steps within the Let step, and they allow configuration of the steps by specifying explicit values for things like volumes and heights. For example, instead of typing the number of microliters into the volume field of an Aspirate step, the name of a variable is inserted. Every time the Aspirate step is executed, the current value of that variable is used as the volume.

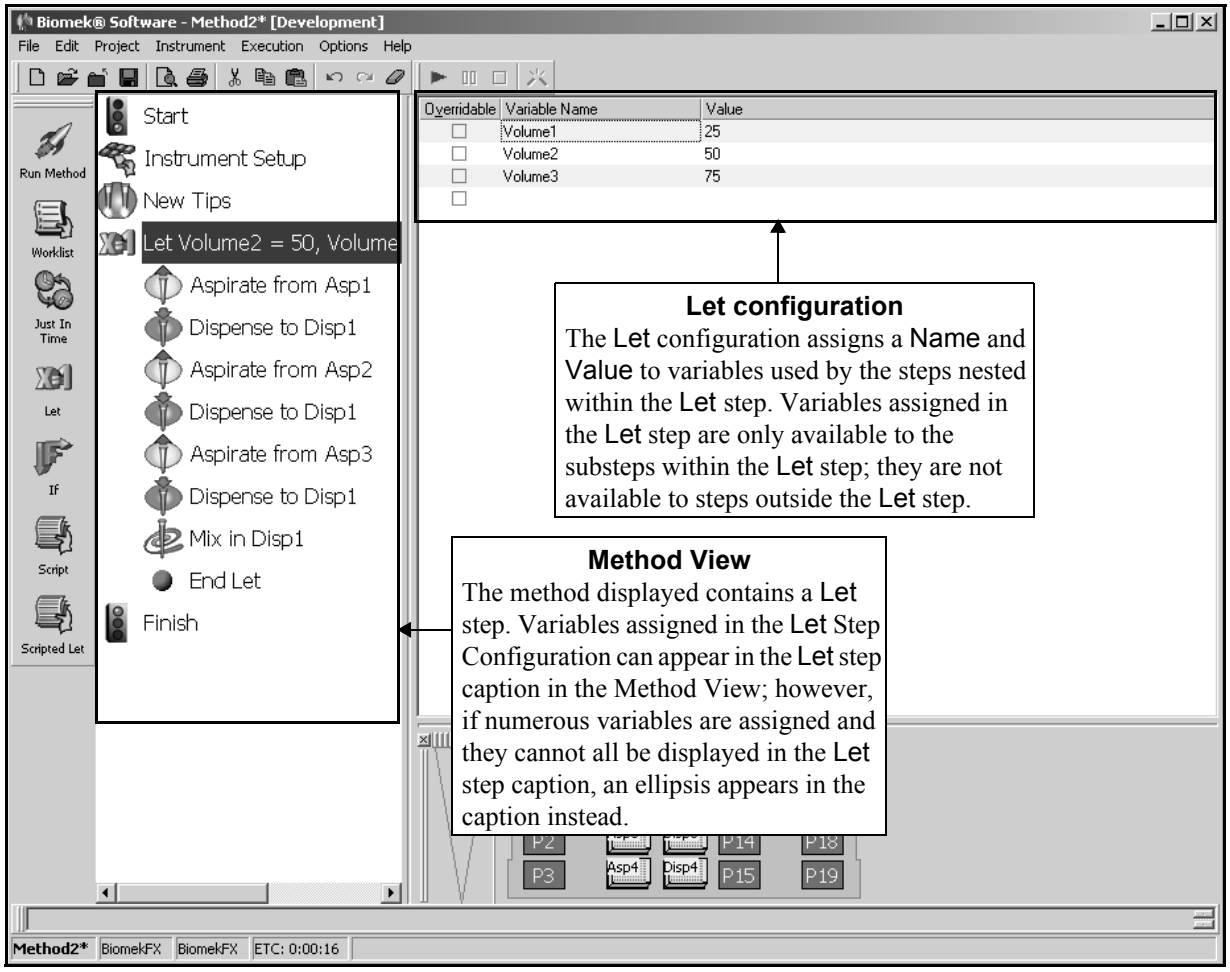
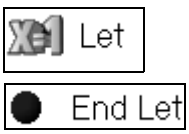


Figure 17-7. Let step and configuration



When the Let step is added to a method, the Let and End Let icons appear (Figure 17-7). Any steps placed between the Let and End Let icons are substeps controlled by the Let step, but they are configured through their individual Step Configurations. Substeps are enqueued for execution in the order of appearance in the Method View; however, it is possible to execute two or more steps simultaneously.

Any of the substeps within the Let step can use variables created in the Let Step Configuration. Only the Name is displayed in the step configuration, not the Value associated with that Name. The Biomek Software automatically uses the associated Value when the step is executed.

17.6.1 Configuring the Let Step

Configuring the Let step involves creating the variables used by the substeps within the Let step (Figure 17-7).

Insert **Let** into the Method View (Figure 17-7).

To configure the Let step:

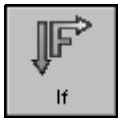
1. Insert the variables desired (refer to Section 13.1, *Overview*).
2. Enter desired steps between Let and End Let icons.
3. Configure the substeps between Let and End Let.

17.7 If Step

The If step controls which steps in a method are executed based on a condition, such as the volume of liquid in a piece of labware. When If is run, Biomek Software tests the If condition, then processes the appropriate block of substeps based on the results of the test.

The substeps of If are:

- Then — substeps following Then are processed if the condition is true.
- Else — substeps following Else are processed if the condition is false.
- End — the End substep terminates each If, Then, and Else block of steps (Figure 17-8).



To insert an If step into a method, insert **If** into the Method View. The If Step Configuration appears (Figure 17-8).

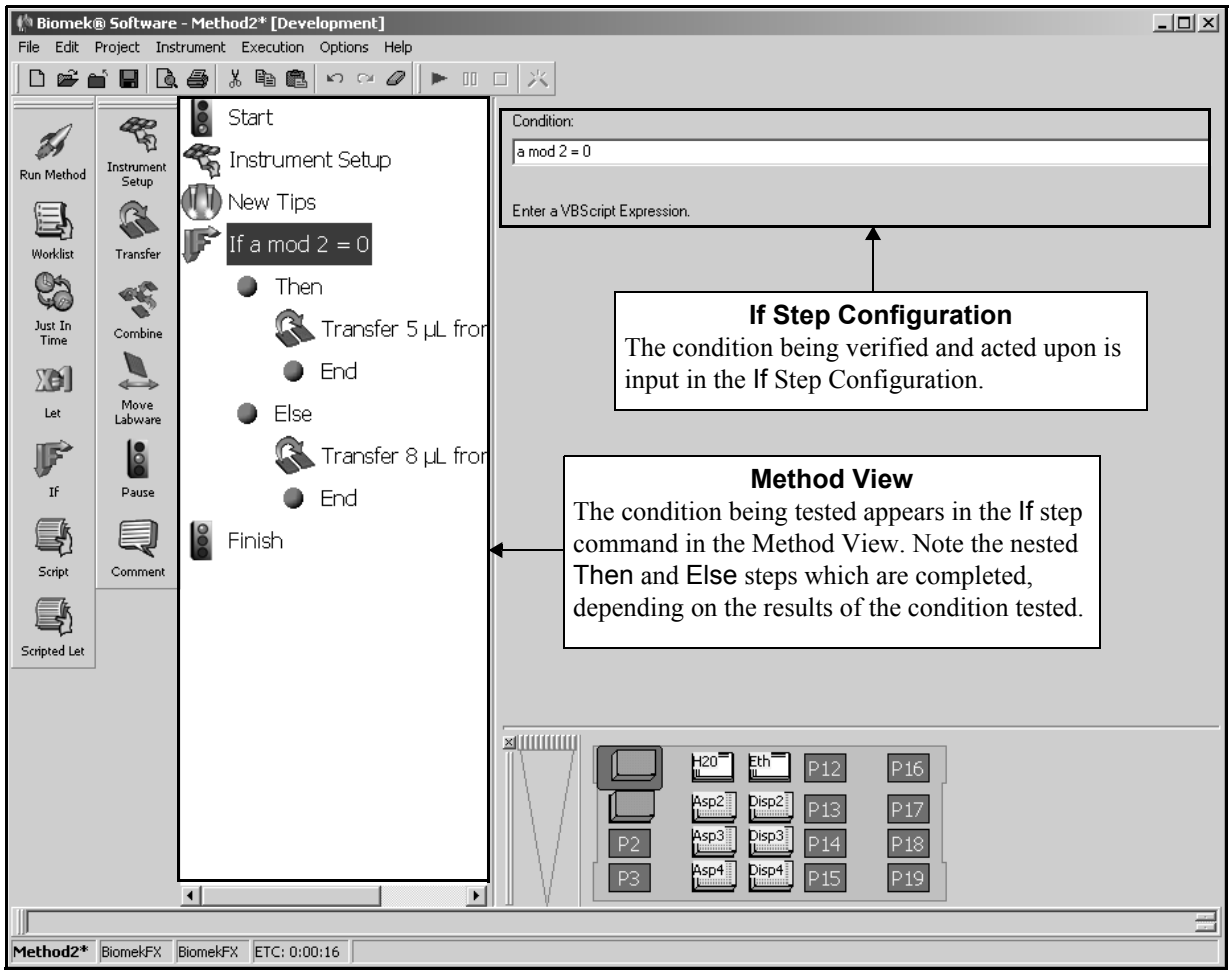


Figure 17-8. If step and configuration

17.7.1 Configuring the If Step

To configure the If step:

1. Enter the **Condition** in the configuration.

   Note: A Condition must be a valid VBScript expression and can refer to variables defined in other steps.

2. Highlight **End** under the Then substep.
3. Add and configure the steps performed if the condition is true.
4. Highlight **End** under the Else substep.
5. Add and configure the steps to perform if the condition is false.

Note: Any steps placed between the Then and End or Else and End icons are configured in their individual Step Configurations using the same procedures as though they were a main step in the method.

17.8 Script Step

Note: The information in this section is intended only to assist in gaining an understanding of what the scripting function does. It is not intended to be a tutorial on scripting. The Script step is provided only for the use of methods developed within Beckman Coulter at this time. This function is not currently supported for end-user applications.

More information is available at //msdn.microsoft.com/scripting and in *VBScript in a Nutshell*, 2nd Edition, Matt Childs, Paul Lomax, and Ron Petrusha 2003, O'Reilly & Associates, Inc.

Note: Refer to Chapter 28, *Scripting*, for other information on scripting.

While the editors and templates in Biomek Software provide the means to perform most operations, it is possible that some highly specialized liquid-handling applications are beyond this scope. Although not an activity typically required by users, Biomek Software uses the Script step for writing script to accommodate these advanced needs.

A Biomek Software script consists of lines of code that provide instructions for instrument operations. The lines of code, or commands, may be typed into the Script Step Configuration. Running the method invokes a Visual Basic® script interpreter that evaluates each line of code and performs the requested operation.

Dragging a Script step from the Method View to the Step Palette makes it available as a step to any method (refer to Chapter 29, *Changing Window Appearance*). To make the values defined in a Let step available to the Script step, place the Script step within the Let step.

The Script step provides a configuration area in which a description of the script step may be entered and lines of code may be written (Figure 17-9).

Insert **Script** into the Method View (Figure 17-9).

Note: Place the Script step within a Let block of steps (refer to Section 17.6, *Let Step*) to use the variables defined in the Let step in the Script.

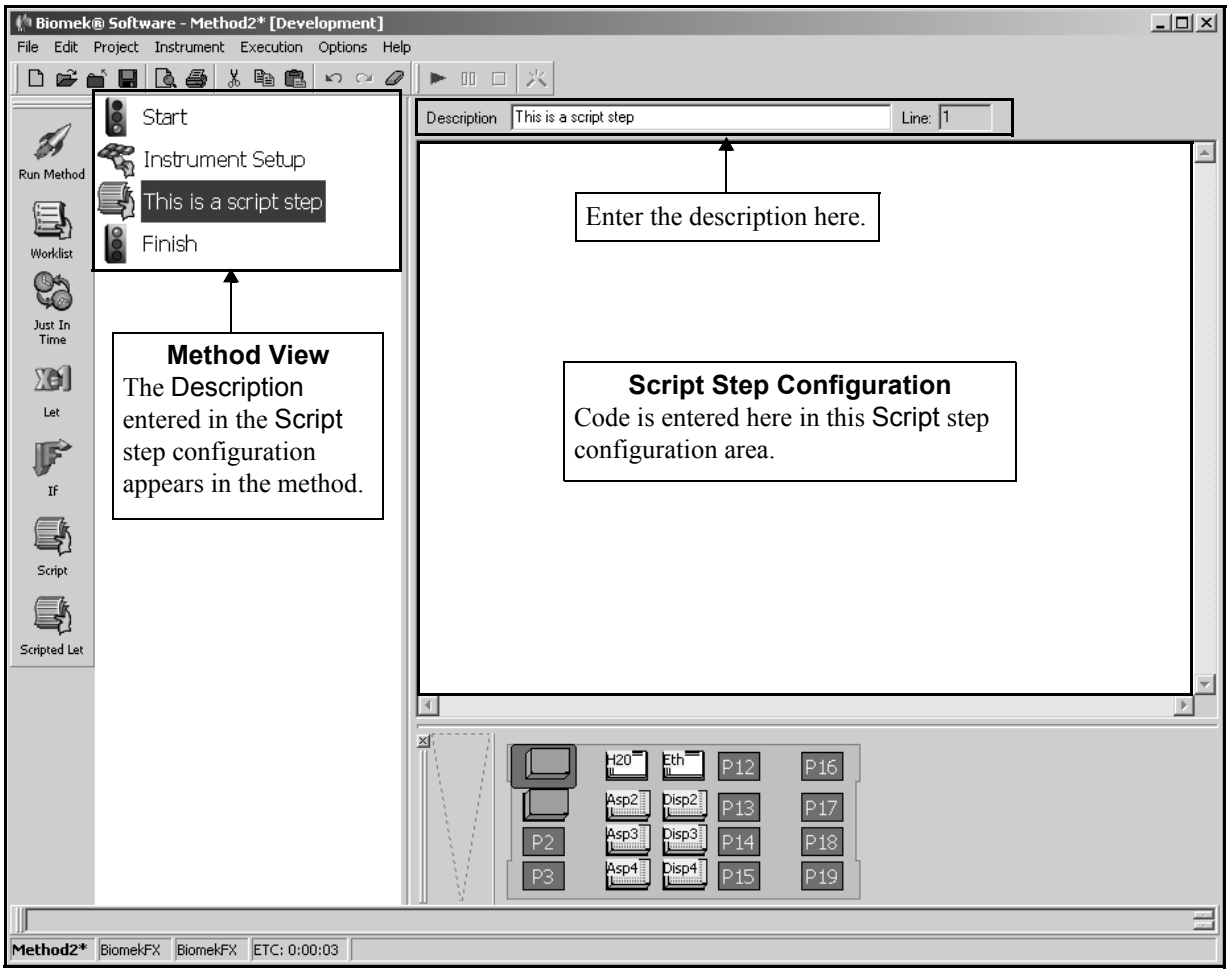


Figure 17-9. Script step and configuration

17.8.1 Configuring the Script Step

To configure the Script step:

1. In **Description**, enter a description for the operation or purpose of the Script Step.

   Note: The Description replaces the word "Script" in the Script step caption in the Method View.

2. Position the cursor in the Script Step Configuration.

   Note: The lines of code can be entered in a word processor and then copied and pasted into the Script Step Configuration using standard Windows™ procedures. Use standard Windows™ techniques for editing scripts.

3. Write and edit the script.

Note: The Biomek Software scripting feature is based on Visual Basic Scripting, a subset of the Microsoft® Visual Basic programming language. Any code interpreted by Visual Basic Scripting can be interpreted by the instrument and may be included in a method. More Visual Basic Scripting information is available at //msdn.microsoft.com/scripting and in the book, *VBScript in a Nutshell*, 2nd ion, Matt Childs, Paul Lomax, and Ron Petrusha 2003, O'Reilly & Associates, Inc. For more specific Biomek Software scripting help, contact Beckman Coulter Technical Support.

17.9 Scripted Let Step

Note: The information in this section is intended only to assist in gaining an understanding of what the scripting function does. It is not intended to be a tutorial on scripting. The Scripted Let step is provided only for the use of methods developed within Beckman Coulter at this time. This function is not currently supported for end-user applications.

More information is available at //msdn.microsoft.com/scripting and in *VBScript in a Nutshell*, 2nd Edition, Matt Childs, Paul Lomax, and Ron Petrusha 2003, O'Reilly & Associates, Inc.

Note: Refer to Chapter 28, *Scripting*, for other information on scripting.

The Scripted Let step is similar to the Script step (refer to Section 17.8, *Script Step*), except it allows for variables created within a Script to be extended outside the Script and used in the method like variables created in a Let step (refer to Section 17.6, *Let Step*). Two additional commands are available to set variables — Extend and WeakExtend.

- Extend — sets the variable name to the specified value for all steps contained within the Scripted Let. The proper syntax for Extend is **Extend "Variable Name", Value**.
- WeakExtend — sets the variable name to the specified value for all steps contained within the Scripted Let step if the specified variable does not already have a value. This is similar to a Let variable with Overridable selected. The proper syntax for WeakExtend is **WeakExtend "Variable Name", Value**.

The Scripted Let step provides a configuration area in which a description of the script step may be entered and lines of code may be written.

Insert **Scripted Let** into the Method View (Figure 17-10).

Note: Place the Scripted Let step within a Let block of steps (refer to Section 17.6, *Let Step*) to use the variables defined in the Let step in the Script.

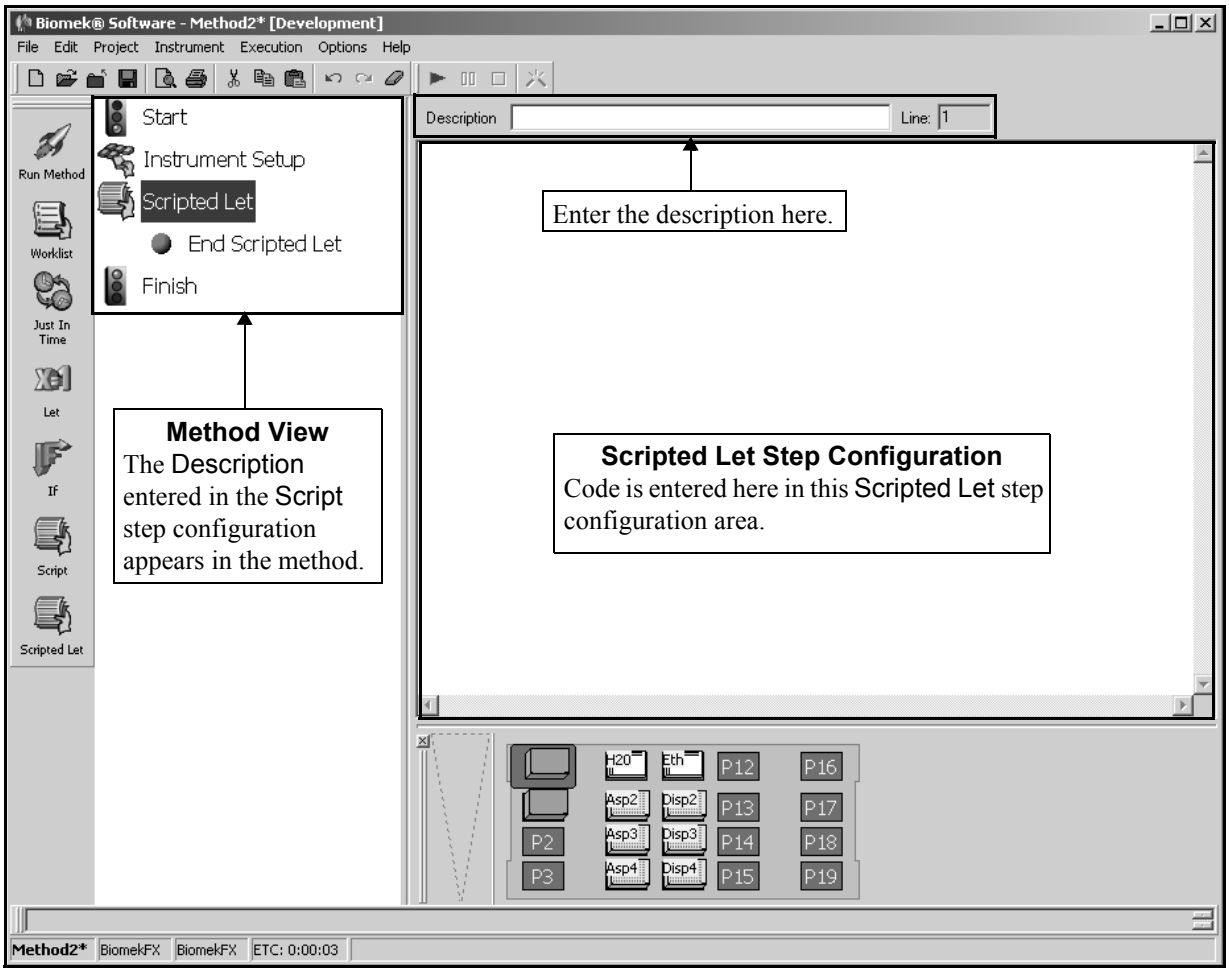


Figure 17-10. Scripted Let step and configuration

17.9.1 Configuring the Scripted Let Step

To configure the Scripted Let step:

1. In **Description**, enter a description for the operation or purpose of the Scripted Let Step.

   Note: The Description replaces the words "Scripted Let" in the Scripted Let step caption in the Method View.

2. Position the cursor in the Scripted Let Step Configuration.

   Note: The lines of code can be entered in a word processor and then copied and pasted into the Scripted Let Step Configuration using standard Windows® procedures. Use standard Windows techniques for editing scripts.

3. Write and edit the script.

   Note: The Biomek Software scripting feature is based on Visual Basic Scripting, a subset of the Microsoft® Visual Basic programming language. Any code interpreted by Visual Basic Scripting can be interpreted by the instrument and may be included in a method. More Visual Basic Scripting information is available at //msdn.microsoft.com/scripting and in the book, *VBScript in a Nutshell*, 2nd Edition, Matt Childs, Paul Lomax, and Ron Petrusha 2003, O'Reilly & Associates, Inc. For more specific Biomek Software scripting help, contact Beckman Coulter Technical Support.

4. Insert any substeps between Scripted Let and End Scripted Let that utilize any variables defined in the Scripted Let.

   Note: Variables extended outside of a script in the Scripted Let step are only available to the substeps within the Scripted Let.

18 Using the Span-8 Step Palette

18.1 Overview

- ***FX, NX-S8*** — Only the Span-8 Pod may be used with steps on the Span-8 step palette.
- ***3000*** — The Serial Dilution, Transfer From File, and Define Pattern steps can all be used with pipetting tools on the Biomek 3000.

Steps on the Span-8 Step Palette provide individual control over liquid-handling functions, including tip handling and pipetting operations, using the Span-8 Pod outside the Transfer and Combine steps. Additional steps, such as Serial Dilution and Transfer From File, configure larger operations involving multiple liquid-handling functions.

The Transfer and Combine steps on the Basic Step Palette are used with the Span-8 Pod to configure larger operations involving multiple liquid-handling functions when strict control of every operation is not necessary.

Note: For information on using and configuring the Transfer and Combine steps using a Span-8 Pod, refer to Section 15.3, *Configuring Transfer and Combine Steps*.

CAUTION: Make sure the correct ALP is chosen when configuring the deck setup in the Deck Editor. ALPs vary in height and failure to choose the correct ALP in the Deck Editor may result in collisions between pod(s) and ALPs during operation.

The steps available in the Span-8 Step Palette are:

- Serial Dilution — performs a series of dilutions on a single microplate.
  - ***3000 —*** Serial Dilution can be used in methods on the Biomek 3000.

- Span-8 Aspirate — aspirates a specified amount of liquid from a single source in preparation for the Span-8 Dispense step.

- Span-8 Dispense — dispenses a specified amount of liquid into destination labware, following the Span-8 Aspirate step.

- Span-8 New Tips — loads new tips to the Span-8 probes.

- Span-8 Tip Discard — unloads tips from the Span-8 probes.

- Span-8 Wash Tips — washes tips by flushing tips with system fluid at a Span-8 Tip Wash ALP or by aspirating and dispensing at a Wash Station 96 ALP. The Span-8 Wash Tips step is also used to purge air from system tubing and syringes during a method.

- Transfer From File — performs well-to-well transfers using a comma-separated data file.
  - ***3000* —** Transfer From File can be used in methods on the Biomek 3000.

- Define Pattern — create a method-specific well pattern manually or by reading well information from a file.
  - ***3000* —** Define Pattern can be used in methods on the Biomek 3000.

When one of the above steps is added to a method, the configuration associated with that step appears on the right side of the Biomek Software main editor, in Step Configuration (Figure 18-1).

Note: Steps not configured appropriately in Step Configuration generate errors when the method is validated or run.

18.2 Displaying the Span-8 Step Palette

In order to add Span-8 steps to a method, display the Span-8 Step Palette (Figure 18-1).

- ***3000*** — Only the Serial Dilution, Transfer From File, and Define Pattern steps are displayed for a Biomek 3000 instrument.

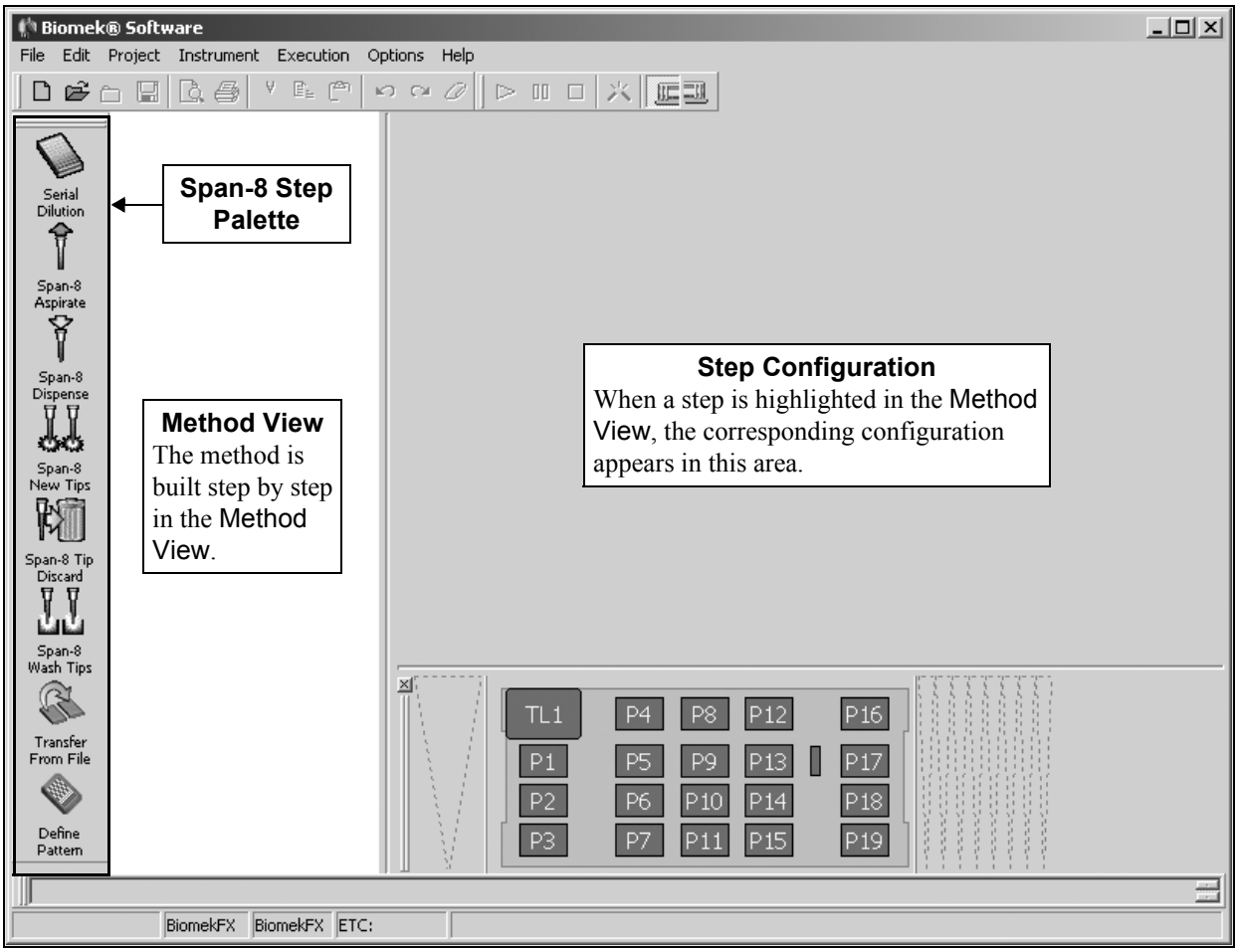


Figure 18-1. Biomek main editor with Span-8 Step Palette displayed

To display the Span-8 Step Palette, complete the following:

- Right-click any empty palette space, and the Step Palette menu appears. Select **Span-8.**

  OR

- From the menu bar, select **Options>Toolbars>Span-8**.

18.3 Serial Dilution Step (including 3000)

The Serial Dilution step is used to perform multiple dilutions of a sample on a single microplate. The Serial Dilution step transfers liquid from wells on a microplate to other wells on the same microplate and may also add diluent to those wells. The microplate may be prepared by the Serial Dilution step or in the same method prior to the Serial Dilution step.

Serial dilution completes multiple dilutions by performing the following actions in sequence:

- Transfer a volume of diluent from the diluent labware to all selected wells except the first row or column (unless specified otherwise).
- Transfer a volume of sample from the first selected well to the next selected well.
- Mix the solution.

Note: The Serial Dilution step does not automatically mix the solution. Select **Customize** to add mixing to the technique or create a new technique in the Technique Editor. Refer to Section 9.3, *Creating New Techniques*, for information on creating and modifying techniques.

- Transfer a volume of solution to the next selected well.
- Mix the solution.
- Repeat transfer and mix operations until all selected wells are used.

Note: The labware may be previously prepared, either by hand or by using the Biomek instrument, with a specific volume of diluent in the selected wells. If the labware is previously prepared, skip the step that adds diluent to the wells.

The Serial Dilution step specifies:

- Pod that performs the dilution.
- Probes that are used during dilution.
- Tips used during dilution.
- Labware type accessed during serial dilution.
- Position of the labware on the deck.
- Liquid type of the labware.
- Wells in the selected labware to use for dilution.
- Volume being diluted.
- Direction in which wells are accessed during dilution.
- Technique.
- Diluent labware type accessed during serial dilution.
- Position of the diluent labware on the deck.
- Liquid type of the diluent labware.
- Wells in the selected diluent labware to use for dilution.
- Dilution ratio.

Insert a **Serial Dilution** step into the method (Figure 18-2).

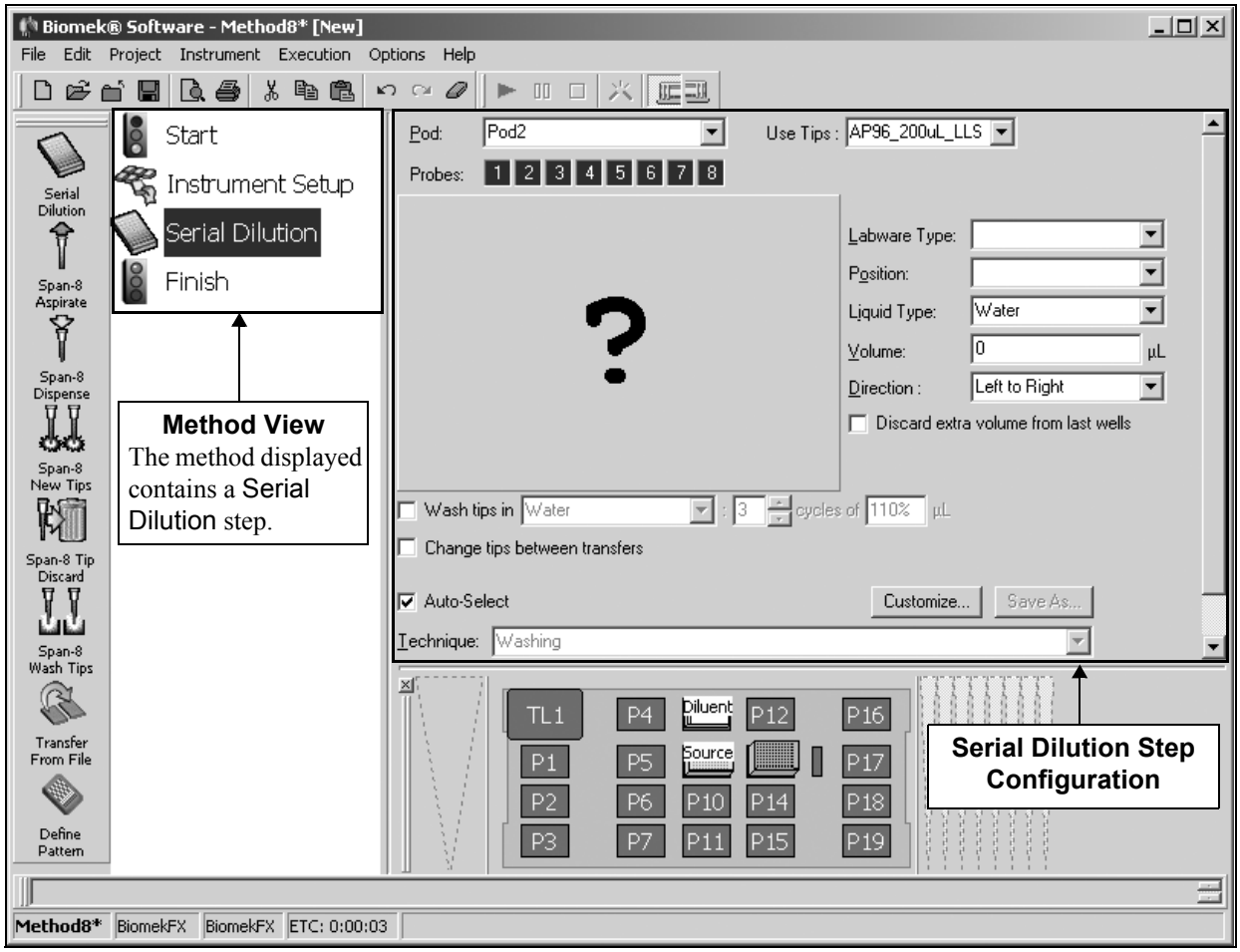


Figure 18-2. Serial Dilution step and configuration

18.3.1 Configuring the Serial Dilution Step

When a Serial Dilution step is added to a method, the Serial Dilution Step Configuration appears (Figure 18-2).

Note: If it is desired to have diluent in any unused wells as a standard, tips can be conserved by using a Transfer step to transfer diluent to the unused wells and selecting **Leave them on** in the Tip Handling configuration.

To configure Serial Dilution:

1. If using a dual-pod ***FX*** instrument, specify the **Pod** performing the dilution operation by selecting a Span-8 Pod from the list. The pod configured as the default pod is displayed in Pod. If the other pod is desired, select the pod from the drop-down list or the Current Deck Display.

   OR

   If using a ***3000***, insert and configure a Load Tool or Change Tool step to load an MP20 or MP200 tool in the method before the Serial Dilution.

   Note: Refer to Section 20.3, *Change Tool Step* or Section 20.4, *Load Tool Step* for information about configuring the desired step.

2. If using a Span-8 pod on the ***FX*** or ***NX-S8***, select the probes used in the dilution by highlighting the desired numbers next to Probes. Any combination of probes may be used as long as all selected probes are using the same type of tips and syringes.

   Note: All disposable tips are selected by default. If there are only fixed tips, all tips are selected by default. For example, if the Span-8 Pod is equipped with fixed tips on probes 1-4 and disposable tips on probes 5-8, probes 5-8 will be selected by default. However, if probes 5-8 are also equipped with fixed tips, all eight probes are selected by default.

3. In **Use Tips**, select the tip type loaded from the drop-down list.

   OR

   Select the tip box from the Current Deck Display with the desired tip type. Selecting tips from the Current Deck Display automatically updates Tips in the Step Configuration.

   - ***FX, NX-S8*** — If the selected Probes are equipped with fixed tips, Use Tips is set to Fixed and is not configurable.

   Note: If tip boxes were assigned names in the Instrument Setup step, enter that name in Use Tips. If tips were not assigned names, select the tip type. It is recommended that tips not be named in the Instrument Setup step because this could restrict the step from locating available tips.

4. Click on the desired piece of labware in the Current Deck Display in which the serial dilution is performed. Information for that piece of labware is entered automatically into the Serial Dilution Step Configuration.

   OR

   Select a **Labware Type** from the list (Figure 18-3).

   Note: The labware contains the sample that is diluted in the first row or column of selected wells, depending on the direction of dilution selected.

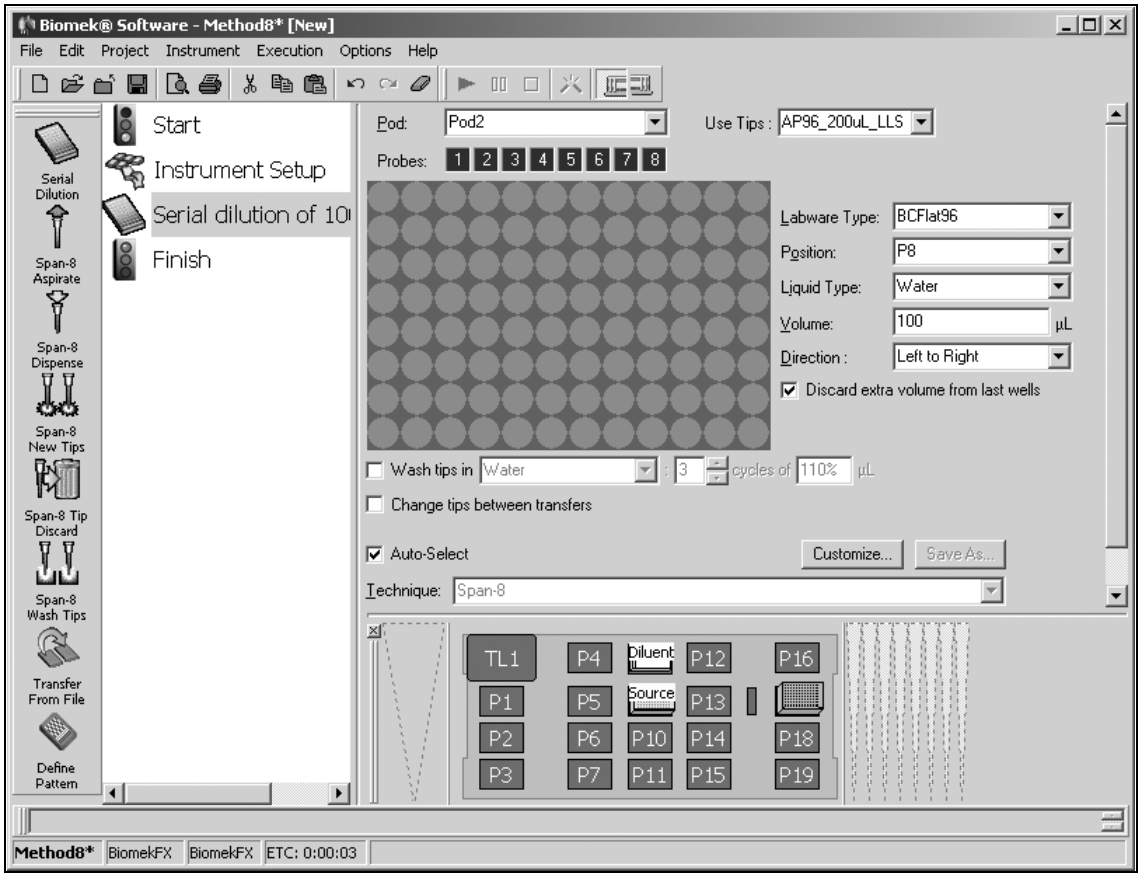


Figure 18-3. Serial Dilution step configuration with labware configured

5. Verify the **Position** of the labware.

   Note: A green outline appears in the Current Deck Display around the selected labware.

6. Select the **Liquid Type** being diluted in the selected labware.
7. Select the wells on the labware to use in the serial dilution. Select the wells according to the procedures described in Chapter 11, *Creating Well Patterns*.

   Note: To zoom in on the labware, double-click on the labware. To call up a menu for Zoom In and a Specify Selection as Text option, right-click on the labware.

   Specify Selection as Text allows the selection of the first well in a microplate

as a target for the dispense operation. Specify Selection as Text may also be used to enter variables or expressions. Wells are numbered left to right and down (for example, the first row is wells 1-12, the second row wells 13-24, etc., for a 96-well microplate).

8. Enter the **Volume** diluted in each well of the selected labware. If using a variable or expression, enter an equal sign (=) followed by the variable name or expression; for example, =AspValue. Otherwise, just enter the desired value.

Note: This is the volume of each diluted solution that is transferred to the next well for the next dilution.

9. Select the **Direction** to dilute. The specified Volume is transferred from each well to the next selected well in the chosen Direction for the next dilution. Available options are:
   - Left to right — dilutes across rows of microplate (Figure 18-4).
   - Top to bottom — dilutes down columns of microplate (Figure 18-5).

➢ ***3000*** — The direction must be Left to right.

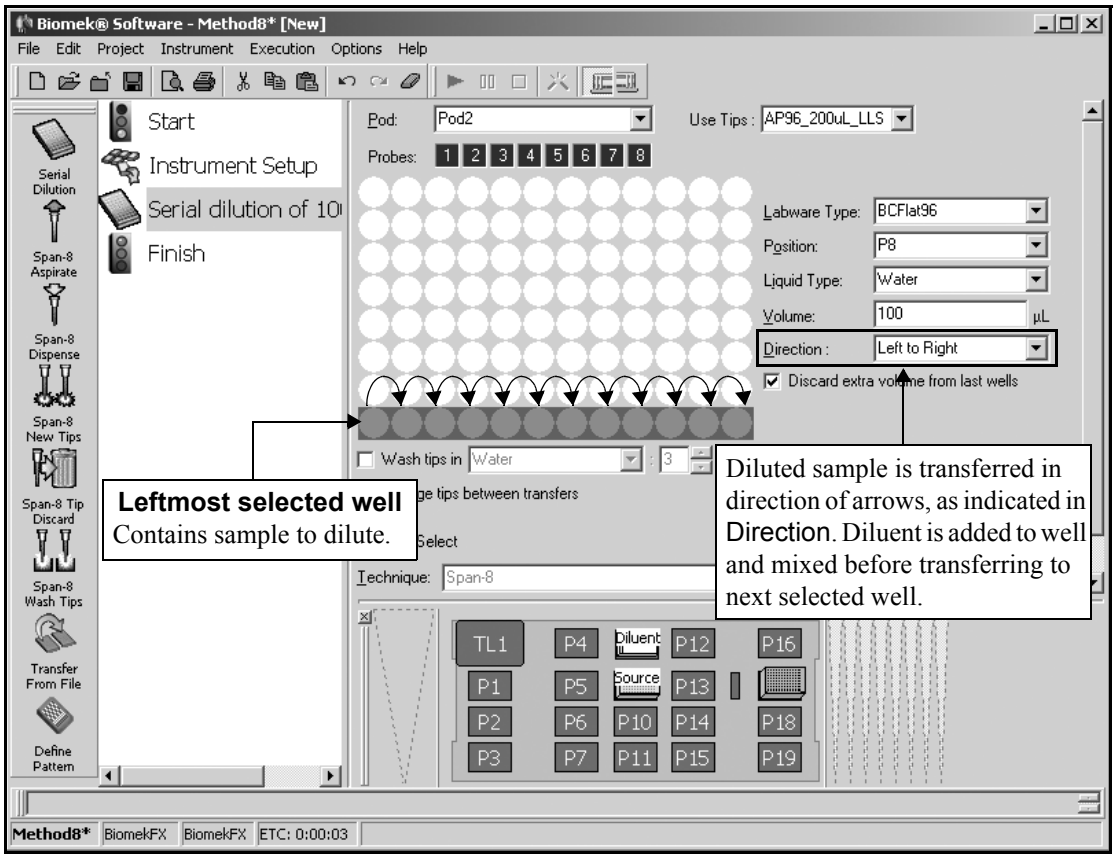


Figure 18-4. Serial Dilution from left to right

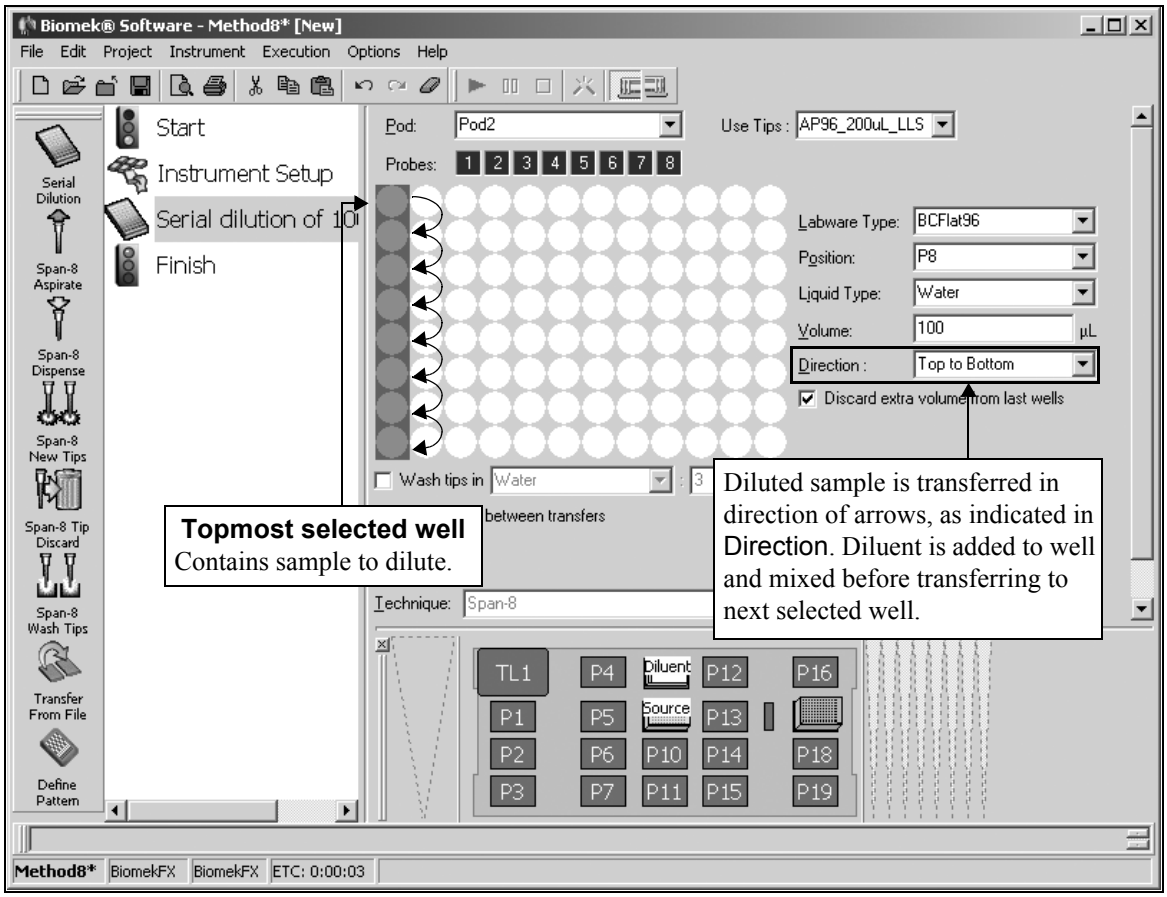


Figure 18-5. Serial Dilution from top to bottom

10. Select **Discard extra volume from last wells** to aspirate the extra Volume from the last wells and discard it at the Span-8 Tip Wash ALP so that each well contains the same volume of solution.

11. If using an ***FX*** or ***NX-S8***, choose **Wash tips in** to use the active 96-Channel Tip Wash ALP to wash the tips.

    ➢ ***3000*** — Tip wash options are not available. Proceed to step 19.

    Note: A WashStation96 ALP must be added to the deck and configured in the Deck Editor before washing can occur. Clicking on a WashStation96 ALP while the Serial Dilution step is being configured places a check in Wash tips in, and populates Wash tips in with the solution configured for the WashStation96 ALP in Labware Properties on the Instrument Setup step.

    Note: If Wash tips in is not selected, proceed to step 15.

12. In **Wash tips in**, select a solution for the wash cycle if the field does not already contain a solution.

    Note: The wash solution specified in the Serial Dilution step must match the solution selected in Labware Properties for the WashStation96 ALP on the Instrument Setup step configuration, or an error occurs.

13. Choose the number of cycles to aspirate and dispense during wash.

14. In **%**, provide the volume of wash fluid to use when washing tips as a percentage of the maximum volume of fluid contained in the tips in previous steps; for example, if the maximum volume of fluid transferred is 50 µL, and the % is set for 110%, the Transfer step washes the tips with 55 µL of solution.

    Note: If the % sign is deleted in the % field, the field label changes to µL. Any value entered is now interpreted as a specific volume, not a percentage.

15. If using an ***FX*** or ***NX-S8*** with fixed tips installed, choose **Wash tips with** to use the passive Span-8 Tip Wash ALP to wash fixed tips.

    Note: A Span-8 Tip Wash ALP must be added to the deck and configured in the Deck Editor before washing can occur. Only fixed tips can be washed with the Span-8 Tip Wash ALP. If using disposable tips and washing is desired, go back to 11. If Wash tips with is not selected, proceed to step 19.

16. In **Wash tips with**, enter the volume of system fluid to use when washing the outside of the tips.

17. In **after dispensing**, enter the volume of system fluid to use when washing the inside of the tips.

18. If using a Span-8 Pod on ***FX***, select **Speed Pump** to use the speed pump when flushing the tips with system fluid, if desired.

    OR

    If using a Span-8 Pod on ***NX-S8***, select **purge pump** to use the purge pump when flushing tips with system fluid, if desired.

    Note: The speed pump or purge pump is an optional device that can be used to shorten the time it takes to wash tips. A speed pump or purge pump must be added as a device and configured with the Span-8 Pod in Hardware Setup to use it when washing tips.

19. Choose **Change tips between transfers** to change tips between transferring diluent and sample.

    Note: Change tips between transfers is available only when disposable tips are installed on all probes.

20. The software automatically selects a Technique based on the liquid type, labware type, tip type, and volume being transferred. To override this selection, deselect **Auto-Select** and choose the desired **Technique**.

    OR

    Choose **Customize** and configure the technique as desired in the Technique Editor.

    Note: For more information on customizing, configuring, and saving a technique, refer to Section 12.3.1, *Understanding Techniques*.

    Note: It is recommended a technique include mixing for best results. Select **Customize** to add mixing to the technique or create a new technique in the Technique Editor. Refer to Section 9.3, *Creating New Techniques*, for information on creating and modifying techniques.

21. If the labware is previously prepared with diluent, select a step that occurs after the Serial Dilution step or the **Finish** step to validate the step configuration.

    OR

    If the labware is not previously prepared with diluent, configure **Diluent Properties**. Proceed to Section 18.3.2, *Configuring Diluent Properties*.

18.3.2 Configuring Diluent Properties

Diluent Properties are configured if the sample microplate is not previously prepared with diluent. The Diluent Properties configuration allows for diluent to be transferred from a piece of labware to the wells used for the dilution.

The Diluent Properties configuration can be collapsed to allow more room during configuration. When collapsed, the diluent properties configuration is displayed as the text Diluent Properties.

To collapse or expand the Diluent Properties configuration, click the arrow to the left of Diluent Properties or the textual display.

To configure Diluent Properties for the Serial Dilution step:

1. Click the arrow to the left of Diluent Properties or the textual display to expand the Diluent Properties configuration (Figure 18-6).

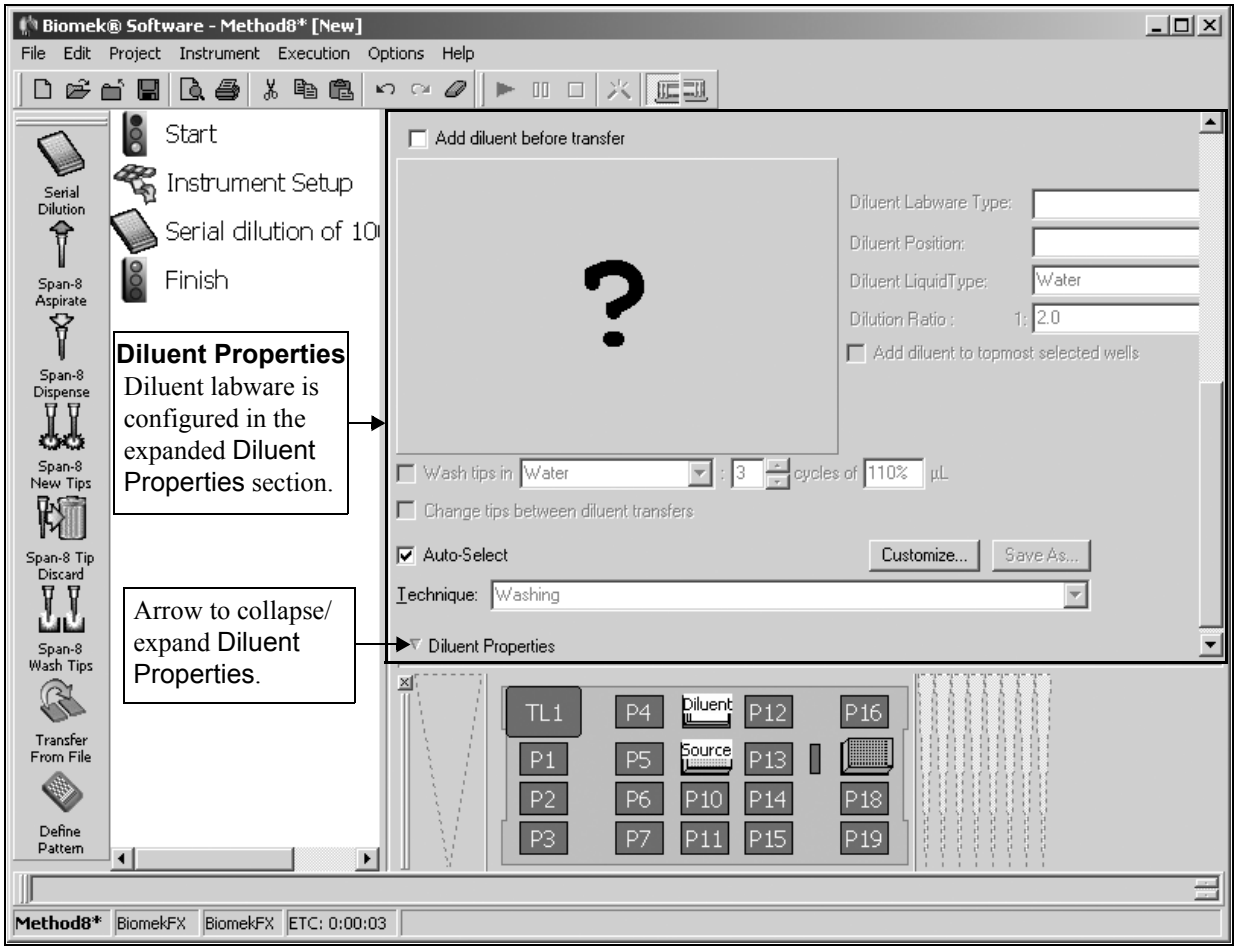


Figure 18-6. Serial Dilution — Diluent Properties configuration

2. Select **Add diluent before transfer** to activate the Diluent Properties configuration.

3. Click on the desired piece of labware in the Current Deck Display to select the labware with the diluent. Information for that piece of labware is entered automatically into the Diluent Properties configuration.

   OR

   Select a **Diluent Labware Type** from the list (Figure 18-7).

Note: Reservoirs are the only labware type valid for diluent retrieval.

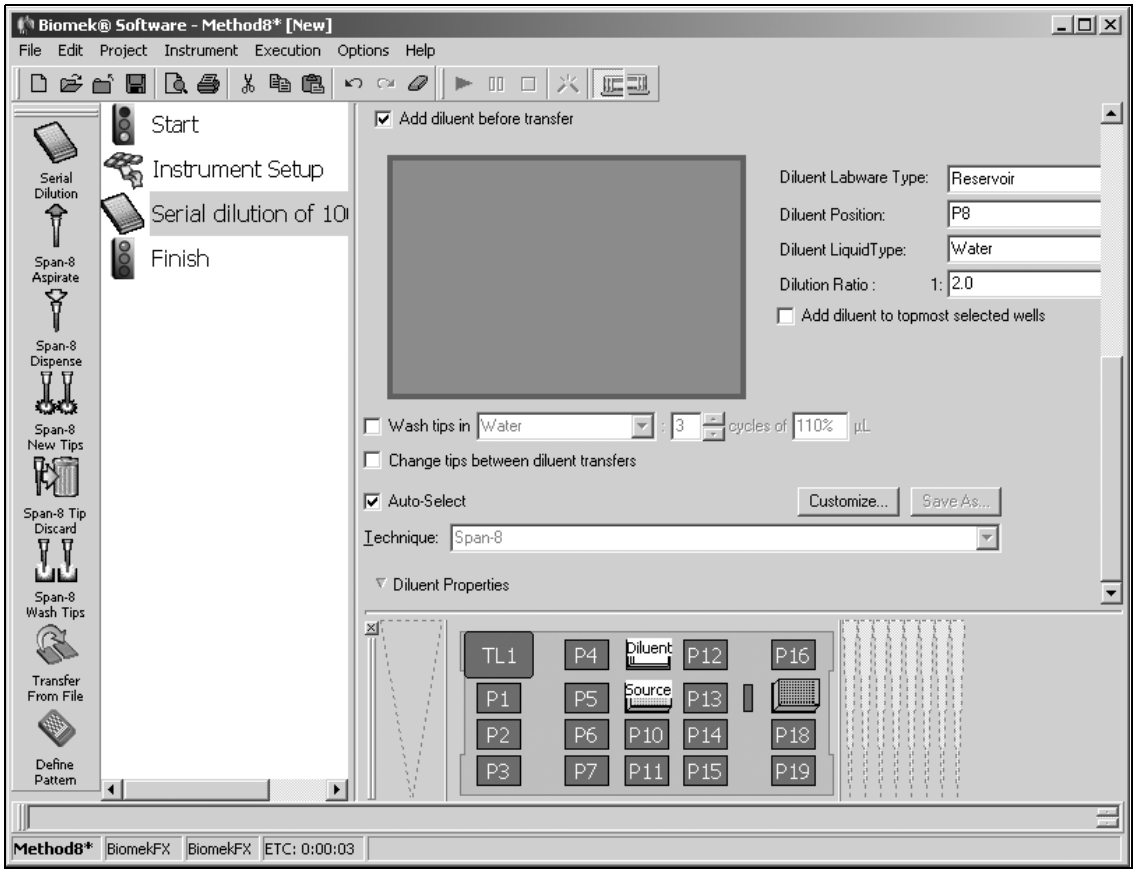


Figure 18-7. Serial Dilution step configuration with diluent labware

4. Verify the **Diluent Position** of the diluent labware.
5. Select the **Diluent Liquid Type** of the diluent in the diluent labware.
6. Enter the desired **Dilution Ratio**. If using a variable, enter an equal sign (=) followed by the variable name; for example, =AspValue. Otherwise, just enter the desired value.

Note: The Dilution Ratio is set up as a ratio of volume of sample to total solution (sample plus diluent) volume. For example, a Dilution Ratio of 1:2 indicates that for every microliter of sample there are two microliters of solution, or a 50 percent dilution (one microliter of diluent added).

7. Select the wells on the labware from which to aspirate diluent. Select the wells according to the procedures described in Chapter 11, *Creating Well Patterns*.

   Note: To zoom in on the labware, double-click on the labware. To call up a menu for Zoom In and a Specify Selection as Text option, right-click on the labware.

   Specify Selection as Text allows the selection of the first well in a microplate as a target for the dispense operation. Specify Selection as Text may also be used to enter variables or expressions. Wells are numbered left to right and top to bottom (for example, the first row is wells 1-12, the second row wells 13-24, etc., for a 96-well microplate).

8. Select **Add Diluent to leftmost/topmost selected wells** if it is desired to use the first selected well for the first dilution. Enough diluent to achieve the entered Dilution Ratio is added to the first selected well.

   Note: If the dilution Direction is configured as **Left to Right**, Add diluent to leftmost selected wells is available (Figure 18-4). If the dilution Direction is configured as **Top to Bottom**, Add diluent to topmost selected wells is available (Figure 18-5).

9. If using an ***FX*** or ***NX-S8***, choose **Wash tips in** to use the active 96-Channel Tip Wash ALP to wash the tips.

   - ***3000*** — Tip wash options are not available. Proceed to step 17.

   Note: A WashStation96 ALP must be added to the deck and configured in the Deck Editor before washing can occur. Clicking on a WashStation96 ALP while the Serial Dilution step is being configured places a check in Wash tips in, and populates Wash tips in with the solution configured for the WashStation96 ALP in Labware Properties on the Instrument Setup step.

   Note: If Wash tips in is not selected, proceed to step 13.

10. In **Wash tips in**, select a solution for the wash cycle if the field does not already contain a solution.

    Note: The wash solution specified in the Serial Dilution step must match the solution selected in Labware Properties for the WashStation96 ALP on the Instrument Setup step configuration, or an error occurs.

11. Choose the number of cycles to aspirate and dispense during wash.

12. In **%**, provide the volume of wash fluid to use when washing tips as a percentage of the maximum volume of fluid contained in the tips in previous steps; for example, if the maximum volume of fluid transferred is 50 µL, and the % is set for 110%, the Transfer step washes the tips with 55 µL of solution.

    Note: If the % sign is deleted in the % field, the field label changes to µL. Any value entered is now interpreted as a specific volume, not a percentage.

13. If using an ***FX*** or ***NX-S8*** with fixed tips installed, choose **Wash tips with** to use the passive Span-8 Tip Wash ALP to wash fixed tips.

    Note: A Span-8 Tip Wash ALP must be added to the deck and configured in the Deck Editor before washing can occur. Only fixed tips can be washed with the Span-8 Tip Wash ALP. If using disposable tips and washing is desired, go back to 9. If Wash tips with is not selected, proceed to step 17.

14. In **Wash tips with**, enter the volume of system fluid to use when washing the outside of the tips.

15. In **after dispensing**, enter the volume of system fluid to use when washing the inside of the tips.

16. If using a Span-8 Pod on ***FX***, select **Speed Pump** to use the speed pump when flushing the tips with system fluid, if desired.

    OR

    If using a Span-8 Pod on ***NX-S8***, select **purge pump** to use the purge pump when flushing tips with system fluid, if desired.

    Note: The speed pump or purge pump is an optional device that can be used to shorten the time it takes to wash tips. A speed pump or purge pump must be added as a device and configured with the Span-8 Pod in Hardware Setup to use it when washing tips.

17. Choose **Change tips between diluent transfers** to change tips between each diluent transfer.

    Note: Change tips between diluent transfers is available only when disposable tips are installed on all probes.

18. The software automatically selects a Technique based on the liquid type, labware type, tip type, and volume being transferred. To override this selection, deselect **Auto-Select** and choose the desired **Technique**.

    OR

    Choose **Customize** and configure the technique as desired in the Technique Editor.

    Note: For more information on customizing, configuring, and saving a technique, refer to Section 12.3.1, *Understanding Techniques*.

    Note: It is recommended to use a technique that includes mixing for best results. Select **Customize** to add mixing to the technique or create a new technique in the Technique Editor.

19. Select a step that occurs after the Serial Dilution step or the **Finish** step to validate the step configuration.

18.4 Span-8 Aspirate Step

The Span-8 Aspirate step (Figure 18-8) removes liquid from source labware in preparation for dispensing to destination labware. The Span-8 Aspirate step is often used in conjunction with the Span-8 Dispense, Span-8 New Tips, and Span-8 Discard Tips steps, but it can be used with any combination of steps. Span-8 Aspirate provides more direct control over pipetting operations than the Transfer or Combine steps because it offers more explicit control over individual probe aspiration volumes and well access.

Note: If the Span-8 Pod is equipped with disposable tips, it is necessary to load tips to the probes using a Span-8 New Tips step prior to aspirating.

The Span-8 Aspirate Step Configuration includes specifying:

- Labware type accessed during aspirate.
- Position of the labware on the deck.
- Type of liquid to aspirate.
- Volume to aspirate.
- Pod that performs the aspirate.
- Probes that are used during aspirate.
- Spacing between probes during aspirate.
- Tip refresh, if desired, and the type of tips used.
- Wells in the selected labware from which to aspirate.
- Technique.
- Pipetting height.

Insert a **Span-8 Aspirate** step into the method (Figure 18-8).

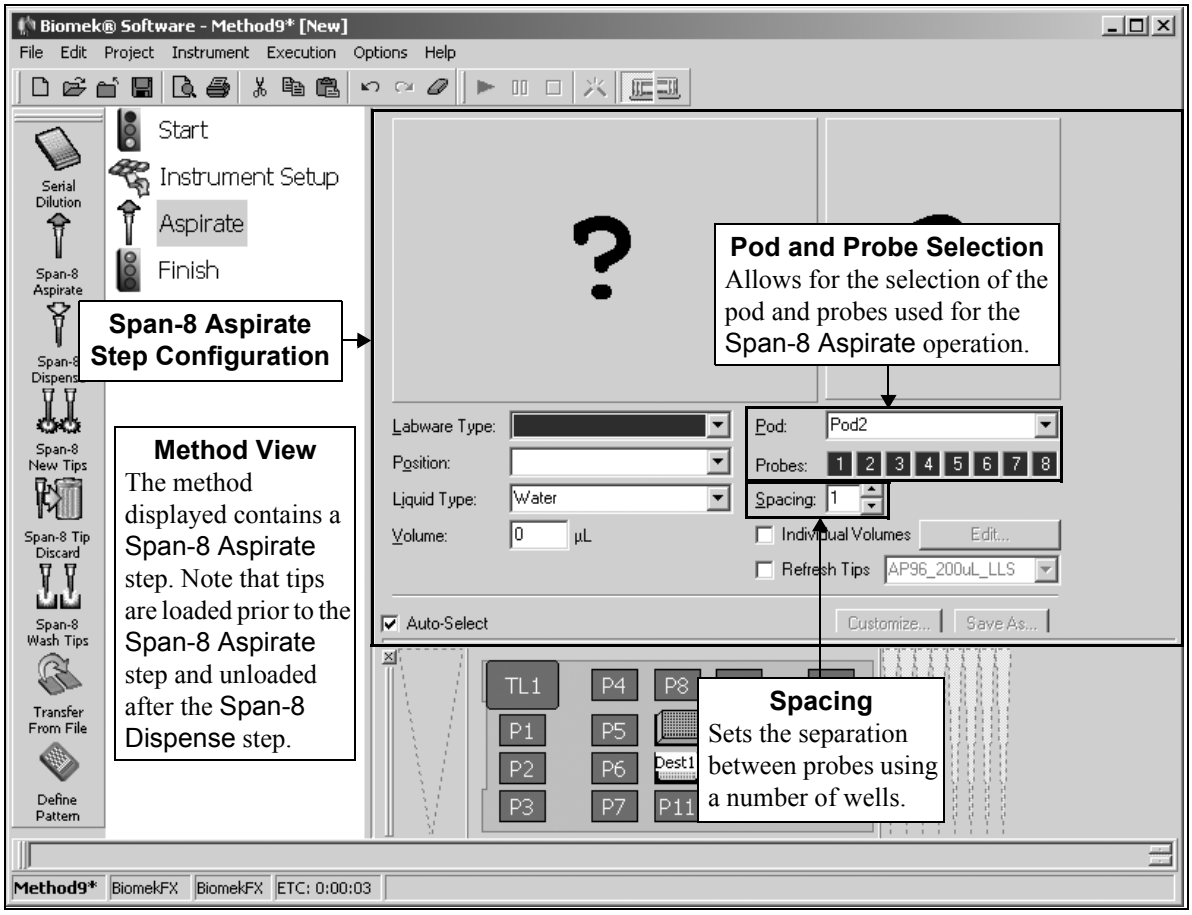


Figure 18-8. Span-8 Aspirate step and configuration

18.4.1 Configuring the Span-8 Aspirate Step

When a Span-8 Aspirate step is added to a method, the Span-8 Aspirate Step Configuration appears (Figure 18-8).

To configure the Span-8 Aspirate step:

1. Click on the desired piece of labware in the Current Deck Display. Information for that piece of labware is entered automatically into the Span-8 Aspirate Step Configuration.

   OR

   Select a **Labware Type** from the drop-down list (Figure 18-9).

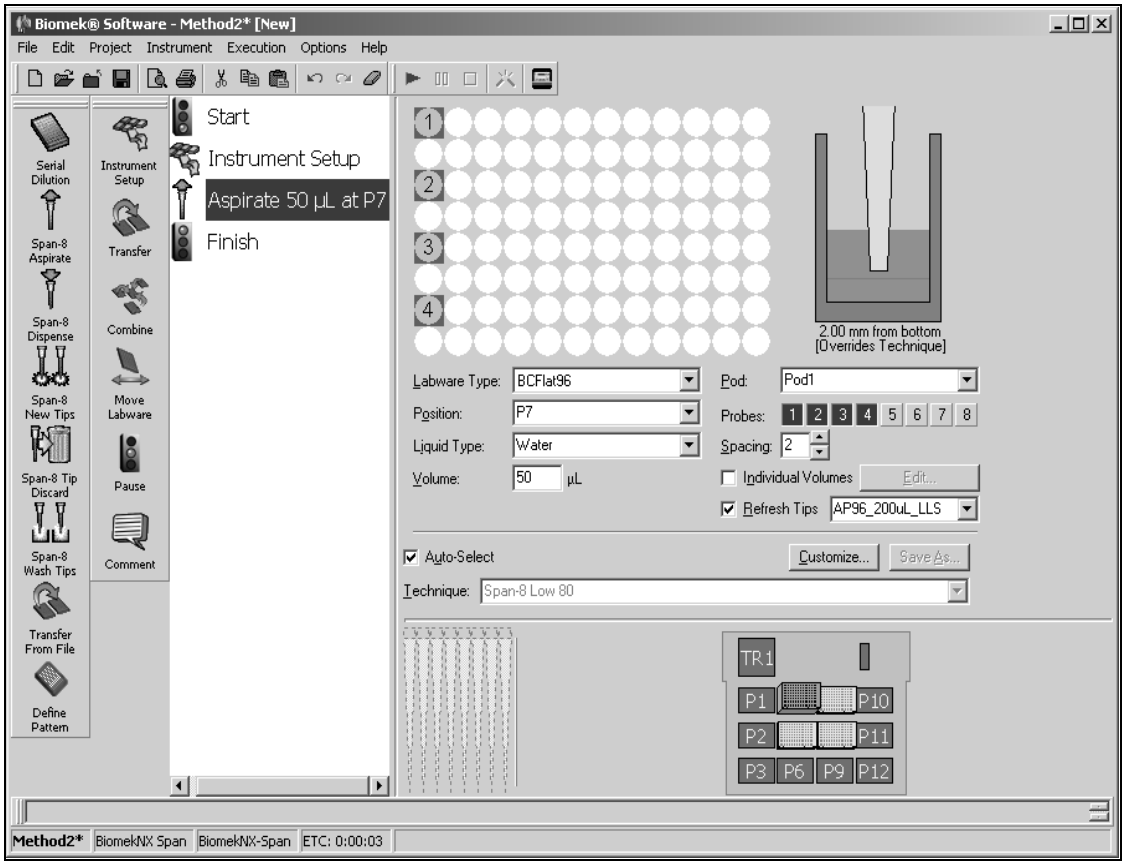


Figure 18-9. Span-8 Aspirate step configuration with labware configured

2. Verify the **Position** of the labware.

   Note: A bright blue outline appears in the Current Deck Display around the selected labware.

3. Select the **Liquid Type** contained in the selected labware.

4. If using a dual-pod ***FX*** instrument, specify the **Pod** performing the aspirate operation by selecting a Span-8 Pod from the list. The pod configured as the default pod is displayed in Pod. If the other pod is desired, select the pod from the drop-down list or the Current Deck Display.

5. Select the **Probes** used in the aspirate step by highlighting the desired probe numbers. Any combination of probes may be used as long as all selected probes are using the same type of tips and syringes.

   Note: All disposable tips are selected by default. If there are only fixed tips, all tips are selected by default. For example, if the Span-8 Pod is equipped with fixed tips on probes 1-4 and disposable tips on probes 5-8, probes 5-8 are selected by default. However, if probes 5-8 are also equipped with fixed tips, all eight probes are selected by default.

6. Select the **Spacing**. Spacing is the number of wells between probes. For example, if a spacing of **3** is selected, the probes hit every third well.

   Note: When aspirating from a 384-well microplate, it is not possible to aspirate from adjacent wells. A minimum spacing of 2 wells is required. When aspirating from some tube racks, it must aspirate from adjacent wells and probe spacing is not possible.

7. Select the wells on the labware to aspirate from by hovering the mouse over the graphic representing the labware. The wells highlighted in yellow indicate the wells accessed based on the selected probes and spacing. Click to select the wells. The wells appear blue after they are selected.

   For example, if aspirating from a 384-well plate, probes 1-4 are selected, and Spacing is set at 4, wells are selected as shown in Figure 18-10.

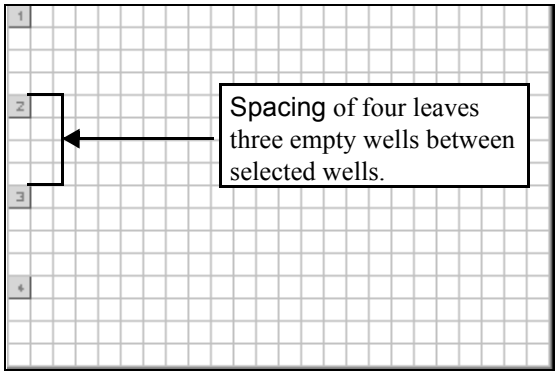


Figure 18-10. Example of how probe and spacing selection affects well selection

   Note: To zoom in on the selected labware, double-click on the labware. To call up a menu for Zoom In and a Specify Selection as Text option, right-click on the labware.

   Specify Selection as Text allows the selection of the first well in a microplate as a target for the aspirate operation. The first selected probe (lowest probe number) aspirates from the specified well. Remaining probes aspirate from wells based on the specified well and Spacing. Specify Selection as Text may also be used to enter variables or expressions. Wells are numbered left to right and down (for example, the first row is wells 1-12, the second row wells 13-24, etc., for a 96-well microplate).

8. Enter the **Volume** aspirated from the selected labware. If using a variable or expression, enter an equal sign (=) followed by the variable name or expression; for example, =AspValue. The Volume is aspirated by all selected Probes.

9. To aspirate a different volume in each probe, select **Individual Volumes** and choose **Edit**. Individual Volumes appears (Figure 18-11).

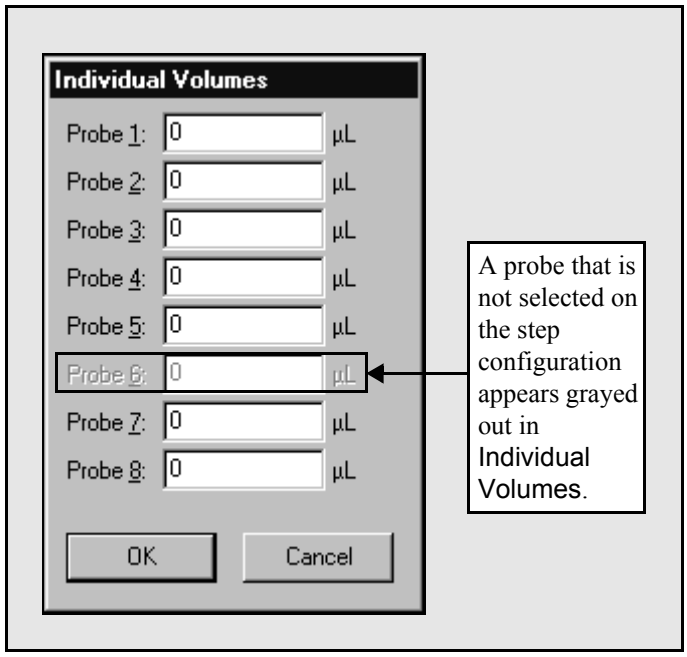


Figure 18-11. Individual Volumes

10. Enter the volume each probe is to aspirate in Individual Volumes. If using a variable or expression, enter an equal sign (=) followed by the variable name or expression; for example, =AspValue. A volume may only be entered for the probes that are selected on the Span-8 Aspirate step configuration. Deselected probes appear grayed out in Individual Volumes.
11. Choose **OK**. Individual Volumes closes.
12. Check **Refresh Tips**, if desired, and specify the **tip type** to load new tips to the pod whether tips are currently loaded or not.

13. The software automatically selects a Technique based on the liquid type, labware type, tip type, and volume being aspirated. To override this selection, deselect **Auto-Select** and select the desired **Technique** (Figure 18-12).

    OR

    Choose **Customize** and configure the technique as desired in the Technique Editor.

Note: For more information on customizing, configuring, and saving a technique, refer to Section 12.3.1, *Understanding Techniques*.

Note: If the technique is auto-selected and the volumes specified differ enough to require different techniques, an aspiration is performed for each unique technique.

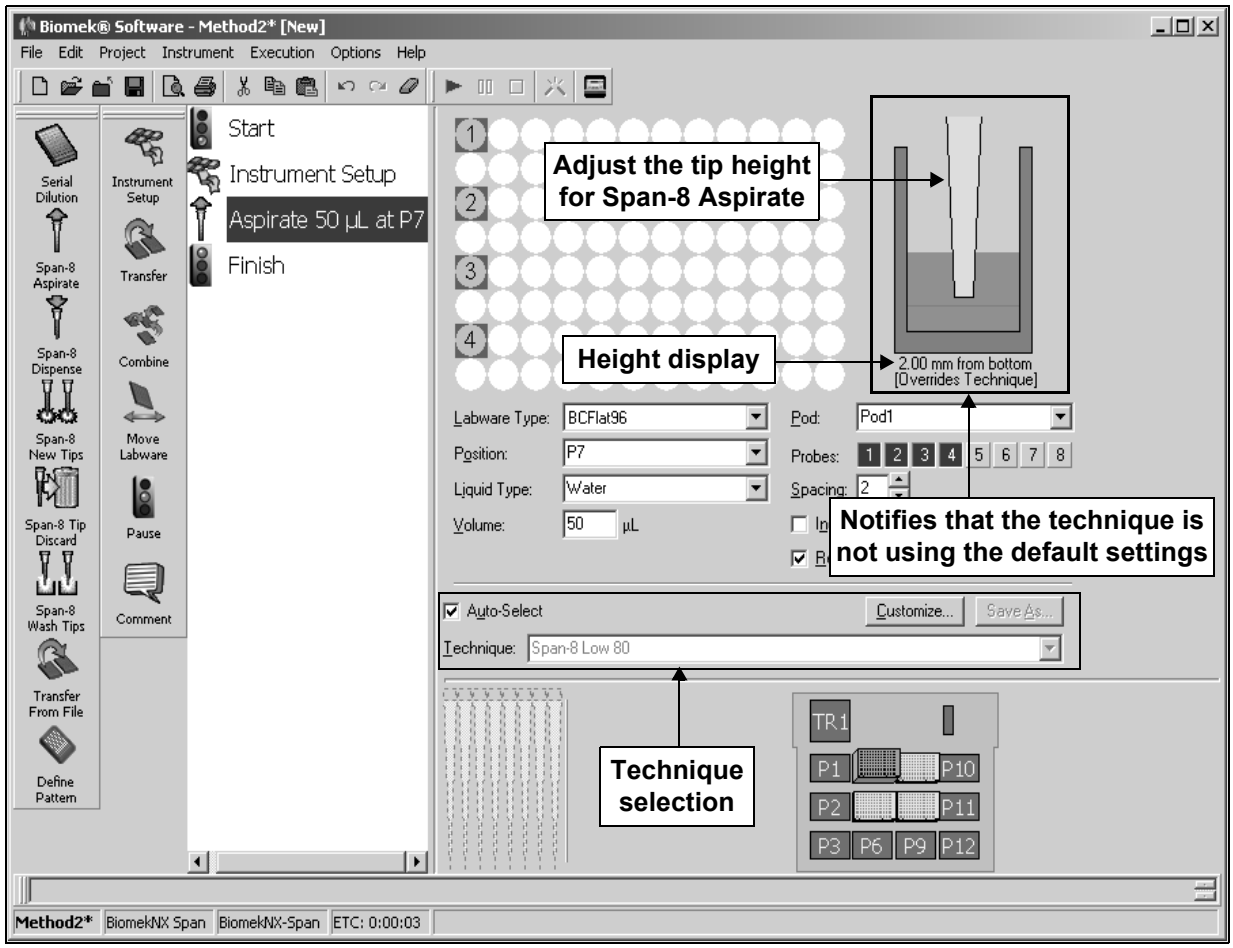


Figure 18-12. Span-8 Aspirate step — Adjusting the aspirate height

14. Leave the tip height as is to use the settings specified in the pipetting technique.

    OR

    Set the aspirate height manually using one of the following techniques:

    - Set the aspirate height by positioning the cursor over the graphic of a tip inside a well (Figure 18-12). Click and drag the graphic up or down. The tip moves with the cursor, and the height displayed below the graphic is adjusted as the graphic is manipulated.

      Note: The cursor changes to a hand when positioned over the graphic.

    - Position the cursor in the graphic of a tip inside a well, and adjust the height using the ↑ and ↓ keys.
    - Right-click on the graphic of a tip inside a well, and a menu appears. Select **Custom Height**, and Custom Height appears (Figure 18-13). Insert the **Height** in millimeters (mm) and, in **from**, select a reference point from the drop-down list.

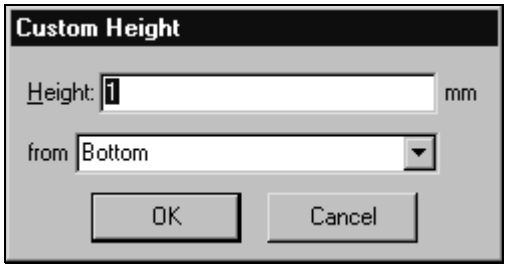


Figure 18-13. Custom Height prompt

Note: The phrase (Overrides Technique) appears below the graphic when the tip height is changed by manipulating the graphic (Figure 18-12), or when the technique is changed with the Customize option.

15. If desired, right-click on the graphic of a tip inside a well and choose how the tip height is measured:

    - **Measure from Liquid** — The tip height is measured from the surface of the liquid in the well.

      Note: With standard tips, Measure from Liquid requires that a known volume of liquid be entered in Labware Properties for the labware to aspirate from. If the volume of liquid is not known, liquid level sensing (LLS) tips must be used to measure the tip height from the surface of the liquid in the well (refer to Section 9.4.5, *Setting Liquid Level Sensing Values (FX, 3000, and NX-S8 only)*).

    - **Measure from Bottom** — The tip height is measured from the bottom of the well.
    - **Measure from Top** — The tip height is measured from the top of the well.

16. Select a step that occurs after the Span-8 Aspirate step or the **Finish** step to validate the step configuration.

18.5 Span-8 Dispense Step

The Span-8 Dispense step dispenses liquid into a single destination labware following aspirate. The Span-8 Dispense step is often used in conjunction with the Span-8 Aspirate, Span-8 New Tips, and Span-8 Discard Tips steps, but it can be used with any combination of steps. Span-8 Dispense provides more direct control over pipetting operations than the Transfer or Combine steps because it offers more explicit control over individual probe dispense volumes and well access.

Tips must be loaded and have liquid in them from a previous step, such as a Span-8 Aspirate step, prior to using a Span-8 Dispense step.

The Span-8 Dispense Step Configuration includes specifying:

- Labware type accessed during dispense.
- Position of the labware on the deck.
- Type of liquid to dispense.
- Volume to dispense.
- Pod that performs the dispense.
- Probes that are used during dispense.
- Spacing of the probes during dispense.
- Empty tips, if desired.
- Wells in the selected labware to dispense.
- Technique.
- Pipetting height.
- Disposal of excess liquid into the reservoir section of the nearest Span-8 Wash ALP.

Insert a **Span-8 Dispense** step into the method (Figure 18-14).

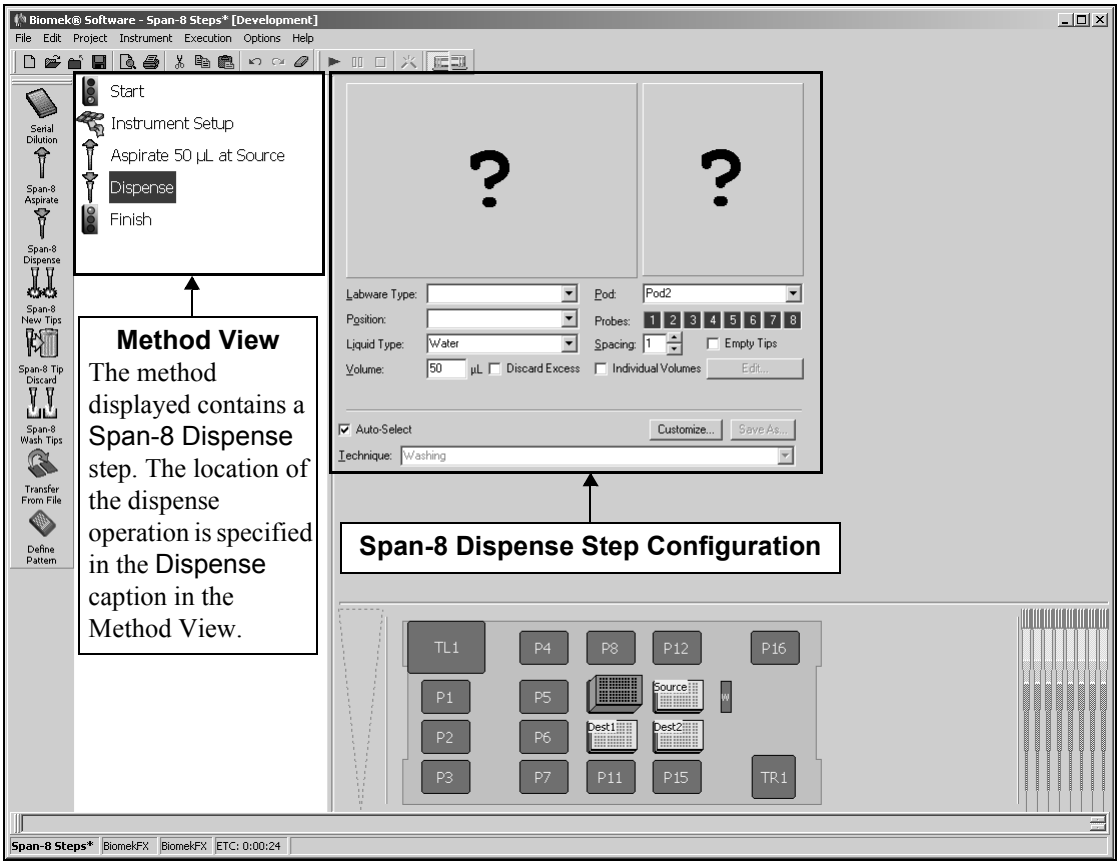


Figure 18-14. Span-8 Dispense step and configuration

18.5.1 Configuring the Span-8 Dispense Step

When a Span-8 Dispense step is added to a method, the Span-8 Dispense Step Configuration appears (Figure 18-14).

To configure the Span-8 Dispense step:

1. Click on the desired piece of labware in the Current Deck Display. Information for that piece of labware is entered automatically into the Span-8 Dispense Step Configuration.

   OR

   Select a **Labware Type** from the list (Figure 18-15).

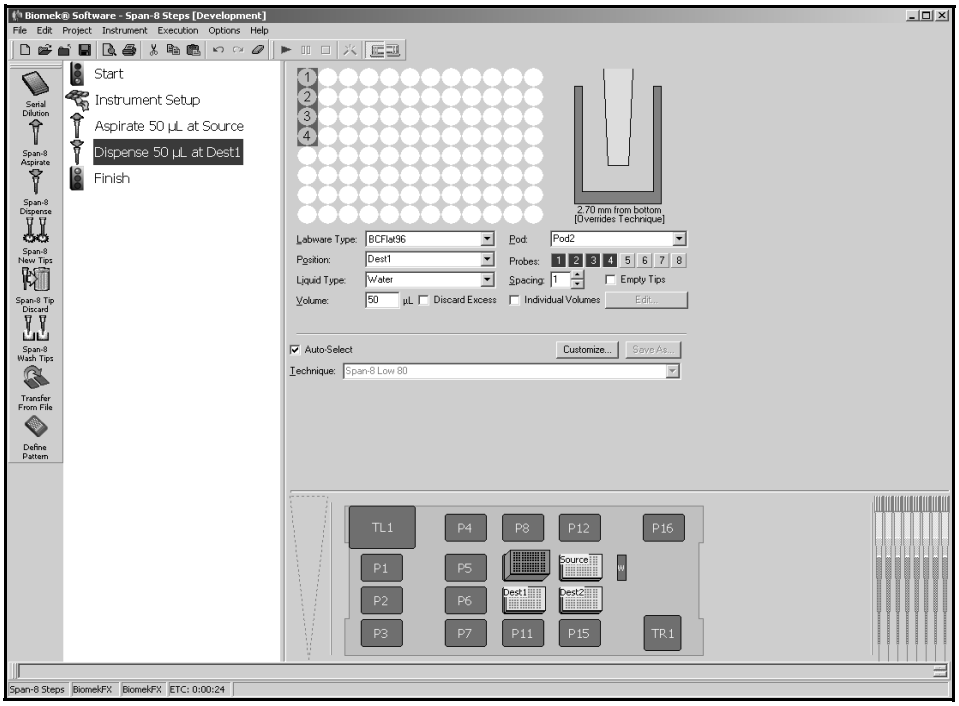


Figure 18-15. Span-8 Dispense step configuration with labware configured

2. Verify the **Position** of the labware.

   Note: A bright yellow outline appears in the Current Deck Display around the selected labware.

3. Select the **Liquid Type** contained in the tips.

4. If using a dual-pod ***FX*** instrument, specify the **Pod** performing the dispense operation by selecting a Span-8 Pod from the list. The pod configured as the default pod is displayed in Pod. If the other pod is desired, select the pod from the drop-down list or the Current Deck Display.

5. Select the **Probes** that will be used in the dispense step by highlighting the desired probe numbers. Any combination of probes may be used as long as all selected probes are using the same type of tips and syringes.

   Note: All disposable tips are selected by default. If there are only fixed tips, all tips are selected by default. For example, if the Span-8 Pod is equipped with fixed tips on probes 1-4 and disposable tips on probes 5-8, probes 5-8 are selected by default. However, if probes 5-8 are also equipped with fixed tips, all eight probes are selected by default.

6. Select the **Spacing**. Spacing is the number of wells between probes. For example, if a spacing of **3** is selected, the probes will hit every third well.

   Note: When dispensing to a 384-well microplate, it is not possible to dispense to adjacent wells. A minimum spacing of 2 wells is required. When dispensing to tube racks, it must dispense to adjacent tubes and probe spacing is not possible.

7. Check **Empty Tips**, if desired, to expel the Trailing Air Gap, the fluid contained in the tip, and the Blow Out all at one time, rather than as separate operations.

   Note: The default setting for Empty Tips is Off.

8. Select the wells on the labware to dispense to by hovering the mouse over the graphic representing the labware. The wells highlighted in yellow indicate the wells accessed based on the selected probes and spacing. Click to select the wells. The wells appear blue after they are selected.

   For example, if dispensing to a 384-well plate, probes 1-4 are selected, and Spacing is set at 4, wells are selected as shown in Figure 18-16.

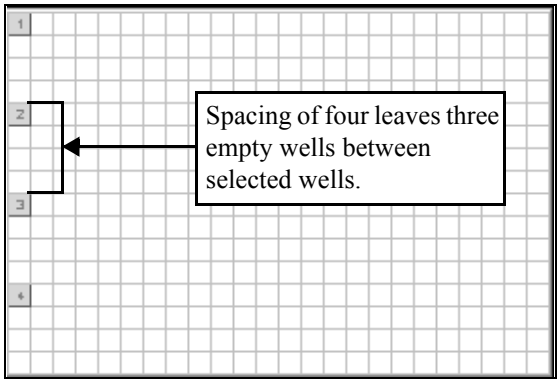


Figure 18-16. Example of how probe and spacing selection affects well selection

Note: To zoom in on the selected labware, double-click on the labware. To call up a menu for Zoom In and a Specify Selection as Text option, right-click on the labware.

Specify Selection as Text allows the selection of the first well in a microplate as a target for the dispense operation. The first selected probe (lowest probe number) dispenses from the specified well. Remaining probes dispense from wells based on the specified well and Spacing. Specify Selection as Text may also be used to enter variables or expressions. Wells are numbered left to right and down (for example, the first row is wells 1-12, the second row wells 13-24, etc., for a 96-well microplate).

9. Enter the **Volume** dispensed to the selected labware. If using a variable or expression, enter an equal sign (=) followed by the variable name or expression; for example, =AspValue. The Volume is dispensed from all selected Probes.
10. To dispense a different volume in each probe, select **Individual Volumes** and choose **Edit**. Individual Volumes appears (Figure 18-17).

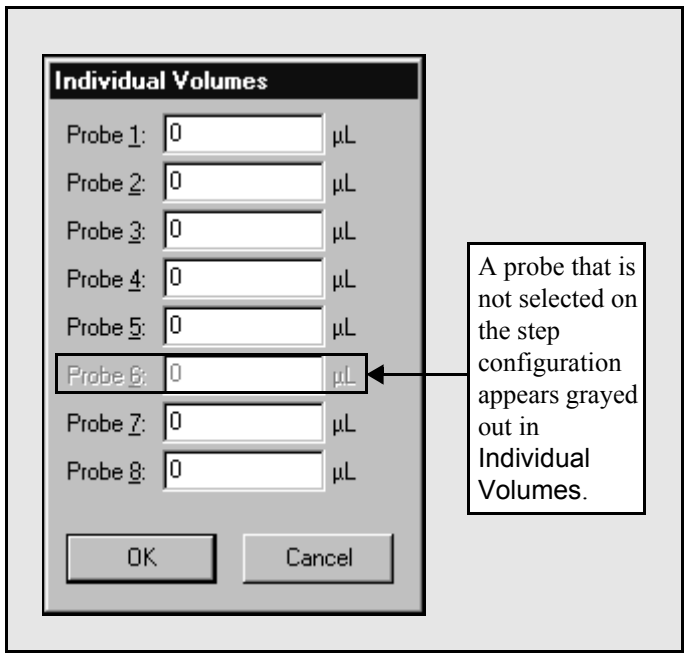


Figure 18-17. Individual Volumes

11. Enter the volume each probe is to dispense in Individual Volumes. If using a variable or expression, enter an equal sign (=) followed by the variable name or expression; for example, =AspValue. A volume may only be entered for the probes that are selected on the Span-8 Dispense step configuration. De-selected probes appear grayed-out in Individual Volumes.
12. Choose **OK**. Individual Volumes closes.

13. The software automatically selects a Technique based on the liquid type, labware type, tip type, and volume being dispensed. To override this selection, deselect **Auto-Select** and select the desired **Technique** (Figure 18-18).

    OR

    Choose **Customize** and configure the technique as desired in the Technique Editor.

Note: For more information on customizing, configuring, and saving a technique, refer to Section 12.3.1, *Understanding Techniques*.

Note: If the technique is auto-selected and the volumes specified differ enough to require different techniques, a dispense is performed for each unique technique.

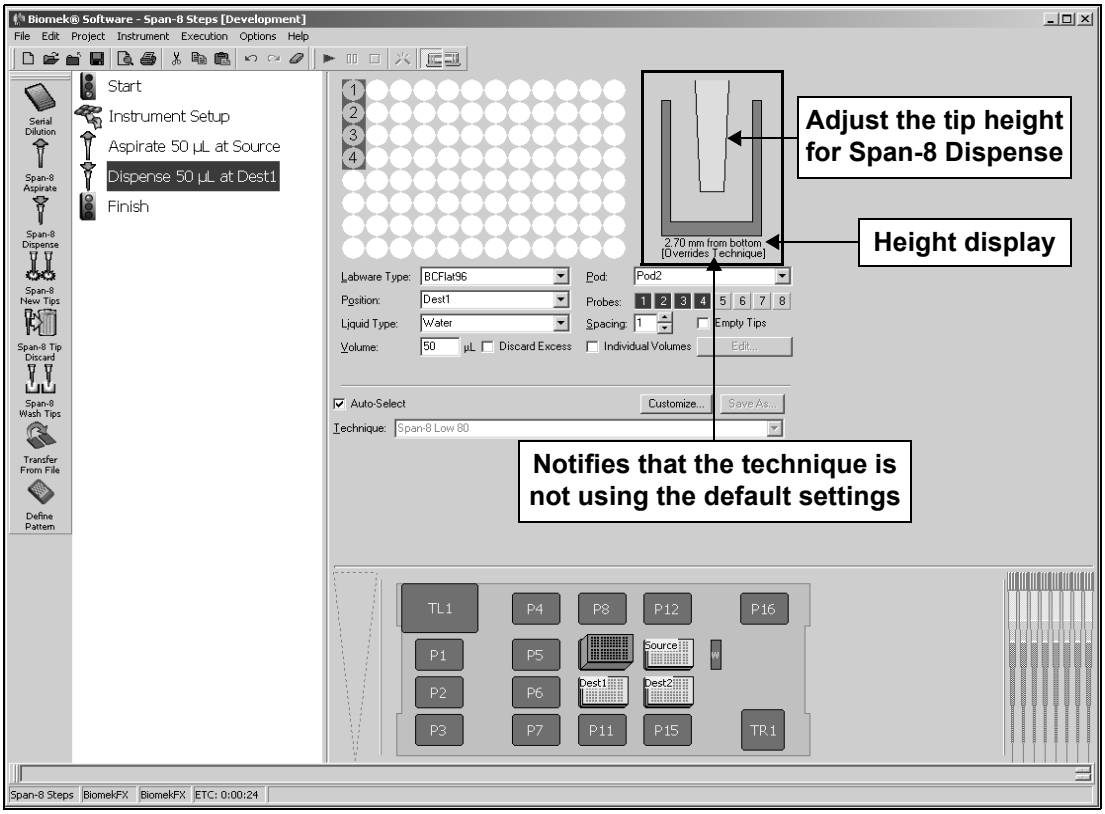


Figure 18-18. Span-8 Dispense step — Adjusting the dispense height

14. Leave the tip height as is to use the settings specified in the pipetting technique.

    OR

    Set the aspirate height manually using one of the following techniques:

    - Set the aspirate height by positioning the cursor over the graphic of a tip inside a well (Figure 18-18). Click and drag the graphic up or down. The tip moves with the cursor, and the height displayed below the graphic is adjusted as the graphic is manipulated.

      Note: The cursor changes to a hand when positioned over the graphic.

    - Position the cursor in the graphic of a tip inside a well, and adjust the height using the ↑ and ↓ keys.
    - Right-click on the graphic of a tip inside a well, and a menu appears. Select **Custom Height**, and Custom Height appears (Figure 18-19). Insert the **Height** in millimeters (mm) and, in **from**, select a reference point from the drop-down list.

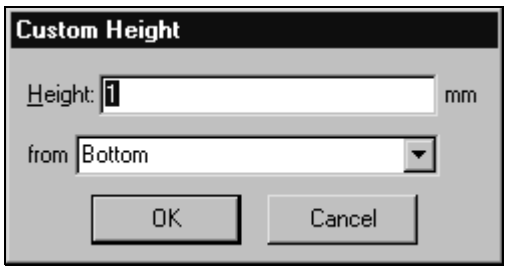


Figure 18-19. Custom Height prompt

Note: The phrase (Overrides Technique) appears below the graphic when the tip height is changed by manipulating the graphic (Figure 18-18), or when the technique is changed with the Customize option.

15. If desired, right-click on the graphic of a tip inside a well and choose how the tip height is measured:
    - **Measure from Liquid** — The tip height is measured from the surface of the liquid in the well.

      Note: With standard tips, Measure from Liquid requires that a known volume of liquid be entered in Labware Properties for the labware to dispense to. If the volume of liquid is not known, liquid level sensing (LLS) tips must be used to measure the tip height from the surface of the liquid in the well.

    - **Measure from Bottom** — The tip height is measured from the bottom of the well.
    - **Measure from Top** — The tip height is measured from the top of the well.
16. Check **Discard Excess** to dispense any excess liquid into the reservoir section of the nearest Span-8 Wash ALP.

    Note: The default setting for Discard Excess is Off.

17. Select a step that occurs after the Span-8 Dispense step or the **Finish** step to validate the step configuration.

18.6 Span-8 New Tips Step

The Span-8 New Tips step instructs the Biomek instrument to load new tips to the Span-8 Pod at a specific point in a method. Tips may also be loaded onto the probes of the Span-8 Pod automatically as part of a Transfer, Combine, or Span-8 Aspirate step. Span-8 New Tips is used when precise tip control is required. Span-8 New Tips is used in conjunction with the Span-8 Discard Tips step (refer to Section 18.7, *Span-8 Tip Discard Step*).

Loading new tips is recommended when:

- Current tips have been used and carryover must be avoided.
- Current tips have manipulated a caustic fluid.
- Current tips are not seated properly.
- Integrity of the current tips is in question.

Insert a **Span-8 New Tips** into the method (Figure 18-20).

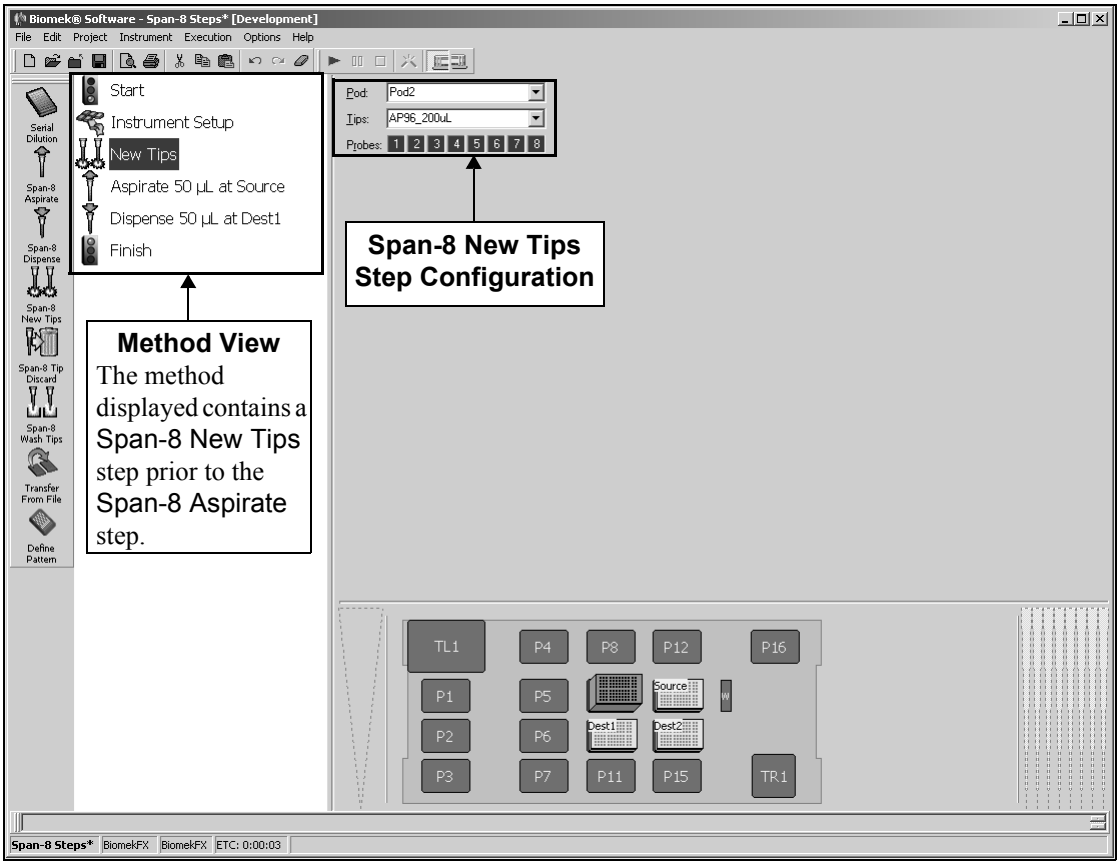


Figure 18-20. Span-8 New Tips step and configuration

18.6.1 Configuring the Span-8 New Tips Step

When a Span-8 New Tips step is added to a method, the Span-8 New Tips Step Configuration appears (Figure 18-20).

To configure Span-8 New Tips:

1. If using a dual-pod ***FX*** instrument, specify the **Pod** requiring new tips by selecting a Span-8 Pod from the list. The pod configured as the default pod is displayed in Pod. If the other pod is desired, select the pod from the drop-down list or the Current Deck Display.
2. Select the **Tips** to load in the Span-8 New Tips step.

   OR

   Select the tip box from the Current Deck Display with the desired tip type. Selecting tips from the Current Deck Display automatically updates Tips in the Step Configuration.

   Note: If tip boxes were assigned names in the Instrument Setup step, enter that name in Tips. If tips were not assigned names, select the tip type. It is recommended that tips not be named in the Instrument Setup step because this could restrict the Span-8 New Tips step from locating available tips.
3. Select the **Probes** that need new tips by highlighting the probe numbers.

   Note: All disposable tips are selected by default. If there are only fixed tips, all tips are selected by default. For example, if the Span-8 Pod is equipped with fixed tips on probes 1-4 and disposable tips on probes 5-8, probes 5-8 will be selected by default. However, if probes 5-8 are also equipped with fixed tips, all eight probes are selected by default.

   Note: Probes equipped with fixed tips cannot have tips loaded.
4. Select a step that occurs after the Span-8 New Tips step or the **Finish** step to validate the step configuration.

18.7 Span-8 Tip Discard Step

The Span-8 Tip Discard step instructs the Biomek instrument to unload tips from a Span-8 Pod at a specific point in a method. Tips may also be discarded from the probes of the Span-8 Pod automatically as part of a Transfer, Combine, or Span-8 Dispense step. Span-8 Tip Discard is used when precise tip control is required. Span-8 Tip Discard is often used in conjunction with the Span-8 New Tips step, but it can be used with any combination of steps.

Span-8 Tip Discard is used when tip integrity is in question or when cross-contamination between labware is a concern. Span-8 Tip Discard can be used in place of the Unload (Tips) option in the Transfer and Combine steps, and is particularly useful with Loop and Worklist steps.

Unloading tips is recommended when:

- Current tips have been used and carryover must be avoided.
- Current tips have manipulated a caustic fluid.
- Current tips are not seated properly.
- Integrity of the current tips is in question.
- To avoid cross-contamination of samples.

Insert a **Span-8 Tip Discard** step into the method (Figure 18-21).

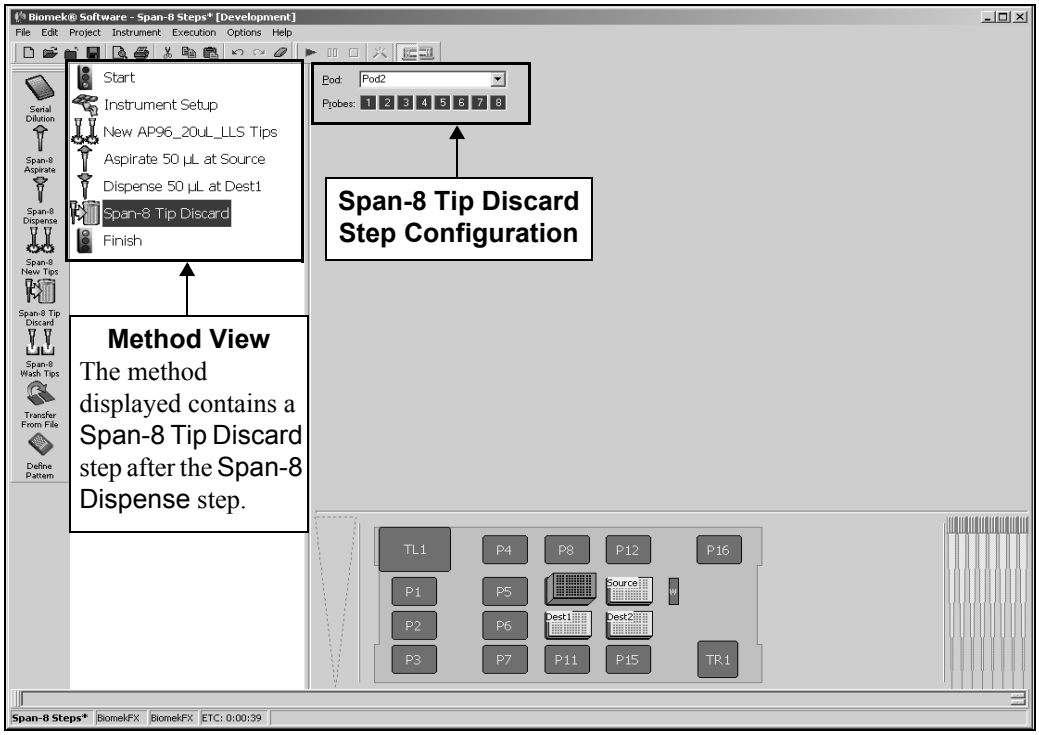


Figure 18-21. Span-8 Tip Discard step and configuration

18.7.1 Configuring the Span-8 Tip Discard Step

When a Span-8 Tip Discard step is added to a method, the Span-8 Tip Discard Step Configuration appears (Figure 18-21).

To configure Span-8 Tip Discard:

1. If using a dual-pod ***FX*** instrument, specify the **Pod** requiring tip removal by selecting a Span-8 Pod from the list. The pod configured as the default pod is displayed in Pod. If the other pod is desired, select the pod from the drop-down list or the Current Deck Display.
2. Select the **Probes** that will discard tips by highlighting the probe numbers.

   Note: All disposable tips are selected by default. If there are only fixed tips, all tips are selected by default. For example, if the Span-8 Pod is equipped with fixed tips on probes 1-4 and disposable tips on probes 5-8, probes 5-8 will be selected by default. However, if probes 5-8 are also equipped with fixed tips, all eight probes are selected by default.

   Note: Probes equipped with fixed tips cannot discard tips.

3. Select a step that occurs after the Span-8 Tip Discard step or the **Finish** step to validate the step configuration.

18.8 Span-8 Wash Tips Step

The Span-8 Wash Tips step flushes fixed tips with system fluid and cleans tips using the Span-8 Tip Wash ALP (refer to the *ALPs User's Manual,* Chapter 18, *Span-8 Tip Wash ALP*), or washes disposable tips by performing multiple aspirate and dispense cycles at a 96-Channel Tip Wash ALP (refer to the *ALPs User's Manual,* Chapter 13, *Multichannel Tip Wash ALPs*). Use the Deck Editor to add and configure the appropriate wash ALP to the deck (refer to Chapter 5, *Preparing and Managing the Deck*).

The Span-8 Wash Tips step can be configured to perform either a passive wash or an active wash. A Passive Wash uses the Span-8 Tip Wash ALP, a Passive ALP, to wash fixed tips. An Active Wash uses a 96-Channel Tip Wash ALP, an Active ALP, to wash disposable or fixed tips.

Note: It is recommended that a Span-8 Wash Tips step be inserted at the start of every method to purge the tubing and syringes of air. If the Span-8 Pod is idle during the method, it may be necessary to insert another Span-8 Wash Tips step into the method immediately before a Span-8 Pod begins to move.

Note: If using a system with mixed fixed and disposable tips, it is necessary to insert separate Span-8 Wash Tips steps to purge each set of four probes used in the method.

The Span-8 Wash Tips Step Configuration includes specifying:

- Pod performing the wash operation.
- Wash station position on the deck.
- Type of wash to perform: Active Wash or Passive Wash.
- Volume of system fluid used in the wash process.
- Technique, liquid type, and number of wash cycles if an Active Wash is chosen.
- Delay before proceeding with method.
- Which probes to wash.

Insert a **Span-8 Wash Tips** step into the method (Figure 18-22).

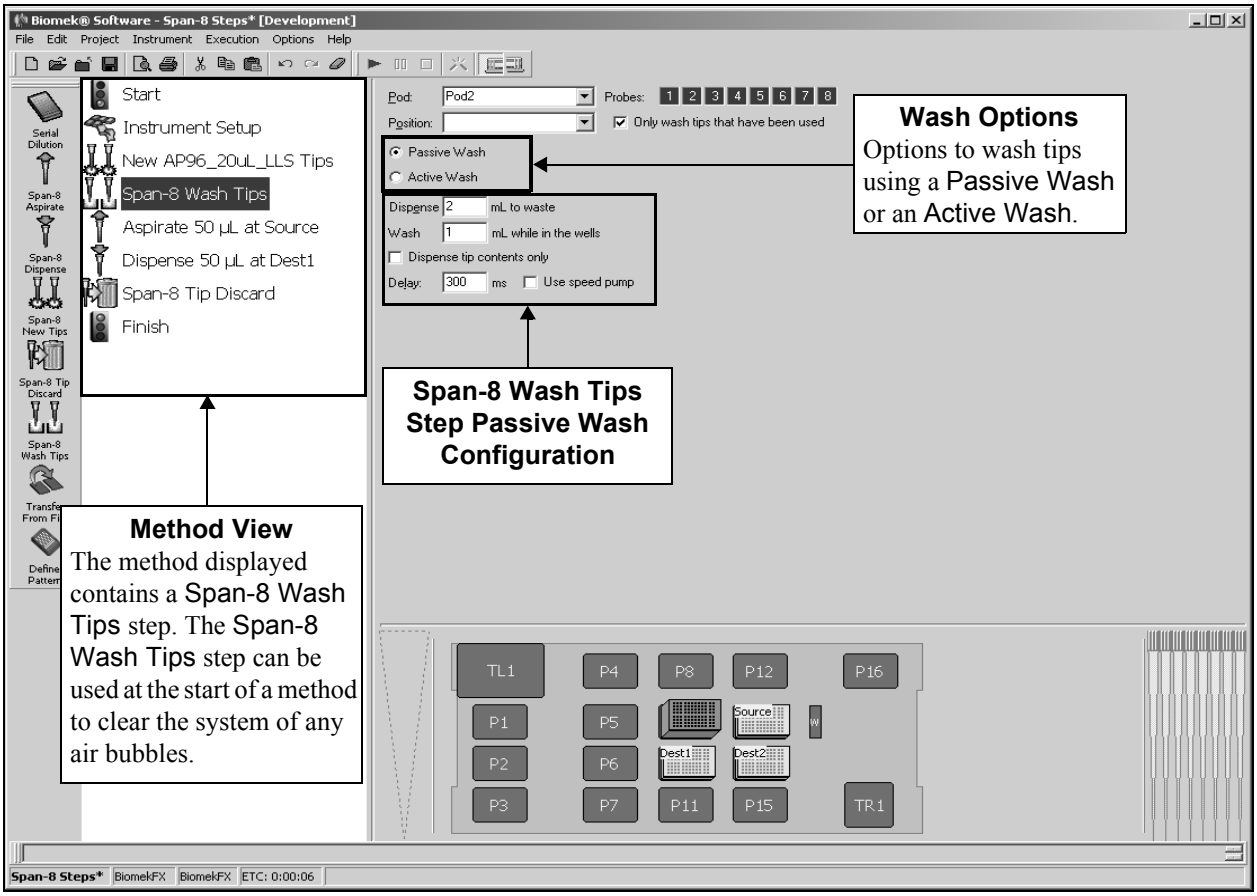


Figure 18-22. Span-8 Wash Tips step — Passive Wash configuration

18.8.1 Configuring the Span-8 Wash Tips Step for a Passive Wash

When a Span-8 Wash Tips step is added to a method, the Span-8 Wash Tips Step Configuration appears (Figure 18-22).

A Passive Wash uses the Span-8 Tip Wash ALP to cleanse fixed tips. To perform a Passive Wash, a Span-8 Tip Wash ALP must be physically on the deck and configured in Instrument Setup (refer to Chapter 4, *Configuring Hardware Setup*) and the Deck Editor (refer to Chapter 5, *Preparing and Managing the Deck*).

The Span-8 Tip Wash ALP has two parts: an open drain for dispensing waste, and eight wells used to clean the tips with system fluid. System fluid washes the inside of the tips and is dispensed through the open drain. Then the tips fit into the wells and the outside of the tips are washed with system fluid.

CAUTION: Do not purge the system without mandrels installed and tubing attached to disposable or fixed tips. Purging the system without the mandrels installed and the tubing attached to tips may cause corrosion in the tip interface.

Note: The Span-8 Wash Tips step Passive Wash can be used at the beginning of a method or during a method in which the Span-8 Pod is idle to purge the tubing and syringes of air rather than using Manual Control.

Note: All disposable tips must be discarded prior to initiating a Span-8 Tip Wash Passive Wash to clean the probes or purge the system.

To configure the Span-8 Wash Tips step for a Passive Wash:

1. If using a dual-pod ***FX*** instrument, specify the **Pod** performing the wash operation by selecting a Span-8 Pod from the list. The pod configured as the default pod is displayed in Pod. If the other pod is desired, select the pod from the drop-down list or the Current Deck Display.
2. Select a **Position** from the drop-down list.

   Note: The Span-8 Wash ALP is added to the deck and configured for use with the Deck Editor (refer to Chapter 5, *Preparing and Managing the Deck*).

   Note: If a wash station is not selected, the closest available wash station is used.
3. Select the **Probes** to wash.

   Note: All disposable tips are selected by default. If there are only fixed tips, all tips are selected by default. For example, if the Span-8 Pod is equipped with fixed tips on probes 1-4 and disposable tips on probes 5-8, probes 5-8 will be selected by default. However, if probes 5-8 are also equipped with fixed tips, all eight probes are selected by default.

   Note: All disposable tips must be discarded prior to initiating a Span-8 Tip Wash Passive Wash to clean the probes or purge the system.
4. Select **Only wash tips that have been used** to automatically wash only the probes have been used. The software determines from the method which probes require washing and washes only those tips.

   Note: When using the Passive Wash to purge the tubing and syringes of air, make sure that Only wash tips that have been used is not selected to flush all probes with system fluid.
5. Select **Passive Wash** to wash the fixed tips using a Span-8 Wash ALP. The Passive Wash configuration appears (Figure 18-22).

   Note: When using the Passive Wash to purge system tubing of air bubbles for probes equipped with disposable tips, make sure that no tips are loaded to the probes.

6. In **Dispense**, enter the volume of system fluid, in milliliters (mL), to use to wash the inside of the tips. The inside of the tips are flushed with the specified volume of system fluid and dispensed into the open drain on the Span-8 Tip Wash ALP.

   Note: When using the Passive Wash to purge the tubing and syringes of air, use approximately 10 to 15 mL of system fluid.

7. In **Wash**, enter the volume of system fluid, in milliliters (mL), to use to wash the outside of the tips. The outside of the tips are washed with the specified volume of system fluid while the tips are positioned in the wells of the Span-8 Tip Wash ALP.

   Note: If Dispense tip contents only is selected, any liquid in the tips is dispensed to the open drain, but the tips are not flushed with system fluid. The Dispense to waste and Wash while in the wells options are unavailable when Dispense tip contents only is selected.

8. In **Delay**, enter the time, in milliseconds (ms), to hold the pod over the Span-8 Wash ALP after each dispense.

   Note: The default Delay is 300 milliseconds (ms).

9. If using a Span-8 Pod on ***FX***, select **Speed Pump** to use the speed pump when flushing the tips with system fluid, if desired.

   OR

   If using a Span-8 Pod on ***NX-S8***, select **purge pump** to use the purge pump when flushing tips with system fluid, if desired.

   Note: The speed pump or purge pump is an optional device that can be used to shorten the time it takes to wash tips. A speed pump or purge pump must be added as a device and configured with the Span-8 Pod in Hardware Setup to use it when washing tips.

10. Select a step that occurs after the Span-8 Wash Tips step or the **Finish** step to validate the step configuration.

18.8.2 Configuring the Span-8 Wash Tips Step for an Active Wash

When a Span-8 Wash Tips step is added to a method, the Span-8 Wash Tips Step Configuration appears (Figure 18-22).

An Active Wash uses the 96-Channel Tip Wash ALP to cleanse disposable or fixed tips. To perform an Active Wash, a 96-Channel Tip Wash ALP must be physically on the deck and configured in Instrument Setup (refer to Chapter 4, *Configuring Hardware Setup*) and the Deck Editor (refer to Chapter 5, *Preparing and Managing the Deck*).

- ***FX*** — In a dual-pod system, the 96-Channel Tip Wash ALP must be located in a deck position accessible by the Span-8 Pod to use Active Wash options.

To configure the Span-8 Wash Tips step for an Active wash:

1. If using a dual-pod ***FX*** instrument, specify the **Pod** performing the wash operation by selecting a Span-8 Pod from the list. The pod configured as the default pod is displayed in Pod. If the other pod is desired, select the pod from the drop-down list or the Current Deck Display.
2. Click on the **Wash Station 96 ALP** in the Current Deck Display. Information for that wash station is entered automatically into the Wash Step Configuration.

   OR

   Select a **Position**.

   Note: The Wash Station 96 ALP is added to the deck and configured for use with the Deck Editor (refer to Chapter 5, *Preparing and Managing the Deck*).

   Note: If a wash station is not selected, the closest available wash station is used.
3. Select the **Probes** to wash.

   Note: All disposable tips are selected by default. If there are only fixed tips, all tips are selected by default. For example, if the Span-8 Pod is equipped with fixed tips on probes 1-4 and disposable tips on probes 5-8, probes 5-8 will be selected by default. However, if probes 5-8 are also equipped with fixed tips, all eight probes are selected by default.
4. Select **Only wash tips that have been used** to automatically wash only the tips that have been used. The software determines from the method which tips require washing and washes only those tips.

5. Select **Active wash** to wash the disposable or fixed tips using a 96-Channel Tip Wash ALP. The Active wash configuration appears (Figure 18-23).

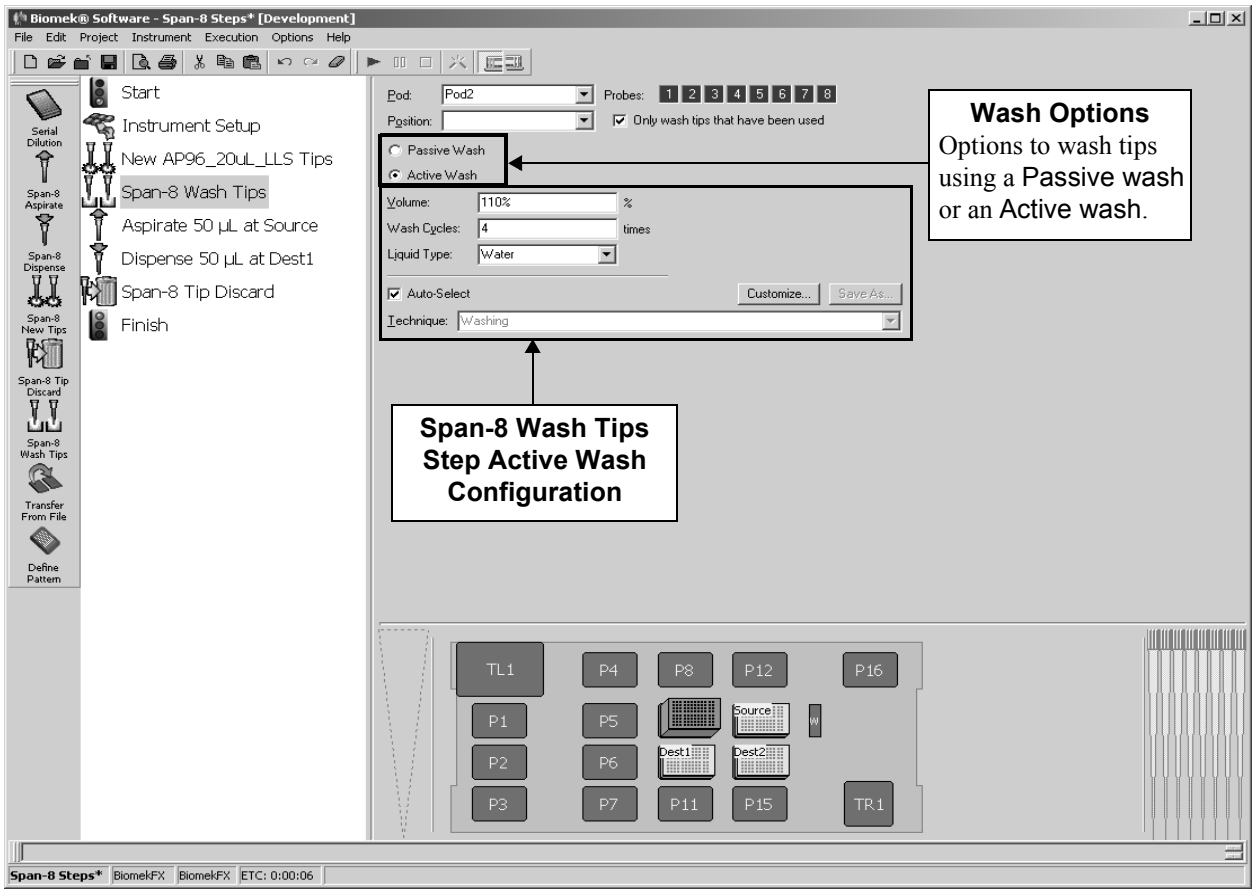


Figure 18-23. Span-8 Wash Tips step — Active Wash configuration

6. Enter the **Volume** of fluid to use when washing the tips.

Note: Enter the volume as a percent (including the percent sign, %) to specify the volume of wash fluid as a percent of the maximum volume of fluid contained in the tips in previous steps. For example, if the maximum volume of fluid transferred is 50 µL, and the % is set for 110%, the Wash step washes the tips with 55 µL of solution. However, if no fluid has been transferred and the volume is entered as a percent, no action is taken and tips are not washed.

7. Specify in Wash Cycles the number of aspirate and dispense operations completed during the wash operation.

8. Verify the **Liquid Type** contained in the selected 96-Channel Tip Wash ALP.

Note: The Liquid Type contained in the 96-Channel Tip Wash ALP is configured in the Instrument Setup step. If the Wash Station is selected from the Current Deck Display, the information is automatically inserted.

9. Select a step that occurs after the Span-8 Wash Tips step or the **Finish** step to validate the step configuration.

18.9 Transfer From File Step (including 3000)

Transfer From File allows a specified volume to be transferred from a specified source well to a specified destination well by reading data from a comma-delimited text file (.txt or .csv). A comma-delimited text file is a text file that specifies the values of a table by separating each column with a comma and each row with a return.

- ***3000*** — Transfer From File may only be used with a single-tip pipette tool.

The Transfer From File configuration specifies:

- Pod that performs the transfer.
- Probes that are used during the transfer.
- Tip handling.
- File properties.
- Source labware.
- Destination labware.
- Transfer details.

Insert a **Transfer From File** step into the Method View. The Transfer From File Step Configuration appears (Figure 18-27).

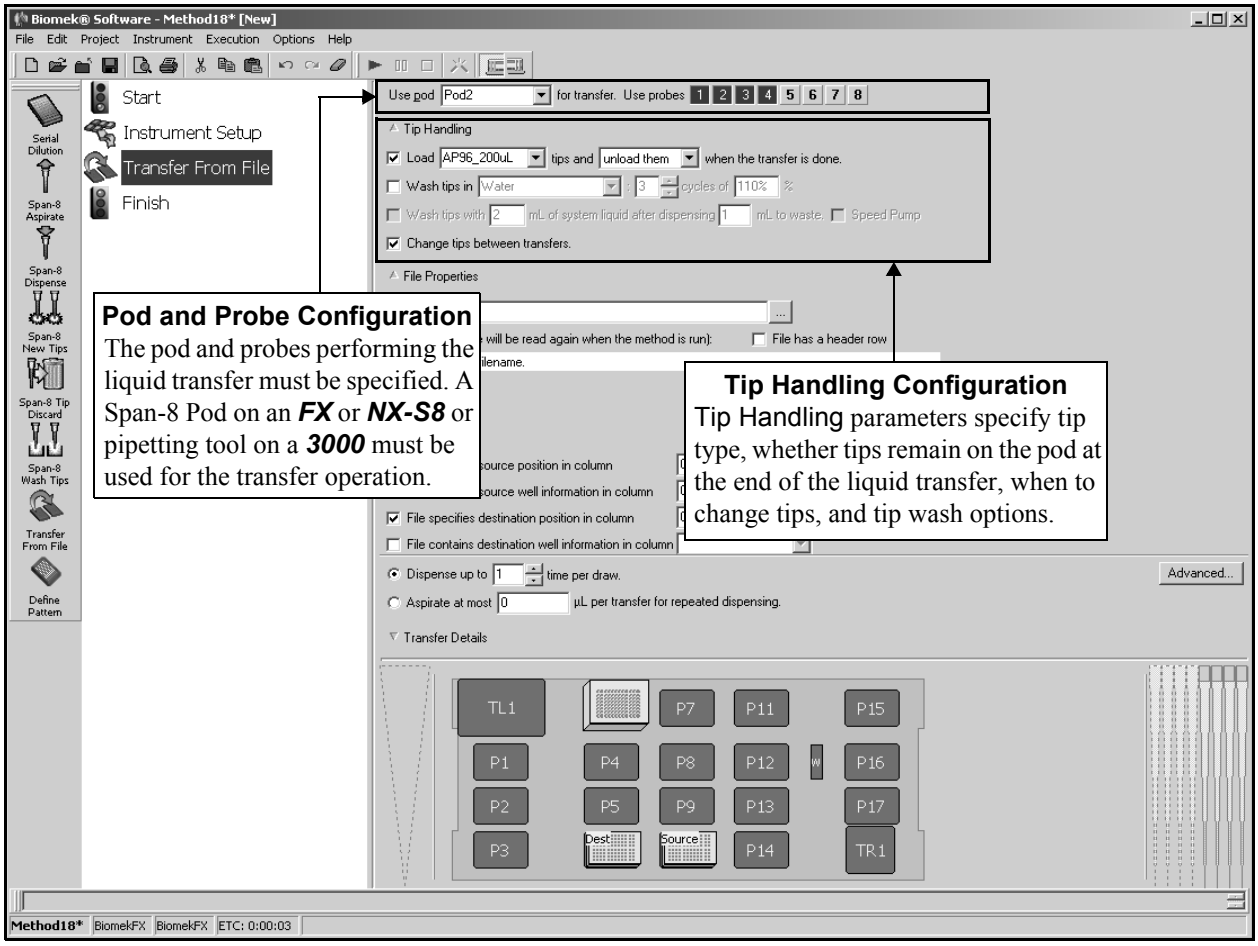


Figure 18-27. Transfer From File step and configuration

18.9.1 Configuring Tip Handling

Configuring Tip Handling in the Transfer From File step is optional, because the Biomek instrument locates and loads clean tips automatically every time a Transfer From File step is initiated. It is recommended, however, that Tip Handling configuration be supplied if cross contamination or conserving consumables is a concern.

Tip Handling is also used to configure washing fixed tips using the Span-8 Wash ALP or disposable tips using the 96-Channel Tip Wash ALP. Refer to Section 18.8, *Span-8 Wash Tips Step*, for more information on washing tips on the Span-8 Pod.

To configure Tip Handling (Figure 18-27) for the Transfer From File step:

1. If using a dual-pod ***FX*** instrument, specify the **Pod** performing the transfer operation. The pod configured as the default pod is displayed in Pod. If the other pod is desired, select the pod from the drop-down list or the Current Deck Display.

   OR

   If using a ***3000***, configure a Load Tool or Change Tool step with a P20 or P200L tool in the method before the Transfer From File.

   Note: Refer to Section 20.3, *Change Tool Step* or Section 20.4, *Load Tool Step* for information about configuring the desired step.

2. If using a Span-8 pod on the ***FX*** or ***NX-S8***, select the probes used in the transfer by clicking the probe numbers in Use Probes. Any combination of probes may be used as long as all selected probes are using the same type of tips and syringes.

   OR

   Right-click any of the probe numbers in **Use Probes** and make a selection from the menu. Options include:

   - Use Disposable Tips — selects all probes with disposable tips.
   - Use Fixed Tips — selects all probes with fixed tips.
   - Use Selection — allows for custom selection.

   Note: Disposable tips are selected by default. If the Span-8 Pod has only fixed tips, all tips are selected by default. For example, if the Span-8 Pod is equipped with fixed tips on probes 1-4 and disposable tips on probes 5-8, probes 5-8 are selected by default. However, if probes 5-8 are also equipped with fixed tips, all eight probes are selected by default.

   Note: If the probes selected are equipped with fixed tips, the Load and unload them/leave them on options (steps 4 and 5) are unavailable and the fixed tips are used for the transfer. Proceed to step 6.

3. If Tip Handling is not already displayed, click the arrow or sentence summary to expand the Tip Handling configuration.

4. Check **Load** and select the type of tips used in the transfer to load tips at the start of the Transfer From File step. If Load is unchecked, the Transfer From File step uses previously loaded tips, rather than loading new tips at the start of the Transfer From File step. Unchecking Load deactivates initial tip loading for the Transfer From File step.

   Note: Tips are selected from the drop-down list, or from the Current Deck Display. If tips are selected via the Current Deck Display, and the tips are named, Load displays the name, not the tip type. If a name was not assigned to the tips, the tip type is displayed in Load.

   It is recommended that tips not be named in the Instrument Setup step, because this could restrict the instrument from locating available tips.

   Note: If Load is checked and the tips loaded on the pod have been used, an error may occur. To increase the number of uses allowed for tips, increase the Load no more than count in the Labware Properties configuration in the Instrument Setup step.

5. To discard tips after the Transfer From File step is completed, select **unload them**.

   OR

   To leave tips on after the Transfer From File step is completed, select **leave them on**.

   Note: The Load and unload them/leave them on fields (steps 4 and 5 above) are useful when multiple Transfer From File steps are used within a method; for example, in the first Transfer From File step, **check Load** and select **leave them on**. In the second Transfer From File step, **uncheck Load** and select **leave them on**. In the third Transfer From File step, **uncheck Load** and select **unload them**. This loads new tips for the first Transfer From File step, uses the same set of tips for all three Transfer From File steps, and unloads the tips when the third Transfer From File step is completed. This is useful when trying to conserve consumables.

6. If using an ***FX*** or ***NX-S8***, choose **Wash tips in** to use the active 96-Channel Tip Wash ALP to wash the tips.

   - ***3000*** — Tip wash options are not available for the Biomek 3000. Proceed to step 14.

   Note: If Wash tips in is not selected, proceed to step 10.

   Note: A WashStation96 ALP must be added to the deck and configured in the Deck Editor before washing can occur. Clicking on a WashStation96 ALP while the Transfer From File step is being configured places a check in Wash tips in, and populates Wash tips in with the solution configured for the WashStation96 ALP in Labware Properties on the Instrument Setup step.

7. In **Wash tips in**, select a solution for the wash cycle if the field does not already contain a solution.

   Note: The wash solution specified in the Transfer From File step must match the solution selected in Labware Properties for the Wash Station ALP on the Instrument Setup step configuration, or an error occurs.

8. Choose the number of cycles to aspirate and dispense during wash.
9. In **%**, provide the volume of wash fluid to use when washing tips as a percentage of the maximum volume of fluid contained in the tips in previous steps; for example, if the maximum volume of fluid transferred is 50 µL, and the % is set for 110%, the Transfer step washes the tips with 55 µL of solution.

   Note: If the % sign is deleted in the % field, the field label changes to µL. Any value entered is now interpreted as a specific volume, not a percentage.

10. If using an ***FX*** or ***NX-S8*** with fixed tips installed, choose **Wash tips with** to use the passive Span-8 Wash ALP to wash fixed tips.

    Note: A Span-8 Wash ALP must be added to the deck and configured in the Deck Editor before washing can occur. Clicking on a Span-8 Wash ALP while the Transfer From File step is being configured places a check in Wash tips with, and uses default values of 2 mL of system liquid after dispensing 1 mL to waste.

    Note: Only fixed tips can be washed with the Span-8 Wash ALP. If using disposable tips or Wash tips with is not selected, proceed to step 14.

11. In **Wash tips with**, enter the volume of system fluid to use when washing the outside of the tips.
12. In **after dispensing**, enter the volume of system fluid to use when washing the inside of the tips.
13. If using a Span-8 Pod on ***FX***, select **Speed Pump** to use the speed pump when flushing the tips with system fluid, if desired.

    OR

    If using a Span-8 Pod on ***NX-S8***, select **purge pump** to use the purge pump when flushing tips with system fluid, if desired.

    Note: The speed pump or purge pump is an optional device that can be used to shorten the time it takes to wash tips. A speed pump or purge pump must be added as a device and configured with the Span-8 Pod in Hardware Setup to use it when washing tips.

14. Select **Change/Wash tips between transfers** to change or wash tips between liquid transfers, if desired.

    Note: If the probes used for transfer are equipped with disposable tips and Wash tips in is not selected, the option to Change tips between transfers is available. If the probes used for transfer are equipped with fixed tips or disposable tips with Wash tips in selected, the option to Wash tips between transfers is available.

The Tip Handling configuration can be collapsed to allow more room during File Properties, Source Labware, and Destination Labware configuration. When collapsed, the Tip Handling configuration is displayed as a sentence summary (Figure 18-28). Use the sentence summary to verify that Tip Handling has been configured appropriately.

To collapse or expand the Tip Handling configuration, click the arrow to the left of Tip Handling or the textual display (Figure 18-28).

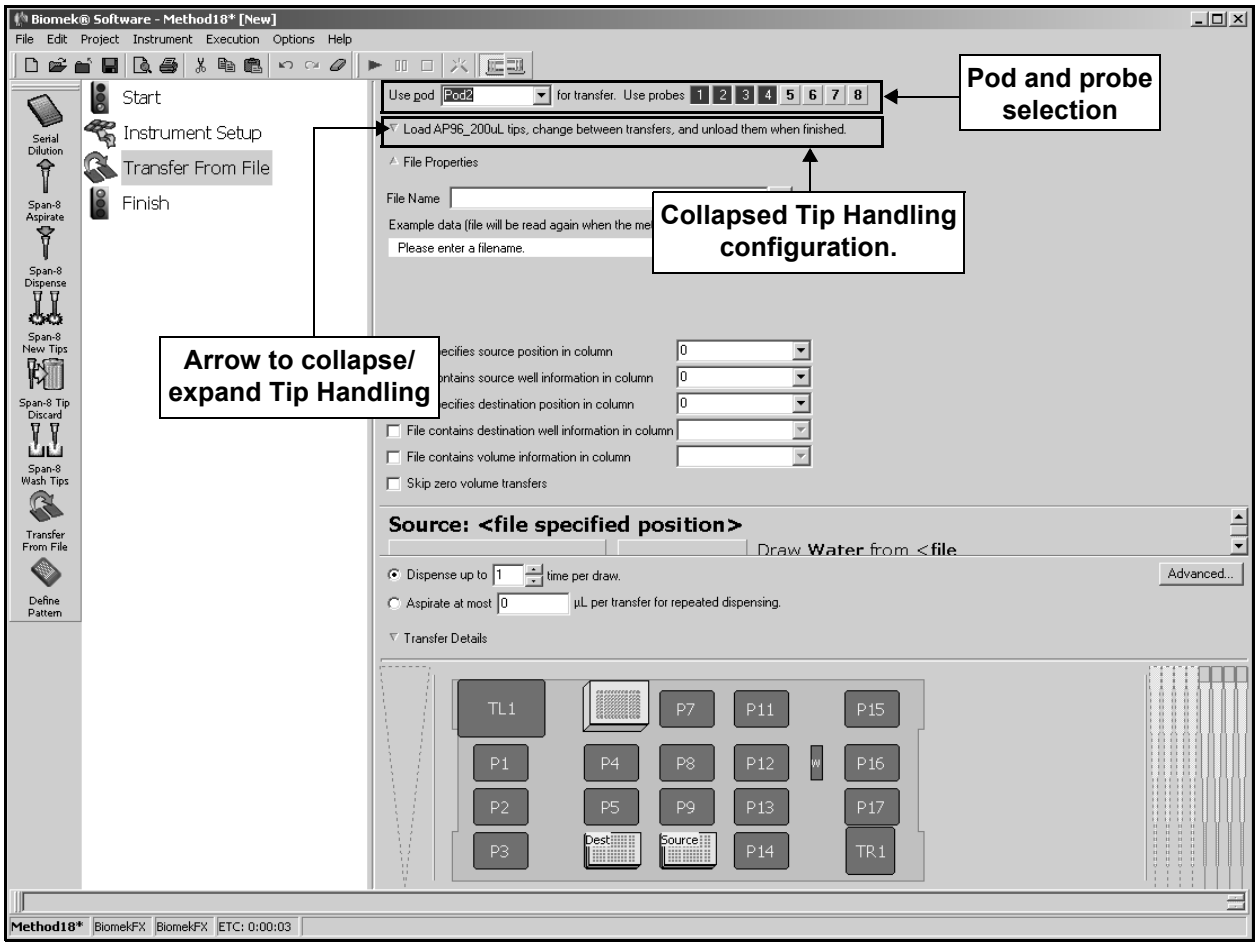


Figure 18-28. Transfer From File step — Tip Handling collapsed

18.9.2 Configuring File Properties

Transfer From File uses a comma-separated value file to configure parts of the transfer operation. The File Properties configuration is needed to specify the file to use and which columns indicate what information.

The file must contain at least information on source wells accessed, but may also specify the position on deck or name of source labware, position on deck or name of destination labware, destination wells accessed, and volume transferred. If all information is specified by the data file, each row is a single well-to-well transfer.

To configure File Properties for the Transfer From File step:

1. If File Properties is not already displayed, click the arrow or textual display to expand the File Properties configuration (Figure 18-29).

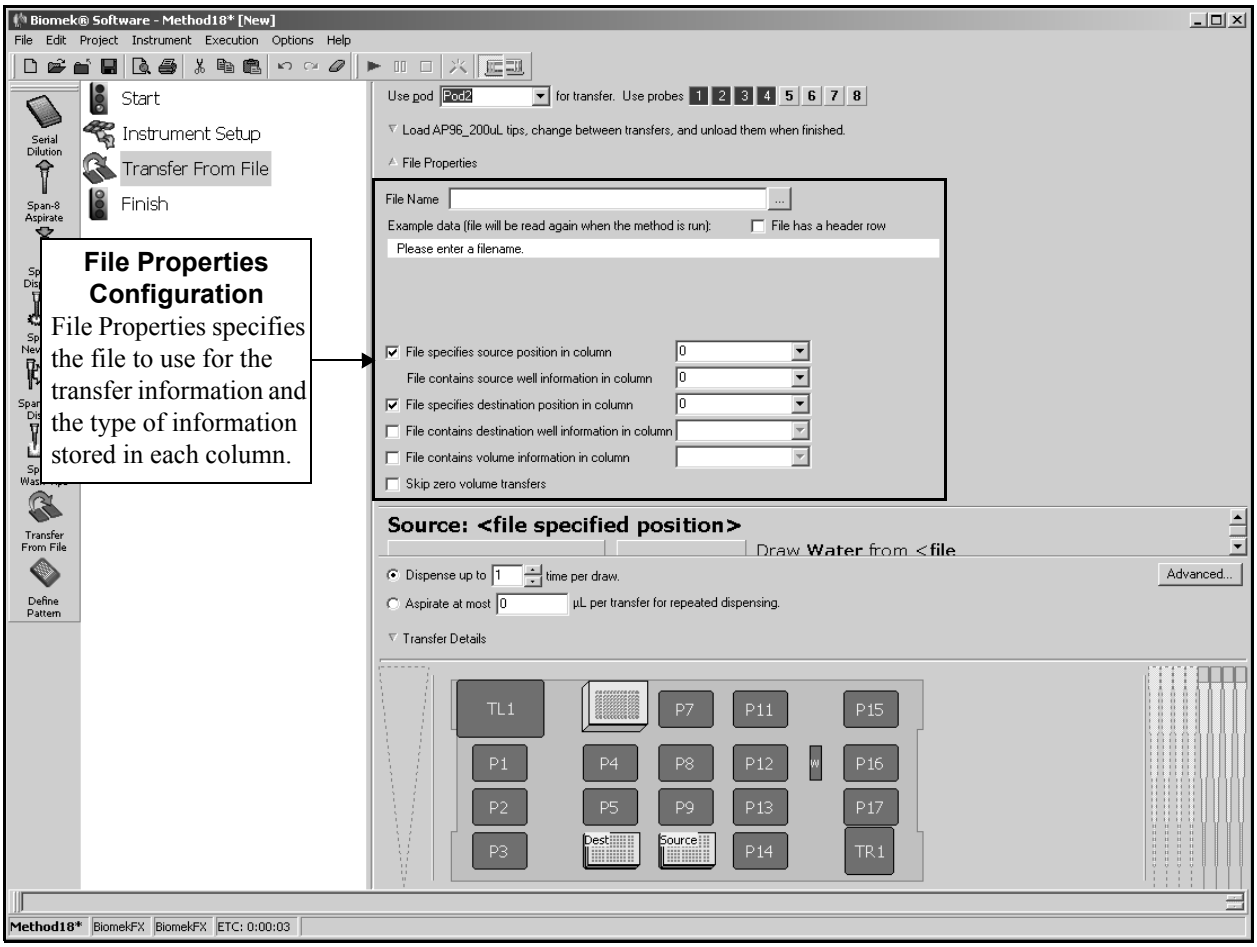


Figure 18-29. Transfer From File — File Properties

2. In **File Name**, enter the full path and file name of the data file from which to read the transfer information.

   OR

   Choose the browse button next to File Name and select the directory and file from which to read the transfer information in Open (Figure 18-30). The selected file is read and Example data is displayed (Figure 18-31).

Note: The data file must be a comma-delimited text file (.txt or .csv).

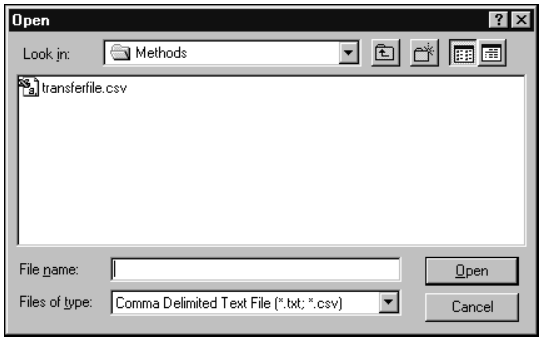


Figure 18-30. Open dialog

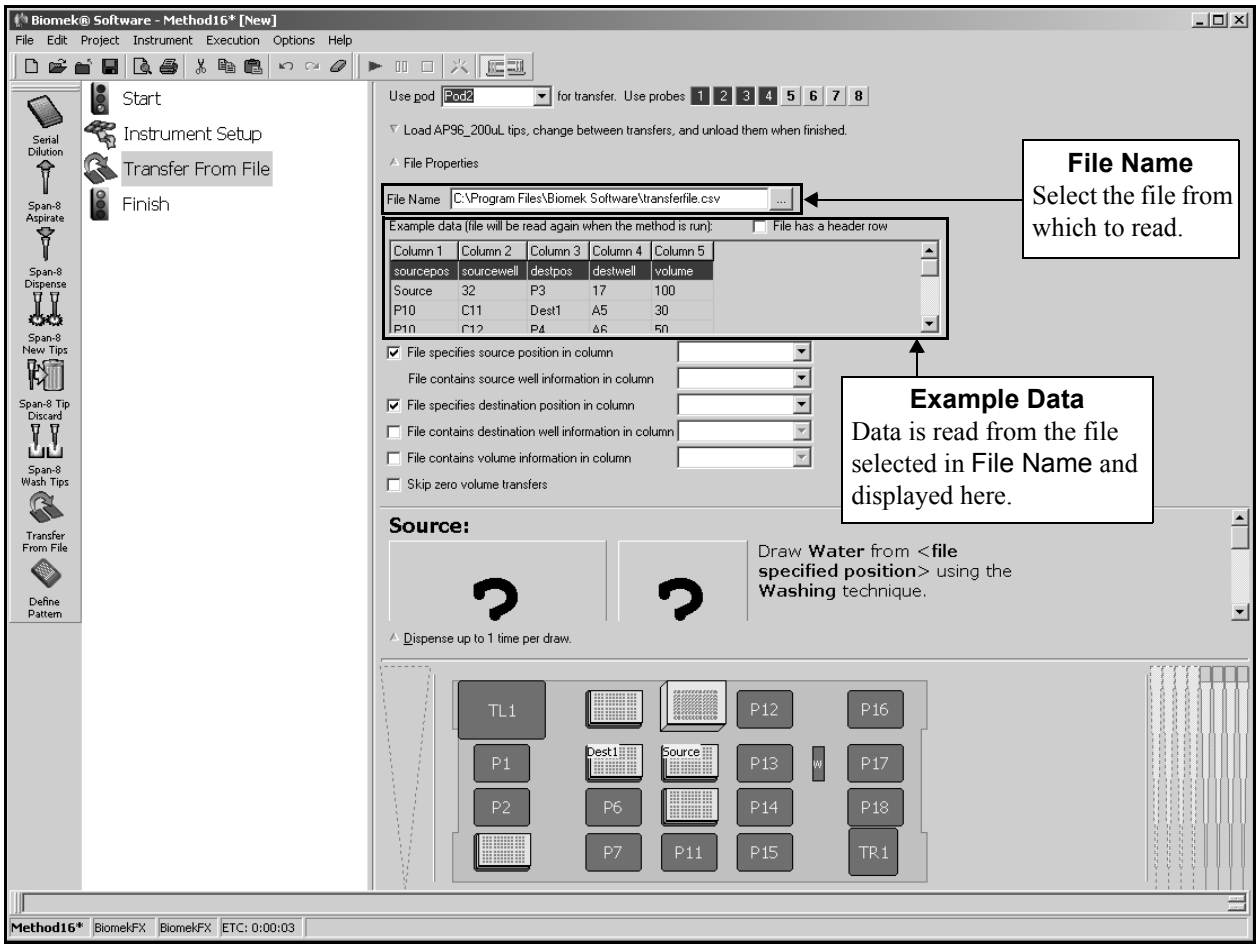


Figure 18-31. Transfer From File — Example data displayed

3. If the file read has a header row identifying the columns, select **File has a header row**. The first row of the data file is used to identify the columns (Figure 18-32).

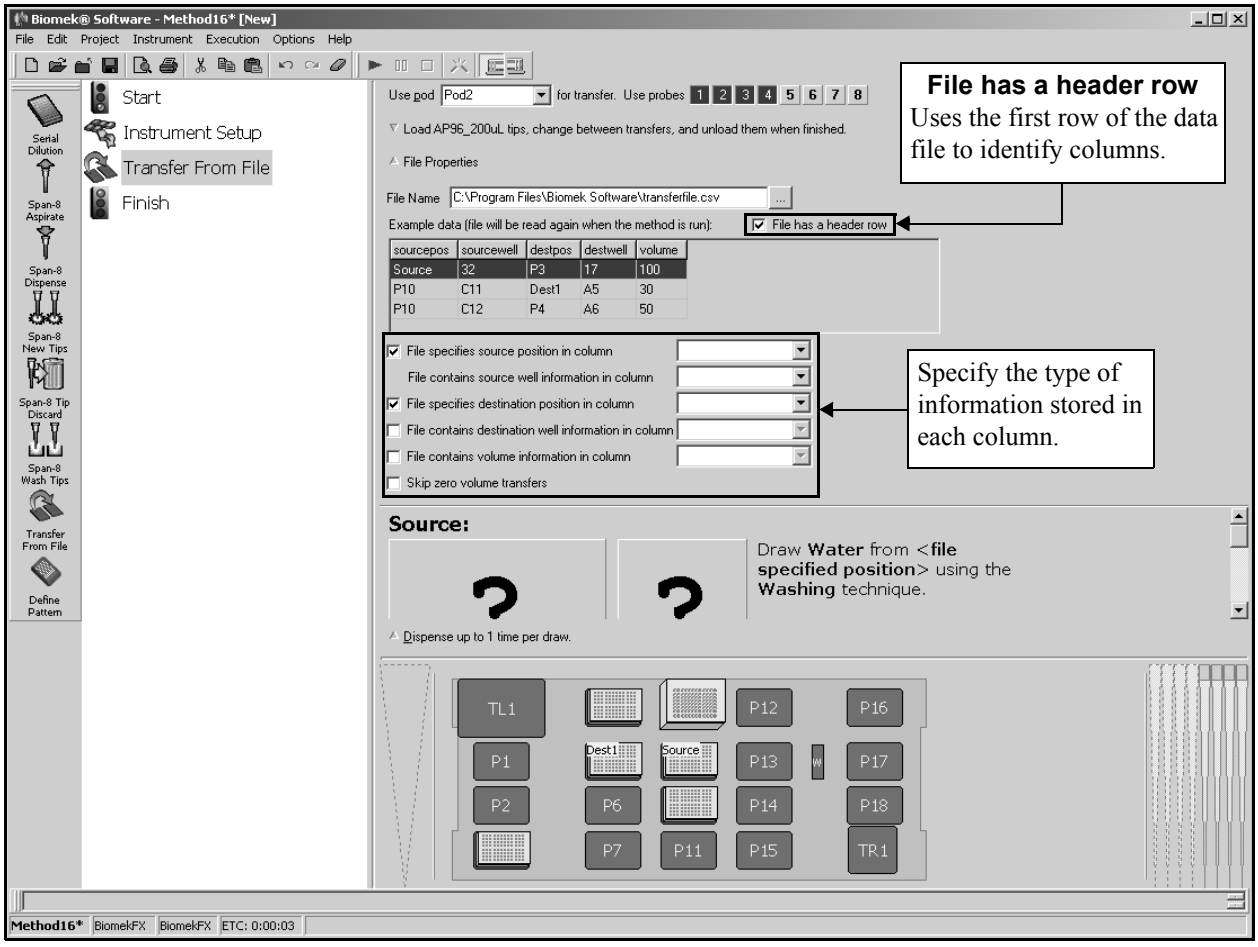


Figure 18-32. Transfer From File — Example data with header row

4. Select **File specifies source position in column** if a column of the data file stores information about the position of source labware and select the desired column from the list.

Note: The source position column may contain either deck positions (P4, P7, etc.) or labware names (Source1, Dest1, etc.). If information is stored as labware names, there must be labware on the deck with the specified labware name (Figure 18-32).

5. In **File contains source well information in column**, select the column of the data file that stores information about source wells from which to transfer from the list.

Note: The source well column may specify wells with either alphanumeric well addresses (A1-H12 for a 96-well plate) or numeric well numbers (1-96 on a 96-well plate). The same data file may contain both alphanumeric and numeric well information (Figure 18-32).

6. Select **File specifies destination position in column** if a column of the data file stores information about the position of destination labware and select the desired column from the list.

   Note: The destination position column may contain either deck positions (P4, P7, etc.) or labware names (Source1, Dest1, etc.). If information is stored as labware names, there must be labware on the deck with the specified labware name (Figure 18-32).

7. Select **File contains destination well information in column** if a column of the data file stores information about destination wells to which to transfer and select the desired column from the list.

   Note: The destination well column may specify wells with either alphanumeric well addresses (A1-H12 for a 96-well plate) or numeric well numbers (1-96 on a 96-well plate). The same data file may contain both alphanumeric and numeric well information.

8. Select **File contains volume information in column** if a column of the data file stores information about the volume to transfer and select the desired column from the list.

   Note: All volumes are specified in microliters (µL).

9. Select **Skip zero volume transfers** to ignore any rows that specify a volume of 0 when performing the Transfer From File step.

The File Properties configuration can be collapsed to allow more room during Source Labware and Destination Labware configuration. When collapsed, the File Properties configuration is displayed as text.

To collapse or expand the File Properties configuration, click the arrow to the left of File Properties or the textual display.

18.9.3 Configuring Source Labware

A ‘source’ is a group of wells accessed at one time by the Biomek instrument to aspirate liquid; for example:

- ***FX, NX-S8***— A Span-8 Pod aspirates from one to eight wells at a time, depending on the selected probes.
- ***3000*** — Using a single-tip pipette tool, aspirates from a single well at a time.

The Transfer From File step configures multiple aspirate and dispense operations using the selected probes to transfer all source wells to the destination labware.

The Source Labware configuration for the Transfer From File step includes choosing:

- the labware type
- the labware location, if not specified by the file
- the liquid type
- the technique
- the pipetting height

Note: Only one piece of Source Labware is configured, because the Transfer From File step moves liquid from a single source to one or more destinations. However, if the source position is specified by the file, multiple sources are accessed for the transfer, but all sources are configured by a single source configuration.

To configure Source Labware for the Transfer From File step:

1. Click on the **Source** configuration area to activate it (Figure 18-33).

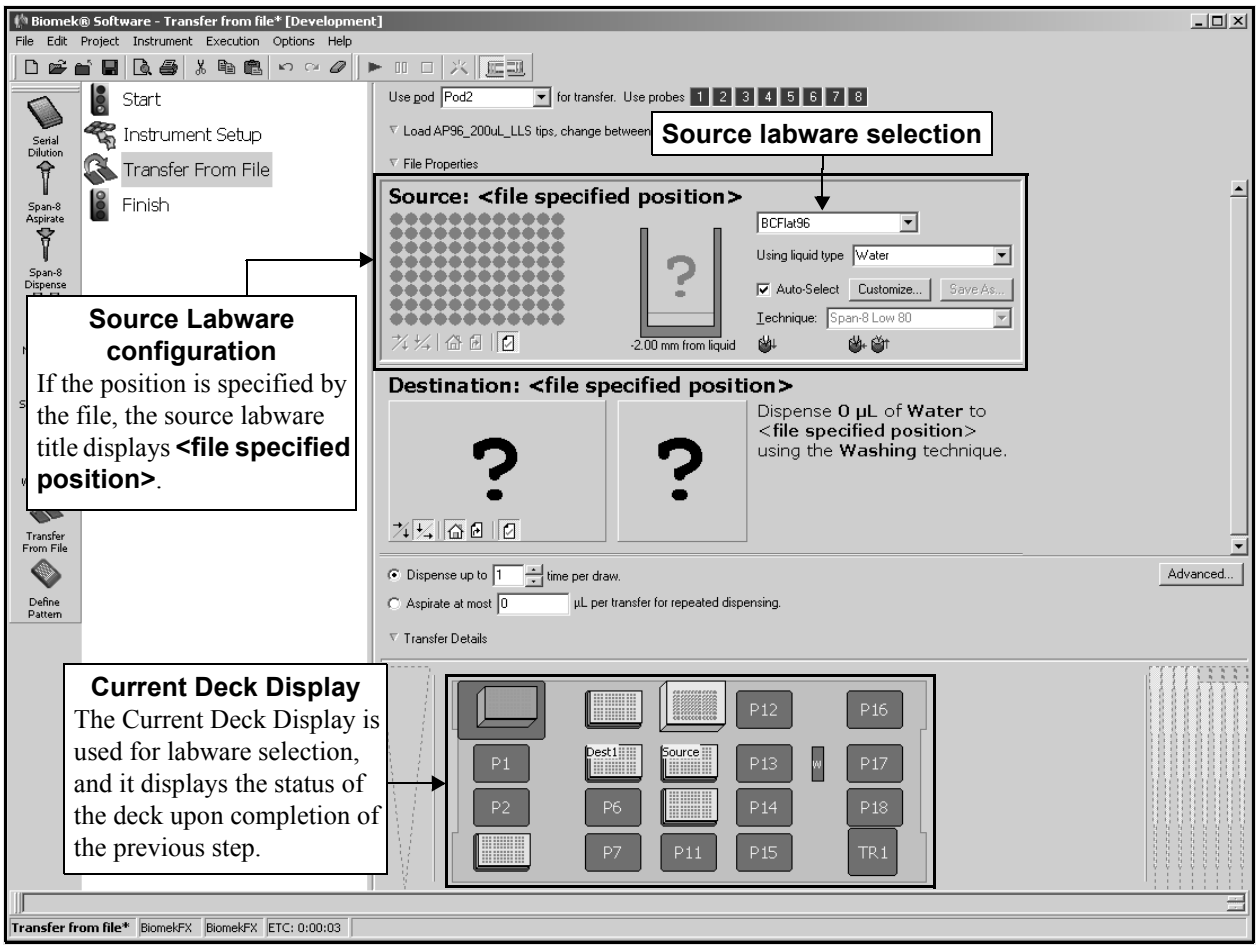


Figure 18-33. Transfer From File step — Source Labware selection

2. If the source position is not specified by the file, click on the desired piece of labware in the Current Deck Display (Figure 18-33). Information for that piece of labware is entered automatically into the Source Labware configuration.

   OR

   If the source position is specified by the data file, select the labware type of the source labware. All sources must use the same labware type.

Note: Reservoirs may not be used as Source Labware.

Note: Once Source Labware has been selected, any subsequent selections become Destination Labware. If an incorrect piece of labware is selected, **right-click on the labware title** and select **Delete** on the menu that appears. If the Source Labware is incorrect, activate the Source Labware configuration by clicking anywhere in the source labware configuration area, and select another piece of labware.

3. Verify the deck position of the labware, if not specified by the data file.

Note: A bright blue outline appears in the Current Deck Display around the labware designated as the Source Labware.

4. In **Using liquid type**, select the type of liquid in the Source Labware (Figure 18-34).

Note: The default liquid type is the liquid type specified as the default in the Liquid Type Editor.

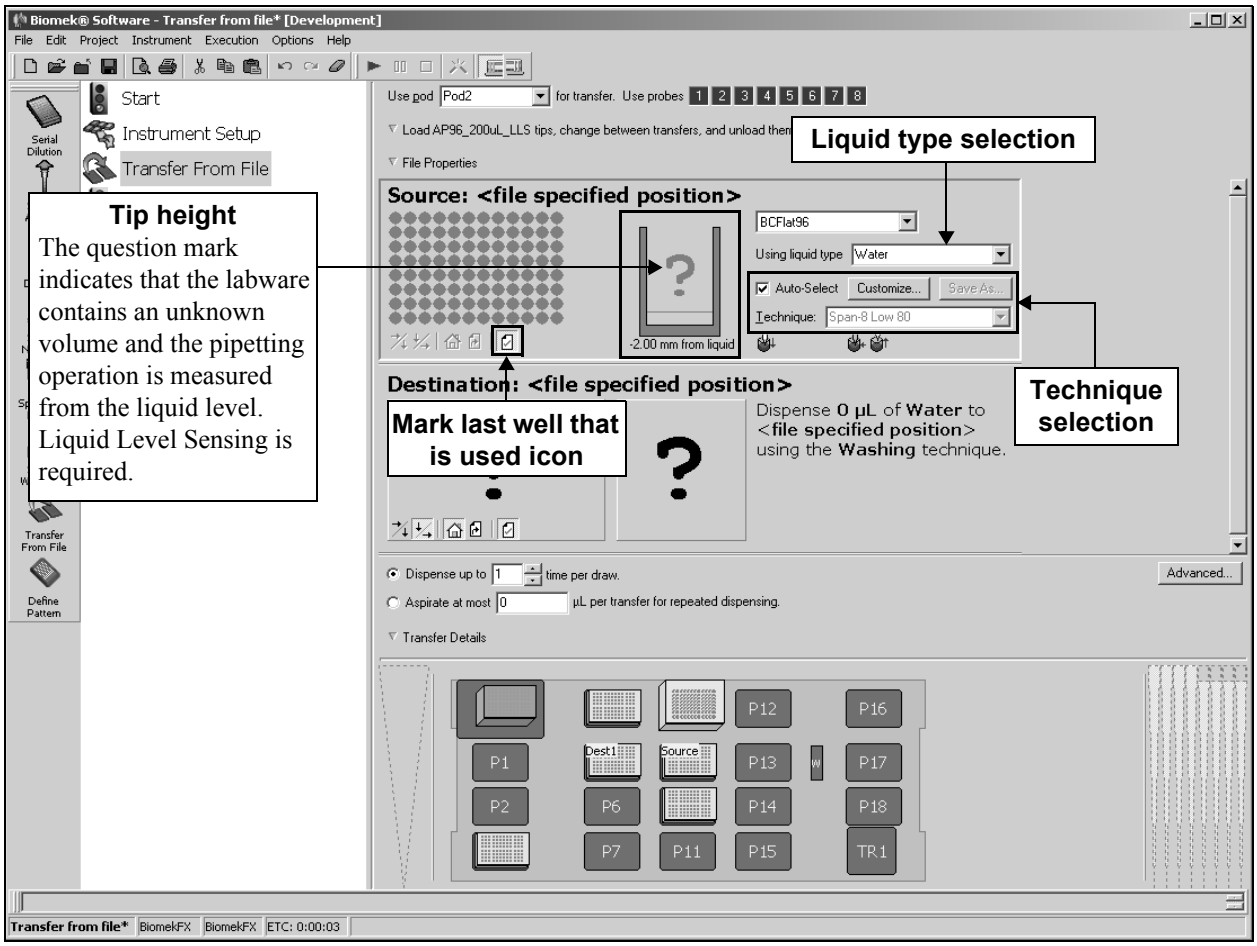


Figure 18-34. Transfer From File step — Source Labware configuration

5. De-select **Mark last well that is used**, if it is not desired to mark wells. This option must be selected to use any options later in the method that make use of marks. For example, if Mark last well that is used is selected and the Transfer From File step runs out of sources before using all destinations, it will mark the last well that had liquid transferred to it. Another Transfer From File step is transferring liquid to the same plate. By selecting **After last marked well** as the Start condition, the first source well will be transferred to the first unused destination well.

Note: Mark last well that is used can also be selected when the labware is zoomed out by using the Set mark button beneath the labware.

Note: Mark last well that is used is selected by default.

6. Keep the auto-selected **Technique** (refer to Section 15.3.2.1, *Auto-Selection of a Technique*).

   Note: The software automatically selects a Technique based on the liquid type, labware type, tip type, and volume being aspirated.

   OR

   Manually select the desired **Technique**, or customize the selected Technique (refer to Section 15.3.2.2, *Customizing and Saving a Technique*).

7. Leave the height as is to use the settings specified in the pipetting technique.

   OR

   Set the aspirate height manually using one of the following techniques:

   - Set the aspirate height by positioning the cursor over the graphic of a tip inside a well. Click and drag the graphic up or down. The tip moves with the cursor, and the height displayed below the graphic is adjusted as the graphic is manipulated.

     Note: The cursor changes to a hand when positioned over the graphic.

   - Position the cursor in the graphic of a tip inside a well, and adjust the height using the ↑ and ↓ keys.
   - Right-click on the graphic of a tip inside a well, and a menu appears. Select **Custom Height**, and Custom Height appears (Figure 18-35). Insert the **Height** in millimeters (mm) and, in **from**, select a reference point from the drop-down list.

Note: The phrase (Overrides Technique) appears below the graphic when the tip height is changed by manipulating the graphic, or when the technique is changed with the Customize option.

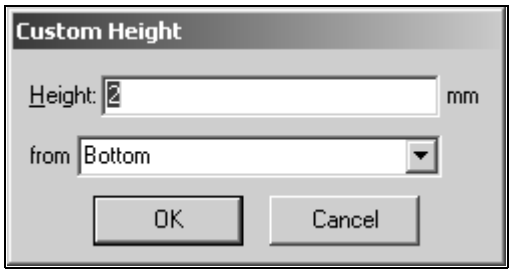


Figure 18-35. Custom Height prompt

18.9.4 Configuring Destination Labware

A ‘destination’ is a group of wells accessed at one time by the Biomek instrument to dispense liquid; for example:

- ***FX, NX-S8*** — A Span-8 Pod dispenses to one to eight wells at a time, depending on the selected probes.
- ***3000*** — Using a single-tip pipette tool, dispenses to a single well at a time.

The Transfer From File step configures multiple aspirate and dispense operations using the selected probes to transfer all source wells to the destination labware when using the Span-8 Pod.

The Destination Labware configuration includes choosing:

- the labware type
- the labware location, if not specified in the data file
- the wells on labware used, if not specified in the data file
- the liquid amount to transfer, if not specified in the data file
- the liquid type
- the technique
- the pipetting height

Note: Multiple pieces of Destination Labware can be configured for the Transfer From File step, because the Transfer step can move liquid from a single source to one or more destinations. However, if the destination position is specified in the data file, all destinations are configured by a single destination configuration.

To configure Destination Labware for the Transfer From File step:

1. If the destination position is not specified by the data file, click on the desired piece of labware in the Current Deck Display. Information for that piece of labware is entered automatically into the Destination Labware configuration.

   OR

   If the destination position is specified by the data file, select the **Destination Labware** type of the destination labware. All destinations must use the same labware type.

   Note: Once the first Destination Labware has been selected, the Source Labware parameters are collapsed to display a sentence summary. To reopen the Source labware parameters, click anywhere in the Source Labware configuration area.

   Note: Subsequent labware selections modify the active Source or Destination Labware configuration. To configure additional Destination Labware, select **Click here to add a destination**, or select outside a labware configuration, and then select another piece of labware from the Current Deck Display. If an incorrect piece of labware is selected, right-click on the labware title and select **Delete** on the menu that appears.

   If either the destination position or destination wells are specified by the data file, additional destinations cannot be configured.

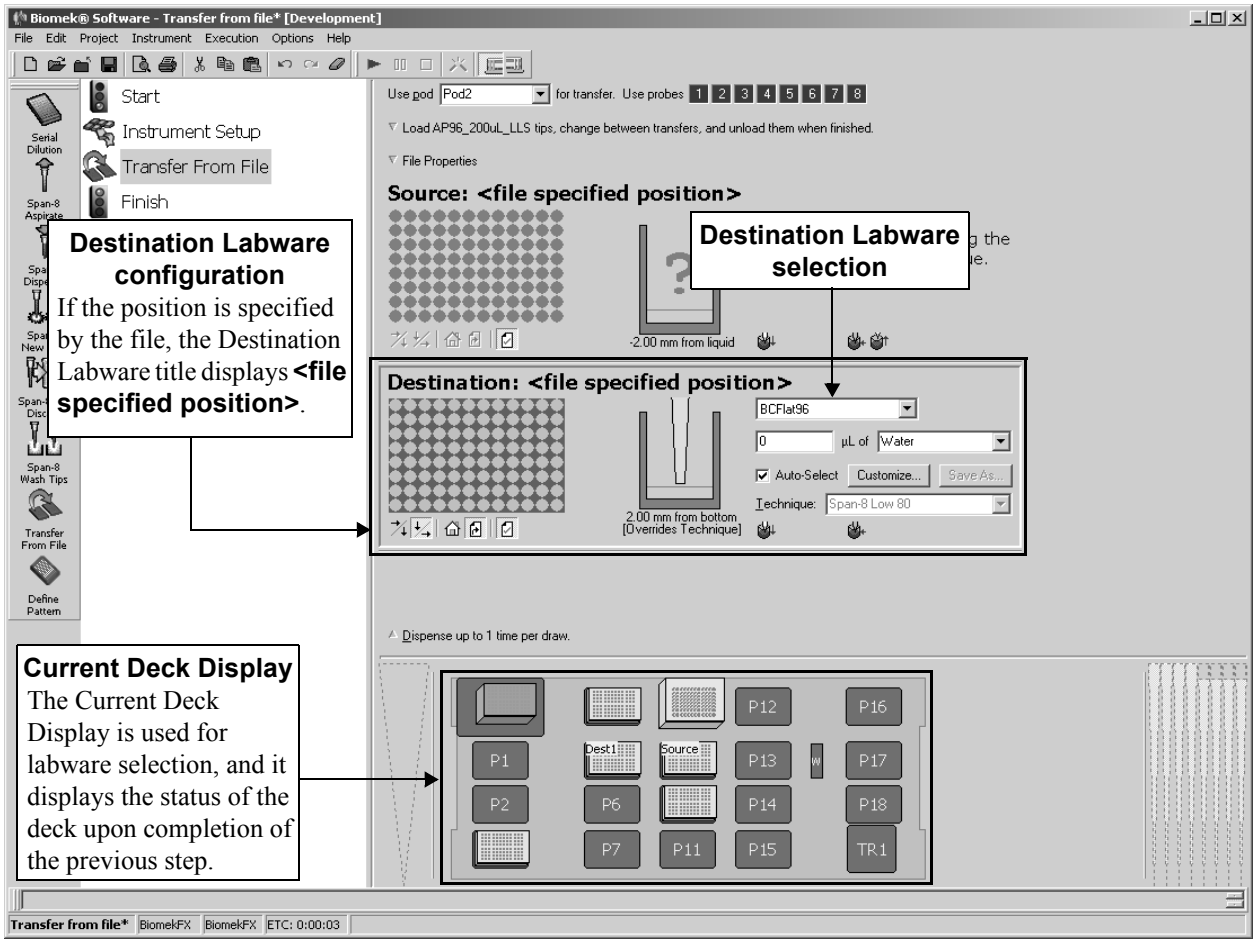


Figure 18-36. Transfer From File step — Destination Labware selection

2. Verify the deck position of the labware, if not specified by the data file.

Note: A bright yellow outline appears in the Current Deck Display around the labware designated as the Destination Labware.

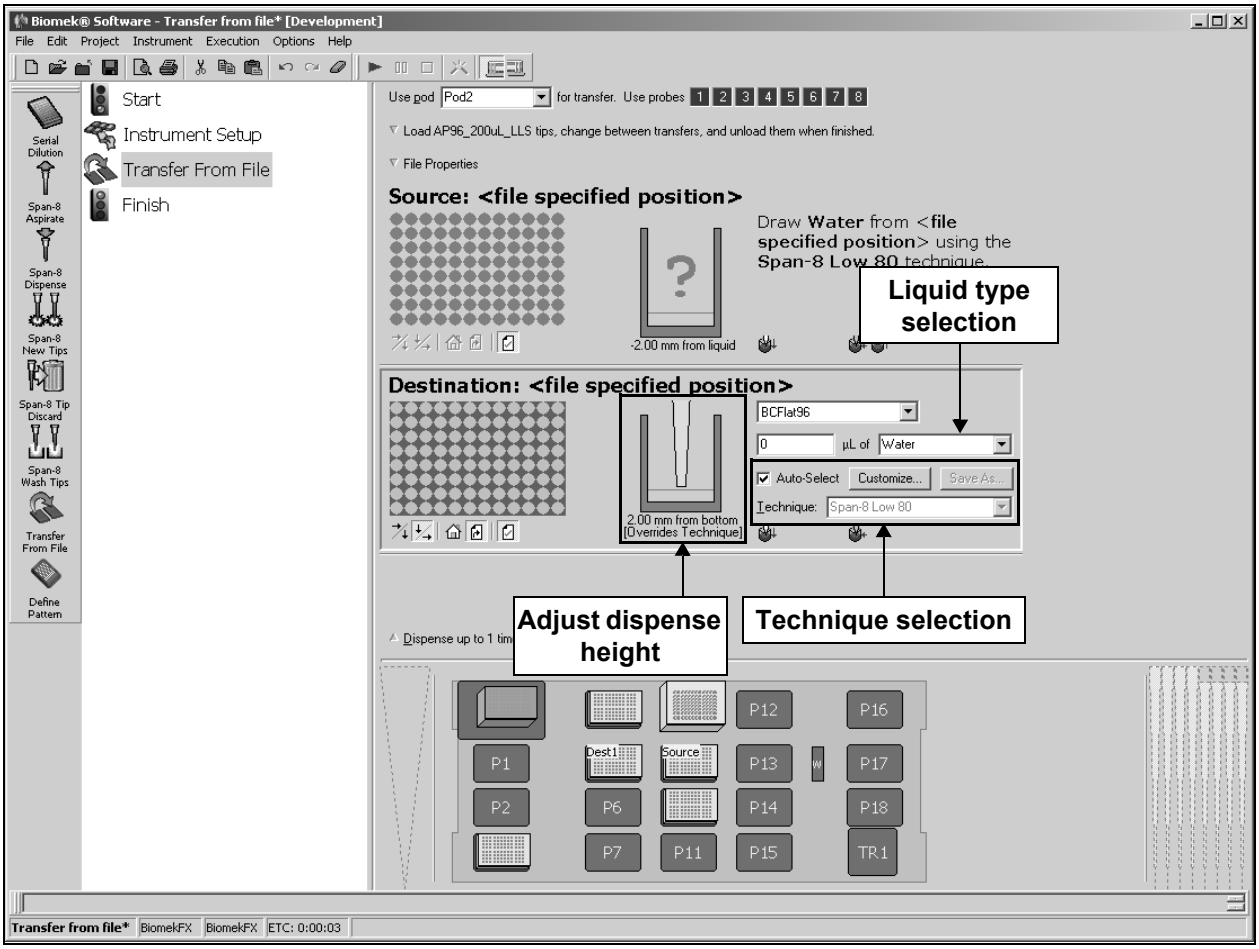


Figure 18-37. Transfer From File step — Destination Labware configuration

3. Enter the amount of liquid (µL) dispensed into the Destination Labware, if not specified by the data file. If using a variable or expression, enter an equal sign (=) followed by the variable name or expression; for example, **=AspValue** (Figure 18-37).
4. Verify that the liquid type indicated is correct. The liquid type dispensed to the Destination Labware should match the liquid type in the Source Labware configuration.
5. Deselect **Mark last well that is used**, if it is not desired to mark wells. This option must be selected to use any options later in the method that make use of marks. For example, if Mark last well that is used is selected and the Transfer From File step runs out of sources before using all destinations, it will mark the last well that had liquid transferred to it. Another Transfer From File step is transferring liquid to the same plate. By selecting **After last marked well** as the Start condition, the first source well will be transferred to the first unused destination well. Mark last well that is used is selected by default.

Note: Mark last well that is used can also be selected when the labware is zoomed out by using the Set mark button beneath the labware.

6. Keep the auto-selected **Technique** (refer to Section 15.3.2.1, *Auto-Selection of a Technique*).

   Note: The software automatically selects a Technique based on the liquid type, labware type, tip type, and volume being aspirated.

   OR

   Manually select the desired **Technique**, or customize the selected Technique (refer to Section 15.3.2.2, *Customizing and Saving a Technique*).

7. Leave the height as is to use the settings specified in the pipetting technique.

   OR

   Set the dispense height manually using one of the following techniques:

   - Set the dispense height by positioning the cursor over the graphic of a tip inside a well. Click and drag the graphic up or down. The tip moves with the cursor, and the height displayed below the graphic is adjusted as the graphic is manipulated.

     Note: The cursor changes to a hand when positioned over the graphic.

   - Position the cursor in the graphic of a tip inside a well, and adjust the height using the ↑ and ↓ keys.
   - Right-click on the graphic of a tip inside a well, and a menu appears. Select **Custom Height**, and Custom Height appears (Figure 18-35). Insert the **Height** in millimeters (mm) and, in **from**, select a reference point from the drop-down list.

   Note: The phrase (Overrides Technique) appears below the graphic when the tip height is changed by manipulating the graphic, or when the technique is changed with the Customize option.

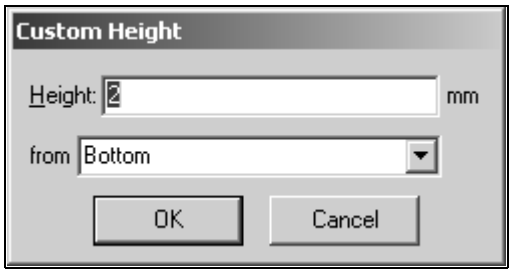


Figure 18-38. Custom Height prompt

8. If destination wells are not specified by the data file, go to Section 18.9.4.1, *Configuring Destination Wells*.
9. Repeat steps 1-8 for each additional piece of Destination Labware if neither destination positions nor destination wells are specified by the data file.

18.9.4.1 Configuring Destination Wells

If destination wells were not specified by the data file, further configuration of the destination labware is required.

To complete the Destination Labware configuration:

1. Double-click the Destination Labware graphic in the step configuration to zoom in on the labware.

   Note: To call up a menu for Zoom In and a Specify Selection as Text option, right-click on the labware.

   Specify Selection as Text allows the selection of wells in a microplate as targets for the transfer operation as comma-delimited text. Wells are numbered left to right and down (for example, the first row is wells 1-12, the second row wells 13-24, etc., for a 96-well plate). Specify Selection as Text may also be used to enter variables or expressions.

2. Select the wells that are destinations for the transfer using one of the following techniques:

   - ***FX, NX-S8*** — Can select individual wells.
   - ***3000*** — A single-tip pipette tool can select individual wells.
     - Choose **Copy Pattern** and select the desired pattern to use a previously defined well pattern created using the Well Patterns Editor (refer to Chapter 11, *Creating Well Patterns*).

       Note: The pattern must be compatible with the head or tool installed.

     - Select **Use pattern** and choose a previously defined pattern from the list to use a pattern created in the Well Patterns Editor or a Define Pattern step.

       Note: Refer to Section 18.10, *Define Pattern Step (including 3000)*, for more information about creating patterns using the Define Pattern step.

     - Define a well pattern using data sets (refer to Section 14.3.1, *Defining Well Patterns Using Data Sets*).
     - Create a custom well pattern from the labware grid by dragging the mouse and using Ctrl and Shift on the keyboard.

       Note: Hold **Shift** and click a well to select additional wells without deselecting any wells. Hold **Ctrl** and click a well to toggle the selection status of selected wells without affecting the status of other wells. If Shift or Ctrl is not held down when selecting wells, any previous selection is deleted.

   Note: To save the pattern, right click the labware graphic and select **Save Pattern** from the menu. Enter a name for the pattern in New Pattern and choose **OK**.

3. Select the **Direction** in which destination wells are mapped to sources. Down first, then left to right is the default selection.

Note: Direction controls how source wells are mapped to the destination, not the physical order in which wells are transferred. The Transfer From File step automatically determines the most efficient way to complete the transfer.

- Down first, then left to right — goes down each column from top to bottom, then goes right to the next column (Figure 18-39)

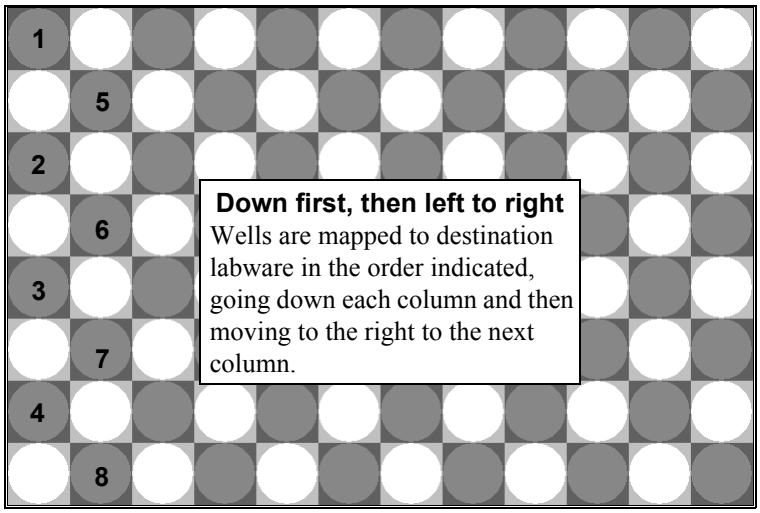


Figure 18-39. Wells accessed down first, then left to right

OR

- To the right first, then top to bottom — goes across each row from left to right, then goes down to the next row (Figure 18-40)

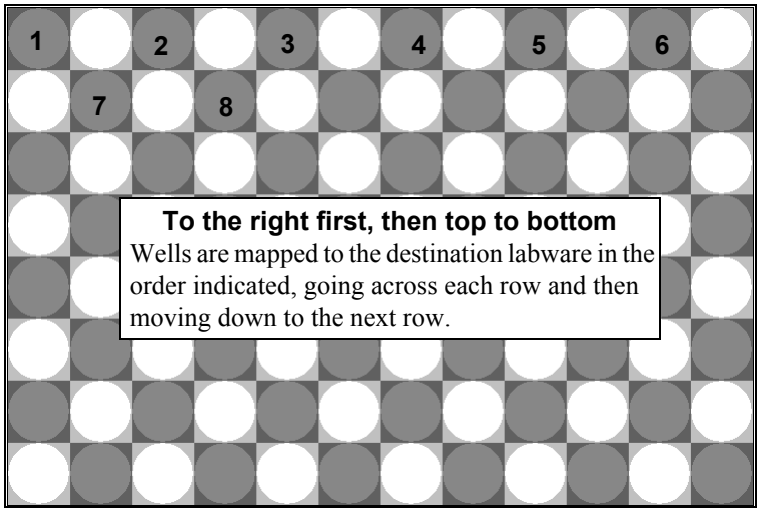


Figure 18-40. Wells accessed to the right first, then top to bottom

Note: The direction can also be selected when the labware is zoomed out by using the Down, then right or Right, then down buttons beneath the labware.

4. Select the first well accessed in **Start**. At first selected well is the default selection.

Note: Start controls how source wells are mapped to the destination, not the physical order in which wells are transferred. The Transfer From File step automatically determines the most efficient way to complete the transfer.

- At first selected well — moves in the selected Direction starting from the first well selected on the labware

  OR

- After last marked well — moves in the selected Direction starting from the first selected well on the labware after the marked well

Note: The selected labware must have marks from a previous step with Mark last well that is used selected.

Note: The start location can also be selected when the labware is zoomed out by using the Start at selection or Start at last mark buttons beneath the labware.

Note: When transferring liquid, the source well in the first row of the data file is transferred to the first accessed destination well, the second source well is transferred to the second accessed destination well, and so forth.

5. Choose **Zoom Out** to return to the step configuration screen.

18.9.5 Configuring Transfer Details

Transfer Details includes specifying:

- a repeat pipetting configuration (Figure 18-41).
- the maximum tolerance in timing between transfer operations (Figure 18-42).

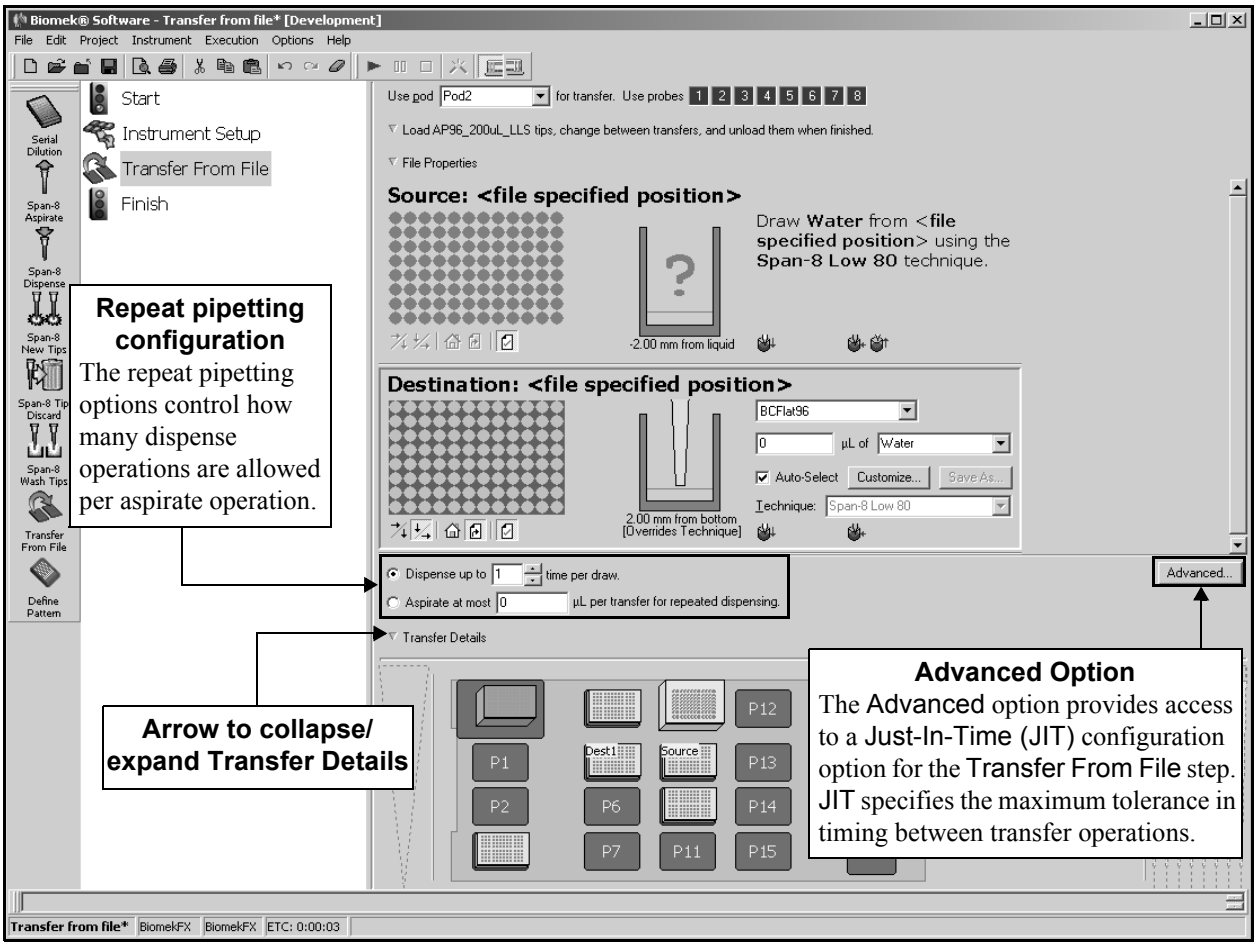


Figure 18-41. Transfer From File step — configuring additional Transfer Details

To configure Transfer Details for the Transfer From File step:

1. Click the arrow or sentence summary below the labware configuration section to expand Transfer Details.
2. Select one of the repeat pipetting configuration options: Dispense up to or Aspirate at most.

Note: Only one repeat pipetting option may be selected. Either Dispense up to or Aspirate at most may be selected, but not both.

3. In **Dispense up to**, select the number of times the Biomek instrument is allowed to dispense per aspirate. For example, if dispensing 75 µL to each of six microplates, three aspirate operations of 150 µL can each dispense into two destinations. In this case, Dispense up to is set to no fewer than two.

   OR

   In **Aspirate at most**, select the maximum volume to aspirate from the source for repeat pipetting. For example, if dispensing 75 µL to each of six microplates, three aspirate operations of 150 µL can each dispense into two destinations. In this case, Aspirate at most is set to no less than 150 µL.

   Note: The default repeat pipetting setting is Dispense up to one time per draw, which does not allow a repeat pipetting operation. Settings of two or more allow repeat pipetting.

4. Click **Advanced** to change the default setting of applying a Just-In-Time (JIT) block to aspirate and dispense operations. The Advanced Options prompt appears (Figure 18-42).

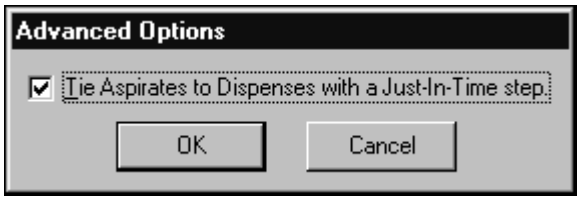


Figure 18-42. Advanced button — JIT Block

5. Uncheck **Tie Aspirate to Dispense with a JIT Block** to deactivate the JIT block.
6. Click **OK** to save any changes.

The Transfer Details configuration can be collapsed to allow more room during Source and Destination Labware configuration. When collapsed, the Transfer Details configuration is displayed as a sentence summary. Use the sentence summary to verify that Transfer Details has been configured appropriately.

To collapse or expand the Transfer Details configuration, click the arrow to the left of Transfer Details or the textual display (Figure 18-41).

18.10 Define Pattern Step (including 3000)

Define Pattern is used to create patterns and assign names to them for use in other steps in the method, such as a Transfer or Combine step. Well patterns defined using the Define Pattern step are method specific and embedded as part of the method.

Embedding the well patterns as part of the method has several advantages:

- Sharing methods among other users is simpler because the pattern information is stored in the method, not in the project.
- Common well patterns can be modified for individual methods without changing the well pattern in the project.
- The pattern definition can be changed while keeping the same pattern name, making it simple to modify methods by changing the well pattern definition. Since the Transfer and Combine steps use the pattern name, changes to the pattern are automatically updated in the Transfer and Combine steps.

Note: This is particularly useful when the pattern is defined by a file using rows that match a bar code or other value. In a Loop step, the pattern could change based on the bar code of the current labware in a group created with a Create Group step. Each iteration of the Loop would transfer using a different pattern as defined by the file in the Define Pattern step.

Insert a **Define Pattern** step into the method. The Define Pattern Step Configuration appears (Figure 18-43).

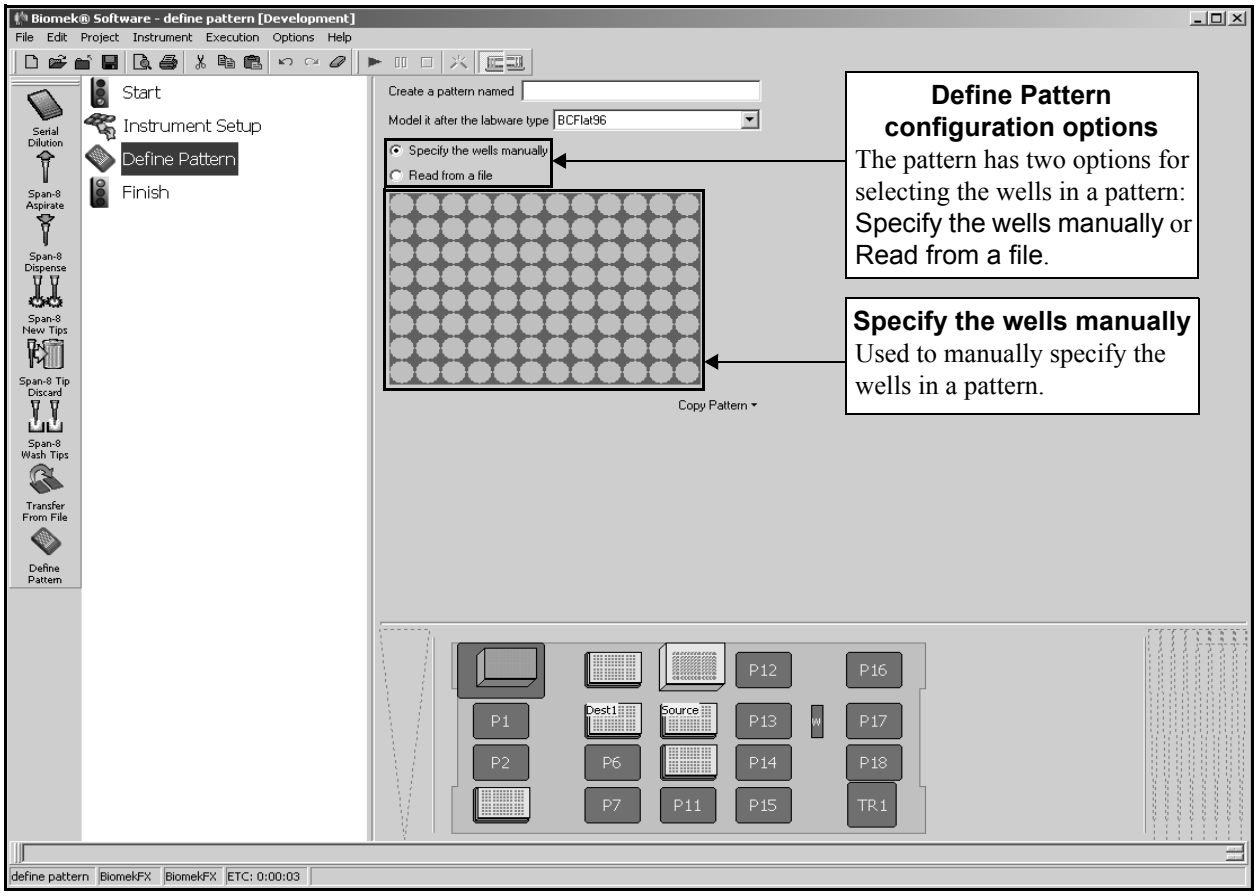


Figure 18-43. Define Pattern step and configuration

Define Pattern has two different configuration options. It can define a pattern by manually specifying wells or reading from a file.

18.10.1 Configuring the Define Pattern Step by Specifying the Wells Manually

To configure the Define Pattern step by manually specifying the wells:

1. In Create a pattern named, enter a name for the pattern.
2. In Model it after the labware type, select the labware type for the pattern.
3. Select **Specify the wells manually**.
4. On the graphic representing the labware, select the wells to be included in the pattern. All wells are selected by default (Figure 18-43).

   Note: Click on a well to select it and deselect the current selection. Hold down **Shift** and click on additional wells to select wells without affecting the current selection. Hold down **Ctrl** and click on wells to toggle wells between selected and deselected without affecting the current selection.

5. To use or modify a well pattern defined in the Well Patterns Editor, select **Copy Pattern** and choose the pattern from the list.

18.10.2 Configuring the Define Pattern Step Reading from a File

To configure the Define Pattern step by reading well information from a file:

1. In Create a pattern named, enter a name for the pattern.
2. In Model it after the labware type, select the labware type for the pattern.
3. Select **Read from a file**. The Read from a file configuration options appear (Figure 18-44).

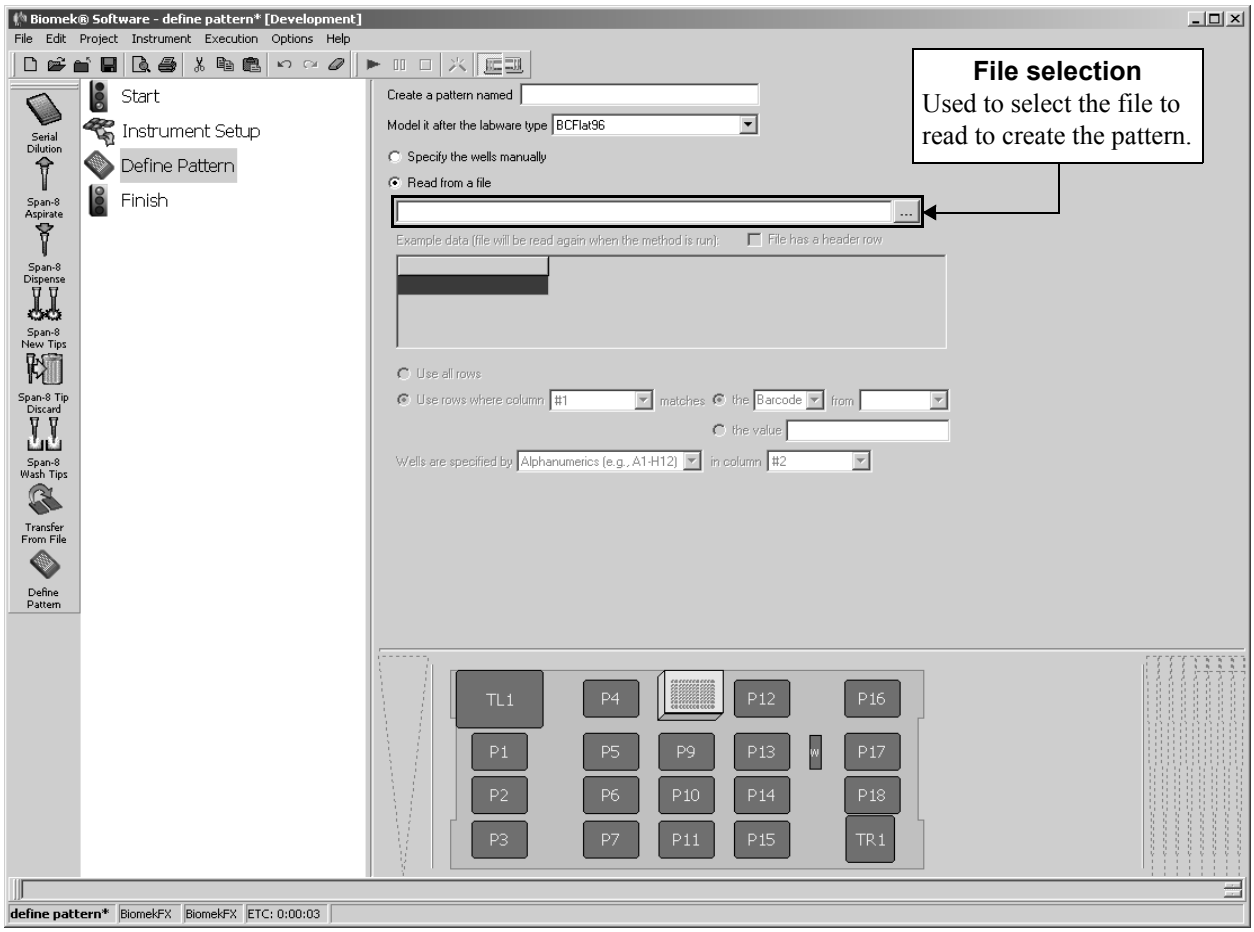


Figure 18-44. Define Pattern step — Read from a file configuration

4. Enter the full path and file name of the data file from which to read the pattern information.

   OR

   Choose the browse button and select the directory and file from which to read the pattern information in Open (Figure 18-45). The selected file is read and Example data is displayed (Figure 18-46).

Note: The data file must be a comma-delimited text file (.txt or .csv).

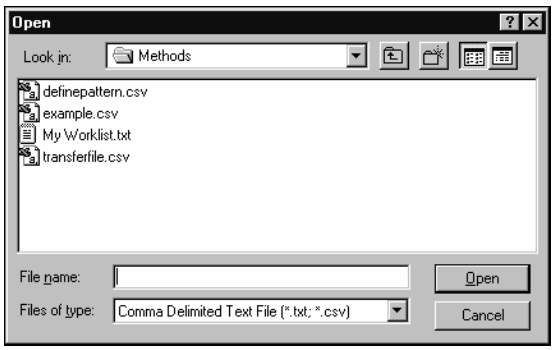


Figure 18-45. Open dialog

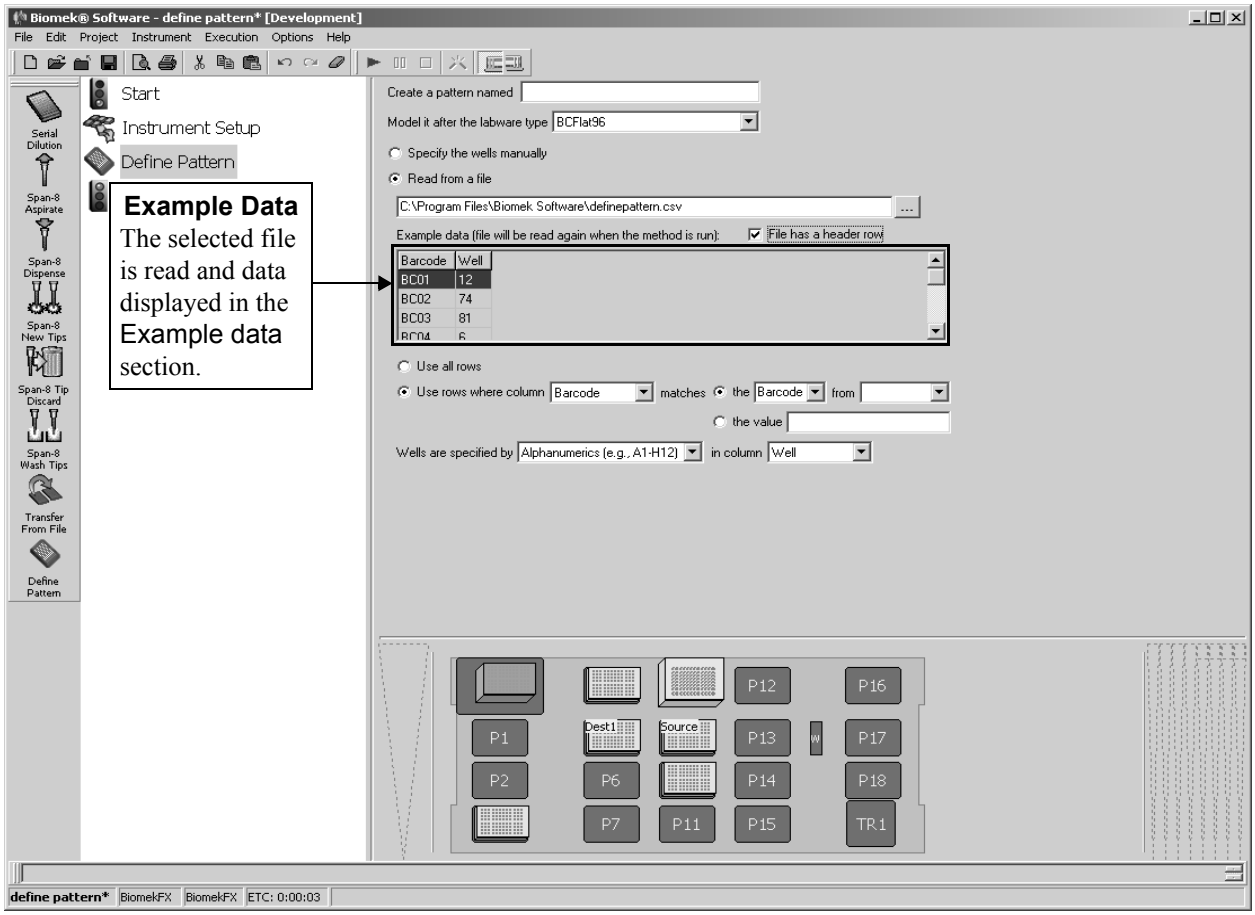


Figure 18-46. Define Pattern step — Example data displayed

5. If the file read has a header row identifying the columns, select **File has a header row**. The first row of the data file is used to identify the columns (Figure 18-47).

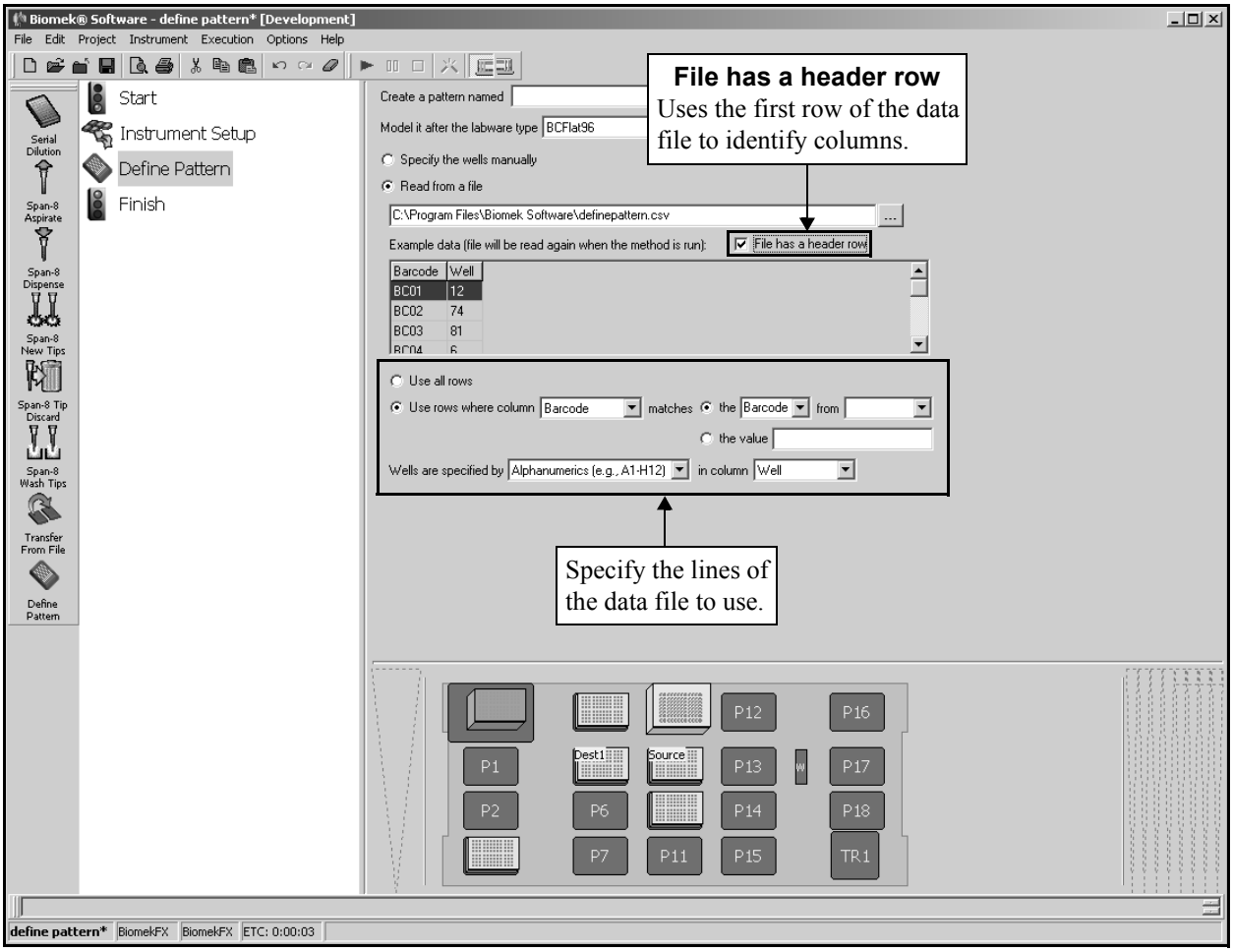


Figure 18-47. Define Pattern step — Example data with header row

6. Beneath the Example data, select which lines from the data file to use when defining the pattern.
   - To use all rows of the data file, select Use all lines.
   - To use specific wells where a certain column matches a specified bar code or value, refer to Section 18.10.2.1, *Specifying Lines to Use*.
7. In Wells are specified by, select whether wells are identified using alphanumeric well addresses (for example, A1-H12 for a 96-well plate) or numeric well numbers (for example, 1-96 for a 96-well plate), and specify the column that contains the well information.
8. Choose a step that occurs after the Define Pattern step or the Finish step to validate the step configuration.

18.10.2.1 Specifying Lines to Use

Sometimes it may be desired to only use specific rows from the data file. For example, if a data file contains information on several plates, the file can be configured to use only the rows pertaining to the current plate using the bar code, deck position, or other factor.

To use selected lines from the data file:

1. Select **Use lines where column** to activate the configuration.
2. In **column matches**, select the column from the data file that must match the specified value to use the row.
3. Select whether the selected column must match the Bar code or Name of the labware selected in **from** and specify a deck position or labware name to match against in from.

   OR

   Select **the value** and enter a variable or expression that must match the column selected.

   The rows that match the specified condition are used to define the well pattern using the column that specifies the well information.

18.10.3 Using a Defined Pattern in a Transfer or Combine Step

Once a pattern has been created using a Define Pattern step, it may be used in any Transfer or Combine step within the method that uses a Span-8 Pod on the ***FX*** or ***NX-S8*** or a pipetting tool on the ***3000***.

To use a defined pattern in a Transfer or Combine step:

1. Select the desired **Transfer** or **Combine** step in the Method View. The step configuration appears.
2. Select the desired **Source** or **Destination** configuration to display the configuration for the selected labware.
3. Double-click the graphic of the labware to zoom in on it.
4. Select **Use pattern** to use a pattern created in a Define Pattern step.

5. Choose the desired pattern created in a Define Pattern step from the list (Figure 18-48). During method run, the configured step uses the specified pattern.

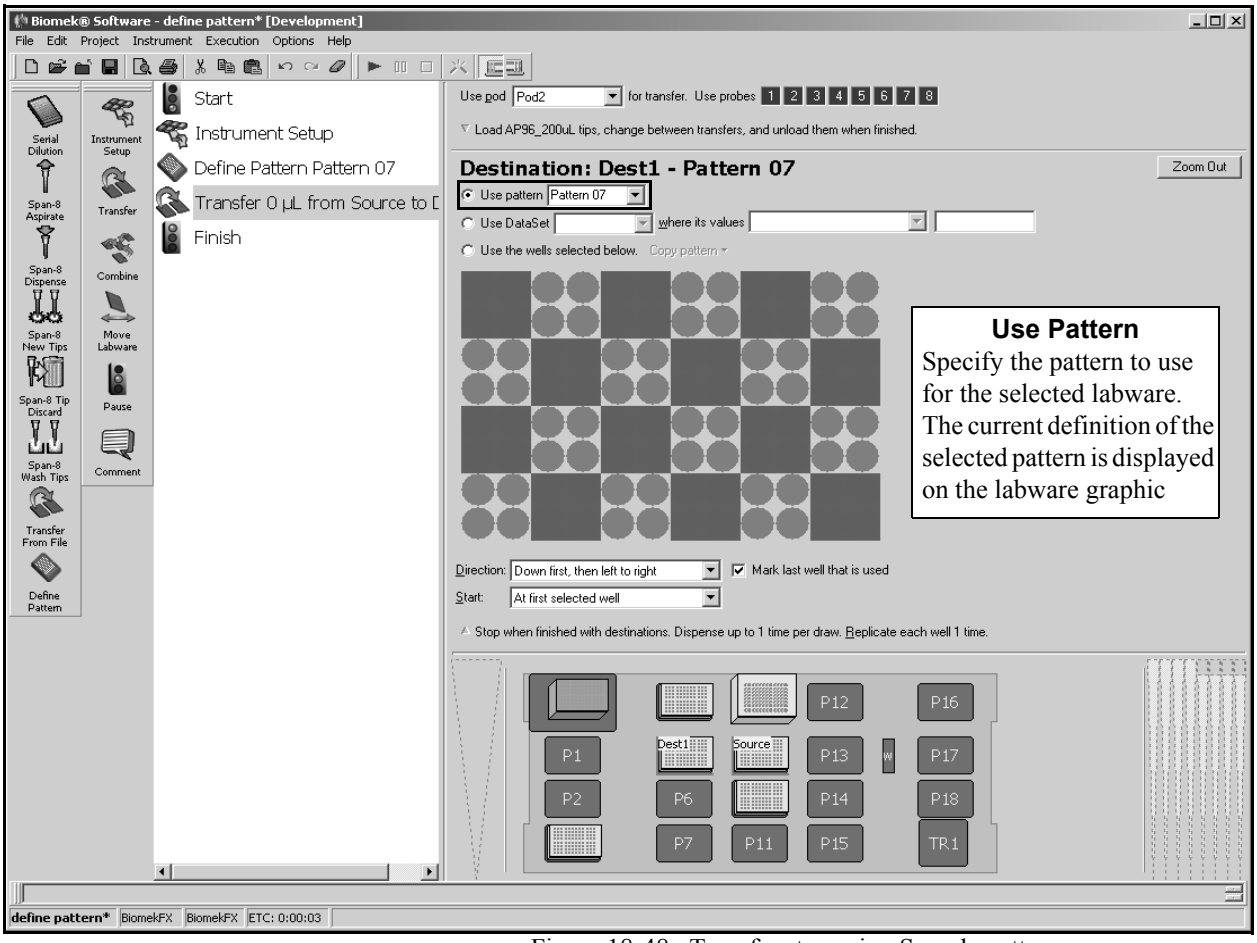


Figure 18-48. Transfer step using Sample pattern

Note: Only patterns that are defined in the current method or from a previously run method that did not clear global variables appear in the list.

6. Choose a step that occurs after the configured Transfer or Combine step or the Finish step to validate the step configuration.

19 Using the HDR Step Palette (FX, 3000 only)

19.1 Overview

CAUTION: Do not attempt to access a 96-Channel or 384-Channel Tip Wash ALP with a Multichannel Pod equipped with an HDR Tool Body. The gripper may crash and damage the pod, HDR Tool Body, or Tip Wash ALP.

The HDR Step Palette provides access to steps used to control the HDR Tool Body on the Biomek FX instrument or the HDR tool on a Biomek 3000 instrument. The HDR steps include the means to transfer liquid, wash pins, and move labware using the HDR Tool Body.

The steps available in HDR Step Palette include:

- HDR Transfer — transfers liquid from a single source to one or more destinations using the HDR Tool Body

- HDR Combine — transfers liquid from a one or more sources to a single destination using the HDR Tool Body

- HDR Tool Cleaning — cleans pins on the HDR Tool Body by dipping the pins in one or more reservoirs and drying them at the HDR Pin Drying ALP

- HDR Move Labware — moves labware using the gripper on the Multichannel Pod with the HDR Tool Body installed.
  - ***3000*** — HDR Move Labware is not available.

Note: In addition to the HDR steps, the Device Action step may be used to control the wash pumps for the circulating reservoirs or the fan for the HDR Pin Drying ALP independently during a method (refer to Section 22.6, *Device Action Step*).

19.2 Displaying the HDR Step Palette

In order to add HDR steps to a method, display the HDR Step Palette (Figure 19-1).

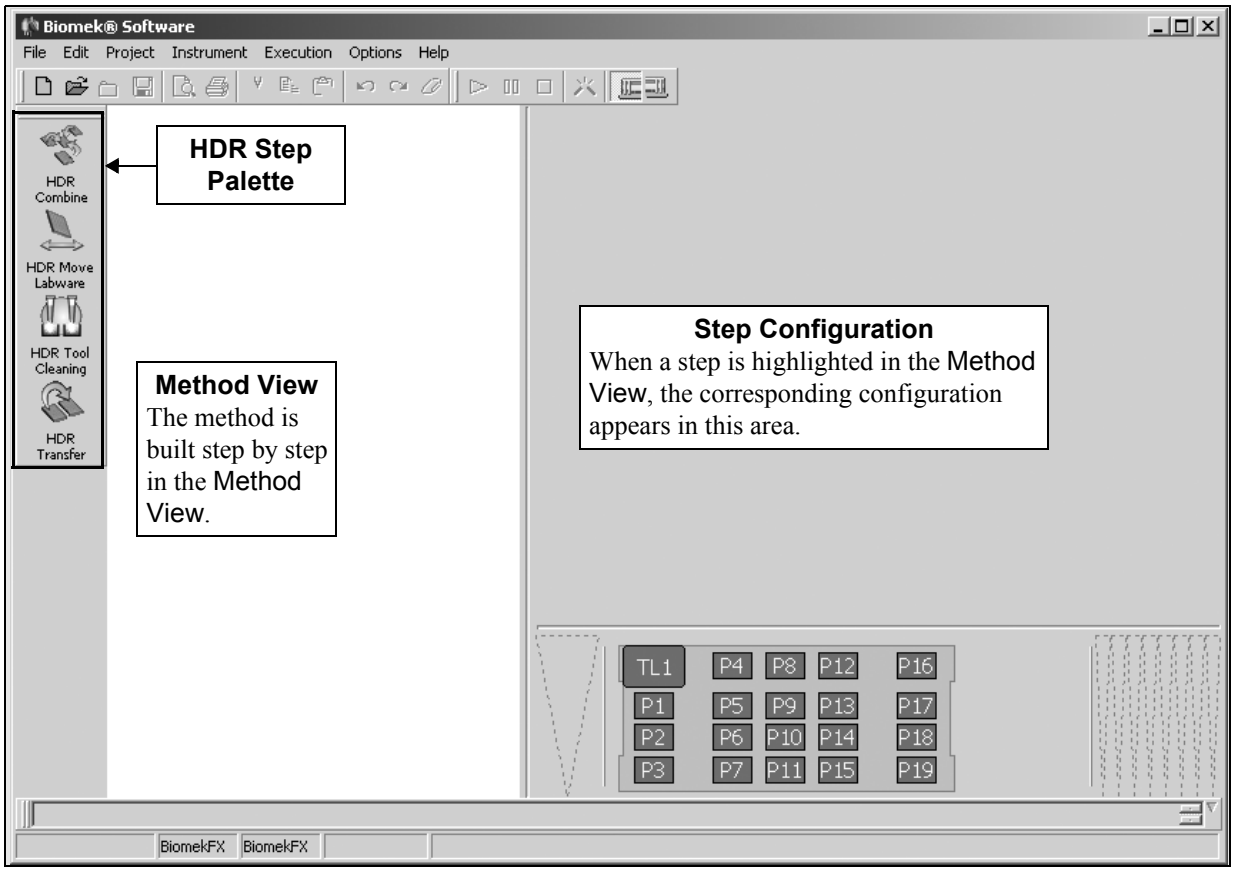


Figure 19-1. Biomek main editor with HDR Step Palette displayed

To display the HDR Step Palette, complete the following:

- Right-click any empty palette space, and the Step Palette menu appears. Select **HDR.**

  OR

- From the menu bar, select **Options>Toolbars>HDR**.

19.3 Using the HDR Transfer and Combine Steps

The HDR Transfer and HDR Combine steps transfer a volume of sample from each well of a source labware to each well of the destination labware. Each destination well may contain up to 36 samples per well in a 6 x 6 array for a 96-well microplate or up to 16 samples per well in a 4 x 4 array for a 384-well microplate.

Note: Only a 384-pin plate with 0.015" post pins can access quadrants of a 1536-well microplate.

The HDR Transfer step transfers liquid from a single source to one or more destinations, while the HDR Combine step transfers liquid from a one or more sources to a single destination.

A liquid transfer operation deposits samples in the same array position of each destination well, starting in the upper left corner position. Each subsequent liquid transfer operation deposits samples in the next available array position, going across each row before moving down to the next row of the array (Figure 19-2).

Figure 19-2. Order of transfer to array positions in destination wells with a 3x3 array

Note: Destination labware should be placed on a Positive Position ALP during gridding applications. Refer to the *ALPs User's Manual,* Chapter 15, *Positive Position ALP*, for more information on the Positive Position ALP.

The HDR Transfer and HDR Combine steps perform liquid-handling functions through the step configuration (Figure 19-3). An HDR Transfer step transfers sources such that each destination receives exactly one source; an HDR Combine step transfers each source to exactly one destination.

- If there are the same number of sources and destinations (wells x array positions), all sources are transferred and each destination receives exactly one source.
- If there are more sources than destinations (wells x array positions), an HDR Transfer step transfers only enough sources so that each destination receives exactly one source (some sources are unused); an HDR Combine step transfers all sources to exactly one destination (some destinations receive more than one source).
- If there are fewer sources than destinations (wells x array positions), an HDR Transfer step transfers all sources until each destinations receives exactly one source (some sources are used multiple times); an HDR Combine step transfers all sources to exactly one destination (not all destinations receive a source).

Note: The HDR Transfer and HDR Combine steps must be used with either a Multichannel Pod equipped with the HDR Tool Body on the Biomek FX instrument, or an HDR tool installed on the head assembly of a Biomek 3000 instrument.

The HDR Transfer or HDR Combine step configuration includes specifying:

- Pod that performs the transfer.
  - ***FX only*** — The pod that performs the transfer is specified.
- Pin washing procedure between transfers, if desired.

Note: Pin washing between transfers requires that a procedure is defined using the Define Procedure step (refer to Section 19.3.1, *Washing Pins Between Transfers*).

- Source labware configuration(s).
- Destination labware configuration(s).

To configure an HDR Transfer step:

1. Insert an HDR Transfer or HDR Combine step into the Method View (Figure 19-3).

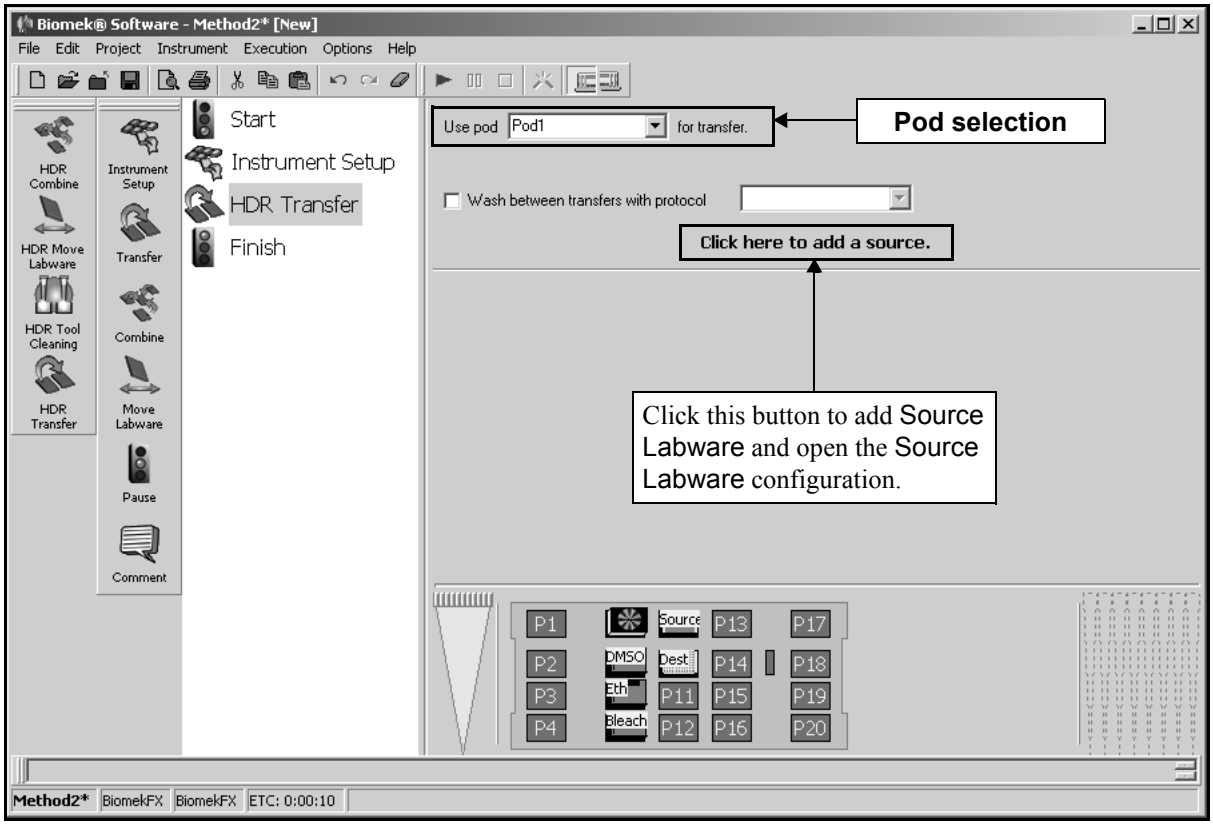


Figure 19-3. HDR Transfer step configuration

2. In Use pod, specify the pod with the HDR Tool Body used to perform the transfer operations.

   ➢ ***3000*** — Use pod does not appear in the step configuration.

3. Select **Wash between transfers with protocol** to wash pins between transfers using a specified procedure.

   Note: Pin washing between transfers requires that a procedure is defined using the Define Procedure step (refer to Section 19.3.1, *Washing Pins Between Transfers*).

4. In Wash between transfers with protocol, select a previously defined procedure to use to wash pins between transfers.

5. Configure Source and Destination labware as described in Sections 19.3.2, *Configuring Source Labware*, and 19.3.3, *Configuring Destination Labware*.

19.3.1 Washing Pins Between Transfers

Pins are washed between transfers in an HDR Transfer or HDR Combine step using a wash procedure defined in a Define Procedure step (refer to Section 21.8.1, *Define Procedure Step*). After defining the procedure, it is selected in the HDR Transfer or HDR Combine step configuration.

To wash pins between transfers in an HDR Transfer or HDR Combine step:

1. Insert a **Define Procedure** step in the Method View. The Define Procedure Step Configuration appears (Figure 19-4).

   Note: Define Procedure is not on any of the default step palettes and must be added to a step palette from the Specialty step category in the Palette Builder. Refer to Section 29.5, *Using the Step Palette Builder*, for more information on adding Define Procedure to a step palette.

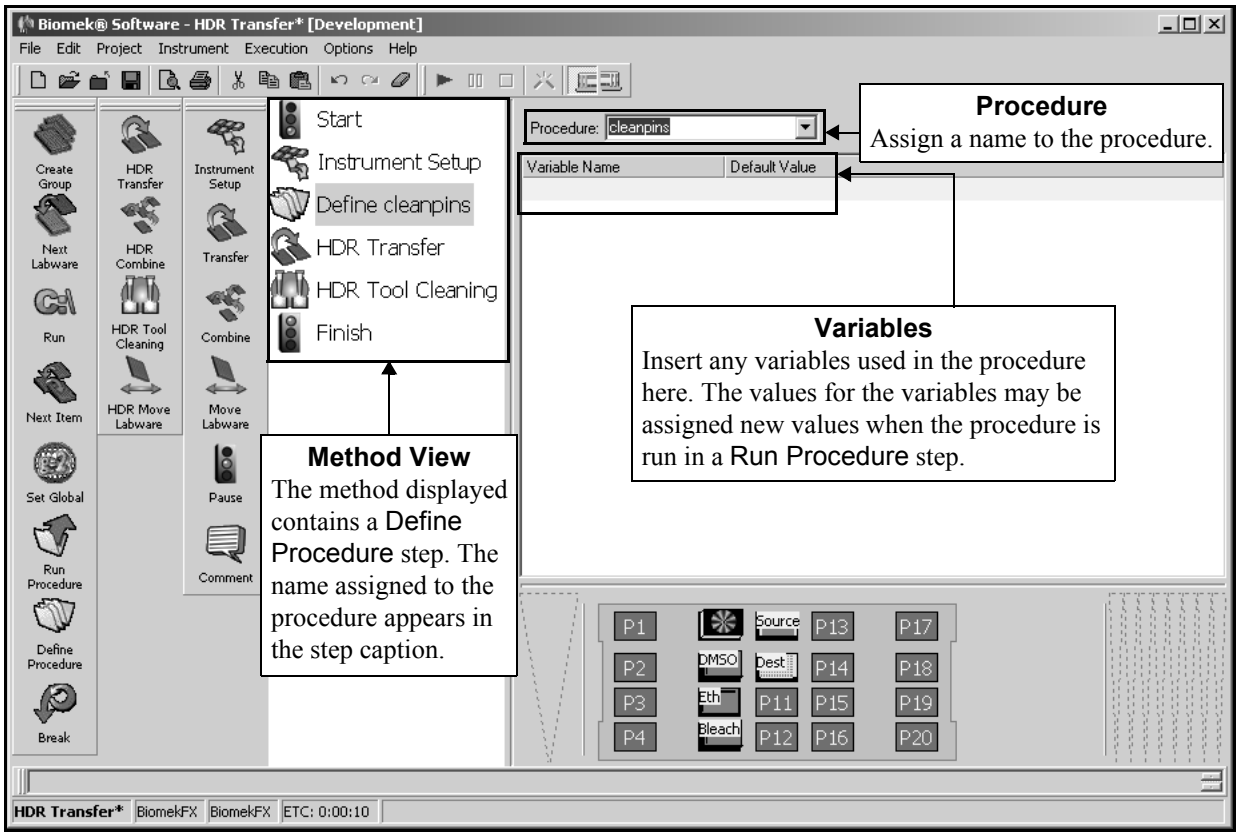


Figure 19-4. Define Procedure step and configuration

2. In **Procedure**, enter a name for the procedure.

   Note: The procedure name may contain only alphanumeric characters and the underscore (_), and is not case-sensitive.

3. Double-click the **Define Procedure** icon in the Method View to open the procedure. The End Procedure icon appears below the Define Procedure icon.
4. Insert the **HDR Tool Cleaning** step between the Define Procedure and End Procedure icons.

5. Configure the **HDR Tool Cleaning** step as desired to perform all pin washing between transfers (refer to Section 19.4, *Using the HDR Tool Cleaning Step*).
6. If desired, insert and configure additional steps between the Define Procedure and End Procedure icons.

   Note: All steps included in this procedure are performed between every transfer of an HDR Transfer or HDR Combine step.

7. Double-click the **Define Procedure** icon in the Method View to collapse the procedure and hide all steps between the Define Procedure and End Procedure icons.

   Note: After defining the procedure and configuring all steps within the procedure as desired, drag it onto one of the step palettes to create a custom step. When writing other methods, insert the custom Define Procedure step into the Method View to use the same pin washing procedure and ensure consistent pin washing across methods.

8. When configuring an HDR Transfer or HDR Combine step, select the procedure created above in Wash between transfers with protocol.

19.3.2 Configuring Source Labware

A 'source' is a group of wells accessed at one time by the HDR Tool Body; for example, a 96-pin plate accesses 96 wells at a time while a 384-pin plate accesses 384 wells at a time.

Note: If configuring a 384-well microplate for access by a 96-pin plate or a 1536-well microplate for access by a 384-pin plate as source labware, any combination of quadrants may be used. For example, if it is desired to transfer liquid from the first, second, and third quadrants but not the fourth, the source labware may be configured to transfer only from those quadrants.

Note: Only a 384-pin plate with 0.015" post pins can access quadrants of a 1536-well microplate.

In the HDR Transfer and HDR Combine steps, the HDR Tool Body dips the pins in the source labware at a specified height for a specified length of time a specified number of times to pick up samples by liquid adhesion.

Note: The volume of sample that adheres to the pins is dependent on many factors, including environmental factors, the liquid type, the surface area of the pins immersed in the sample, the length of time the pins are in contact with the sample, pin washing technique, and dryness of the pins. Conduct tests to determine the optimal settings to transfer the desired volume of a specific liquid type with a specific pin size.

The Source Labware configuration for the Transfer step includes choosing:

- Labware type
- Labware location
- Dipping configuration
- Quadrants used, if applicable

Note: Quadrants are applicable when accessing a 384-well microplate using a 96-pin plate or a 1536-well microplate using a 384-pin plate. Only a 384-pin plate with 0.015" post pins can access quadrants of a 1536-well microplate.

Note: A single source is configured for the HDR Transfer step, because the HDR Transfer step moves liquid from a single source to one or more destinations. Multiple sources can be configured for the HDR Combine step, because the HDR Combine step moves liquid from multiple sources to a single destination.

To configure Source Labware for the HDR Transfer and HDR Combine steps:

CAUTION: Do not access labware positioned on a 1 x 5 Passive ALP with the HDR Tool Body. The gripper may crash into the ALP.

CAUTION: Do not access labware on a Stirring ALP with the HDR Tool Body. The magnetic stirrer may bend the pins or interfere with the liquid transfer performance of the pins.

1. Select **Click here to add a source** (Figure 19-3). The Source Labware configuration appears (Figure 19-5).

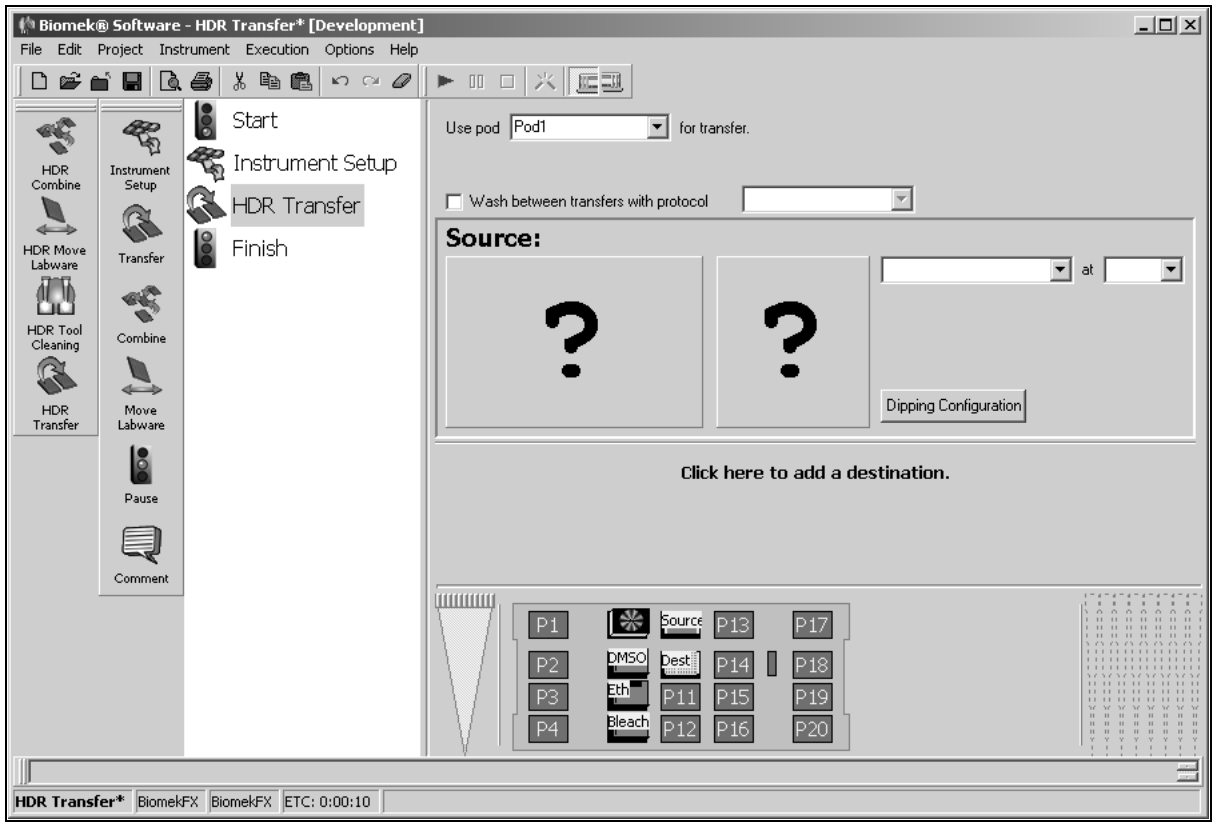


Figure 19-5. HDR Transfer step — Source Labware configuration

2. Click on the desired piece of labware in the Current Deck Display. The labware type and position for that piece of labware is entered automatically into the Source Labware configuration (Figure 19-6).

   OR

   Select a **Source Labware** type and specify the deck position.

Note: To configure additional Source Labware for an HDR Combine step, select **Click here to add a source**, and then select another piece of labware from the Current Deck Display. If an incorrect piece of labware is selected, right-click on the labware title and select **Delete** on the menu that appears, or change the Source Labware selection by clicking anywhere in the source labware configuration area, and selecting another piece of labware.

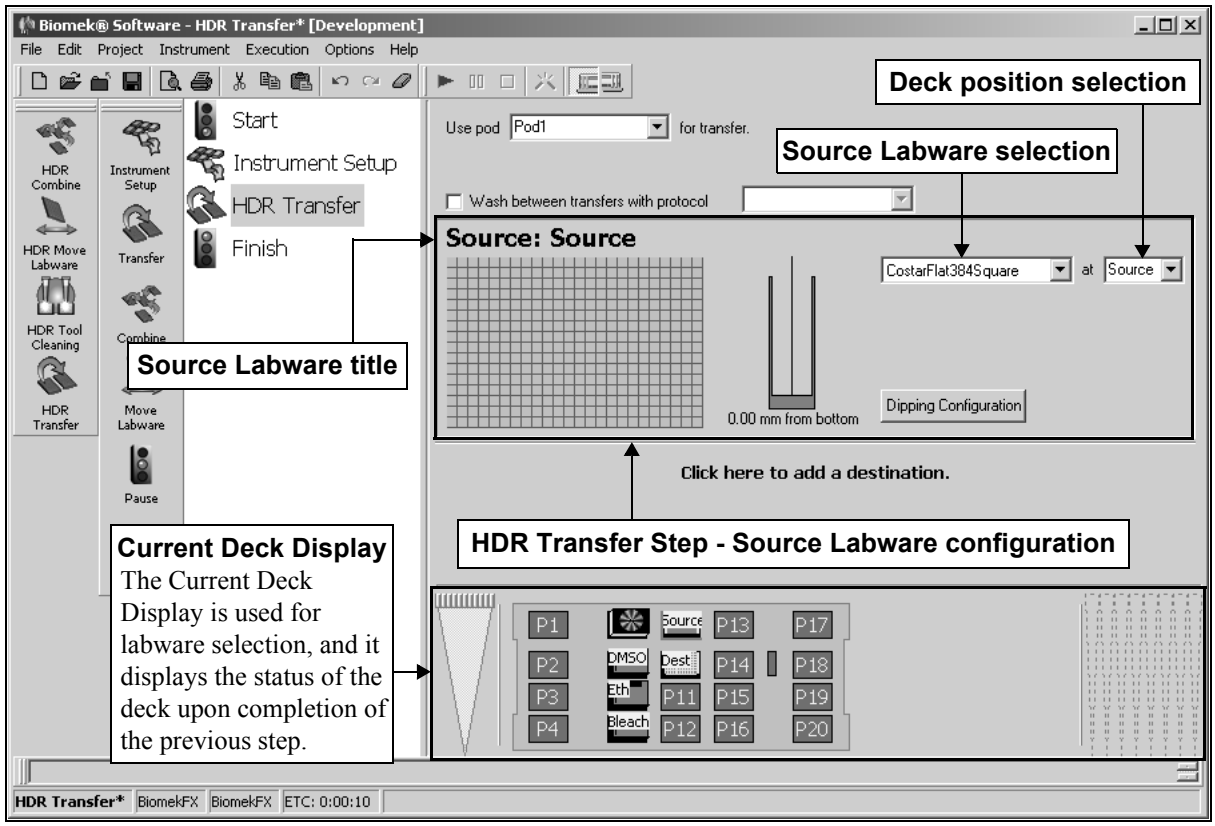


Figure 19-6. HDR Transfer step — Source Labware selected

3. Verify the deck position of the labware.

Note: A bright blue outline appears in the Current Deck Display around the labware designated as the Source Labware.

4. To specify quadrants in a microplate to access, double-click the source labware in the step configuration to zoom in on the labware.

   Note: To call up a menu for Zoom In and a Specify Selection as Text option, right-click on the labware.

   Specify Selection as Text allows selection of quadrants as targets for aspirate and dispense operations. Specify Selection as Text may also be used to enter variables or expressions (refer to Section 13.2, *Using Variables* and Section 13.3, *Using Expressions*).

   Note: Specify Selection as Text is not applicable for 96-well microplates, reservoirs, or 384-well microplates accessed by a 384-channel pod.

5. Select the desired quadrant(s) on the zoomed-in graphic of the labware.

   Note: Selecting any well automatically selects all wells in that quadrant.

   Note: To select multiple quadrants, click and drag over the desired quadrants or hold down **Ctrl** or **Shift** and select the desired quadrants.

6. Choose **Zoom Out** to return to the step configuration screen.

7. Choose **Dipping Configuration** to configure the dipping operation. Dipping Configuration appears (Figure 19-7).

   Note: The Dipping Configuration is similar to a pipetting technique. It specifies the method in which liquid is picked up by the pins.

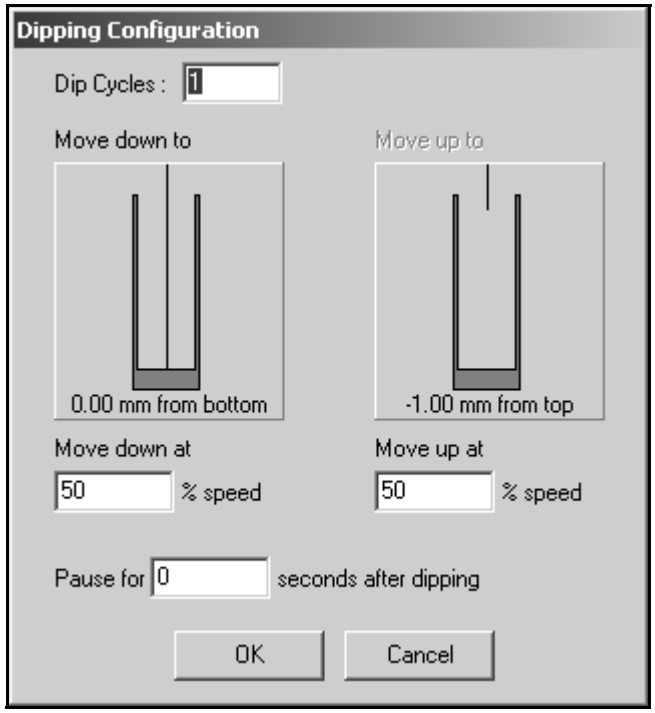


Figure 19-7. Dipping Configuration

8. In Dip Cycles, enter the number of times the pins should descend into the wells to pick up liquid.

   Note: For Dip Cycles greater than **1**, Move up to must be configured.

9. In Move down to, specify the height the pins descend to for each dipping cycle.

   Note: By default, Move down to is measured from bottom of the well. To measure from top of the well or from liquid, right click the graphic of the pin in the well and make the desired selection from the menu.

   Note: The Move down to height can go as much as 2 mm below the bottom of the well as long as the pod can descend that far. Descending below the bottom of the well potentially corrects for any slight imperfections in the labware or ALP heights and can be done safely because the pin push plate is in a floating position, allowing the pins to move up and down freely without resistance. To specify a height below the bottom of the well, right-click the graphic of the pin in the well and select Custom Height. Enter a negative value in Custom Height to move the pins below the bottom of the well.

10. In Move down at, enter the speed of the descent of the HDR Tool Body as a percentage of the maximum speed of the pod.

11. In Move up to, specify the height the pins ascend to between each dipping cycle.

    Note: If Dip Cycles is set to **1**, Move up to is disabled.

    Note: By default, Move up to is measured from bottom of the well. To measure from top of the well or from liquid, right click the graphic of the pin in the well and make the desired selection from the menu.

12. In Move up at, enter the speed of the ascent of the HDR Tool Body as a percentage of the maximum speed of the pod.

13. In Pause for, enter the length of time the pod pauses at the down position for each Dip Cycle to pick up liquid.

14. Choose **OK** to save the Dipping Configuration and return to the source labware configuration.

15. Leave the pin height as is to use the settings for the Move down to height specified in the Dipping Configuration.

    OR

    Set the pin height manually using one of the following methods:

    - Position the cursor over the graphic of a pin inside a well. Click and drag the graphic up or down. The pin moves with the cursor, and the height displayed below the graphic is adjusted as the graphic is manipulated.
    - Select the graphic of a pin inside a well, and use the ↑ and ↓ keys. The textual representation of the height, which is displayed below the graphic, adjusts in 0.1 millimeter (mm) increments.
    - Right-click on the graphic of a pin inside a well, and a menu appears. Select **Custom Height**, and Custom Height appears (Figure 19-8). Insert the **Height** in millimeters (mm) and, in **from**, select a reference point from the drop-down list. Choose **OK**.

Note: The cursor changes to a hand when positioned over the graphic.

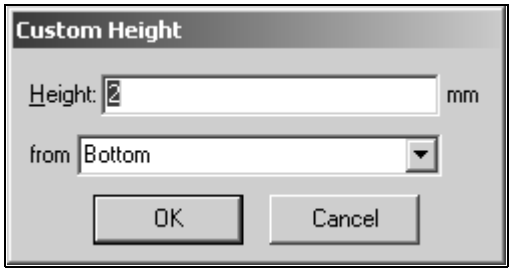


Figure 19-8. Custom Height prompt

16. Repeat steps 1 to 15 for each additional piece of Source Labware.

Note: A Destination Labware must be selected before additional Source Labware can be configured.

19.3.3 Configuring Destination Labware

A ‘destination’ is a group of wells accessed at one time by the HDR Tool Body; for example, a 96-pin plate accesses 96 wells at a time while a 384-pin plate accesses 384 wells at a time.

Destination wells may be configured to hold an array of destination sites, allowing for a greater number of samples on a single microplate. All destination wells must have the same array configuration.

Note: If configuring a 384-well microplate using a 96-pin plate or a 1536-well microplate using a 384-pin plate as source labware, any combination of quadrants may be used. For example, if it is desired to transfer liquid to the first, second, and third quadrants but not the fourth, the destination labware may be configured to transfer only to those quadrants.

- ***3000*** — 1536-well plates are not used.

Note: Only a 384-pin plate with 0.015” post pins can access quadrants of a 1536-well microplate.

In the HDR Transfer and HDR Combine steps, the HDR Tool Body dips the pins in the destination labware at a specified height for a specified length of time a specified number of times to deposit samples by liquid adhesion. Multiple samples can be deposited in a single destination well in an array format.

Note: The volume of sample that deposits from the pins to the destination labware is dependent on many factors, including environmental factors, the liquid type, the surface area of the pins in contact with the labware, and the length of time the pins are in contact with the labware. Conduct tests to determine the optimal settings to transfer the desired volume of a specific liquid type with a specific pin size.

The Destination Labware configuration includes choosing:

- Labware type
- Labware location
- Dipping configuration
- Array configuration for gridding

  Note: Destination labware should be placed on a Positive Position ALP during gridding applications. Refer to the *ALPs User’s Manual,* Chapter 15, *Positive Position ALP*, for more information on the Positive Position ALP.

- Quadrants used, if applicable

  Note: Quadrants are applicable when accessing a 384-well microplate using a 96-pin plate or a 1536-well microplate using a 384-pin plate. Only a 384-pin plate with 0.015” post pins can access quadrants of a 1536-well microplate.

  - ***3000*** — 1536-well plates are not used.

Note: Multiple destinations can be configured for the HDR Transfer step, because the HDR Transfer step moves liquid from a single source to one or more destinations. A single destination is configured for the HDR Combine step, because the HDR Combine step moves liquid from one or more sources to a single destination.

To configure Destination Labware for the HDR Transfer step:

CAUTION: Do not access labware positioned on a 1 x 5 Passive ALP with the HDR Tool Body. The gripper may crash with the ALP.

CAUTION: Do not access labware on a Stirring ALP with the HDR Tool Body. The magnetic stirrer may bend the pins or interfere with the liquid transfer performance of the pins.

1. Select **Click here to add a destination** (Figure 19-9). The Destination Labware configuration appears.

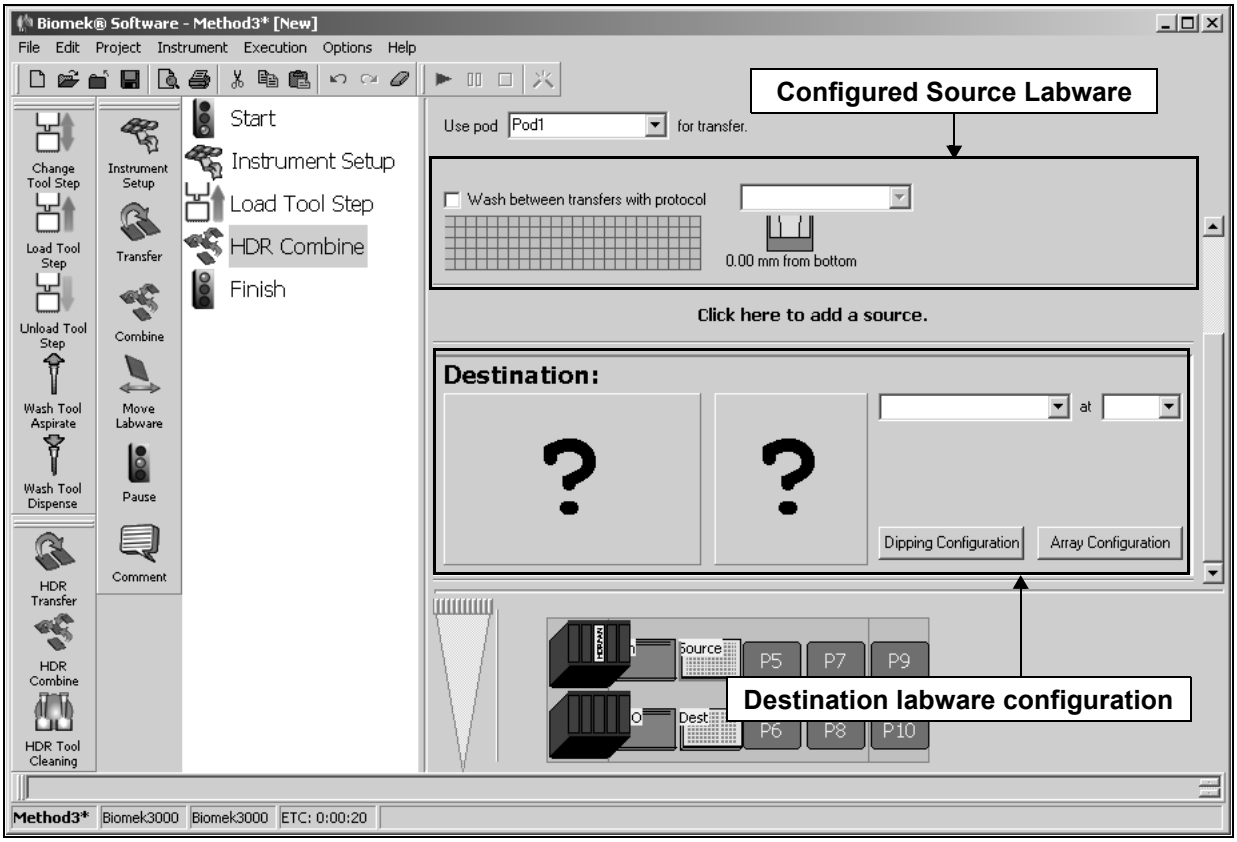


Figure 19-9. HDR Transfer step — Adding Destination Labware

2. Click on the desired piece of labware in the Current Deck Display. The labware type and position for that piece of labware is entered automatically into the Destination Labware configuration (Figure 19-6).

   OR

   Select a **Destination Labware** type and specify the deck position.

Note: Once the Destination Labware has been selected, the Source Labware parameters are collapsed to display a sentence summary. To reopen the Source labware parameters, click anywhere in the Source Labware configuration area.

Note: To configure additional Destination Labware for an HDR Transfer step, select **Click here to add a destination**, and then select another piece of labware from the Current Deck Display. If an incorrect piece of labware is selected, right-click on the labware title and select **Delete** on the menu that appears, or change the Destination Labware selection by clicking anywhere in the destination labware configuration area, and selecting another piece of labware.

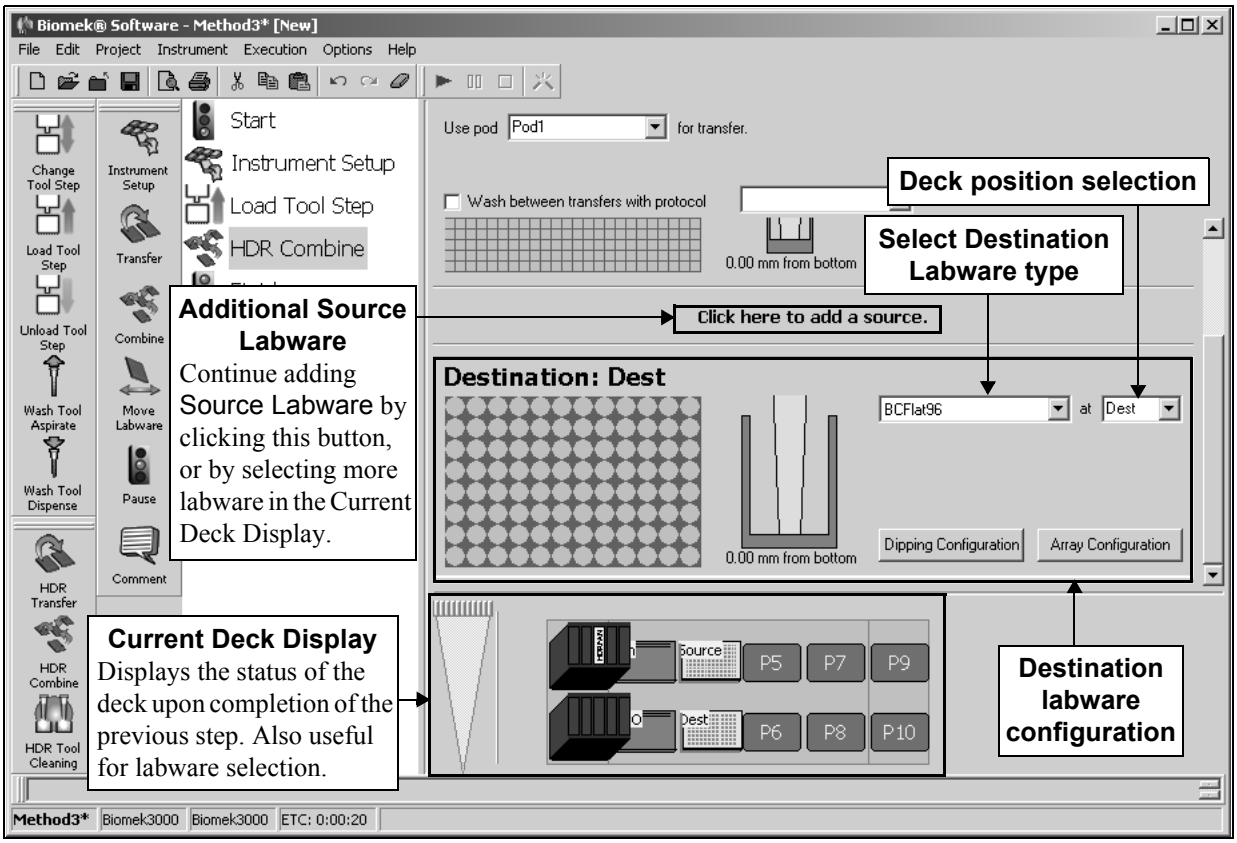


Figure 19-10. HDR Combine step — Destination Labware configuration

3. Verify the deck position of the labware.

Note: A bright yellow outline appears in the Current Deck Display around labware designated as Destination Labware.

4. To specify the quadrants of a microplate to access, double-click the destination labware in the step configuration to zoom in on the labware.

   Note: To call up a menu for Zoom and a Specify Selection as Text option, right-click on the labware.

   Specify Selection as Text allows selection of quadrants as targets for aspirate and dispense operations. Specify Selection as Text may also be used to enter variables or expressions (refer to Section 13.2, *Using Variables* and Section 13.3, *Using Expressions*).

   Note: Specify Selection as Text is not applicable for 96-well microplates, reservoirs, or 384-well microplates accessed by a 384-pin plate.

5. Select the desired quadrant(s) on the zoomed-in graphic of the labware.

   Note: Selecting any well automatically selects all wells in that quadrant.

   Note: To select multiple quadrants, click and drag over the desired quadrants or hold down **Ctrl** or **Shift** and select the desired quadrants.

6. Choose **Zoom Out** to return to the step configuration screen.
7. Choose **Dipping Configuration** to configure the operation. Dipping Configuration appears (Figure 19-11).

   Note: The Dipping Configuration is similar to a pipetting technique. It specifies the method in which liquid is deposited by the pins.

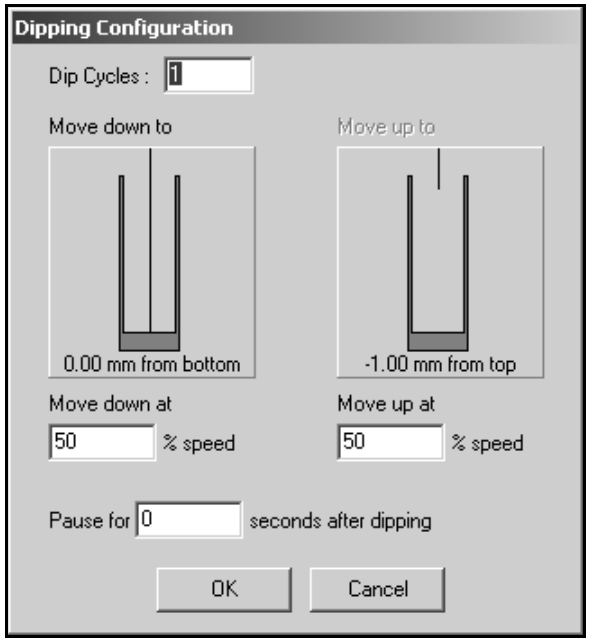


Figure 19-11. Dipping Configuration

8. In Dip Cycles, enter the number of times the pins should descend into the wells to deposit liquid.

   Note: For Dip Cycles greater than **1**, Move up to must be configured.

9. In Move down to, specify the height the pins descend to for each dipping cycle.

   Note: By default, Move down to is measured from bottom of the well. To measure from top of the well or from liquid, right click the graphic of the pin in the well and make the desired selection from the menu.

   Note: The Move down to height can go as much as 2 mm below the bottom of the well as long as the pod can descend that far. Descending below the bottom of the well potentially corrects for any slight imperfections in the labware or deck position heights and can be done safely because the pin push plate is in a floating position, allowing the pins to move up and down freely without resistance. To specify a height below the bottom of the well, right-click the graphic of the pin in the well and select Custom Height. Enter a negative value in Custom Height to move the pins below the bottom of the well.

10. In Move down at, enter the speed of the descent of the HDR Tool Body as a percentage of the maximum speed of the pod.

11. In Move up to, specify the height the pins ascend to between each dipping cycle.

    Note: If Dip Cycles is set to **1**, Move up to is disabled.

    Note: By default, Move up to is measured from bottom of the well. To measure from top of the well or from liquid, right click the graphic of the pin in the well and make the desired selection from the menu.

12. In Move up at, enter the speed at which the HDR Tool Body moves up as a percentage of the maximum speed of the pod.

13. In Pause for, enter the length of time the pod pauses at the down position for each Dip Cycle to deposit liquid.

14. Choose **OK** to save the Dipping Configuration and return to the source labware configuration.

15. Choose **Array Configuration** to configure arrays for the destination wells. Array Configuration appears (Figure 19-12).

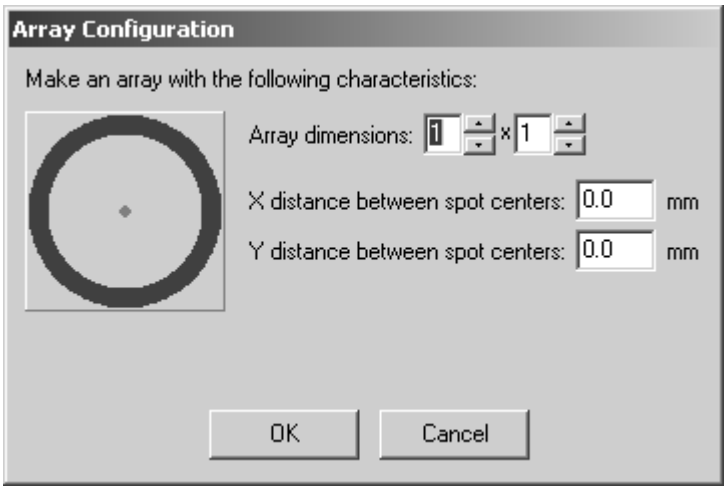


Figure 19-12. Array Configuration

Note: It is recommended that destination labware is placed on a Positive Position ALP during gridding applications for best results. Refer to the *ALPs User's Manual,* Chapter 15, *Positive Position ALP*, for more information on the Positive Position ALP.

16. In Array dimensions, select the desired size of the array. The first value changes the number of rows in the array and the second value changes the number of columns in the array.

Note: The maximum Array dimension is **6x6** when transferring to a 96-well microplate or **4x4** when transferring to a 384-well microplate.

17. In X distance between spot centers, enter the distance in millimeters (mm) between the centers of adjacent spots in each row.

Note: The X distance between spot centers updates automatically as the second value in Array dimensions changes.

18. In Y distance between spot centers, enter the distance in millimeters (mm) between the centers of adjacent spots in each column.

Note: The Y distance between spot centers updates automatically as the first value in Array dimensions changes.

19. Choose **OK** to save the Array Configuration and return to the Destination Labware configuration.

20. Leave the pin height as is to use the settings for the Move down to height specified in the Dipping Configuration.

    OR

    Set the pin height manually using one of the following methods:

    - Position the cursor over the graphic of a pin inside a well. Click and drag the graphic up or down. The pin moves with the cursor, and the height displayed below the graphic is adjusted as the graphic is manipulated.

      Note: The cursor changes to a hand when positioned over the graphic.

    - Select the graphic of a pin inside a well, and use the ↑ and ↓ keys. The textual representation of the height, which is displayed below the graphic, adjusts in 0.1 millimeter (mm) increments.
    - Right-click on the graphic of a pin inside a well, and a menu appears. Select **Custom Height**, and Custom Height appears (Figure 19-8). Insert the **Height** in millimeters (mm) and, in **from**, select a reference point from the drop-down list. Choose **OK**.

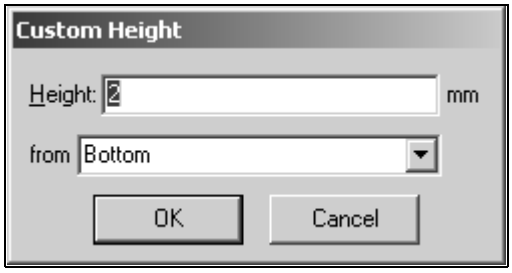


Figure 19-13. Custom Height prompt

21. For an HDR Transfer step, repeat steps 1 to 20 for each additional piece of Destination Labware.

19.4 Using the HDR Tool Cleaning Step

The HDR Tool Cleaning step washes pins on the HDR Tool Body. The HDR Tool Cleaning step uses a "dunk and dry" methodology to wash pins by dipping the pins in one or more reservoirs with wash solutions and drying the pins over a fan.

Note: To clean pins between transfers of an HDR Transfer or HDR Combine step, the HDR Tool Cleaning step must be inserted in a Define Procedure step.

The HDR Tool Cleaning step configuration is similar to that of the HDR Transfer or HDR Combine step. Instead of Source and Destination configurations, however, a series of wash operations — either dipping the pins into a wash reservoir or drying the pins at the HDR Pin Drying ALP — are configured. Cleaning operations are performed in the order they are configured.

The HDR Tool Cleaning step configuration includes specifying:

- Pod that performs the cleaning operations.
- Cleaning operation configuration(s).

To configure an HDR Tool Cleaning step:

1. Insert an HDR Tool Cleaning step into the Method View (Figure 19-14).

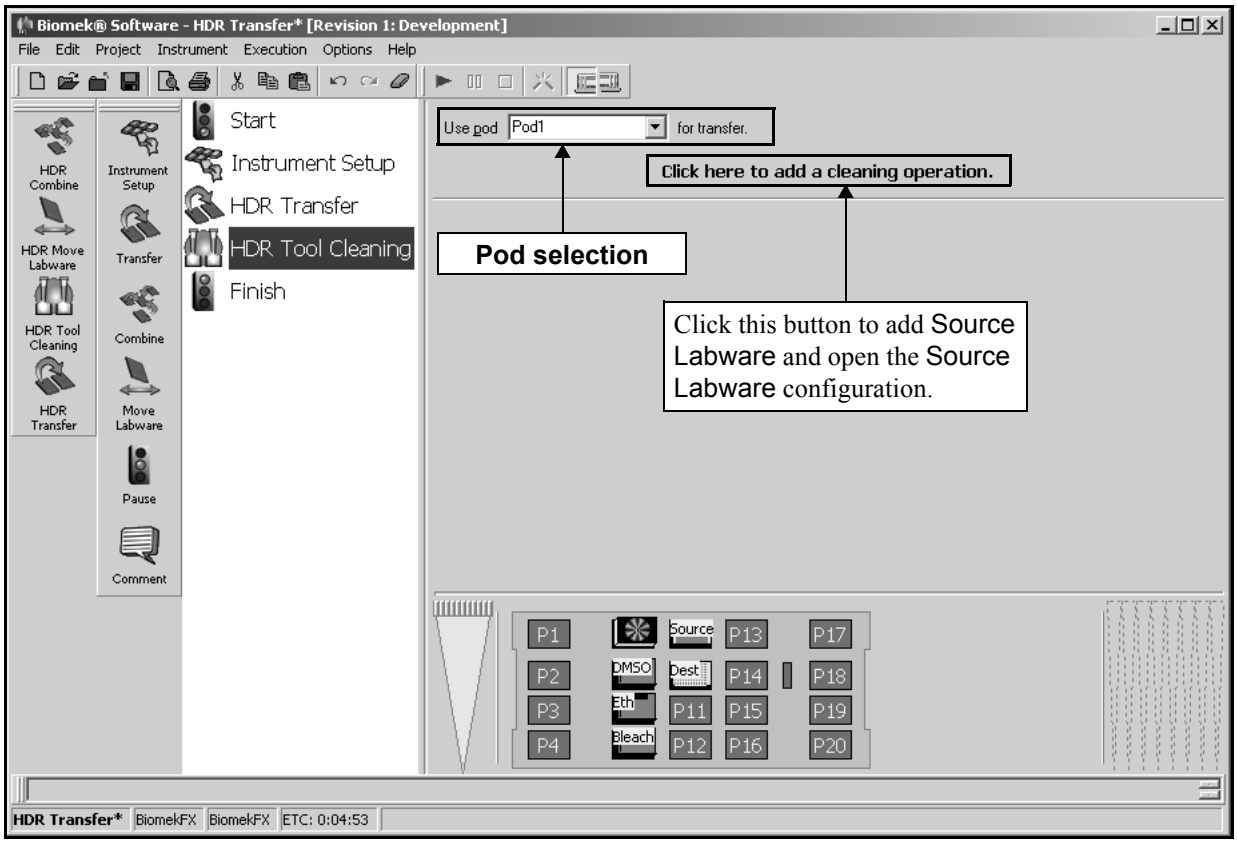


Figure 19-14. HDR Tool Cleaning step configuration

2. In Use pod, specify the pod with the HDR Tool Body used to perform the transfer operations.

   ➢ ***3000*** — Use pod does not appear in the step configuration.

3. Configure Cleaning Operations as described in Section 19.4.1, *Configuring Cleaning Operations*.

19.4.1 Configuring Cleaning Operations

The HDR Tool Cleaning step is configured through a series of cleaning operations. There are two types of Cleaning Operations:

- Wash Operations — pins are dipped in wash solution in a reservoir, deep-well microplate, or other labware type (refer to Section 19.4.1.1, *Configuring a Wash Operation*).
- Drying Operations — pins are air-dried by a fan at the HDR Pin Drying ALP on a Biomek FX instrument or the HDR Fan on the tool rack on a Biomek 3000 instrument (refer to Section 19.4.1.2, *Configuring a Drying Operation*).

As many Cleaning Operations as desired can be configured in the HDR Tool Cleaning step.

Note: Cleaning operations are performed in the order they are listed in the step configuration.

19.4.1.1 Configuring a Wash Operation

A Wash operation dips pins in a piece of labware a specified number of times for a specified length of time. Usually a reservoir is used as Wash labware, but pins can be dipped in any labware type.

To configure a wash operation for the HDR Tool Cleaning step:

CAUTION: Do not attempt to access a 96-Channel or 384-Channel Tip Wash ALP with a Multichannel Pod equipped with an HDR Tool Body. The gripper may crash and damage the pod, HDR Tool Body, or Tip Wash ALP.

CAUTION: Do not access labware positioned on a 1 x 5 Passive ALP with the HDR Tool Body. The gripper may crash with the ALP.

CAUTION: Do not access labware on a Stirring ALP with the HDR Tool Body. The magnetic stirrer may bend the pins or interfere with the liquid transfer performance of the pins.

1. Select **Click here to add a cleaning operation** (Figure 19-14). The Cleaning Operation configuration appears.

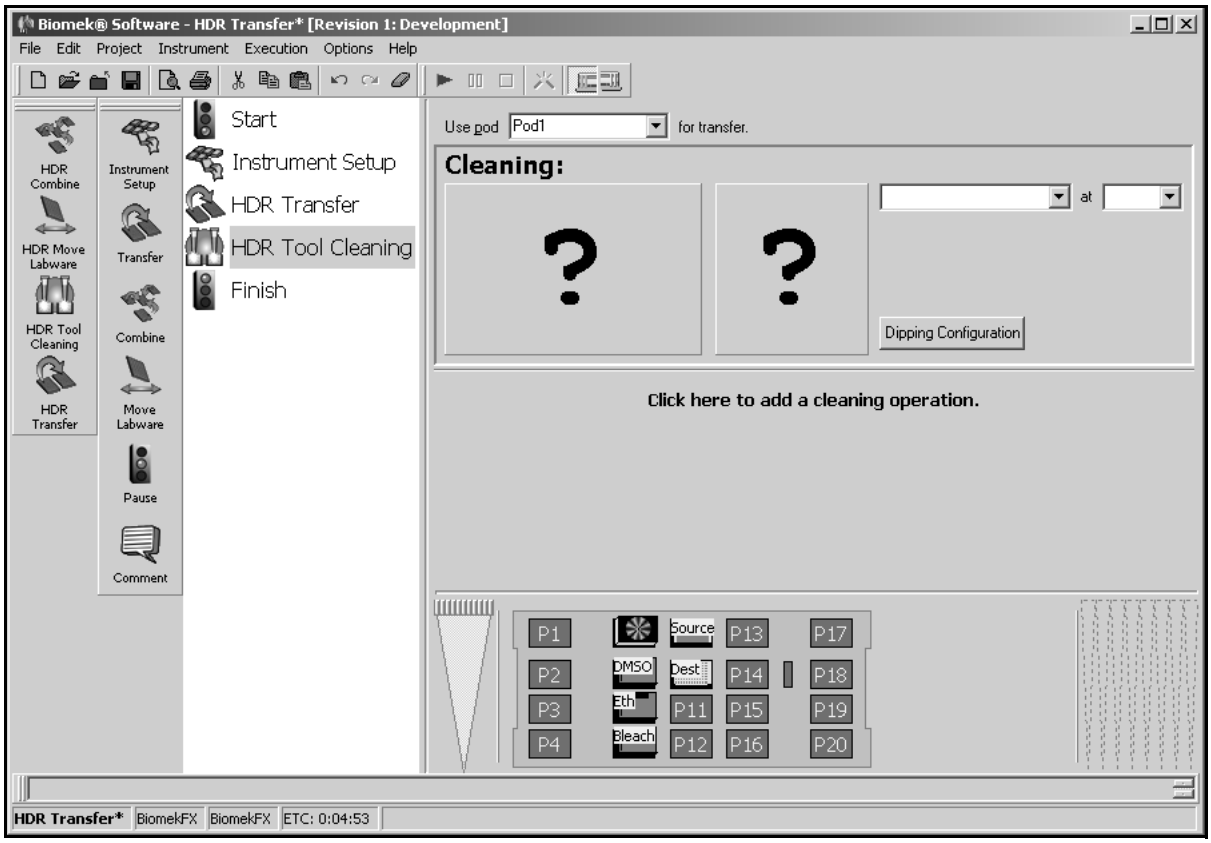


Figure 19-15. HDR Tool Cleaning step — new cleaning operation configuration

2. Click on the piece of labware with the desired wash solution in the Current Deck Display. The labware type and position for that piece of labware is entered automatically into the Cleaning Operation configuration (Figure 19-14).

Note: If the selected labware is named, the name of the labware appears instead of the deck position.

OR

Select a **Cleaning** Labware type (Figure 19-14) and deck position.

Note: Subsequent labware selections modify the active Cleaning Operation configuration. To configure additional Cleaning Operations, select **Click here to add a cleaning operation**, or select outside a cleaning operation configuration, and then select another piece of labware from the Current Deck Display. If an incorrect piece of labware is selected, right-click on the labware title and select **Delete** on the menu that appears.

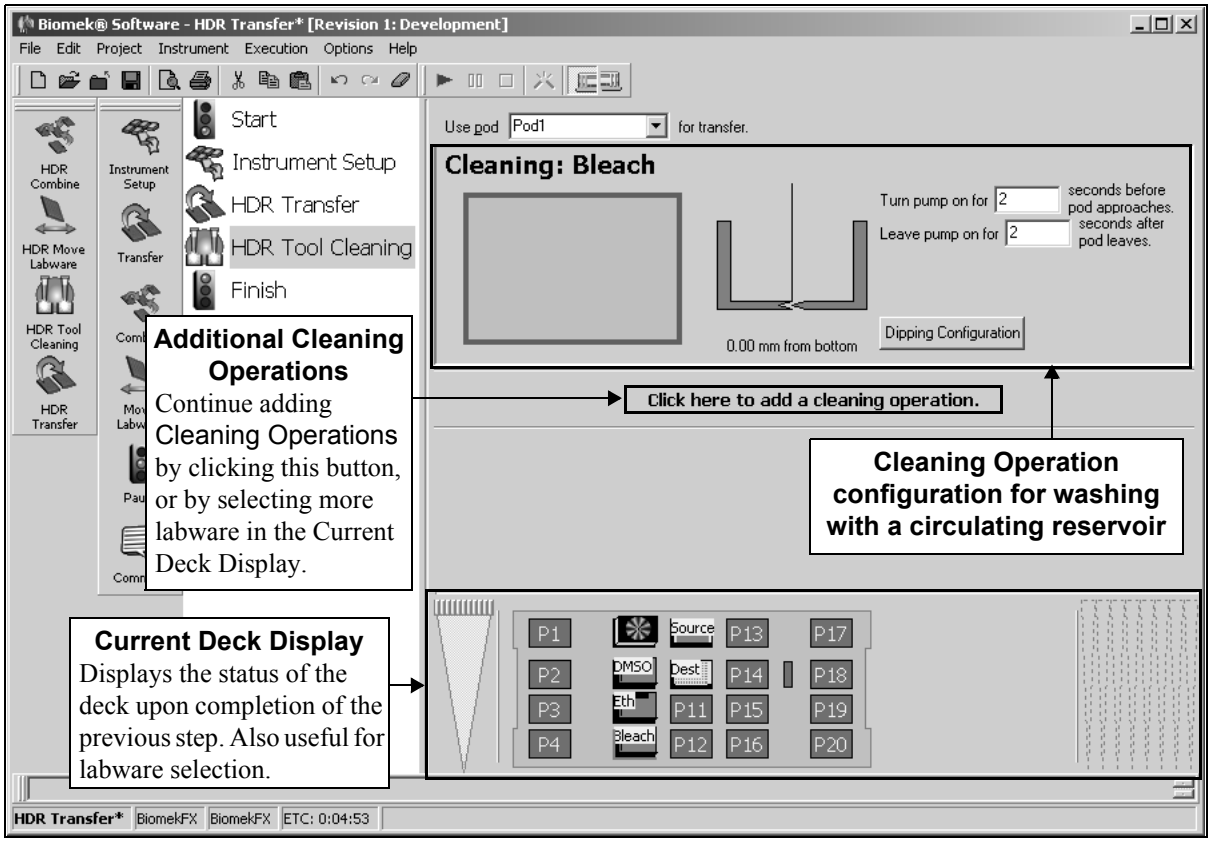


Figure 19-16. HDR Tool Cleaning step — configuration for a wash operation

3. If the Cleaning labware selected is a static reservoir or microplate, verify the labware type and deck position of the labware.

   Note: A bright blue outline appears in the Current Deck Display around the labware designated for the first Cleaning operation; a yellow outline appears in the Current Deck Display around labware designated for any subsequent Cleaning operations.

   OR

   On an ***FX*** instrument, if the Cleaning labware selected is a circulating reservoir (Figure 19-14):

   - In Turn pump on for, enter the length of time in seconds to turn the wash pump on before the HDR Tool Body moves to the circulating reservoir.

     Note: The default value for Turn pump on for is **2** seconds.

   - In Leave pump on for, enter the length of time in seconds to leave the wash pump on after the HDR Tool Body moves away from the circulating reservoir.

     Note: The default value for Leave pump on for is **2** seconds.

4. To specify the quadrants of a microplate to access, double-click the source labware in the step configuration to zoom in on the labware.

   Note: To call up a menu for Zoom and a Specify Selection as Text option, right-click on the labware.

   Specify Selection as Text allows selection of quadrants as targets for aspirate and dispense operations. Specify Selection as Text may also be used to enter variables or expressions (refer to Section 13.2, *Using Variables* and Section 13.3, *Using Expressions*).

   Note: Specify Selection as Text is not applicable for 96-well microplates, reservoirs, or 384-well microplates accessed by a 384-pin plate.

5. Select the desired quadrant(s) on the zoomed-in graphic of the labware.

   Note: Selecting any well automatically selects all wells in that quadrant.

   Note: To select multiple quadrants, click and drag over the desired quadrants or hold down **Ctrl** or **Shift** and select the desired quadrants.

6. Choose **Zoom Out** to return to the step configuration screen.

7. Choose **Dipping Configuration** to configure the wash operation. Dipping Configuration appears (Figure 19-17).

Note: The Dipping Configuration is similar to a pipetting technique. It specifies the method in which pins are washed.

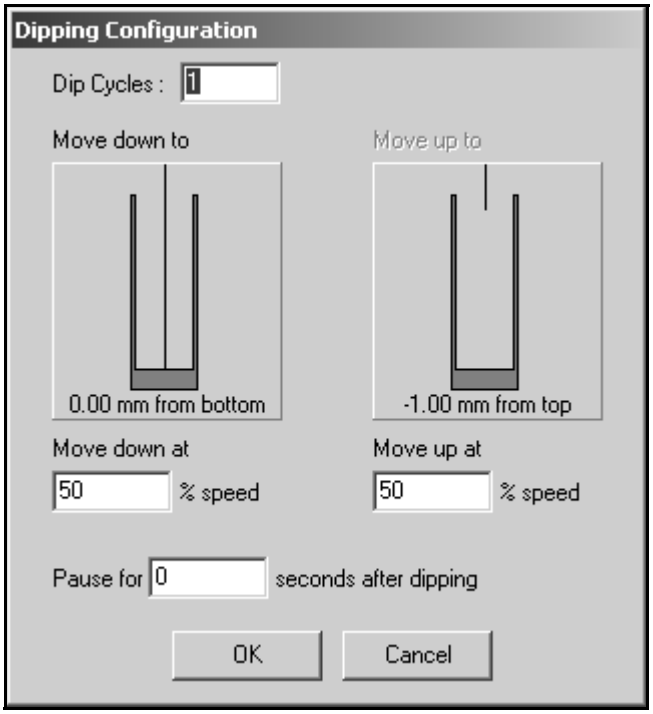


Figure 19-17. Dipping Configuration

8. In Dip Cycles, enter the number of times the pins should descend into the wells.

Note: For Dip Cycles greater than **1**, Move up to must be configured.

9. In Move down to, specify the height the pins descend to for each dipping cycle.

Note: By default, Move down to is measured from bottom of the well. To measure from top of the well or from liquid, right click the graphic of the pin in the well and make the desired selection from the menu.

Note: The Move down to height can go as much as 2 mm below the bottom of the well as long as the pod can descend that far. Descending below the bottom of the well potentially corrects for any slight imperfections in the labware or deck position heights and can be done safely because the pin push plate is in a floating position, allowing the pins to move up and down freely without resistance. To specify a height below the bottom of the well, right-click the graphic of the pin in the well and select Custom Height. Enter a negative value in Custom Height to move the pins below the bottom of the well.

10. In Move down at, enter the speed of the descent of the HDR Tool Body as a percentage of the maximum speed of the pod.

11. In Move up to, specify the height the pins ascend to between each dipping cycle.

    Note: If Dip Cycles is set to **1**, Move up to is disabled.

    Note: By default, Move up to is measured from bottom of the well. To measure from top of the well or from liquid, right click the graphic of the pin in the well and make the desired selection from the menu.

12. In Move up at, enter the speed at which the HDR Tool Body moves up as a percentage of the maximum speed of the pod.
13. In Pause for, enter the length of time the pod pauses at the down position for each Dip Cycle to wash pins.
14. Choose **OK** to save the Dipping Configuration and return to the source labware configuration.
15. Leave the pin height as is to use the settings for the Move down to height specified in the Dipping Configuration.

    OR

    Set the pin height manually using one of the following methods:

    - Position the cursor over the graphic of a pin inside a well. Click and drag the graphic up or down. The pin moves with the cursor, and the height displayed below the graphic is adjusted as the graphic is manipulated.

      Note: The cursor changes to a hand when positioned over the graphic.

    - Selecting the graphic of a pin inside a well, and use the ↑ and ↓ keys. The textual representation of the height, which is displayed below the graphic, adjusts in 0.1 millimeter (mm) increments.
    - Right-click on the graphic of a pin inside a well, and a menu appears. Select **Custom Height**, and Custom Height appears (Figure 19-8). Insert the **Height** in millimeters (mm) and, in **from**, select a reference point from the drop-down list. Choose **OK**.

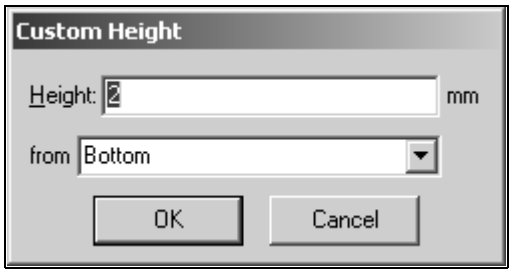


Figure 19-18. Custom Height prompt

16. Configure additional Cleaning Operations following the procedures in Sections 19.4.1.1, *Configuring a Wash Operation* and 19.4.1.2, *Configuring a Drying Operation*.

19.4.1.2 Configuring a Drying Operation

To configure a drying operation for the HDR Tool Cleaning step:

1. Select **Click here to add a cleaning/drying operation**. The Cleaning Operation configuration appears (Figure 19-19).

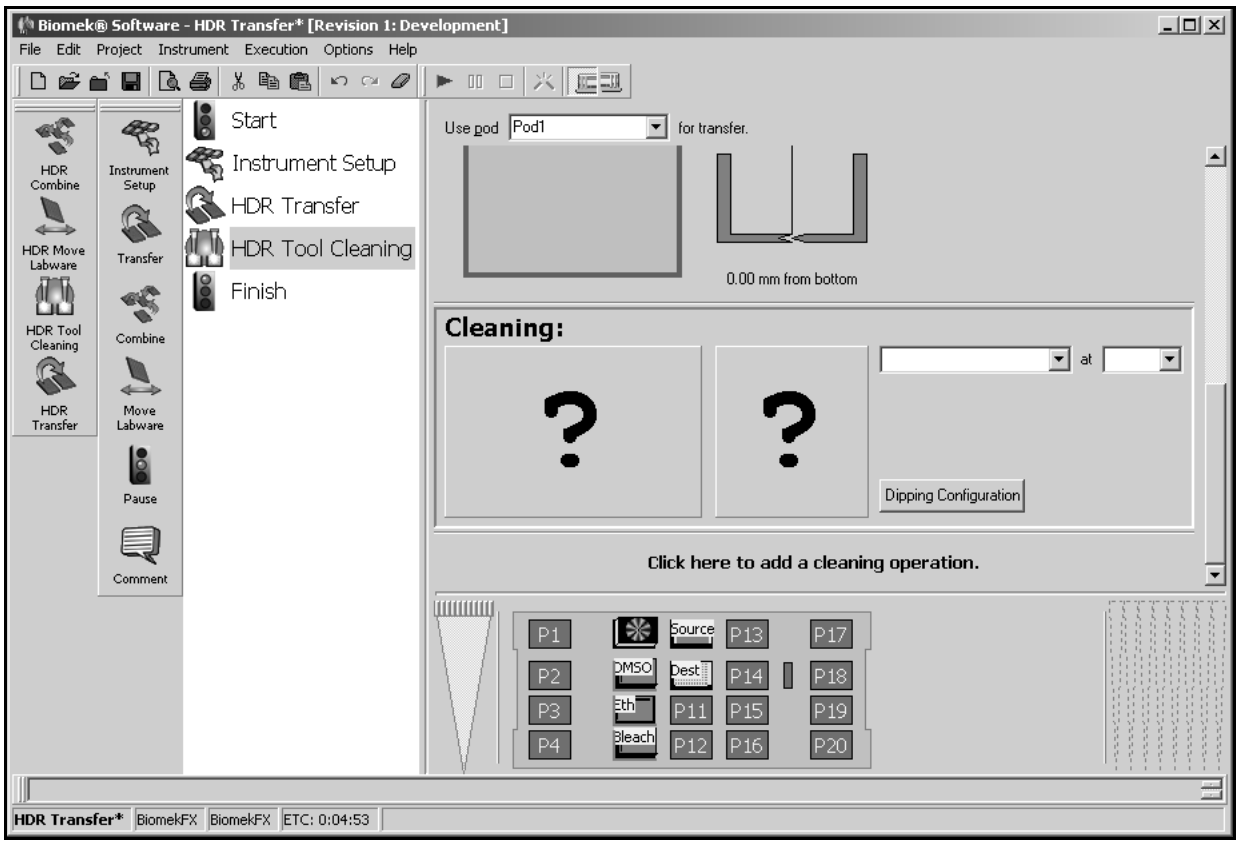


Figure 19-19. HDR Tool Cleaning step — new cleaning operation configuration

2. Click on the position with the fan (either the HDR Pin Drying ALP on the Biomek FX instrument or the tool rack with the HDRFan tool installed on the Biomek 3000 instrument) in the Current Deck Display. Information for the fan is entered automatically into the Cleaning Operation configuration.

Note: Subsequent labware selections modify the active Cleaning Operation configuration. To configure additional Cleaning Operations, select **Click here to add a cleaning operation**, or select outside a cleaning operation configuration, and then select another piece of labware from the Current Deck Display. If an incorrect piece of labware is selected, right-click on the labware title and select **Delete** on the menu that appears.

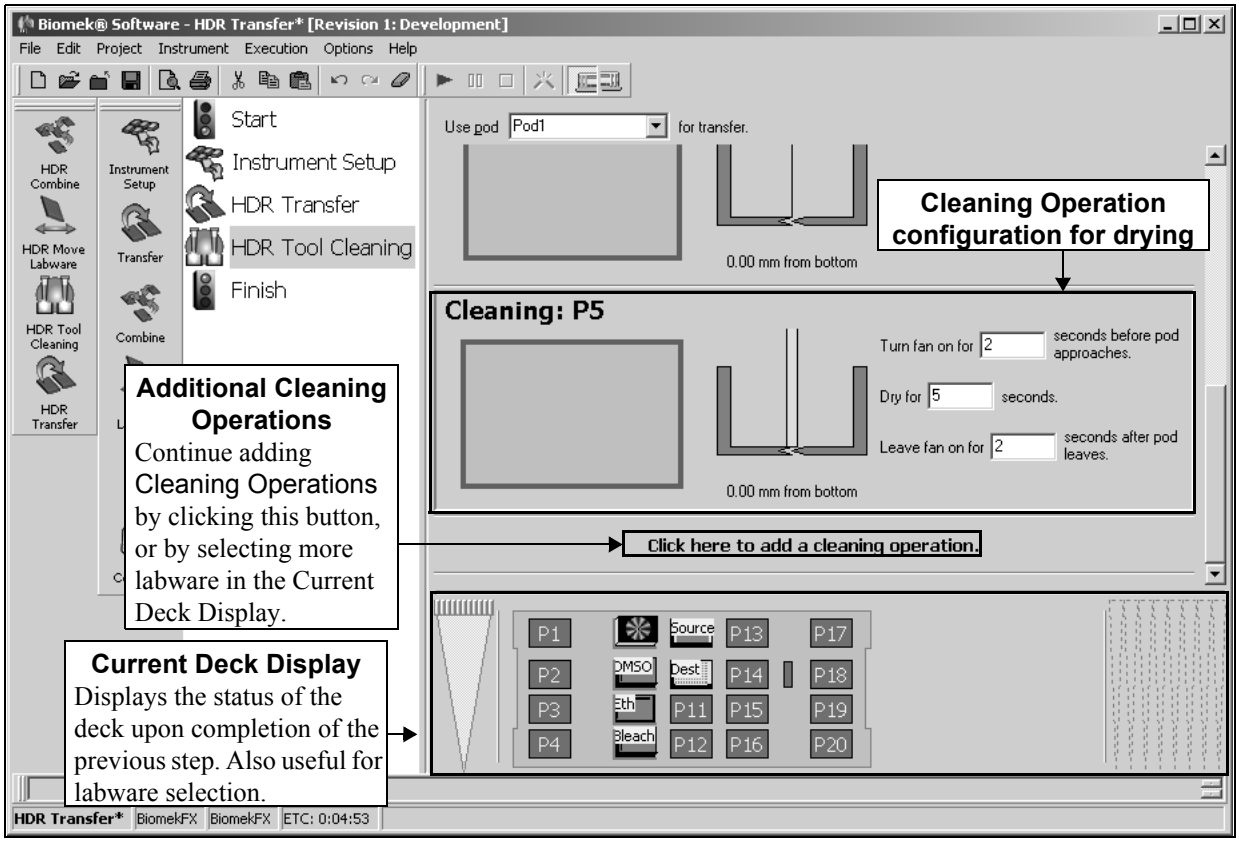


Figure 19-20. HDR Tool Cleaning step — configuration for a drying operation

3. In Turn fan on for, enter the length of time in seconds to turn the fan on before the HDR Tool Body moves to the HDR Pin Drying ALP.

Note: The default value for Turn fan on for is **2** seconds.

- ***3000*** — Turn on for is not available because the fan unit is not controlled by Biomek Software.

4. In Dry for, enter the length of time in seconds to keep the HDR Tool Body at the HDR Pin Drying ALP to dry.

Note: The default value for Dry for is **5** seconds.

5. In Leave fan on for, enter the length of time in seconds to leave the fan on after the HDR Tool Body moves away from the HDR Pin Drying ALP.

Note: The default value for Leave fan on for is **2** seconds.

➢ ***3000*** — Leave on for is not available because the fan unit is not controlled by Biomek Software.

6. Leave the pin height as is to use the default setting.

   OR

   Set the pin height manually using one of the following methods:

   - Position the cursor over the graphic of a pin inside a well. Click and drag the graphic up or down. The pin moves with the cursor, and the height displayed below the graphic is adjusted as the graphic is manipulated.
   - Selecting the graphic of a pin inside a well, and use the ↑ and ↓ keys. The textual representation of the height, which is displayed below the graphic, adjusts in 0.1 millimeter (mm) increments.
   - Right-click on the graphic of a pin inside a well, and a menu appears. Select **Custom Height**, and Custom Height appears (Figure 19-8). Insert the **Height** in millimeters (mm) and, in **from**, select a reference point from the drop-down list. Choose **OK**.

Note: The cursor changes to a hand when positioned over the graphic.

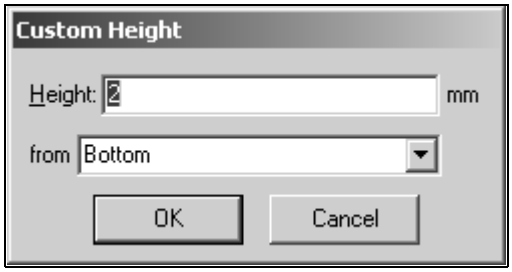


Figure 19-21. Custom Height prompt

7. Configure additional Cleaning Operations following the procedures in Sections 19.4.1.1, *Configuring a Wash Operation* and 19.4.1.2, *Configuring a Drying Operation*.

19.5 Using the HDR Move Labware Step (FX only)

The HDR Move Labware step moves labware from one position on the Biomek FX deck to another position. HDR Move Labware can also remove labware from the deck by placing it in a Disposal ALP or moving it to an external hardware device without halting the Biomek FX or the method, and without causing a light curtain violation.

Note: The HDR Move Labware step should be used only when moving labware with a Multichannel Pod that has the HDR Tool Body installed. If the pod is equipped with any other multichannel head, use the Move Labware step found on the Basic Step Palette (refer to Section 15.4, *Move Labware Step*). A validation error results if the inappropriate Move Labware step is used.

Insert an HDR Move Labware step into the Method View (Figure 19-22).

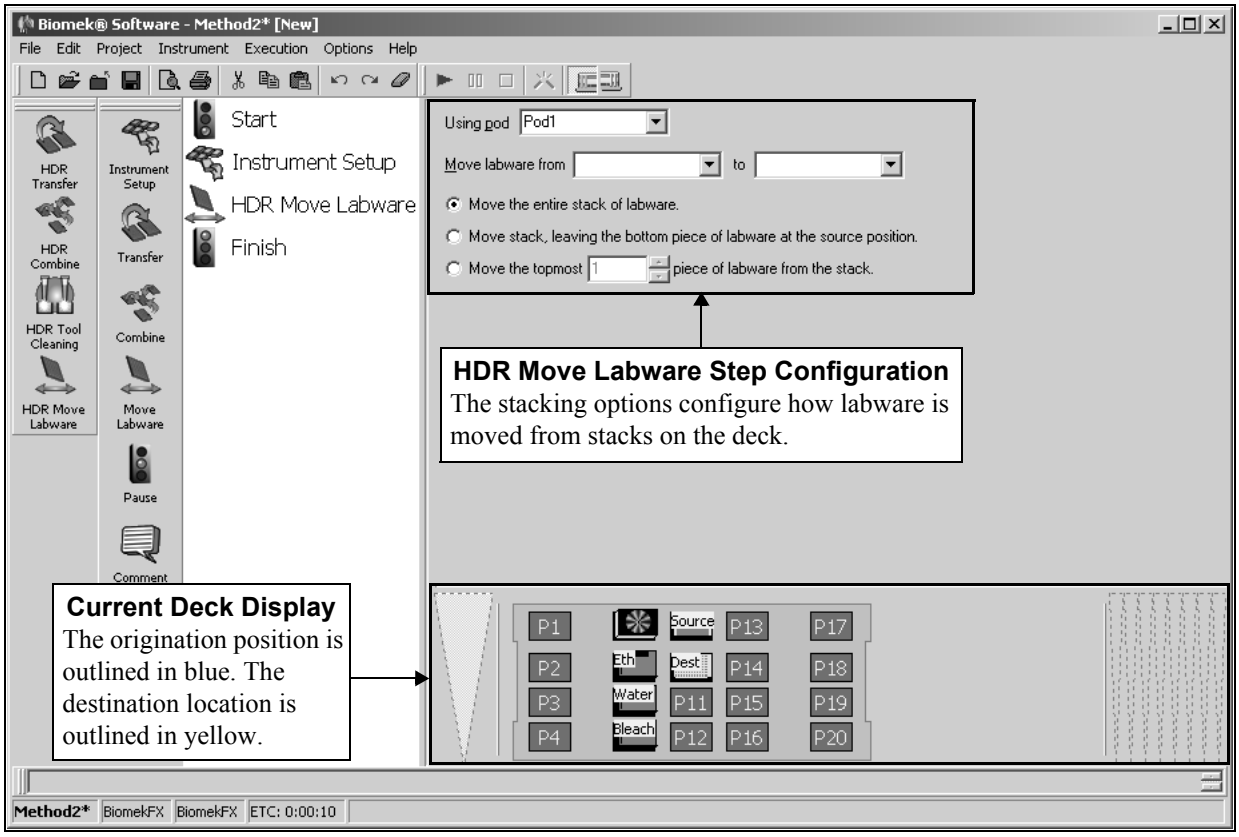


Figure 19-22. HDR Move Labware step and configuration

19.5.1 Configuring the HDR Move Labware Step

To configure an HDR Move Labware step, complete the following steps:

CAUTION: Make sure the correct ALP is chosen when configuring the deck setup in the Deck Editor. ALPs vary in height, and failure to choose each ALP correctly in the software may result in collisions between pod(s) and ALPs during operation.

CAUTION: Do not access labware positioned on a 1 x 5 Passive ALP with the HDR Tool Body. The gripper may crash with the ALP.

1. In Using Pod, select the pod moving the labware.

   Note: In Using Pod, Pod1 is the default for a one-pod Biomek FX system. In a two-pod Biomek FX system, the pod configured as the default pod is displayed in Using Pod. If the other pod is desired, select the pod from the drop-down list. Only a Multichannel Pod with the HDR Tool Body installed may use the HDR Move Labware step.

2. In Move labware from, select the original deck position for the labware from the Current Deck Display. This instructs the Biomek FX to Move labware from a specific deck position in preparation for leaving it at a final destination.

3. In to, select the final deck position for the labware from the Current Deck Display. This instructs the Biomek FX to move the labware to a final deck position.

4. Select the desired option for moving stacked labware:

   - **Move the entire stack of labware** — moves all labware in the stack; this option should be selected when moving a single unstacked piece of labware.
   - **Move stack, leaving the bottom piece of labware at the source position** — moves all labware in the stack except for the bottom piece.

     Note: Selecting Move stack, leaving the bottom piece of labware at the source position when the source deck position contains only one piece of labware results in an error.

   - **Move the topmost . . .piece(s) of labware from the stack —** moves only the specified number of labware from the top of the stack.

   Note: Refer to Section 7.3.6.4.1, *Biomek Stacking Rules*, for complete information on using stacks with the Biomek FX instrument.

20 Using the Biomek 3000 Step Palette

20.1 Overview

The Biomek 3000 Step Palette provides steps for use specifically with a Biomek 3000 workstation, including tool loading and unloading and aspirate and dispense operations with the Wash System.

The steps available in the Biomek 3000 Step Palette are:

- Change Tool — unloads the tool currently loaded on the Biomek 3000 head assembly to an empty tool rack position and loads the specified tool.

- Load Tool — locates the specified tool on the deck and loads it to the Biomek 3000 head assembly.

- Unload Tool — unloads the tool currently loaded on the Biomek 3000 head assembly to an empty tool rack position.

- Remove to Waste — aspirates liquid to waste using a wash tool.

- Bulk Dispense — performs a bulk dispense operation from a wash liquid container using a wash tool.

- Purge Wash Tool — purges the tubing of the wash system and wash tool.

- Wash Plate — perform a plate washing operation using a wash tool.

When one of the above steps is added to a method, the configuration for the step appears on the right side of the Biomek main editor, in step configuration (Figure 20-1).

Note: Steps not configured appropriately in Step Configuration generate errors when the method is validated or run.

20.2 Displaying the Biomek 3000 Step Palette

In order to add Biomek 3000 steps to a method, display the Biomek 3000 Step Palette (Figure 20-1).

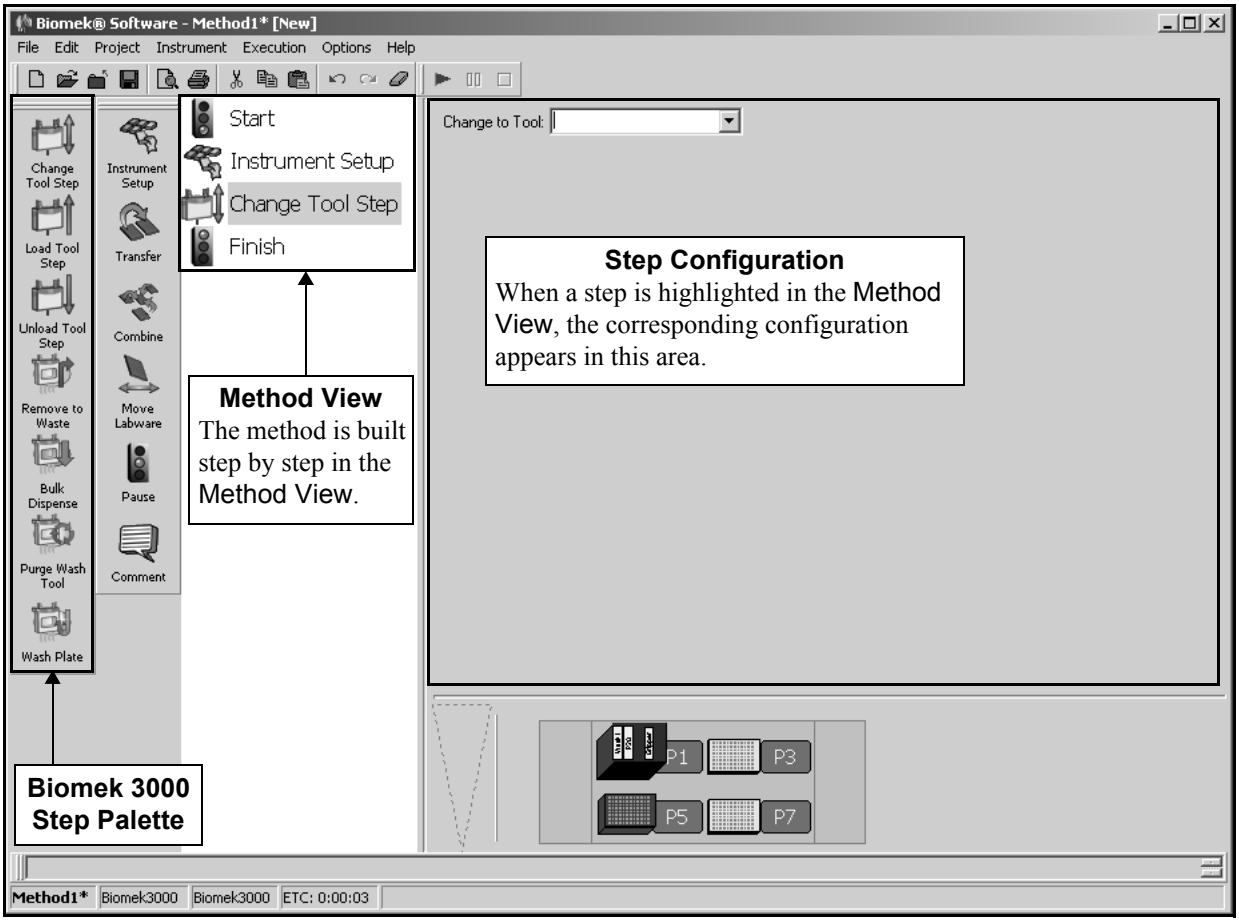


Figure 20-1. Biomek Software main editor with Biomek 3000 Step Palette displayed

To display the Biomek 3000 Step Palette, complete the following:

- Right-click any empty palette space, and the Step Palette menu appears. Select **Biomek3000**.

  OR

- From the toolbar, select **Options>Toolbars>Biomek3000**.

20.3 Change Tool Step

The Change Tool step is used to instruct the Biomek 3000 workstation to unload the tool installed on the head assembly and load a different tool. The Biomek 3000 workstation automatically locates an empty tool rack position, unloads the tool at the empty position, locates the desired tool, and loads the tool to the head assembly.

Note: The Transfer, Combine, and Move Labware steps automatically change to an appropriate tool to perform the operation. However, if a specific tool is desired for an operation, a Change Tool or Load Tool step should be inserted prior to the operation to guarantee the desired tool is used.

Insert a Change Tool step into the method. The Change Tool step configuration appears (Figure 20-2).

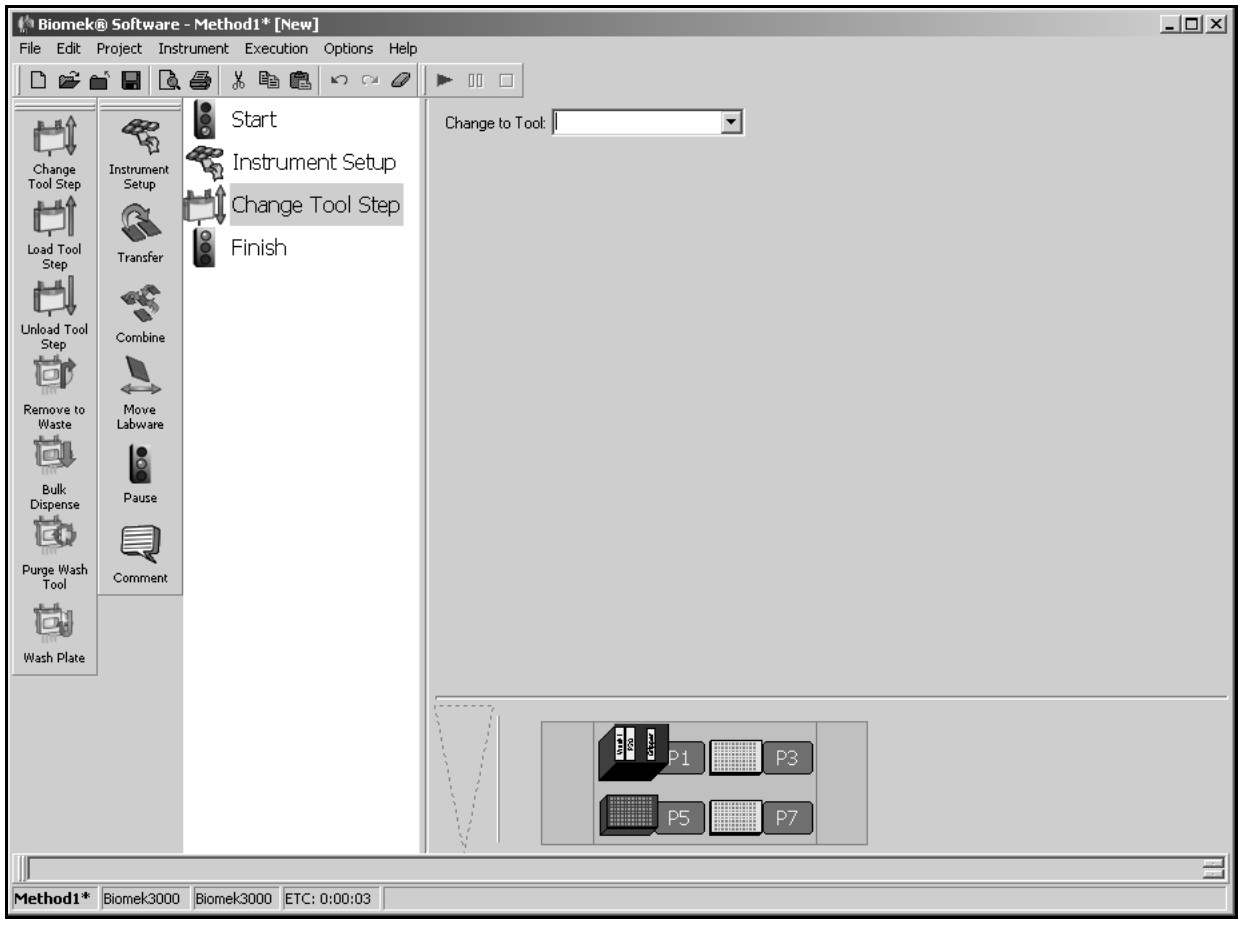


Figure 20-2. Changing tools during a method

To configure the Change Tool step configuration:

1. In Change to Tool, specify the tool to load after unloading the current tool. All tools located on the deck in a tool rack (as configured in Labware Properties for the tool rack in an Instrument Setup step) are available for selection.
2. Select a step that occurs after the Change Tool step or the **Finish** step to validate the step configuration.

20.4 Load Tool Step

The Load Tool step is used to instruct the Biomek 3000 workstation to load a tool to the Biomek 3000 head assembly when no tool is currently installed. The Biomek 3000 workstation automatically locates the desired tool in a tool rack and loads the tool to the head assembly.

Note: The Transfer, Combine, and Move Labware steps will automatically change to an appropriate tool to perform the operation. However, if a specific tool is desired for an operation, a Change Tool or Load Tool step should be inserted prior to the operation to guarantee the desired tool is used.

Insert a Load Tool step into the method. The Load Tool step configuration appears (Figure 20-3).

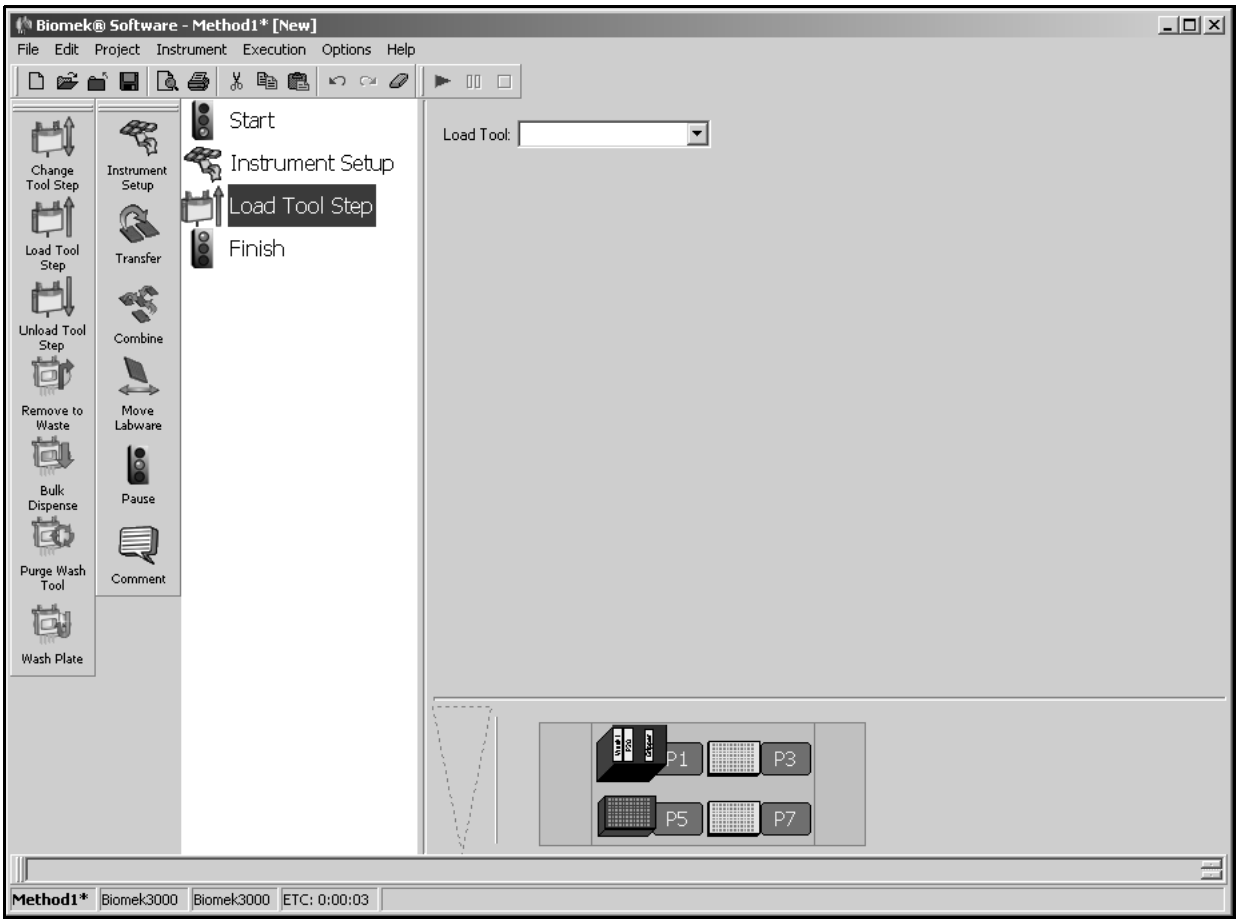


Figure 20-3. Loading tool during a method

To configure the Load Tool step configuration:

1. In Load Tool, specify the tool to load to the head assembly. All tools that are located on the deck in a tool rack (as configured in the Labware Properties for the tool rack in an Instrument Setup step) are available for selection.
2. If the tool selected in Load Tool is a wash tool, in Liquid, select the liquid type to purge the tubing and wash tool with after loading the tool. Biomek Software automatically performs a purge operation similar to a *Purge Wash Tool Step* (Section 20.8) with the selected Liquid when the tool is loaded.

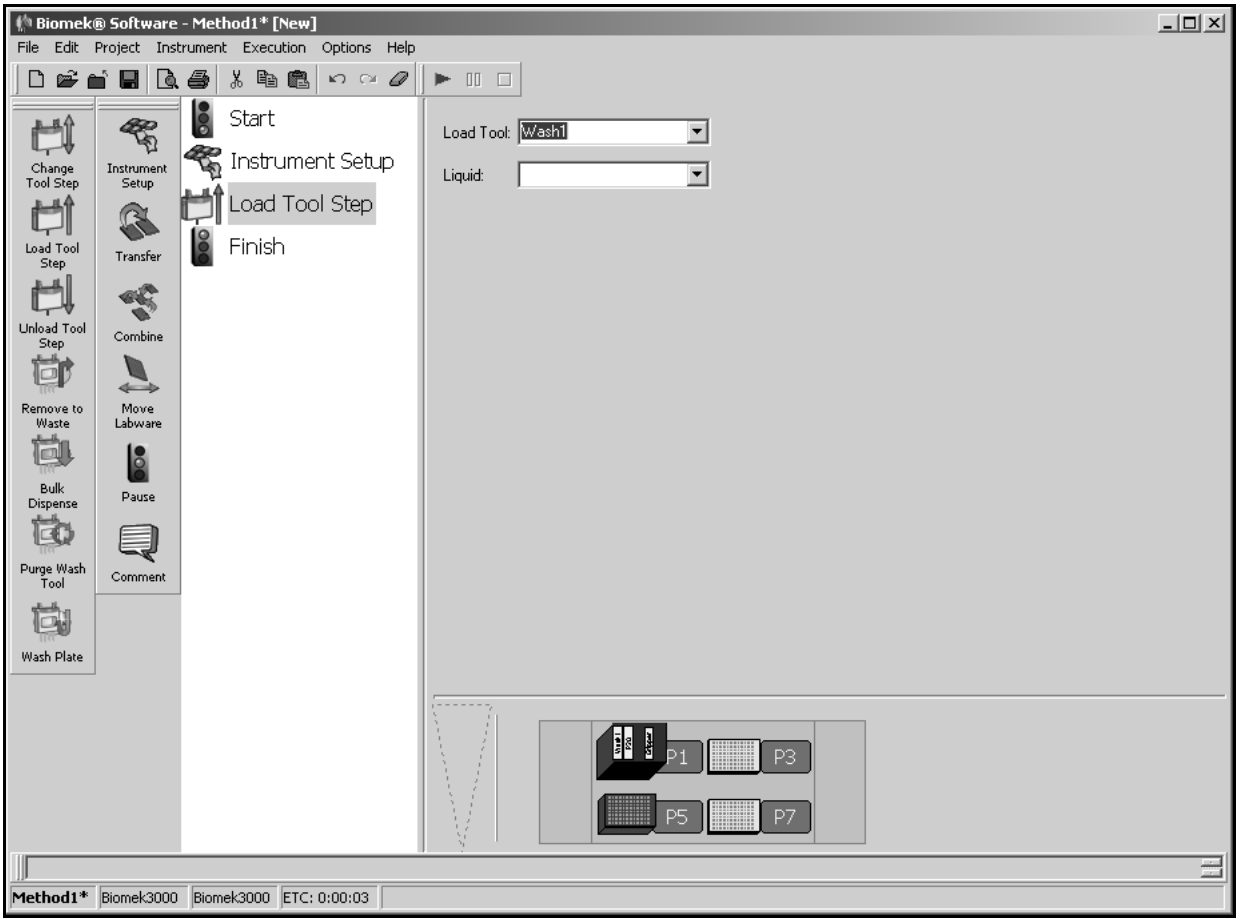


Figure 20-4. Load Tool step configuration with wash tool selected

3. Select a step that occurs after the Load Tool step or the **Finish** step to validate the step configuration.

20.5 Unload Tool Step

The Unload Tool step is used to instruct the Biomek 3000 workstation to unload the tool installed on the head assembly. The Biomek 3000 workstation automatically locates an empty tool rack position and unloads the tool at the empty position.

A tool must be unloaded before loading a new tool. Many steps, such as Transfer, Combine, and Move Labware automatically unload the current tool and load a more appropriate tool for the operation It is only necessary to use an Unload Tool step when it is desired to unload the current tool prior to loading a specific tool to the head assembly using a Load Tool step.

Note: The Biomek 3000 head assembly can be instructed to automatically unload any tools installed at the end of a method in the Finish step.

Insert an Unload Tool step into the method. The Unload Tool step configuration appears (Figure 20-5).

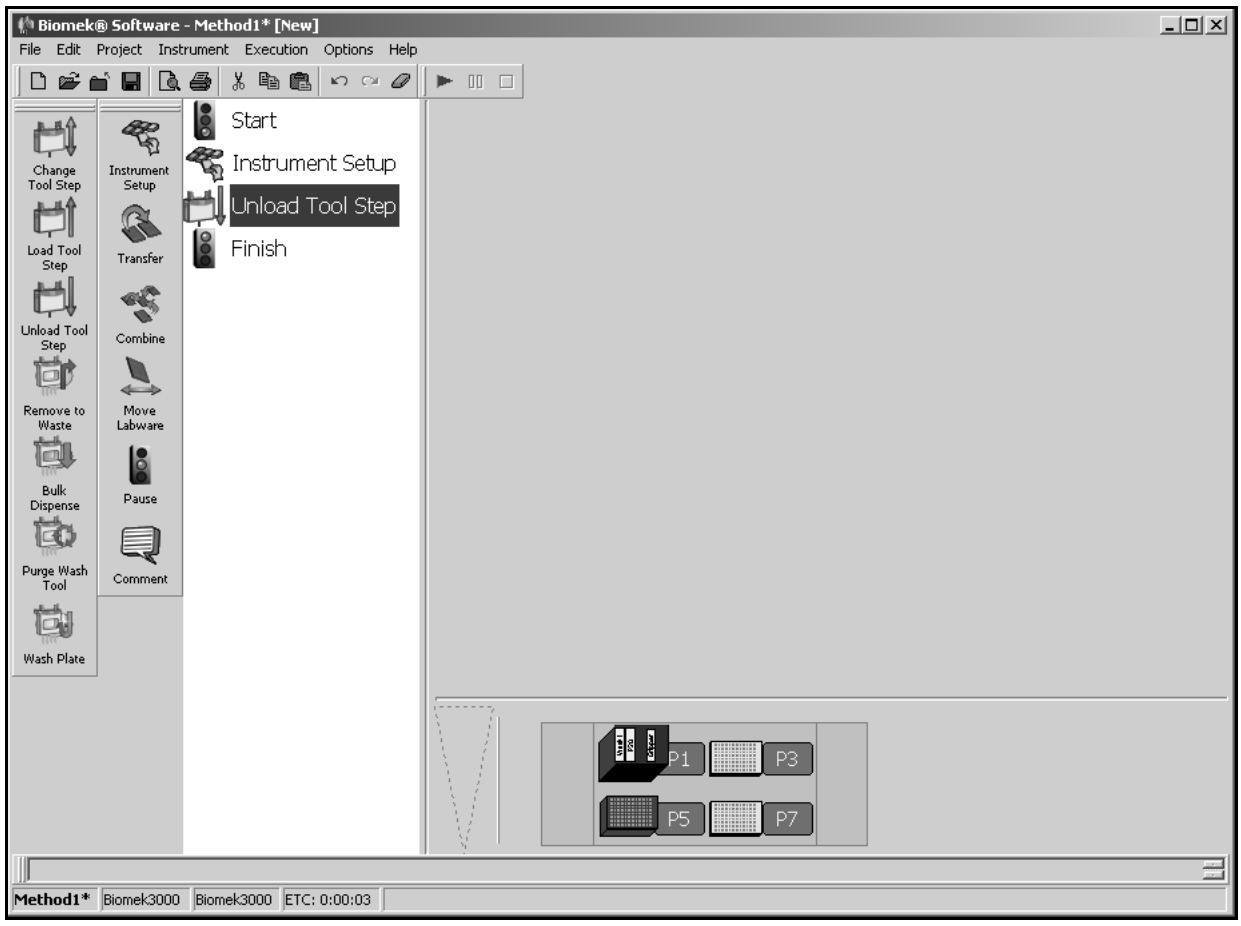


Figure 20-5. Unloading a tool during a method

The Unload Tool step requires no additional configuration. Select a step that occurs after the Unload Tool step or the **Finish** step to validate the step configuration.

20.6 Remove to Waste Step

The Remove to Waste step is used to aspirate liquid using a single-channel or eight-channel wash tool to an off-deck waste container. The wash tools has two needles for each channel: a long aspiration needle and a shorter dispense needle. Liquid is aspirated from the wells using the aspiration needles by applying a vacuum for a specified amount of time and removed to an off-deck waste container.

Note: A Wash Unit must be installed on the Biomek 3000 workstation and connected to an external vacuum pump or vacuum source to aspirate liquid using the Remove to Waste step.

Insert a Remove to Waste step into the method. The Remove to Waste step configuration appears (Figure 20-6).

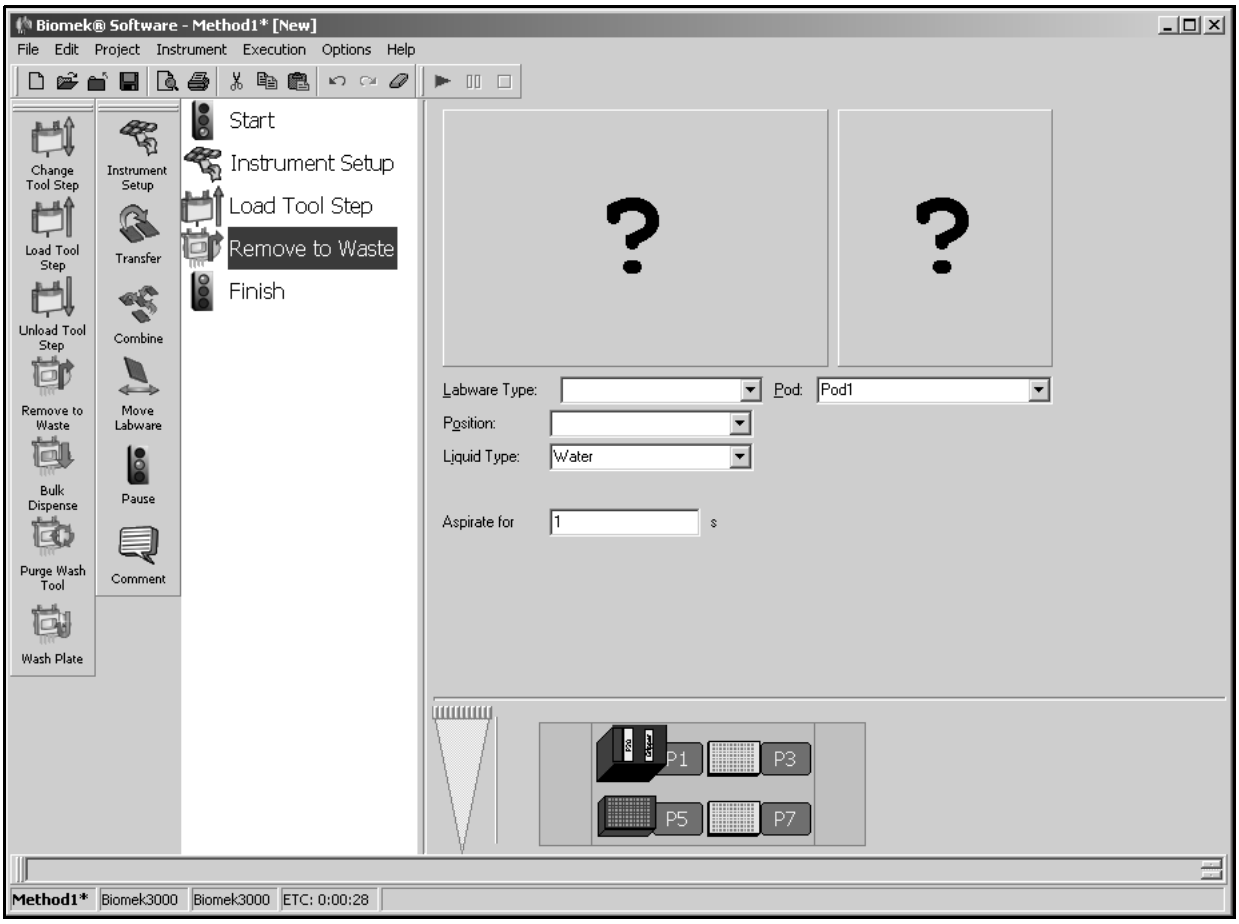


Figure 20-6. Remove to Waste step configuration

Note: A wash tool must be loaded onto the Biomek 3000 head assembly using either a Load Tool or Change Tool step prior to the Remove to Waste step.

Note: If a 6-port valve is installed with the Wash Unit, a Device Action step must be inserted to configure the wash liquids available from each port.

To configure the Remove to Waste step:

1. Click on the desired piece of labware in the Current Deck Display. The Labware Type and Position for that piece of labware is entered automatically into the Remove to Waste step configuration.

   OR

   Select a **Labware Type** and **Position** from the drop-down list.

2. On the plate map, select the wells from which to aspirate liquid to waste.

   Note: Hold **Shift** and click a well to select additional wells without deselecting any wells. Hold **Ctrl** and click a well to toggle the selection status of selected wells without affecting the status of other wells. If Shift or Ctrl is not held down when selecting wells, any previous selection is deleted.

3. In Liquid Type, select the liquid type to aspirate.
4. In Aspirate for, enter the length of time in seconds to apply vacuum and aspirate liquid to waste for each well.
5. Select a step that occurs after the Remove to Waste step or the **Finish** step to validate the step configuration.

20.7 Bulk Dispense Step

The Bulk Dispense step is used to dispense liquid using a single-channel or eight-channel wash tool. The wash tools have two needles for each channel: a long aspiration needle and a shorter dispense needle. Liquid is dispensed from the source wash liquid container through the dispense needles. The volume dispensed is limited only by the amount of liquid in the source container.

After dispensing, a Backup Volume is aspirated by the dispense needles to prevent droplets from forming on the dispense needles. The Backup Volume is set in Hardware Setup (refer to the *Biomek® 3000 Laboratory Automation Workstation User's Manual,* Section 12.4.3, *Configuring Wash Tools*).

Note: A Wash Unit must be installed on the Biomek 3000 workstation to dispense liquid using the Bulk Dispense step.

Insert a Bulk Dispense step into the method. The Bulk Dispense step configuration appears (Figure 20-7).

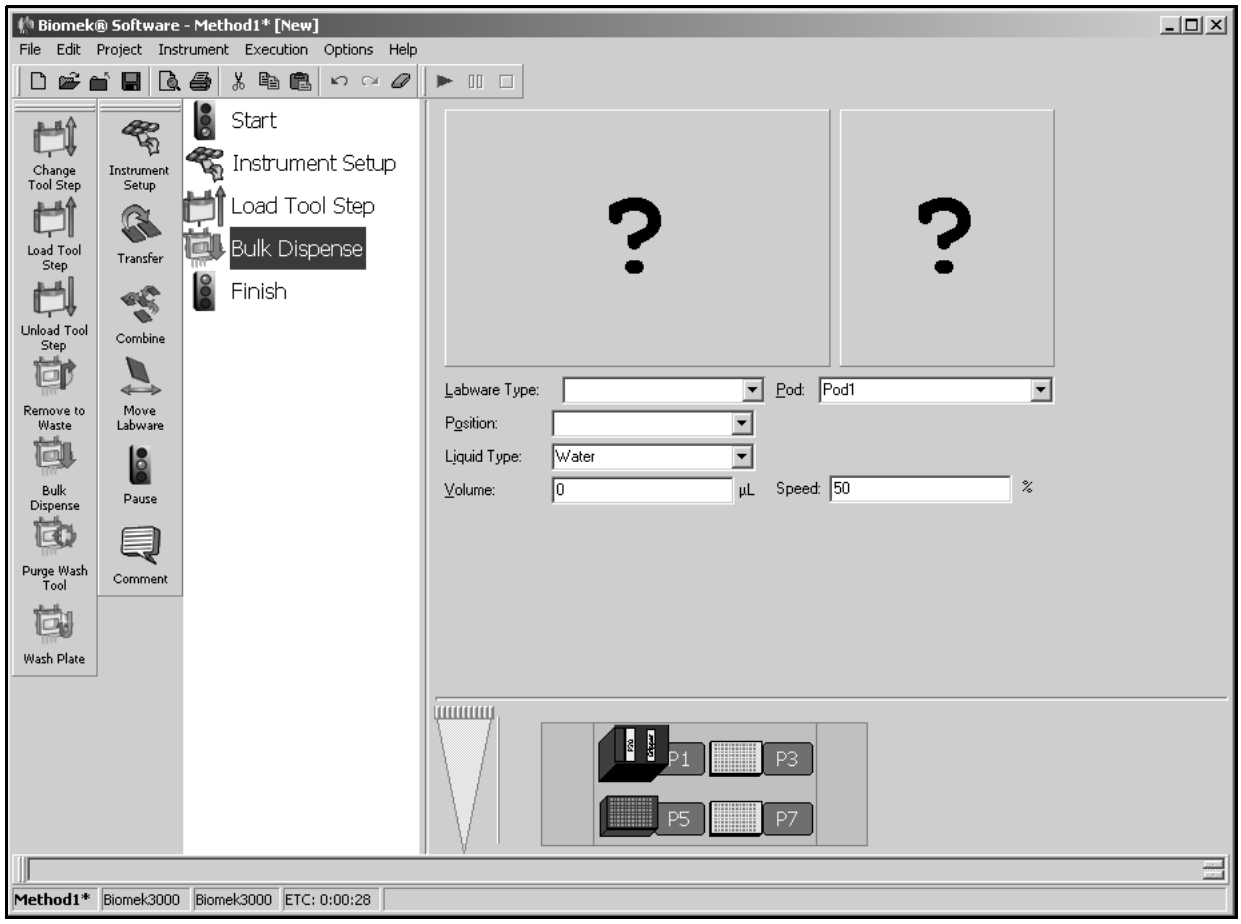


Figure 20-7. Bulk Dispense step configuration

Note: A wash tool must be loaded onto the Biomek 3000 head assembly using either a Load Tool or Change Tool step prior to the Bulk Dispense step.

Note: If a 6-port valve is installed with the Wash Unit, a Device Action step must be inserted to configure the wash liquids available from each port.

To configure the Bulk Dispense step:

1. Click on the desired piece of labware in the Current Deck Display. The Labware Type and Position for that piece of labware is entered automatically into the Bulk Dispense step configuration.

   OR

   Select a **Labware Type** and **Position** from the drop-down list.

2. On the plate map, select the wells from which to aspirate liquid to waste.

   Note: Hold **Shift** and click a well to select additional wells without deselecting any wells. Hold **Ctrl** and click a well to toggle the selection status of selected wells without affecting the status of other wells. If Shift or Ctrl is not held down when selecting wells, any previous selection is deleted.

3. In Liquid Type, select the liquid type to dispense.

   Note: If using the Wash Tool Dispense step with a six-port valve, the liquid type must be one of the liquid types configured for the six-port valve in the Device Action step.

4. In Volume, enter the volume to dispense in microliters (µL).
5. In Speed, enter the speed at which to dispense.
6. Select a step that occurs after the Bulk Dispense step or the **Finish** step to validate the step configuration.

20.8 Purge Wash Tool Step

The Purge Wash Tool step is used to rinse the tubing and needles of the tools before use. A purge is automatically performed when a wash tool is loaded or when liquids are switched using the 6-port valve. The Purge Wash Tool step enables another purge to occur at any time during a method. The Purge Wash Tool step is useful for rinsing the tubing and wash tool when changing wash liquids using a 6-port valve.

During a purge, a wash liquid is dispensed through the dispense tubing and dispense needles on the wash tool. At the same time, wash liquid is aspirated using the aspirate needles on the wash tool and removed to waste through the aspirate tubing. The purge process effectively rinses the wash system tubing and wash tool, preparing it for use with the specified wash liquid.

After a purge operation, the dispense needles aspirate a Return Volume to prevent droplets from forming on the dispense needles. The Return Volume is set in Hardware Setup (refer to the *Biomek® 3000 Laboratory Automation Workstation User's Manual,* Section 12.4.3, *Configuring Wash Tools*).

Note: It is recommended to insert a Purge Wash Tool step using distilled or deionized water at the end of each method that uses the wash tool to maintain the wash system.

Note: A Wash Unit must be installed on the Biomek 3000 workstation to purge using the Purge Wash Tool step.

Insert a Purge Wash Tool step into the method. The Purge Wash Tool step configuration appears (Figure 20-8).

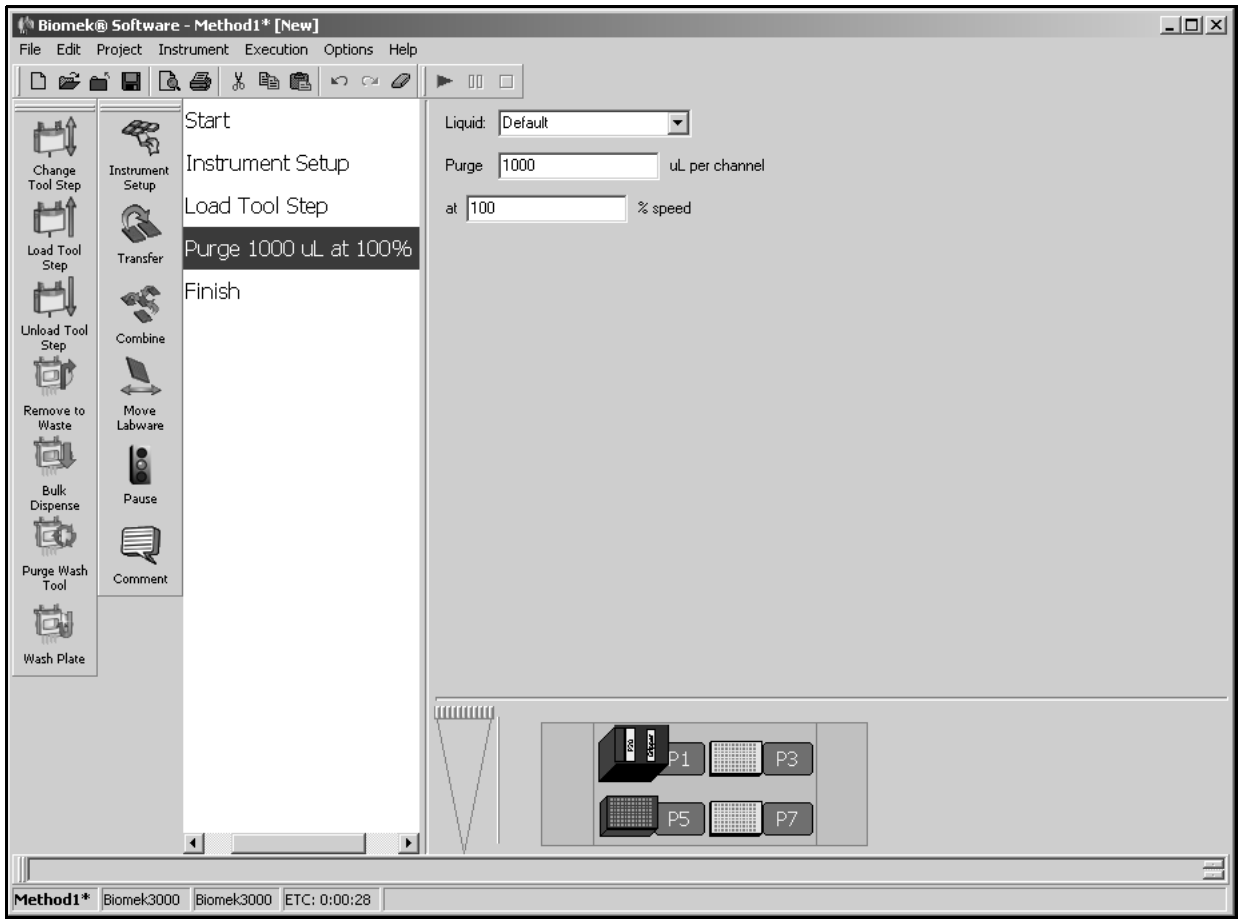


Figure 20-8. Wash Tool Purge step configuration

Note: A wash tool must be loaded onto the Biomek 3000 head assembly using either a Load Tool or Change Tool step prior to the Wash Tool Purge step.

Note: If a 6-port valve is installed with the Wash Unit, a Device Action step must be inserted to configure the wash liquids available from each port.

To configure the Purge Wash Tool step:

1. In Liquid, select the liquid type to use for the purge.

   Note: If using the Wash Tool Dispense step with a six-port valve, the liquid type must be one of the liquid types configured for the six-port valve in the Device Action step.

2. In Purge, enter the volume to dispense from each channel in microliters (µL).
3. In Speed, enter the speed at which to purge.
4. Select a step that occurs after the Purge Wash Tool step or the **Finish** step to validate the step configuration.

20.9 Wash Plate Step

The Wash Plate step is used to perform plate washing operations using a wash tool on the Biomek 3000 head assembly. Plate washing is performed as part of many assays to remove any unbound substrates before further processing.

A typical plate washing procedure performs the following actions:

- dispense liquid into wells from dispense needles on the wash tool.
- after dispensing, aspirate a Backup Volume with dispense needles to prevent droplets from forming on the dispense needles. The Backup Volume is set in Hardware Setup (refer to the *Biomek® 3000 Laboratory Automation Workstation User's Manual,* Section 12.4.3, *Configuring Wash Tools*).
- pause for a specified length of time.
- aspirate liquid from the wells using the aspirate needles on the wash tool and remove it to waste.
- repeat a specified number of times.

Note: A Wash Unit must be installed on the Biomek 3000 workstation to wash plates using the Wash Plate step.

Insert a Wash Plate step into the method. The Wash Plate step configuration appears (Figure 20-9).

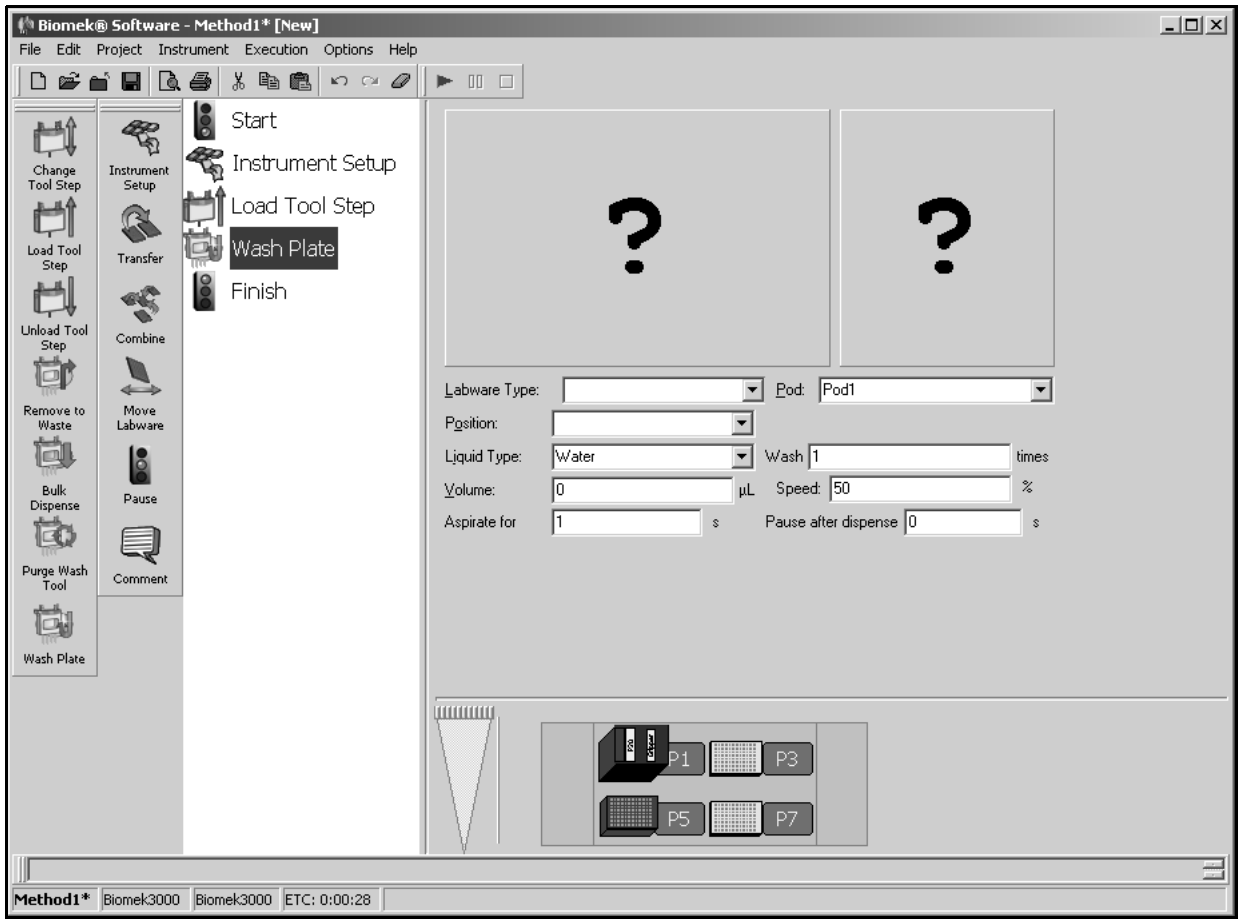


Figure 20-9. Wash Plate step configuration

To configure the Wash Plate step:

Note: A wash tool must be loaded onto the Biomek 3000 head assembly using either a Load Tool or Change Tool step prior to the Wash Plate step.

Note: If a 6-port valve is installed with the Wash Unit, a Device Action step must be inserted to configure the wash liquids available from each port (refer to Section 22.6.1.1, *Configuring the Device Action Step for 6-Port Valve (3000 only)*).

1. Click on the desired piece of labware in the Current Deck Display. The Labware Type and Position for that piece of labware is entered automatically into the Wash Plate step configuration.

   OR

   Select a **Labware Type** and **Position** from the drop-down list.

2. On the plate map, select the wells of the microplate to wash.

   Note: Hold **Shift** and click a well to select additional wells without deselecting any wells. Hold **Ctrl** and click a well to toggle the selection status of selected wells without affecting the status of other wells. If Shift or Ctrl is not held down when selecting wells, any previous selection is deleted. Wells are selected individually or in rows, depending on the wash tool used.

3. In Liquid Type, select the liquid type to use for plate washing.

   Note: If using the Wash Plate step with a 6-port valve, the liquid type must be one of the liquid types configured for the 6-port valve in the Device Action step.

4. In Wash ... times, enter the number of cycles to perform to wash the plate.
5. In Volume, enter the volume to dispense to each well from the dispense needles during each cycle of the plate wash in microliters (µL).
6. In Speed, enter the speed at which to dispense.
7. In Aspirate for, enter the length of time in seconds to apply vacuum and aspirate liquid to waste for each well using the aspirate needles.
8. In Pause after dispense, enter the length of time after the dispense to pause before beginning the aspirate operation.
9. Select a step that occurs after the Wash Plate step or the **Finish** step to validate the step configuration.

21 Using the Specialty Step Palette

21.1 Overview

The steps presented in the Specialty Step Palette allow more control over methods. These steps are used to:

- Set variables and make non-incremental changes to variables.
- Break out of loops.
- Create and use groups of labware.
- Run executables.
- Define and run procedures.

Note: The steps available in the Specialty Step Palette do not use the pod directly and may be used with any single or dual-pod configuration.

Steps available in Specialty include:

- Create Group — creates a group of labware.

- Next Labware — accesses the next piece of labware in a group of labware created using Create Group.

- Run Program — runs any executable file during a method.

- Next Item — binds a series of values to a global variable.

- Set Global — defines a global variable that can be used in subsequent steps of a method.

- Run Procedure — runs a series of steps previously created in a Define Procedure step.

- Define Procedure — creates a series of steps that can be run at any point during a method using a Run Procedure step.

- Break — breaks out of one or more loops.

21.2 Displaying the Speciality Step Palette

To add specialty steps to a method, display the Specialty Step Palette (Figure 21-1).

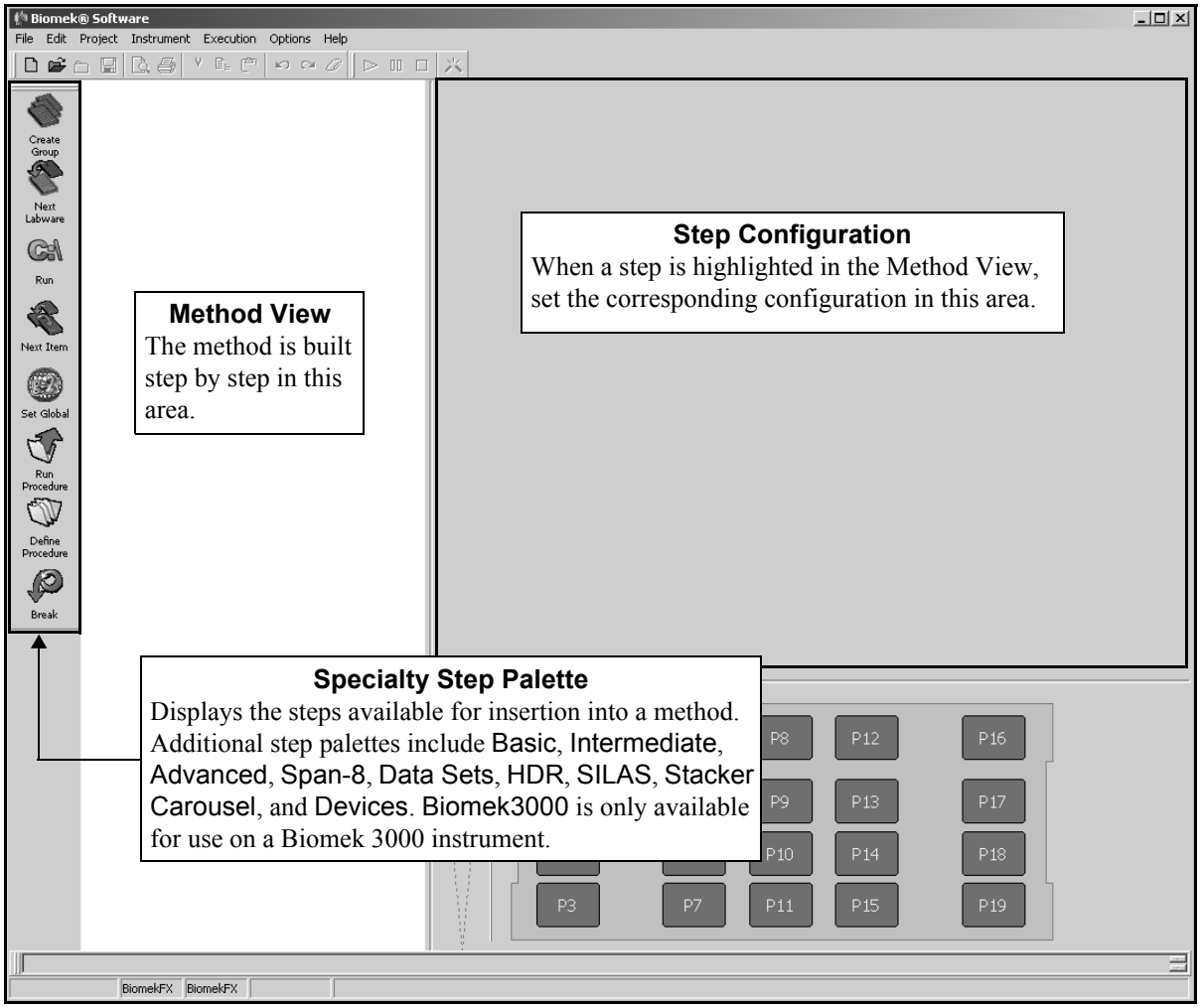


Figure 21-1. Biomek Software main editor with Specialty Step Palette displayed

To display the Specialty Step Palette:

- Right-click any empty palette space, and select **Specialty** from the menu.

  OR

- From the toolbar, select **Options>Toolbars>Specialty**.

21.3 Create Group Step

The Create Group step creates and names a group of labware that may be accessed during a method run using a Next Labware step.

21.3.1 Configuring the Create Group Step

To insert a Create Group step into a method, insert the **Create Group** in the Method View. The Create Group Step Configuration appears (Figure 21-2).

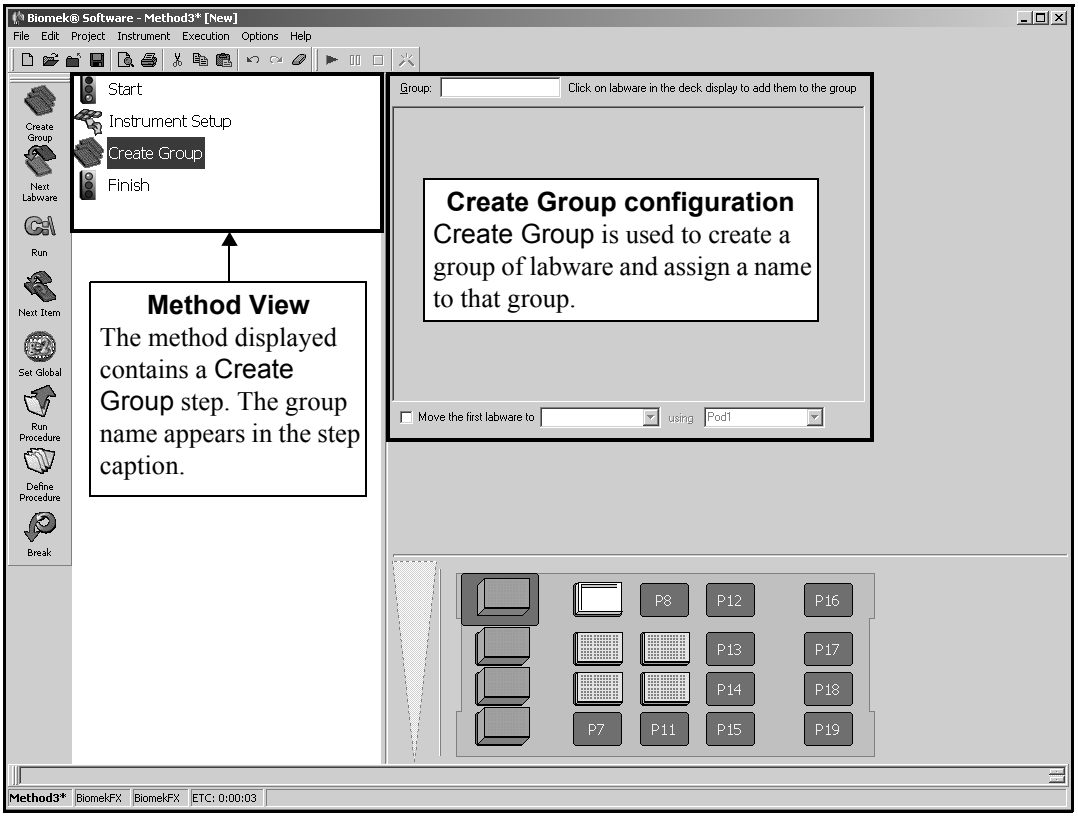


Figure 21-2. Create Group step and configuration

To configure the Create Group step:

1. In **Group**, enter a name for the group of labware (Figure 21-3).
2. Click on labware in the Current Deck Display to add them to the group.

Note: Choose Delete to remove the labware from the group.

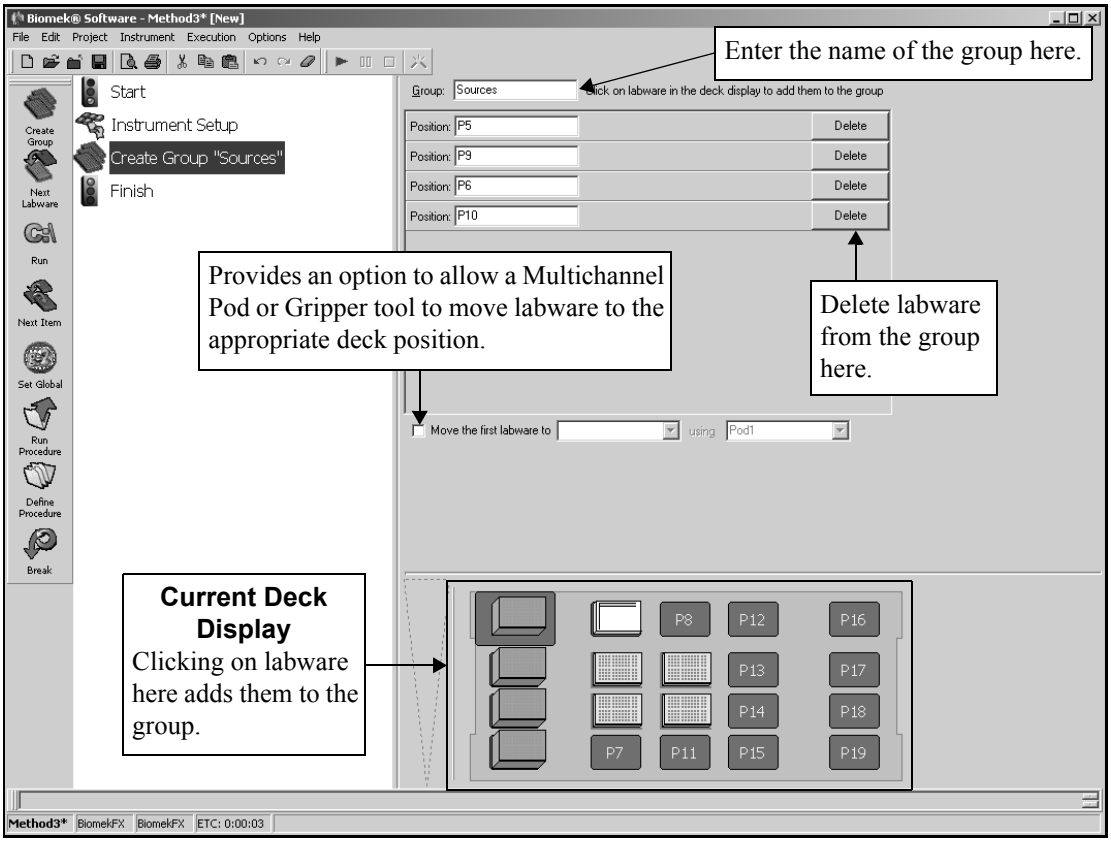


Figure 21-3. Create Group step configuration with labware added

3. Choose **Move the first labware to** to allow the pod to move labware to a specific position, if desired.

Note: Selecting Move the first labware to is equivalent to inserting a Next Labware step right after the Create Group step. The group variable is assigned the value of the first labware in the group and is moved to the specified position.

- ***FX*** — When selecting Move the first labware to, the chosen pod must be a Multichannel Pod; these pods have a gripper that can grasp and move labware.
- ***3000***, ***NX-S8*** — To use a gripper tool, it must be installed in Hardware Setup, configured in Instrument Setup, and available on the deck.

4. If Move the first labware to is selected, select the deck position to which to move the first labware.

   Note: Click on any empty deck position in Current Deck Display. Move the first labware to is selected, and the deck position chosen in the Current Deck Display is selected.

   If a deck position is not selected, it leaves the labware at its current location.

5. If Move the first labware to is selected, select the pod used to move the first labware to the selected position.

   Note: Choosing the position and pod is a necessary option if a Stacker Carousel presents a piece of labware that must be moved to a deck position.

   - ***FX*** — The chosen pod must be a Multichannel Pod; these pods have a gripper that can grasp and move labware.
   - ***3000***, ***NX-S8*** — To use a gripper tool, it must be installed in Hardware Setup, configured in Instrument Setup, and available on the deck.

21.4 Next Labware Step

Next Labware assigns the next labware in the group as the value of the global variable created in the Create Group step. The global variable created in the Create Group step is not assigned a value until a Next Labware step has assigned a value to the global variable. The Next Labware step also has options to get the next labware only when a pattern is completed or to break out of the current loop when all labware is used.

21.4.1 Configuring the Next Labware Step

Insert the **Next Labware** step in the Method View. The Next Labware Step Configuration appears (Figure 21-4)

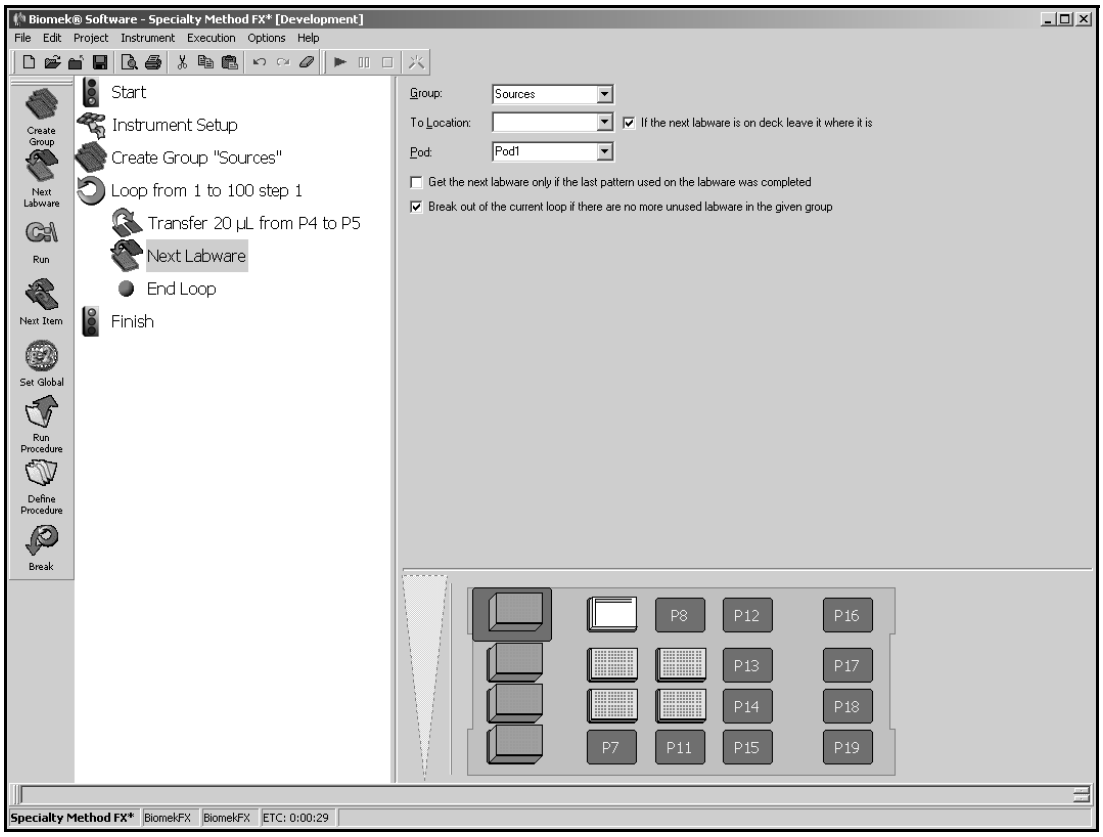


Figure 21-4. Next Labware step and configuration

To configure the Next Labware step:

1. Choose the **Group** from the pull-down menu.

   Note: All the groups created in the current method are listed.

2. In **To Location**, choose the deck position to which the next listed labware in the selected Group is moved by selecting from the list

   OR

   Click on the empty deck position in the Current Deck Display.

3. Check **If the labware is on deck leave it where it is** to leave the labware in its current location instead of moving it to the To Location, if desired.
4. Choose the **Pod** moving the labware to the specified To Location.

Note: Choosing the position and pod is necessary when a Stacker Carousel presents a piece of labware that must be moved to a deck position.

- ***FX*** — On the Biomek FX, the chosen pod must be a Multichannel Pod; these pods have a gripper that can grasp and move labware.
- ***3000***, ***NX-S8*** — To use a gripper tool, it must be installed in Hardware Setup, configured in Instrument Setup, and available on the deck.

5. Choose **Get the next labware only if the last pattern used on the labware was completed** to allow the next piece of labware in the group to be accessed only if all the selected wells on the current piece of labware have been accessed in a Transfer or Combine step.
6. Choose **Break out of the current loop if there are no more unused labware in the given group** to break out of the current loop and allow the method to continue when all the labware in the group has been accessed.

21.4.2 Using Group Variables in a Method

Group names configured in a Create Group step and assigned a value with a Next Labware step may be used in any deck position field in any step within the method.

To use a group variable in another step:

1. Select a field that requires a deck position in the desired step configuration. For example, the group Sources is used to specify the deck location of the destination for the Transfer step (Figure 21-5).
2. Enter the group name, preceded by an equal sign. For example, **=Sources** in the at field of the destination in the Transfer step indicates a volume is transferred to the labware at the deck position indicated by the group variable Sources.

Note: Group names may be used in any field where a deck position is a valid value for that field.

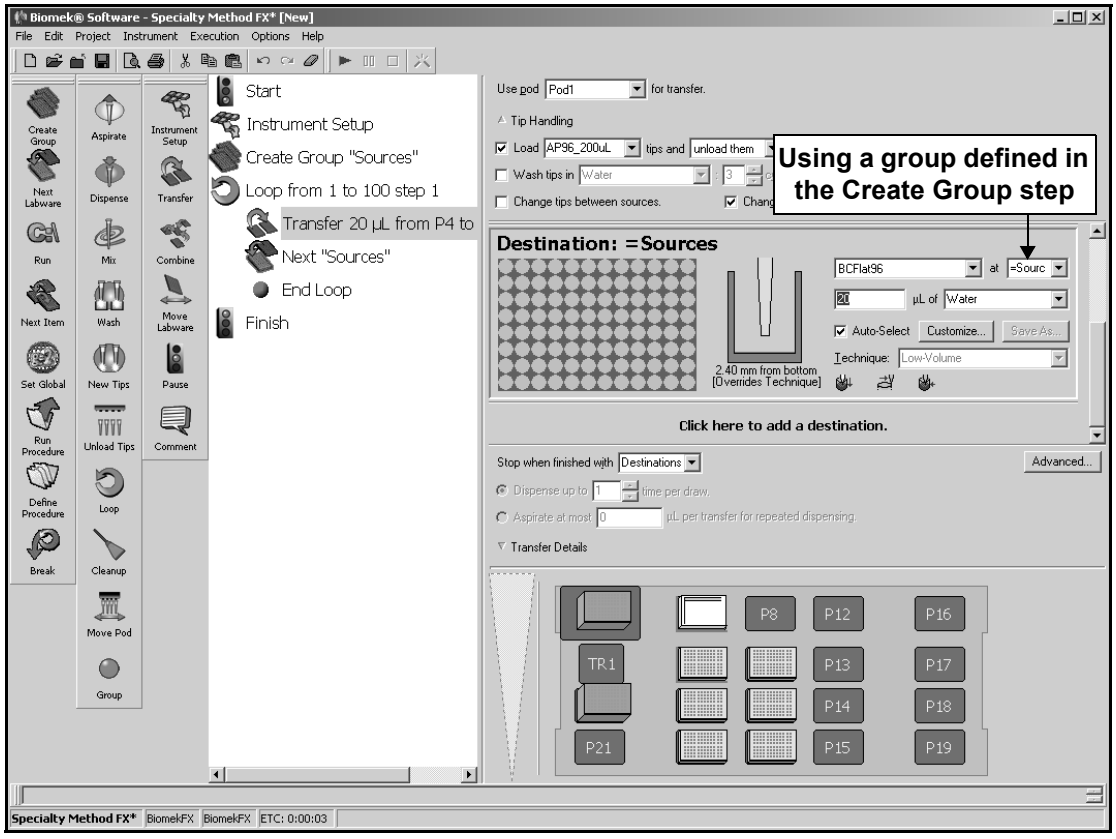


Figure 21-5. Transfer step using the Sources group defined in a Create Group step

21.5 Run Program Step

Run Program executes any application within a method. It can be used, for example, to run a custom data logger, display a read-me file or special instructions at specified times during a method, or access a database.

21.5.1 Configuring the Run Program Step

Insert the **Run Program** step in the Method View. The Run Program Step Configuration appears (Figure 21-6).

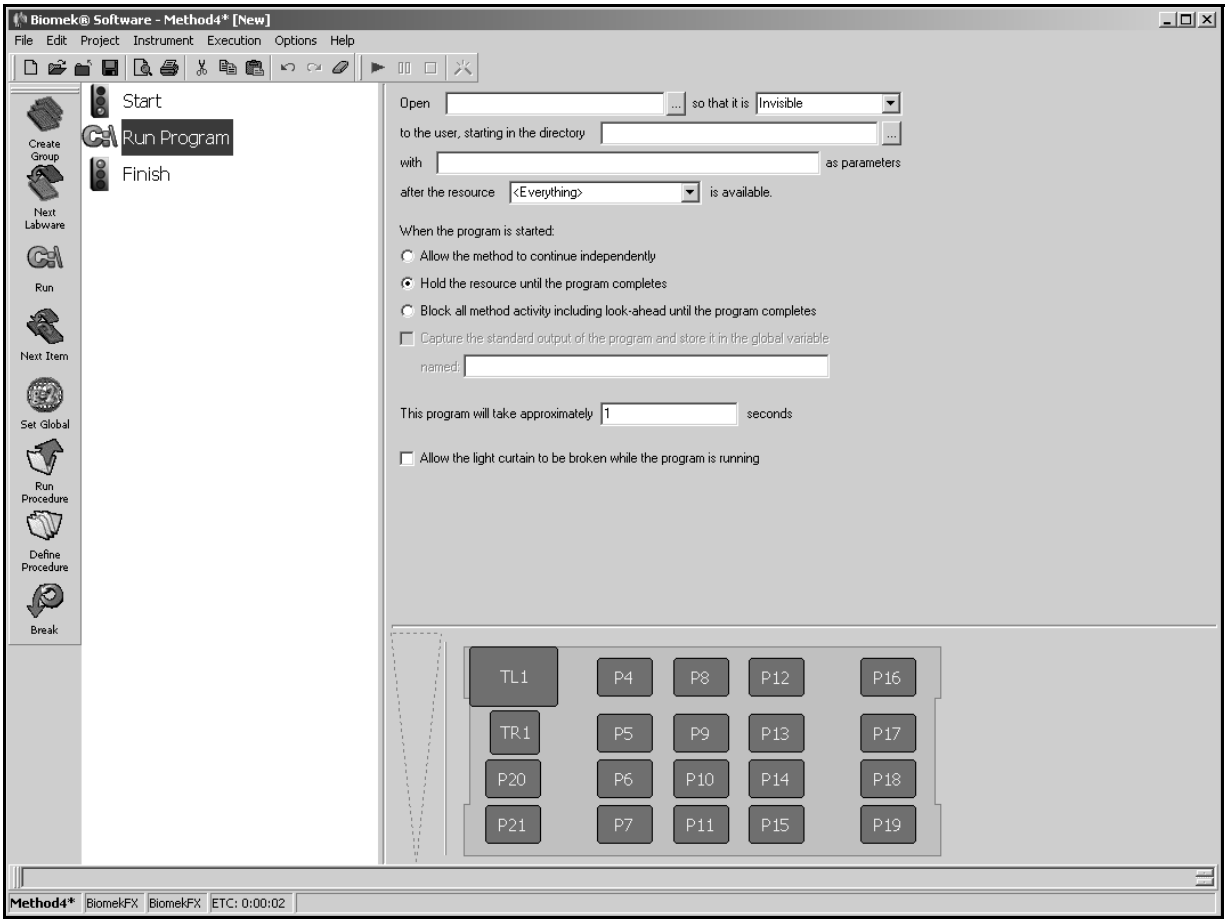


Figure 21-6. Run Program step and configuration

To configure the Run Program step:

1. In Open, enter the full path and file name for the program to execute during method run

   OR

   Choose **Browse** and select the desired program from Open.

   Note: Any executable file (.exe, .bat, etc.) in any accessible directory (local or network) may be selected in the Run Program step. Web sites can be accessed (http://www.beckmancoulter.com) or email (mailto:jdoe@example.com) sent.

2. Select how the program should be run in so that it is. Options are Visible or Invisible.

   Note: Any application that is Visible is run and displayed in a visible window. Any application that is Invisible is run in the background with no visual display. Certain executables, such as Notepad or Calculator, cannot be executed as Invisible.

3. In starting in the directory, specify the directory to search for the parameter entered in with.

   Note: When the Run Program step is executed, it searches the indicated directory for the specified parameter. Results depend on the application run and whether or not the specified parameter is found.

4. In with, enter any parameters used when running the program. For example, if the selected program is Microsoft® Word, the full path and file name of a Word document can be entered as a parameter. The program runs and opens the Word file entered as a parameter in with.

5. In after the resource, select a pod, deck position, or ALP. The program executes when the selected resource is available.

   Note: Select **<Everything>** to run the program when everything on the deck is available.

6. Make a selection in When a program is started:

   - **Allow the method to continue independently** — after starting the program, the method continues independent from the program; that is, it does not wait for the program to finish before continuing with the method. This is useful for displaying nonfatal information.
   - **Hold the resource until the program completes** — the selected resource is paused while the program is running and may not be accessed until the program is finished and closed.
   - **Block all method activity including look-ahead until the program completes** — the method pauses and waits for the program to finish before enqueueing the next step and continuing with the method. This is useful when data from the executable is used to make choices in a Biomek method; for example, a LIMS system driving a hit picking method.

7. In This program will take approximately, enter the estimated length of time to run the program in seconds.

   Note: The time entered in This program will take approximately is only used to calculate the ETC and does not affect the method run or actual run time for the method.

8. If desired, select **Allow the light curtain to be broken while the program is running**. While the program is running, the Biomek instrument is paused and the light curtain may be broken without causing an error. This is useful for integrating third-party devices onto a Biomek system.

   Note: Allow the light curtain to be broken while the program is running is available when the resource <Everything> is selected and Allow the method to continue independently is deselected.

   - ***3000*** — Does not have light curtain.

9. Select a step that occurs after the Run Program step or the Finish step to validate the step configuration.

21.6 Next Item Step

The Next Item step is used to iterate over a sequence of values. When configured, the Next Item step names a global variable, provides a list of VB script expressions, and specifies behavior when the list is exhausted.

When the Next Item step is used in a method, the named global variable may be assigned a new value. Each expression is evaluated to form a list of values.

If the named global variable is not assigned a value, it is assigned the first value of the list. If the global variable is assigned a value, the step searches for a matching value in the list and performs one of the following actions based on the results of the search:

- If a match is found, the global variable is assigned the next value in the list.
- If the matching value is the last value in the list, the action to take when the list is exhausted is applied.
- If no match is found, the global variable is assigned the first value in the list.

Note: Use a Set Global step prior to the first appearance of a Next Item step to create the variable used in the Next Item step and assign it no value (leave the Value field empty). This guarantees that the first Next Item step assigns the first value in the list to the variable.

The Next Item step is often used with a Loop step, with the value of the variable changing with each iteration of the loop.

Note: Refer to Section 16.9, *Loop Step*, for more information on using the Loop step.

21.6.1 Configuring the Next Item Step

Insert **Next Item** into the Method View. The Next Item Step Configuration appears (Figure 21-7).

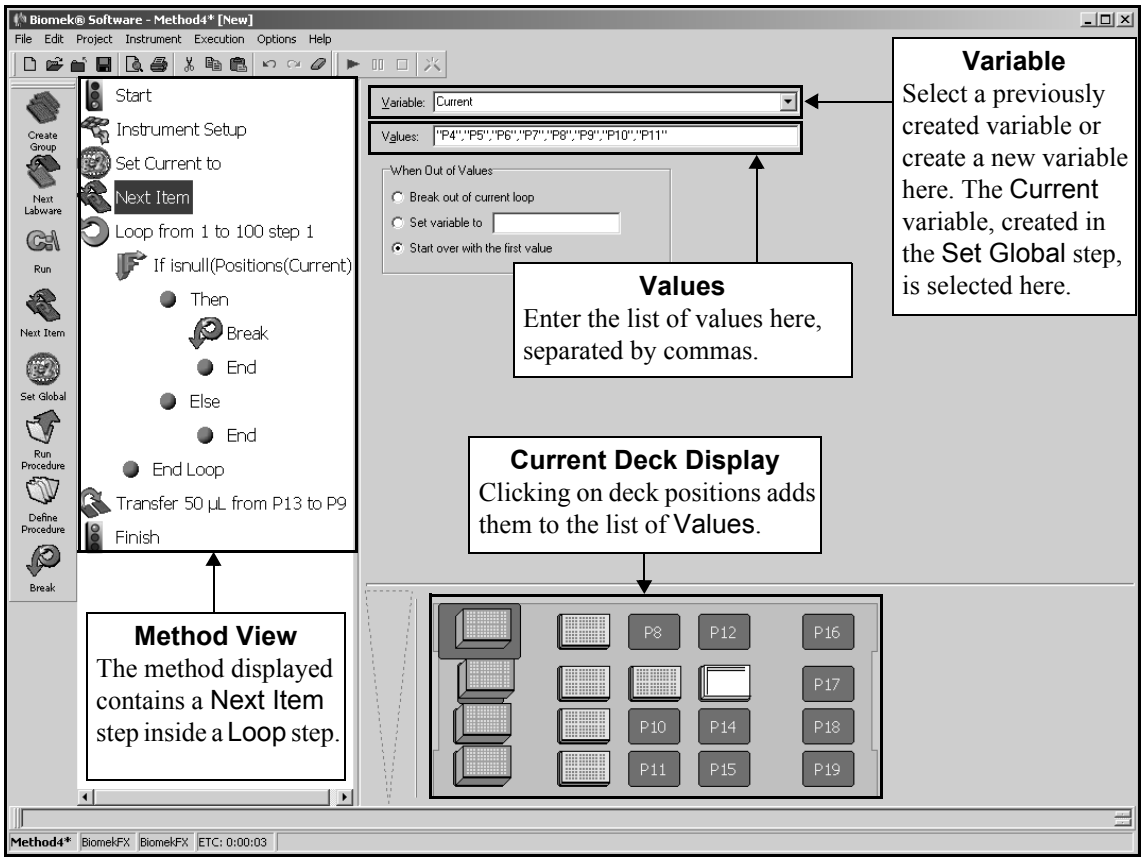


Figure 21-7. Next Item step and configuration

To configure the Next Item step:

1. Select a previously defined **Variable**

   OR

   Enter a new **Variable** name.

2. Enter the **Values** of the Variable, separating each with a comma.

Note: Deck positions must be entered in double quotes. For example, deck position P4 is entered as **"P4"** in Values. Deck positions may also be entered by clicking on each position in the Current Deck Display.

Note: All Values must be unique. If a value is repeated in the list, an error occurs during validation.

3. Indicate the action to take when all values have been used:
    - Break out of current loop — ends the current loop and continues with the method; Next Item must be placed inside a Loop step or a procedure that is run from inside a Loop step to use this option
    - Set variable to — sets the variable to a specified value and uses that value for the variable
    - Start over with the first value — sets the variable to the first value and continues; loops the Next Item values

21.7 Set Global Step

The Set Global step is used to create a global variable accessible to all steps following the Set Global step in a method. It allows steps to be parameterized by specifying explicit values for fields like volumes and heights. For example, instead of typing the number of microliters into the volume field of an Aspirate step, the name of a variable is inserted. Every time the Aspirate step is executed, the current value of that variable is used as the volume.

Any of the steps following the Set Global step can use variables created in the Set Global Step Configuration. A step uses a global variable by referencing it in its step configuration. The Biomek Software automatically uses the associated value when the step is executed.

Note: For information on variables and expressions, refer to Chapter 13, *Using Variables and Expressions in a Method*.

21.7.1 Configuring the Set Global Step

Configuring the Set Global step involves naming the variable and setting its initial value.

Insert **Set Global** into the Method View. The Set Global Step Configuration appears (Figure 21-8).

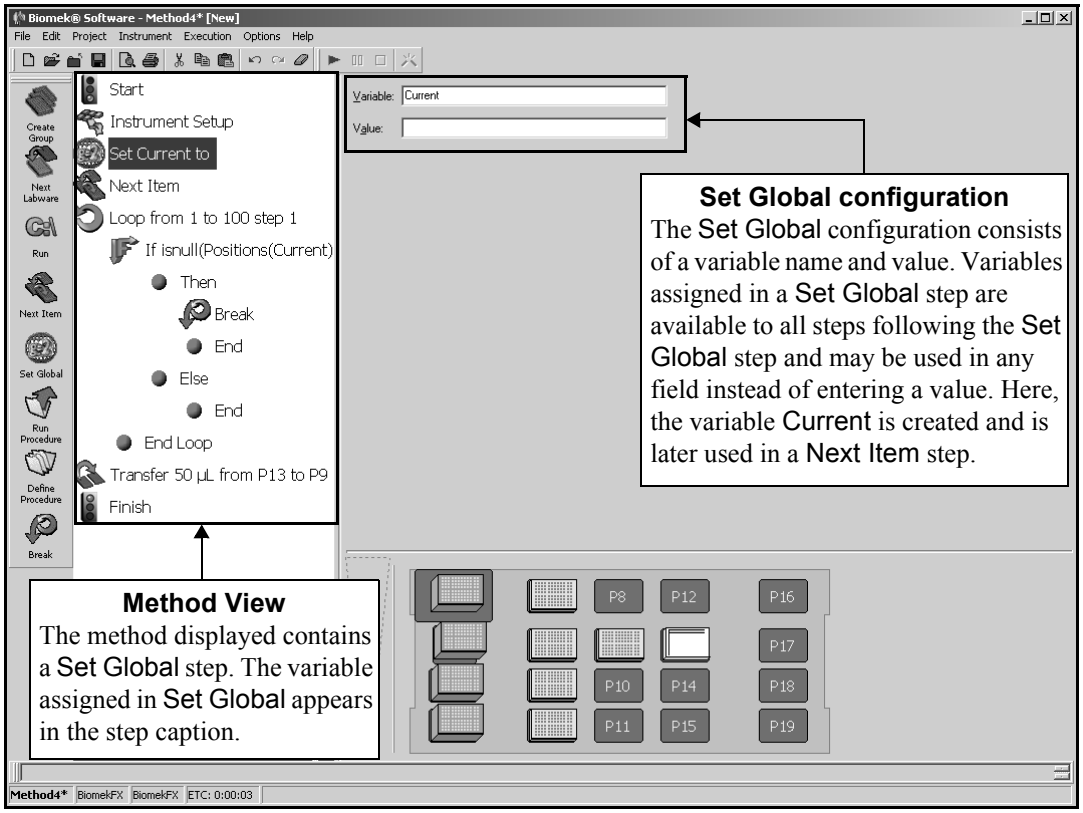


Figure 21-8. Set Global step and configuration

To configure the Set Global step:

1. Select **Set Global** in the Method View. The Set Global Step Configuration appears.
2. Enter the **Variable** name (refer to Chapter 13, *Using Variables and Expressions in a Method*).
3. Enter the desired **Value** for the Variable.

Note: The value of the variable is assigned the appropriate units when used in a step configuration. For example, if a variable AspValue with a value of 10 is used in the Volume field of a Transfer step, the software interprets this as 10 microliters (µL).

Note: Deck positions must be entered in double quotes. For example, deck position P4 is entered as **"P4"** in Values.

21.8 Defining and Running Procedures

The Define Procedure and Run Procedure steps are used to create a series of steps that may be used multiple times in a method. A procedure is created by adding and configuring steps within a Define Procedure step.

Variables may be created in the Define Procedure step and used to configure the steps in the procedure. Variables created in the Define Procedure step configuration can be overridden in the Run Procedure step configuration.

Multiple procedures can be defined in a method, and a procedure can be run multiple times within a method.

The advantages of using procedures are:

- The ability to run the same steps multiple times within a method but configuring them only once
- The size of the current method is controlled which reduces confusion by listing only the Run Procedure step in the Method View, not all of the steps accessed by the Run Procedure step

21.8.1 Define Procedure Step

The Define Procedure step is used to create procedures that may be called any time during a method with a Run Procedure step.

When the Define Procedure step is added to a method, the Define Procedure icon appears. Double-click the icon to expand the procedure and display the End Procedure icon. Any steps placed between the Define Procedure and End Procedure icons are run when the procedure is called with a Run Procedure step. These steps are configured through their individual step configurations.

The procedure may be collapsed to conserve space in the Method View by double-clicking the Define Procedure icon.

21.8.1.1 Configuring the Define Procedure Step

Insert **Define Procedure** in the Method View. The Define Procedure Step Configuration appears (Figure 21-9). Define Procedure is added to a method collapsed.

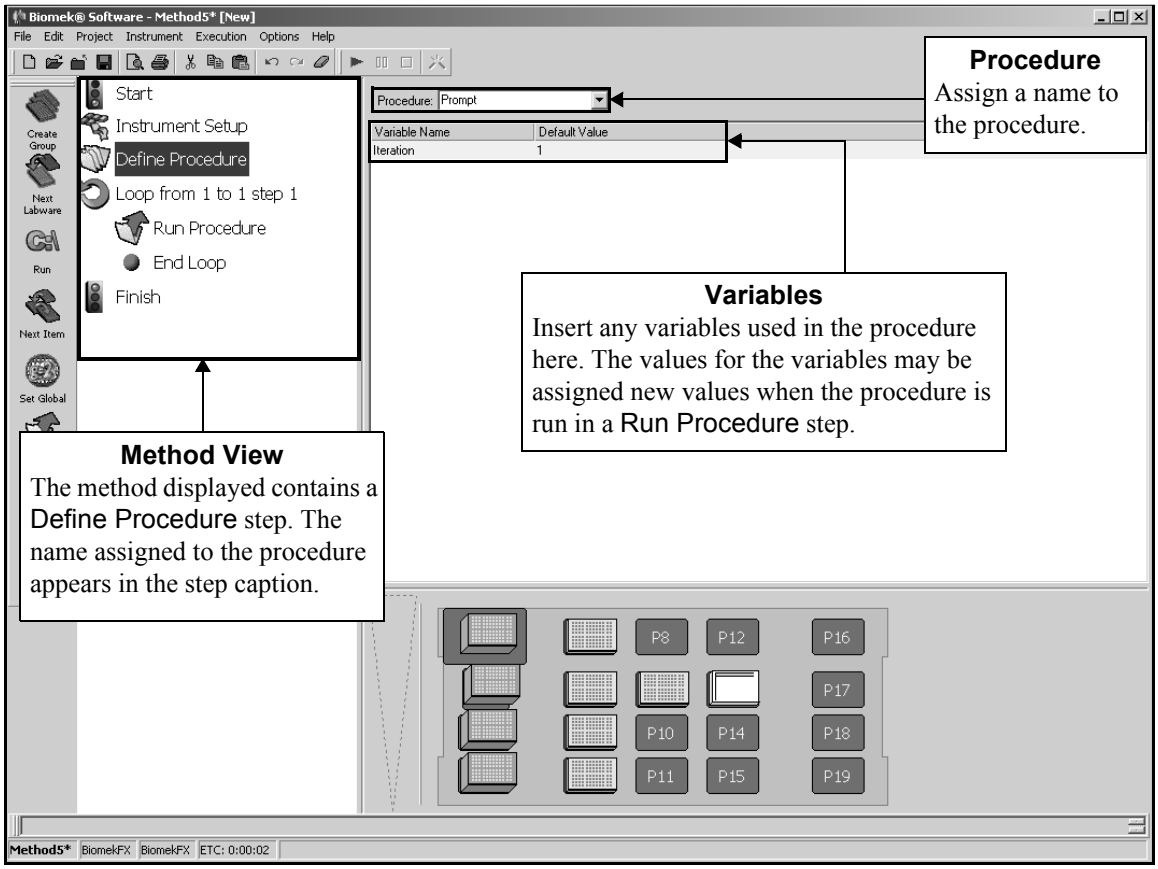


Figure 21-9. Define Procedure step and configuration

To configure the Define Procedure step:

1. In **Procedure**, enter a name for the procedure.

   Note: The procedure name may contain only alphanumeric characters and the underscore (_), and are not case-sensitive.

2. Insert the variables desired (refer to Chapter 13, *Using Variables and Expressions in a Method*).

   Note: Variables created in a Define Procedure step are accessible only to the substeps within that procedure.

3. Double-click the **Define Procedure** icon in the Method View to open the procedure. The End Procedure icon appears below the Define Procedure icon.
4. Insert the desired steps between Define Procedure and End Procedure.
5. Configure the steps between Define Procedure and End Procedure as desired.
6. Double-click the **Define Procedure** icon to collapse the procedure and hide all steps between the Define Procedure and End Procedure icons.

21.8.2 Run Procedure Step

The Run Procedure step executes a procedure previously created with the Define Procedure step. The step inserts all of the steps from the referenced procedure into the current method at the point the Run Procedure step appears. The called procedure then behaves exactly as if the steps were configured at the point where the procedure is called.

The Run Procedure step may also assign new values to variables created in the called procedure. These values override any value configured in the Define Procedure step. This allows a procedure to be used as a template that can be customized each time it is performed by a Run Procedure step by changing the values of the variables.

21.8.2.1 Configuring the Run Procedure Step

Insert **Run Procedure** in the Method View. The Run Procedure Step Configuration appears (Figure 21-10).

Note: The procedure to run in a Run Procedure step must be defined in a Define Procedure step earlier in the method. or in a previously run method that did not clear all global variables in the Finish step

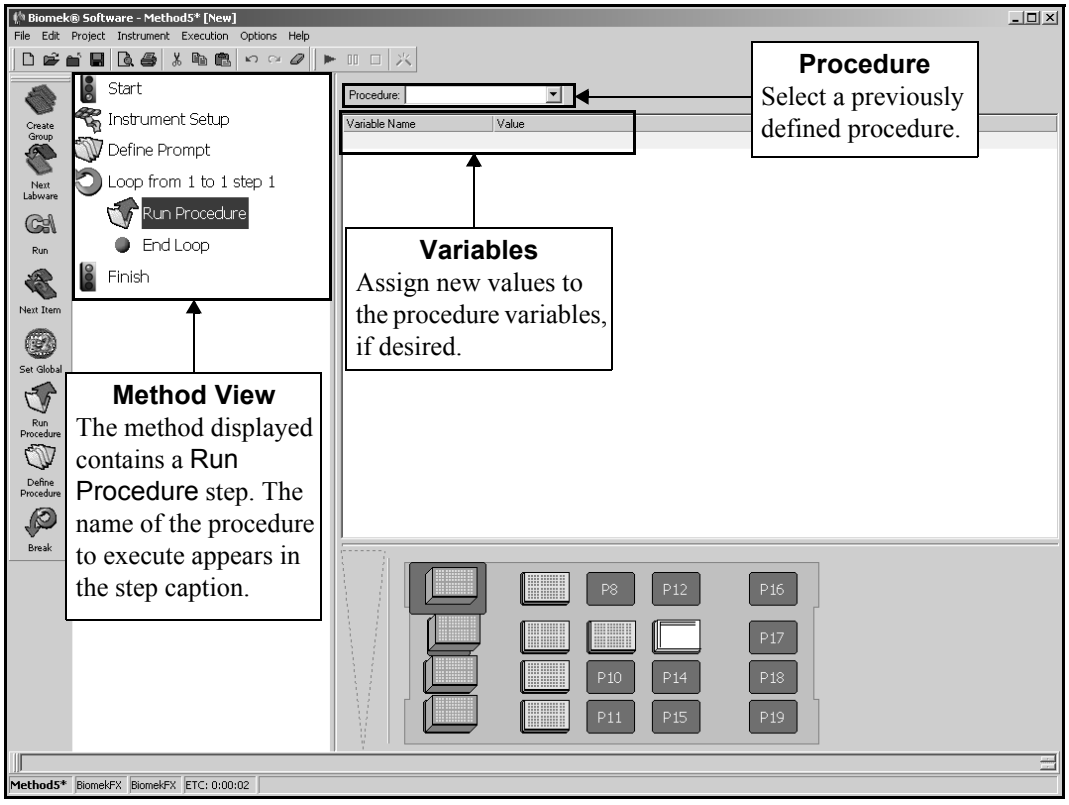


Figure 21-10. Run Procedure step and configuration

1. Select the desired procedure from the list of defined procedures. The variables used in that procedure are displayed.
2. Enter the desired values for the variables (refer to Chapter 13, *Using Variables and Expressions in a Method*).

Note: Variables in a Run Procedure step are accessible only to the called procedure.

21.9 Break Step

The Break step is used to break out of one or more loops during a method. Break is usually used as part of an If step to break out of a Loop under certain conditions. When Break is placed under the Then substep and the If statement is true, the Break step ends the Loop.

Note: The Break step must be placed inside of a Loop step or a procedure run from inside a Loop step or errors are generated during validation or method run.

Note: Refer to Section 16.9, *Loop Step*, for more information on using a Loop step. Refer to Section 17.7, *If Step*, for more information on using an If Step.

21.9.1 Configuring the Break Step

To insert a Break step into a method, insert the **Break** step inside a Loop step in the Method View. The Break Step Configuration appears (Figure 21-11).

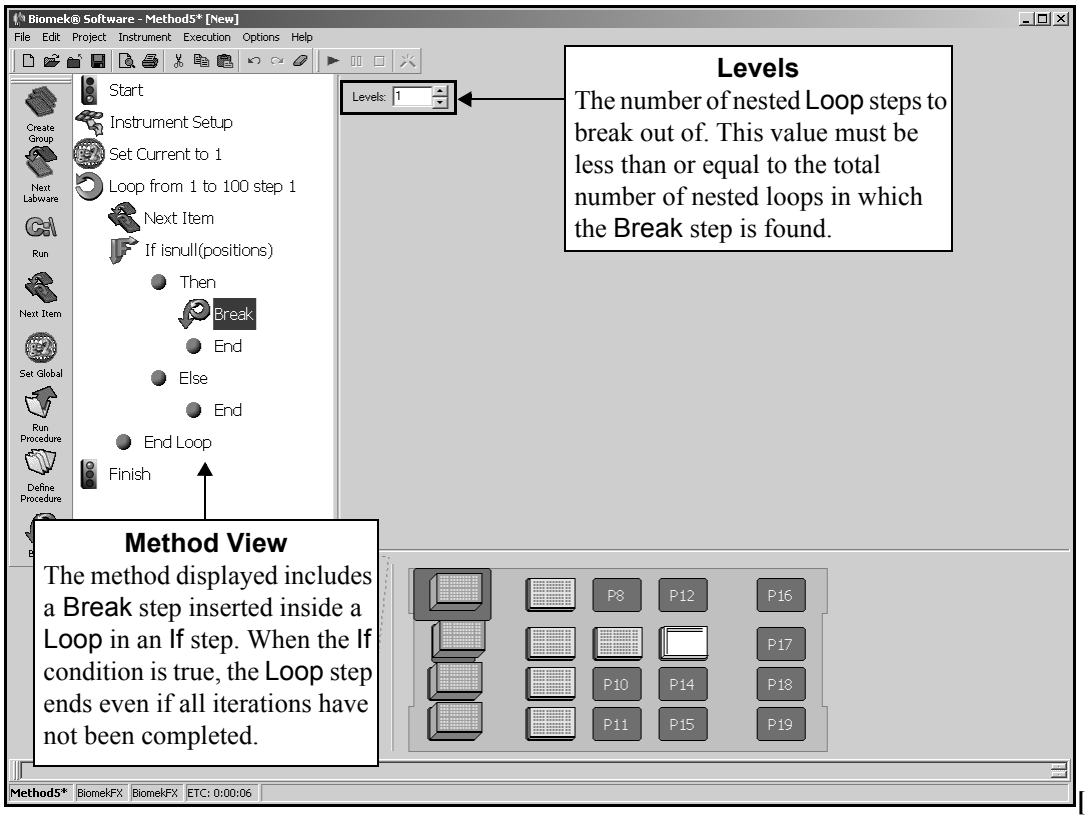


Figure 21-11. Break step and configuration

To configure the Break step:

Select the number of **Levels** to break out of.

Note: Levels refers to the number of nested Loop steps that are discontinued. Break terminates the number of Loop steps specified in Levels and continues with the method.

For example, a method contains a Loop step that contains a second Loop step nested. Within the second Loop step is an If step with a Break step with Levels set at **2** under the Then branch. When the If statement in the second Loop step is true, the Break step terminates both Loop steps and continues with the method. If Levels was set to **1**, the Break step terminates the second Loop step and continues with the first Loop step.

Note: There must be a number of nested Loop steps greater than or equal to the number of Levels or an error occurs during method validation and run.

22 Using the Devices Step Palette

22.1 Overview

The steps presented in the Devices Step Palette (Figure 22-1) integrate active ALPs and other devices with the Biomek instrument. The integration allows Biomek Software to control the device.

After an active ALP or device is integrated, Biomek Software understands the attributes of the device, displays the configuration for the device, and receives information for operating the device.

Note: Devices must be installed and configured in Hardware Setup. Refer to the instrument hardware manual for more information.

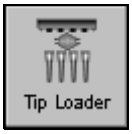
Note: Devices must also be configured on the deck in the Deck Editor (refer to Chapter 5, *Preparing and Managing the Deck*).

The steps displayed on the Devices Step Palette include:

- SPE — allows a method to easily assemble and disassemble the stack of labware required for an SPE operation.

- Device Setup — configures labware contained in external devices that hold multiple pieces of labware.

- Device Action — controls devices during a method run.
  - ***FX*** — controls devices and active ALPs such as the Tip Wash ALP or Stirring ALP.
  - ***3000*** — controls devices such as the autolatch, 6-port valve, vacuum, Wash System, and MicroMix.
  - ***NX*** — controls devices and active ALPs such as the Source/Waste Sensor and Drainable/Refillable Reservoir ALP.



- Tip Loader — configures a Tip Loader ALP location and status.
  - ***FX***, ***NX-MC*** — The Tip Loader ALP is used *only* with a Multichannel Pod.

The following step is displayed when a SILAS device and the software associated with it are installed on the system:

- SILAS™ Module step — controls operation of the associated SILAS Module, such as a barcode reader or a SILAS consumer that has been added to a step palette.

Note: The icon for a SILAS Module step varies according to the device the step represents; for example, a Barcode Reader SILAS Module step displays an icon of a barcode reader.

When a device integration step is added to a method, the configuration associated with that step appears on the right side of the Biomek main editor in Step Configuration (Figure 22-1). Steps not configured appropriately can generate errors when the method is validated or run.

22.2 Displaying the Devices Step Palette

In order to add device steps to a method, the Devices Step Palette must be displayed (Figure 22-1).

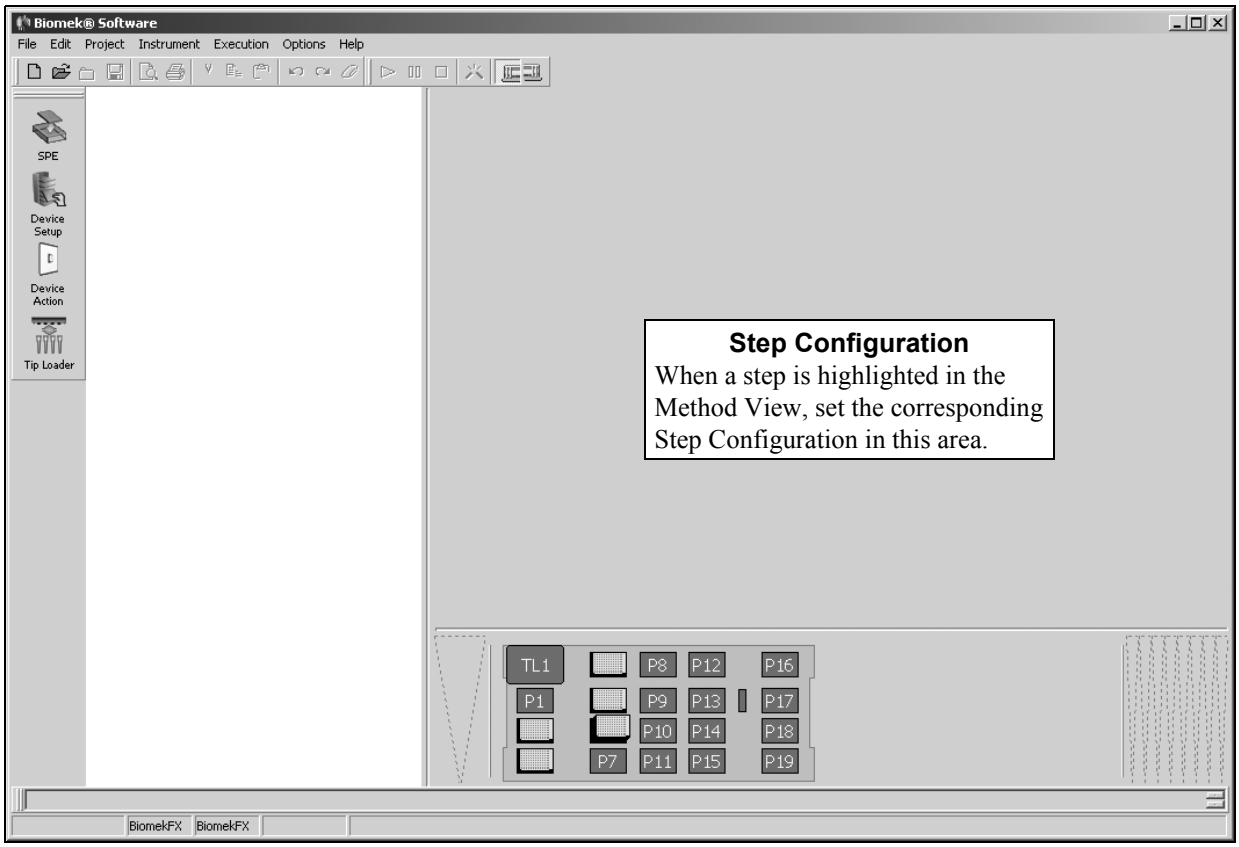


Figure 22-1. Main editor for a Biomek FX with Devices Step Palette displayed

To display the Devices Step Palette, complete the following:

- Right-click any empty palette space, and the Step Palette menu appears. Select **Devices** from the menu.

  OR

- From the toolbar, select **Options>Toolbars>Devices**

22.3 SPE Step

The Solid Phase Extraction (SPE) ALP applies a vacuum to remove liquid from a filter microplate. The SPE step is a convenient way of executing the assembly and disassembly of the SPE ALP system. The configuration for the SPE step informs Biomek Software of the:

- Operation required of the SPE step (Figure 22-2)
- Location of the filtered microplate used by the SPE ALP
- Locations of the SPE vacuum manifold and receiver
- Location of the SPE ALP on the deck
- Pod constructing/destroying the SPE stack
  - ***FX***, ***NX-MC*** — The SPE step is for use with a Multichannel Pod; the gripper must be used to assemble and disassemble the SPE ALP.
  - ***3000*** — A gripper tool must be installed and configured on the deck.
  - ***NX-S8*** — The SPE step may only be used on the NX Span-8 with gripper; the gripper must be used to assemble and disassemble the SPE ALP.

Note: The SPE ALP can only be used on a DNA Preparation Deck Layout and occupies two deck positions.

Insert a SPE step into the Method View (Figure 22-2).

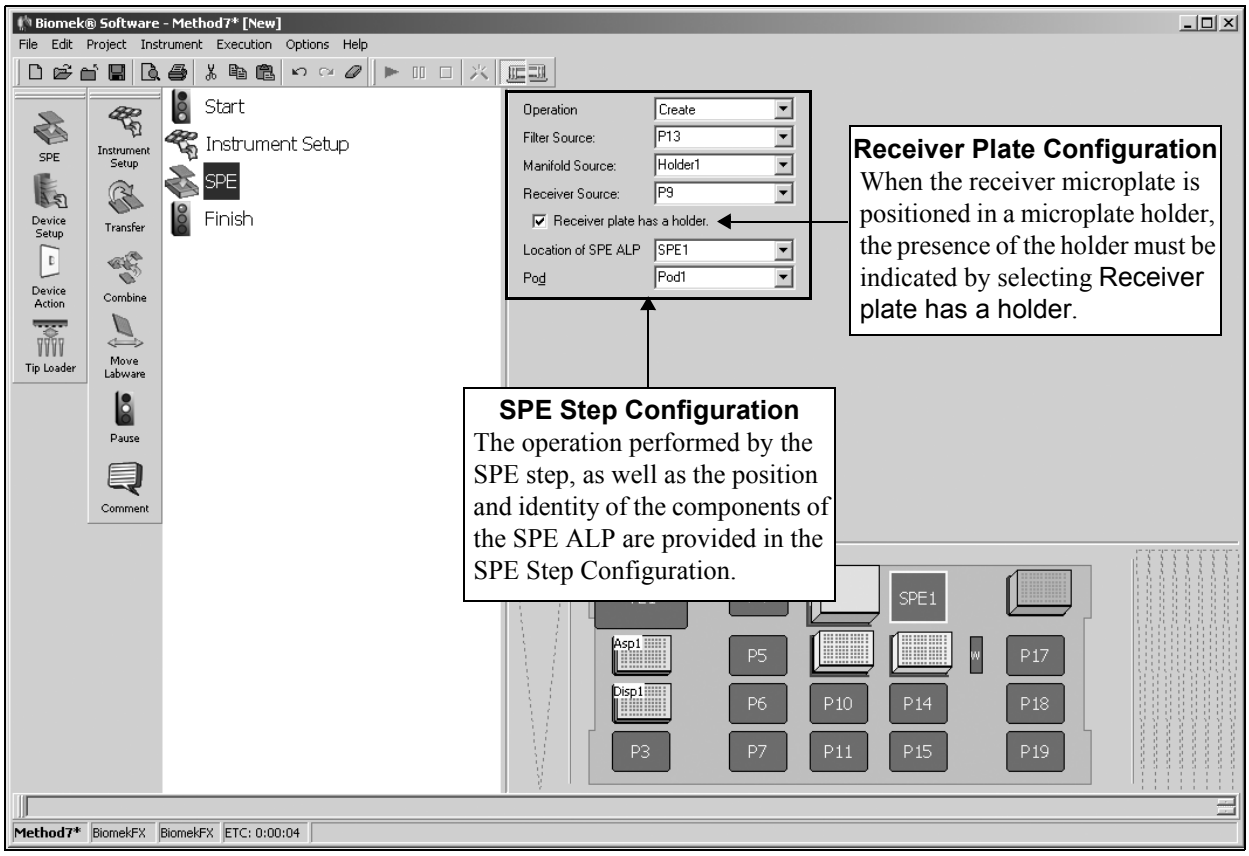


Figure 22-2. SPE step and configuration

22.3.1 Configuring the SPE Step

When an SPE step is added to a method, the SPE Step Configuration appears (Figure 22-2).

To configure the SPE step:

1. Select the **Operation** performed by the SPE ALP from the options listed below:
   - Create — assembles the various pieces of an SPE stack
   - Destroy — disassembles an SPE stack
2. Select the location of the **Filter Source** used by the SPE stack. The Filter Source is the location on the deck of the filtered microplate that is placed on top of the SPE ALP stack.
3. Select the location of the **Manifold Source** for the SPE stack. The Manifold Source is the location of the Manifold, which is referred to as the Collar in the *ALPs User's Manual* (refer to the *ALPs User's Manual,* Chapter 16, *Solid Phase Extraction (SPE) Vacuum Manifold ALP*).

4. Select the location of the **Receiver Source** for the SPE stack. The Receiver Source is any filtered microplate that is positioned inside the SPE Collar and the SPE ALP. If no receiver microplate is defined, the fluid flows through the source filtered microplate into the SPE ALP Base. The fluid is removed from the base via the vacuum hose (refer to the *ALPs User's Manual,* Chapter 16, *Solid Phase Extraction (SPE) Vacuum Manifold ALP*).

   Note: Filter Source, Manifold Source, and Receiver Source all change to Destination when Operation is set to Destroy.

5. Select **Receiver plate has a holder** if the receiving microplate is positioned in a Filter Holder. The Filter Holder is used to keep the tips of a filtered microplate from touching the base of an ALP stand. A filter microplate without a Filter Holder can be positioned inside a 1x1 ALP without damaging the microplate.

   Note: Labware, including the Filter Holder, is positioned on the Deck Layout in the Instrument Setup step.

6. Select the **Location of SPE ALP** on the Biomek deck.

7. Specify the **Pod** accessing the SPE stack.

   Note: In Pod, Pod1 is the default for a one-pod Biomek system. In a two-pod system, the pod configured as the default pod is displayed in Pod. If the other pod is desired, select the pod from the drop-down list.

8. Select a step that occurs after the SPE step or the **Finish** step to validate the step configuration.

22.4 Using External Devices with Biomek Laboratory Automation Workstations

External devices may be used during a method run. In order to use these devices in a method, there are three components that must be configured for proper operation of the device. These components are:

- Device Editor — sets the attributes of the device within the Biomek Software (refer to Section 22.4.1, *Configuring Devices Using the Device Editor*).
- Device Setup Step — configures the labware within a device for use in a method (refer to Section 22.5, *Device Setup Step*).
- SILAS Module — configures the operation of the device for the method (refer to Section 22.8.1, *Configuring the SILAS Module*).

22.4.1 Configuring Devices Using the Device Editor

Use the Device Editor to configure external devices for use with the Biomek instrument. Each external device may contain different setup options, such as the number and type of labware the device is capable of holding. In order to use the device, this information must be provided through the Device Editor.

Note: For specific operating instructions for external devices, refer to the user's manual for each specific device.

To open the Device Editor:

Choose **Instrument>Device Editor**. Device Editor appears (Figure 22-3).

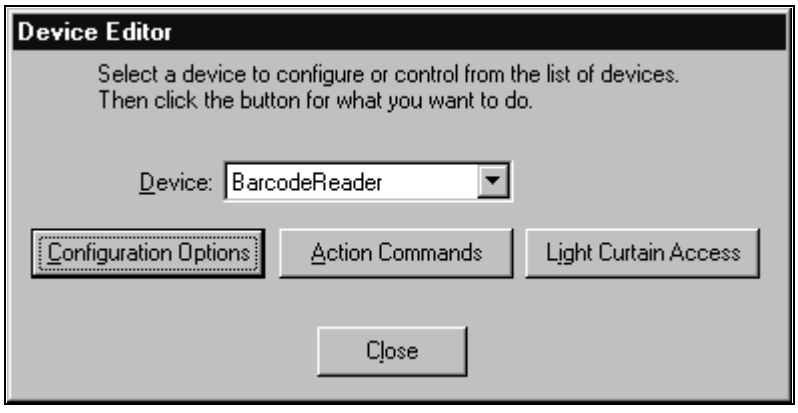


Figure 22-3. Device Editor

To configure a device for use with the Biomek instrument:

1. In Device, select an installed device.
2. Choose the desired option:
   - **Configuration Options** — configures the device to be used with the Biomek instrument. Refer to the device user's manual for more information about available options.
   - **Action Commands** — select and manually operate individual device operations. Refer to the device user's manual for more information about availble operations.
   - **Light Curtain Access** (Figure 22-4) — allows light curtain violations caused by a device action to be ignored.

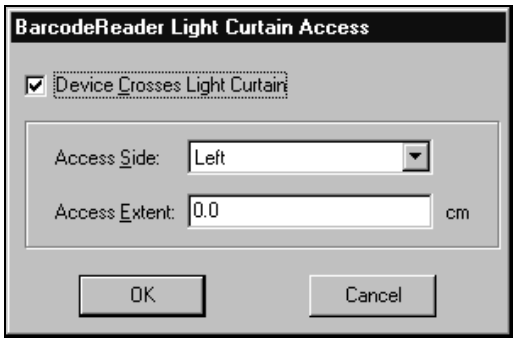


Figure 22-4. Light Curtain Access configuration

To configure Light Curtain Access:

- ***FX***, ***NX*** — Device Crosses Light Curtain is deselected by default. When selected, light curtain violation parameters must be specified. Light curtain violations occurring within the specified parameters are ignored; violations occuring outside the parameters stop the method run or action in progress.
- ***3000*** — does not have a light curtain.

1. Select **Device Crosses Light Curtain** to enable Light Curtain Access.
2. In Access Side, choose the side of the deck where the device action passes through the light curtain: **Left**, **Center**, **Right**.
3. In Access Extent, enter the extent in centimeters that the device passes through the light curtain.
4. Choose **OK** to close Light Curtain Access and save changes.

   OR

   Choose **Cancel** to close Light Curtain Access without saving changes. Device Editor appears.

22.5 Device Setup Step

The Device Setup step is used to configure the labware contained in multiple slot external devices, such as a carousel (Figure 22-5). A Device Setup step only configures one device, so multiple Device Setup steps must be used when multiple external devices are used.

Device Setup is used to select the type of labware contained in each slot in the device, and it allows the Labware Properties to be set for each piece of labware in the device.

Note: The software included with an external device must be installed before the device can be configured in the Device Setup step and accessed by the Biomek instrument.

Insert a Device Setup step into the Method View (Figure 22-5).

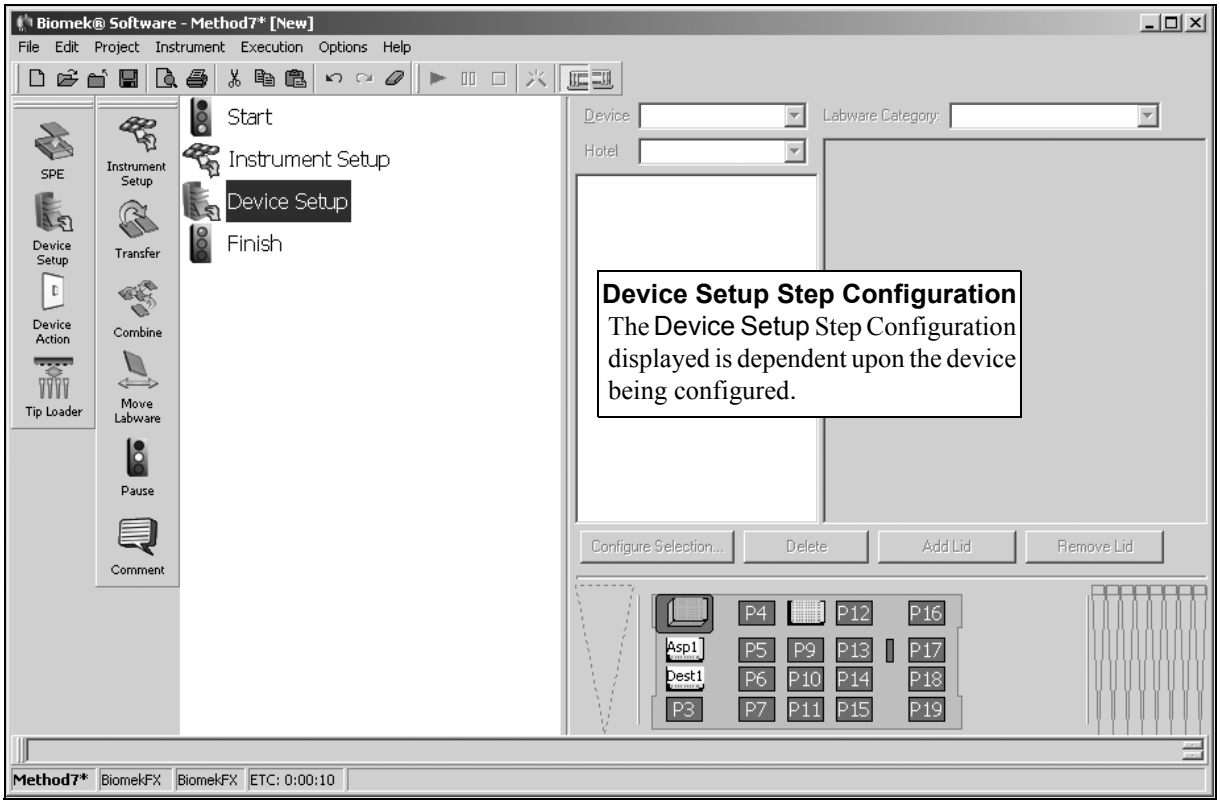


Figure 22-5. Device Setup step and configuration

22.5.1 Configuring the Device Setup Step

When a Device Setup step is inserted into a method, the Device Setup Step Configuration appears (Figure 22-5). The Device Setup Step Configuration includes:

- Configure Selection — displays the Labware Properties for the selected piece of labware.
- Delete — removes labware from the selected slot.
- Add Lid — communicates to the software that a lid is included with a piece of labware, such as a tip box or microplate with a lid. When Add Lid is applied to any piece of labware, an asterisk appears next to the labware indicating that a lid is present.
- Remove Lid — communicates to the software that a lid has been removed from the labware. When Remove Lid is applied to any piece of labware with an asterisk next to its name, the asterisk disappears indicating that a lid is no longer present.

To configure the Device Setup step:

1. Select the **Device** from the options listed. The configuration for the device is displayed in Step Configuration.
2. Select a **Labware Category**.
3. Select a position, or multiple positions, within the configuration of the device to populate with labware.
4. Select a piece of labware from the graphical labware display.

   OR

   Drag and drop a piece of labware from the graphical labware display to the desired position in the device.
5. Right-click a piece of labware in the Step Configuration and select **Configure Selection**. Labware Properties appears for the type of labware being configured (Figure 22-6 and Figure 22-7). Use Labware Properties to configure each piece of labware within the device (refer to Section 22.5.1.1, *Configuring Labware Properties for Tips and Labware*).
6. Choose **OK** to save Labware Properties and return to the Device Setup Step Configuration.
7. Use **Add Lid** and **Remove Lid** as necessary to configure the lid status for the labware in the device.

Note: When Add Lid is selected, it indicates that a lid is included with a piece of labware. An asterisk appears next to the labware in the graphical representation of the stack (Figure 22-5).

When Remove Lids is used on a piece of labware preceded by an asterisk, the asterisk disappears indicating that the lids are not present.

22.5.1.1 Configuring Labware Properties for Tips and Labware

Specific tips and labware used in a method can be configured using Labware Properties. The information provided in Labware Properties is used when a pipetting technique is selected, and when tips are loaded and unloaded.

To access Labware Properties:

Double-click on a piece of labware in the Device Setup Step Configuration.

OR

Choose **Configure Selection**.

OR

Right-click on a piece of labware in the Device Setup Step Configuration, and choose **Configure Selection**. Labware Properties appears (Figure 22-6).

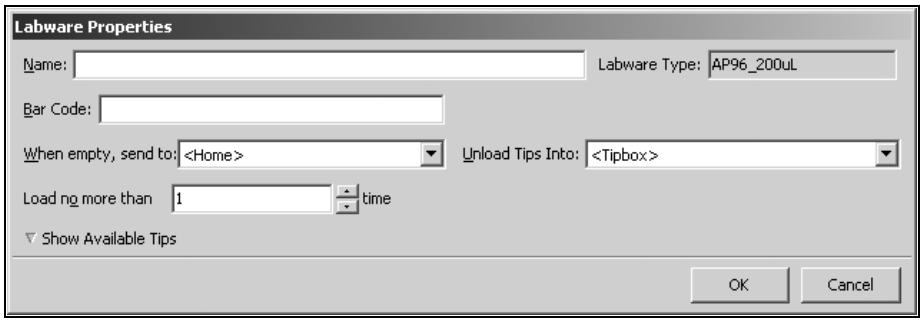


Figure 22-6. Labware Properties for tips

22.5.1.1.1 Configuring Labware Properties for Tips

When the labware selected for configuration is tip box, Labware Properties provides the ability to configure (Figure 22-6):

- Name assigned to the tip box
- Bar code
- Where to dispose of tips
- Where to dispose of tip boxes
- Maximum number of times tips can be loaded
- Available tips

Note: Variables and expressions may entered in any field that can be configured. Refer to Chapter 13, *Using Variables and Expressions in a Method*, for more information on using variables and expressions.

To configure Labware Properties:

1. In Labware Type, verify the tip type.
2. In Name, enter name for the tip box, if applicable.

   OR

   Leave Name blank. When Name is blank, tips are accessed by the information displayed in the Labware Type field.

   Note: Naming tip boxes forces the instrument to look for a specific box of tips, rather than any tip box containing the specified tip type, located anywhere on the deck. Multiple tip boxes can be given the same name. This is used to create a pool of tip boxes for a specific use.

3. In Bar Code, enter the bar code.

   Note: Use the bar code field to identify a specific tip box in certain methods, such as plate replication. This field may be left blank.

4. In When empty, send to, select a final destination for the tip box at the end of the method.
5. In Unload Tips Into, select the location reserved for tip disposal.
6. In Load no more than, enter the number of times tips can be loaded onto the pod during the method.
7. Choose Show Available Tips to display a graphic of the tip box (Figure 22-7).

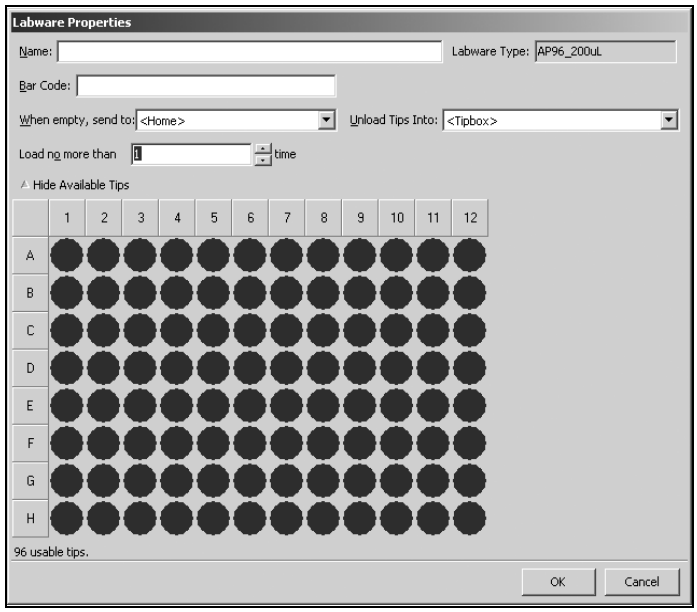


Figure 22-7. Labware Properties for tips with available tips shown

8. On the graphic of the tip box, select the usable tips. This can be used to indicate missing tips or tips that are otherwise not used in the method. By default, all tips are selected.

9. Choose **Hide Available Tips** to collapse the graphic of the tipbox.
10. Choose **OK** to save Labware Properties and return to the Device Setup step configuration.

22.5.1.1.2 Configuring Labware Properties for Labware

For labware other than tip boxes, Labware Properties provides the ability to configure (Figure 22-8):

- Name assigned to the labware
- Bar code
- Maximum volume per well
- Volume for each well, if known
- Liquid type

Note: Variables and expressions may entered in any field that can be configured. Refer to Chapter 13, *Using Variables and Expressions in a Method*, for more information on using variables and expressions.

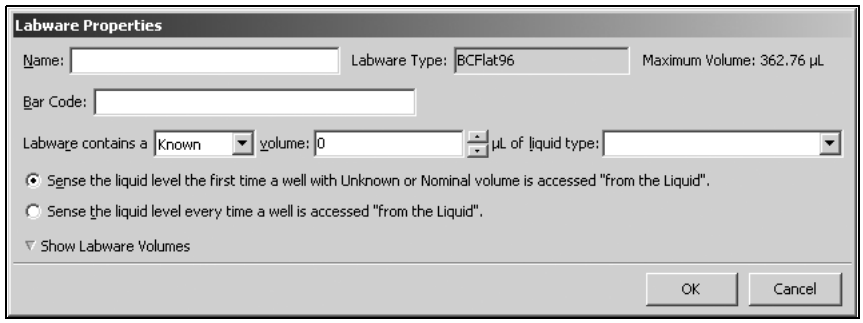


Figure 22-8. Labware Properties for microplates, reservoirs, and tube racks

To configure Labware Properties:

1. Verify the Labware Type.
2. In Name, enter a name for the labware.

   Note: When a deck is populated by numerous pieces of labware, naming labware is recommended. Names should be descriptive of the contents of the labware or the work being accomplished during the method. Naming labware in a meaningful fashion may reduce confusion.

3. In Bar Code, enter the bar code.

   Note: Use the bar code field to identify a specific plate in certain methods, such as plate replication. This field may be left blank.

4. Make a selection in **Labware contains**. Options are Unknown, Nominal, and Known. This information is used by many of the techniques supplied with Biomek Software which aspirate or dispense liquid a certain offset from the liquid level. Some pods or tools can detect the liquid level using liquid-level sensing technology.

    - If Known is selected, the liquid level is not detected during method run and the entered value is used during validation and method run. Known Volume should be supplied whenever possible.
    - If Unknown is selected, the liquid level is detected during method run if required by the technique, and the wells are assumed to be full when validating the method.
    - If Nominal is selected, the liquid level is detected during method run, but the volume in the wells is assumed to be the entered value when validating the method.

5. Enter the **Volume**, if Nominal or Known Volume is selected. A value entered in Volume is assigned to all wells.

6. Select the Liquid Type contained in the labware. The liquid type is useful information when Biomek Software auto-selects a technique for any aspirate and dispense operations acted upon this piece of labware. The technique auto-selected to aspirate and dispense the liquid is selected based on the physical factors of the liquid, as well as the physical attributes of the labware. For more information on liquid types, refer to Chapter 8, *Understanding and Creating Liquid Types*.

7. Select **Sense the liquid level the first time a well with Unknown or Nominal volume is accessed "from the Liquid"** to use liquid level sensing to determine the liquid level only the first time it accesses a well with an Unknown or Nominal volume from the liquid. Any instances the same well on the piece of labware is accessed, the liquid level is calculated internally based on the result of the earlier liquid level sense and the amount aspirated or dispensed to the well in previous steps.

    OR

    Select **Sense the liquid level every time a well is accessed "from the Liquid"** to use liquid level sensing to determine the liquid level every time it accesses a well with an Unknown or Nominal volume from the liquid.

Note: Liquid level sensing options only apply if the pod or tool accessing the labware is capable of sensing the liquid level. If not, the option selected is ignored.

---

8. If the labware does not contain uniform volumes, choose **Show Labware Volumes** to display a graphic of the labware (Figure 22-9).

Note: If Known Volume or Nominal Volume was selected in **Labware contains a**, Show Labware Volumes activates.

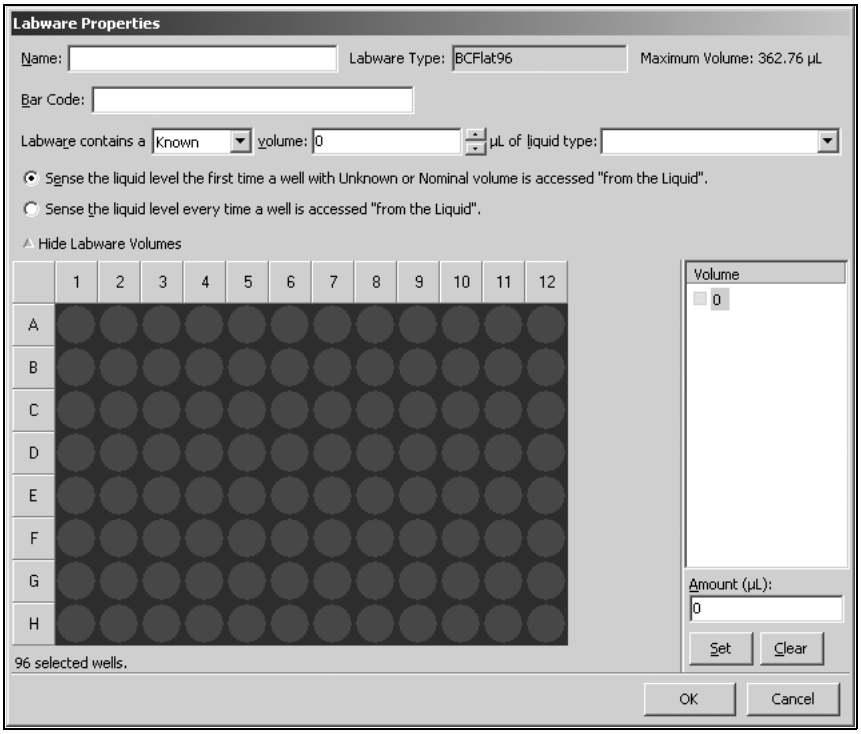


Figure 22-9. Labware Properties for 96-well microplate Labware Volumes shown

9. Select the desired wells on the graphic.

Note: Hold down Ctrl to toggle wells between selected and deselected without affecting the selection status of other wells.

10. Enter the volume to assign to the currently selected wells in **Amount**.
11. Choose **Set** to assign the current Amount to the currently selected wells. The wells are given a color code that corresponds to the list of set volumes under Volume.

Note: Clear sets the volume for all wells back to zero.

12. Repeat steps 10-12 until all desired wells have been assigned the desired volume.
13. Choose **Hide Labware Volumes** to collapse the graphic of the labware.
14. Choose **OK** to save Labware Properties and return to the Device Setup step configuration.

22.6 Device Action Step

The Device Action step is used to configure the actions of active ALPs and devices.

- ***FX*** — controls actions, such as operating the wash pump for the Wash ALP, stirring actions for the Stirring ALP, shaking actions for the Microplate Shaking ALP, and positioning actions for the Positive Position ALP.
- ***3000*** — controls devices, such as the autolatch, 6-port valve, vacuum, Wash System, and MicroMix.
- ***NX*** — controls devices and active ALPs, such as the Source/Waste Sensor and Drainable/Refillable Reservoir ALP.

Note: Any devices installed in Hardware Setup, except Tip Loaders and Device Controllers, are listed under Device in the Device Action Step Configuration.

Insert a **Device Action** step into the Method View (Figure 22-10).

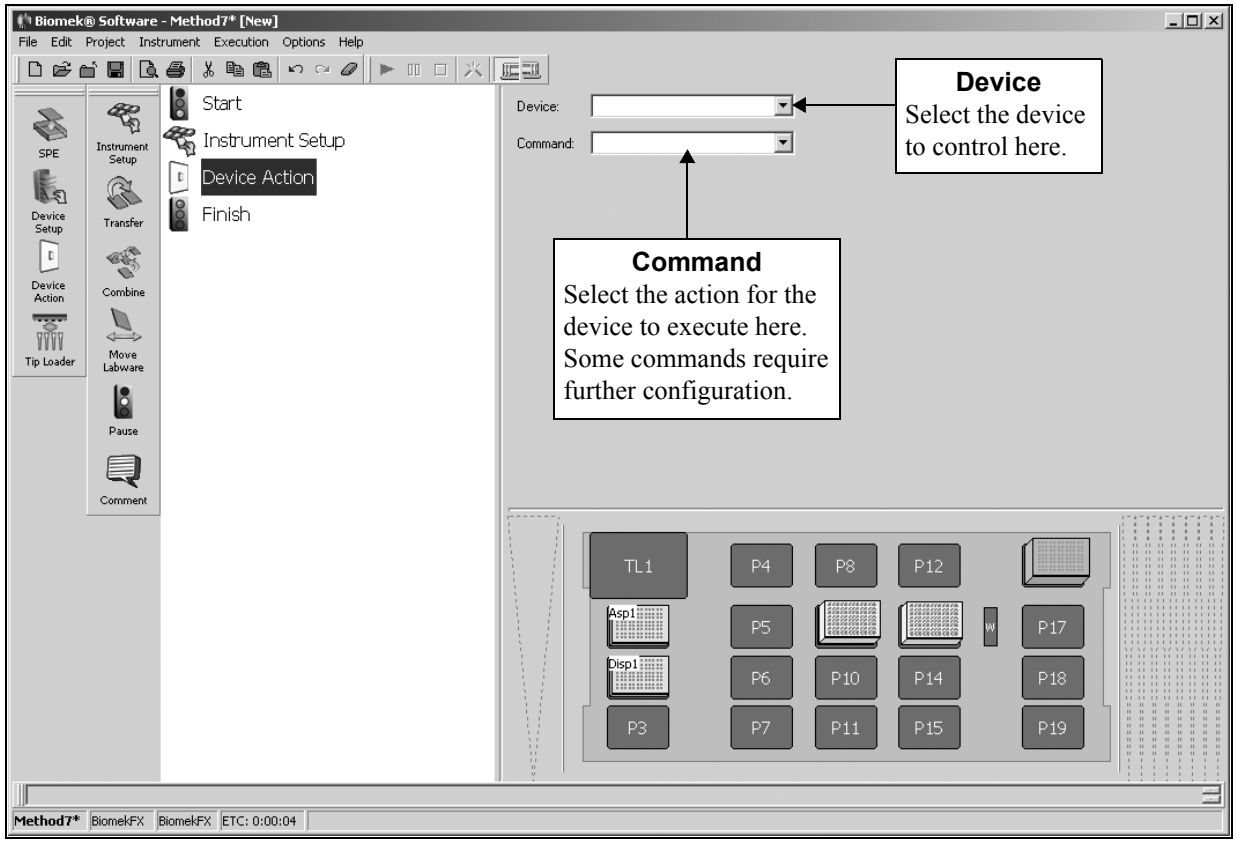


Figure 22-10. Device Action step and configuration

22.6.1 Configuring the Device Action Step

When Device Action is added to a method, the associated configuration appears.

The configuration options available for the Device Action step depend upon the device selected for configuration.

The Device Action step is used to control the following ALPs and devices:

- *Configuring the Device Action Step for 6-Port Valve (3000 only)* (Section 22.6.1.1).
- *Configuring the Device Action Step for an Autolatch (3000 only)* (Section 22.6.1.2).
- *Configuring the Device Action Step for a Drainable/Refillable Reservoir ALP (FX, NX only)* (Section 22.6.1.3).
- *Configuring the Device Action Step for the MicroMix (3000 only)* (Section 22.6.1.4).
- *Configuring the Device Action Step for the Microplate Shaking ALP (FX, NX only)* (Section 22.6.1.5).
- *Configuring the Device Action Step for a Multichannel Tip Wash ALP (FX, NX-MC only)* (Section 22.6.1.6).
- *Configuring the Device Action Step for a Positive Position ALP (FX, NX only)* (Section 22.6.1.7).
- *Configuring the Device Action Step for a Source/Waste Sensor (FX and NX only)* (Section 22.6.1.8)
- *Configuring the Device Action Step for a Speed Pump (FX only)* (Section 22.6.1.9).
- *Configuring the Device Action Step for the Stirring ALP (FX, NX only)* (Section 22.6.1.10).
- *Configuring the Device Action Step for the Vacuum (3000 only)* (Section 22.6.1.11).
- *Configuring the Device Action Step for the Wash System (3000 only)* (Section 22.6.1.12).

22.6.1.1 Configuring the Device Action Step for 6-Port Valve (3000 only)

To configure the Device Action step for the 6-port valve:

1. From **Device**, select the 6-port valve performing the required operation.

   Note: Biomek Software refers to the 6-port valve as SixPortValve.

   OR

2. Click on the 6-port valve in the Current Deck Display to select it. The configuration for the 6-port valve appears (Figure 22-11).

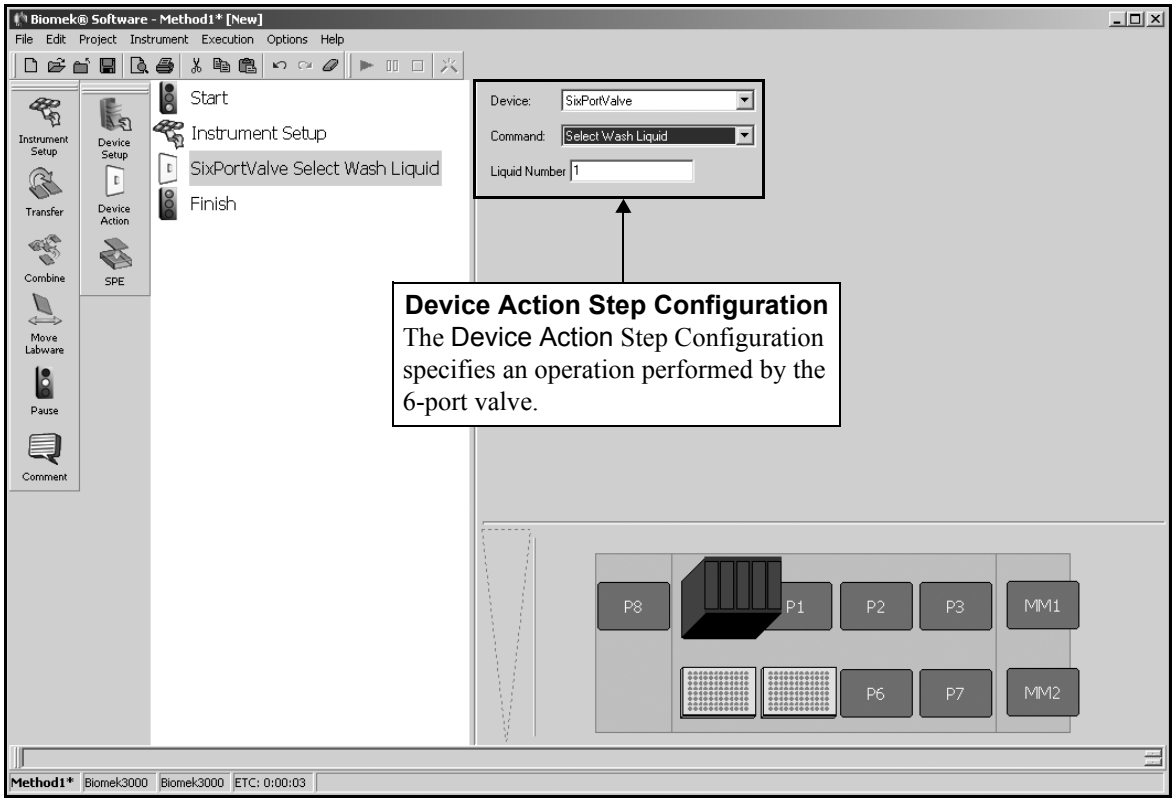


Figure 22-11. Device Action step for the 6-port valve

3. In **Command**, choose:
   - Select Wash Liquid — to enter the liquid number in Liquid Number.
   - Device Setup — to select the liquid type for the six ports from the drop-down menus. Figure 22-12 appears.

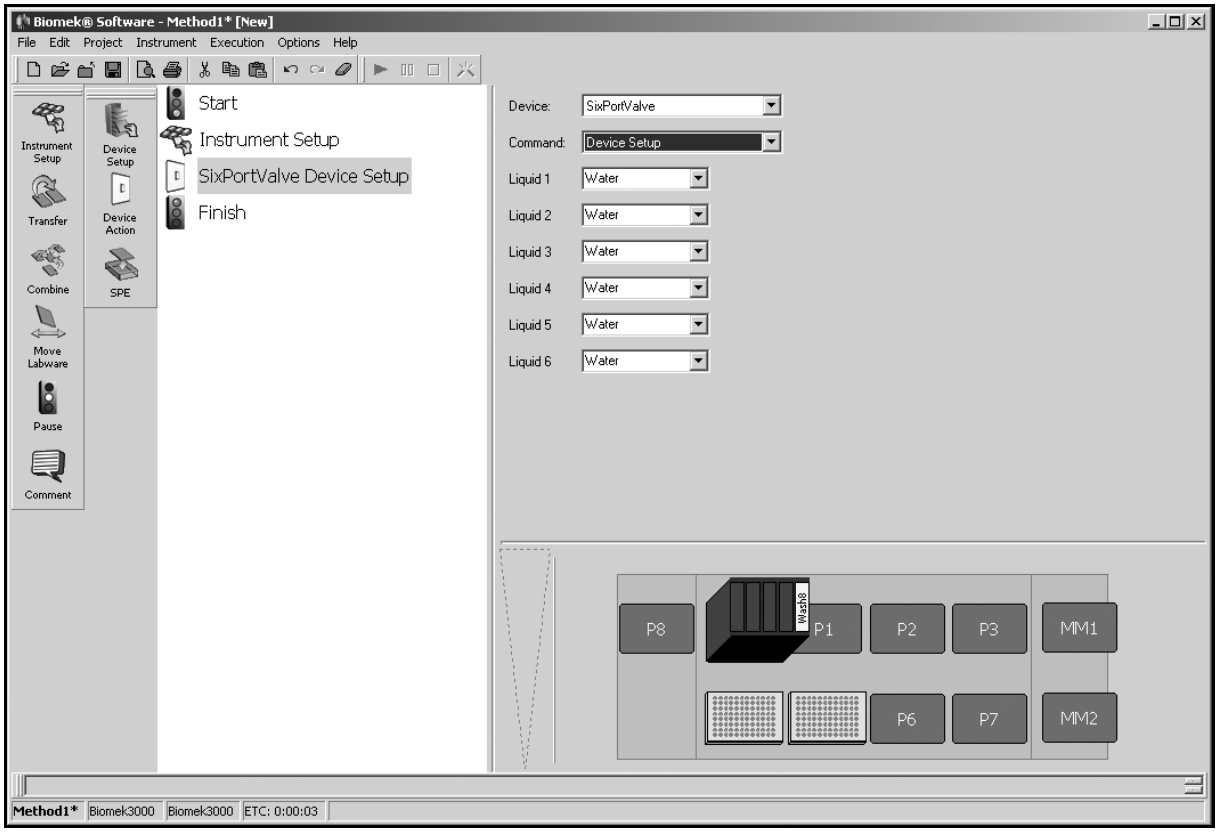


Figure 22-12. Device Action step for the 6-port valve with Device Setup chosen

22.6.1.2 Configuring the Device Action Step for an Autolatch (3000 only)

To configure the Device Action step for the Auto-Latching Tip Rack Holder or autolatch:

1. From **Device**, select the autolatch performing the required operation.

   OR

   Click on the autolatch in the Current Deck Display to select it. The configuration for the autolatch appears (Figure 22-13).

Note: The deck position has a blue border in the Current Deck Display and is displayed to the right of Device.

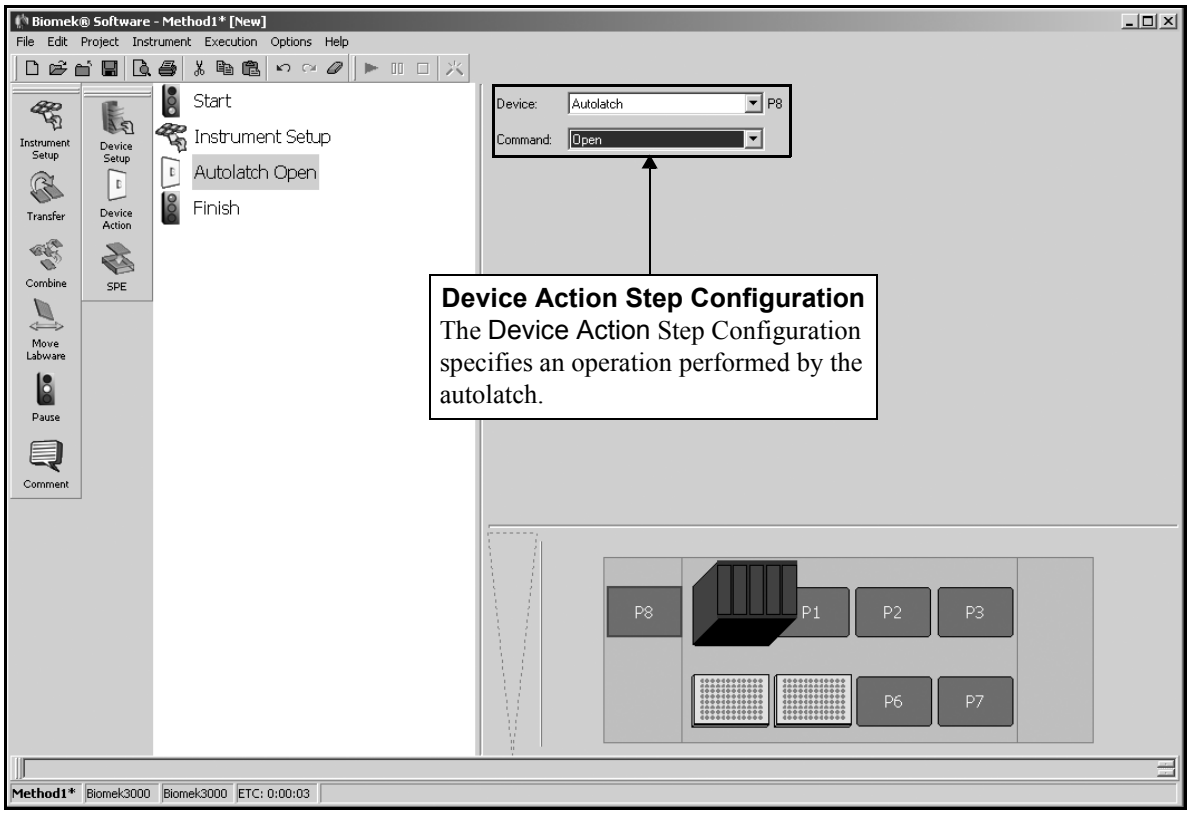


Figure 22-13. Device Action step for the autolatch

2. In **Command**, indicate the desired state for the autolatch: Open or Close.

22.6.1.3 Configuring the Device Action Step for a Drainable/Refillable Reservoir ALP (FX, NX only)

To configure the Device Action step for the Drainable/Refillable Reservoir ALP:

1. From **Device**, select the Drainable/Refillable Reservoir ALP performing the operation.

   Note: Biomek Software refers to the ALP as DrainableRefillableReservoir.

   OR

   Click on the desired ALP in the Current Deck Display. The deck position is highlighted by a blue border and named to the right of Device. The configuration for the ALP appears (Figure 22-14).

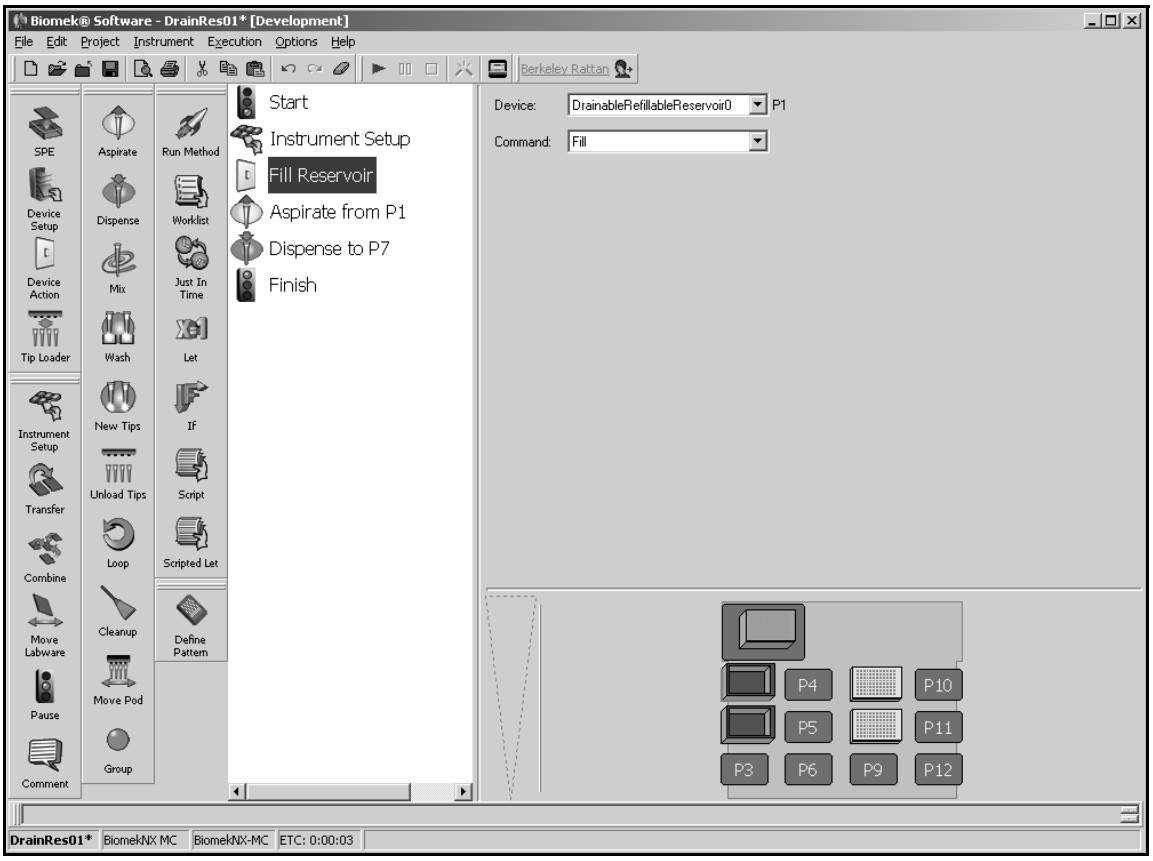


Figure 22-14. Device Action step for the Drainable/Refillable Reservoir ALP

2. In Command, choose the operation performed by the ALP:
   - **Fill** — fills the reservoir to the maximum level.
   - **Drain** — drains the reservoir.
   - **AssertSensor** — has the sensor check for the presence of liquid in the reservoir. Sensor State appears in the configuration.
   - **AutoFill** — keeps the reservoir supplied with liquid during the method run. AutoFill should be appears in the configuration.

3. If AssertSensor is selected, in Sensor State, choose
   - **On** — allows the method run to proceed when sufficient liquid is detected in the reservoir.
   - **Off** — allows the method run to proceed when liquid is not detected in the reservoir.
4. If AutoFill is the selected Command, in AutoFill should be, choose:
   - **On** — turns AutoFill on for the duration of the method run.
   - **Off** — turns AutoFill off. Liquid remains in the reservoir.

Note: To turn off AutoFill and drain the reservoir, insert a Device Action step configured to Drain the reservoir. Draining the reservoir is useful for reducing evaporation during a long pause in a method run. For example, insert a Device Action step configured to Drain the reservoir right before the pause. When the pause ends, insert a Device Action step configured to turn AutoFill On. The reservoir will be supplied with liquid during subsequent pipetting operations in the method run.

22.6.1.4 Configuring the Device Action Step for the MicroMix (3000 only)

To configure the Device Action step for the MicroMix:

1. From **Device**, select the MicroMix performing the required operation.

   OR

   Click on the MicroMix in the Current Deck Display to select it. The configuration for the MicroMix appears.

   Note: The deck position has a blue border in the Current Deck Display and is displayed to the right of Device.

2. In **Command**, choose:
   - Shake — to configure a shake operation (refer to Section 22.6.1.4.1, *Configuring Shake*).
   - Custom Shake — to configure a custom shake operation (refer to Section 22.6.1.4.2, *Configuring Custom Shake*).
   - On — to turn on the MicroMix
   - Off — to turn off the MicroMix.

22.6.1.4.1 Configuring Shake

To configure a shake operation for the MicroMix:

1. In **Command**, choose Shake.

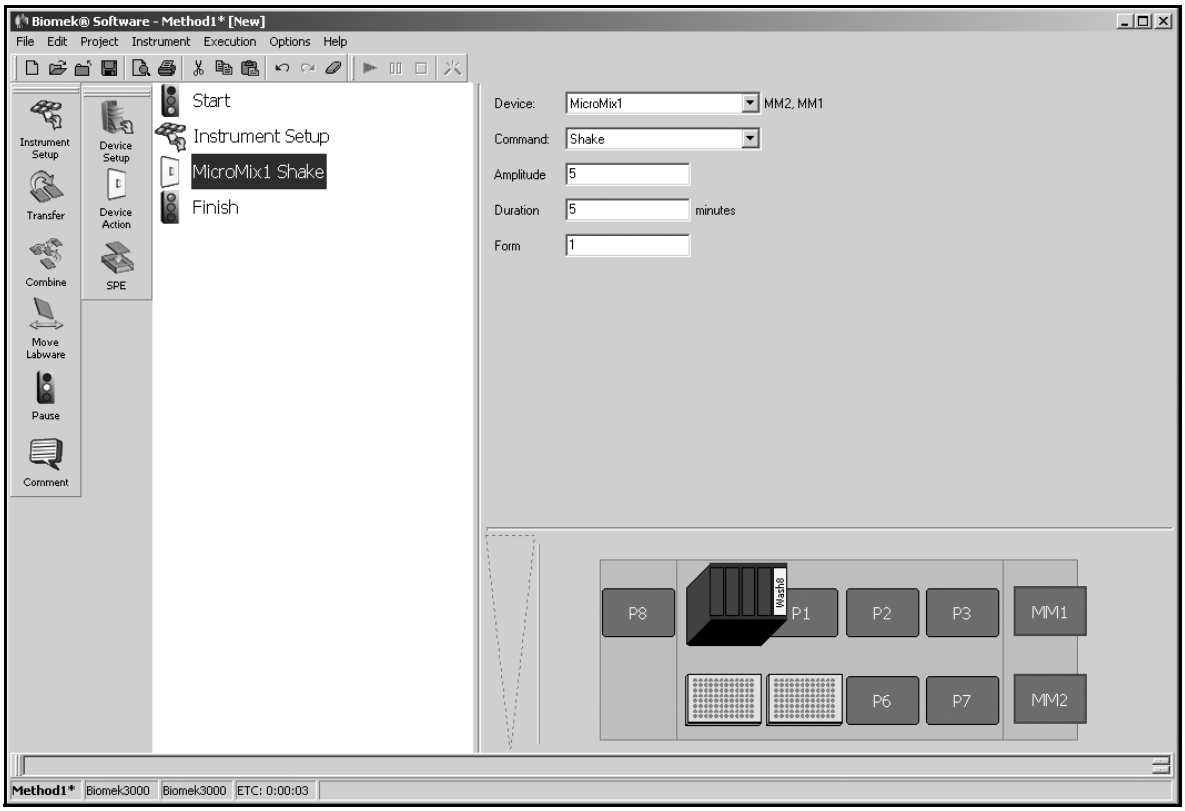


Figure 22-15. Device Action step for the MicroMix with Shake chosen

2. In **Amplitude**, enter the magnitude of power.

   Note: The selection for Amplitude ranges from 1 to 9; the minimum amplitude is 1 and the maximum is 9.

3. In **Duration**, enter the time in minutes.
4. In **Form**, enter the form number.

   Note: Sixty Forms (preset shaking cycle patterns) are available. See the *Appendix* in the *MicroMix 5 Shaker User's Manual* for a list of the available forms.

22.6.1.4.2 Configuring Custom Shake

To configure a custom shake operation:

1. In **Command**, choose Custom Shake (Figure 22-16).

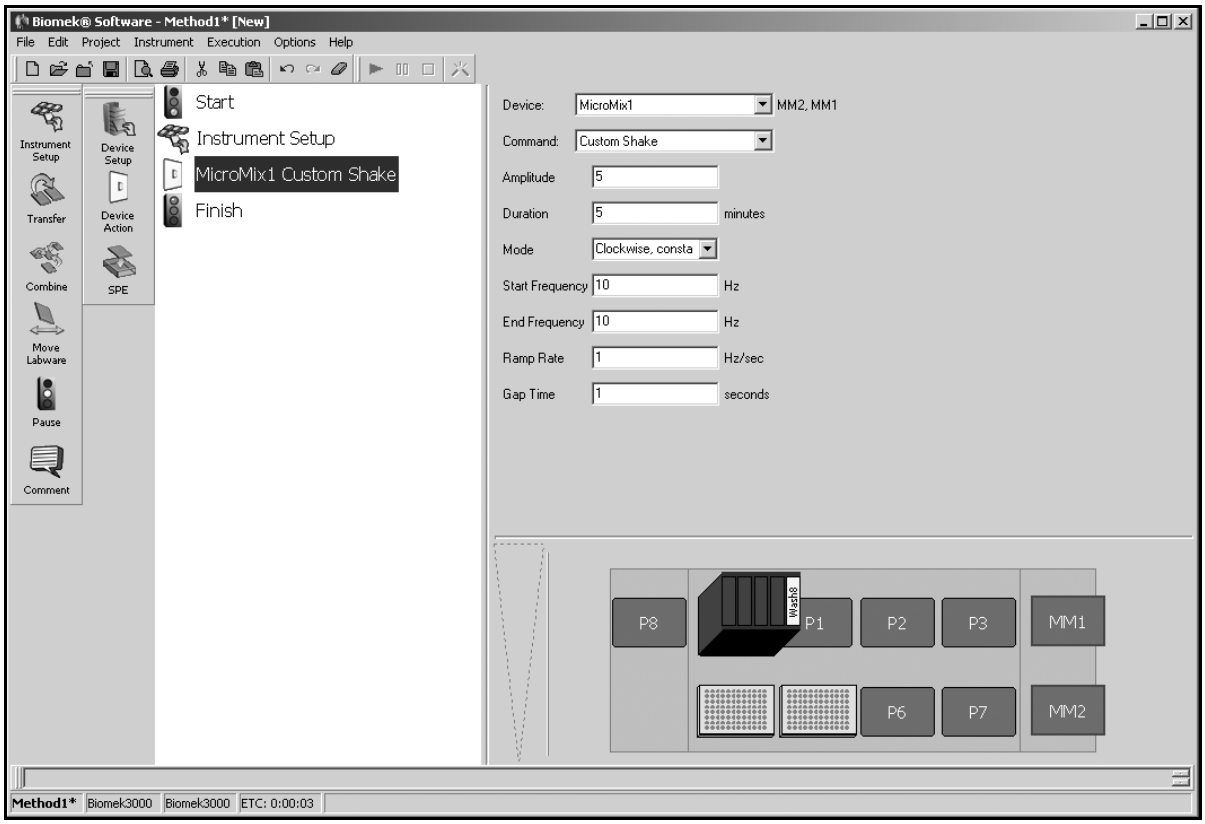


Figure 22-16. Device Action step for the MicroMix with Custom Shake chosen

2. In **Amplitude**, enter the magnitude of power.

   Note: The selection for Amplitude ranges from 1 to 9; the minimum amplitude is 1 and the maximum is 9.

3. In **Duration**, enter the time in minutes.
4. In **Mode**, choose one of the following:
   - Clockwise, constant direction, constant speed.
   - Counter-clockwise, constant direction, constant speed.
   - Ramp frequency up, ramp frequency down, gap, change direction.
   - Ramp frequency up, gap, change direction, ramp frequency down, gap, change direction.

5. In **Start Frequency**, enter the starting orbital speed.

   Note: The allowable range of Start Frequency is 10 to 30.

6. In **End Frequency**, enter the ending orbital speed.

   Note: The allowable range of End Frequency is 10 to 30.

7. In **Ramp rate**, enter the speed of change from the Start Frequency to the End Frequency.

   Note: The allowable range of Ramp rate is 1 to 250.

8. In **Gap time**, enter the non-shaking period prior to change of direction in seconds.

   Note: The allowable range of Gap time is 0 to 2.55.

22.6.1.5 Configuring the Device Action Step for the Microplate Shaking ALP (FX, NX only)

To configure the Device Action step for the Microplate Shaking ALP (Figure 22-17):

1. From **Device**, select the Microplate Shaking ALP performing the required operation.

   Note: The Biomek Software refers to the Microplate Shaking ALP as ShakerALP.

   OR

   Click on the Microplate Shaking ALP on the Current Deck Display to select it. The configuration for the Microplate Shaking ALP appears (Figure 22-17).

   Note: The deck position has a blue border in the Current Deck Display and is displayed to the right of Device.

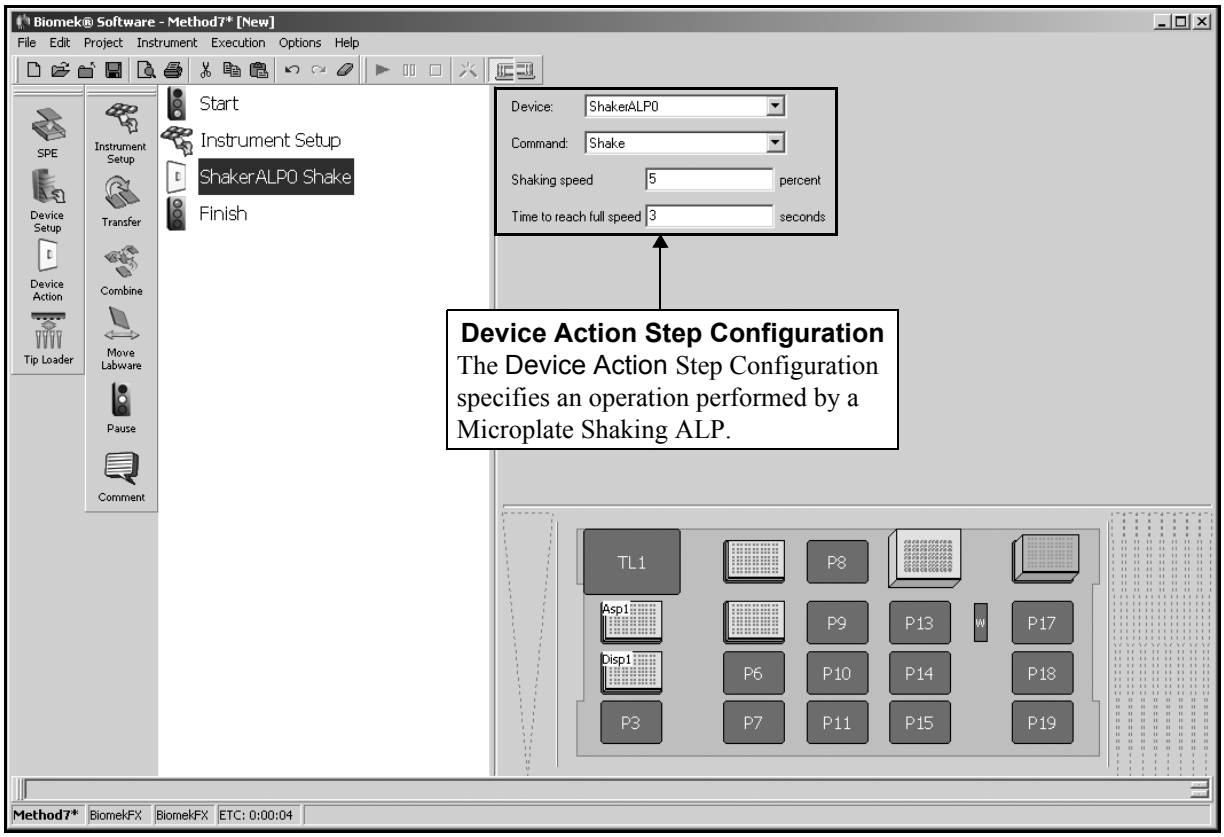


Figure 22-17. Device Action step for the Microplate Shaking ALP

2. In **Command**, indicate the operation performed by the device: Shake, Timed Shake, Off, Clamp, or Unclamp.

   Note: Shake and Timed Shake activate the Microplate Shaker ALP and require further configuration, as described below. Off deactivates the Microplate Shaker ALP and does not require further configuration. Clamp and Unclamp tighten and loosen the clamp on the Microplate Shaker ALP and do not require further configuration.

3. Select the **Shaking speed**, which is in the range of 1-100 indicating a percentage of the Microplate Shaking ALP's maximum shaking speed.

4. In **Time to reach full speed**, select how long (in seconds) it should take to reach the full shaking speed.

   Note: The Microplate Shaking ALP stops shaking automatically when pipetting to or from the ALP and restarts when the pipetting operation is finished. The Microplate Shaking ALP stops shaking when a gripper operation is performed, but does not restart when the operation is completed. The Microplate Shaking ALP stops shaking when the Finish step is executed.

5. For a Timed Shake action only, select how long (in seconds) to shake the microplate in **Time to shake**.

22.6.1.6 Configuring the Device Action Step for a Multichannel Tip Wash ALP (FX, NX-MC only)

To configure the Device Action step for the wash pump associated with a Multichannel Tip Wash ALP (Figure 22-18):

Note: A Multichannel Tip Wash ALP may be a 96-Channel or 384-Channel Tip Wash ALP.

1. From **Device**, select the wash pump associated with the Multichannel Tip Wash ALP performing the required operation.

   OR

   Click on the Multichannel Tip Wash ALP in the Current Deck Display to select it. The configuration for the Multichannel Tip Wash ALP appears (Figure 22-18)

   Note: The deck position has a blue border in the Current Deck Display and is displayed to the right of Device.

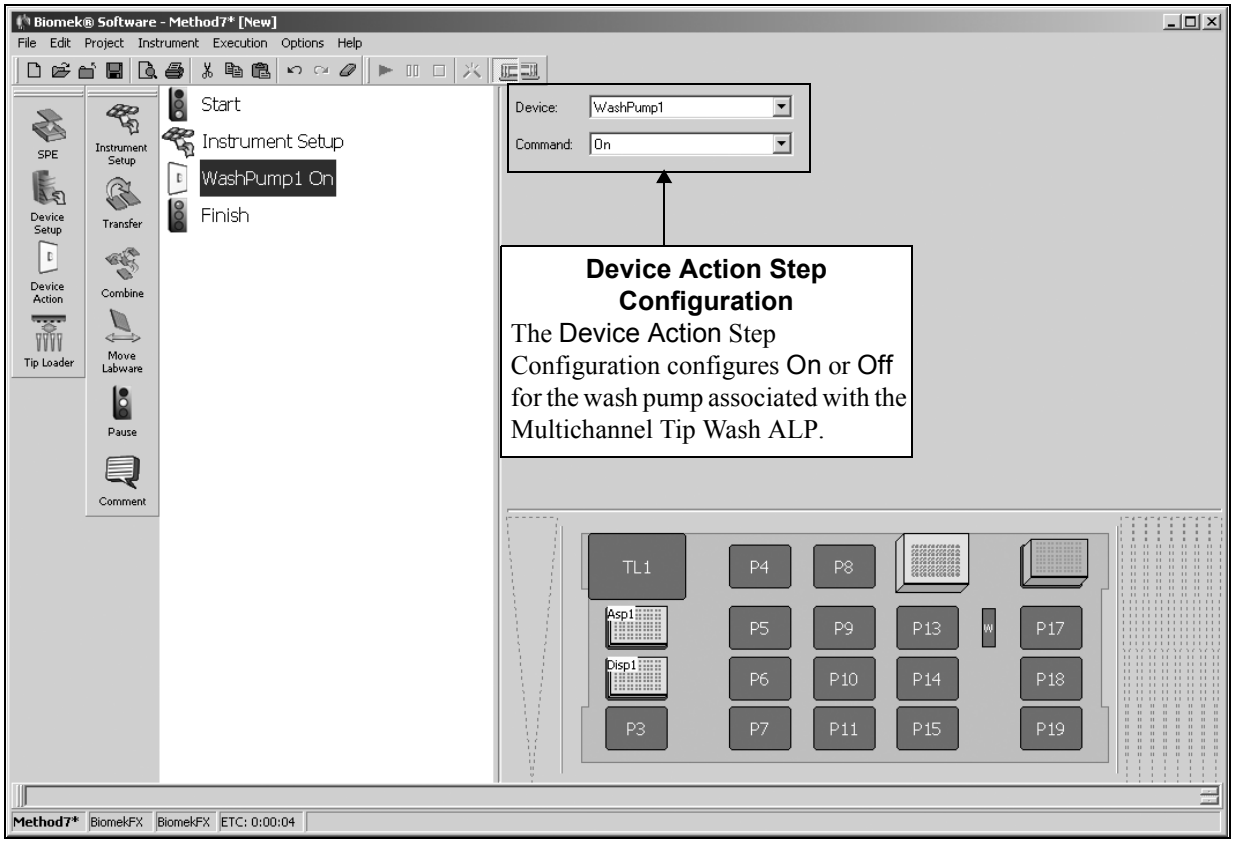


Figure 22-18. Device Action step for a Multichannel Tip Wash ALP

2. In **Command**, indicate the desired state for the Multichannel Tip Wash ALP: On or Off.

   Note: The Multichannel Tip Wash ALP stops washing when the Finish step is executed.

22.6.1.7 Configuring the Device Action Step for a Positive Position ALP (FX, NX only)

To configure the Device Action step for the Positive Position ALP:

1. From **Device**, select the Positive Position ALP performing the required operation.

   OR

   Click on the Positive Position ALP in the Current Deck Display to select it. The configuration for the Positive Position ALP appears (Figure 22-19).

Note: The deck position has a blue border in the Current Deck Display and is displayed to the right of Device.

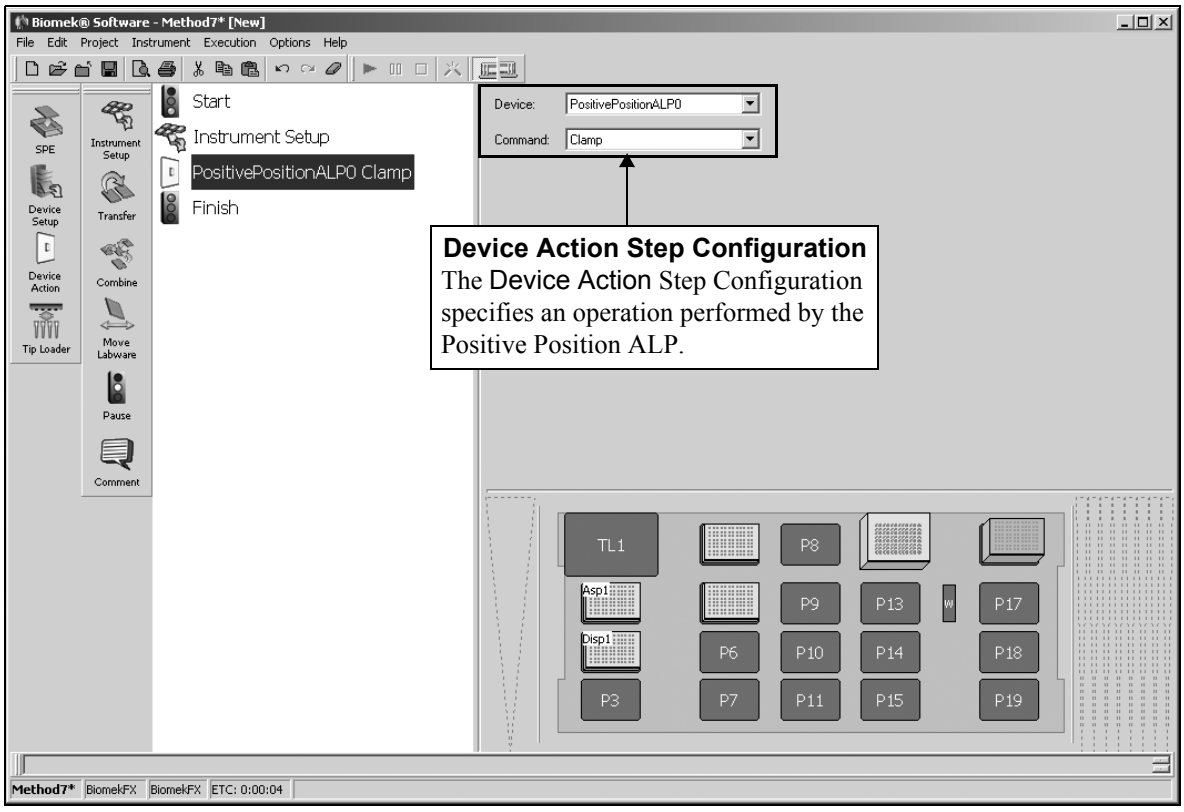


Figure 22-19. Device Action Step for the Positive Position ALP

2. In **Command**, indicate the desired action for the Positive Position ALP:
   - Clamp — tightens the clamp to hold the labware in place
   - Unclamp — releases the clamp to allow the labware to be removed from the ALP
   - VerifyLabware — verifies that labware is currently on the Positive Position ALP; an error displays and the method stops if no labware is found
   - VerifyNoLabware — verifies that there is currently no labware on the Positive Position ALP; an error displays and the method stops if labware is found

22.6.1.8 Configuring the Device Action Step for a Source/ Waste Sensor (FX and NX only)

To configure the Device Action step for a Source/Waste Sensor:

1. From Device, select the **SourceWasteSensor** performing the operation. Configuration options for the sensor appear (Figure 22-20).

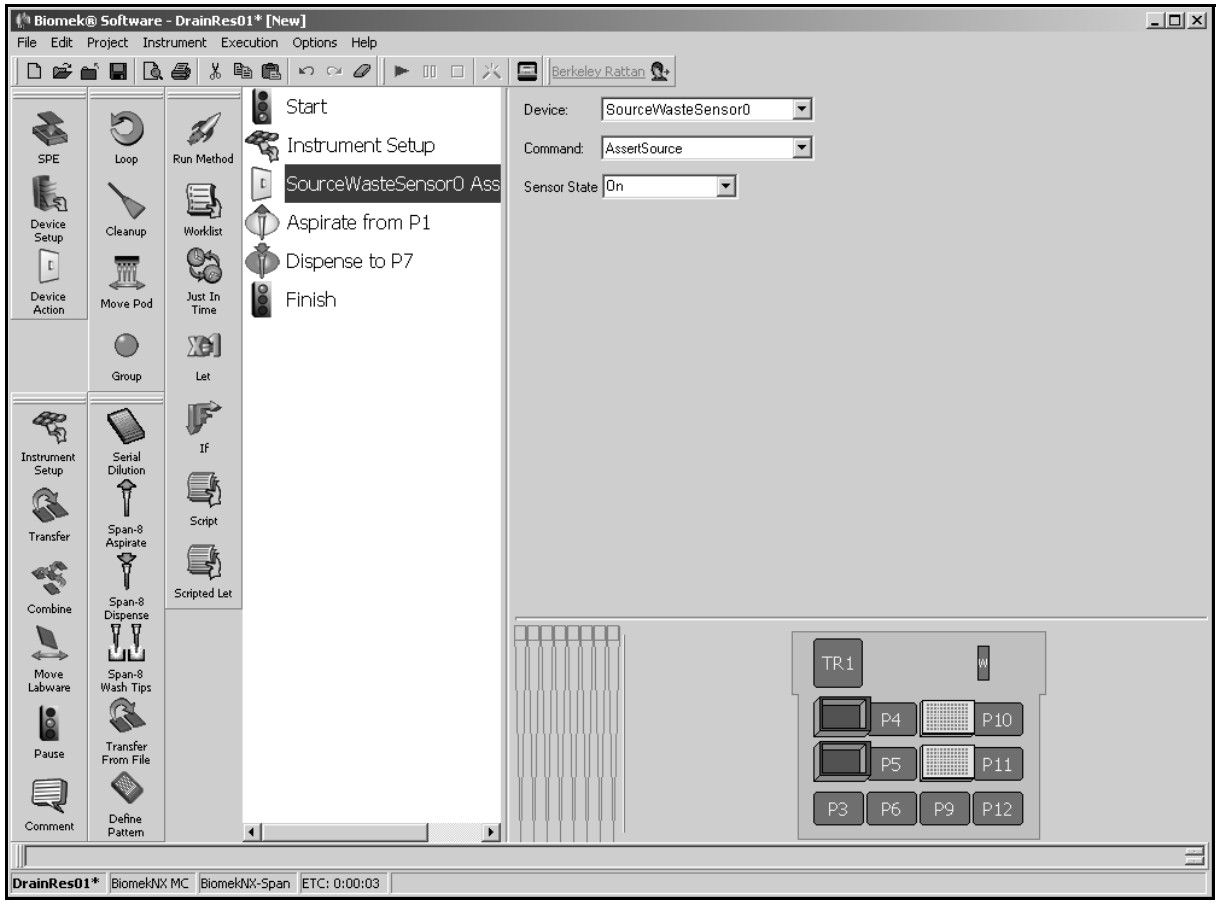


Figure 22-20. Device Action for a Source/Waste Sensor

2. In Command, select the operation to perform:
   - **AssertSource** — has the source container sensor check for the presence of liquid.
   - **AssertWaste** — has the waste container sensor check for the presence of liquid.
3. In Sensor State, set the sensor action:
   - **On** — allows the method run to continue if sufficient liquid is detected in the source container, or if the liquid level in the waste container is sufficiently low.
   - **Off** — allows the method run to continue when insufficient liquid is detected in the source container, or if the waste container is filled to the maximum level allowed.

22.6.1.9 Configuring the Device Action Step for a Speed Pump (FX only)

The Speed Pump is used in conjunction with the Span-8 Wash ALP. To configure the Device Action step for the Speed Pump:

1. From **Device**, select the Speed Pump performing the required operation.

   OR

   Click on the Span-8 Wash ALP in the Current Deck Display to select it. The configuration for the Speed Pump appears (Figure 22-21).

Note: The deck position has a blue border in the Current Deck Display and is displayed to the right of Device.

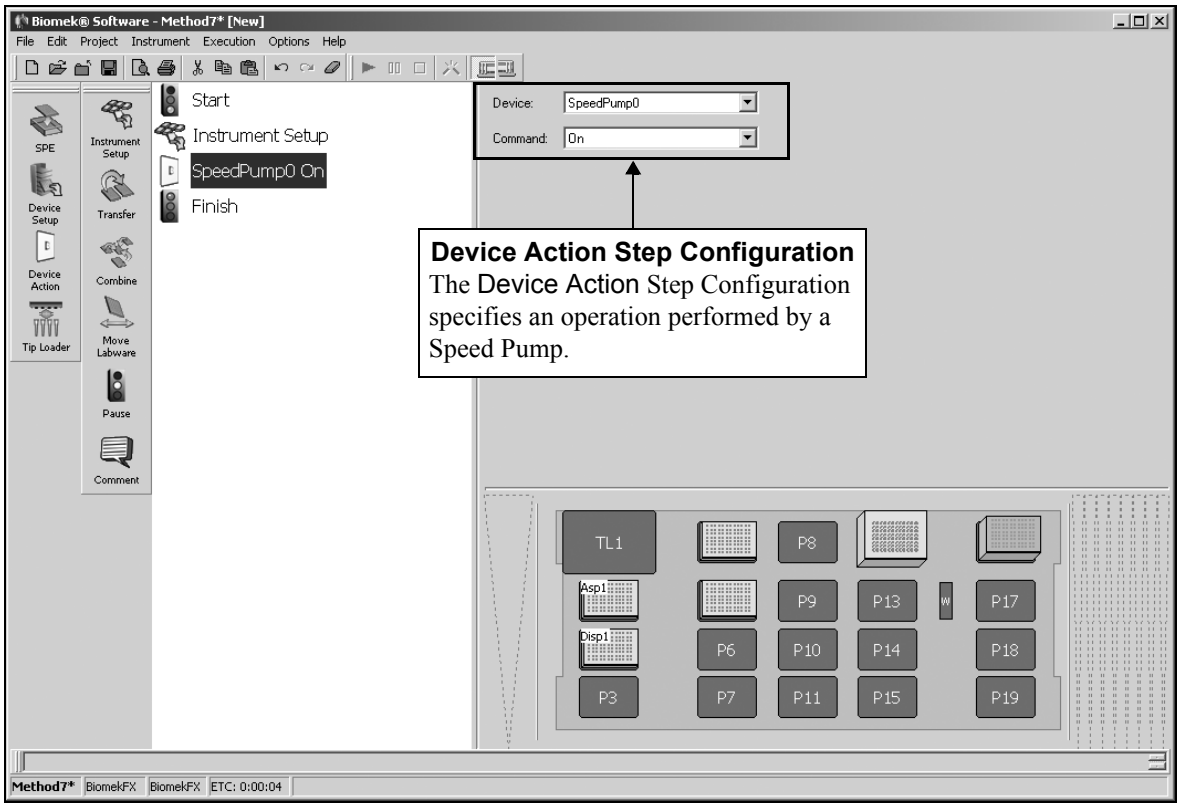


Figure 22-21. Device Action step for the Speed Pump

2. In **Command**, indicate the desired state for the Wash Station ALP: On or Off.

Note: The Speed Pump stops when the Finish step is executed.

22.6.1.10 Configuring the Device Action Step for the Stirring ALP (FX, NX only)

CAUTION: When setting the height for pipetting operations on the Stirring ALP, the presence of the stir bar must be taken into consideration. Pipetting operations that do not account for the height of the stir bar could damage the tips.

To configure the Device Action step for the Stirring ALP (Figure 22-22):

1. From **Device**, select the Stirring ALP performing the required operation.

   Note: Biomek Software refers to the Stirring ALP as StirrerALP.

   OR

   Click on the Stirring ALP on the Current Deck Display to select it. The configuration for the Stirring ALP appears (Figure 22-22).

   Note: The deck position has a blue border in the Current Deck Display and is displayed to the right of Device.

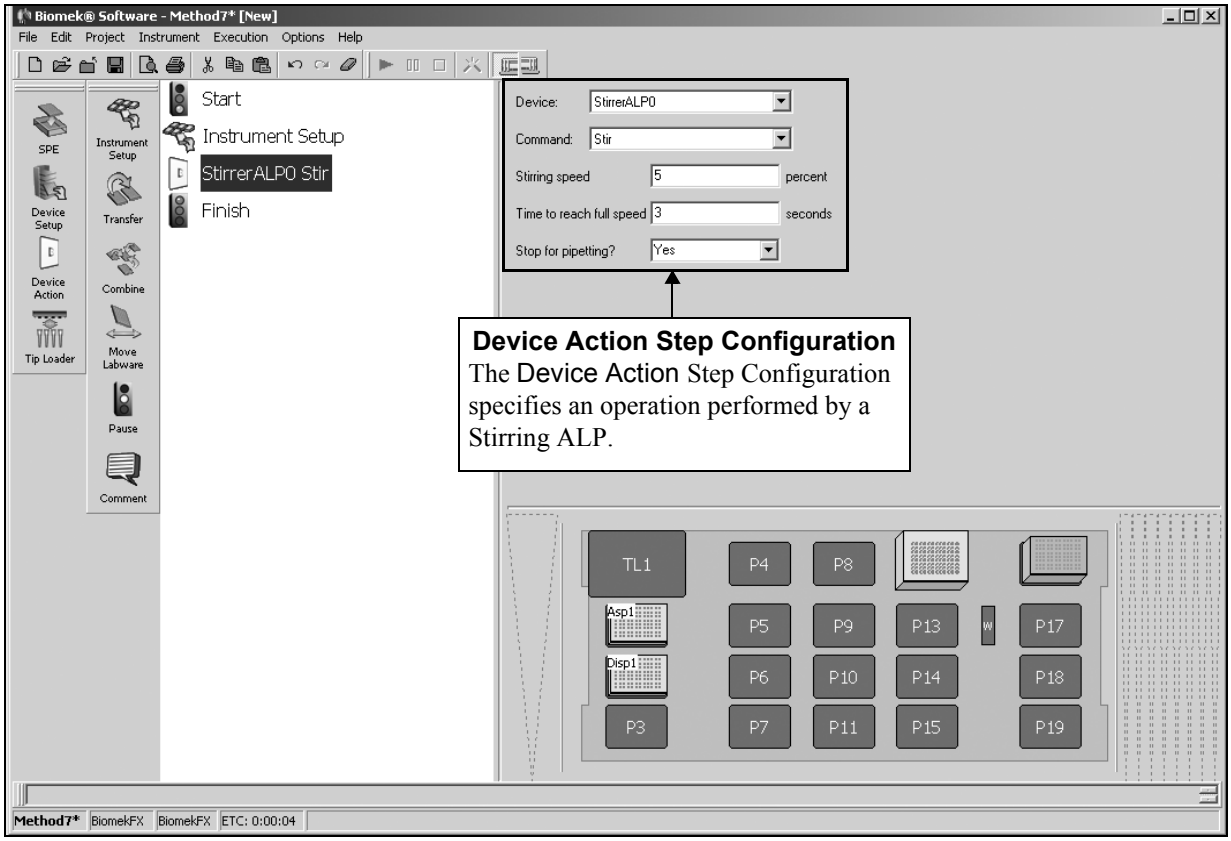


Figure 22-22. Device Action step for the Stirring ALP

2. In **Command**, indicate the operation performed by the device: Stir or Off.

   Note: The Stir command requires further configuration, as described below. Off deactivates the Stirring ALP and does not require further configuration.

3. Select the **Stirring speed**, which is in the range of 1-100 indicating a percentage of the Stirring ALP's maximum stirring speed.

4. In **Time to reach full speed**, select how long (in seconds) it should take to reach the full stirring speed.
5. In **Stop for Pipetting?**, select whether or not to stop the stirring operation for pipetting. If Yes is selected, when performing pipetting operations to labware on the Stirring ALP it stops stirring while the tips access the labware and resumes stirring when finished.

Note: The Stirring ALP stops stirring when the Finish step is executed.

22.6.1.11 Configuring the Device Action Step for the Vacuum (3000 only)

To configure the Device Action step for the vacuum:

1. From **Device**, select the vacuum performing the required operation.

   OR

   Click on the vacuum in the Current Deck Display to select it. The configuration for the vacuum appears (Figure 22-23).

Note: The deck position has a blue border in the Current Deck Display and is displayed to the right of Device.

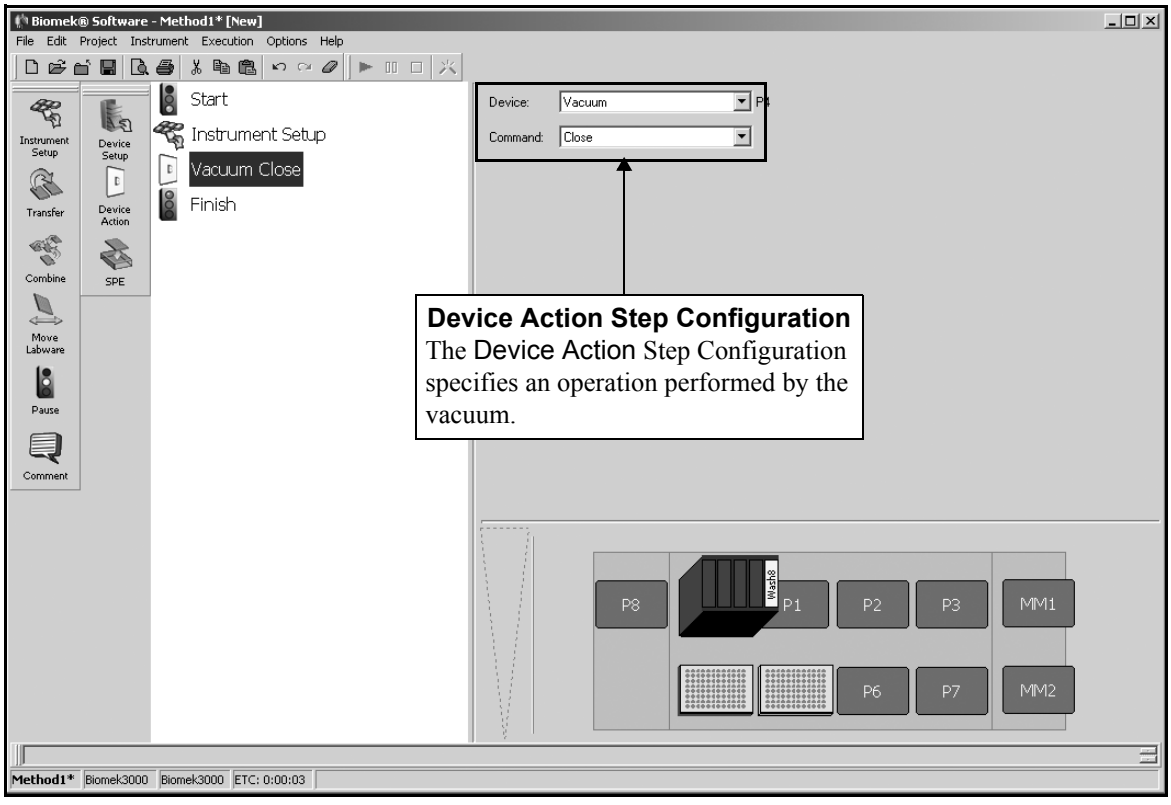


Figure 22-23. Device Action step for the vacuum

2. In **Command**, choose:
   - Close — to close the vacuum.
   - Open — to open the vacuum.
   - Timed Vacuum — to select the vacuum time in seconds. Figure 22-24 appears.

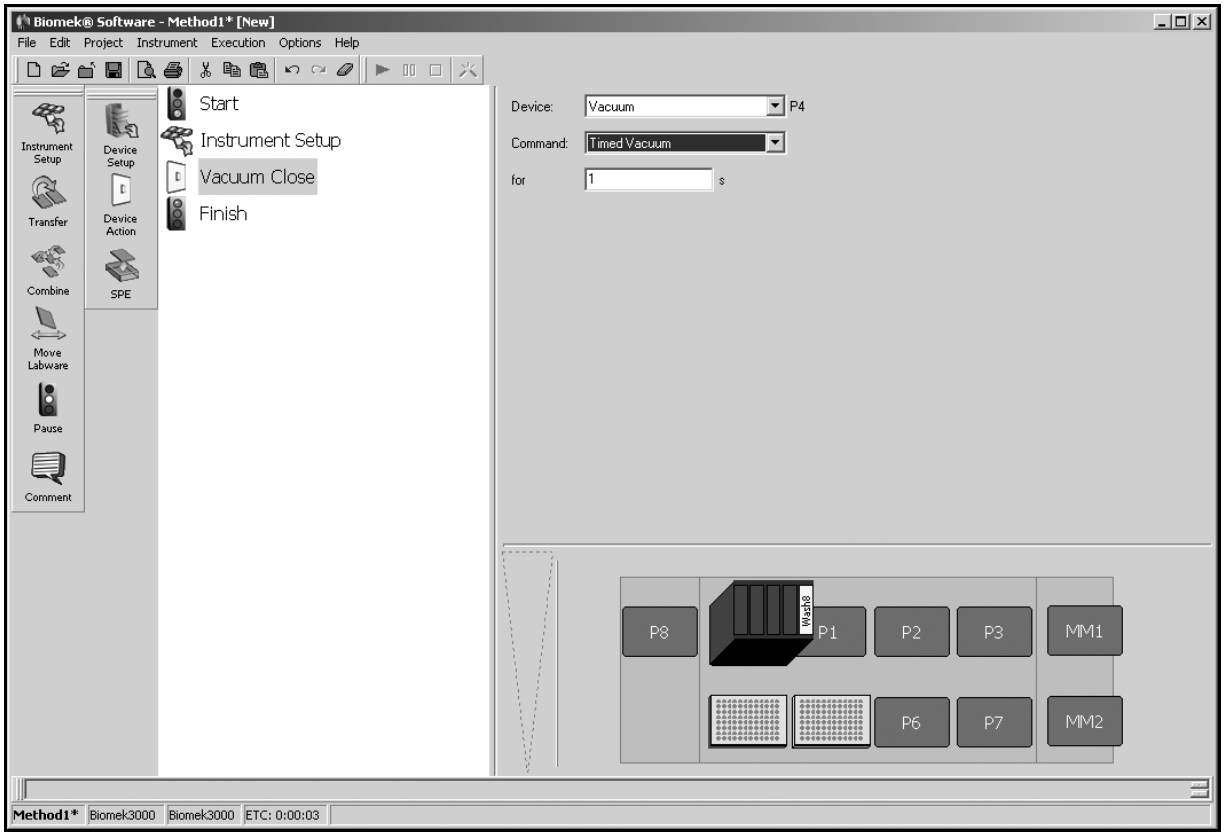


Figure 22-24. Device Action for the vacuum with Timed Vacuum chosen

22.6.1.12 Configuring the Device Action Step for the Wash System (3000 only)

To configure the Device Action step for the Wash System:

1. From **Device**, select the Wash System performing the required operation.

   OR

   Click on the Wash System in the Current Deck Display to select it. The configuration for the Wash System appears (Figure 22-25).

Note: The deck position has a blue border in the Current Deck Display and is displayed to the right of Device.

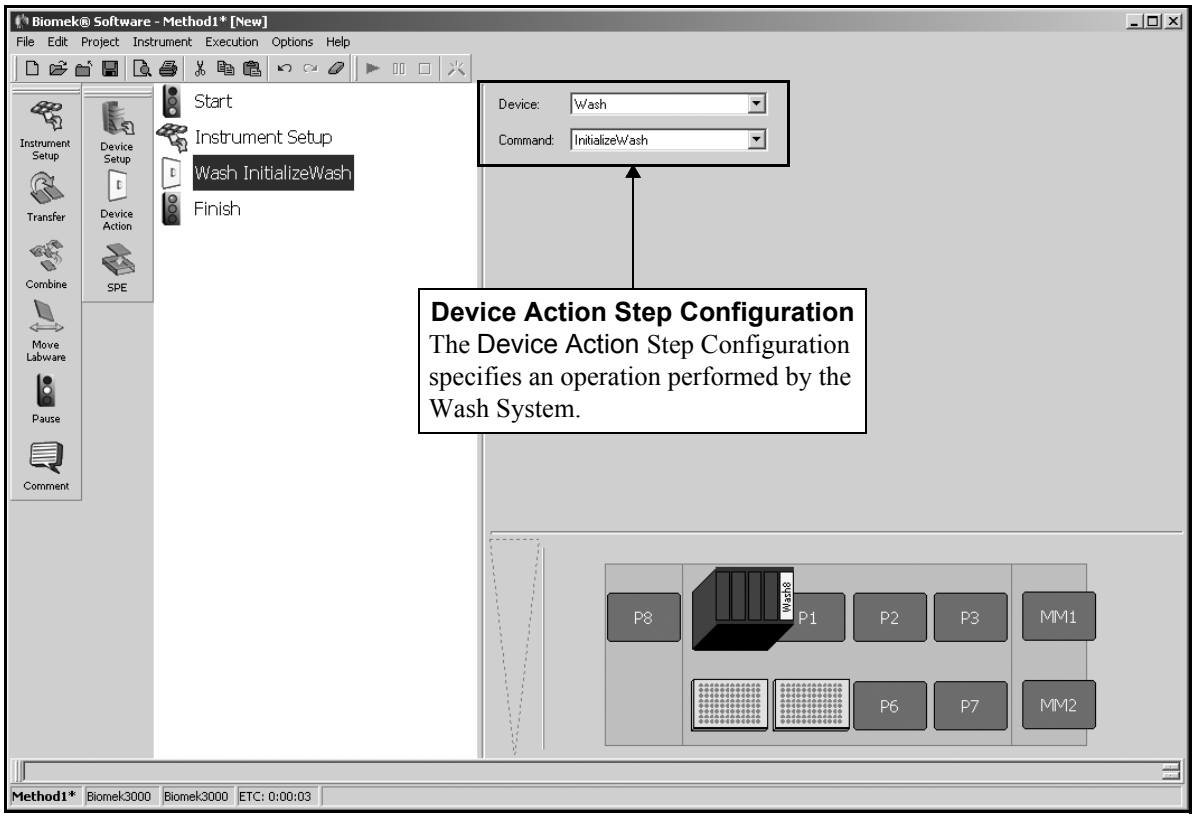


Figure 22-25. Device Action for the Wash System

2. In **Command**, choose:
   - InitializeWash — to initialize the wash.
   - Latch — to open or close the latch on the wash by choosing **Open** or **Close** from Direction (Figure 22-26).
   - Aspirate — to aspirate the wash liquid by entering **Speed** and **Volume** (Figure 22-27).
   - Dispense — to dispense the wash liquid by entering **Speed** and **Volume** (Figure 22-27).

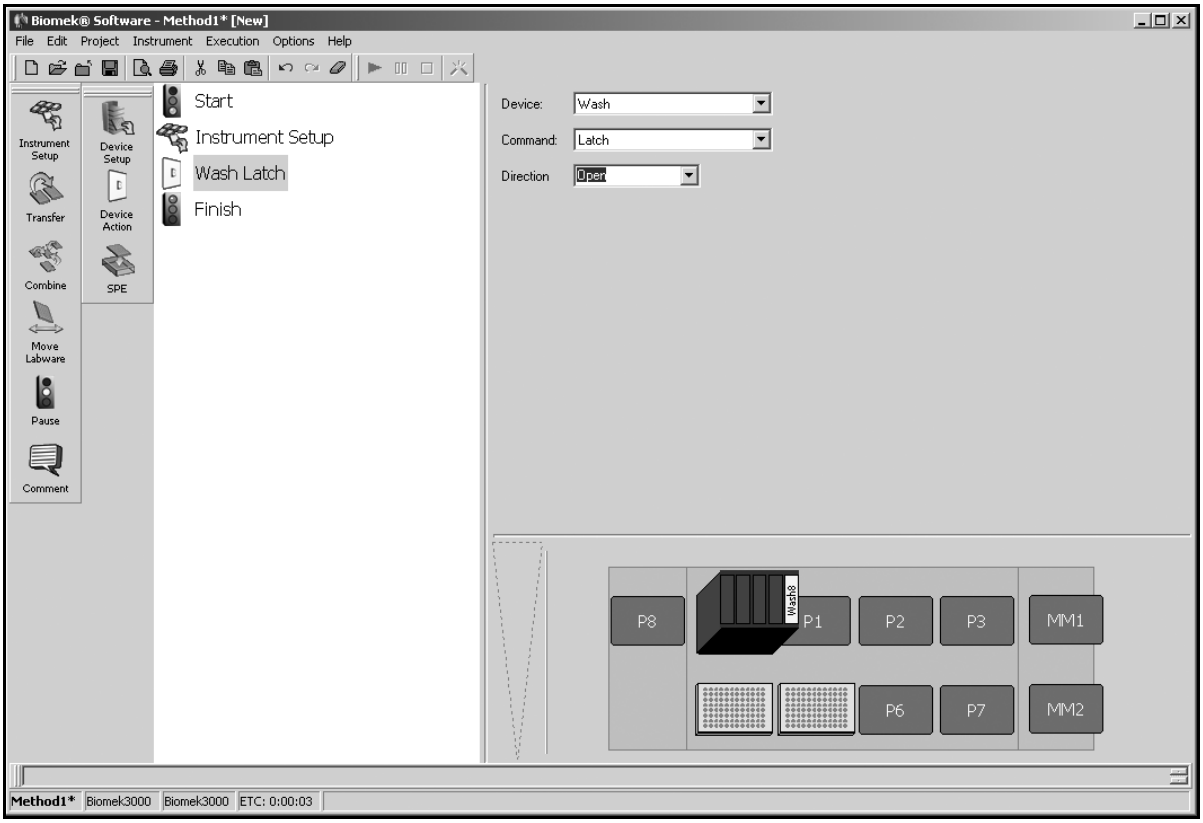


Figure 22-26. Device Action for the Wash System with Latch chosen

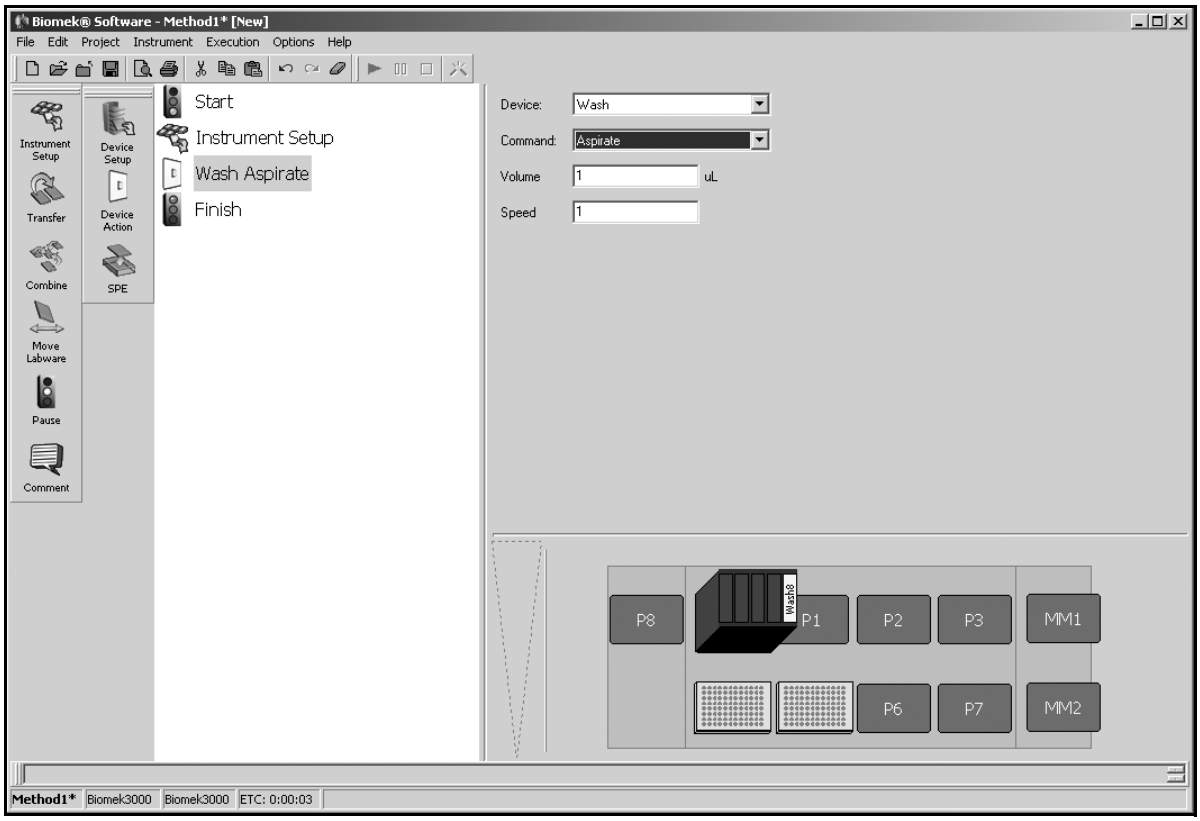


Figure 22-27. Device Action for the Wash System with Aspirate chosen

22.7 Tip Loader Step (FX, NX-MC only)

The Tip Loader step provides more control over a Tip Loader ALP than other steps using the Tip Loader ALP, such as New Tips and Unload Tips (Figure 22-28).

- ***FX*** — the Tip Loader is used only for loading and unloading tips to a Multichannel Pod.

The Tip Loader step is used when precise control over tip loading and unloading is required, such as when performing multiple aspirate and dispense operations with each operation requiring a specific set of tips.

Note: A usable tip box must be present on the Tip Loader ALP before using the Tip Loader step. The Tip Loader step does not automatically locate a tip box prior to performing an operation.

Insert a Tip Loader step into the Method View (Figure 22-28).

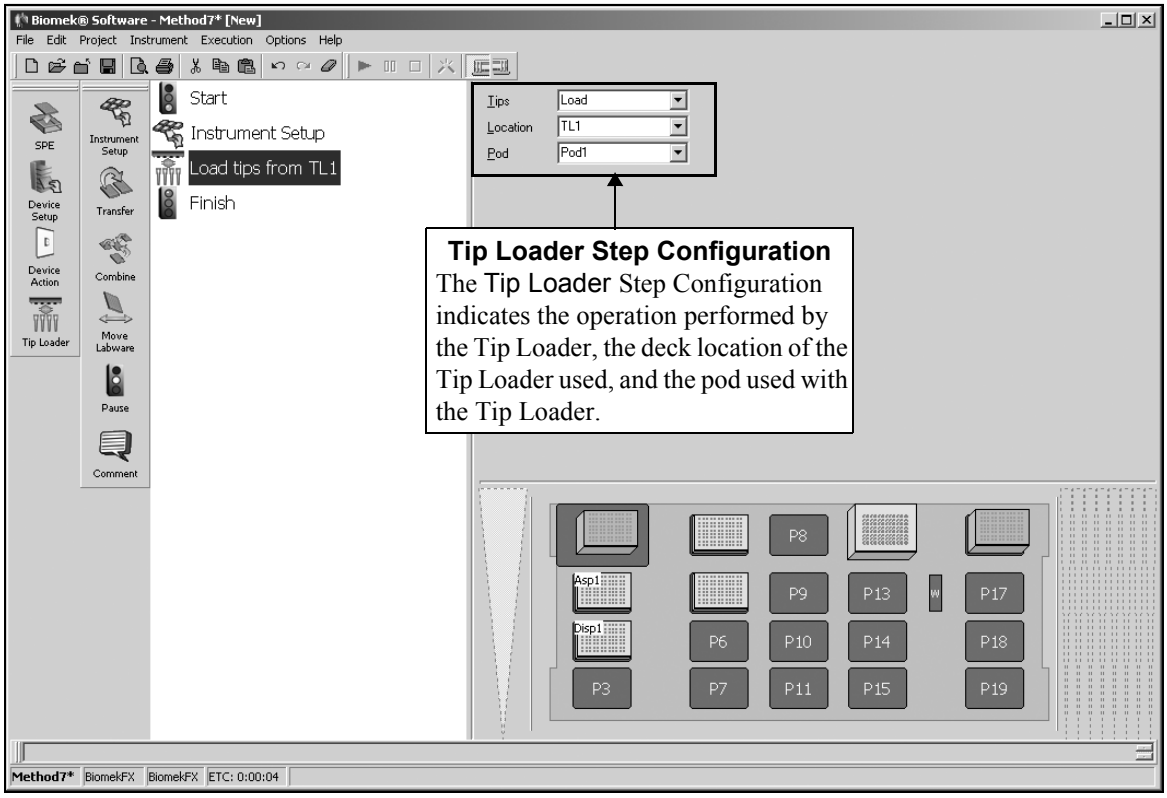


Figure 22-28. Tip Loader step and configuration

22.7.1 Configuring the Tip Loader Step

When the Tip Loader step is added to a method, the associated configuration appears (Figure 22-28).

To configure Tip Loader:

1. In Tips, specify whether to **Load** or **Unload** tips.

   Note: If the Tips field indicates that a load is performed, the Tip Loader caption in Method View indicates the operation with "Load 96 Tips from …"; however, if Unload is requested, the caption reads, "Unload 96 Tips from …".

2. Specify the **Location** of the Tip Loader on the deck.
3. Specify the **Pod** performing the tip load operation from the drop-down list.

   OR

   Select the **Pod** from the Current Deck Display. The tip diagram on the left of the Current Deck Display represents Pod1, while the tip on the right represents Pod2. Selecting a pod from the Current Deck Display automatically updates Pod in the Step Configuration.

   - ***FX*** — The pod can be selected from the Current Deck Display only if the instrument has two Multichannel Pods; Span-8 Pod cannot be used with this step.

     Note: In Pod, Pod1 is the default for a single-pod system. In a dual-pod system, the pod configured as the default pod is initially displayed in Pod.

22.8 SILAS Module Step

Any external device requiring a SILAS module for operation during a method is configured using a SILAS step. SILAS steps operate devices on a Biomek deck during a method run by communicating between Biomek Software and the SILAS modules.

22.8.1 Configuring the SILAS Module

Note: Before inserting a SILAS step into a method, it must be placed on a step palette. Refer to Chapter 29, *Changing Window Appearance*, for more information.

When configuring a SILAS Module, any required labware movement must be known and the appropriate selection must be made. All SILAS modules for external devices are configured using the same procedure, but some devices may have additional fields to configure.

To configure a SILAS Module Step:

1. Insert a SILAS Module Step into the method in the Method View (Figure 22-29).

   Note: The SILAS Module Step is labeled according to the device it represents; for example, the SILAS Module Step for the barcode reader is labeled as a Barcode Reader step.

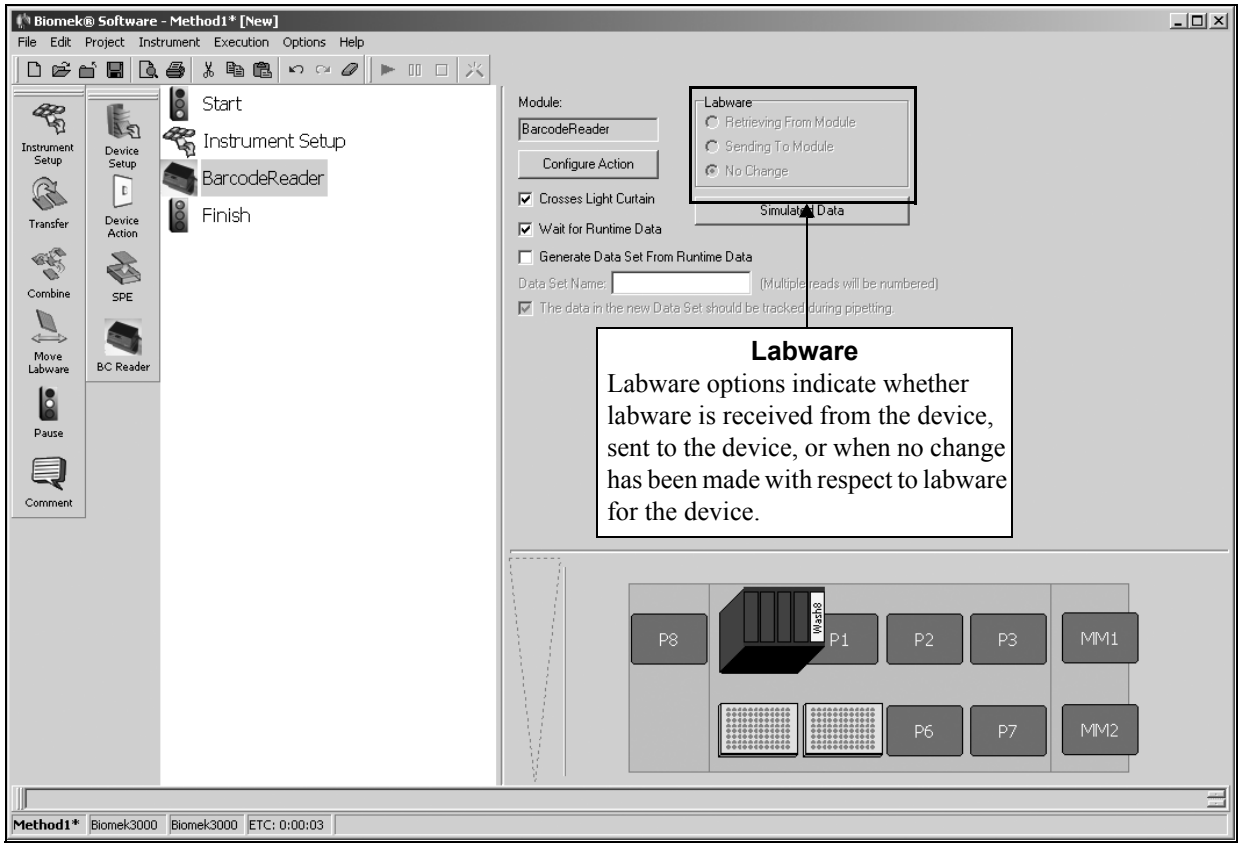


Figure 22-29. A Barcode Reader SILAS Module Step inserted in a method

2. Select **Configure Action**. Configure the operation of the device as desired.

3. Select **Update** after completing the action configuration.
4. Select the appropriate **Labware** movement.

   Labware options include:

   - Retrieving From Module — retrieves labware from the device
   - Sending To Module — sends labware from the deck to the device
   - No Change — labware remains in the current position after operations are completed

5. Select **Crosses Light Curtain** if the action taken by the device causes something to cross the light curtain. If selected, the instrument disables the light curtain while this command is executing.

   ➢ ***3000*** — This instrument does not have a light curtain.

   Note: Refer to Section 22.4.1, *Configuring Devices Using the Device Editor*, to configure the Crosses Light Curtain option.

6. Select **Wait for Runtime Data,** if required. Wait for Runtime Data allows Biomek Software to use data resulting from an action to make decisions on operations. Refer to Section 22.8.2, *Configuring Runtime Data*, for more information.

   Note: When Wait for Runtime Data is checked, the Biomek instrument will not validate beyond this step until it is completed.

22.8.2 Configuring Runtime Data

Runtime Data allows Biomek Software to read specific data about labware and to perform operations that meet specific criteria during a method. For example, the results of a bar code read can determine the specific operations performed on the labware using an If step.

Note: Information entered in Runtime Data Defaults during method validation is used because real data has not yet been obtained by Biomek Software.

To configure and use Runtime Data:

1. Select **Simulated Data**. Runtime Data Defaults appears (Figure 22-30).

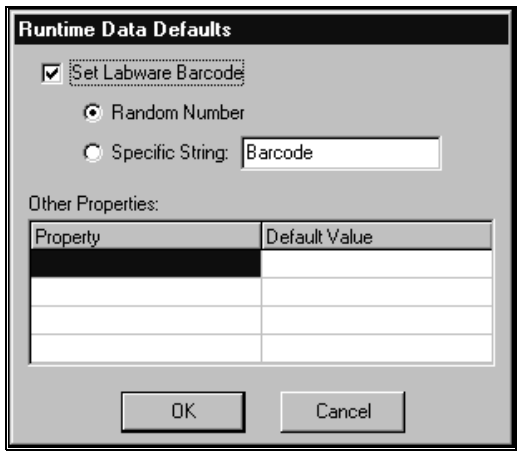


Figure 22-30. Runtime Data Defaults

2. Choose **Set Labware Barcode** to provide data for future decisions.
3. Choose one of the following:
   - **Random Number** — sets the Barcode property to a random number
   - **Specific String** — sets the Barcode property to the string indicated
4. In the **Property** field, enter the name of the property to set.
5. Enter the **Default Value** for the property when the property is not present for the labware.
6. Choose **OK** when configuration is complete.

22.8.3 Creating Data Sets from SILAS Messages

Data sets can be created from messages sent by a SILAS step for a device. For example, the results of a measurement from a microplate reader can be stored in a data set created from the SILAS step.

To create a data set from a SILAS message using a SILAS step:

1. Insert the desired SILAS step into the Method View.

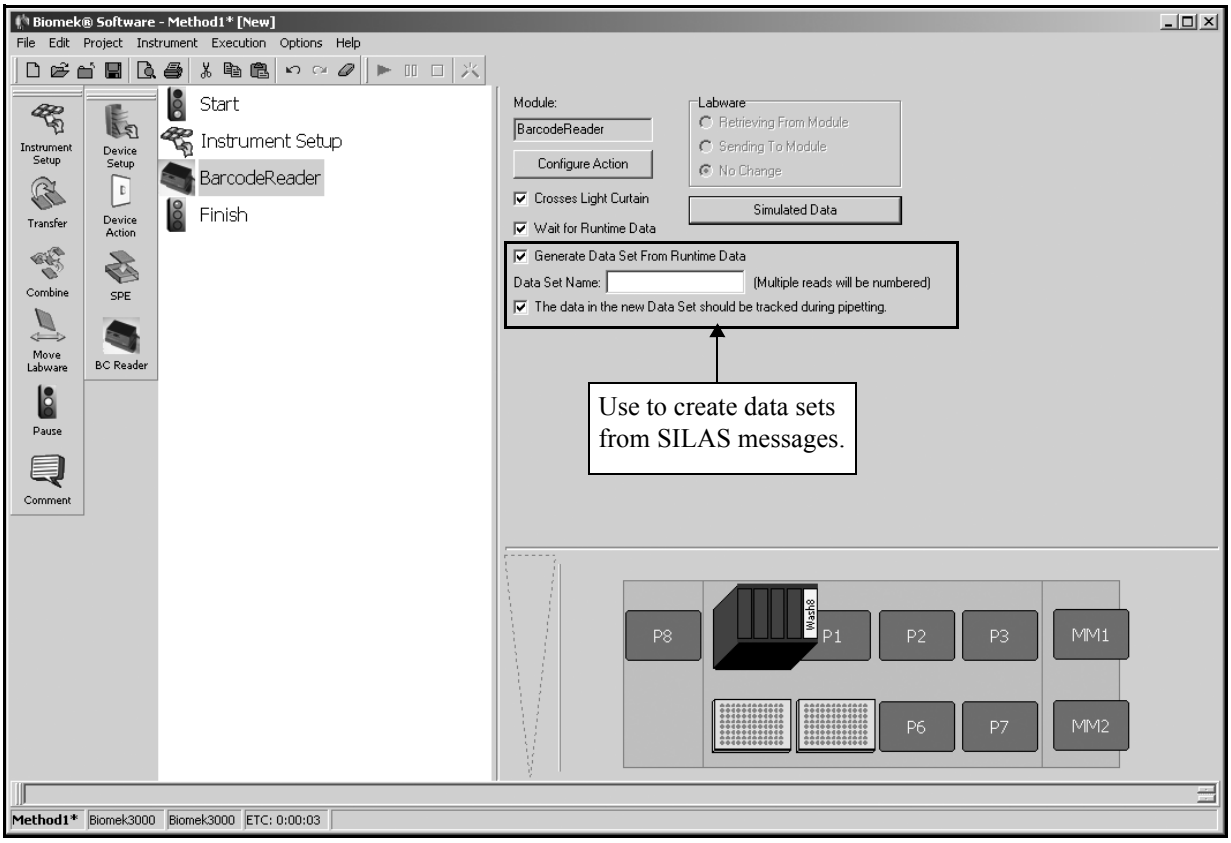


Figure 22-31. SILAS step with data sets chosen

2. Select **Configure Action** and configure the action of the device as desired.
3. Select **Wait for Runtime Data,** if required. Wait for Runtime Data allows Biomek Software to use data resulting from an action to make decisions on operations (refer to Section 22.8.2, *Configuring Runtime Data*).

   Note: When Wait for Runtime Data is checked, the Biomek instrument will not validate beyond this step until the step is completed.

4. Select **Generate Data Set From Runtime Data** to create a data set from the results of the configured action.
5. In Data Set Name, enter a name for the data set.

   Note: If the configured action produces more than one result per well, such as a multiple wavelength or kinetic read, a data set is created for each result and the Data Set Name is appended with an incremental number; for example, DataSet1, DataSet2, DataSet3, and so forth.

6. Select **The data in the new Data Set should be tracked during pipetting** to allow the system to track the data during pipetting operations.
7. Choose **Simulated Data**. Runtime Data Defaults appears (Figure 22-32).

Note: Information entered in Runtime Data Defaults during method validation is used because real data has not yet been obtained by Biomek Software (refer to Section 22.8.2, *Configuring Runtime Data*).

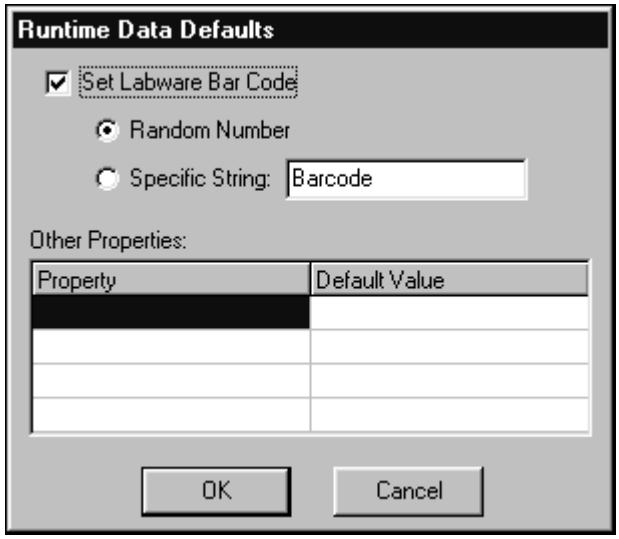


Figure 22-32. Runtime Data Defaults

8. In Property, enter the Data Set Name.
9. In Default Value, enter a default value to use for the data set during method validation. This value is used for all wells on the plate.

Note: At run time, the actual values of the data set will be used. The Default Value is only used for method validation.

23 Using the Stacker Carousel Step Palette

23.1 Overview

Steps on the Stacker Carousel Step Palette allow labware to be moved to and from the Stacker Carousel and the Biomek deck. The Stacker Carousel and steps expand labware capacity and increase walk-away automation during a method.

Note: Refer to the hardware manual for the specific instrument for detailed information on integrating and framing a Stacker Carousel on a Biomek Laboratory Automation Workstation.

The steps available in the Stacker Carousel Step Palette are:

- Present — configures from which hotel labware is presented to the deck and bar code reading options.

- Stacker Setup — configures the placement and properties of labware in the hotels on the Stacker Carousel.

- Store — configures to which hotel labware is stored from the deck.

23.2 Displaying the Stacker Carousel Step Palette

In order to use the Stacker Carousel steps in a method, display the Stacker Carousel Step Palette (Figure 23-1).

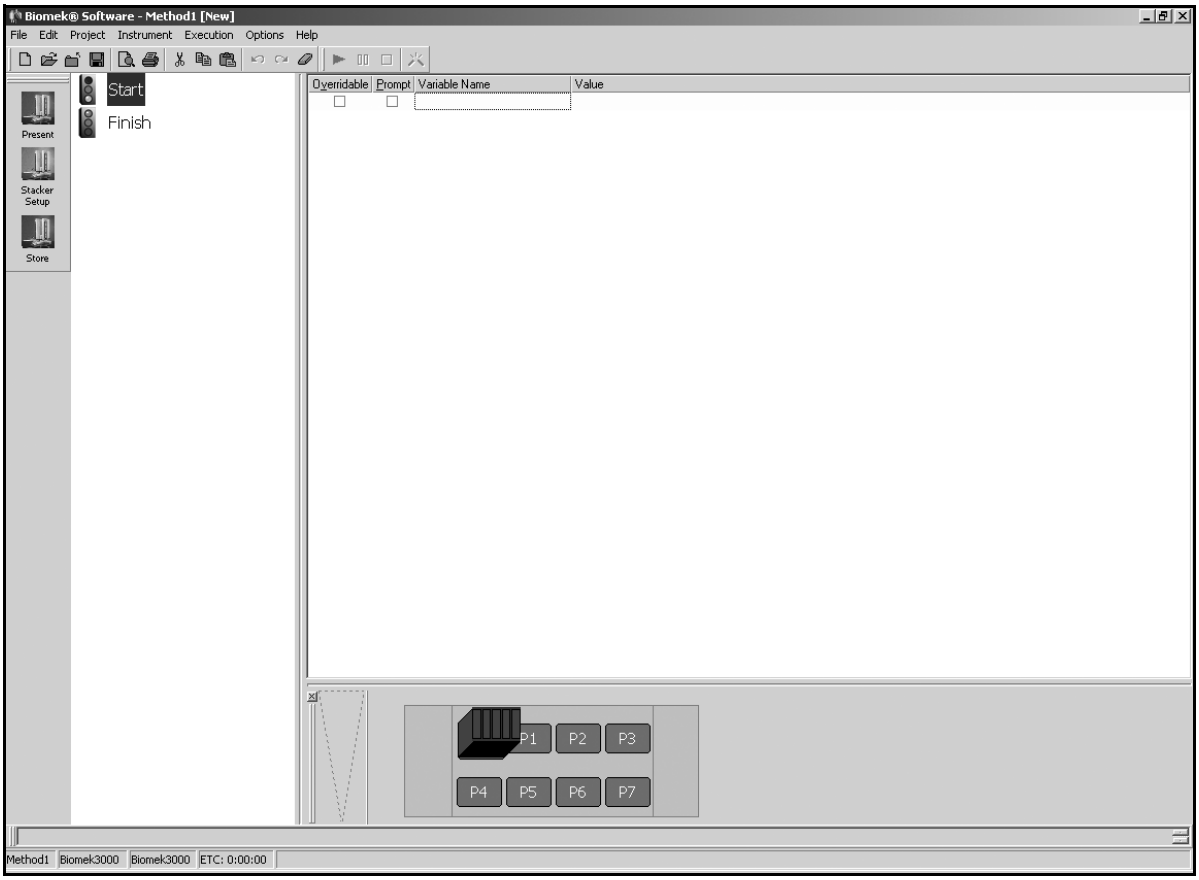


Figure 23-1. Biomek main editor with Stacker Carousel Step Palette displayed

To display the Stacker Carousel Step Palette, complete the following:

- Right-click any empty palette space and the step palette menu appears. Select **StackerCarousel**.

  OR

- From the toolbar, select **Options>Toolbars>StackerCarousel**.

23.3 Using the Stacker Setup Step

Use the Stacker Setup step to:

- configure the placement of labware in the hotels on the Stacker Carousel.
- configure the properties of the labware in the hotels.

23.3.1 Configuring the Placement of Labware in the Hotels

To configure the placement of labware in the hotels, labware is dragged from the Labware Category and dropped onto the slots of the hotels. As labware is dragged to the slot, the options Drop One, Fill Slot, and Fill Stack appear to allow the hotel to be quickly configured with labware.

The slots in hotels visually indicate the pieces of labware contained in each slot. A piece of labware that cannot be placed in a particular slot due to the configuration rules cannot be dropped into the slot (refer to Section 23.3.1.1, *Following the Rules to Configure the Placement of Labware in Hotels*).

23.3.1.1 Following the Rules to Configure the Placement of Labware in Hotels

These rules must be followed to configure the placement of labware in the hotels:

- Labware cannot be placed in a None hotel.
- Labware that cannot be stacked cannot be substacked. For example, in normal operation a tipbox cannot be stacked on a BCFlat96 plate, so in the Stacker Setup step, a tipbox cannot be substacked on a BCFlat96 plate in a hotel.

  Note: Substacking refers to stacking labware in the same slot of the hotel.

- Labware that is taller than the hotel's slot height cannot be placed in the hotel.
- A substack of labware that is taller than the hotel's slot height cannot be placed in hotel.
- A substack of labware cannot be placed in an HD (high-density) hotel.

To configure the placement of labware in the hotels on the Stacker Carousel:

1. Drag and drop a **Stacker Setup** step into the Method View (Figure 23-2).

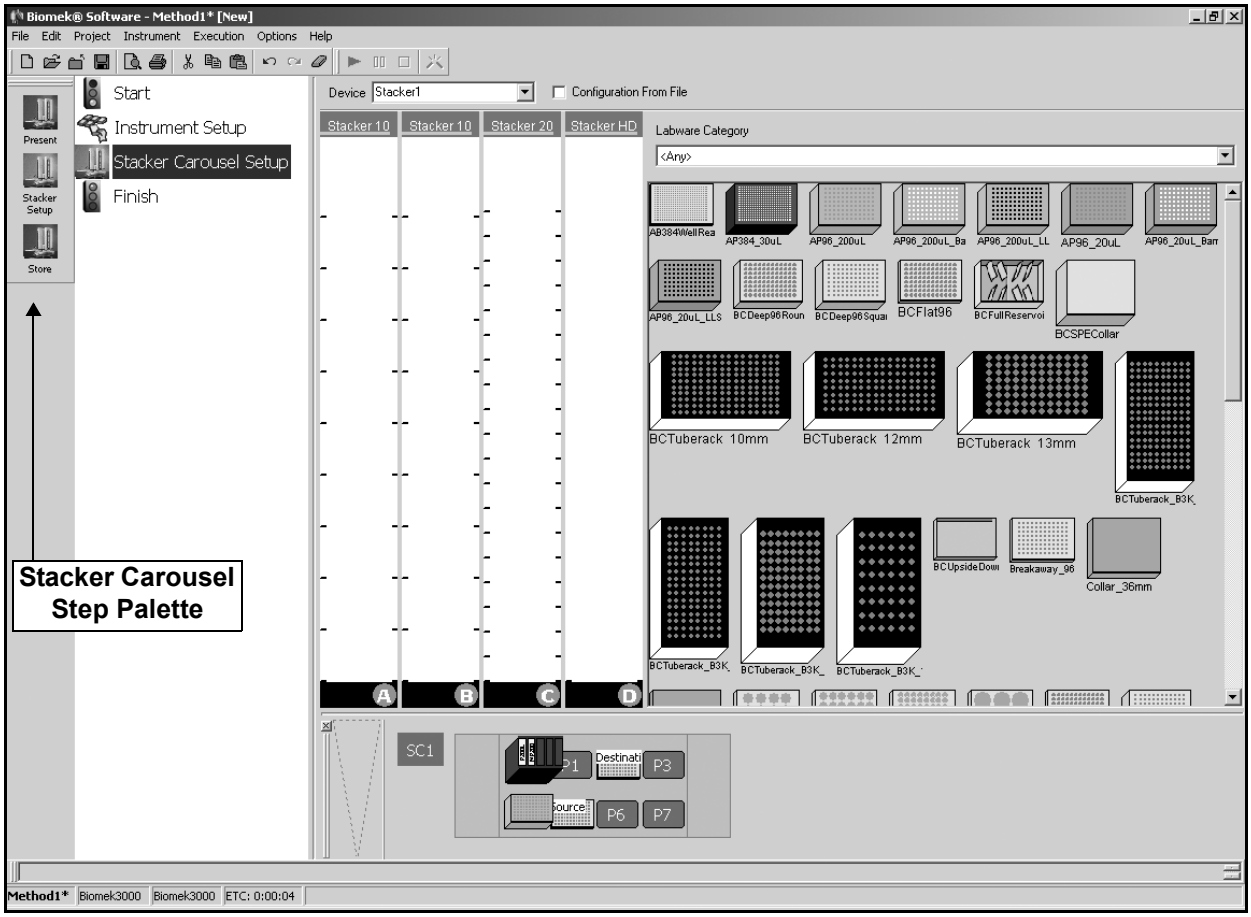


Figure 23-2. Stacker Setup step configuration

2. Choose the appropriate Stacker Carousel in **Device**.

Note: Multiple Stacker Carousels may be installed on a Biomek instrument.

Note: The Stacker Carousel must be installed and configured in Hardware Setup to appear in Device. Refer to the hardware manual for the specific instrument for detailed information on integrating and framing a Stacker Carousel on a Biomek instrument.

3. Drag and drop labware into the slots of the desired hotels.

Note: As labware is dropped into a slot, a dialog with options Drop One, Fill Slot, and Fill Stack appears (Figure 23-3). Choose one.

Figure 23-3. Dialog to drop labware into hotels

OR

Check **Configuration from File** to use a stacker configuration from a .csv file. **File** and **Browse** appear to allow the desired file to be chosen.

Note: Comma-Separated Value Files (.csv) (Table 23-1) are files that include data from a table that can be imported into another application. In this case, the .csv file used with the Stacker Setup step must contain Hotel, Slot, and LabwareType, and it may contain Name, LiquidType, UnloadTipsInto, BoxFinalLocation, Volume, BarCode, and SlotOrder.

Table 23-1. Example of a Comma-Separated Value File

Hotel	Slot	Slot Order	Labware Type	Name	Volume	Liquid Type	Bar Code	Unload TipsInto	BoxFinal Location
A	3	1	AP96200µL			na		<Tipbox>	<Home>
A	1	1	BCFlat96	Dest1		Water			
A	2	1	BCFlat96	Dest2	120	Water			
A	4	1	BCFlat96	Dest3	130	Water			
B	1	1	BCFlat96		110	Water			
B	2	1	BCFlat96		120	Water			
B	3	1	BCFlat96		130	Water			
B	4	1	BCFlat96		140	Water			
B	5	1	BCFlat96		150	Water			
B	6	1	BCFlat96		160	Water			
C	1	1	BCFlat96			Water			
D	1	1	BCFlat96			Water			

23.3.2 Configuring the Properties of the Labware in the Hotels

Each piece of labware in a hotel that will eventually be brought onto the instrument deck is configured using Labware Properties. The information provided in Labware Properties is used when a technique is selected, and when tips are loaded and unloaded.

To access Labware Properties:

1. Double-click on a piece of labware in the Stacker Setup.

   OR

   Right-click on a piece of labware in the Stacker Setup to open the menu to Labware Properties (Figure 23-4).

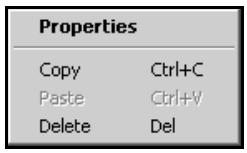


Figure 23-4. Menu accessing Labware Properties

Note: Right-clicking a piece of labware also provides the options of **Copy**, **Paste**, and **Delete** to populate the hotels with labware. Choosing **Copy** after labware has been configured in Labware Properties allows configured labware to be copied. Then choosing **Paste** allows a copied version of the configured labware to be pasted into another space on a hotel. Choosing **Delete** will delete the labware from the hotel.

Note: Right-clicking a tip box also provides the option of **Remove Tips** to configure an empty tip box.

The configuration options in Labware Properties provide the following information, if it applies to the type of labware selected:

- Name assigned to a piece of labware, if desired
- Labware type
- Maximum volume per well
- Bar code
- Volume for each well, if known
- Liquid type
- Where to dispose of tips
- Where to dispose of tip boxes
- Maximum number of times tips can be loaded
- Available tips

Note: Variables and expressions may be entered in any field that can be configured. Refer to Chapter 13, *Using Variables and Expressions in a Method*, for more information on using variables and expressions.

23.3.2.1 Configuring Tip Properties

When the labware selected for configuration is a tip box, Labware Properties provides the ability to configure the following information

1. Double-click the tip box to configure in the Stacker Setup Display

   OR

   Right-click the tip box to configure in the Stacker Setup Display and select **Properties** from the menu. Labware Properties for tips appears (Figure 23-5):

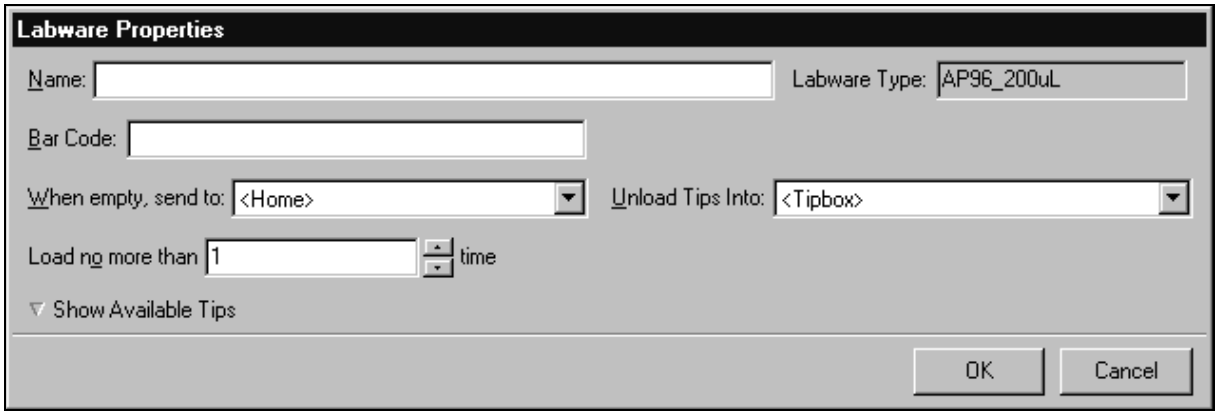


Figure 23-5. Labware Properties for a tip box

2. In **Name**, enter the name that is assigned or will be assigned to the tip box in the Stacker Setup step, if applicable.

   OR

   Leave Name blank. When Name is blank, tips are accessed by the information displayed in the Labware Type field.

   Note: Naming tip boxes forces the instrument to look for a specific box of tips, rather than any tip box containing the specified tip type located anywhere on the deck.

   Note: Multiple tip boxes can be given the same name. This is used to create a pool of tip boxes for a specific use.

3. In Labware Type, verify the tip type.
4. In Bar Code, enter the bar code.

   Note: Use the bar code field to identify a specific tip box in certain methods, such as plate replication. This field may be left blank.

5. In When empty, send to, select a final destination for the tip box at the end of the method.
6. In Unload Tips Into, select the location reserved for tip disposal.
7. In Load no more than, enter the number of times tips can be loaded onto the pod during the method.

8. Choose **Show Available Tips** to display a graphic of the tip box (Figure 23-6).

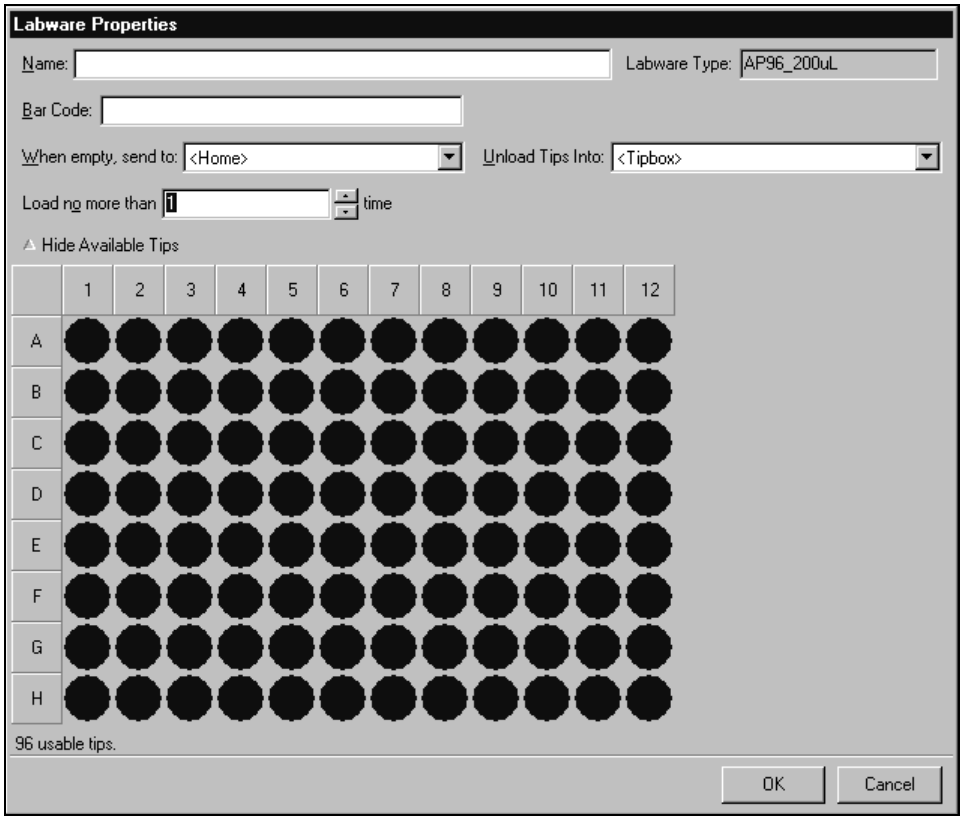


Figure 23-6. Labware Properties for tips with Show Available Tips activated

9. On the graphic of the tip box, select the usable tips. By default, all tips are selected.

Note: This can be used to indicate missing tips or tips that are otherwise not to be used in the method.

10. Choose **Hide Available Tips** to collapse the graphic of the tip box.
11. Choose **OK** to save Labware Properties.

23.3.2.2 Configuring Labware Properties

When the labware selected for configuration is a microplate or small tube rack, Labware Properties provides the ability to configure the following information:

1. Double-click the piece of labware to configure in the Stacker Setup Display

   OR

   Right-click the piece of labware to configure in the Stacker Setup Display and select **Properties** from the menu. Labware Properties for microplates, reservoirs, and tube racks appears (Figure 23-7).

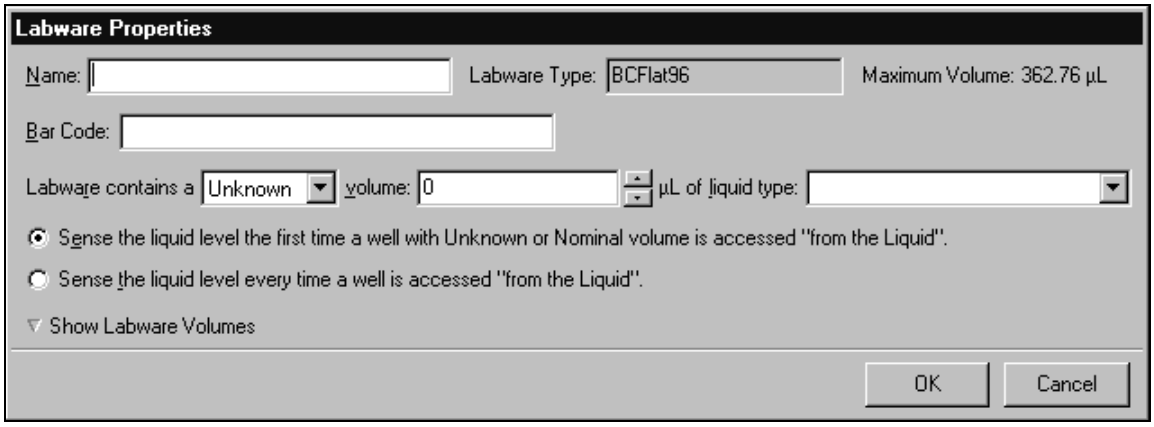


Figure 23-7. Labware Properties for microplates, reservoirs, and tube racks

2. Verify the Labware Type.
3. In **Name**, enter a name for the labware.

   Note: When a deck is populated by numerous pieces of labware, naming labware is recommended. Names should be descriptive of the contents of the labware or the work being accomplished during the method. Naming labware in a meaningful fashion may reduce confusion.

4. In **Bar Code**, enter the bar code.

   Note: Use the bar code field to identify a specific plate in certain methods, such as plate replication. This field may be left blank.

5. Make a selection in **Labware contains**. Options are Unknown, Nominal, and Known. This information is used by many of the techniques supplied with Biomek Software which aspirate or dispense liquid a certain offset from the liquid level. Some pods or tools can detect the liquid level using liquid-level sensing technology.
    - If Known is selected, the liquid level is not detected during method run and the entered value is used during validation and method run. Known Volume should be supplied whenever possible.
    - If Unknown is selected, the liquid level is detected during method run if required by the technique, and the wells are assumed to be full when validating the method.
    - If Nominal is selected, the liquid level is detected during method run, but the volume in the wells is assumed to be the entered value when validating the method.
6. Enter the **Volume**, if Nominal or Known volume is selected.

    Note: A value entered in Volume is assigned to all wells.

7. Select the **Liquid Type** contained in the labware. The liquid type is useful information when Biomek Software auto-selects a pipetting technique for any aspirate and dispense operations acted upon this piece of labware. The pipetting technique auto-selected to aspirate and dispense the liquid is selected based on the physical factors of the liquid, as well as the physical attributes of the labware. For more information on liquid types, refer to Chapter 8, *Understanding and Creating Liquid Types*.
8. Select **Sense the liquid level the first time a well with Unknown or Nominal volume is accessed "from the Liquid"** to use liquid level sensing to determine the liquid level only the first time it accesses a well with an Unknown or Nominal volume from the liquid. Any instances the same well on the piece of labware is accessed, the liquid level is calculated internally based on the result of the earlier liquid level sense and the amount aspirated or dispensed to the well in previous steps.

    OR

    Select **Sense the liquid level every time a well is accessed "from the Liquid"** to use liquid level sensing to determine the liquid level every time it accesses a well with an Unknown or Nominal volume from the liquid.

    Note: Liquid level sensing options only apply if the pod or tool accessing the labware is capable of sensing the liquid level. If not, the option selected is ignored.

9. If the labware does not contain uniform volumes, choose **Show Labware Volumes** to display a graphic of the labware (Figure 23-8).

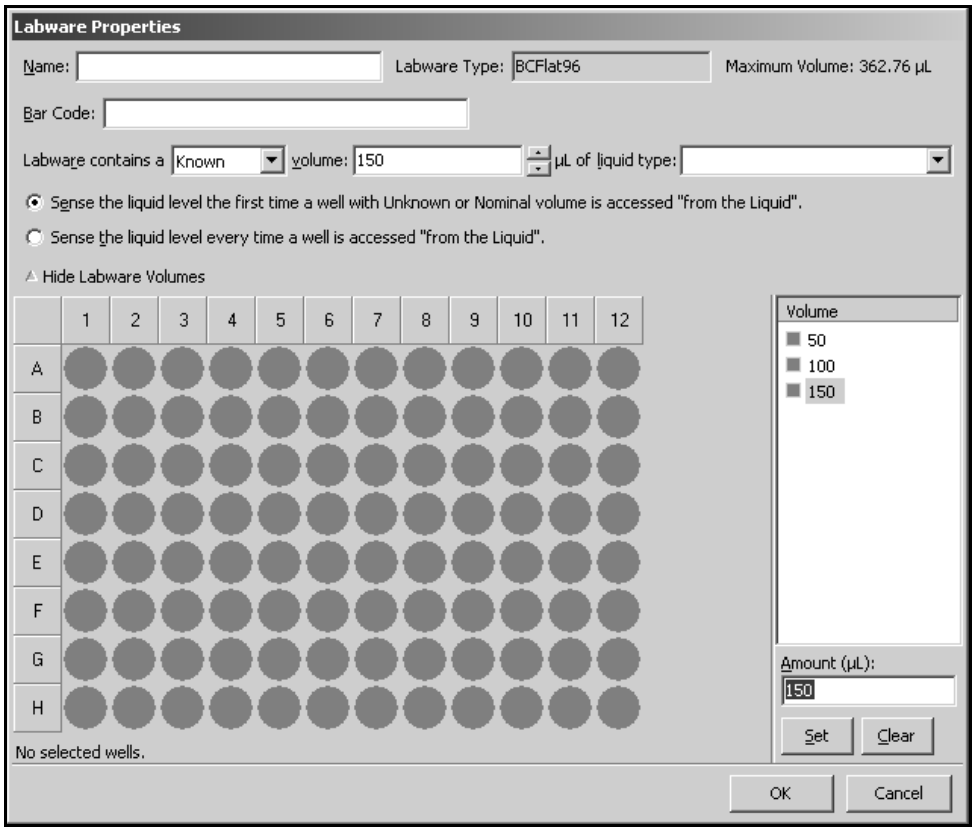


Figure 23-8. Labware Properties for microplates, reservoirs, or tube racks with Show Labware Volumes activated

Note: Show Labware Volumes may appear different depending on the number of wells on the selected labware. The graphic shown is for a 96-well microplate.

10. Select the desired wells on the graphic.

    Note: Hold down Ctrl to toggle wells between selected and deselected without affecting the selection status of other wells.

    Note: Clicking on a column or row heading selects all wells in that column or row.

11. Enter the volume to assign to the currently selected wells in **Amount**.
12. Choose **Set** to assign the current Amount to the currently selected wells. The wells are given a color code that corresponds to the list of set volumes under Volume.
13. Repeat steps 10-12 until all desired wells have been assigned the desired volume.

    Note: Clear sets the volume for all wells back to zero.

14. Choose **Hide Labware Volumes** to collapse the graphic of the labware.
15. Choose **OK** to save Labware Properties and return to the Stacker Setup step configuration.

23.4 Using the Present Step

Use the Present step for:

- *Configuring from which Hotel Labware is Presented* (Section 23.4.1).
- *Configuring Bar Code Reading Options* (Section 23.4.2).

23.4.1 Configuring from which Hotel Labware is Presented

To configure a Present step in a method:

1. Drag and drop a **Present** step into the Method View.
2. Choose a hotel and the desired stacker carousel from **Present labware from hotel. . .of . . .** . The chosen hotel is highlighted (Figure 23-9).

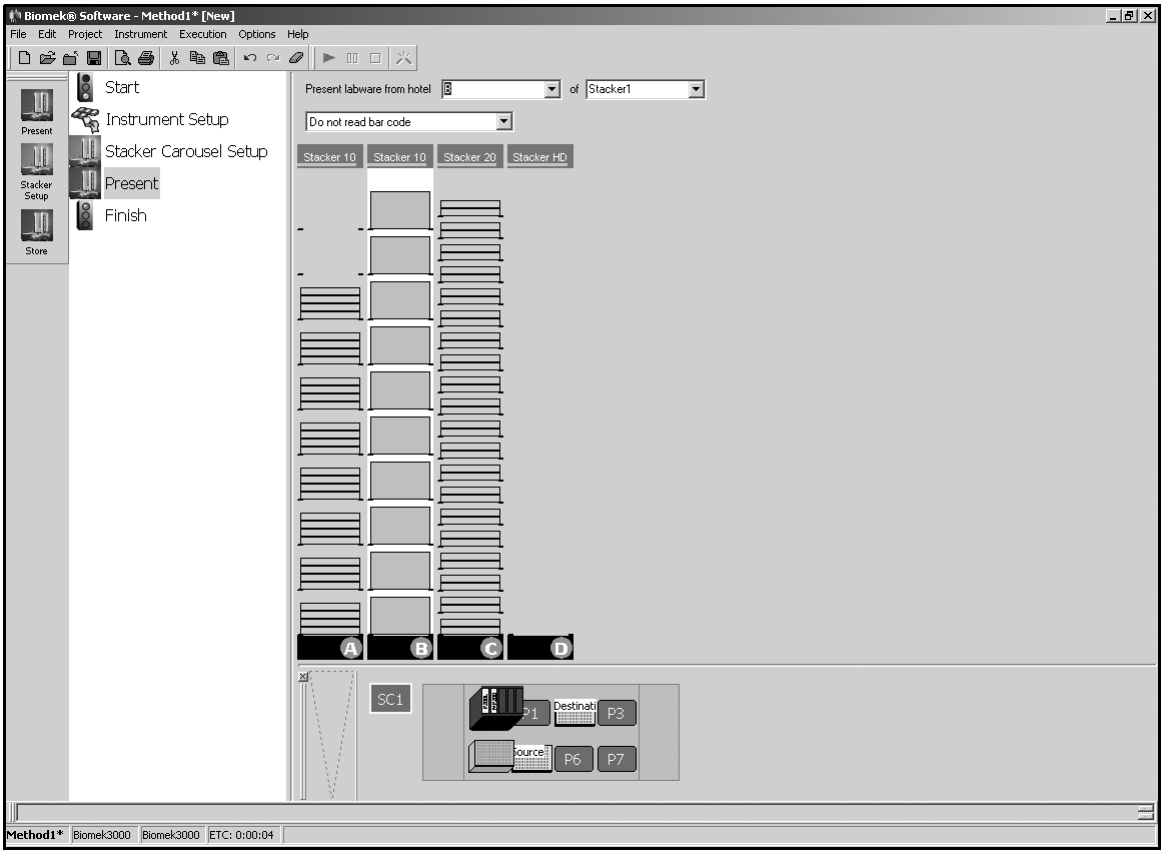


Figure 23-9. Present Step configuration

Note: Multiple Stacker Carousels may be installed on a Biomek instrument.

3. Choose **Do not read bar code**, **Read bar code for logging**, or **Read bar code for decision making** (refer to Section 23.4.2, *Configuring Bar Code Reading Options*).

Note: The step in the Method View is more descriptive once the step is configured and Finish selected; for example "Present from hotel B of Stacker 1."

23.4.2 Configuring Bar Code Reading Options

The bar code reading options available in the Present step are defined as follows:

- Do not read bar code — the bar code is not read when the Stacker Carousel presents the plate.
- Read bar code for logging — the bar code is captured in the pipetting logs (refer to Sections 26.2.3, *Pipetting Log*, 26.2.4, *Span8Pipetting Log (FX, NX-S8 only)*, and 26.3.6, *UnifiedPipetting Log Contents*).
- Read bar code for decision making — the results of the bar code read determine the next operation of the method. The software waits for the results of the bar code before continuing method execution.

Note: Because the Read bar code for decision making option creates a dependent operation (similar to the If Step and Then and Else), it impacts the validation process during method building. The method validation stops at this point as it waits for the results of the bar code read before it continues; however, since there is no actual bar code read during validation the software does not know what operation to validate next. To make sure the validation process finishes satisfactorily, in Read bar code for decision making using. . . for method validation, type in a value to use as the bar code during method validation.

For example, to check for an exact bar code, use the If step with the condition
`=(Labware("SC1").Properties.Barcode="SRC")`
or to check for plates whose bar code begin with SRC, use the If Step with the condition
`=(Left(Labware("SC1").Properties.Barcode,3)="SRC").`

23.5 Using the Store Step

Use the Store step to configure to which hotel on the Stacker Carousel labware is stored from the deck.

To configure a Store step in a method:

1. Drag and drop a **Store** step into the Method View.
2. Choose a hotel and the desired stacker carousel from **Store labware in hotel. . .of . . .** . The chosen hotel is highlighted (Figure 23-10).

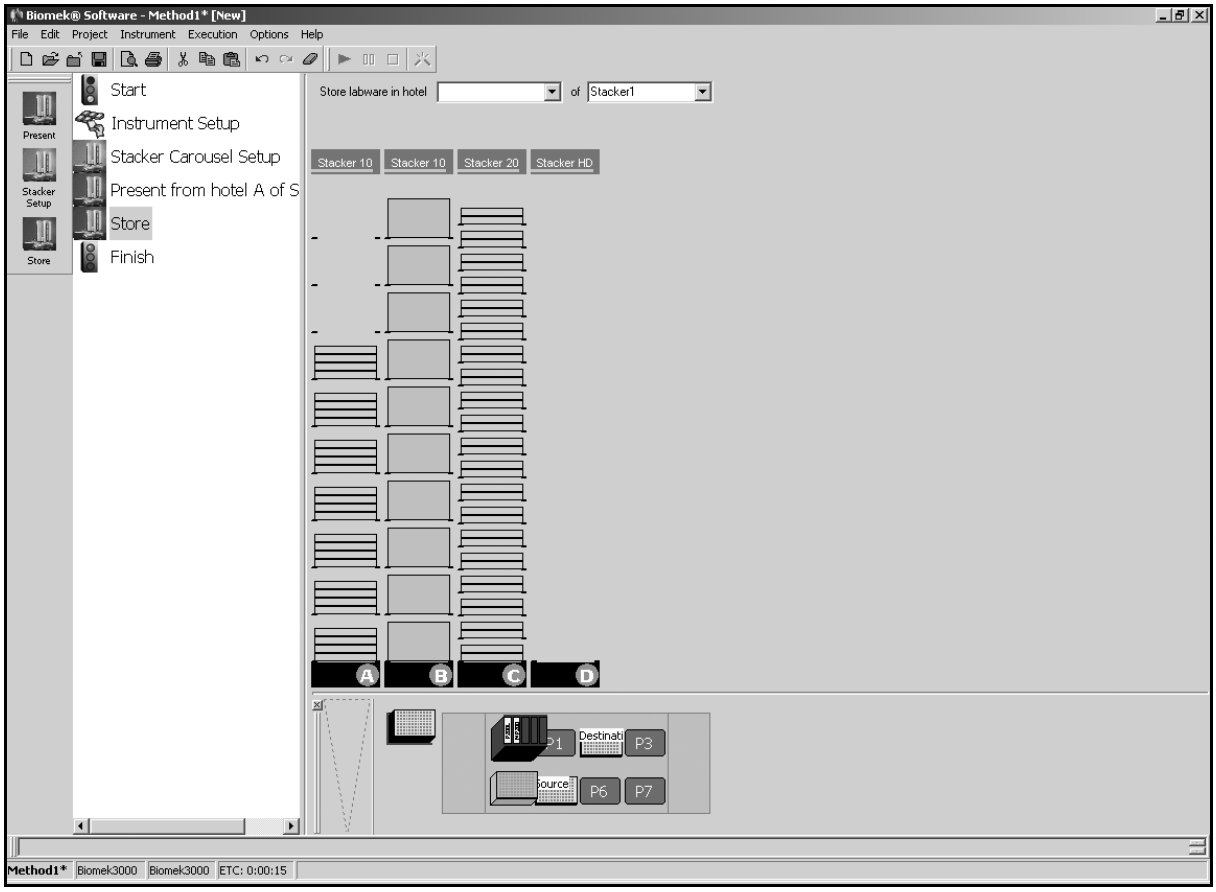


Figure 23-10. Store Step configuration

Note: The step in the Method View is more descriptive once the step is configured and Finish selected; for example "Store to hotel B of Stacker 1."

24 Using the Data Sets Step Palette

24.1 Overview

Steps on the Data Sets Step Palette allow data sets to be created, managed, used, and reported in Biomek methods. Data sets allow sample tracking which means the contents of the plate or tube are known at any time in the method and decisions may be made during transfer or pipetting operations based on the contents of the plate or tube.

Note: Refer to Chapter 14, *Using Sample Tracking and Data Sets in a Method*, for more information on using sample tracking and data sets in a method.

The steps available on the Data Sets are:

- Create Data Set — specifies data in a data set.

- Data Set Management — renames, removes, copies, or modifies the properties of a data set.

- Data Set Processing — applies a transformation expression to an existing data set to create a new data set.

- Reporting — generates a report on data sets at any point during a method.

24.2 Displaying the Data Sets Step Palette

In order to add data set steps to a method, display the Data Sets Step Palette (Figure 24-1).

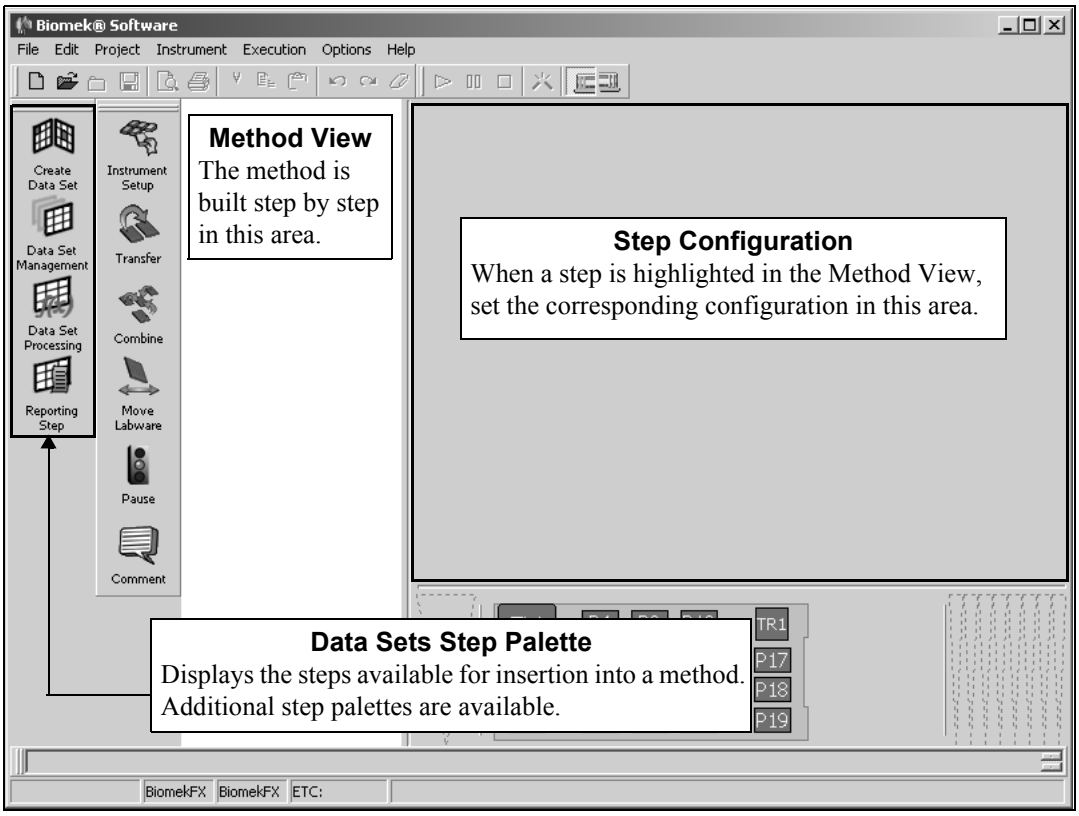


Figure 24-1. Biomek Software main editor with Advanced Step Palette displayed

To display the Data Sets Step Palette:

- Right-click any empty palette space, and select **DataSets** from the menu.

  OR

- From the toolbar, select **Options>Toolbars>DataSets**.

24.3 Configuring the Create Data Set Step

The Create Data Set step is used to create data sets from a text file or a database table. The specified file or database table is read and compared to either the plate bar code and well number of the plate or a data set specifying the sample ID. Data sets are created from the specified columns of the file or database table using the rows that matched the plate bar code and well number or data set specifying the sample ID.

Note: The text file must reside on the local computer.

Note: SQL Server 2000 SP3 is the version requirement to import the datatbase table.

Insert a Create Data Set step into the Method View (Figure 24-2).

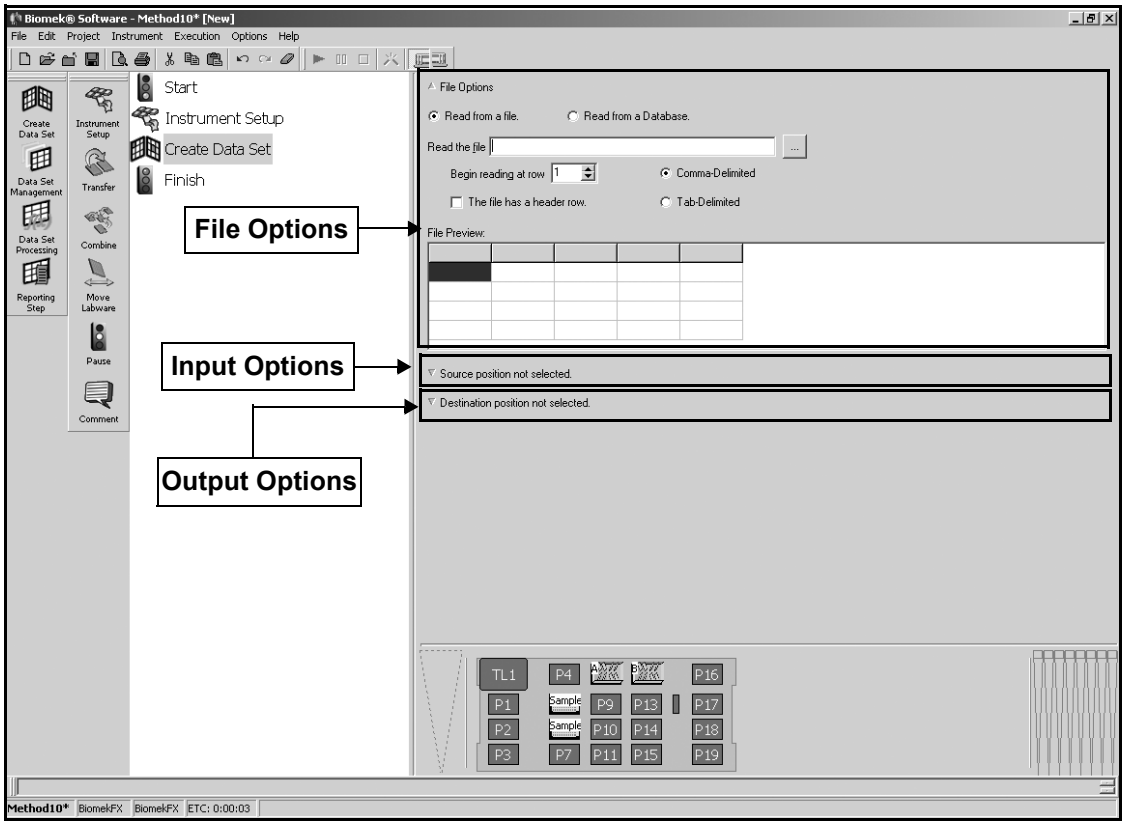


Figure 24-2. Create Data Set step configuration

The Create Data Set step consists of three collapsible configuration areas. Each area can be collapsed or expanded independently from each other to display the configuration options for that section (Figure 24-2). To collapse or expand any of the configuration areas, click on the sentence summary.

Configuring the Create Data Set step includes configuring:

- the file or database to read (refer to Section 24.3.1, *Configuring File Options*).
- the columns of the file or database table to compare (refer to Section 24.3.2, *Configuring Input Options*).
- the columns of the file or database table used to create data sets (refer to Section 24.3.3, *Configuring Output Options*).

24.3.1 Configuring File Options

File Options is used to select a comma- or tab-delimited text file (refer to Section 24.3.1.1, *Reading from a Text File*) or a database table (refer to Section 24.3.1.2, *Reading From a Database Table*) to use to create data sets for a piece of labware.

24.3.1.1 Reading from a Text File

To configure File Options to read from a file:

1. If not expanded, select the sentence summary to display File Options (Figure 24-3).

Note: By default, File Options is expanded when a Create Data Set step is inserted.

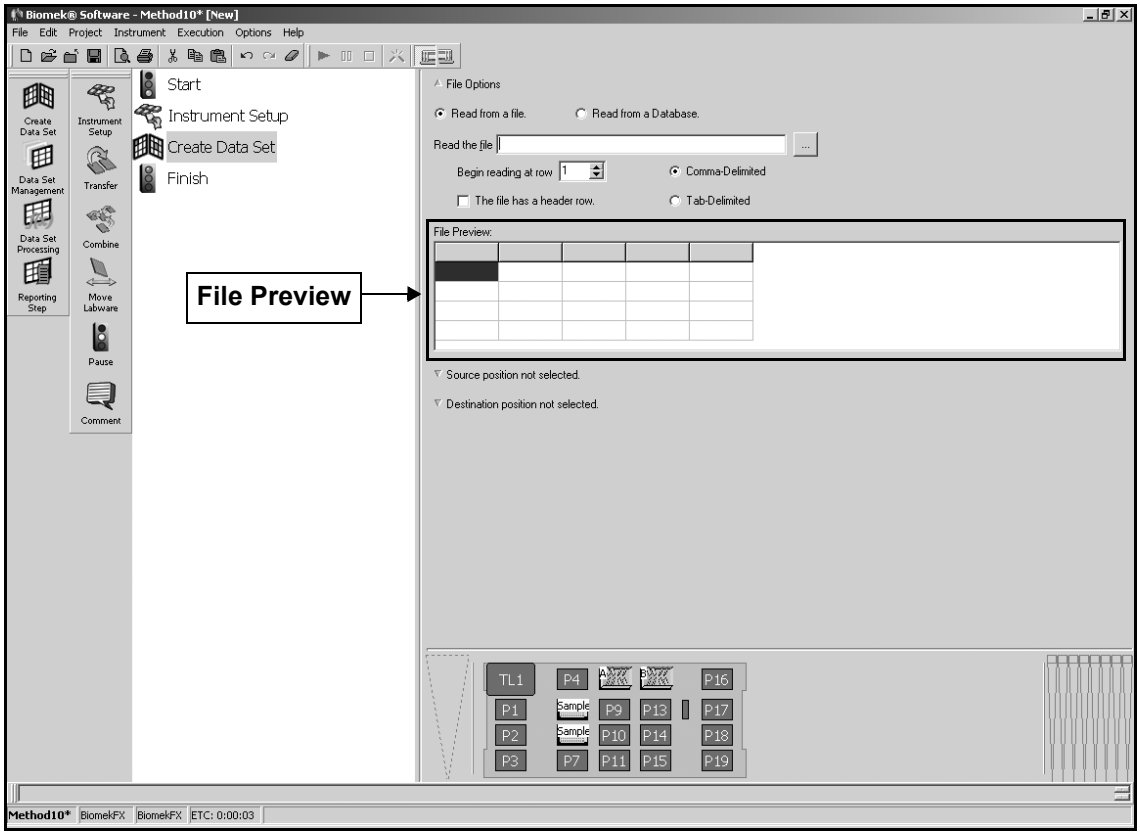


Figure 24-3. Create Data Set step — File Options displayed

2. Under File Options, select **Read from a file**.
3. In Read the file, enter the full directory path and file name of the text file to read and press **Enter**. The first four rows of the selected data file are displayed in File Preview.

Note: Browse to select the file using standard Windows techniques.

Note: The text file must reside on the local computer.

4. In Begin reading at row, select the first row of the data file that should be read. File Preview updates.

5. Select **The file has a header row** if a header row is included in the data file. The first row that is read is used for column headings in File Preview (Figure 24-3). For example, if Begin reading at row is set to 5 and The file has a header row is selected, the contents of row 5 are used as the column headings.

   Note: If The file has a header row is not selected, column headings are given a generic label Column#.

6. Select the appropriate file type option: Comma-Delimited or Tab-Delimited. File Preview updates accordingly.

24.3.1.2 Reading From a Database Table

File Options can be configured to read data from a database table stored in the SQL Server database.

Note: SQL Server is a Microsoft product that allows queries and provides analysis, and is required to run Biomek Software. The installation of this product is the responsibility of the user and is not supported by Beckman Coulter Service Engineers. SQL Server 2000 SP3 is the version requirement.

To configure File Options to read from a database:

1. If necessary, select the sentence summary to display File Options (Figure 24-4).

   Note: File Options is expanded when a Create Data Set step is inserted.

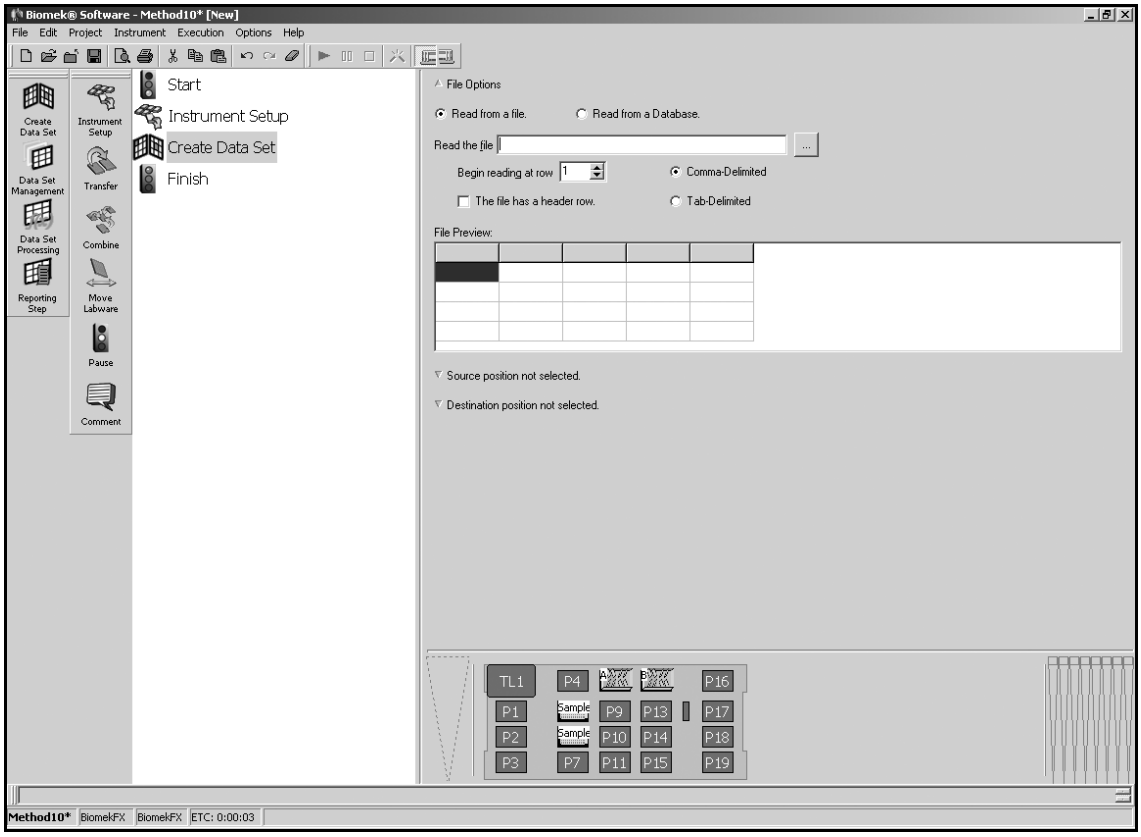


Figure 24-4. Create Data Set step — File Options displayed

2. Under File Options, select **Read from a Database**. File Options changes to display the database options (Figure 24-5).

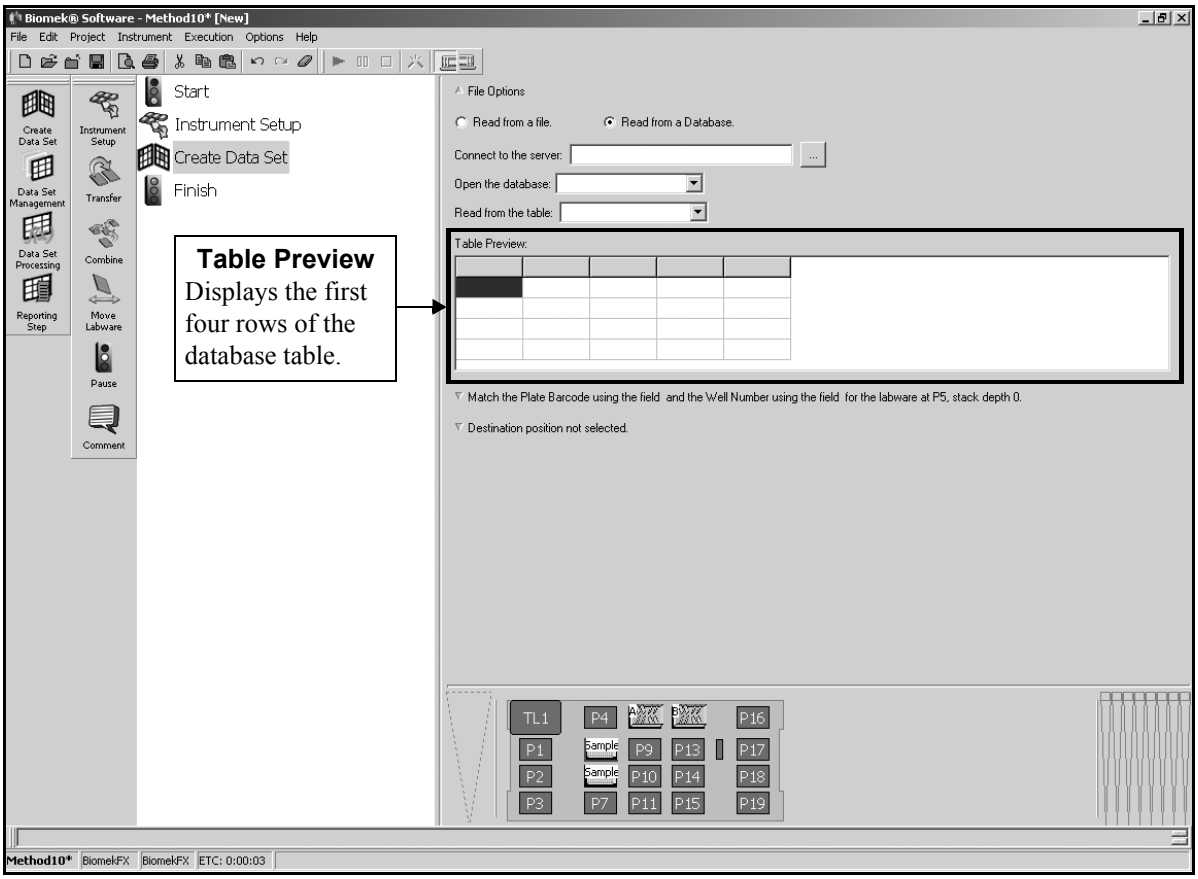


Figure 24-5. Reading from a database

3. Browse to find the location of the desired database on that server. SQL Server Connection (Figure 24-6) appears on top of the Create Data Set step configuration.

Note: SQL Server is a Microsoft product that allows queries and provides analysis. The installation of this product is the responsibility of the user and is not supported by Beckman Coulter Service Engineers. SQL Server 2000 SP3 is the version requirement.

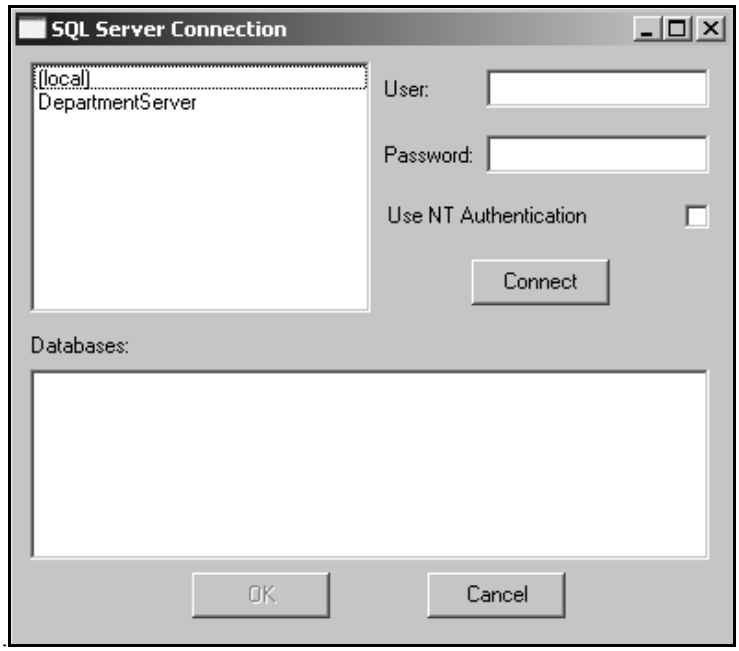


Figure 24-6. SQL Server Connection

4. Select the desired server from the list of servers on the left.
5. Enter the **User** name and **Password** to log in to the selected server.

   OR

   Select **Use NT Authentication**.

Note: The administrator of the SQL Server Connection sets the logging protocol for user and password or NT authentication.

6. Choose **Connect**. A list of the available databases appears in Databases (Figure 24-7).

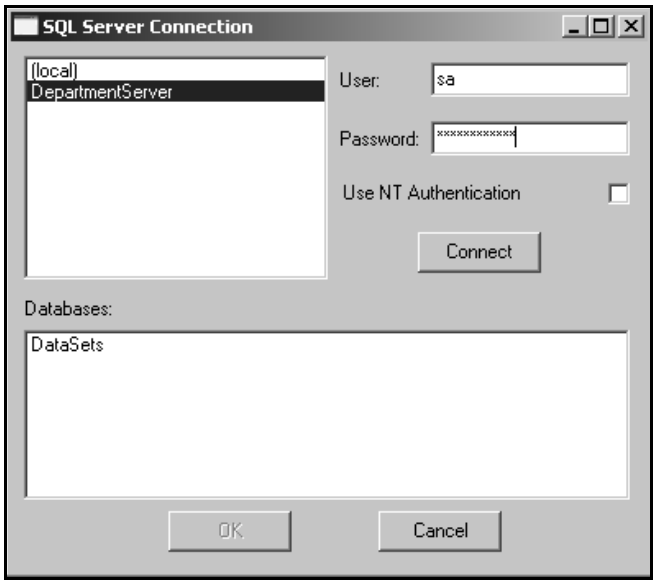


Figure 24-7. Connected to SQL Server

7. In Databases, select the desired database found on the server to use to create data sets.

   OR

   Repeat steps 3-6 to connect to a different server, if desired.

8. Choose **OK** to accept the server and close SQL Server Connection.

9. In Read from the table (Figure 24-5), select the database table to read. The first four rows of the selected database table are displayed in Table Preview (Figure 24-5).

24.3.2 Configuring Input Options

Input Options (Figure 24-9) is used to configure the columns of the file or database table to compare to the plate bar code and well number or data set specifying the sample ID of the specified plate. Rows that match the plate bar code and well number or data set specifying the sample ID are used to create the data set(s).

By default, Input Options is collapsed when a Create Data Set is inserted into a method (Figure 24-8).

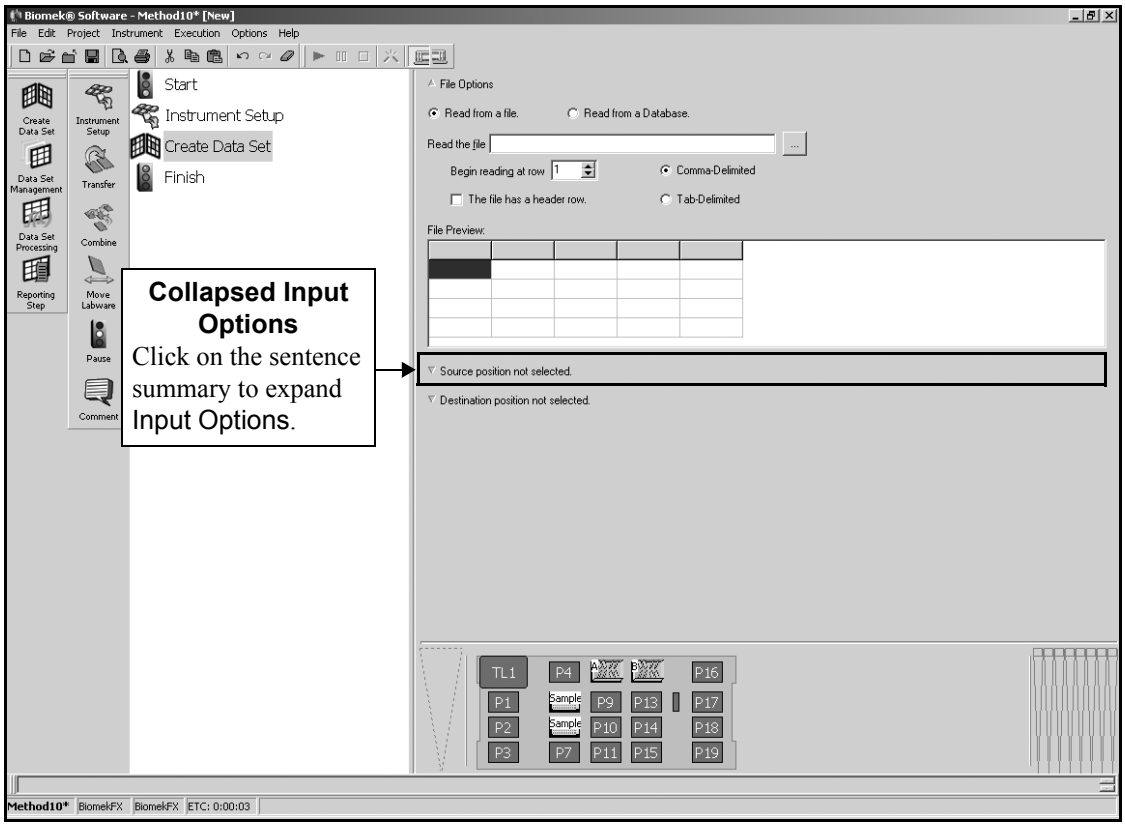


Figure 24-8. Create Data Set step — expanding Input Options

Click on the sentence summary to expand Input Options (Figure 24-9).

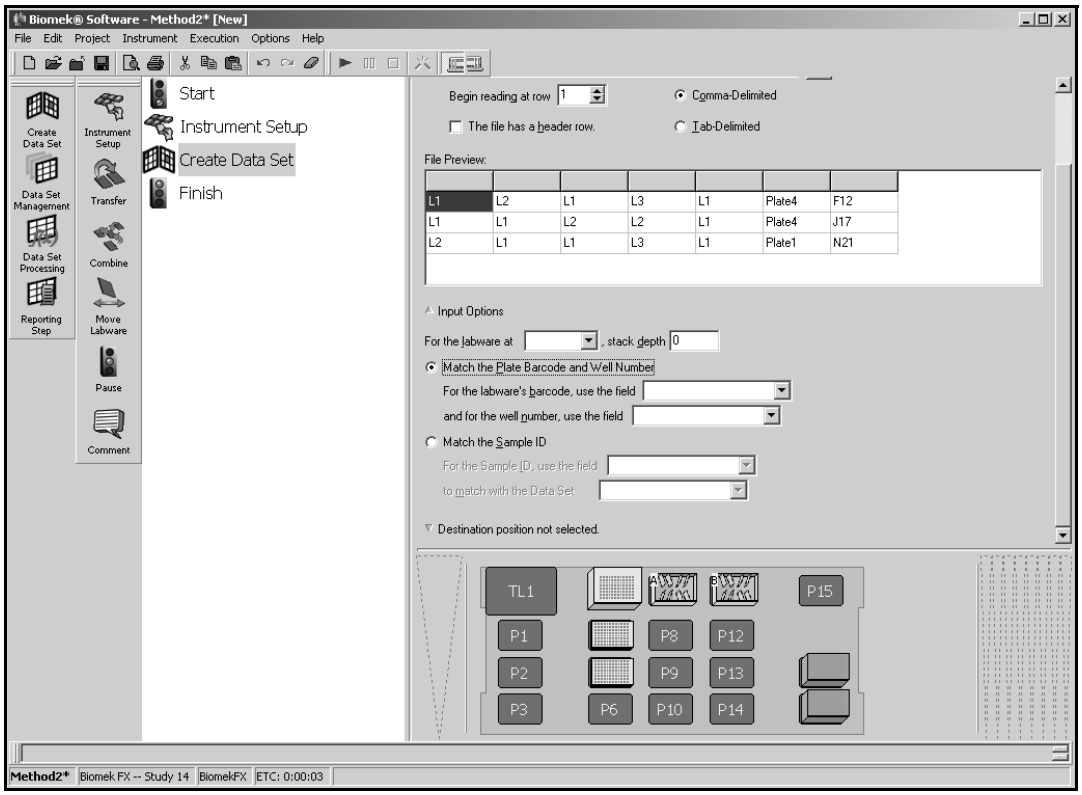


Figure 24-9. Create Data Set step — Input Options displayed

24.3.2.1 Matching Plate Bar Code and Well Number

The specified file or database table is compared to the plate bar code and well number to determine which rows of the file or database table to use to create the data set. Only the rows of the file or database table that match the plate bar code are used. The column for well number is used to assign the correct value of the data set to each well.

To configure Input Options to match the plate bar code and well number:

1. In For the labware at, select the deck position of the labware to compare the plate bar code and well number or data set specifying the sample ID to the file or database table (Figure 24-9).

   OR

   Click on the desired labware in the Current Deck Display.

2. If the labware is in a stack, enter the **stack depth**.

   Note: Depth refers to a specific piece of labware in a stack. To use the top piece of labware, enter **0**; to use the second from the top piece of labware, enter **1**; to use the third from the top piece of labware, enter **2**; and so on. Refer to Section 7.3.6.4.1, *Biomek Stacking Rules*, for information on using stacks.

3. Select **Match the Plate Barcode and Well Number** to compare the plate bar code and well number of the selected plate to the file or database table (Figure 24-9).

4. In For the labware's barcode, use the field, select the column of the file or database table to compare to the plate bar code.

   Note: For the labware's barcode, use the field is optional. If no field is specified, all rows of the file or database table are assumed to apply to that plate. If a well number is repeated, the last row of the file or database table to use that well number is used.

5. In and for the well number, use the field, select the column of the file or database table to compare to the well number.

24.3.2.2 Matching Sample IDs

The specified file or database table is compared to a data set that specified the sample IDs for the selected plate to determine which rows of the file or database table to use to create the data set. Only the rows of the file or database table that match one of the sample IDs on the plate are used to create data sets.

To configure Input Options to match the plate bar code and well number:

1. In For the labware at, select the deck position of the labware to compare the plate bar code and well number or data set specifying the sample ID to the file or database table (Figure 24-10).

   OR

   Click on the desired labware in the Current Deck Display.

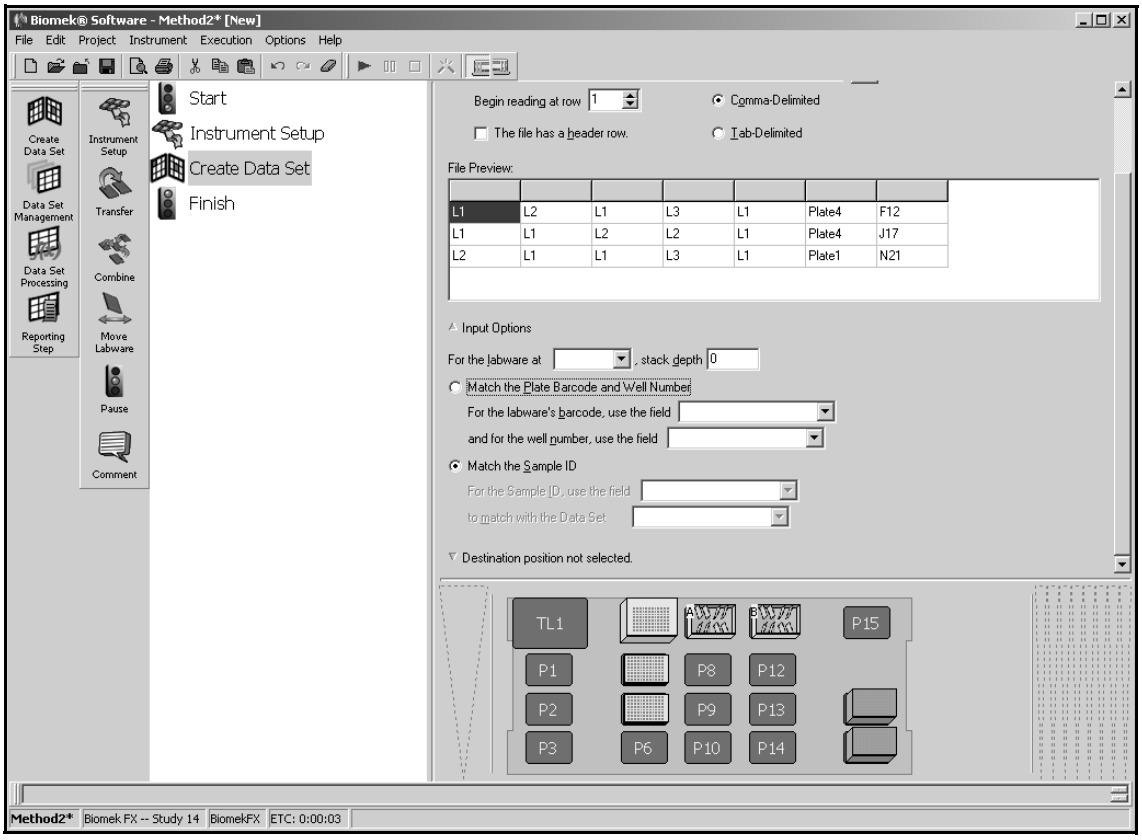


Figure 24-10. Create Data Set step — Input Options displayed

2. If the labware is in a stack, enter the **stack depth**.

   Note: Depth refers to a specific piece of labware in a stack. To use the top piece of labware, enter **0**; to use the second from the top piece of labware, enter **1**; to use the third from the top piece of labware, enter **2**; and so on. Refer to Section 7.3.6.4.1, *Biomek Stacking Rules*, for information on using stacks.

3. Select **Match the Sample ID** to compare a data set specifying the sample IDs for the selected plate to the file or database table (Figure 24-10).
4. In For the Sample ID, use the field, select the column of the file or database table to compare to the data set specifying sample IDs for the plate.
5. In to match with the Data Set, select the data set that specifies the sample IDs for the plate.

24.3.3 Configuring Output Options

Output Options is used to configure the plate for which data sets are created and to specify the columns of the file or database table to use to create data sets.

By default, Output Options is collapsed when a Create Data Set is inserted into the Method View.

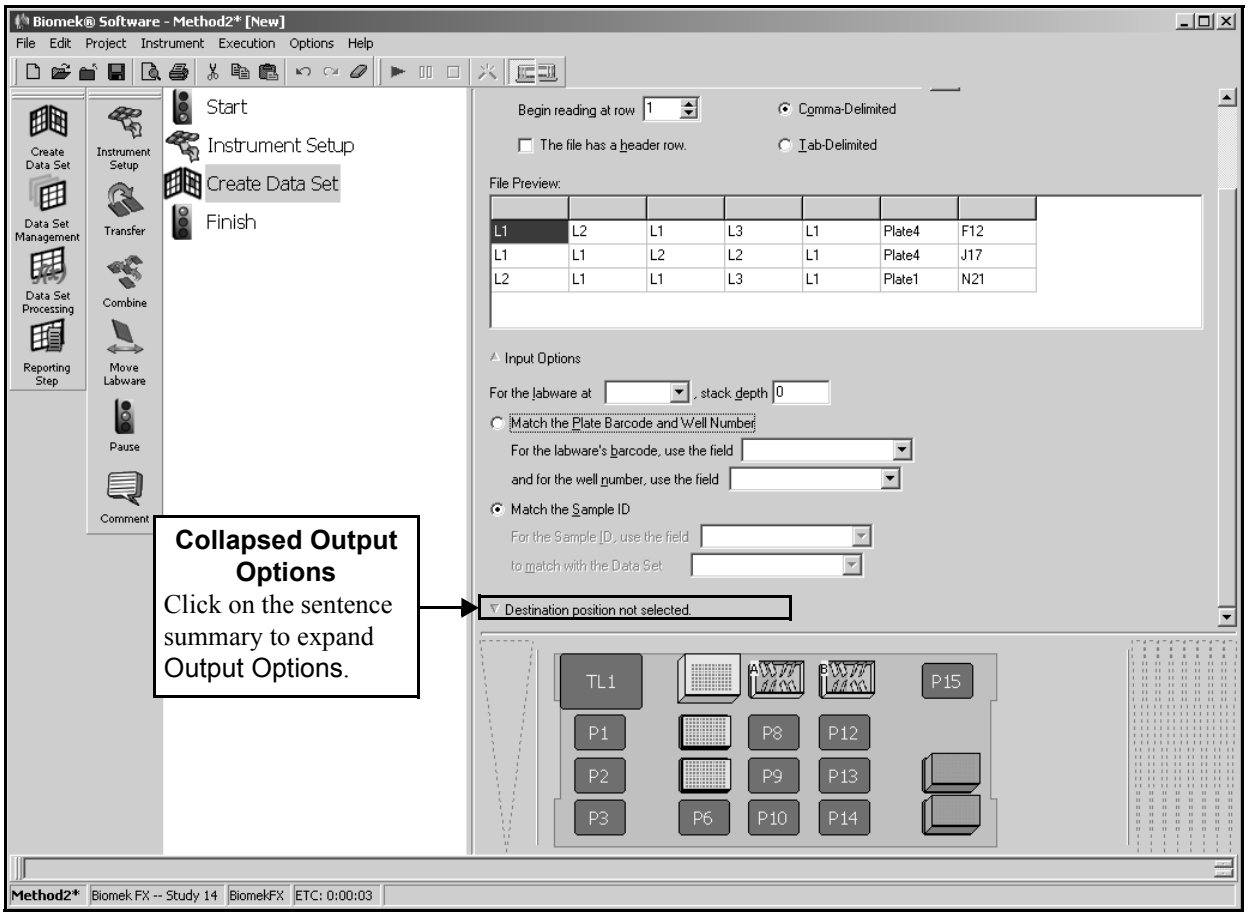


Figure 24-11. Create Data Set step — expanding Output Options

To configure Output Options:

1. Click on the sentence summary to expand the Output Options configuration (Figure 24-12).

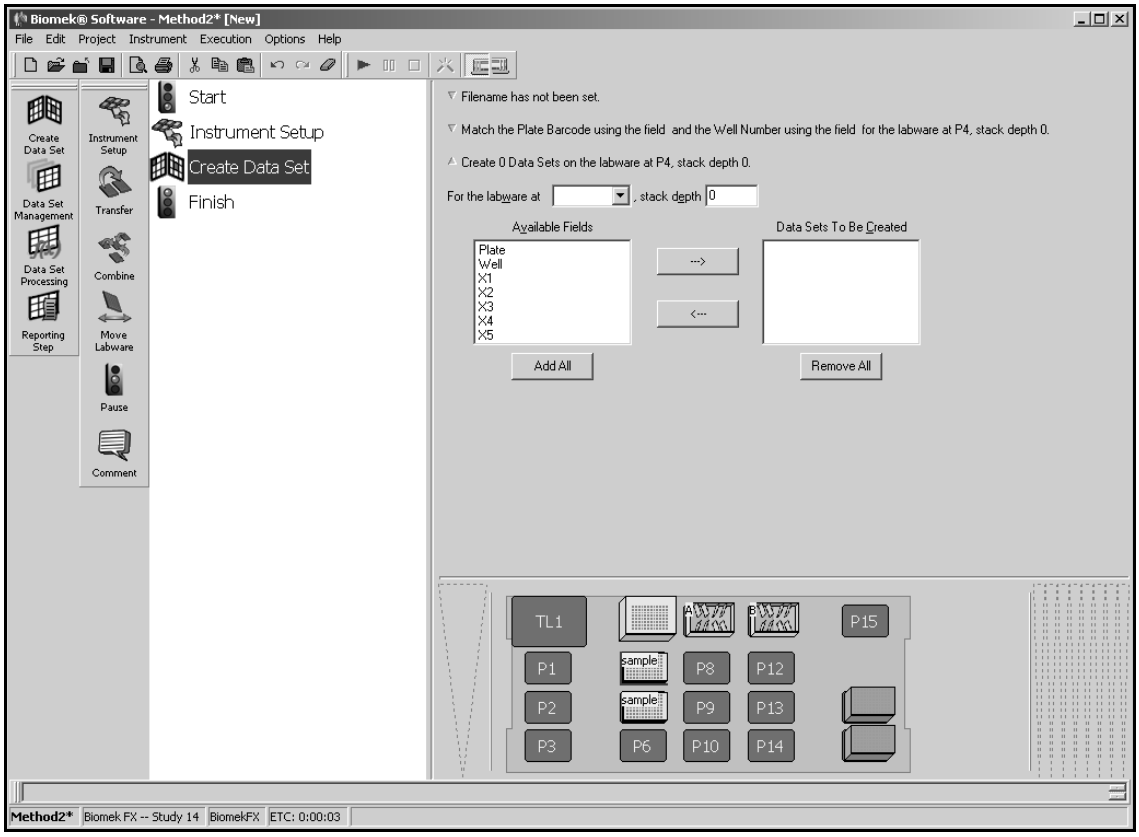


Figure 24-12. Create Data Set step — Output Options

2. In For the labware at, select the deck position of the labware for which data sets are created.

   OR

   Click on the desired labware in the Current Deck Display.

3. If the labware is in a stack, enter the **stack depth**.

   Note: Depth refers to a specific piece of labware in a stack. To use the top piece of labware, enter **0**; to use the second from the top piece of labware, enter **1**; to use the third from the top piece of labware, enter **2**; and so on. Refer to Section 7.3.6.4.1, *Biomek Stacking Rules*, for information on using stacks.

4. Under Available Fields, select the desired columns from the file or database table from which to create data sets. The selected fields appear highlighted.

5. Select **--->** to move the selected fields to Data Sets to be Created.

   Note: To add all columns from Available Fields to Data Sets to be Created, select **Add All**.

6. To remove an option from Data Sets to be Created, select the desired data set to remove and select **<---**. The selected field(s) are moved back to Available Fields.

   Note: To remove all columns from Data Sets to be Created, select **Remove All**.

24.3.3.1 Setting Data Set Properties

Properties for each data set can be modified in Output Options by right-clicking on the data set name under Data Sets To Be Created. Properties that can be modified are:

- data set name
- including the data set in reports
- tracking the data set during pipetting

To modify properties of a data set:

1. In Data Sets To Be Created, right-click the desired data set. The data set properties menu appears.

Figure 24-13. Changing data set properties

2. Select the desired option from the menu:
   - Select **Set Destination Name** and enter a new name for the data set to rename the data set.
   - Select **Include in Reports** to allow the data set to be included in the reports chosen in the Reporting (refer to Section 24.6, *Configuring the Reporting Step*) or Finish steps (refer to Section 12.2.2, *Configuring the Finish Step*).
   - Select **Track Data While Pipetting** to allow the system to track the data during pipetting operations.

     Note: When Track Data While Pipetting is selected, the data set is copied to the destination labware during pipetting.

3. Repeat steps 1 and 2 to select additional options, if desired.

24.4 Configuring the Data Set Management Step

The Data Set Management step is used to manage data sets that have been created automatically or created using the Instrument Setup step, the Create Data Set step, the SILAS step, or Visual Basic scripting.

Note: Data sets are not created or processed in the Data Set Management step.

Managing data sets includes using the Data Set Management step for:

- *Copying a Data Set* (Section 24.4.1).
- *Renaming a Data Set* (Section 24.4.2).
- *Removing a Data Set* (Section 24.4.3).
- *Changing the Properties of a Data Set* (Section 24.4.4).

24.4.1 Copying a Data Set

To copy a data set:

1. Insert a **Data Set Management** step into the Method View. The Data Set Management step configuration appears (Figure 24-14).

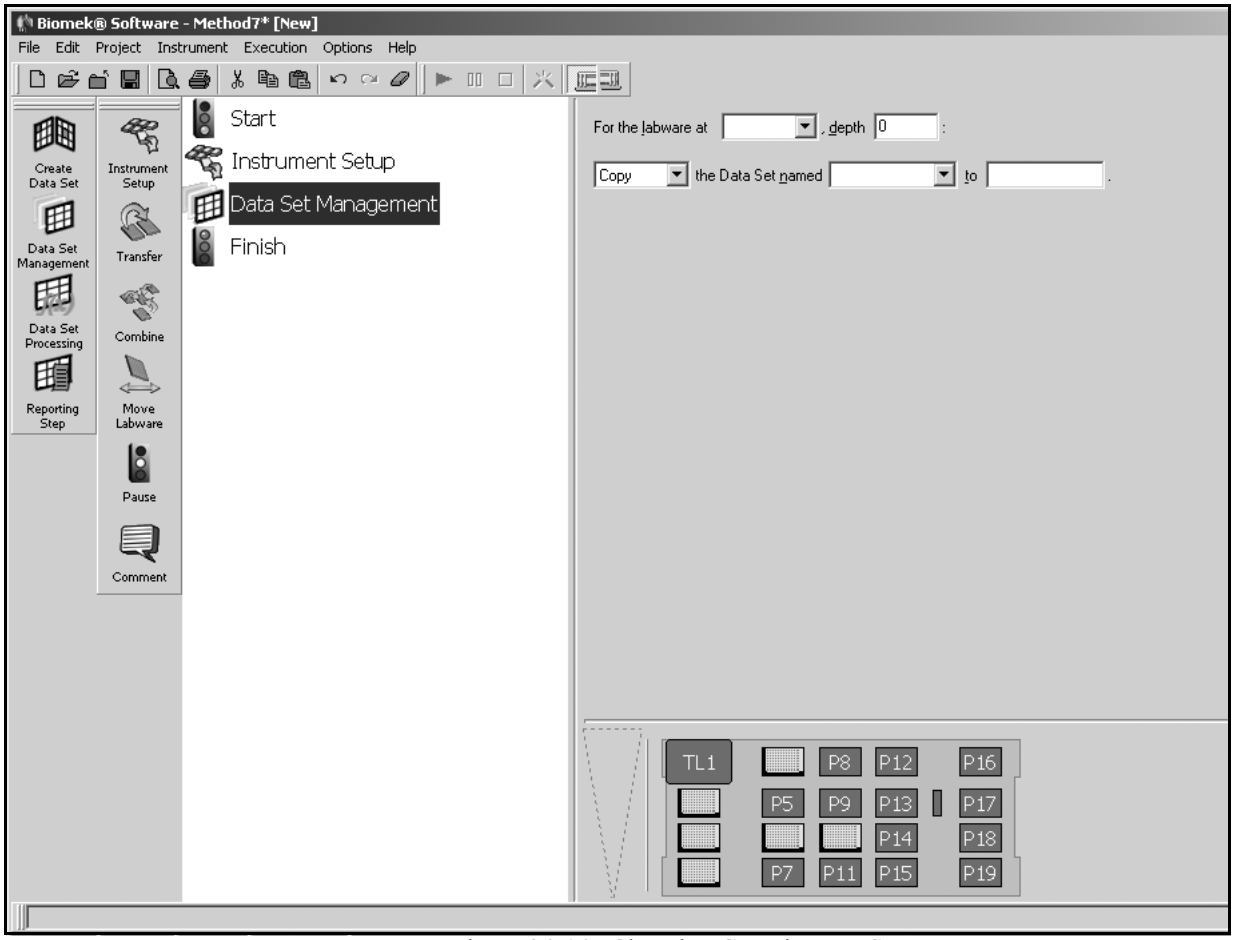


Figure 24-14. Choosing Copy in Data Set Management step

2. From **For the labware at**, choose the labware where the data set is copied.
3. If in a stack, enter the **depth** of the labware.

Note: Depth refers to a specific piece of labware in a stack. To use the top piece of labware, enter **0**; to use the second from the top piece of labware, enter **1**; to use the third from the top piece of labware, enter **2**; and so on. Refer to Section 7.3.6.4.1, *Biomek Stacking Rules*, for information on using stacks.

4. From the drop-down menu, choose **Copy**.
5. From **the Data Set named**, choose the data set to copy.

Note: Each data set must have a unique name. The method displays an error during validation if two data sets have the same name.

6. At **to**, enter the name of the copied data set. A copy of the data set is created with the entered name.

24.4.2 Renaming a Data Set

Rename renames a data set. Renaming data sets is an important function for sample tracking because only one data set named Sample ID can exist on a single piece of labware. When another data set is created from the Instrument Setup step using sample IDs, it overwrites the previous data set.

Rename a data set when sample IDs from the Instrument Setup are necessary for a transfer operation and then another set of sample IDs is necessary for a second transfer operation. For example, the name of the first Sample ID data set can be used to maintain a record of the first transfer operation and then the second Sample ID data set may be renamed before the second transfer operation.

Note: Each data set must have a unique name. The method displays an error during validation if two data sets have the same name.

Note: Refer to Section 15.2.6, *Creating the SampleID Data Set Using the Instrument Setup Step*, for more information on creating the Sample ID data set using the Instrument Setup step.

To rename a data set:

1. Insert a **Data Set Management** step into the Method View. The Data Set Management step configuration appears (Figure 24-14).
2. From **For the labware at**, choose the labware where the data set is renamed.
3. If in a stack, enter the **depth** of the labware.

Note: Depth refers to a specific piece of labware in a stack. To use the top piece of labware, enter **0**; to use the second from the top piece of labware, enter **1**; to use the third from the top piece of labware, enter **2**; and so on. Refer to Section 7.3.6.4.1, *Biomek Stacking Rules*, for information on using stacks.

4. From the drop-down menu, choose **Rename**. Figure 24-15 appears.

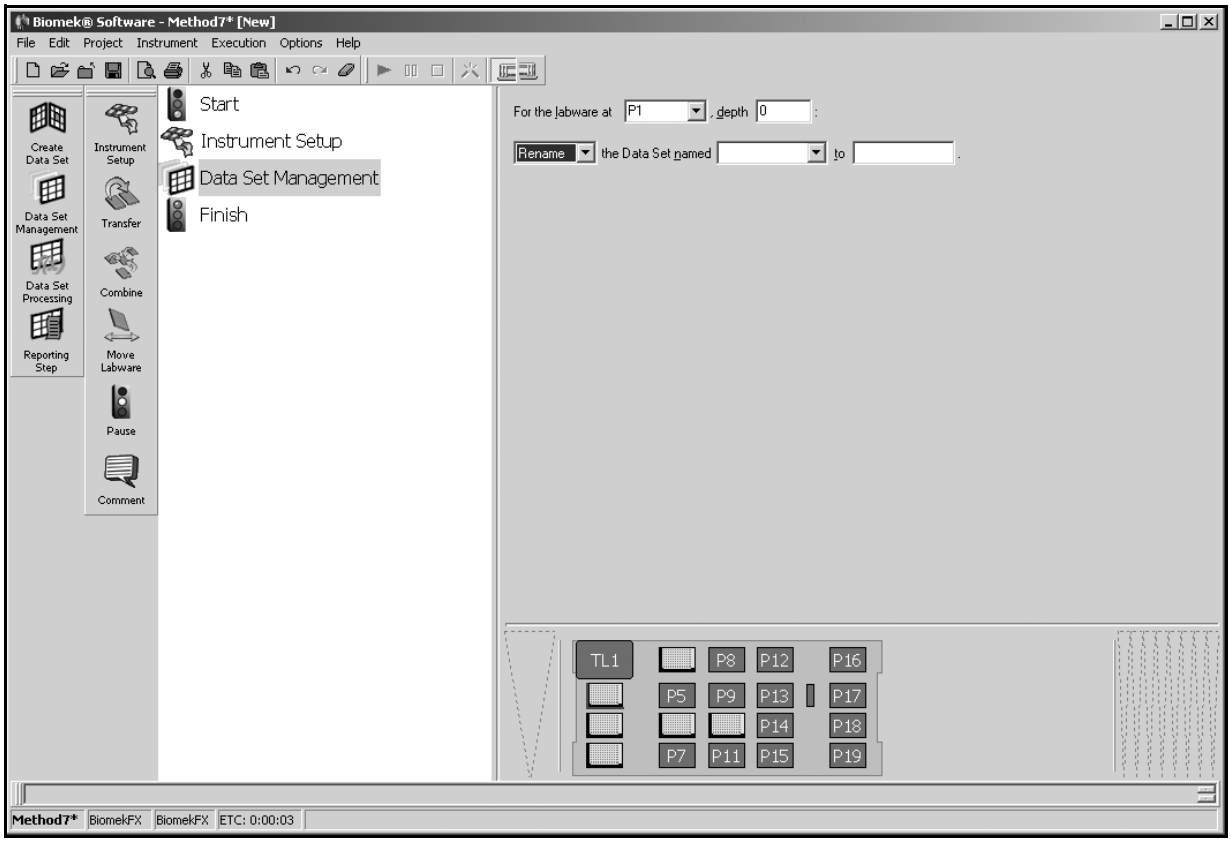


Figure 24-15. Choosing Rename in Data Set Management step

5. From **the Data Set named**, choose the data set to rename.

Note: Each data set must have a unique name. The method displays an error during validation if two data sets have the same name.

6. At **to**, enter the new name of the data set. The data set is renamed.

24.4.3 Removing a Data Set

When a data set is no longer needed, it may be removed.

To remove a data set:

1. Insert a **Data Set Management** step into the Method View. The Data Set Management step configuration appears (Figure 24-14).
2. From **For the labware at**, choose the labware where the data set is removed.
3. If in a stack, enter the **depth** of the labware.

   Note: Depth refers to a specific piece of labware in a stack. To use the top piece of labware, enter **0**; to use the second from the top piece of labware, enter **1**; to use the third from the top piece of labware, enter **2**; and so on. Refer to Section 7.3.6.4.1, *Biomek Stacking Rules*, for information on using stacks.

4. From the drop-down menu, choose **Remove**. Figure 24-16 appears.

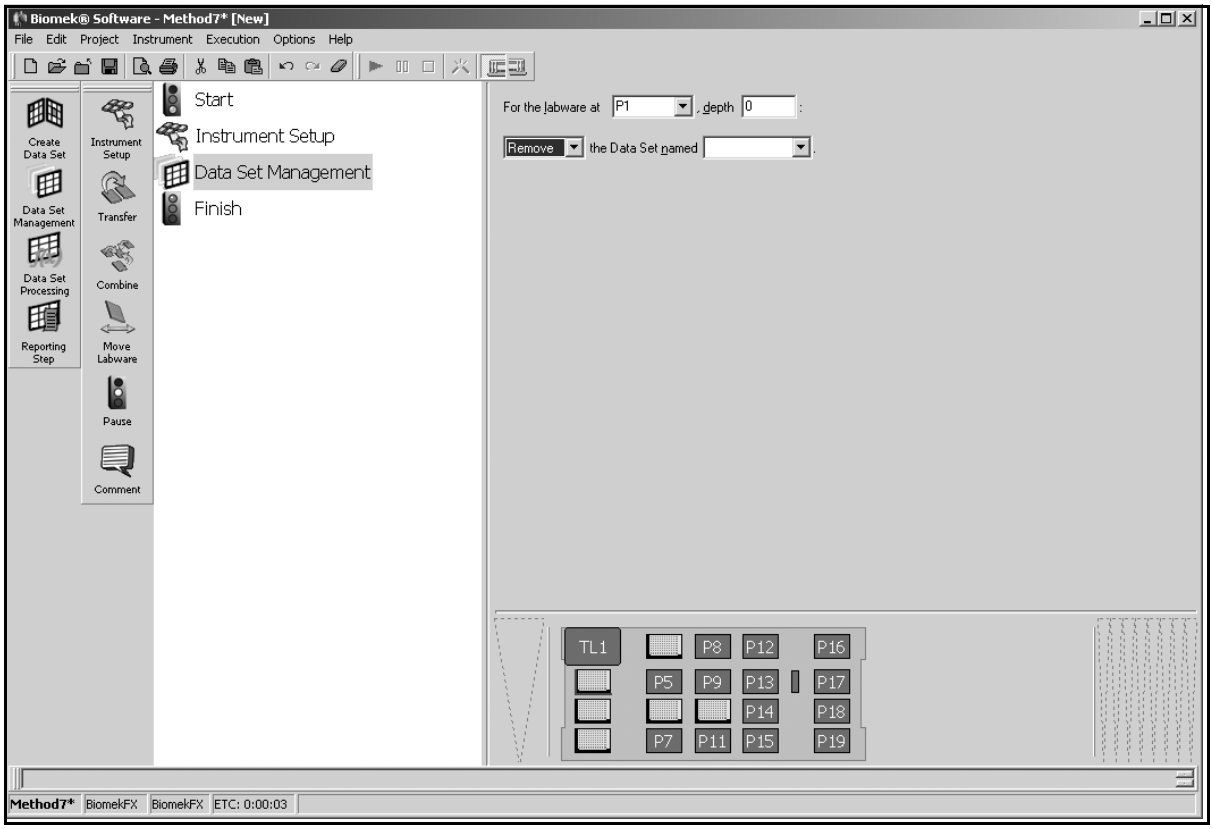


Figure 24-16. Choosing Remove in Data Set Management step

5. From **the Data Set named**, choose the data set to remove. The data set is removed.

24.4.4 Changing the Properties of a Data Set

When Change is chosen in the Data Set Management step, two options are available:

- Including or not including the data set in reports.
- Tracking or not tracking the data in the data sets during pipetting.

To change the reporting properties of a data set:

1. Insert a **Data Set Management** step into the Method View. The Data Set Management step configuration appears (Figure 24-14).
2. From **For the labware at**, choose the labware where the data set properties are changed.
3. If in a stack, enter the **depth** of the labware.

   Note: Depth refers to a specific piece of labware in a stack. To use the top piece of labware, enter **0**; to use the second from the top piece of labware, enter **1**; to use the third from the top piece of labware, enter **2**; and so on. Refer to Section 7.3.6.4.1, *Biomek Stacking Rules*, for information on using stacks.

4. From the drop-down menu, choose **Change**. Figure 24-17 appears.

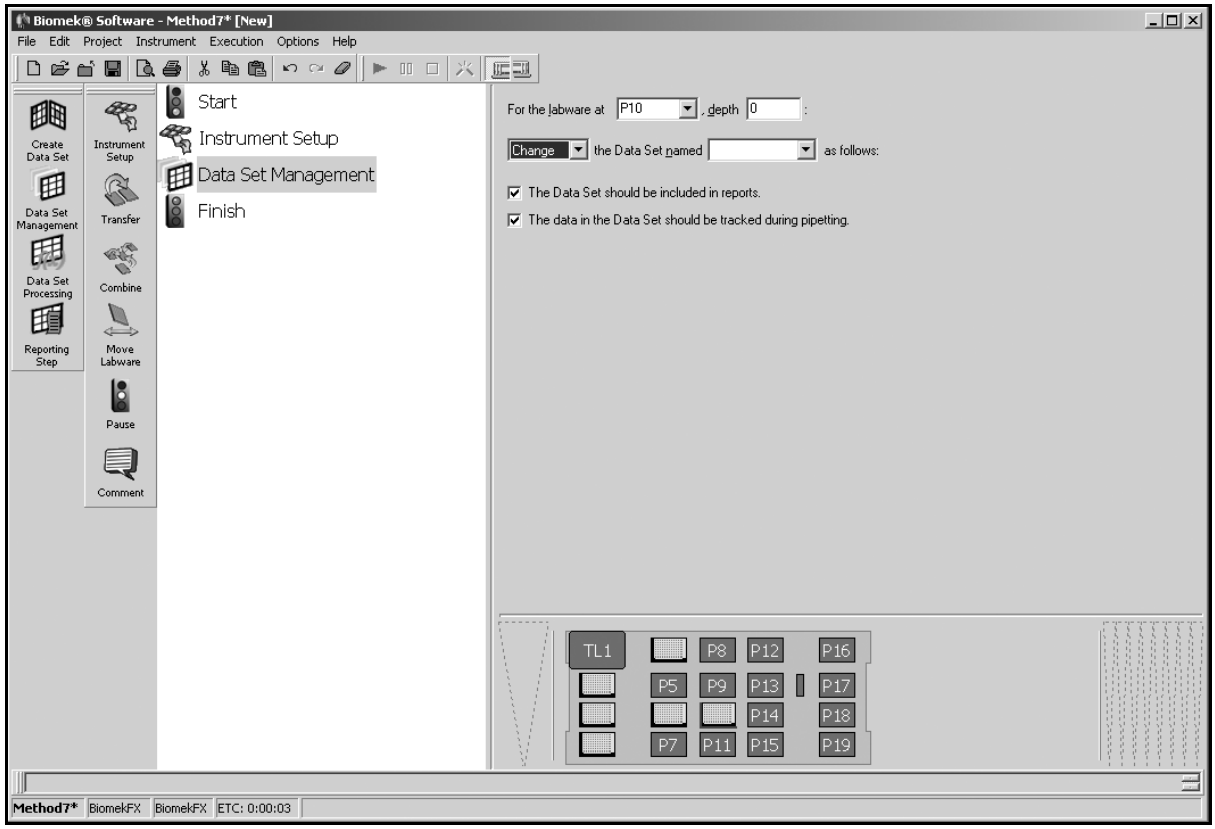


Figure 24-17. Change chosen on Data Set Management step configuration

5. From **the Data Set named**, choose the data set to be changed.

6. Ensure **The Data Set should be included in reports** is checked to allow the data set to be included in the reports chosen in the Reporting or Finish steps.
7. Ensure **The data in the Data Set should be tracked during pipetting** is checked to allow the system to track the data during pipetting operations.

Note: If the data set applies only to the source labware and should not be tracked, do not check The data in the new Data Set should be tracked during pipetting. Not checking this option may be useful for complex methods that use data sets, but may not require the data set to be transferred to the destination labware.

24.5 Configuring the Data Set Processing Step

The Data Set Processing step allows a transformation expression to be applied to an existing data set to create a new data set. The expression is applied to each well or tube in the destination data set and the result is stored in the corresponding well or tube of the newly created data set.

Note: A transformation expression is an operation stated in symbolic form (refer to Section 24.5.1, *Understanding Expressions*).

Note: The destination data set is the result of the transformation expression applied to the existing data set.

The applied expression may result in numeric or Boolean values for the new data set (Table 24-2). These values are presented in a report on data sets that is configured in the Reporting (refer to Section 24.6, *Configuring the Reporting Step*) or Finish steps (refer to Section 12.2.2, *Configuring the Finish Step*).

Note: Boolean values are expressed as True or False in the reports configured in the Reporting or Finish steps.

Insert a **Data Set Processing** step into the Method View. The Data Set Processing step configuration appears (Figure 24-18).

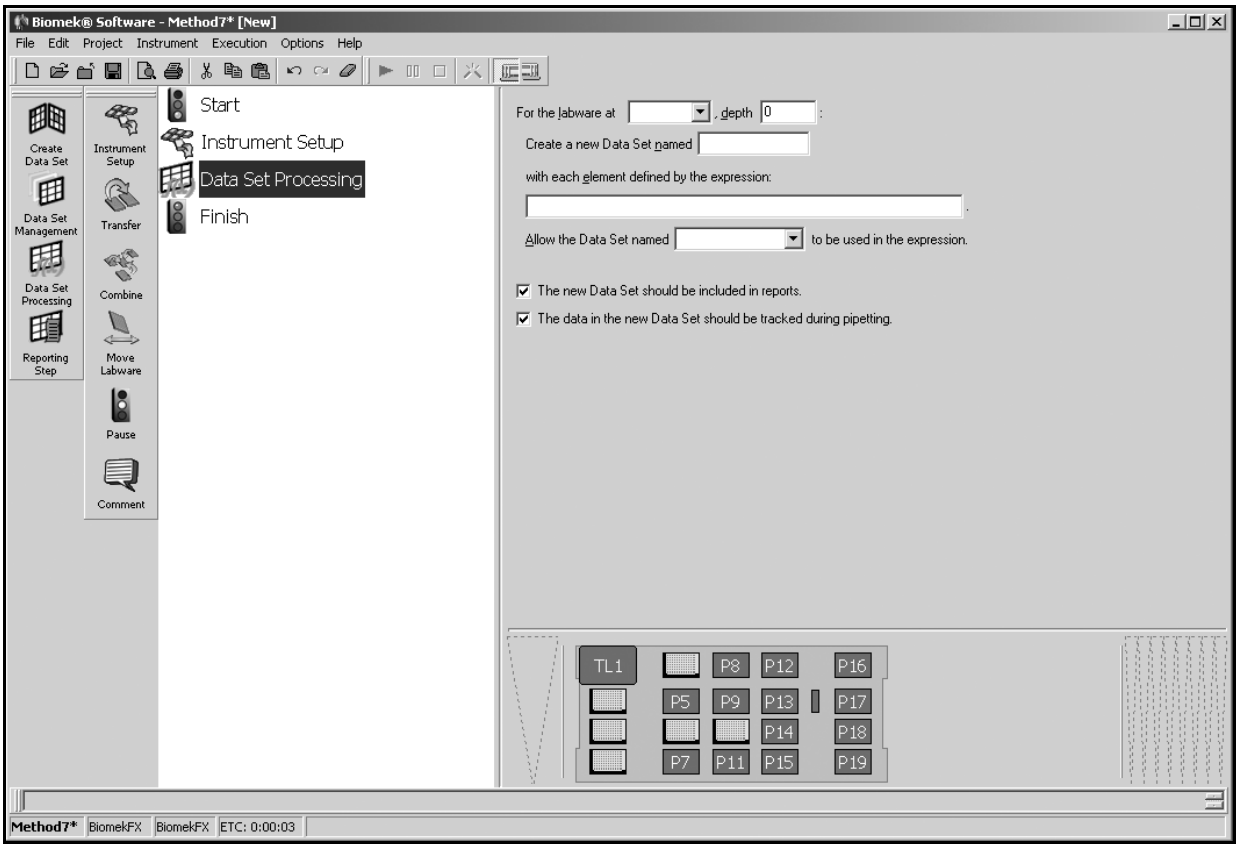


Figure 24-18. Data Set Processing step configuration

To configure the Data Set Processing step:

1. At **For the labware at**, choose the labware where the new data set is located.
2. If in a stack, enter the **depth** of the labware.

   Note: Depth refers to a specific piece of labware in a stack. To use the top piece of labware, enter **0**; to use the second from the top piece of labware, enter **1**; to use the third from the top piece of labware, enter **2**; and so on. Refer to Section 7.3.6.4.1, *Biomek Stacking Rules*, for information on using stacks.

3. In Create a new Data Set named, enter the name of the new data set.

   Note: Each data set must have a unique name. The method displays an error during validation if two data sets have the same name.

4. In with each element defined by the expression:, enter the expression.

   Note: Refer to Section 24.5.1, *Understanding Expressions*, for information on common symbols used in expressions.

   Note: An equal (=) sign must precede the expression entered in the Data Processing step.

5. At Allow the Data Set named. . . to be used in the expression, choose the previously created data set to be used in the expression.

   Note: The previously created data sets are available for selection.

   Note: Leave Allow the Data Set named. . .to be used in the expression blank to not use an existing data set as the basis for the transformation.

6. Ensure **The new Data Set should be included in reports** is checked to allow the new data set to be included in reports chosen in the Reporting or Finish steps.
7. Ensure **The data in the new Data Set should be tracked during pipetting** is checked to allow the data from the new data set to be tracked during pipetting operations.

   Note: If the expression is applied only to the source labware and should not be tracked, do not check The data in the new Data Set should be tracked during pipetting. Not checking this option may be useful for complex methods that use data sets, but may not require the data set to be tracked.

24.5.1 Understanding Expressions

Expressions, using symbols, allow a customized operation to be performed in the Data Set Processing step.

Using expressions in the Data Set Processing step includes understanding:

- some common symbols necessary to create an expression (Table 24-1).
- results of expressions on data sets (Table 24-2).

Note: An equal (=) sign must precede an expression entered in the Data Set Processing step.

Note: Refer to Section 13.3, *Using Expressions*, for more information on using expressions.

Table 24-1. Some common symbols used in expressions

Symbol	Definition
+	addition
-	subtraction
*	multiplication
/	division; returns a rational number
\	integer division; returns an integer, no remainder; for example, 13 \ 5 returns a value of 2
a MOD b	returns the remainder after a is divided by b; for example, 13 MOD 5 returns a value of 3
>	greater than
<	less than
=	equal to
< >	not equal to
^	exponentiation; for example, a ^ b = a^b

Table 24-2. Some expressions and the results

Expression	Result
= DataSetName > 5	creates a new data set where each element is True if the value in the existing data set is greater than 5 and False if the value is less than or equal to 5
= DataSetName * 1.05	creates a new data set where each value is the product of the existing data set multiplied by 1.05

Note: Element refers to the value associated with a well or tube.

24.6 Configuring the Reporting Step

The Reporting step (refer to Section 24.6, *Configuring the Reporting Step*) allows a report to be generated on data sets at any point during a method. While specifying the data desired from the data sets may be accomplished in the Create Data Set, Data Set Management, Data Set Processing, and Script steps, the report style and saved location of the report are chosen in the Reporting step.

The report contains data from all data sets that are configured to be included in reports and the type may be selected from four styles (refer to Section 24.6.1, *Report Styles*).

Since the Volume data set (refer to Section 14.2.1, *Understanding the Volume Data Set*) is reported in every report, the volume in each well in a microplate or tube in a rack can be tracked throughout a method if a Reporting step is inserted after every transfer or pipetting operation.

Note: The report style and saved location of the report on data sets generated at the end of a method may also be chosen in the Finish step (refer to Section 12.2.2, *Configuring the Finish Step*).

Insert a **Reporting** step into the Method View. The Reporting step configuration appears (Figure 24-19).

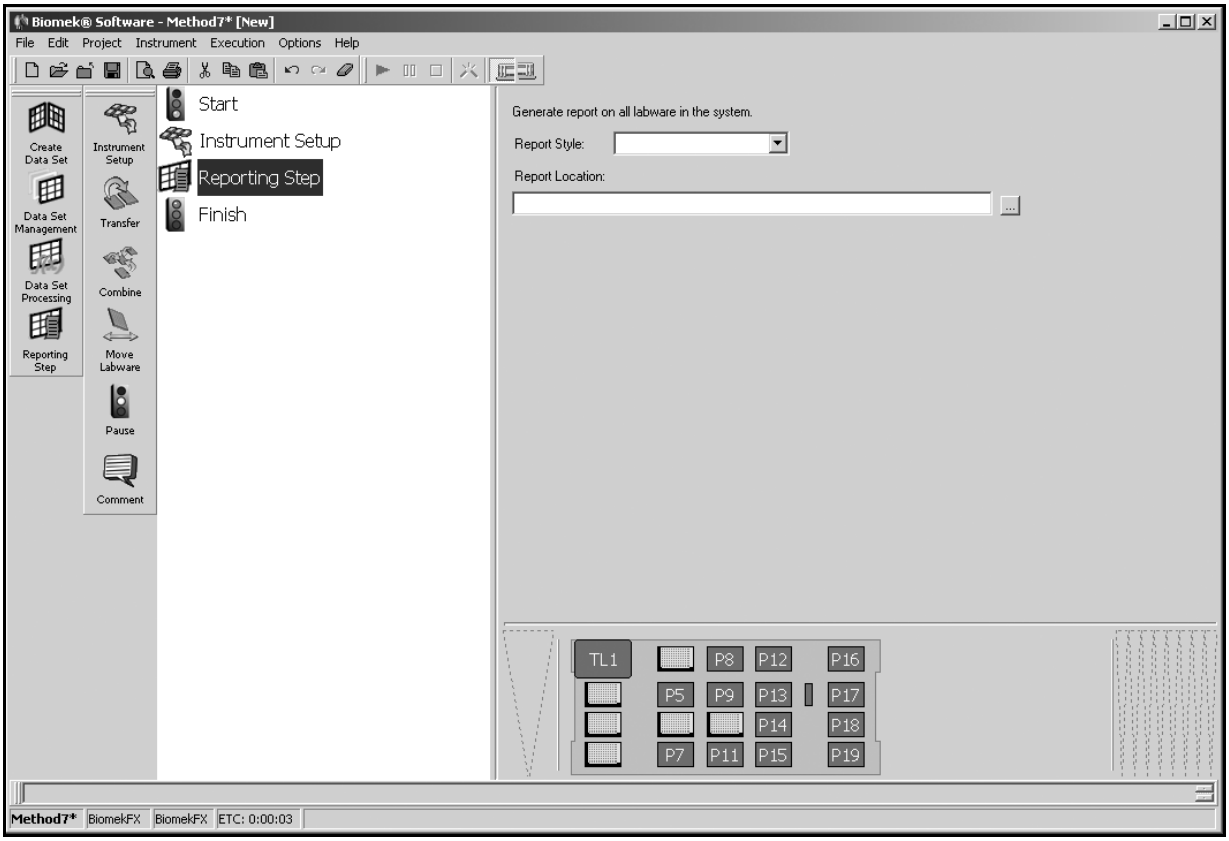


Figure 24-19. Reporting step configuration

To choose the report style and location of the report:

1. From **Report Style**, choose one of the following:
   - Text File
   - Per-Plate HTML Files
   - Per-Plate Text Files
   - SQL Server (refer to Section 24.6.2, *Configuring a SQL Server Report Style*)

   Note: Refer to Section 24.6.1, *Report Styles*, for examples and information on the types of reports that may be generated.

2. In **Report Location**, browse to find the location where the file is to be saved. The Reporting step is configured.

24.6.1 Report Styles

The report styles on data sets that may be generated are:

- Text File — a single text file listing all plates in the system. The columns in this file include the SequentialID, plate name, plate bar code, well number, sample ID (if the SampleID data set is created), and volume. A column for each data set that has reporting enabled is also included (Figure 24-20).

  Note: The SequentialID is a number assigned to each plate. This number is the only way to identify a plate in a report if the plate name or bar code were not specified.

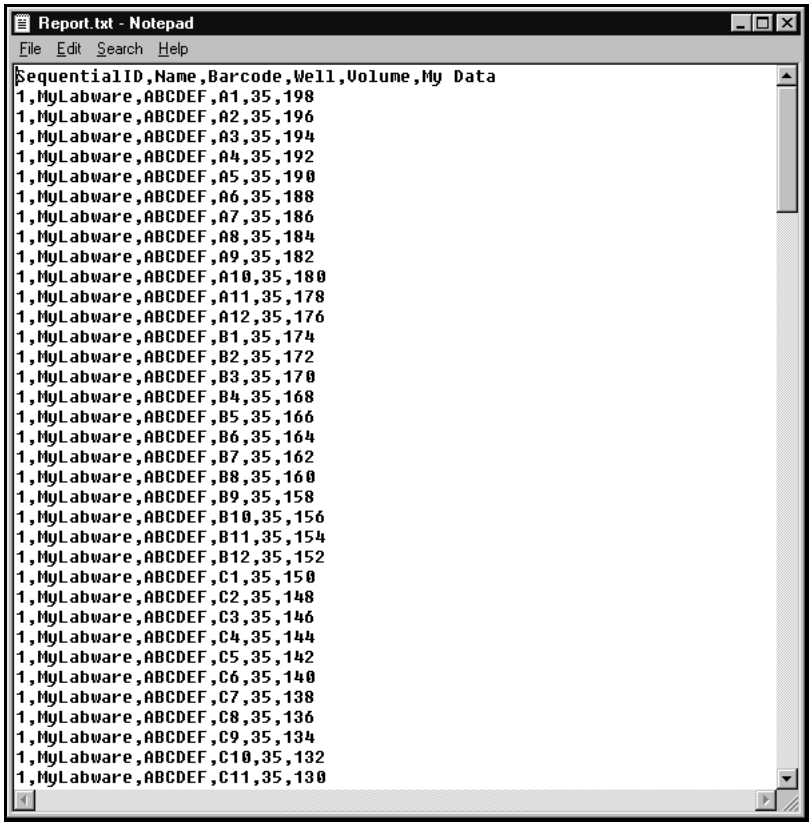
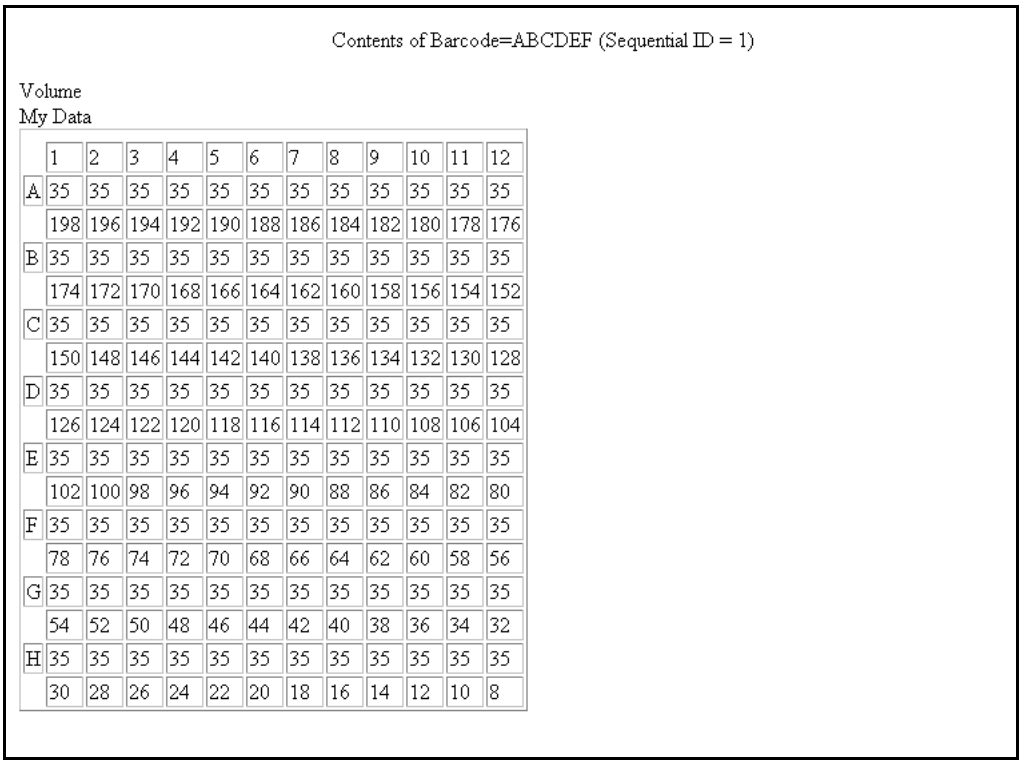


Figure 24-20. Report saved as Text File

- Per-Plate HTML Files — a folder containing an HTML file for each plate in the system. Each file contains the plate name, plate bar code, and an HTML table indexed by well number that includes the sample ID (if the SampleID data set is created) and volume. An entry for each data set that has reporting enabled is also included. The SequentialID is listed at the top of the file (Figure 24-21).

Note: The SequentialID is a number assigned to each plate. This number is the only way to identify a plate in a report if the plate name or bar code were not specified.



Contents of Barcode=ABCDEF (Sequential ID = 1)

Volume
My Data

	1	2	3	4	5	6	7	8	9	10	11	12
A	35	35	35	35	35	35	35	35	35	35	35	35
	198	196	194	192	190	188	186	184	182	180	178	176
B	35	35	35	35	35	35	35	35	35	35	35	35
	174	172	170	168	166	164	162	160	158	156	154	152
C	35	35	35	35	35	35	35	35	35	35	35	35
	150	148	146	144	142	140	138	136	134	132	130	128
D	35	35	35	35	35	35	35	35	35	35	35	35
	126	124	122	120	118	116	114	112	110	108	106	104
E	35	35	35	35	35	35	35	35	35	35	35	35
	102	100	98	96	94	92	90	88	86	84	82	80
F	35	35	35	35	35	35	35	35	35	35	35	35
	78	76	74	72	70	68	66	64	62	60	58	56
G	35	35	35	35	35	35	35	35	35	35	35	35
	54	52	50	48	46	44	42	40	38	36	34	32
H	35	35	35	35	35	35	35	35	35	35	35	35
	30	28	26	24	22	20	18	16	14	12	10	8

Figure 24-21. Report saved as Per-Plate HTML Files

- Per-Plate Text Files — a folder containing a text file for each plate in the system. Each file contains the SequentialID, plate name, plate bar code, and columns that include the well number, and sample ID (if the SampleID data set is created). A column for each data set that has reporting enabled is also included.

  Note: The SequentialID is a number assigned to each plate. This number is the only way to identify a plate in a report if the plate name or bar code were not specified.

  Note: The text files in the folder for each plate in the system look similar to Figure 24-20.

- SQL Server — a single database table listing all plates in the system. The columns of this table include the SequentialID, plate name, plate bar code, well number, and sample ID (if the SampleID data set is created). A column for each data set that has reporting enabled is also included. The table is created with a time-date stamp appended to the name (Figure 24-22).

  Note: The SequentialID is a number assigned to each plate. This number is the only way to identify a plate in a report if the plate name or bar code were not specified.

  Note: SQL Server is a Microsoft product that allows queries and provides analysis. The installation of this product is the responsibility of the user and is not supported by Beckman Coulter Service Engineers. SQL Server 2000 SP3 is the version requirement.

  Note: Refer to Section 24.6.2, *Configuring a SQL Server Report Style*, for specific information on configuring a SQL Server report.

Data in Table 'MyTable09_17_2002_14_25_53' in 'DataSets' on 'W...

SequentialID	Name	Barcode	Well	Volume
1		BARCODE11	A1	0
1		BARCODE11	A2	0
1		BARCODE11	A3	0
1		BARCODE11	A4	0
1		BARCODE11	A5	0
1		BARCODE11	A6	0
1		BARCODE11	A7	0
1		BARCODE11	A8	0
1		BARCODE11	A9	0
1		BARCODE11	A10	0
1		BARCODE11	A11	0
1		BARCODE11	A12	0
1		BARCODE11	B1	0
1		BARCODE11	B2	0
1		BARCODE11	B3	0
1		BARCODE11	B4	0
1		BARCODE11	B5	0
1		BARCODE11	B6	0

Figure 24-22. Report saved as SQL Server

24.6.2 Configuring a SQL Server Report Style

When SQL Server is chosen as the report style, the server, database, and table name are configured.

Note: SQL Server is a Microsoft product that allows queries and provides analysis. The installation of this product is the responsibility of the user and is not supported by Beckman Coulter Service Engineers. SQL Server 2000 SP3 is the version requirement.

Note: Refer to Figure 24-22 for an example of a SQL Server report style.

To configure a SQL server report style:

1. In Report Style, choose **SQL Server**. Figure 24-23 appears.

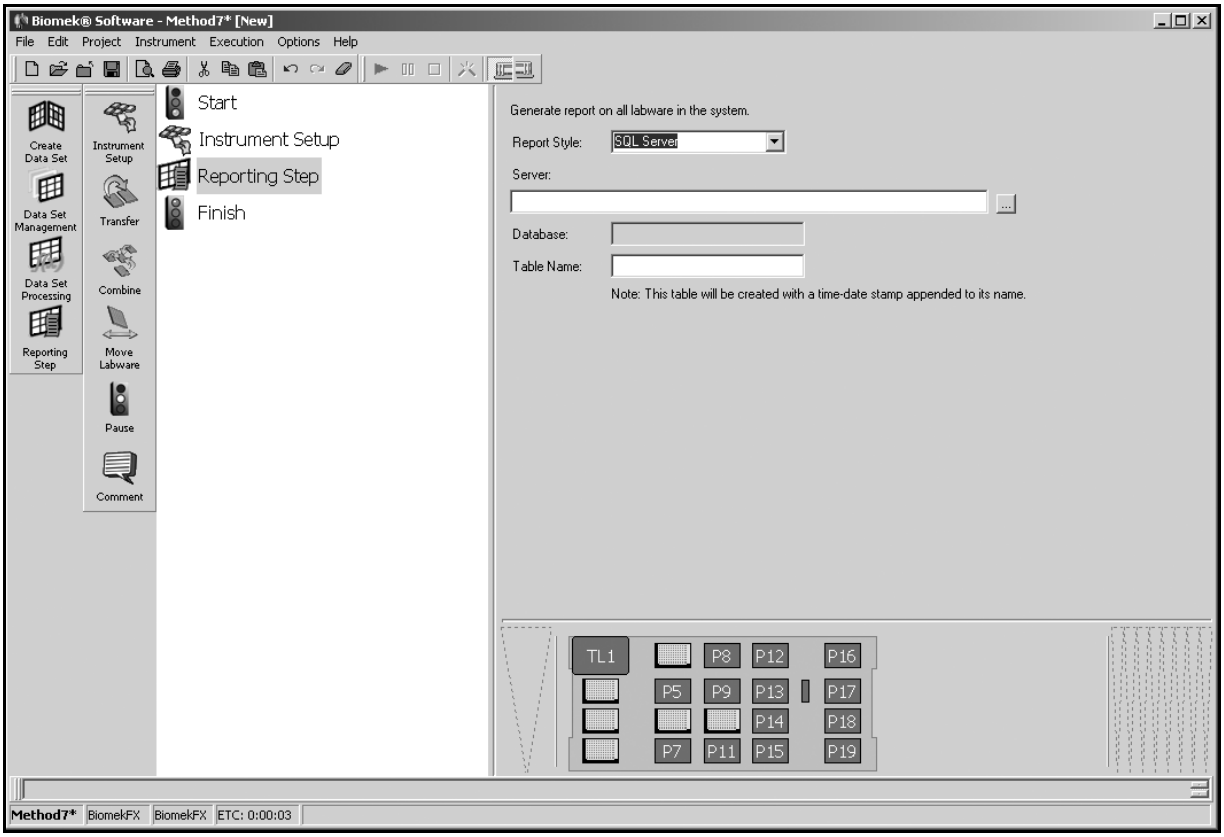


Figure 24-23. SQL Server report style chosen

2. Browse to find the location of the desired database on that server. SQL Server Connection (Figure 24-24) appears on top of the Reporting step configuration.

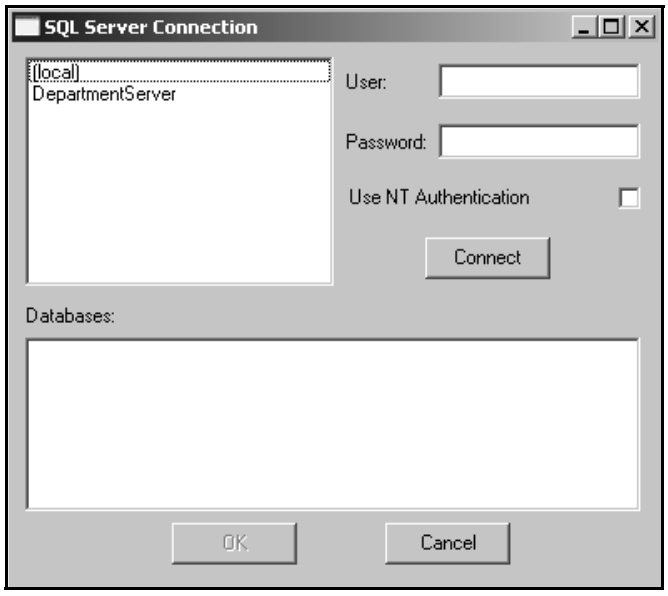


Figure 24-24. SQL Server Connection

3. Highlight the desired server.
4. Enter the **User** and **Password**.

   OR

   Check **Use NT Authentication**.

Note: The administrator of the SQL Server Connection sets the logging protocol for user and password or NT authentication.

5. Choose **Connect**. A list of the available databases appears in Databases (Figure 24-25).

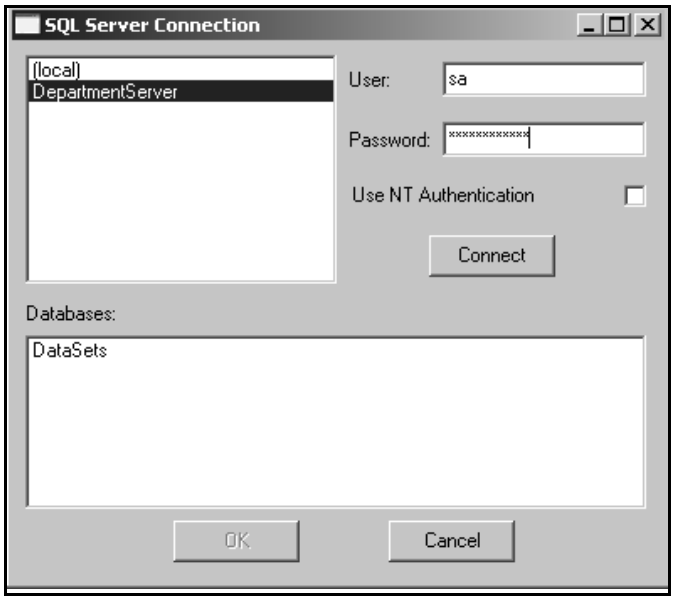


Figure 24-25. List of databases in SQL Server Connection

6. From **Databases**, highlight the desired database.

7. Choose **OK**. SQL Server Connection closes and the chosen server and database are entered in the Reporting step configuration.

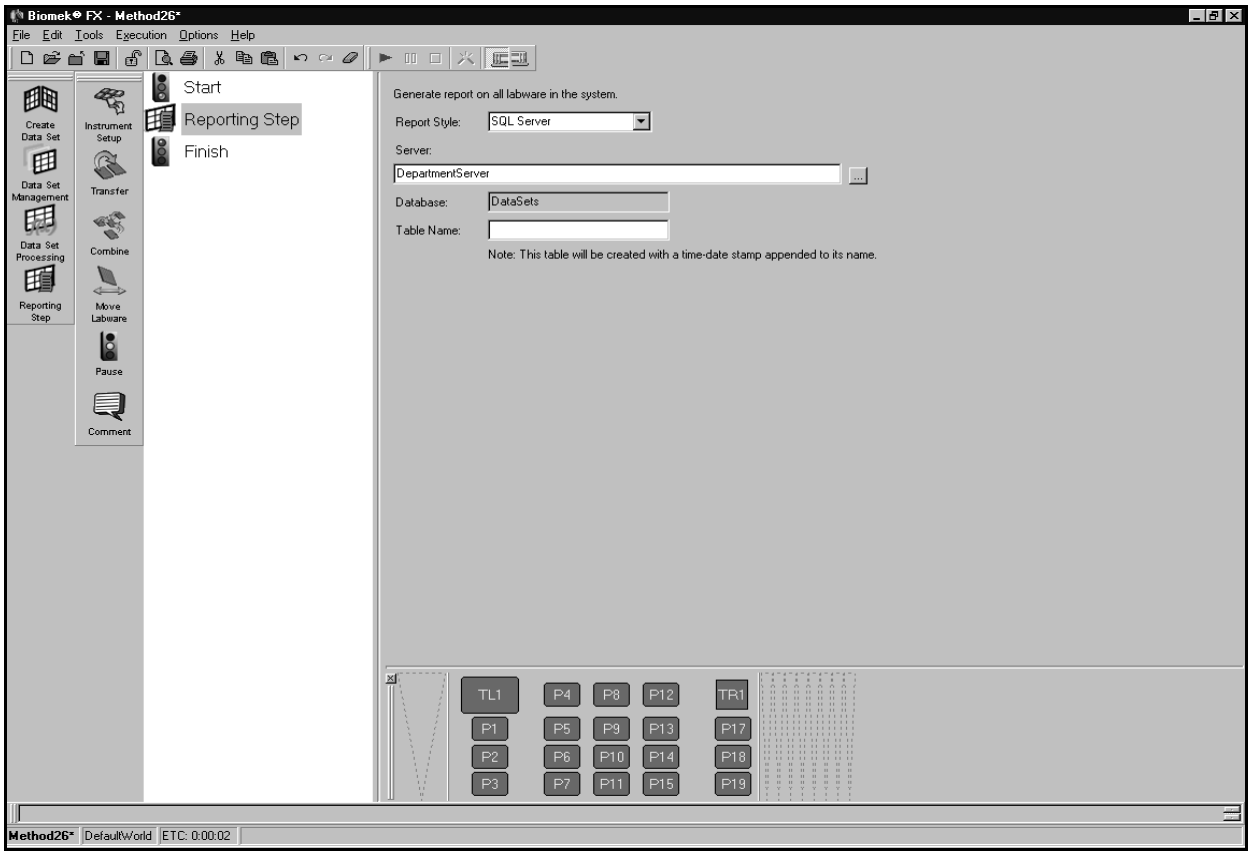


Figure 24-26. Server and database chosen

8. From the Reporting step configuration (Figure 24-19), enter the name of the **Table Name**.

Note: Table names must begin with a letter, and only letters, numbers and underscores (_) can be used.

Note: The table is created with a time-date stamp appended to the name.

25 Handling and Preventing Errors

25.1 Overview

Biomek Software provides extensive error handling and error prevention capabilities to help make sure the method being built, edited, set up, and run executes appropriately. Included in the Biomek Software error handling and prevention capabilities are:

- Error notification and cause messages.
- Error recovery options.
- Constant internal validation during method building and editing.
- Internal validation before running a method.

25.1.1 Error Message Overview

There are several types of error messages that may display while building and running methods using Biomek Software. The types of error messages generated depend on the type of error that has occurred. While errors may originate from more than one source, most errors fall into the following general categories:

- *Configuration Errors* (Section 25.2) — occur when a device or step is not configured correctly during method development or instrument configuration.
- *Validation Errors* (Section 25.3) — occur when a method or step is validating.
- *Manual Control Errors* (Section 25.4) — occur when a manual control movement requested of the ALPs, bridge, pod, head, or gripper is not compatible with Biomek instrument capabilities.
- *Run-Time Errors* (Section 25.5) — occur while a method is running.
- *Light Curtain Errors* (Section 25.6) — occur when there is a light curtain violation.
- *Liquid Level Sensing Errors* (Section 25.7) — occur while attempting to determine the liquid level in a piece of labware during a method run.

- *Clot Detection Error Message (NX-S8 only)* (Section 25.8) — occurs when a clot has been detected
- *Multiple Error Messages* (Section 25.9) — numerous errors may occur during validation or method run.
- *Observed Errors* (Section 25.10) — an error observed by the operator as the method runs.

25.1.2 Error Recovery Overview

Error recovery is the process of making changes to ensure a method can be completed. When changes are made and no subsequent errors are detected, the method completes. Depending on the conditions causing the error, the error message displays the appropriate error recovery options available.

Error recovery options may include:

- Fixing the error and continuing the method from the point of interruption.
- Stopping the current method, making modifications, and running the entire method from the beginning.
- Ignoring the error and continuing with the method.
- If a method using a dual-pod **FX** instrument is in progress when an error occurs, one pod can continue its tasks as long as its operations are not dependent upon the pod with the error.

25.1.3 Error Prevention Overview

Errors may be prevented by validating a method during the method-building process. Validation detects a large class of common errors before they occur by internally simulating the method prior to execution. This internal simulation provides an opportunity to change the method before it is run.

Operations for validating a method include:

- Validating the method immediately before a run starts by selecting Validate the current method before running it in Preferences.
- Individually validating steps by highlighting subsequent steps or the Finish step in the Method View.
- Individually validating operations by using the Single Step tool, available from the Execution menu.

25.2 Configuration Errors

Configuration errors occur when steps, labware, or devices are not configured correctly during method development or system setup.

25.2.1 Configuration Error Messages

When a configuration error is encountered during system setup, an error message may be displayed immediately (Figure 25-1).

Figure 25-1. Example of a configuration error generated due to a Liquid Type Editor configuration problem

A configuration error notification can also be generated as soon as a device configuration entry is made; for example, an incorrect entry in the Deck Editor appears red rather than black (Figure 25-2).

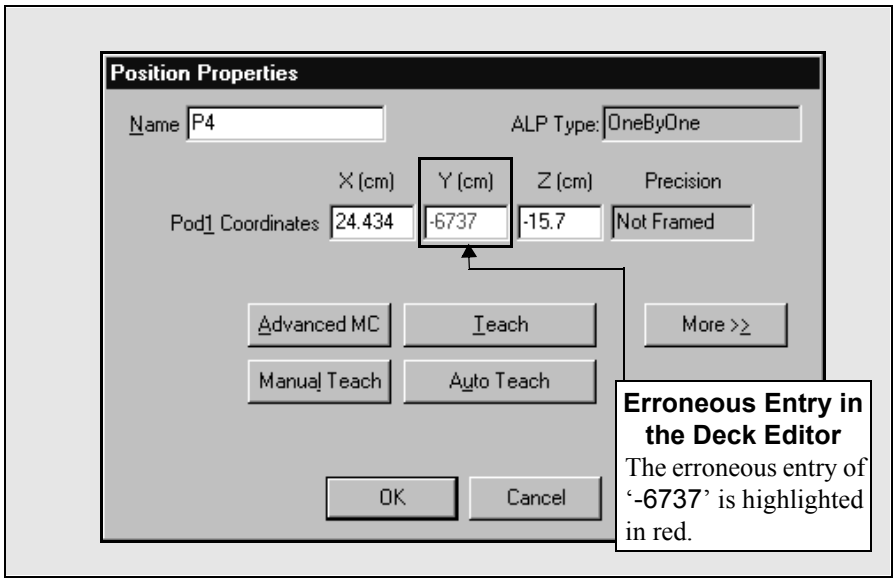


Figure 25-2. Example of a configuration error generated from the Deck Editor

When a step is not configured correctly, the step causing the error is highlighted in red in the Method View (Figure 25-3), and a message describing the error in detail is displayed at the bottom of the Biomek method editor and in a tool tip when the cursor is hovered over the step.

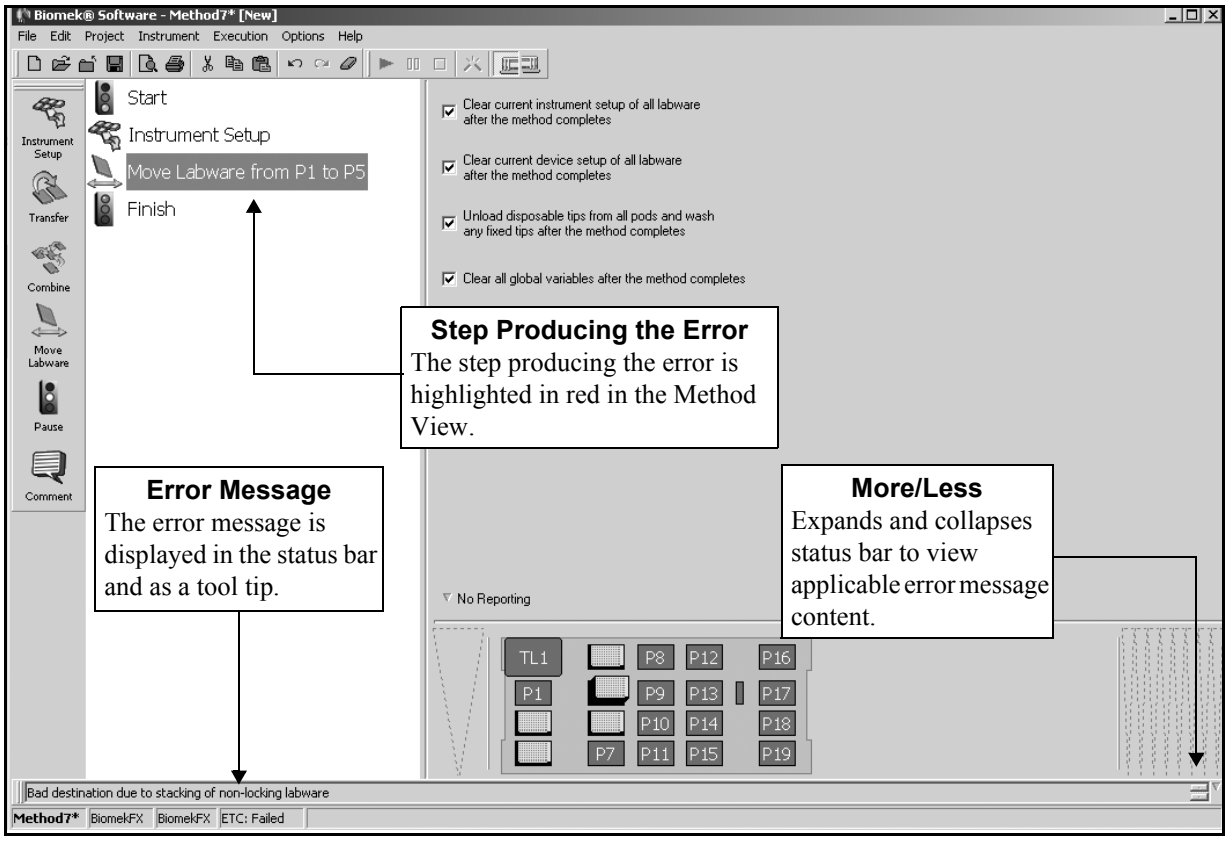


Figure 25-3. Example of an error generated during method validation because a step is not configured correctly

Note: The Error Message status bar may be hidden by choosing **Options>Toolbars** and deselecting **Method Error**.

To view multiple lines for a long error message, click the **More** button (Figure 25-3) to expand the error display to show the entire error message (Figure 25-4).

Click the **Less** button (Figure 25-4) to collapse the error display back to a single line (Figure 25-3).

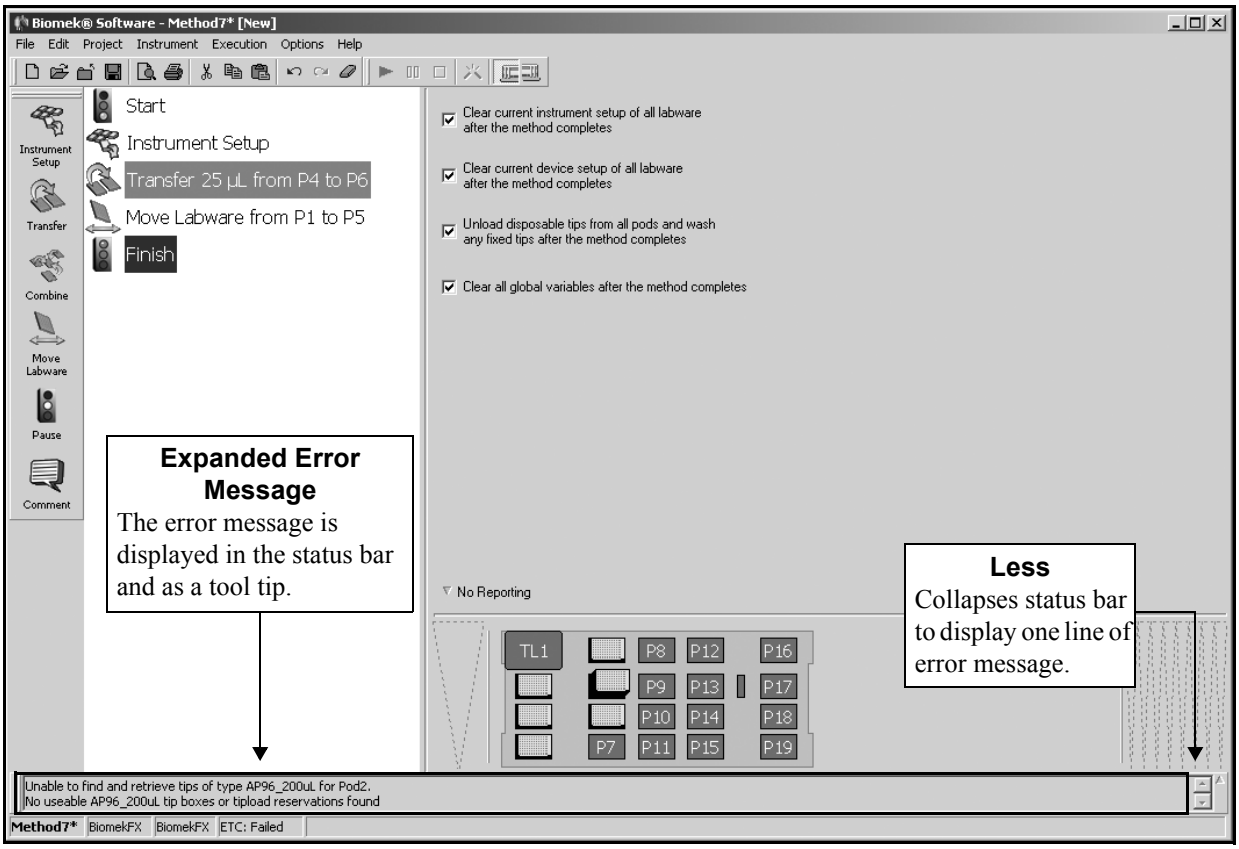


Figure 25-4. Example of an expanded error message

25.2.2 Recovering from Configuration Errors

To recover from configuration errors, ensure that all of the facts pertaining to the step, labware, or device configuration have been supplied and are acceptable values. For example, make sure that volumes do not exceed the maximum capacity of the specified tips or labware.

25.3 Validation Errors

Validating a method prior to execution internally simulates the method to test for errors. If an error is detected during validation, an error message displays information about the error.

Note: In this section, validation refers only to running methods in simulation mode to test for step or instrument configuration errors. It does not refer to validating a revision of a method using Beckman Coulter Accounts & Permissions. Refer to Section 12.15, *Checking Out a Method* for more information about validating checked in revisions of methods.

Note: Validation errors can occur due to step configuration or instrument configuration errors, as noted in Section 25.2, *Configuration Errors*.

25.3.1 Validation Error Messages

Errors encountered during validation may display the following information in the error messages:

- Source
- Type
- Cause
- Location
- Error Code
- Recovery Option(s)
- Date and Time

25.3.2 Validating a Method Before Run

When Validate the current method before running it is checked in Preferences (Figure 25-5), a method is internally simulated to test for errors when the method is run. If no errors are detected during this validation, the method is executed. If an error is encountered during this validation, the process stops and an error message displays information about the nature of the error.

When Validate the current method before running it is selected, the first step causing an error is highlighted in the Method View (Figure 25-6). Validate the current method before running it is enabled by default.

To prevent the system from slowing down due to unnecessary memory consumption, use Look ahead up to [1800] seconds in the method while it is running (refer to Section 25.3.2.1, *Using Look ahead up to [1800] seconds in the method while it is running*).

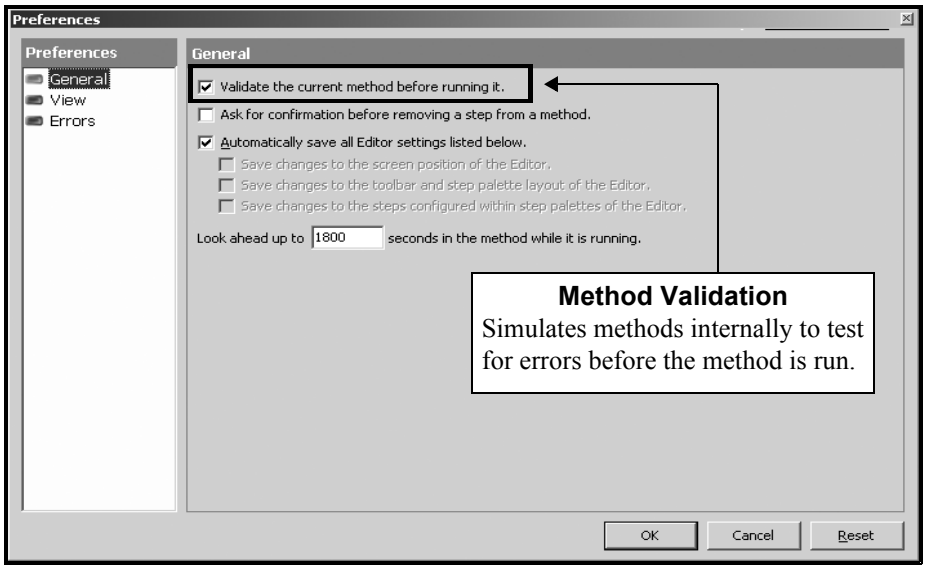


Figure 25-5. Validate the current method before running it option in Preferences

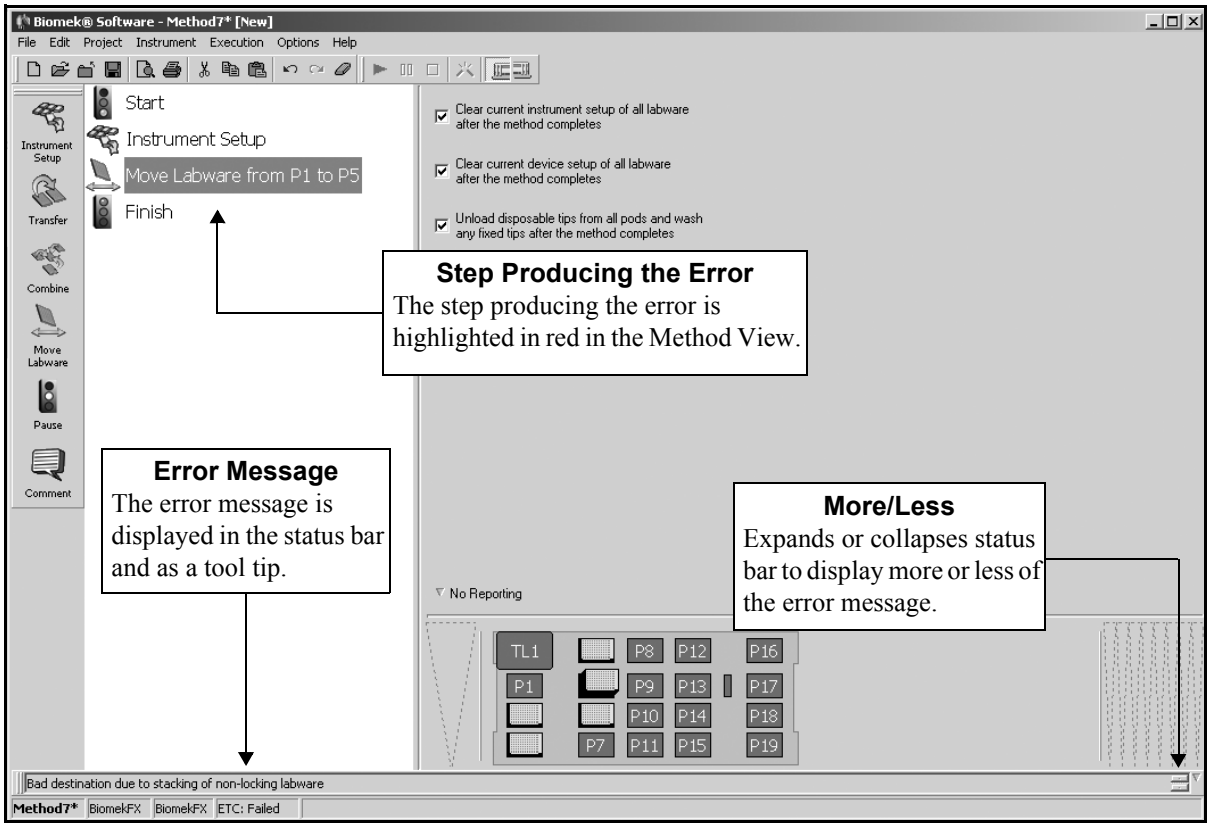


Figure 25-6. Example of a validation error message generated during method development as a result of incomplete step configuration

To use Validate the current method before running it:

1. From the toolbar, choose **Options>Preferences**. Preferences appears (Figure 25-5).
2. Make sure **Validate the current method before running it** is checked.
3. Choose **OK**.
4. Run the method.

Note: Validating a complex or lengthy method could result in occupying system resources for a long period of time. Validate the current method before running it can be disabled prior to running a previously validated method, or a method not requiring validation, by using Options>Preferences and deselecting Validate the current method before running it.

25.3.2.1 Using Look ahead up to [1800] seconds in the method while it is running

When a method is run, the software translates the steps of the method into "to do" lists of actions to be performed on each device. This translation process occurs while the method is running. Since methods can be arbitrarily long, the lists of actions can consume large amounts of computer memory, possibly slowing the system.

To prevent unnecessary slowing of the system due to memory consumption, the Look ahead up to [1800] seconds in the method while it is running option in Preferences (Figure 25-5) designates a time-based governor for suspending the translation process. The time in seconds entered into Look ahead up to [1800] seconds in the method while it is running is a threshold at which the translation process may be suspended so that the "to do" lists do not become too large. If each currently active device requires more than the time-designated threshold to complete its "to do" list, the suspension may occur. (The translation process is never suspended during a Just In Time step.) Once the system determines that some device may finish its list earlier than this threshold, it automatically resumes the translation process.

Note: To prevent problems with executing actions that should occur simultaneously, such as in a dual-pod system, it is important to enter a high enough Look ahead up to [1800] seconds in the method while it is running time.

25.3.2.2 Validation Error Messages Detected During Method Development

During method building, Biomek Software validates constantly. Errors that are detected during this process are displayed when a subsequent step in the method is highlighted. When the Finish step is highlighted, the entire method is validated.The step causing the error is highlighted in red in the Method View, and a message describing the error in detail is displayed in the status bar at the bottom of the method editor as well as a tool tip when the mouse pointer is hovered over the step.

25.3.2.3 Validation Error Messages Detected During Method Run

Validation errors may also be detected during method execution. The display of the error message depends on whether Validate the current method before running it is selected or not (refer to Section 25.3.2, *Validating a Method Before Run*).

If Validate the current method before running it is selected, the method is validated before it starts. If an error is found, it displays an error message similar to Figure 25-7.

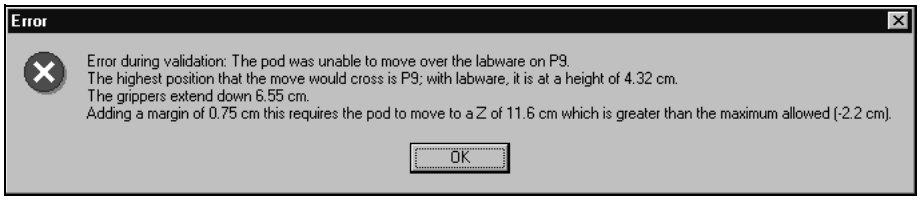


Figure 25-7. Example of a validation error message detected before method run

If a method has not been previously validated and the Validate the current method before running it option is not selected, it displays an error message similar to Figure 25-8.

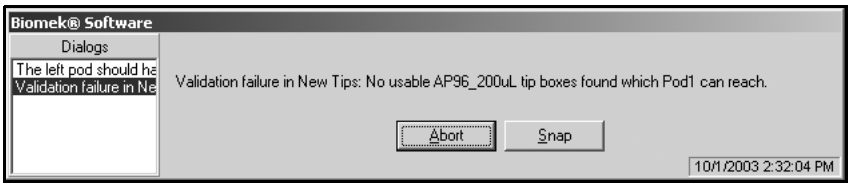


Figure 25-8. Example of a validation error message detected during method run

25.3.3 Recovering from Validation Errors

To recover from Validation errors encountered during method execution, choose one of the options provided on the error message. Validation error messages have either the OK recovery option or both Abort and Snap recovery options.

Validation error message recovery options include:

- Abort — stops the method after Biomek instrument completes the move in progress.
- Snap — stops the method after Biomek instrument completes the move in progress and creates a Continuation method (refer to Section 25.11.2, *Snapping a Continuation*).
- If the method is in the process of performing a move, such as aspirating or dispensing, the Biomek instrument completes the move; however, the instrument may not complete the entire step. For example, if the Biomek instrument is in the process of performing a Transfer step and an error occurs while it is aspirating, selecting Abort or Snap results in completing the aspiration but not the Transfer step.
  - ***3000*** — Snapping a Continuation is not available.
- OK — stops the method, allowing changes.

Note: OK is presented only as an option for a validation error detected before the run has started if Validate the current method before running it is turned on (refer to Section 25.3.2, *Validating a Method Before Run*).

25.3.3.1 Choosing Abort

Choose Abort to stop a method after completing the move in progress and leave the method open for editing.

To use Abort:

1. Read the error message to determine the cause of the problem.
2. Choose **Abort** to make the necessary changes in the original method file.

25.3.3.2 Choosing Snap (not available on a 3000)

Snap allows the method to be modified without changing the original method. When Snap is chosen, a Continuation method is created. A Continuation method is a new method consisting of the step causing the error, any steps not yet completed, and, if applicable, any incomplete substeps of the step which generated the error (refer to Section 25.11.2, *Snapping a Continuation*).

To use Snap:

1. Read the error message to determine the cause of the problem.
2. Choose **Snap** to create a Continuation method (refer to Section 25.11.2, *Snapping a Continuation*).

25.4 Manual Control Errors

Manual Control errors occur when a manual control movement requested of the bridge, pod, head, or gripper is not compatible with Biomek instrument capabilities.

25.4.1 Manual Control Error Messages and Recovery

Manual Control errors have only one recovery option, and that is to choose OK on the error message (Figure 25-9). Manual Control error messages should be carefully read to determine whether the problem lies in the hardware or software. Once that determination has been made, appropriate changes can be made to recover from the error.

To recover from Manual Control errors:

1. Read the error message to determine the problem.
2. Choose **OK**, then make the necessary changes.

Figure 25-9. Example of a Manual Control error because the Biomek FX tried to move the pod too far on the Z axis

25.5 Run-Time Errors

Run-Time errors result from problems that occur while a method is executing; for example, tips cannot load because the tiploader rods are not operating correctly. Run-Time error recovery options are presented on each error message.

25.5.1 Run-Time Error Messages

Run-Time error messages (Figure 25-10 and Figure 25-14) display the:

- Source
- Device
- Error Message
- Error Number
- Recovery Option(s)
- Date and Time

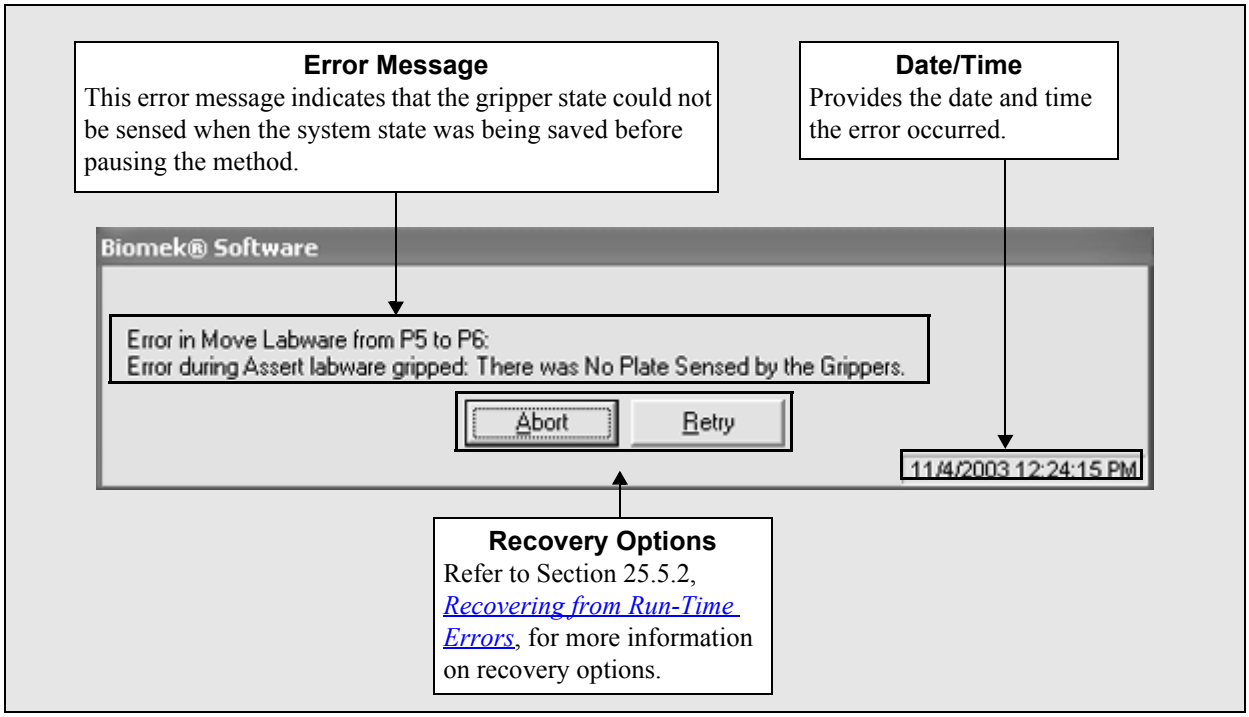


Figure 25-10. An example of a Run-Time error due to undetermined gripper state

25.5.2 Recovering from Run-Time Errors

To recover from errors, choose one of the Recovery Options and correct the problem that caused the error.

The options available for recovering are:

- Abort — stops the method after Biomek instrument completes the move in progress.
- Retry — attempts to complete the move in progress when the error was encountered and complete the method (refer to Section 25.5.2.2, *Choosing Retry*).

WARNING: The Ignore error recovery option is potentially dangerous since almost every action depends upon the successful completion of previous actions. Choose Ignore at your own risk.

- Ignore — skips the move in progress and proceeds with the rest of the method, if possible (refer to Section 25.5.2.3, *Choosing Ignore*).
- Snap — stops the method after the Biomek instrument completes the move in progress and creates a Continuation method (refer to Section 25.10.1.3, *Snapping a Continuation (not available on a 3000)*).

Note: If the method is in the process of performing a move, such as aspirating or dispensing, the Biomek instrument completes the move; however, the instrument may not complete the entire step. For example, if the Biomek instrument is in the process of performing a Transfer step and an error occurs while it is aspirating, selecting Abort or Snap results in completing the aspiration but not the remainder of the Transfer step.

➢ ***3000*** — Snapping a Continuation is not available.

After the errors are corrected, the method can be rerun or continued from where the error occurred.

25.5.2.1 Choosing Abort

Choose Abort to stop a method after completing the move in progress and leave the method open for editing.

To recover from errors using Abort:

1. Read the error message to determine the cause of the problem.
2. Choose **Abort** to make the necessary changes in the original method file.

25.5.2.2 Choosing Retry

Choose Retry to attempt to complete the step that is in progress when the error was encountered. If the step is completed successfully, the method continues.

CAUTION: Resuming a method assumes that the Biomek instrument is in the same state as when the error occurred. The pod may be moved to deal with a problem, but no changes can be made to the Biomek instrument deck.

To recover from errors using Retry:

1. Read the error message to determine the cause of the problem.
2. Examine the instrument to verify it is safe to restart the method.
3. Choose **Retry**. The instrument attempts to perform the move in progress when the error occurred, and, if successful, the method continues. If the method cannot continue after choosing Retry, another error message appears.

25.5.2.3 Choosing Ignore

WARNING: The Ignore error recovery option is potentially dangerous since almost every action depends upon the successful completion of previous actions. Choose Ignore at your own risk.

Choose Ignore to bypass the error and proceed with the method. The move in progress when the hardware error is detected does not complete, but the method attempts to continue the run.

To recover from errors using Ignore:

1. Read the error message to determine the cause of the problem.
2. Choose **Ignore**. The error is ignored, and the method continues to run, if possible. If the method cannot continue after choosing Ignore, another error message appears.

Note: Ignore may be useful for failed SILAS steps such as failed bar code reads or device time-out errors that do actually complete.

25.5.2.4 Choosing Snap (not available on a 3000)

Snap allows the method to be modified without changing the original method. When Snap is chosen, a Continuation method is created (refer to Section 25.11, *Using Continuations (not available on a 3000)*).

To recover from errors using Snap:

1. Read the error message to determine the cause of the problem.
2. Choose **Snap** to create a Continuation method (refer to Section 25.11.2, *Snapping a Continuation*).

25.6 Light Curtain Errors

The light curtain is a perimeter diffuse-reflective safety component that stops the Biomek FX or Biomek NX instrument when objects more than one inch in diameter penetrate the light curtains protective zone. Light curtain errors occur when an object penetrates (or violates) the light curtain protective zone and a light curtain error message is displayed.

- ***3000*** — Does not have a light curtain, although pressing the STOP button on the front rail of the instrument allows recovery options similar to those for a light curtain violation (refer to Section 25.6.3, *Using the Stop Button on the Biomek 3000*).

A light curtain violation does not stop the entire instrument. Certain on-deck devices and all devices controlled by SILAS may continue to operate despite a light curtain violation. However, new commands will not be issued once a light curtain violation has occurred and the system will come to a stop once all currently issued commands are completed.

25.6.1 Light Curtain Error Messages

Light curtain error messages appear when there is a light curtain violation. The light curtain error message displays:

- a graphic.
- an OK button.
- error message text.

25.6.2 Recovery Options for Light Curtain Errors

Light curtain errors can be recovered from by:

- Removing the obstruction and responding to the light curtain error message.
- Aborting a method during a light curtain violation using the buttons on the toolbar.
- Snapping a continuation during a light curtain violation using the buttons on the toolbar.

Note: If a light curtain violation occurs during a pause, the light curtain error must be resolved before the method can be resumed.

25.6.2.1 Removing the Obstruction and Responding to the Light Curtain Error Message

When a light curtain error message appears, the following text is displayed in the error:

"A light curtain violation has occurred. When you are clear of the light curtain, press OK. The pods will move back to where they were before the light curtain violation and the method will resume. If you wish to abort the method, you may press the stop button on the toolbar."

To recover from a light curtain error message:

1. Remove the violating object from the light curtain.
2. Click **OK**. The pod position is restored to its position before the light curtain violation and the method continues. If the light curtain violation remains, another error message is displayed.

Note: The system will not check or restore the position of the D axis. More specifically, the system will not resume a pipetting action from the point the light curtain error occurred. The entire pipetting operation must be restarted; it cannot be completed from where it left off.

- **FX** — If using a dual-pod system, each pod will be moved back to position one at a time to avoid collisions.

25.6.2.2 Aborting a Method During a Light Curtain Violation

Abort stops the method and leaves it open for editing. The method may not be continued from the point the error occurred.

To abort during a light curtain violation, click **Abort** on the toolbar.

25.6.2.3 Snapping a Continuation During a Light Curtain Violation

Snap stops the method and creates a Continuation method. A Continuation method allows the method to be modified without changing the original method.

To snap a continuation during a light curtain violation, click **Snap Continuation** on the toolbar. A Recovery step is inserted at the start of the continuation method that will restore pod positions.

CAUTION: The partially completed steps assume the pods are in the same position they were in when the method was halted. Removing the Recovery step without also removing these partially completed steps could result in a crash.

If it is not desired for the pod(s) to restore position, delete the Recovery step and any partially complete steps that come after it in the continuation.

Note: For more information about continuations, refer to Section 25.11, *Using Continuations (not available on a 3000)*.

25.6.3 Using the Stop Button on the Biomek 3000

Pressing the emergency STOP button on the front rail of the Biomek 3000 stops movement of the bridge and head assembly.

When the STOP button is pressed, Figure 25-11 appears.

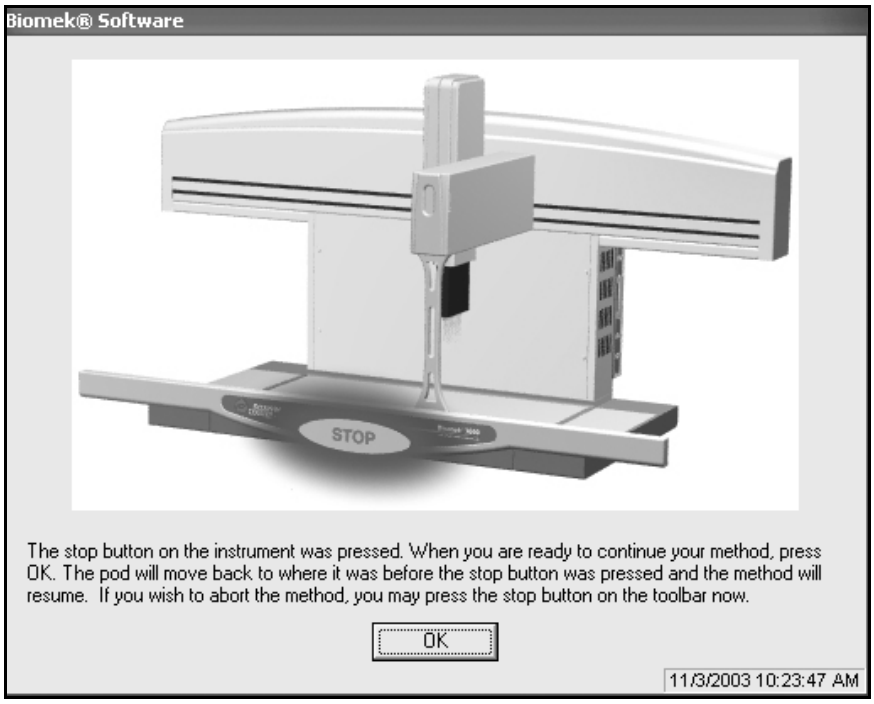


Figure 25-11. Choosing STOP on the front rail of the Biomek 3000

Two options are possible after pressing the emergency STOP:

- Choose **OK** to resume the method.

  Note: If the STOP button is pressed while a tool is being loaded, the instrument must be homed before the method is resumed.

- From the toolbar, choose **Execution>Stop** to abort the method.

25.7 Liquid Level Sensing Errors

The technologies for Liquid Level Sensing are different on the Biomek FX and NX instruments and the Biomek 3000 which accounts for the difference in error messages and recovery options for the instruments.

25.7.1 Liquid Level Sensing on the FX and NX-S8

If the liquid level in a piece of labware is not known, the Span-8 Pod can determine the liquid level when Liquid Level Sensing (LLS) capable tips are used.

LLS tips are used to determine the liquid level in a piece of labware by detecting a shift in the capacitance of a probe. The LLS tip moves to a specified height within a well and then slowly moves down into the well. When the tip contacts liquid, there is a large change in the capacitance detected. The liquid level is sensed by determining the height at which this change in capacitance occurs.

25.7.2 Liquid Level Sensing on the Biomek 3000

The P200L Single-Tip Pipette Tool includes patented technology that sonically detects the liquid level. Liquid level sensing is performed using an acoustic process involving a transmitter and receiver within the single-channel tools. The transmitter emits a sound wave through the tip that bounces back when it contacts liquid. The receiver detects the wave as it bounces back past the end of the tip.

25.7.3 Recovering from Liquid Level Sensing Errors

Liquid level sensing error messages appear when no liquid is sensed or when the amount of liquid sensed is incompatible with the operation performed. Liquid level sensing error messages display one of the following error messages:

> “There is insufficient volume in well ## for this operation. Check mandrel # before continuing.”
>
> “There is too much volume in well ## for this operation. Check mandrel # before continuing.”
>
> “Validation failure in Move to #. Consecutive senses did not provide a stable value. This can be caused by bubbles in the well or by the meniscus of the liquid.”

Liquid level sensing errors display a variety of recovery options in the error message, based on the instrument and type of liquid level sensing error encountered.

25.7.3.1 No Liquid is Detected on a FX or NX-S8

When no liquid is detected on a FX or NX-S8, the error message provides information on the probes (mandrel) generating the error and the following recovery options:

- Seek Again — Repeats liquid level sensing operation.
- Seek Slower— Repeats liquid level sensing with tip descending into the labware at a slower rate of speed.
- Move Up — Positions tip higher in well and repeats liquid level sensing.
- Snap [a Continuation] — Stops the method after the instrument completes the move in progress and creates a Continuation method (refer to Section 25.11, *Using Continuations (not available on a 3000)*).
- Abort — Stops the method after the instrument completes the move in progress.

25.7.3.2 Liquid Level Sensing Returning an Unstable Value on a FX or NX-S8

When a consistent value is not detected after numerous attempts to verify the liquid level on a FX or NX-S8, the error message (Figure 25-12) provides information on the pipetting operation generating the error, specific information on the error received, possible causes for the error, and the following recovery options:

- Abort — Stops the method after the instrument completes the move in progress
- Snap [a Continuation] — Stops the method after the instrument completes the move in progress and creates a Continuation method (refer to Section 25.11, *Using Continuations (not available on a 3000)*)

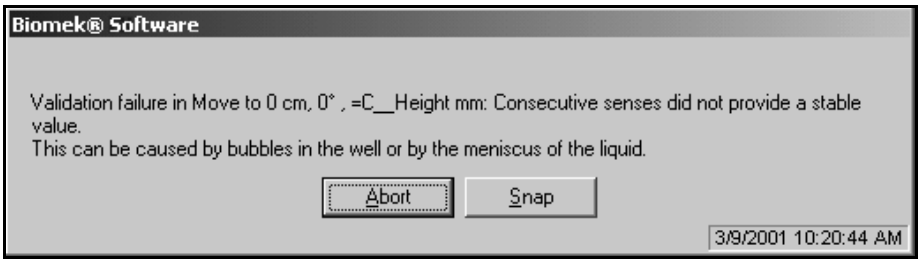


Figure 25-12. Inconsistent liquid level value detected error message

25.7.3.3 Liquid Level is Incompatible with the Operation

When the liquid level detected is incompatible with the pipetting operation, the error message is dependent on the instrument type (refer to Section 25.7.3.3.1, *Incompatible Pipetting Operation on a FX or NX-S8* and 25.7.3.3.2, *Incompatible Pipetting Operation on a 3000*) and provides information on the specific probe (mandrel) generating the error and recovery options.

25.7.3.3.1 Incompatible Pipetting Operation on a FX or NX-S8

The following recovery options are available:

- Seek Again — Repeats liquid level sensing operation.
- Pipette Air — Pipettes air when liquid is not available.
- Pipette From Bottom — Moves tip to bottom of well and continues pipetting operation.
- Snap [a Continuation] — Stops the method after the instrument completes the move in progress and creates a Continuation method (refer to Section 25.11, *Using Continuations (not available on a 3000)*).
- Abort — Stops the method after the instrument completes the move in progress.

25.7.3.3.2 Incompatible Pipetting Operation on a 3000

The following recovery options are available:

- Pipette Air — Pipettes air when liquid is not available.
- Pipette From Bottom — Moves tip to bottom of well and continue pipetting operation.
- Abort — Stops the method after the instrument completes the move in progress.

25.8 Clot Detection Error Message (NX-S8 only)

In order for clots to be detected, conductive disposable tips (called LLS in the Tip Type Editor) or fixed tips must be used and the technique must include clot detection. Biomek Software views the detection of a clot as an error and provides recovery options when a clot is detected.

25.8.1 Retrying Has Not Resolved the Clot

If the clot has not been resolved by retrying and Prompt user for further input is selected in the technique, an error message appears providing information on the probes (mandrel) generating the error and the following recovery options:

- Dispense, Aspirate Again, then Retry Detection — Dispenses the liquid back into the well, aspirates again, and retries clot detection.
- Ignore and Continue — Ignores the error and continues the method.

Note: Ignoring the error and continuing the method when a clot exists may contaminate the deck.

- Snap [a Continuation}— Stops the method after the instrument completes the move in progress and creates a Continuation method (refer to Section 25.11, *Using Continuations (not available on a 3000)*).
- Abort — Stops the method after the instrument completes the move in progress.

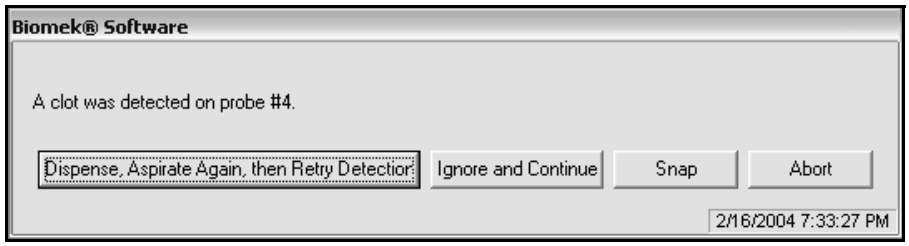


Figure 25-13. Clot detection error

25.9 Multiple Error Messages

When multiple error messages are generated during method validation, a dialog appears in the Instrument Setup prompt that contains a list of the errors (Figure 25-14). Specific information about each error in the list is displayed in the message area by highlighting the message in the error list. Recovery options for each message are also displayed.

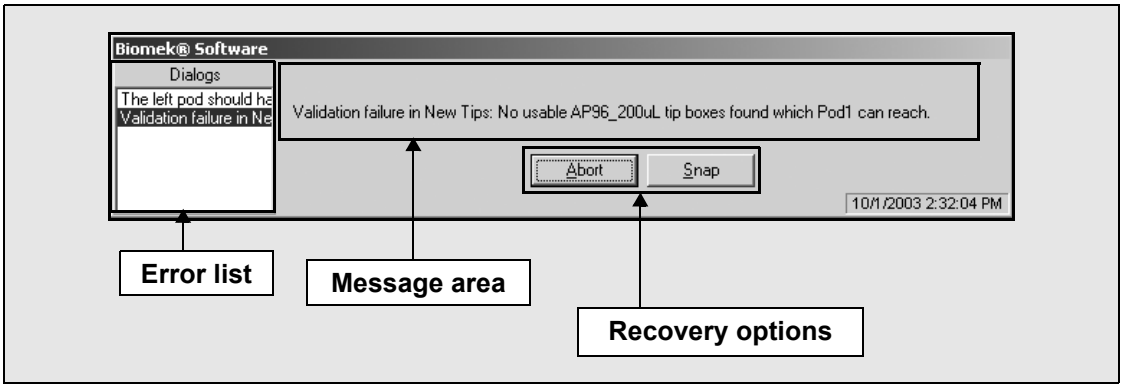


Figure 25-14. Error message dialog with multiple errors

When multiple errors are encountered, the error messages appear in prompts similar to the examples displayed in Figure 25-15 and Figure 25-16.

Figure 25-15. An example of multiple error messages

Figure 25-16. An example of multiple error message generated during Run-Time

25.9.1 Recovering from Multiple Errors

Multiple error messages should be read carefully to determine where the problem lies: in the hardware, software, or in the method. Once that determination has been made, appropriate changes can be made to recover from the errors. Errors can be resolved in any order. Refer to Section 25.5.2, *Recovering from Run-Time Errors*, for more information on error recovery options.

25.10 Observed Errors

Occasionally, errors are observed while watching the Biomek instrument execute a run. For example, the instrument may attempt to aspirate from an empty or missing microplate.

Observed errors may result from setup, hardware, or software issues.

25.10.1 Recovering from Observed Errors

The Biomek Software provides three options for recovering from observed errors while the method is running:

- Pause — halts a method without causing a light curtain violation.
- Stop — halts a method when there is no intent to resume the method from the point where it was stopped.
- Snap — stops the method after Biomek instrument completes the move in progress and creates a Continuation method (refer to Section 25.11, *Using Continuations (not available on a 3000)*).
  - ***3000*** — Snapping a Continuation is not available.

25.10.1.1 Pausing a Method

Use Pause to halt a method without causing a light curtain violation. Pause causes the method to halt after the Biomek instrument has completed the move in progress. For example, if the Biomek instrument is in the process of loading tips when Pause is selected, it finishes loading the tips before the system halts. When the method is resumed, it continues as though it were never halted.

Note: A method cannot be edited during a pause.

Use one of the following procedures to pause a method:

CAUTION: No changes to the Biomek instrument state are permitted while a method is paused. Changes can be made to the labware contents, but not the deck or the Biomek devices.

1. Choose **Execution>Pause**.

   OR

   Choose **Pause** on the toolbar. The instrument completes the move in progress, stops, and deactivates the light curtain.

2. Make the necessary changes to correct the observed error.
3. To resume the method run, choose **Pause** again. The light curtain is reactivated, and the method resumes from the point where it was paused.

25.10.1.2 Stopping a Method

WARNING: The light curtain is a safety device. Use it to stop a method only in an emergency.

Use Stop to halt a method during its run when there is no intent to resume method execution. If the pod is in the process of a move, the operation is not completed. Since the method is halted, this option allows edits to the method or changes to the hardware and deck.

Note: Stop may not halt operations already in progress on external devices, such as Stacker Carousels.

Use one of the following procedures to stop a method during a run:

- Choose **Execution>Stop**.

  OR

- Choose **Stop** on the toolbar.

  OR

  - ***FX, NX-S8*** — Break (violate) the light curtain by no more than one inch, and Abort (refer to Section 25.6, *Light Curtain Errors*).

  OR

  - ***3000*** — Press the STOP button on the front of the instrument (refer to Section 25.6.3, *Using the Stop Button on the Biomek 3000*) and choose Stop from the toolbar.

Note: Use standard procedures to rerun the method.

25.10.1.3 Snapping a Continuation (not available on a 3000)

Another way to recover from observed errors is by snapping a Continuation. Snapping a Continuation stops the current method and allows corrections in the middle of a method run. The method can be restarted from the point where the method was halted.

To snap a continuation, choose **Snap** to create a Continuation (refer to Section 25.11, *Using Continuations (not available on a 3000)*).

25.11 Using Continuations (not available on a 3000)

Continuation methods allow error recovery or method modification after a method has begun execution. A Continuation is a temporary method with steps generated automatically that complete the original method from the point at which the Continuation method was snapped. A Continuation method is displayed in the Method View and can be edited; however, it cannot be saved and used as a regular method.

- **FX** — If two pods are in use, one pod can continue to perform operations after an error occurs on the other pod. In this case, it is acceptable to allow the pod that is still performing operations to complete what it can before snapping a Continuation.

Note: When Beckman Coulter Accounts & Permissions is enabled, only users with permission to run the method may snap, edit, and run continuations (refer to Chapter 2, *Using Accounts & Permissions*).

25.11.1 Characteristics of Continuations

Continuation methods have several distinct characteristics such as:

- A Continuation method may not have a Start step.
- Icons for steps unavailable for editing appear gray, not colored. If a step containing multiple operations, such as Transfer or Combine, is in progress when a Continuation method is created, the incomplete operations are displayed as substeps under the main step at the start of the Continuation method in a Recovery Step (Figure 25-17). For example, if the Transfer step is in progress when a Continuation is snapped, the first step in the Continuation method is Transfer. Double-click on the Transfer step to view the substeps.

  Note: For light curtain violations, the Recovery step also includes steps to restore the pod to its position when the Light Curtain violation occurred.

- When a Continuation method is run successfully, the Continuation automatically closes.
- Only the last Continuation method generated is saved. Each subsequent Continuation method overwrites the previous Continuation method.

WARNING: To eliminate the possibility of replacing a Continuation method before corrections are made, it is recommended that a Continuation method be edited and run as soon as it is created.

- A Continuation method that contains a partially completed loop appears as one or more Loop steps. The first Loop is the partially completed loop iterations, while the last Loop step represents the remaining iterations of the loop. The number appearing with the first Loop indicates the iteration number the loop was on when the Continuation method was created (Figure 25-17).

Note: There are many dependencies among actions taken by different steps; therefore, take great care in modifying steps or substeps in a Continuation method.

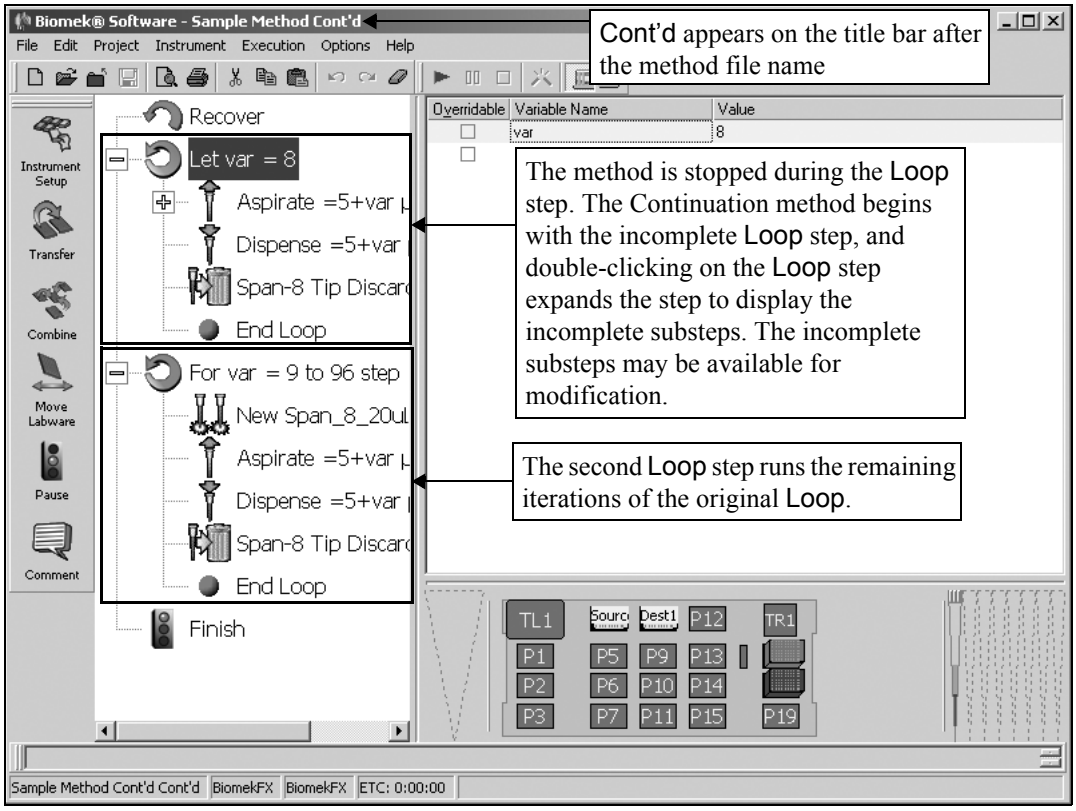


Figure 25-17. A Continuation method snapped during a Loop step

25.11.2 Snapping a Continuation

CAUTION: A Continuation method assumes that the instrument is in the same state as when the Continuation was snapped. If this is not true, the Continuation method must be edited to account for the changes.

A Continuation method is a temporary method created when Snap is chosen on an error message or when Snap Continuation is chosen from the toolbar during a method run.

To abort the current method and create a Continuation method:

1. Choose **Execution>Snap Continuation**. Snap Continuation Information appears (Figure 25-18).

   OR

   Choose **Snap** from an error dialog.

   OR

   Choose **Snap Continuation** on the toolbar. Snap Continuation Information appears (Figure 25-18).

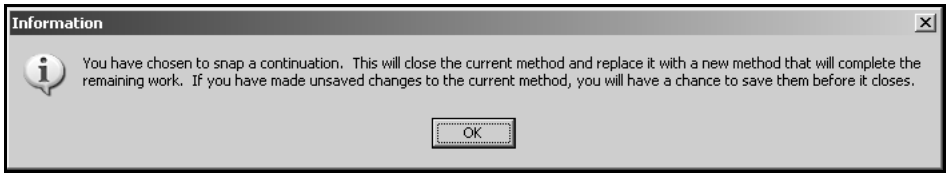


Figure 25-18. Snap Continuation Information

2. Choose **OK**. The Confirm prompt (Figure 25-19) appears if there are unsaved changes in the original method.

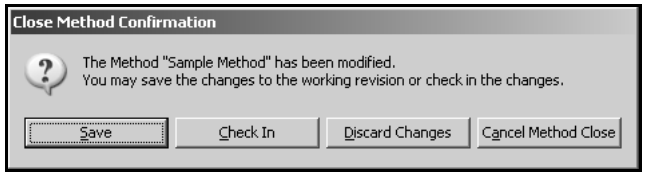


Figure 25-19. Confirm saving changes to method

3. If prompted to save, choose from among the following options:
    - Choose **Save** to save and close the current method and to open the Continuation method.

      Note: Refer to Section 12.9, *Saving a Method* for more information. After the method is saved, the Continuation method opens.

    - Choose **Check In** to save and check in the method and open the Continuation method.

      Note: Refer to Section 12.10, *Checking In a Method*, for more information. After the method is saved and checked in, the Continuation method opens.

    - Choose **Discard Changes** to close the original method without saving the changes. Any unsaved changes in the method are lost and the Continuation opens and is active for editing.
    - Choose **Cancel Method Close** to keep the original method active without saving and create a Continuation method for later use (refer to Section 25.11.3, *Loading and Running a Continuation*).

    Note: Once the Continuation method is opened, the title changes in the titlebar indicating that the Continuation method is now active; for example, <Method Name> Cont'd.

    Note: To access a Continuation method that is saved but not executed, follow the procedures outlined in Section 25.11.3, *Loading and Running a Continuation*.

4. Edit the **Continuation** method as needed (perhaps to correct an error).
5. Run the **Continuation** method.
6. Repeat steps 1 through 5 as many times as necessary to correct all errors.

When the Continuation method is run successfully, the Continuation method closes and cannot be loaded and run again.

25.11.3 Loading and Running a Continuation

If the Cancel Method Close option is chosen when snapping a Continuation (refer to Section 25.11.2, *Snapping a Continuation*), a Continuation method is created and saved for later use. To use the Continuation method later, it must be loaded.

Note: Continuation methods performed successfully are automatically deleted. Load Continuation is available only if a Continuation method exists. If a second Continuation is snapped before the first Continuation method is run, the first Continuation method is lost.

To load and run a Continuation method:

1. Choose **File>Load Continuation**. The Continuation method loads and appears in Method View.
2. Edit the Continuation method by adding, deleting, and editing steps.
3.  Run the **Continuation**.

   Note: If the Continuation method runs successfully, the Continuation method closes, and the Continuation is deleted. If further errors occur while running the Continuation method, handle them as outlined in this chapter.

25.12 Performing Single Operations Within Steps

The Single Step option performs single operations within Biomek steps, such as Aspirate or New Tips. Single Step pauses the Biomek instrument between each operation in a step, allowing visual verification that the operation is correct. Performing single operations can help when fine tuning a method.

To open Single Step:

Choose **Execution>Single Step**. Single Step appears (Figure 25-20):

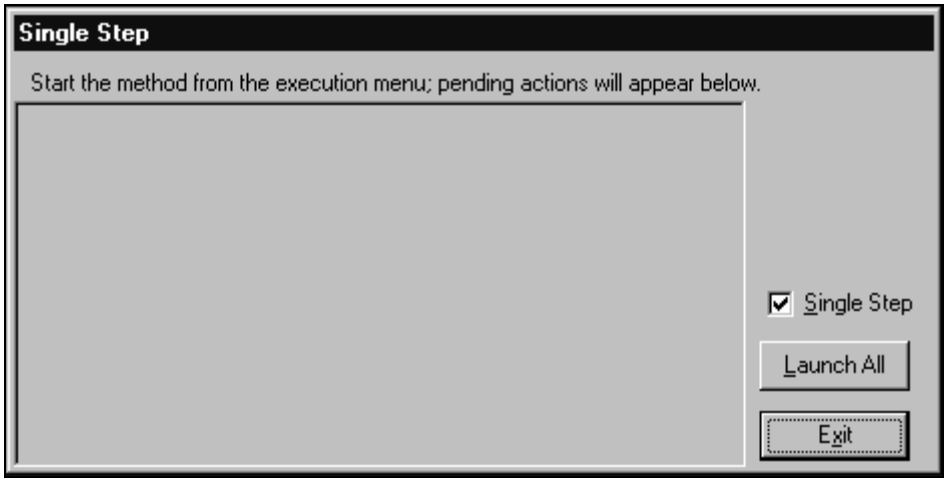


Figure 25-20. Single Step prompt

Single Step allows a method to be executed, one operation at a time. For example, to visually verify that tips are loading properly, use Single Step to walk through the New Tips step operation by operation. It is important to move slowly when using Single Step. Moving too quickly through the method may by-pass steps that need verification.

When visually verifying steps using Single Step, there are multiple operations that occur. For example, the New Tips step may walk through operations that include:

- Moving to a tip box.
- Extending the gripper.
- Gripping the tip box.
- Lifting the tip box.
- Moving to the tip loader.
- Placing the tip box on the tip loader.
- Retracting the gripper.
- Preparing to load tips.
- Loading Tips.

To run a method using Single Step:

1. Open the Single Step prompt. This can be done during a method run.
2. Start the method using the Start button on the toolbar. The method will stop for the first movement of a pod or bridge and the prompt will display the operation to perform (Figure 25-21).

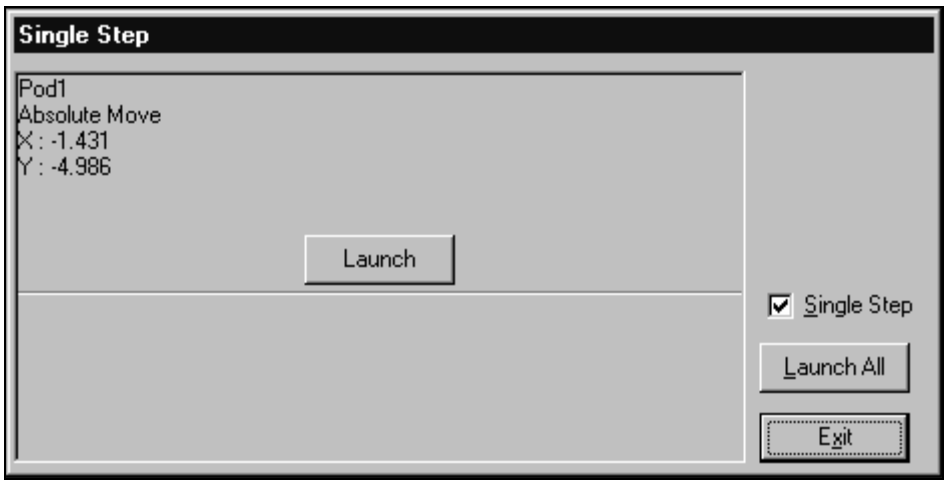


Figure 25-21. First move of method using Single Step

3. To perform the next move, choose **Launch**.
4. To perform all steps in the method after verifying the desired steps, uncheck **Single Step**.

   Note: Choose **Launch All** to launch all operations listed in the Single Step prompt. When there is more than one Launch button available, Launch All simultaneously presses all the Launch buttons.

5. Choose **Exit** to leave Single Step at any time.

26 Generating and Using Log Data

26.1 Overview

Logs provide text records of a method run. The contents of the text record, or log file, is based upon the type of log requested. Logs include information on liquid transfer operations, errors, and gripper movements, as well as information contained in data sets.

Log types include:

- Details — captures every operation that occurs during a method run, including Instrument Setup, absolute moves, pod movements, and gripper movements.
- Errors — captures any errors that occur during a method run.
- Pipetting — captures pipetting operations completed by a pod during a method run, deck location, and labware name or type.
  - ***FX*** — available only for instruments with a Multichannel pod.
  - ***3000*** — available with all pipetting tools.
  - ***NX-MC*** — available for this instrument.
  - ***NX-S8*** — not available for this instrument.
- Span8Pipetting — captures only Span-8 pipetting operations that occur during a method run, including location and labware name or type.
- Span8Transfer — captures only Span-8 transfer operations that occur during a method run, including location and labware name or type.
  - ***FX*** — Span8Pipetting and Span8Transfer are available only for instruments with a Span-8 pod.
  - ***3000***, ***NX-MC*** — Span8Pipetting and Span8Transfer are not available for these instruments.
  - ***NX-S8*** — available for this instrument.

Note: The addition of SampleID data sets also allows the Span8Pipetting and Span8Transfer logs to include well identification information.

- UnifiedPipetting — captures pipetting operations, along with Sample IDs for wells, performed by any pod, including information on the where the aspirate or dispense operation occurs.
- UnifiedTransfer — captures transfer operations, along with Sample IDs for wells, performed by any pod, including information on the source and destination labware.

Log files are used to generate reports and capture the history of a method run. Log files can be printed using a standard text editor or by inserting them into a spreadsheet program, such as Microsoft® Excel.

26.2 Types of Logs

The seven types of logs available capture either a complete account of a method or specific operations that occur during a method run. The type of log captured is indicated by the file name in the Logs subdirectory. Logs is a subdirectory of the Biomek directory.

To access Logs:

Browse to C:\Documents and Settings\All Users\Documents\Biomek\Logs.

OR

Choose **Start>Beckman Coulter>Tools>Biomek Files** to open the Biomek directory and access Logs.

Examples of the naming procedures for log files are:

- Details — Details03-09-2000 17.11.20.log
- Errors — Errors03-27-2000 10.27.41.log
- Pipetting — Pipetting03-09-200 17.11.20.log
- Span8Pipetting — Span8Pipetting03-05-2001 16.51.18.log
- Span8Transfer — Span8Transfer03-05-2001 16.51.18.log
- UnifiedPipetting — UnifiedPipetting09-27-2002 12.11.41.log
- UnifiedTransfer — UnifiedTransfer09-27-2002 12.11.41.log

26.2.1 Details Log

The Details log provides comprehensive information about each move made by the Biomek instrument. It is used when trying to identify and correct movement problems for any pod.

Refer to Section 26.3.1, *Details Log Contents*, for specific information about the Details Log contents.

Note: The default setting for the Details log is Off.

Note: The Details log is most useful to Beckman Coulter Service Engineers when troubleshooting an instrument.

26.2.2 Errors Log

The Errors log lists any errors or interruptions that occur during a method run. It is used to get the exact error message to include in a report or a discussion with Technical Support.

Refer to Section 26.3.2, *Errors Log Contents*, for specific information about the Errors log contents.

Note: The default setting for the Errors log is On.

26.2.3 Pipetting Log

The Pipetting log lists aspirate and dispense operations that are executed during a method run. It is used when validating a method or generating a comprehensive report about the pipetting operations used during a method.

- ***FX*** — available only for instruments with a Multichannel pod.
- ***3000*** — available with all pipetting tools.
- ***NX-MC*** — available for this instrument.
- ***NX-S8*** — not available with this instrument.

Refer to Section 26.3.3, *Pipetting Log Contents*, for specific information about the Pipetting log contents.

Note: The default setting for the Pipetting log is Off.

26.2.4 Span8Pipetting Log (FX, NX-S8 only)

The Span8Pipetting log lists aspirate and dispense operations performed by the Span-8 Pod during a method run. It is used when validating a method or generating a comprehensive report about Span-8 pipetting operations used during a method. The SampleID data sets allows the Span-8Pipetting log to include the sample ID assigned in the Instrument Setup step for wells on labware. The sample ID is captured in the Well Identification field.

Refer to Section 26.3.4, *Span-8Pipetting Log Contents (FX, NX-S8 only)*, for specific information about the Span8Pipetting Log contents.

- ***FX*** — default setting is On when a Span-8 Pod is installed and configured in Instrument Setup. However, a Span8Pipetting log is available only after a method has been run with a Span-8 pod.
- ***NX-S8*** — default setting is On. However, a Span8Pipetting log is available only after a method has been run with a Span-8 pod.

26.2.5 Span8Transfer Log (FX, NX-S8 only)

The Span8Transfer log lists liquid transfer operations performed by the Span-8 Pod during a method run. It is used when validating a method or generating a comprehensive report about Span-8 liquid transfer operations used during a method. The SampleID data sets allows the Span-8Transfer log to include the sample ID assigned in the Instrument Setup step for wells on labware. The sample ID is captured in the Well Identification field.

Refer to Section 26.3.5, *Span-8Transfer Log Contents (FX, NX-S8 only)*, for specific information about the Span8Transfer Log contents.

- ***FX*** — default setting is On when a Span-8 Pod is installed and configured in Instrument Setup. However, a Span8Pipetting log is available only after a method has been run with a Span-8 pod.
- ***NX-S8*** — default setting is On. However, a Span8Pipetting log is available only after a method has been run with a Span-8 pod.

26.2.6 UnifiedPipetting Log

The UnifiedPipetting log lists aspirate and dispense operations, along with Sample IDs for wells, performed by any pod. It includes information on the labware where the aspirate or dispense operation occurs and is used when validating a method or generating a comprehensive report about pipetting operations used during a method.

Refer to Section 26.3.6, *UnifiedPipetting Log Contents*, for specific information about the UnifiedPipetting log contents.

Note: The default setting for the UnifiedPipetting log is Off.

26.2.7 UnifiedTransfer Log

The UnifiedTransfer log lists transfer operations, along with Sample IDs for wells, performed by any pod. It includes information on the source and destination labware and is used when validating a method or generating a comprehensive report about liquid transfer operations used during a method.

Refer to Section 26.3.7, *UnifiedTransfer Log Contents*, for specific information about the UnifiedTransfer log contents.

Note: The default setting for the UnifiedTransfer log is Off.

26.3 Log Contents

Each of the logs provide specific types of information; however, all log files provide the following information in their header:

- Method name and file path.
- User.
- Method start date and time.
- Unit serial number.
- Pod serial number.
- Last date the pod was validated (by a Beckman Coulter Service Engineer).
- A blank line (used as a separation between the header and the information captured during the method run).

Each line below the header can contain the following information:

- Date the information was captured.
- Time the information was captured.
- Information captured during the method run that is specific to the type of log requested.

Note: The information captured during the method run is based on the type of log generated. More specifically, when a Pipetting Log is generated, pipetting information such as the pod performing the operation, the type of pipetting operation performed, and the labware position and name are captured, along with other pipetting specific information.

The last line of a log file contains the date and time the method run ended.

26.3.1 Details Log Contents

Each line below the header of a Details log contains the following information:

- Date/Time — when the error occurred.
- Action Completed — action performed by the Biomek instrument.
- Device Completing the Action — the device performing the action (if applicable).

26.3.2 Errors Log Contents

Each line below the header of an Errors log contains the following information:

- Date/Time — when the error occurred.
- Error Description — provides the exact error message.

26.3.3 Pipetting Log Contents

Each line below the header of a Pipetting log contains the following information:

- Date/Time — when the error occurred.
- Pod Name — which pod performed the operation (Pod1 or Pod2).
- Position — the location on the deck (P1, P2...).
- Labware Name — name assigned to the labware in Labware Properties.
- Labware Barcode — barcode assigned to the labware in Labware Properties.
- Labware Section — the quadrant accessed.

  Note: Quadrants are numbered 1 through 4. A 96 well microplate is always Quadrant 1.

- Amount — the amount of fluid pipetted.

Note: If no information was supplied for a particular field, the field is blank in the Pipetting log.

26.3.4 Span-8Pipetting Log Contents (FX, NX-S8 only)

Each line below the header of a Span-8Pipetting log contains the following information:

- Date/Time — when the error occurred.
- Pod Name — which pod performed the operation (Pod1 or Pod2).
- Operation — the pipetting operation performed (aspirate or dispense).
- Position — the location on the deck (P1, P2...).
- Labware Name — name assigned to the labware in Labware Properties.
- Labware Barcode — barcode assigned to the labware in Labware Properties.
- Well Number — the well number pipetted to or from.

  Note: Wells are numbered left to right, top to bottom for all types of labware (Figure 26-1).

- Well Identification — sample ID assigned in the Instrument Setup step for wells on labware.
- Probe Number — the probe used for the pipetting operation.

  Note: Probes are numbered 1 through 8, from the back of the Biomek instrument to the front.

- Amount — the amount of fluid pipetted.
- Technique — the name of the technique used to govern the pipetting operation, or Custom if a customized technique was used.

Note: If no information was supplied for a particular field, the field is blank in the Span-8Pipetting log.

	1	2	3	4	5	6	7	8	9	10	11	12
A	1	2	3	4	5	6	7	8	9	10	11	12
B	13	14	15	16	17	18	19	20	21	22	23	24
C	25	26	27	28	29	30	31	32	33	34	35	36
D												
E												
F												
G												
H												

Figure 26-1. Well numbering in log files

26.3.5 Span-8Transfer Log Contents (FX, NX-S8 only)

Each line below the header of a Span-8Transfer log contains the following information:

- Date/Time — when the error occurred.
- Pod Name — which pod performed the operation (Pod1 or Pod2).
- Source Position — location of the source labware for the pipetting operation.
- Source Labware Name — name assigned to the source labware in Labware Properties.
- Source Well Number — the number of the well pipetted from in the source labware.

  Note: Wells are numbered left to right, top to bottom for all types of labware (Figure 26-1).

- Source Well Identification — sample ID assigned in the Instrument Setup step for wells on labware.
- Destination Position — location of the destination labware for the pipetting operation.
- Destination Labware Name — name assigned to the destination labware in Labware Properties.

- Destination Well Number — the number of the well pipetted to in the destination labware.

  Note: Wells are numbered left to right, top to bottom for all types of labware (Figure 26-1).

- Destination Well Identification —sample ID assigned in the Instrument Setup step for wells on labware.
- Probe Number — the probe used for the pipetting operation.

  Note: Probes are numbered 1 through 8, from the back of the Biomek instrument to the front.

- Amount — the amount of fluid pipetted.
- Technique — the name of the technique used to govern the pipetting operation, or Custom if a customized technique was used.

Note: If no information was supplied for a particular field, the field is blank in the Span-8Transfer log.

26.3.6 UnifiedPipetting Log Contents

Each line below the header of a UnifiedPipetting log (Figure 26-2) contains the following information:

- Date/Time — when the pipetting operation occurred.
- Pod Name — which pod performed the pipetting operation (Pod1 or Pod2).
- Type of Pipetting Operation — aspirate or dispense.
- Source Position — location of the source labware for the pipetting operation.
- Labware Name — name assigned to the labware in Labware Properties.
- Labware Bar Code — bar code assigned to the labware in Labware Properties.
- Labware Well Number— number of the well pipetted from in the labware.

  Note: Wells are numbered left to right, top to bottom for all types of labware (Figure 26-1).

- Labware Sample ID for Well — sample ID assigned in Instrument Setup step for well for labware.
- Probe or Tip Number — probe or tip used for the pipetting operation.
  - ***FX*** — probes for the Span-8 Pod are numbered 1 through 8, from the back the instrument to the front. Tips for the Multichannel Pod are numbered left to right, top to bottom (like well numbering) for all types of labware.
  - ***3000*** — Tips for the Multi-Tip Pipette Tools are numbered 1 through 8, from the back of the Biomek instrument to the front.
  - ***NX-MC*** — tips for the Multichannel Pod are numbered left to right, top to bottom (like well numbering) for all types of labware.
  - ***NX-S8*** — probes for the Span-8 Pod are numbered 1 through 8, from the back the instrument to the front.

- Volume — amount of fluid pipetted.
- Technique — the name of the technique used to govern the pipetting operation, or Custom if a customized technique was used.

Note: If no information was supplied for a particular field, the field is blank in the UnifiedPipetting log.

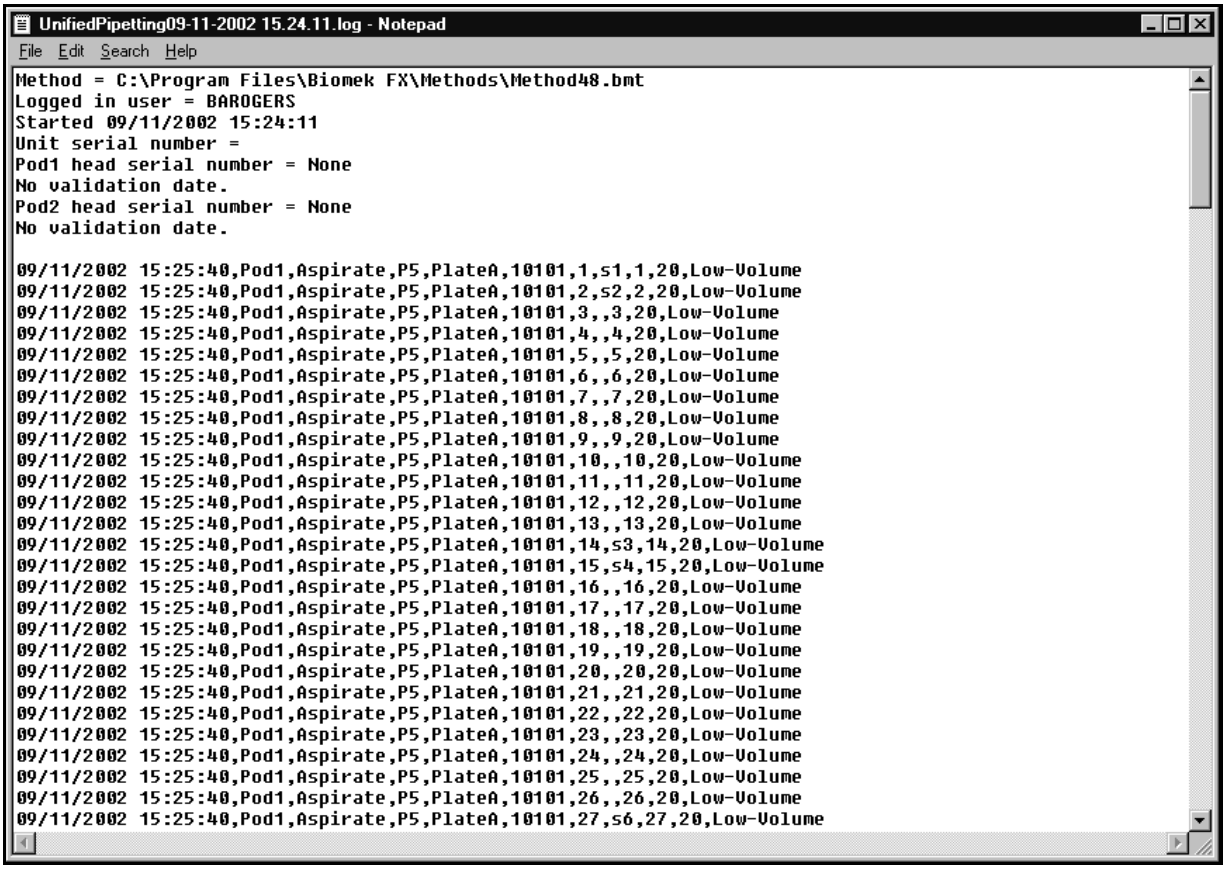


Figure 26-2. UnifiedPipetting log

26.3.7 UnifiedTransfer Log Contents

Each line below the head of a UnifiedTransfer log (Figure 26-3) contains the following information:

- Date/Time — when the transfer occurred.
- Pod Name — which pod performed the transfer (Pod1 or Pod2).
- Source Position — location of the source labware for the transfer operation.
- Source Labware Name — name assigned to the source labware in Labware Properties.
- Source Labware Bar Code — bar code assigned to the source labware in Labware Properties.
- Source Labware Well — number of the well pipetted from in the source labware.

  Note: Wells are numbered left to right, top to bottom for all types of labware (Figure 26-1).

- Source Labware Sample ID for Well — sample ID assigned in Instrument Setup step for well for source labware.
- Destination Position — location of the destination labware for the transfer operation.
- Destination Labware Name — name assigned to the destination labware in Labware Properties.
- Destination Labware Bar Code — bar code assigned to the destination labware in Labware Properties.
- Destination Labware Well — the number of the well transferred to in the destination labware.
- Destination Labware Sample ID for Well — sample ID assigned in Instrument Setup step for well for destination labware.

- Probe or tip number — probe or tip used for the transfer operation.
  - ***FX*** — probes for the Span-8 Pod are numbered 1 through 8, from the back the instrument to the front. Tips for the Multichannel Pod are numbered left to right, top to bottom (like well numbering) for all types of labware.
  - ***3000*** — Tips for the Multi-Tip Pipette Tools are numbered 1 through 8, from the back of the Biomek instrument to the front.
  - ***NX-MC*** — tips for the Multichannel Pod are numbered left to right, top to bottom (like well numbering) for all types of labware.
  - ***NX-S8*** — probes for the Span-8 Pod are numbered 1 through 8, from the back the instrument to the front.
- Volume — amount of fluid transferred.

Note: If no information was supplied for a particular field, the field is blank in the UnifiedTransfer log.

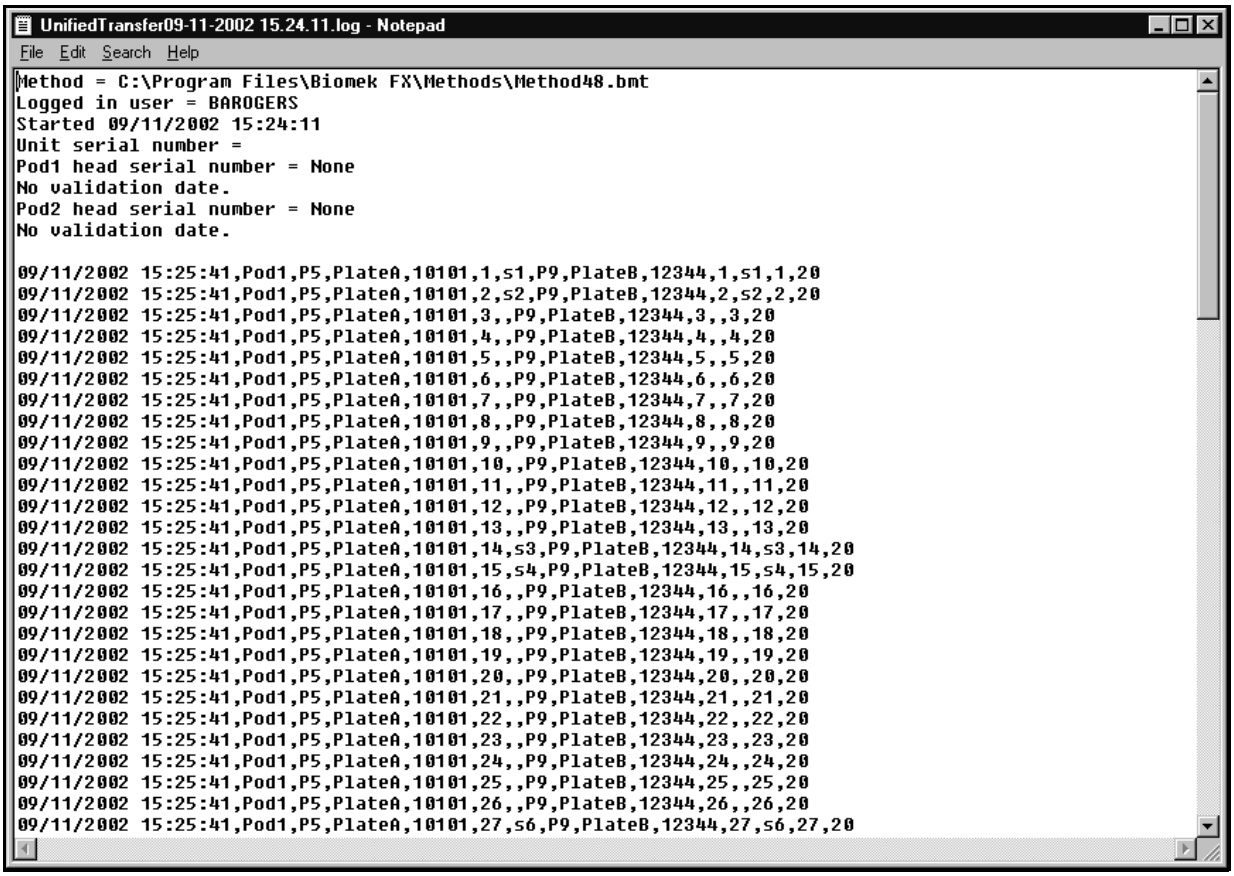


Figure 26-3. UnifiedTransfer log

26.4 Selecting Log Types

To generate log(s) during a method run, the only information required is a selection of the type of log(s) desired.

To select log(s):

1. Choose **Options>Log Configuration**. Log Configuration appears (Figure 26-4).

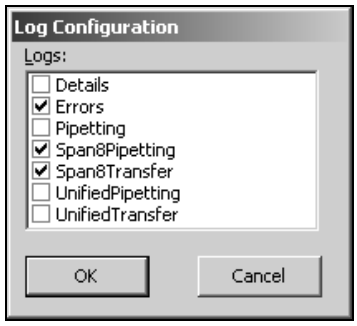


Figure 26-4. Select the log type(s) generated here

Note: The default setting for Errors is On. The default settings for Details, Pipetting, UnifiedPipetting,and UnifiedTransfer logs are Off.

- ***FX*** — Span8Pipetting and Span8Transfer logs only appear when a Span-8 Pod is installed and configured for use and after a method has been run with a Span-8 pod. When these conditions are met, the default settings for the Span8Pipetting and Span8Transfer logs are On.
- ***3000***, ***NX-MC*** — Span8Pipetting and Span8Transfer logs are not available for these instruments.
- ***NX-S8*** — Span8Pipetting and Span8Transfer logs only appear after a method has been run. The default settings for the Span8Pipetting and Span8Transfer logs are On.

2. Check the logs desired.

26.5 Viewing Log Files

View log files when creating reports or obtaining detailed information about a method. Log files are viewed in a standard text processor, such as Notepad (Figure 26-5), or in a spreadsheet, such as Microsoft Excel (Figure 26-6).

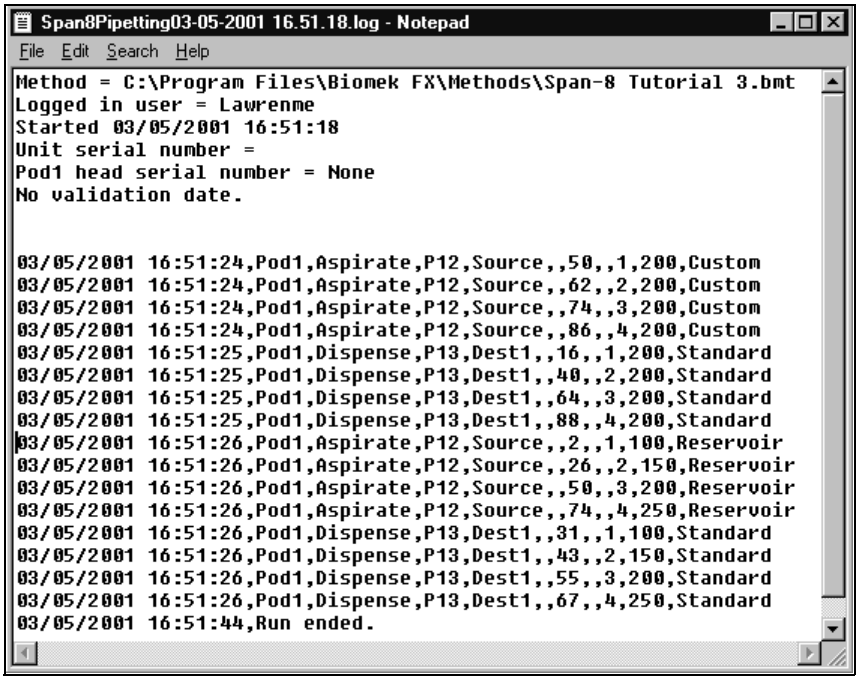


Figure 26-5. Span8Pipetting Log viewed in Notepad

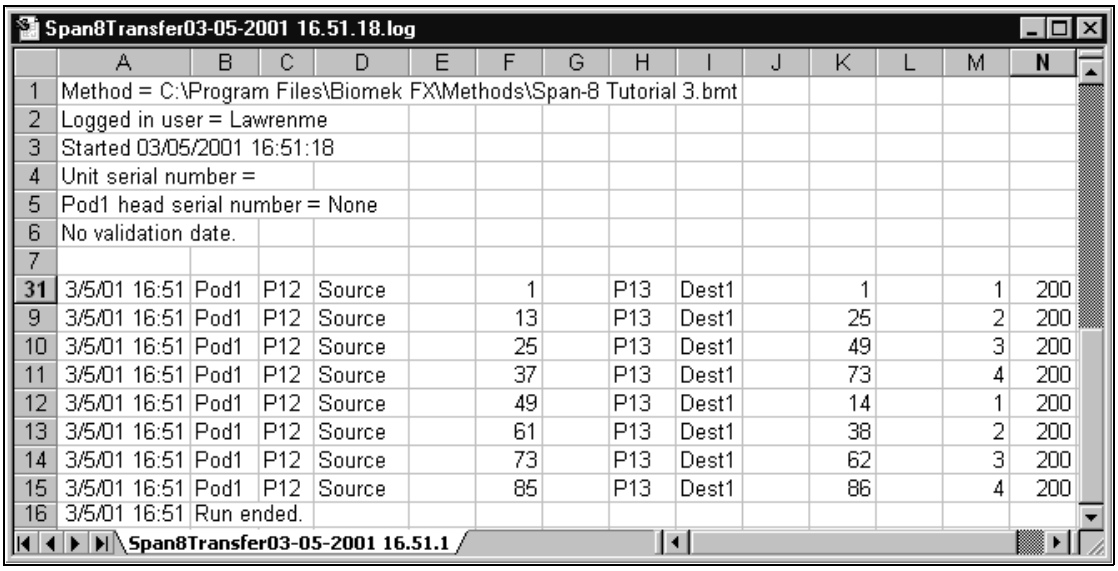


Figure 26-6. Span8Transfer Log viewed in Microsoft Excel

27 Using Manual Control

27.1 Overview

Manual Control and Advanced Manual Control are used to control:

- Movement of the bridge, head, and gripper independently of a method.
- Pod when framing the deck or gripper and recovering from errors.
- Device Controllers and ALPs on a Biomek FX or Biomek NX manually.
- Devices on a Biomek 3000 manually.

For information on manually controlling Biomek instruments, ALPs, or other devices through Manual Control, refer to the appropriate hardware user's manual:

- ***FX*** — *Biomek® FX Laboratory Automation Workstation User's Manual*
- ***3000*** — *Biomek® 3000 Laboratory Automation Workstation User's Manual*
- ***NX-MC*** — *Biomek® NX Multichannel Laboratory Automation Workstation User's Manual*
- ***NX-S8*** — *Biomek® NX Span-8 Laboratory Automation Workstation User's Manual*

Refer to the *ALPs User's Manual* or the appropriate integration manual for information on using Manual Control with specific ALPs or devices.

27.2 Accessing Manual Control

To open Manual Control, choose **Instrument>Manual Control**. An Information dialog (Figure 27-1) appears briefly as the connection is made with the Biomek instrument, immediately followed by Manual Control (Figure 27-2).

Note: Manual Control is available only when a method is not being executed. If a need for manual control is realized during a method run, stop the method using the Stop button or Snap Continuation button (refer to Chapter 25.11.2, *Snapping a Continuation*) on the toolbar before accessing Manual Control.

- ***3000*** — Snapping a Continuation is not available.

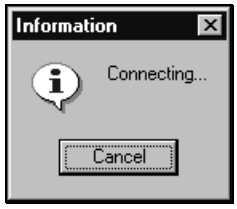


Figure 27-1. Confirms Manual Control is connecting

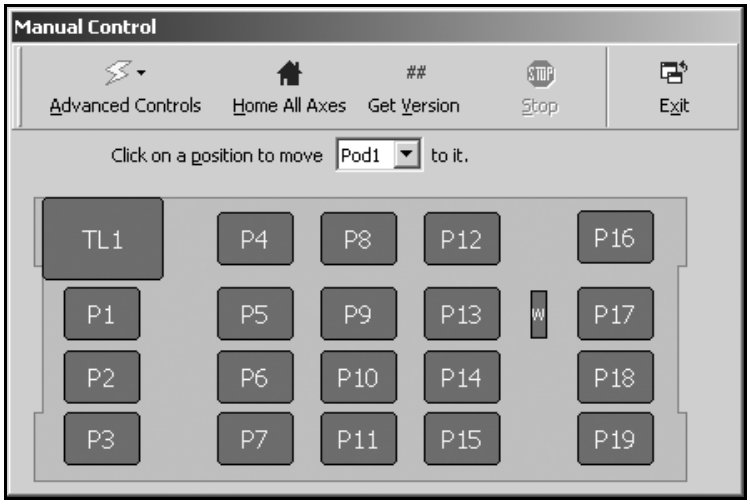


Figure 27-2. Manual Control

27.3 Understanding the Options in Manual Control

Table 27-1 lists and describes the options in Manual Control:

Table 27-1. Manual Control Options

Option	Description
Advanced Controls	Accesses Advanced Manual Control which allows a pod, ALP, or device to be selected. Refer to the specific hardware manual for details on using Advanced Manual Control for a device.
Home All Axes	Gives the instrument a point of reference from which to make subsequent moves. For a single-pod system, home position is left, back. For a dual-pod system, home position for the first (left) pod is left, back and for the second (right) pod is right, back. **Note:** Pods should be homed each time the instrument is powered on. Depending on the type of pods on the system, a Warning appears. After confirming that the actions have been addressed properly, choose **OK**.
Get Version	Shows the current firmware version for installed devices, pods, and devices (Figure 27-3).
Stop	Stops a pod once movement has started after selecting the desired pod from Click on a position to move.
Click on a position to move	Moves the pod to a specific deck position after selecting the desired pod. Manual Control moves the pod to the top of the Z axis, then centers it over the selected position.
Exit	Closes Manual Control.

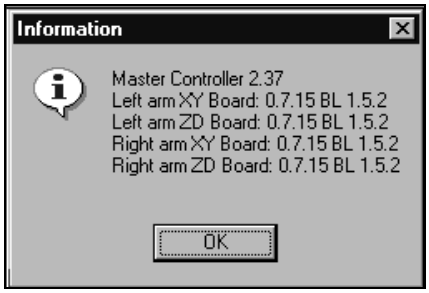


Figure 27-3. Information displaying firmware version

28 Scripting

28.1 Overview

The Biomek scripting feature is based on Visual Basic Scripting, a subset of the Microsoft® Visual Basic programming language. Any Visual Basic Scripting code can be interpreted by Biomek Software and may be included in a method.

Note: For more Visual Basic Scripting information, go to http://msdn.microsoft.com/scripting.

The Advanced Step Palette provides a Script step and a Scripted Let step, which provide a configuration area in which code can be entered. These steps invoke a Visual Basic Scripting Engine that evaluates the code.

The Script step and Scripted Let step expose objects that are used internally by Biomek Software. This is accomplished through the use of Microsoft's Component Object Model (COM).

Data from a reader or LIMS file in a .csv file format may be translated into a data set using scripting. The data sets created from scripting behave like any other data set created in the Create Data Set step, from sample IDs in the Instrument Setup step, or in the SILAS step.

The sections in this chapter include:

- refer to Section 28.2, *Using the Script Steps*
- refer to Section 28.3, *Scripting Data Sets*

28.2 Using the Script Steps

A Script step, available from the Advanced Step Palette, provides a configuration area in which a description of the script step may be entered, and lines of code may be written.

Note: Refer to Section 17.8, *Script Step*, for information on configuring a Script step.

A Scripted Let step is also available from the Advanced Step Palette and provides a configuration area in which a description of the script step may be entered, and lines of code may be written. However, two additional commands may be entered in the Scripted Let step that allow for variables created in the script to be extended outside of the script and used in configuring other steps in the method. These two new commands are:

- Extend — sets the variable name to the specified value for all steps contained within the Scripted Let. The proper syntax for Extend is **Extend "Variable Name", Value**.
- WeakExtend — sets the variable name to the specified value for all steps contained within the Scripted Let step if the specified variable does not already have a value. This is similar to a Let variable with Overridable selected. The proper syntax for WeakExtend is **WeakExtend "Variable Name", Value**.

Note: Refer to Section 17.9, *Scripted Let Step*, for information on configuring a Scripted Let step.

28.3 Scripting Data Sets

Note: The information in this section requires an advanced skill level; it is not intended to offer instructions on learning VBScript. Scripting data sets is not supported by Beckman Coulter Service Engineers; however, information is available at http://msdn.microsoft.com/library/default.asp and in VBScript in a Nutshell: A Desktop Quick Reference, 2nd Edition, Matt Childs, Paul Lomax, and Ron Petrusha 2003, O'Reilly & Associates, Inc.

Data from a reader or LIMS file in a .csv file format may be translated into a data set using scripting. The data sets created from scripting behave like any other data set created in the Create Data Set step, from sample IDs in the Instrument Setup step, or in the SILAS step.

The procedure (refer to Section 28.3.1, *Procedure to Script Data Sets*) to script data sets includes:

- Creating a new data set to hold imported data.
- Opening a .csv file.
- Translating data from a .csv file to a new data set called Sample ID.
- Placing the translated data (the new data set called Sample ID) into the new data set to hold imported data.

28.3.1 Procedure to Script Data Sets

Execute the following script code:

```
' Create a new Data Set to hold our imported data.
Set DestinationDataSet = Labware("P5").DataSets.Add("SampleID")
' Create the Windows file system object. This object will allow us
' to find our data file on the disk.
Set FileSystemObject = CreateObject("Scripting.FileSystemObject")
' Check to see if the file is on the disk.
If Not FileSystemObject.FileExists("c:\demodata.csv") Then
  ' Call the system's error creator. This will cause a sensible
  ' error message to be shown to the person running the method.
  ' The first parameter is an error code number. 500 was chosen
  ' because it is not already in use by Windows.
  ' The second parameter is the source of the error.
  ' The third parameter is the description of the error.
  Err.Raise 500, "My Import Script", "File does not exist."
End If
' Open the data file.
Set FileStream = FileSystemObject.OpenTextFile("c:\demodata.csv")
' Loop over the rows in the file.
For i = 0 To 7
  ' Read a line out of the file.
  RowLine = File.Stream.ReadLine
  ' Split the values in the line into an array of values, using
  ' the comma as a delimiter.
  ' Note that the array contains values 0, 1, ..., 11.
  RowDataArray = Split(Rowline, ",")
  ' Loop over the columns in the row.
  For j = 0 To 11
    ' Put the data from the array into our new Data Set.
    ' The expression "(i*12) + (j+1)" converts from the 0-based
    ' loop variables to well identifiers.
    DestinationDataSet((i*12) + (j+1)) = RowDataArray(j)
  Next ' end the column loop
Next ' end the row loop
' Close the file when we're done.
FileStream.Close
```

29 Changing Window Appearance

29.1 Overview

The Biomek main editor (Figure 29-1) contains the basic tools necessary to create and run methods; however, there may be times when additional tools are needed. To address this situation, steps and step palettes may be added to the main editor as necessary. These additional steps and step palettes provide more functionality when creating and running methods. By using Preferences (Figure 29-12) and Step Palette Builder (Figure 29-2), the look of the main editor can be changed to fit the needs of the laboratory.

Preferences is used to alter the Method View and change the size of the steps (or step buttons) in a step palette. For example, graph lines and + and - buttons may be added to the Method View (Figure 29-1), and toolbar and step palette positions may be saved automatically when the appropriate settings are checked in Preferences.

The Step Palette Builder allows the addition, removal, and manipulation of steps on the step palettes. Steps may be added to any step palette or combined into a new step palette. Individual devices, such as an incubator, operating with a SILAS module must be added to a step palette after the SILAS module has been installed so the device can be used in a method and controlled by Biomek Software.

Note: The Current Deck Display can be manipulated like a toolbar, except it can be docked only below the user interface area.

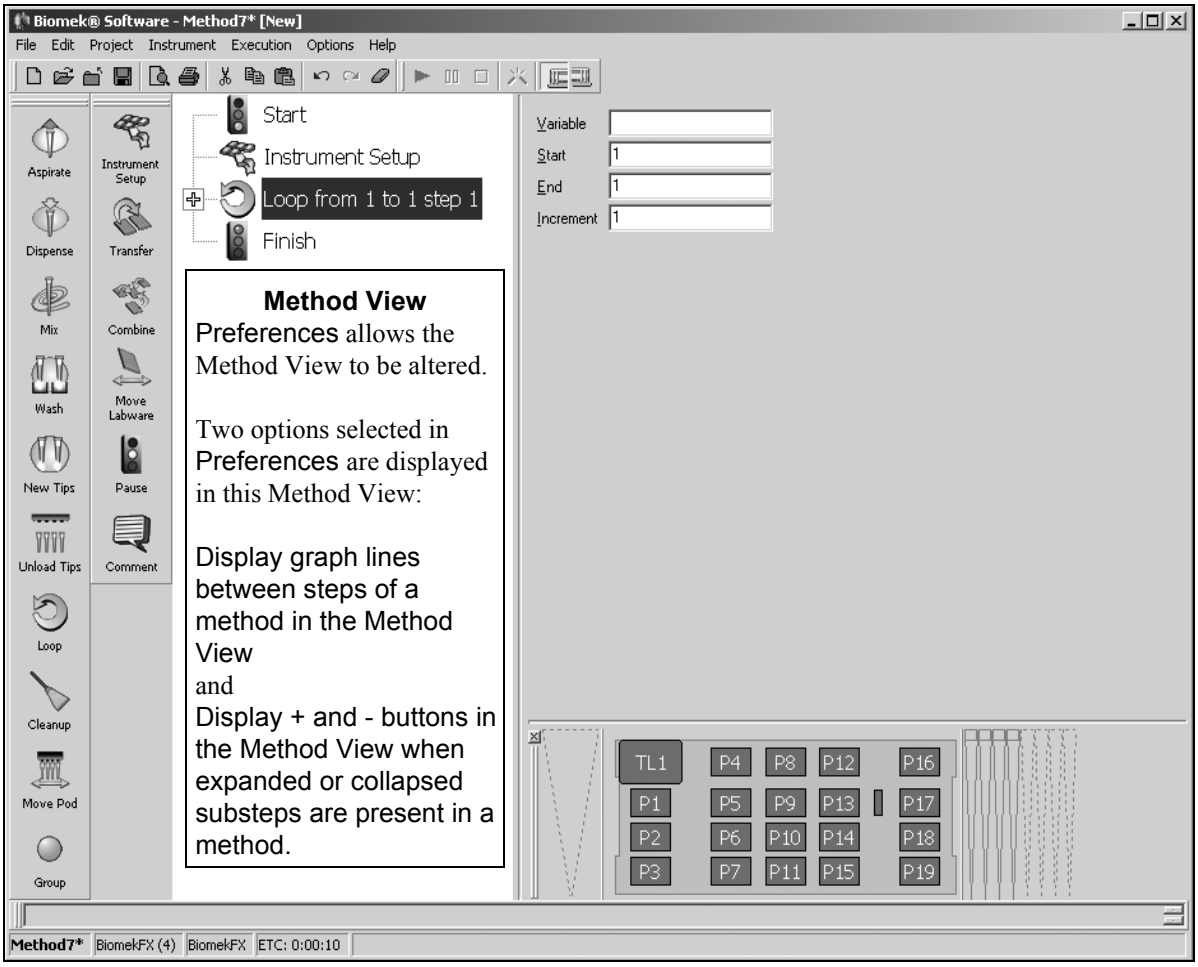


Figure 29-1. Main editor for a Biomek FX

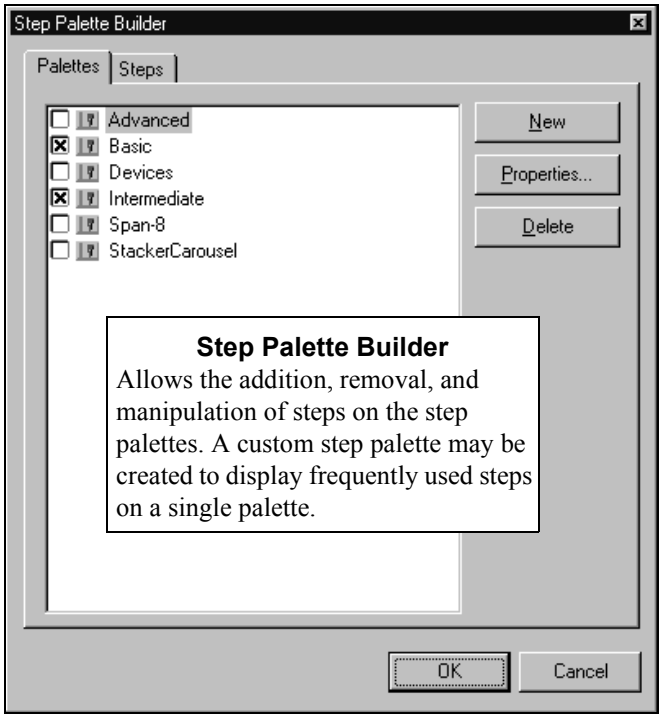


Figure 29-2. Step Palette Builder

Note: The available step palettes in the Step Palette Builder are based on the instrument.

- ***3000*** — the Span-8 Step Palette is available because the Serial Dilution, Transfer from File, and Define Pattern steps may be used with the instrument.

29.2 Changing Display Preferences

Preferences allows the main editor appearance to be customized. Preferences allows the customization of the main editor using options organized under General, View, and Errors.

To customize the appearance of the main editor:

1. Choose **Options>Preferences...**. Preferences appears (Figure 29-3).

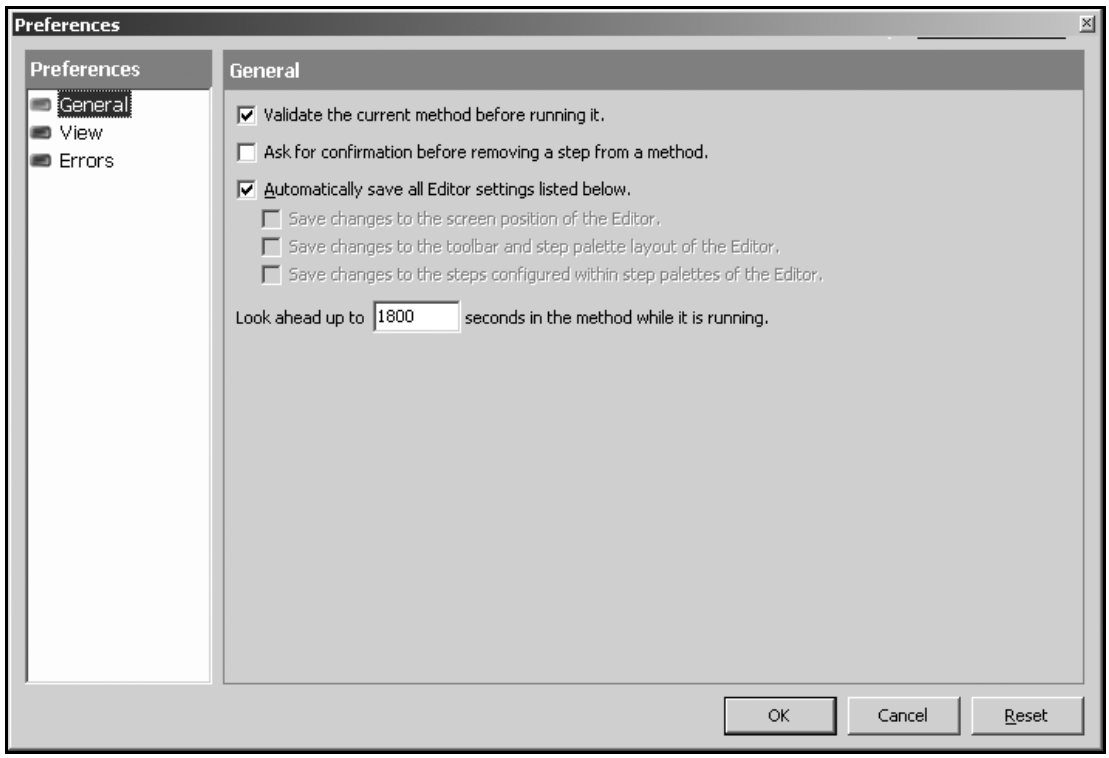


Figure 29-3. Preferences

2. Choose **General** to configure options concerning validating and saving methods (refer to Section 29.2.1, *Configuring General Options*).

   OR

   Choose **View** to configure options concerning the appearance of the Method View (refer to Section 29.2.2, *Configuring View Options*).

   OR

   Choose **Errors** to configure options concerning the notifications of errors (refer to Section 29.2.3, *Configuring Errors Options*).

29.2.1 Configuring General Options

General options concern validating and saving methods.

To configure General options:

1. From Preferences, highlight **General** (Figure 29-3).
2. Check the desired options using Table 29-1.
3. Choose **OK** to save the checked options.

   OR

   Choose **Cancel** to cancel the checked options.

   OR

   Choose **Reset** to reset all customizations, including custom labware, toolbar/palette organization, options chosen in Preferences, and position of the main editor.

Table 29-1. General options

Option	Description
Validate the current method before running it.	Simulates methods internally to test for errors before the method is run. If no errors are detected, the method is executed. If an error is detected, the process stops and an error message displays information about the error.
Ask for confirmation before removing a step from a method.	Displays a confirmation prompt when deleting a step from a method (Figure 29-4).
Automatically save all Editor settings listed below.	Automatically saves the following three settings. (Enabled by default.)
Save changes to the screen position of the Editor.	When checked, automatically saves the size and position of the editor on the screen. (Available when Automatically save all Editor settings listed below is not selected.)
Save changes to the toolbar and step palette layout of the Editor.	When checked, automatically saves toolbar and step palette size, arrangement, and location. (Available when Automatically save all Editor settings listed below is not selected.)

Table 29-1. General options (Continued)

Option	Description
Save changes to the steps configured within step palettes of the Editor.	When checked, automatically saves steps on step palette (modified by Palette Builder).(Available when Automatically save all Editor settings listed below is not selected.)
Look ahead up to [1800] seconds in the method while it is running.	To prevent the system from bogging down due to unnecessary memory consumption, the software translate the steps of the method into "to do" lists of actions. This option prevents the software from bogging down by designating a length of time for suspending the translation process (refer to Section 25.3.2.1, *Using Look ahead up to [1800] seconds in the method while it is running*).

Note: When Automatically save all Editor settings listed below is not selected, and when Save changes to the screen position of the Editor, Save changes to the toolbar and step palette layout of the Editor, and Save changes to the steps configured within step palettes of the Editor are also not selected, the main editor opens at default size with the last saved configuration for the editor, toolbars, and palettes.

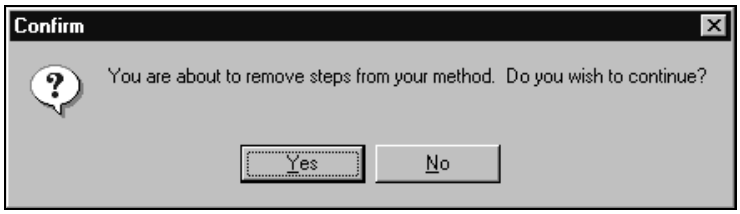


Figure 29-4. Confirm to delete steps from a method

29.2.2 Configuring View Options

View options concern the appearance of the Method View.

To configure View options:

1. From Preferences, highlight **View** (Figure 29-5).

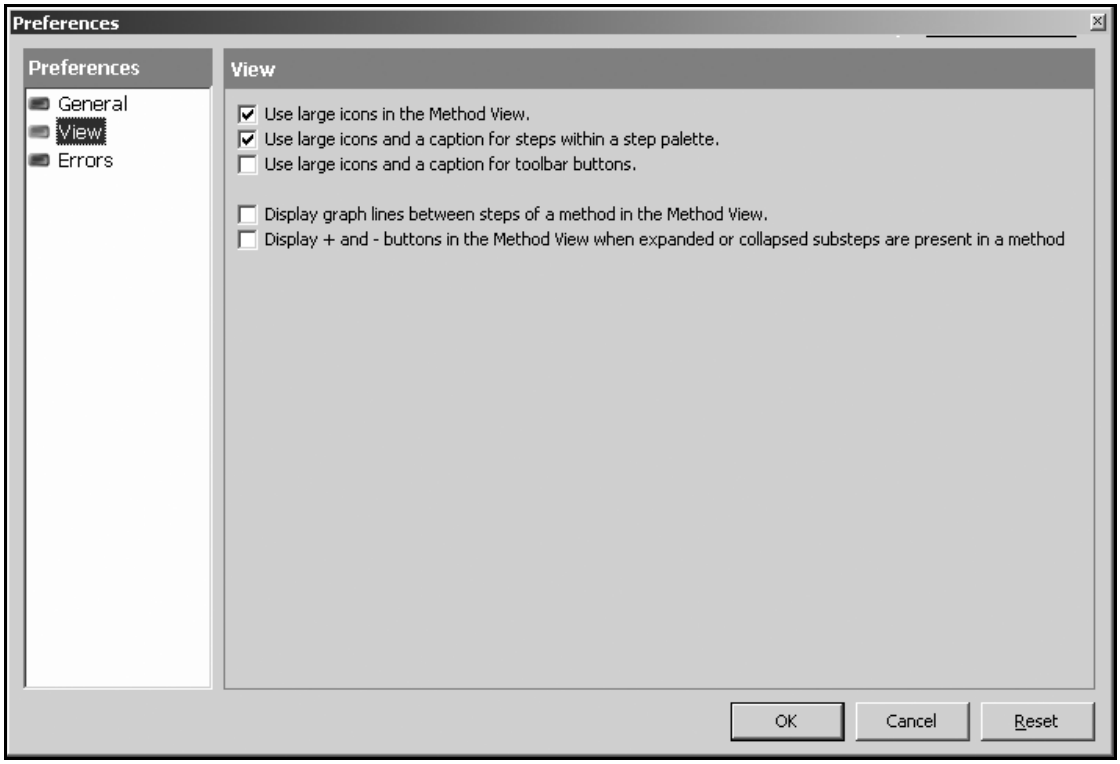


Figure 29-5. Preferences - View

2. Check the desired options using Table 29-2.
3. Choose **OK** to save the checked options.

   OR

   Choose **Cancel** to cancel the checked options.

   OR

   Choose **Reset** to reset all customizations, including custom labware, toolbar/palette organization, options chosen in Preferences, and position of the main editor.

Table 29-2. View Options

Option	Description
Use large icons in the Method View.	Displays text and icons in the Method View in a larger size. (Enabled by default.)
Use large icons and a caption for steps within a step palette.	Displays large icons with labels (descriptive text) under the steps on the step palettes. (Enabled by default.)
Use large icons and a caption for toolbar buttons.	Displays large toolbars with labels (descriptive text) when checked.
Display graph lines between steps of a method in the Method View.	Displays lines which connect steps in the Method View when checked.
Display + and - buttons in the Method View when expanded or collapsed substeps are present in a method.	Displays + and - in front of steps such as Loop which contain nested steps. Click the + or - to expand or collapse the main step.

29.2.3 Configuring Errors Options

Error options concern the notifications of errors. An option to play a .wav file when an error occurs is available while another option allows a program, such as an .exe file, to be run when an error occurs.

To configure Errors options:

1. From Preferences, highlight **Errors** (Figure 29-6).

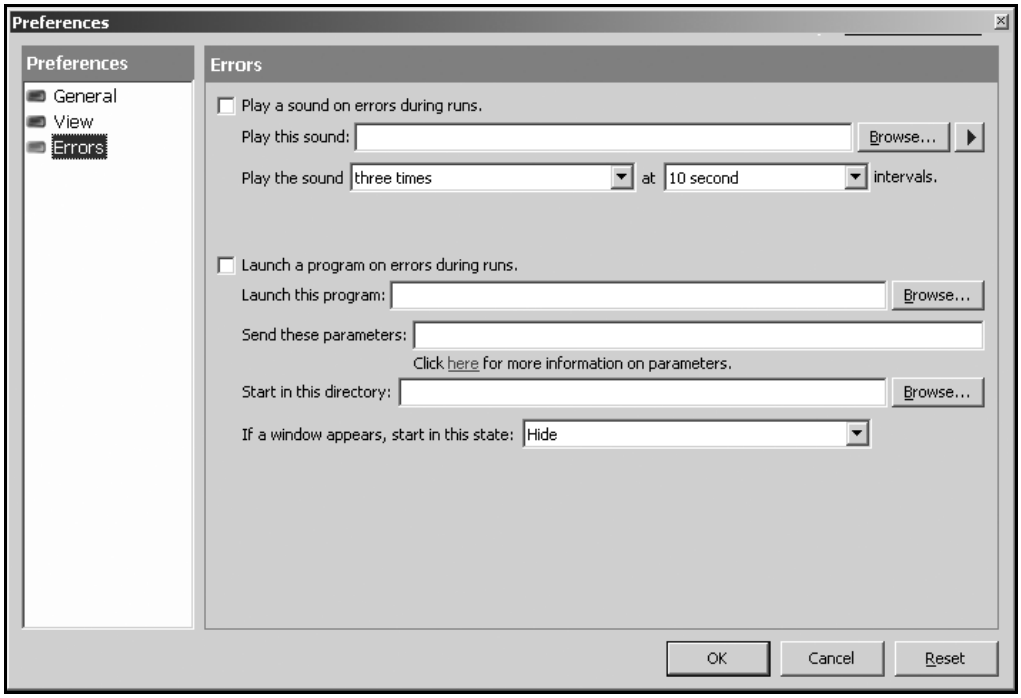


Figure 29-6. Preferences - Errors

2. Choose **Play a sound on errors during runs** to run a .wav file when an error message appears.
3. In Play this sound, use **Browse** to find the desired .wav file.
4. Choose the desired .wav file. The desired file appears in Play this sound.
5. From Play the sound, choose one of the following options from the drop-down menu to play the sound the desired number of times when an error message appears:
    - once
    - twice
    - three times
    - repeatedly until dismissed

6. From intervals, choose one of the following options from the drop-down menu to play the sound at the desired intervals when an error message appears:
   - 10 second
   - 1
   - 5
   - 30
   - 1 minute
   - 5 minute
7. Choose **Launch a program on errors during runs** to run an .exe file when an error message appears.
8. In Launch this program, use Browse to find the desired .exe file.
9. Choose the desired file. The desired file appears in Launch this program.
10. In Send these parameters, enter the desired parameters using the information displayed in Figure 29-7.

Note: Choose **click here** to display Parameter Information (Figure 29-7). Choose **OK** to close Parameter Information. Highlighting the Parameter and Value and choosing OK does not enter the desired parameter; the desired parameters must be manually entered in Send these parameters.

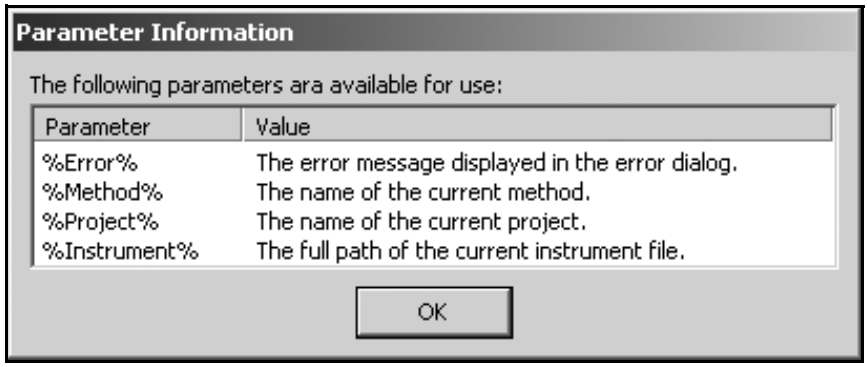


Figure 29-7. Parameter Information

11. In Start in this directory, use **Browse** to start browsing in the desired directory.
12. From If a window appears, start in this state, choose one of the following options from the drop-down menu to display the style of the program:
    - Don't care — the message appears in the default style of the program.
    - Maximize — the message appears in the maximized state of the program.
    - Minimize — the message appears in the minimized state of the program.
13. Choose **OK** to save the checked options.

    OR

    Choose **Cancel** to cancel the checked options.

    OR

    Choose **Reset** to reset all customizations, including custom labware, toolbar organization, options chosen in Preferences, and position of the main editor.

29.3 Toggling Toolbars and Step Palettes

The Biomek main editor provides toolbars and step palettes to allow quick access to method-building tools. Descriptions of the options in Toolbars are shown in Table 29-3.

To toggle toolbars and step palettes on and off:

1. Choose **Options>Toolbars**. A submenu appears listing the toolbars and step palettes (Figure 29-8).

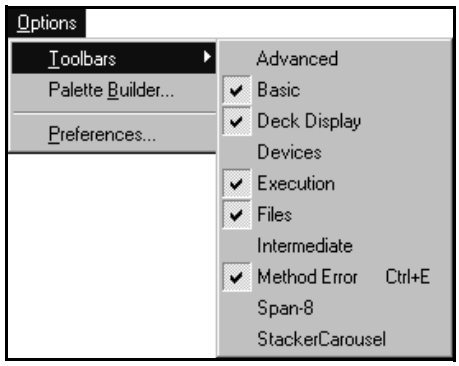


Figure 29-8. Options for step palettes and toolbars

Note: The available step palettes in the Step Palette Builder are based on the instrument.

- ***3000*** — the Span-8 Step Palette is available because the Serial Dilution, Transfer from File, and Define Pattern steps may be used with the instrument.

Note: Any custom step palettes created with the Step Palette Builder also appear in the submenu (refer to Section 29.5.4, *Creating a New Step Palette*).

OR

Right-click in a gray area around the toolbars or step palettes. A menu listing only the step palettes appears (Figure 29-9).

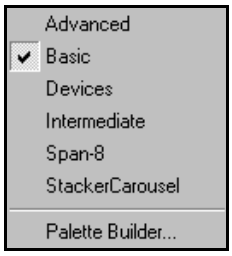


Figure 29-9. Step palette menu for a Biomek FX

Note: The step palette menu is based on the instrument; for example.

Note: Any custom step palettes created with the Step Palette Builder also appear in the submenu (refer to Section 29.5.4, *Creating a New Step Palette*).

2. Choose the desired toolbar or step palette to toggle it on or off. The corresponding toolbar or step palette appears or is hidden from view.

Note: A check to the left of a toolbar or step palette in **Options>Toolbars** indicates that it is currently displayed.

Note: Use the Step Palette Builder as an alternative method for displaying and hiding step palettes (refer to Section 29.5.2, *Displaying and Hiding Step Palettes*).

Table 29-3. Toolbar Options

Option	Description
Advanced	Toggles on or off the Advanced Step Palette.
Basic	Toggles on or off the Basic Step Palette (Figure 29-10).
Biomek3000	Toggles on or off the Biomek 3000 Step Palette.
Deck Display	Toggles on or off the Deck Display (Figure 29-10).
Devices	Toggles on or off the Devices Step Palette.
Execution	Toggles on or off the part of the toolbar that is associated with the running of methods (Figure 29-10).
Files	Toggles on or off the part of the toolbar that is associated with the building of methods (Figure 29-10).
Intermediate	Toggles on or off the Intermediate Step Palette.
Method Error	Toggles on or off the description of errors (Figure 29-10).
Span-8	Toggles on or off the Span-8 Step Palette. ➢ ***3000*** — the Span-8 Step Palette is available because the Serial Dilution, Transfer from File, and Define Pattern steps may be used with the instrument.
Specialty	Toggles on or off the Specialty Step Palette.
StackerCarousel	Toggles on or off the Stacker Carousel Step Palette.

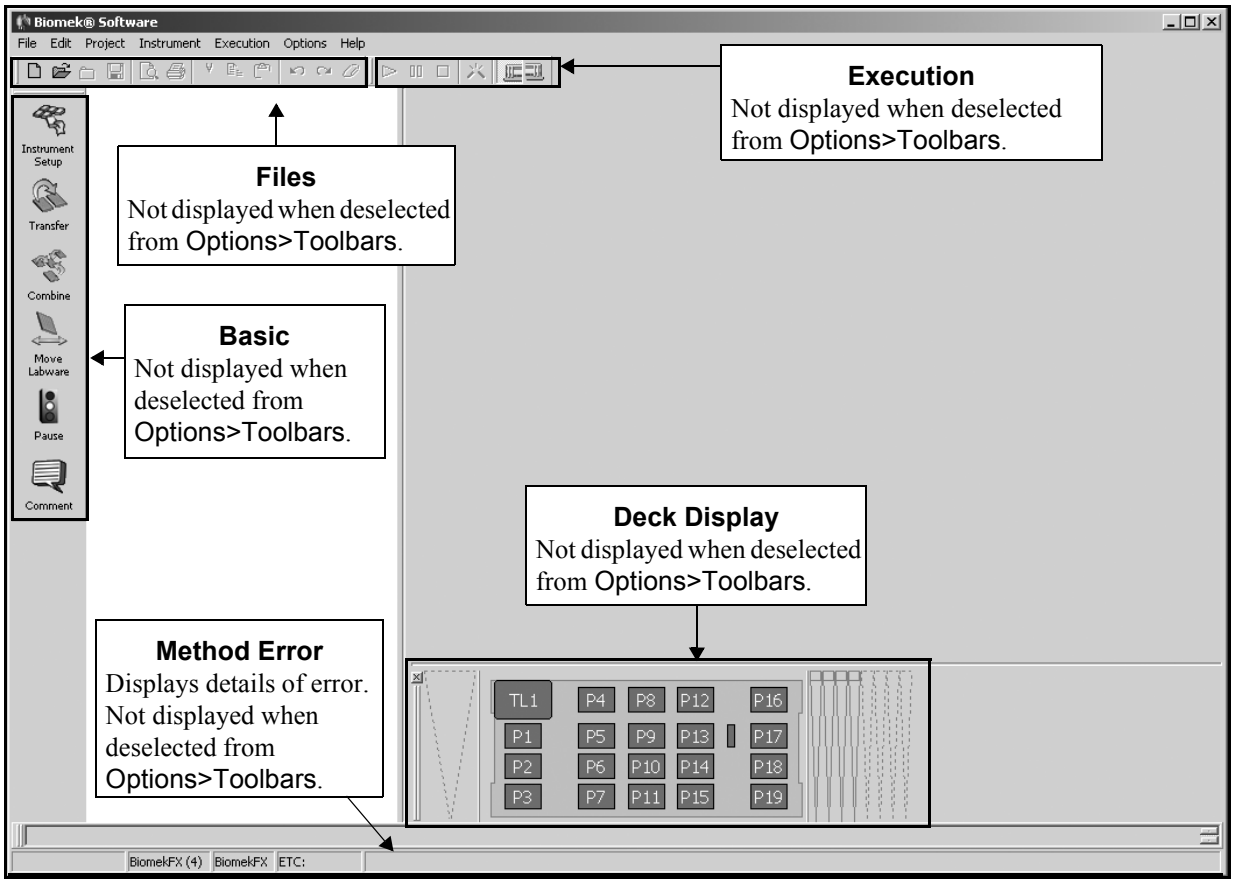


Figure 29-10. Main editor with default toolbar options displayed

29.4 Customizing Step Palettes

Customize a step palette to add custom steps, change the view of the step palettes, or modify tool tips and labels of any step.

29.4.1 Displaying Large Step Palette and Toolbar Views

Labels for toolbars and step palettes can be displayed using Preferences. The Large Step Palette View and the Large Toolbar View display labels for the steps and tools (Figure 29-11).

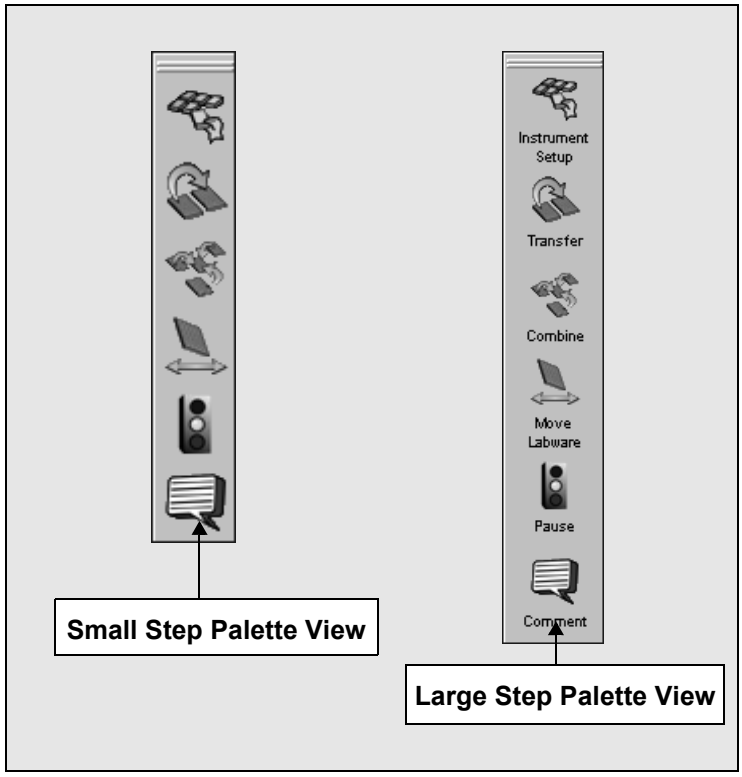


Figure 29-11. Step palette views with and without labels

To toggle the step palette view:

1. Choose **Options>Preferences>View**. Figure 29-12 appears.

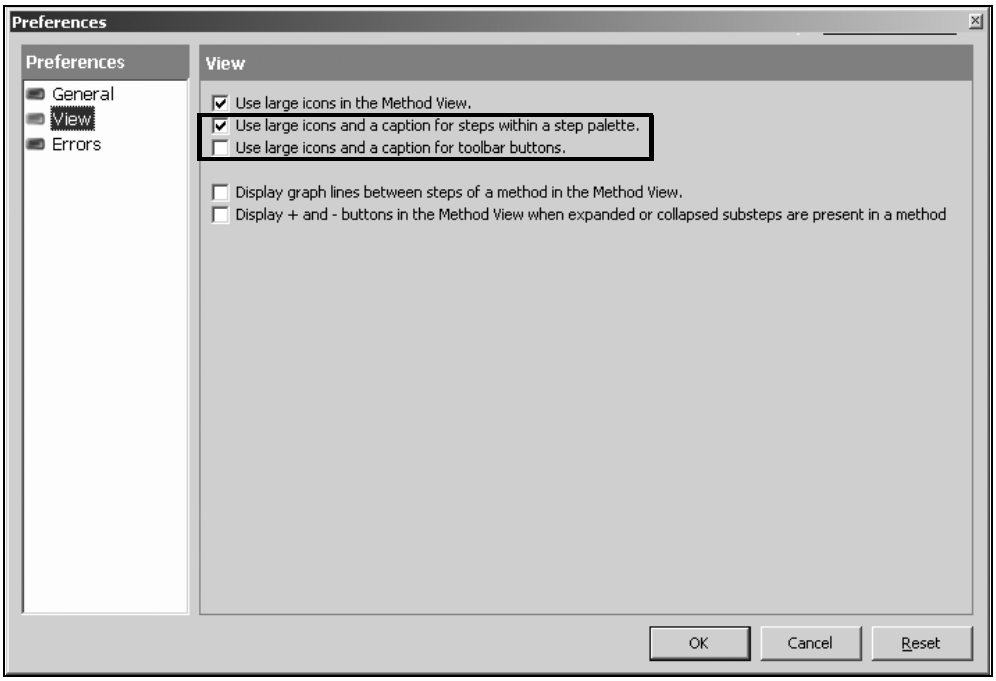


Figure 29-12. Preferences — main editor setting options

2. Choose **Use large icons and a caption for steps within a step palette** to toggle the step labels (Figure 29-12).

   Note: The default for Use large icons and a caption for steps within a step palette is On.

3. Choose **Use large icons and a caption for toolbar buttons** to toggle the toolbar labels.

   Note: The default for Use large icons and a caption for toolbar buttons is Off.

4. Choose **OK**.

29.4.2 Changing Step Properties

Change the properties associated with each step to make the step purpose easier to identify, or to distinguish custom, configured steps from standard steps. Each step has three properties:

- Tool Tip — brief tip on the steps usage that displays when the mouse pointer hovers over the step.
- Label — text describing operations of a step.
- Bitmap — graphic displayed on the step button.

To change step properties:

1. On the step palette, right-click on the desired step.
2. Choose **Properties**. Step Properties appears (Figure 29-13).

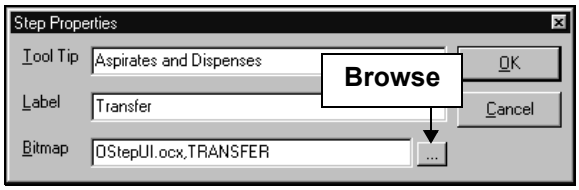


Figure 29-13. Step Properties

3. In Tool Tip, enter a new **Tool Tip**.
4. In Label, enter a new **Label**.
5. In Bitmap, choose a different graphic for the step button by clicking on **Browse**, and selecting the desired bitmap.
6. Choose **Open** to accept the new bitmap and return to Step Properties.
7. Choose **OK** to save changes to the Step Properties and return to the main editor.

29.4.3 Modifying a Step Caption in Method View

A step caption may be modified in the Method View. This allows differentiation of the steps by their captions.

To change a step caption in the Method View:

1. Highlight the desired step in the Method View.
2. Right-click on the step to open a menu.
3. Select **Change Caption**. Edit Step Caption appears (Figure 29-14).

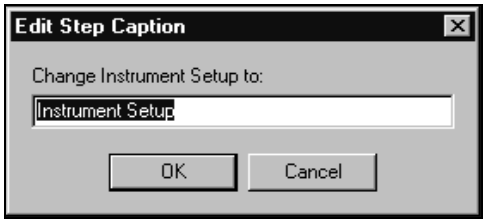


Figure 29-14. Change the step caption in Edit Step Caption

4. Enter the new step caption for the step.
5. Choose **OK**. The new caption appears at the appropriate spot in the Method View.

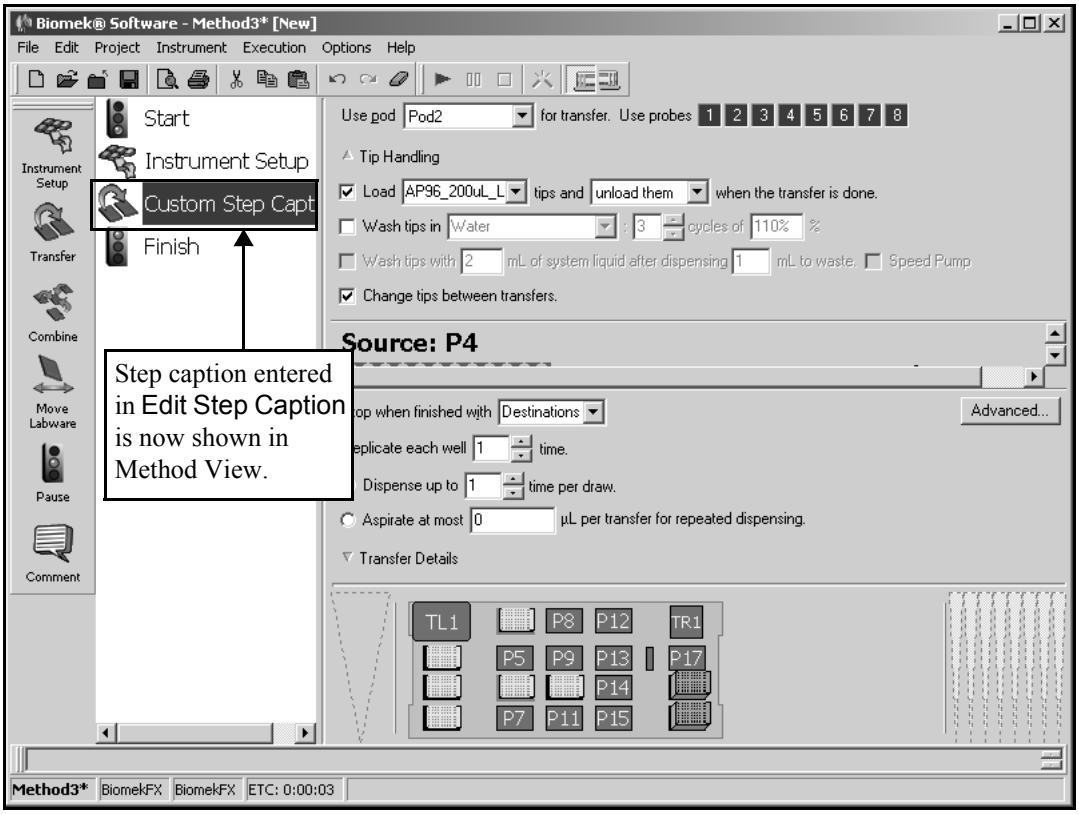


Figure 29-15. Modified step caption in Method View

29.5 Using the Step Palette Builder

The Step Palette Builder is used to create, delete, and modify step palettes. If a step is no longer needed on a step palette, it can be removed easily with the Step Palette Builder.

Use the Step Palette Builder to:

- Display a step palette.
- Hide a step palette.
- Add steps.
- Remove steps.
- Rearrange steps.
- Create a step palette.
- Modify step palette properties.
- Delete a step palette.

29.5.1 Accessing the Step Palette Builder

To access the Step Palette Builder:

Choose **Options>Palette Builder...**.Step Palette Builder appears (Figure 29-16).

OR

1. Right-click in a gray area around the toolbars or step palettes. A menu listing available step palettes appears (Figure 29-9).
2. Choose **Palette Builder...**.Step Palette Builder appears (Figure 29-16).

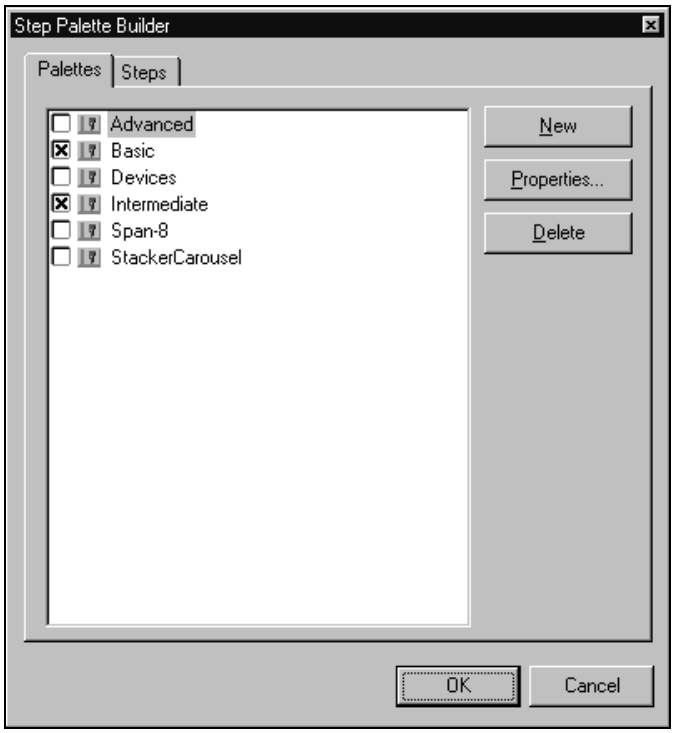


Figure 29-16. Step Palette Builder

Note: The Step Palette Builder is based on the instrument.

- ***3000*** — the Span-8 Step Palette is available because the Serial Dilution, Transfer from File, and Define Pattern steps may be used with the instrument.

29.5.2 Displaying and Hiding Step Palettes

Display and hide step palettes using the Step Palette Builder.

To display or hide a step palette:

1. Choose **Options>Palette Builder...**.Step Palette Builder appears (Figure 29-16).

   OR

   Right-click in a gray area around the toolbars or step palettes. A menu listing available step palettes appears (Figure 29-9). Choose **Palette Builder...**.Step Palette Builder appears (Figure 29-16).

2. In the Step Palette Builder, click on the check box to the left of the desired palette to toggle the display on and off.

3. Choose **OK**. The selected step palettes are displayed or hidden from the Biomek main editor.

Note: As an alternative method for toggling a step palette on or off, use the Options>Toolbars menu (refer to Section 29.3, *Toggling Toolbars and Step Palettes*). This alternative method is available only when Palette Builder is not open.

29.5.3 Customizing Step Palettes

There are two main sources for steps added to step palettes:

- With Step Palette Builder not open, steps can be moved from the Method View onto a step palette.
- With Step Palette Builder open, steps can be moved from the Step Palette Builder to a step palette or moved between palettes.

Note: In order to use a SILAS module, such as the bar code reader, it must be placed on a step palette.

29.5.3.1 Adding Non-Configured Steps to a Step Palette

To add steps to a step palette:

1. Choose **Options>Palette Builder...**.Step Palette Builder appears (Figure 29-16).

   OR

   Right-click in a gray area around the toolbars or step palettes. A menu listing available step palettes appears (Figure 29-9). Choose **Palette Builder...**.Step Palette Builder appears (Figure 29-16).

2. Choose the **Steps** tab (Figure 29-17).

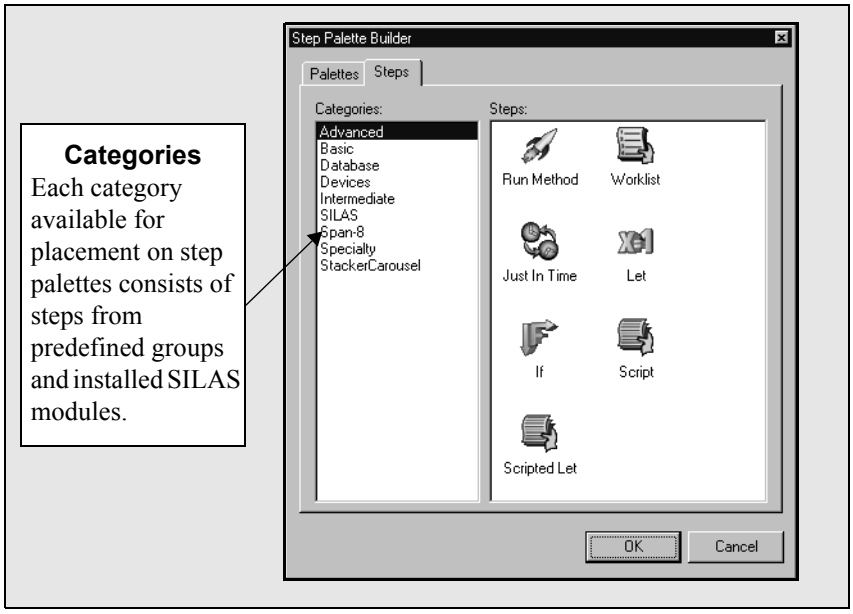


Figure 29-17. Step Palette — Steps tab

3. In Categories, choose the desired category of steps. Steps from the selected category appear on the right side of the Step Palette Builder.

   Note: Multiple selections can be highlighted at once in the Steps tab by holding down Ctrl or Shift.

4. Drag the desired step from Steps to a step palette on the main editor. The step is added to the step palette.

   OR

   Drag the desired step from one palette to another on the main editor.

5. From the Step Palette Builder, choose **OK**.

29.5.3.2 Adding Configured Steps to a Step Palette

If a step configuration used in a method is to be used several times in various methods, add it to a step palette to save time during the method building process. By adding a configured step, any subsequent uses of the same configuration are added to a method easily.

To add configured steps to a step palette:

1. Configure the step in the Method View.
2. Highlight the step to add to the step palette.
3. Drag the step to the desired step palette. The addition of the step must be confirmed before it is added to the palette (Figure 29-18).

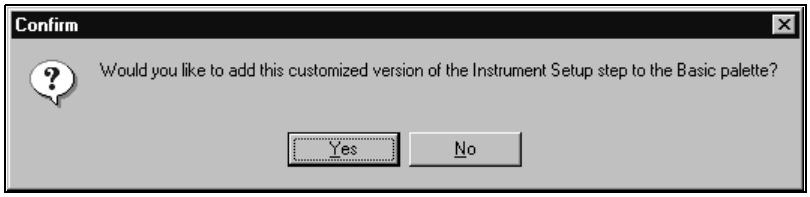


Figure 29-18. Confirmation for adding a step to a step palette

29.5.3.3 Rearranging Steps on a Step Palette

To rearrange steps on a step palette:

1. Choose **Options>Palette Builder...**.Step Palette Builder appears (Figure 30-12).

   OR

   Right-click in a gray area around the toolbars or step palettes. A menu listing available step palettes appears (Figure 29-9). Choose **Palette Builder...**.Step Palette Builder appears (Figure 29-16).

2. Drag and drop the desired step on the step below the desired location on the palette. The step inserts itself above the step on which it was dropped.
3. From the Step Palette Builder, choose **OK**.

29.5.3.4 Removing Steps From a Step Palette

Remove steps no longer needed to keep step palettes manageable.

To remove steps from a step palette:

1. Choose **Options>Palette Builder...**.Step Palette Builder appears (Figure 29-16).

   OR

   Right-click in a gray area around the toolbars or step palettes. A menu listing available step palettes appears (Figure 29-9). Choose **Palette Builder...**. Step Palette Builder appears (Figure 29-16).

2. Drag and drop the desired step to a location where a step palette is not present.
3. From the Step Palette Builder, choose **OK**.

29.5.4 Creating a New Step Palette

Create custom step palettes to display frequently used or commonly used configured steps on a single palette.

To create a step palette:

1. Choose **Options>Palette Builder...**.Step Palette Builder appears (Figure 29-16).

   OR

   Right-click in a gray area around the toolbars or step palettes. A menu listing available step palettes appears (Figure 29-9). Choose **Palette Builder...**.Step Palette Builder appears (Figure 29-16).

2. Choose **New**. A new step palette appears in the upper left corner of the main editor (Figure 29-19).

Figure 29-19. New Step Palette

3. Change the new palettes properties (refer to Section 29.5.5, *Modifying Step Palette Properties*).
4. Add steps to the step palette (refer to Section 29.5.3.1, *Adding Non-Configured Steps to a Step Palette*).
5. From the Step Palette Builder, choose **OK**.

29.5.5 Modifying Step Palette Properties

The Step Palette Properties is the Name of the palette that appears in the Step Palette Builder and in Options>Toolbars.

To change a step palettes properties:

1. Choose **Options>Palette Builder...**.Step Palette Builder appears (Figure 29-16).

   OR

   Right-click in a gray area around the toolbars or step palettes. A menu listing available step palettes appears (Figure 29-9). Choose **Palette Builder...**.Step Palette Builder appears (Figure 29-16).

2. Select the desired palette.
3. Choose **Properties....** Palette Properties appears (Figure 29-20).

Figure 29-20. Palette Properties

4. Type a descriptive name for the step palette.

   Note: All alphanumeric and non-alphanumeric characters are allowed in palette names.

5. From Palette Properties, choose **OK** to save the name.
6. From Step Palette Builder, choose **OK**.

29.5.6 Deleting a Step Palette

Delete any step palettes that are no longer needed.

To delete a step palette:

1. Choose **Options>Palette Builder...**.Step Palette Builder appears (Figure 29-16).

   OR

   Right-click in a gray area around the toolbars or step palettes. A menu listing available step palettes appears (Figure 29-9). Choose **Palette Builder...**.Step Palette Builder appears (Figure 29-16).

2. Select the desired palette.
3. Choose **Delete**. The step palette is removed from the main editor.

   Note: Deleting a step palette cannot be undone. There is no confirmation for deleting a step palette. If a step palette is accidentally deleted, choose **Cancel** in Step Palette Builder.

4. Choose **OK**.

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