Affymetrix®
Laboratory Information Management System (LIMS)

LIMS Manager User's Guide

Version 3.0

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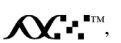
Affymetrix®, GeneChip®, EASI™,  ,  ,  , HuSNP™, GenFlex™, Jaguar™, MicroDB™, 417™, 418™, 427™, 428™, Pin-and-Ring™, Flying Objective™, NetAffx™ and CustomExpress™ are trademarks owned or used by Affymetrix, Inc.

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Contents

1

Chapter 1

Getting Started

Welcome to Affymetrix® Laboratory Information Management System (LIMS). LIMS Manager v 3.0 is a stand-alone database application designed to assist the system administrator in managing the data created by Affymetrix® Microarray Suite (formerly GeneChip® Analysis Suite). LIMS Manager imports and archives probe array data, provides security and allows the system administrator to assign users and set user privileges.

This chapter provides you with the information you need to get started with Affymetrix® LIMS Manager, including system requirements and installation procedures. Additionally, an overview of LIMS Manager and other Affymetrix® software applications is presented.

System Requirements

To use Affymetrix® LIMS Manager your system must meet the following hardware and software minimum requirements:

- 500 MHz Processor
- 128 MB RAM
- Microsoft Windows NT® or Windows 2000 Workstation
- Available space on hard drive = 1 GB
- Microsoft® Internet Explorer 5.5 with SP2
- Microsoft® Data Access Components (MDAC) 2.5 SP1

Installing LIMS Manager

During the installation of Affymetrix® LIMS Manager 3.0 previous version(s) are not removed. If installed in the same directory, the installation program overwrites the previous version's files.

After completing the installation of LIMS Manager 3.0, the program asks you to reboot the system. Restart the computer. Upon logging in, the system registers information into the registry and displays a message on screen informing you that the installation has finished.

✔ Note

You must be logged in as administrator to install the LIMS Manager 3.0 software.

LIMS Manager 3.0 is not required to run MAS 5.0 in LIMS mode.

The screen captures depicted in this manual may not exactly match the windows displayed on your screen.

▲ WARNING

If at any time during the installation a dialog box with a red 'X' appears, this indicates that you logged on with a username that does not have the local administrative privileges required to install the software. Log out and log back in under a user name with proper privileges.

1. Insert the Affymetrix® LIMS 3.0 Client CD-ROM.

   If the autorun feature does not start the program:

   a. Click **Start** → **Run**.

   b. Type <*cd drive letter*>:\setup.exe.

   c. Click **OK**.

   ⇒ A splash screen is displayed, followed by the Welcome window **(Figure 1.1)**.

Figure 1.1
Welcome window

2. Click **Next**.

   ⇒ Several consecutive Software License Agreement windows appear.

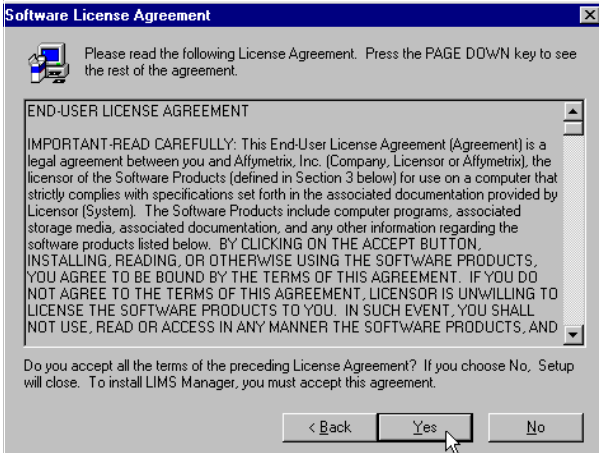


Figure 1.2
Software License Agreement window

3. Review the contents and click **Yes** in each window to accept the terms of the licensing agreement.

   ⇒ A Question window appears regarding the path location in reference to an upgrade **(Figure 1.3)**.

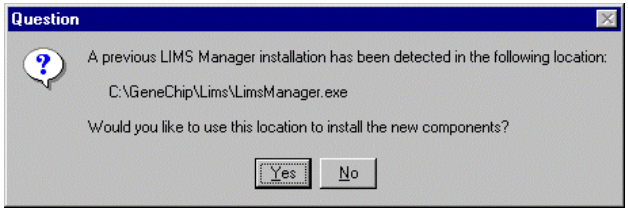


Figure 1.3
Question window

✔ Note

For upgrades, we recommended that you install LIMS Manager v 3.0 in the same location as the previous version and overwrite the existing files.

4. If this is an upgrade you are asked if you want the latest version of LIMS Manager in the same location as the previous version.

   - Click **Yes** to install in defined location.

     ⇒ The files from the previous version are overwritten.

   - Click **No** to install in new location. In the dialog box that appears, define the new path location desired.

   ⇒ The Choose Destination Location window appears **(Figure 1.4)**.

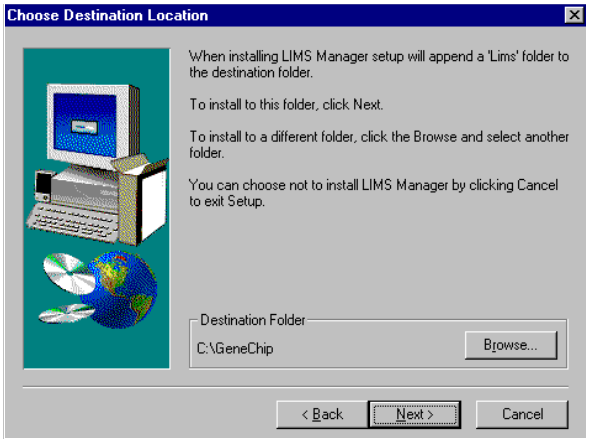


Figure 1.4
Choose Destination Location window

5. Select the destination to install LIMS Manager 3.0. Click **Next**. C:\GeneChip is the default location.
   ⇒ Files are copied.
6. Click **Next**.
   ⇒ The Select Components window appears **(Figure 1.5)**.

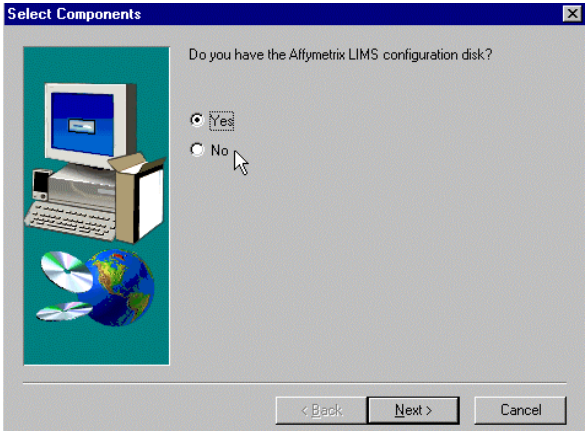


Figure 1.5
Select Components window - configuration disk

7. Select **Yes** if you have the LIMS configuration disk, **No** if you do not.
8. If **Yes**, go to step 9. If **No**, go to step 11.
9. Browse to the location of LIMS configuration disk.

   The file needed is called **GeneChipDB.ini** and resides on the LIMS server. The file is located at <server>\gclims\library. Browse to the file location.

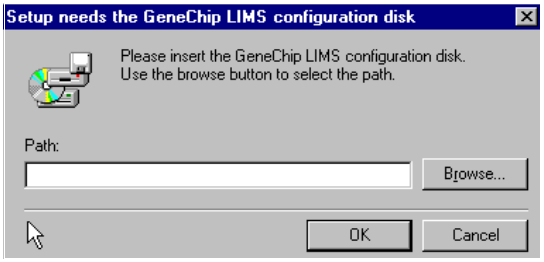


Figure 1.6
Browse to File Location

10. Click **OK**. Go to step 14.
11. Enter the name of the LIMS server and click **Next** **(Figure 1.7)**.

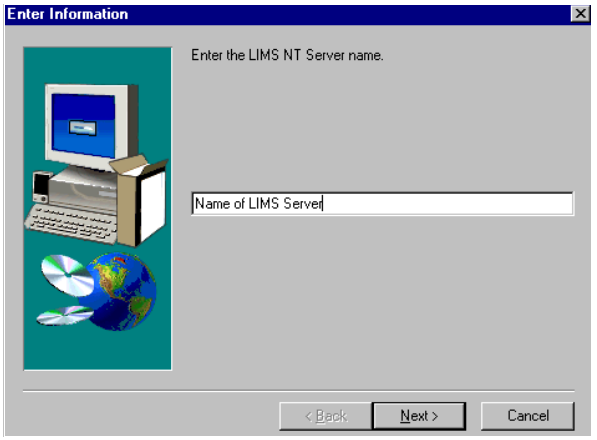


Figure 1.7
Enter Information window - enter LIMS server name

12. Enter the name of the domain the server resides on with the global group name that contains the LIMS users. (Domain Name\Global Group) **(Figure 1.8)**.

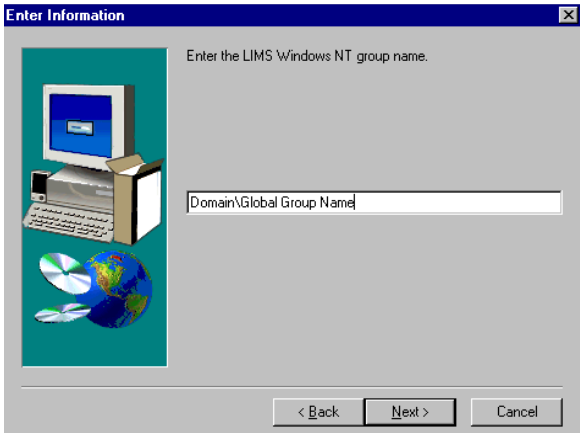


Figure 1.8
Enter Information window - enter global group name

13. Click **Next**.

    ⇒ The Setup Not Complete window appears.

14. Select **Yes, I want to restart my computer now** to complete the installation.

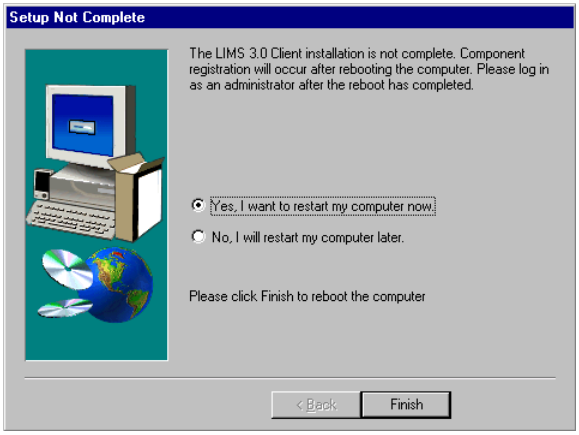


Figure 1.9
Reboot to continue installation

15. Log in as an administrator to complete the installation.
16. Click **Finish** in the Setup dialog box.

LIMS Manager Overview

Affymetrix® LIMS Manager v 3.0 is the software tool that provides you with a convenient way to manage your GeneChip® expression data. Improved performance in process database, improved access security throughout and improved query performance are just some of the features new in version 3.0 designed to enhance the management capabilities of LIMS Manager.

Features in Version 3.0

- Improved query performance for better database access
- Improved database management and data security features
- Improved access security throughout, including administrator defined user access level for added data security
- Easily track experiment status
- Ability to import historical data from a local hard drive or an external storage device (ZIP, JAZ, CD-ROM) and store on LIMS server
- Supports experiment and sample attribution
- Support for new data analysis algorithms
- Expanded Oracle® database support to include Oracle 8.1.7 - both publish and process database
- Expanded Microsoft® SQL database support to include SQL 2000 - both publish and process database
- Support for Microsoft Windows NT® and Microsoft® Windows 2000

Workflow-Based Tracking

Affymetrix® LIMS Manager software tracks experiments and processes. Its database provides storage and management for expression data.

You can access experimental data from any workstation on the network through the Affymetrix® LIMS server. Each user with access to the LIMS system can set up samples, experiments and publish data.

The LIMS Manager software processes experimental data through a workflow-based tracking system. The software tracks the stages of sample registration, experiment setup, hybridization, scan, grid alignment, analysis processes and publishing. This tracking allows you to follow the status of an experiment from sample preparation through analysis.

Data Security

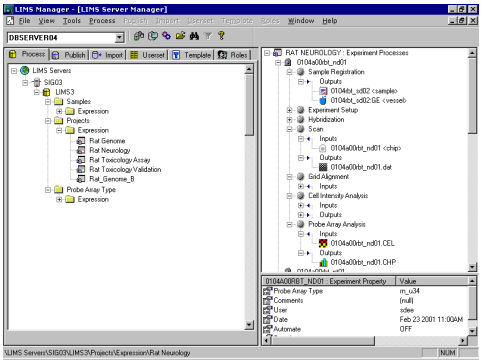
The Affymetrix® LIMS software incorporates data security from the Windows 2000 computer. The logon name verifies that the user has access to the Affymetrix® LIMS database.

Users can access the Affymetrix® LIMS database only if they have been granted authorization. Access is provided to the LIMS server by requesting privileges from the system administrator who is responsible for assigning users' rights and permissions.

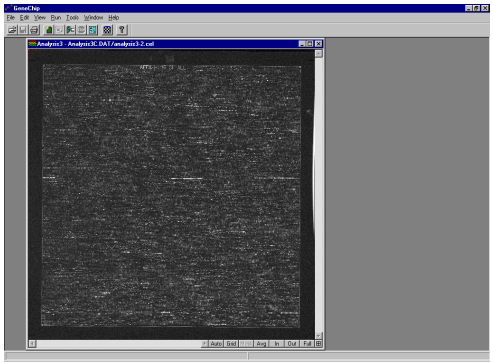
LIMS protects users' data from unauthorized changes. A user who creates, generates and analyzes an experiment is the original owner of the data. With security settings defined in the Roles tab, a user who is not the owner of the data will only have read access but is allowed to create new analyses without overwriting the original data. Security settings can also specify that only the owner of the data can overwrite the original data files.

LIMS and Affymetrix® Software Applications

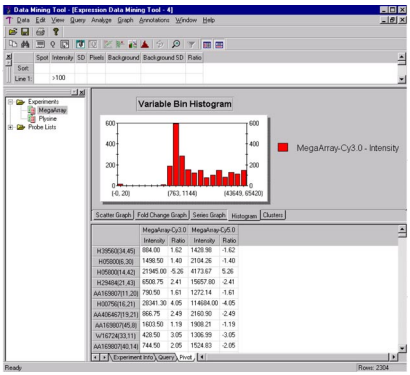
Affymetrix® LIMS Manager is the second of three software tools from Affymetrix for gene expression analysis **(Figure 1.10)**.



Affymetrix® LIMS Manager



Affymetrix® Microarray Suite



Affymetrix® Data Mining Tool

Figure 1.10
Affymetrix® software applications for expression analysis

Use Affymetrix® Microarray Suite to create, analyze and publish expression analysis data files. Next, import these files to a server database using LIMS Manager. Finally, access the publish database using Affymetrix® Data Mining Tool (DMT) to further analyze the data by filtering, pivoting and graphing. All three products are separate Windows applications available from Affymetrix.

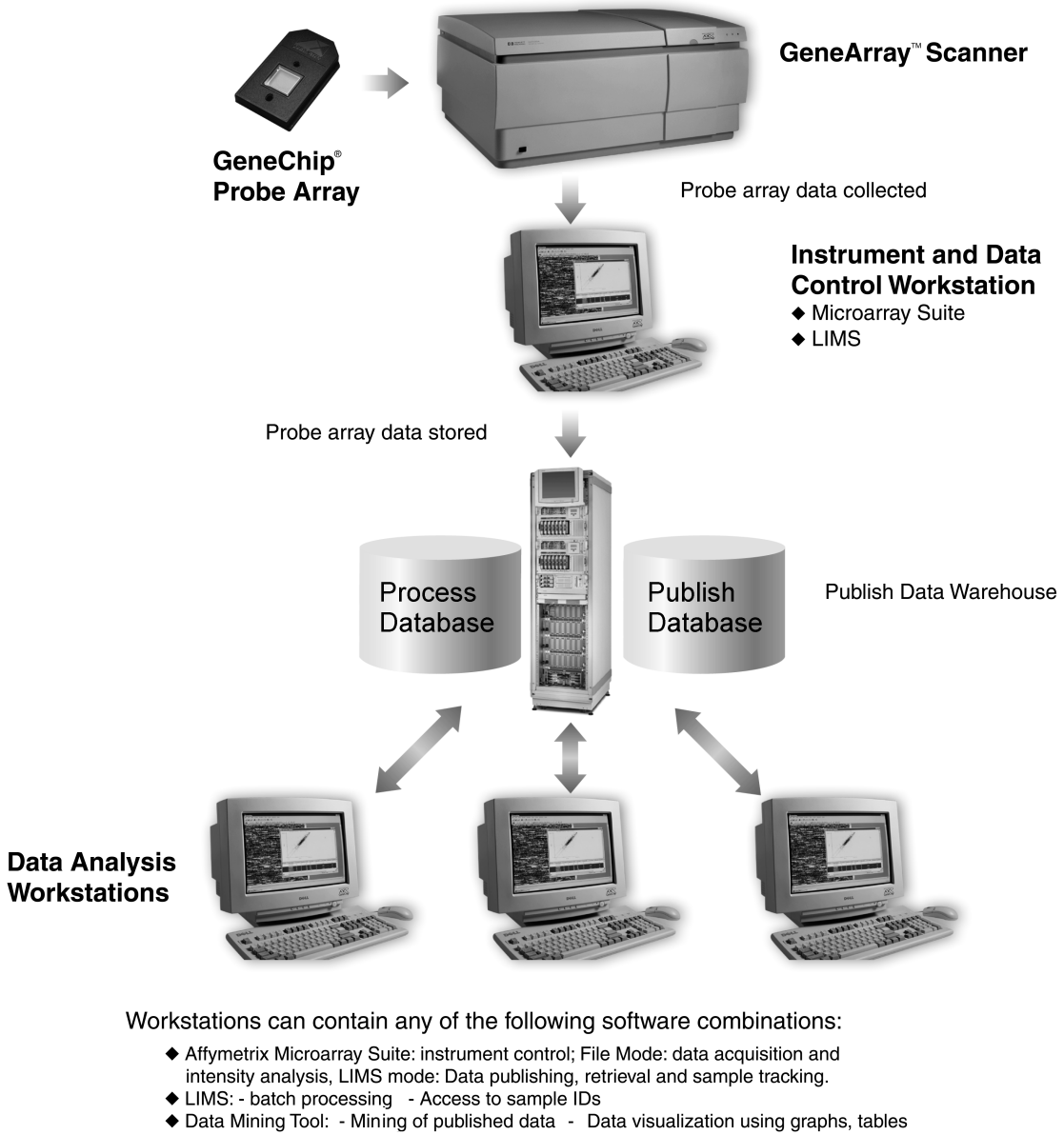


Figure 1.11
GeneChip® Probe Array data flow

Summary

The Affymetrix® LIMS and Data Mining Tool applications ensure that multiple users have simultaneous access to the database from any workstation. When used together, Affymetrix® Microarray Suite, Affymetrix® LIMS and Affymetrix® Data Mining Tool software applications generate experimental and research data for scientific analysis. Using these powerful tools in conjunction, users are able to review and analyze data in a robust and dynamic manner.

User Interface Orientation

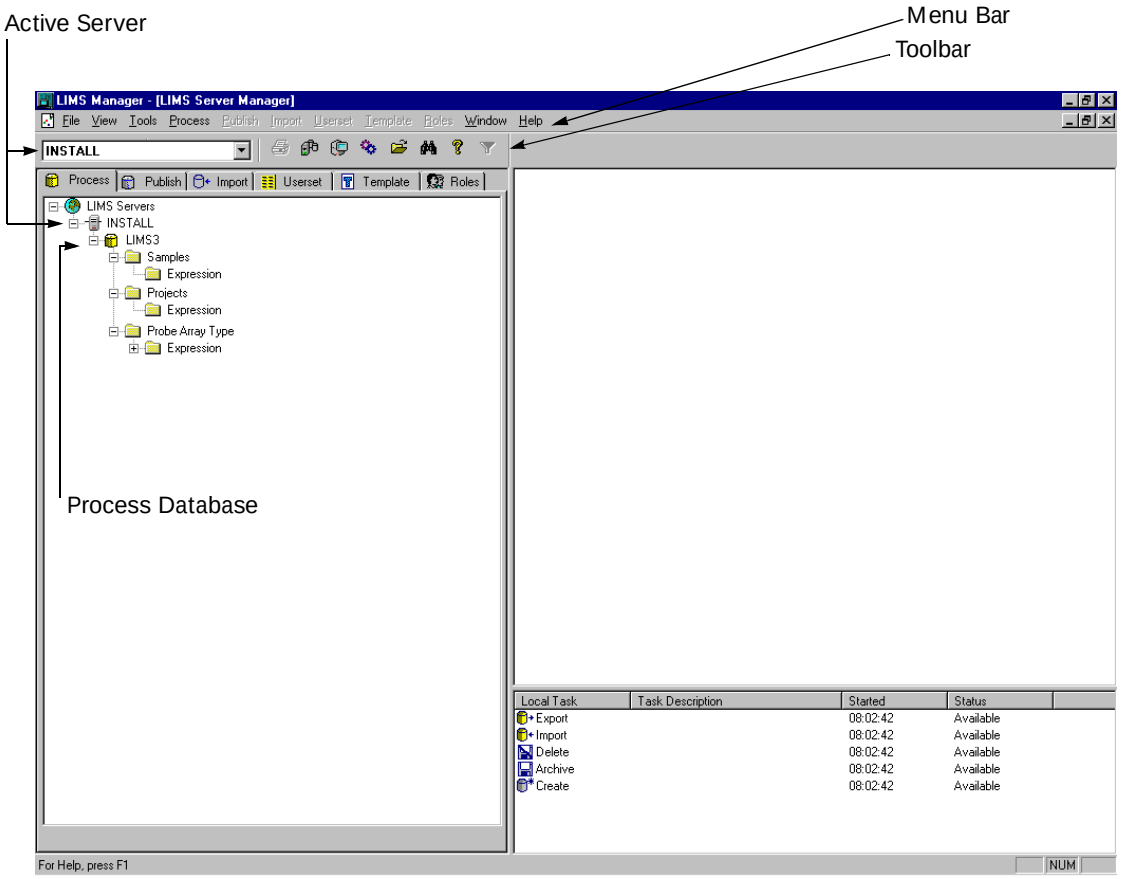


Figure 1.12
LIMS Manager interface

Icons Used in LIMS

Table 1.1
LIMS Manager Icons

	Sample		Template		Properties Information
	Project		Global		Gray bullet indicates processes that have been completed.
	Experiment Information / .exp file		Server		Green bullet indicates processes waiting to commence.
	Image of Scanned Probe Array / .dat file		Process Database (yellow)		Red check mark on .exp, .dat, .cel or .chp icon(s) indicates that the file already exists in the Publish Database.
	Averaged Intensities / .cel file		Publish Database (gray)		Export Status
	Analysis Output / .chp file		Import to Database		Import Status
	Probe Array type		Domain		Delete Status
	Chip		User Group		Archive Status
	Vessel		User		Create Publish Database Status
	Userset		Role		Filter

Tool/Toolbar Items

Most toolbar or **Tool** menu items are available across all tabs. Detailed descriptions of these commands are presented in subsequent sections of this manual.

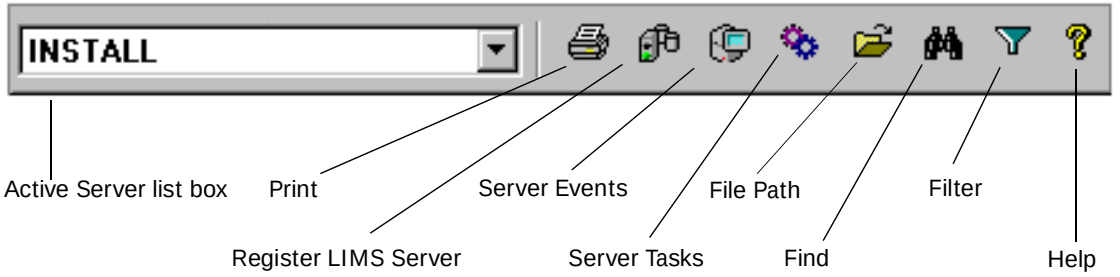


Figure 1.13
LIMS Toolbar

Glossary

The following terms are used frequently throughout this manual. For your convenience the terms are listed under the tabs where they are most frequently found.

File and Object Types Across All Tabs

Automate	Automate is a monitored task whose status, either on or off, is viewed in the **Local Task** pane. **Automate On** indicates LIMS is automatically tracking an experiment through data analysis after a scan of the probe array has successfully completed.
.cel	The .cel averaged intensity file. Also known as “cell” file, this file is automatically created after grid alignment. The cell averaging analysis calculates the average intensities of each cell and assigns it an x and y coordinate, and can be used to re-analyze data with different algorithm patterns. The .cel file is one of two file types you can migrate to a publish database using Affymetrix® Microarray Suite.
.chp	Also known as a “chip” file, this analysis file is the output generated by the analysis of a .dat and .cel file. The .chp is the second of two file types you can migrate to a publish database using Affymetrix® Microarray Suite.

.dat	The .dat file is the image of the scanned probe array and is created by the analysis.
.exp	The .exp file is created by the user and contains information defined by the experiment template used. The experiment name becomes the file name for subsequent files generated in the analysis. The **Import** function presents the concept of moving files and on this tab there is an experiment (.exp) file. The process database contains files and data, but does not contain experiment files; only experiment and sample data.
Sample	A set of experiments.

Tab-Specific Terminology

Active Server	Several LIMS servers may be registered. The active server refers to the LIMS server where the displayed process database resides.
Archive	To move files from the process database and send to an external location.
Export	To copy data from the process database and send to an external location.
Process Database	Database residing on server containing experiment and sample data. Only one process database exists per server.
Project	A set of experiments with a common bond and grouped together by their affiliation to a project. Creation of the project is accomplished during the sample registration process in Affymetrix® Microarray Suite.
Unarchive	Restoring files to the process database.

Affymetrix® Analysis Data Model	The Affymetrix® Analysis Data Model is the relational database schema Affymetrix uses to store experiment data so that results may be filtered and mined by analysis tools. Previously referred to as the GATC data model, the Affymetrix® Analysis Data Model includes additional tables to support mapping, spotted arrays and new expression results [1]. The Affymetrix® Analysis Data Model is publicly available to support open access to experiment information generated and managed by Affymetrix® software.
Intensities	See .cel file on page 18.
Publish Database	An Affymetrix® Analysis Data Model database residing on a server containing select process data that have been published. You may have several publish databases on a single server.
Publish	Publishing is the act of migrating sample data to a Microsoft® SQL or Oracle® publish database and is a function of Microarray Suite v 4.0 or above.

Create Sample	Creating a sample captures sample information and is used to identify the relationship of the .exp and analysis files being imported.
Import	Importing copies data files created in Affymetrix® Microarray Suite and stored on a local hard drive and moves them into the process database.

1 Affymetrix® LIMS Manager 3.0 does not support mapping or spotted array data.

Userset	A userset is a predefined prarameter set used when running an expression analysis.
Independent Parameter	Defined in the userset, independent parameters are static settings not influenced by probe array selection.
Dependent Parameter	Defined in the userset, dependent parameters are settings that are specific to the particular probe array type selected.

Activate	**Activate** is a command that restores an inactive (deactivated) template or attribute.
Template	A template is a form created by the administrator in LIMS to define the attributes and values for both the experiment and sample registration process. The registration process is a function of Affymetrix® Microarray Suite.
Deactivate	On the **Template** tab, the **Deactivate** command does not permanently remove an existing template or attribute. The deactivate action only renders the item inactive. The item does not appear in Affymetrix® Microarray Suite until the **Activate** command is used.

Privilege	Privileges are the functions or permissions used for defining roles.
Role Definitions	The name used to identify the first branch listed under the server where role names are identified.
Role	A **Role** is a defined set of access privileges.
User Definitions	The name used to identify the branch under the process database where role membership is defined.

Documentation

This manual provides a detailed outline for all tasks associated with Affymetrix® LIMS Manager.

Additionally, the LIMS Manager installation CD includes an electronic version of this user's guide. The on-line documentation is presented in Adobe Acrobat® format (a .pdf file) and is readable with the Adobe Acrobat® Reader software, available free from Adobe at http://www.adobe.com. The electronic user's guide is printable, searchable and fully indexed.

Conventions Used

Various conventions are used throughout the manual to help illustrate the procedures described. Explanations of these conventions are provided below.

Steps

Instructions for procedures are written in a step format. Immediately following the step number is the action to be performed. On the line below the step there may be the following symbol: ⇒. This symbol defines the system response or consequence as a result of user action; what you see and what has happened that you may not see.

Following the response, additional information pertaining to the step may be found and is presented in paragraph format.
For example:

9. Click **Yes** to continue.

   ⇒ The **Delete** task proceeds.
   In the lower right pane the status is displayed.

   To view more information pertaining to the delete task, right-click **Delete** and select **View Task Log** from the shortcut menu.

Font Styles

Bold fonts indicate names of commands, buttons or options within a dialog box. When asked to enter specific information, such input appears in italics within the procedure being outlined.
For example:

1. To select another server, enter the server name in the **Oracle Alias** box.
2. Enter *DMT_2_Tutorial* in the **Publish Database** box, then click **Register**.

   ⇒ The tutorial database is available to DMT.

Screen Captures

The steps outlining procedures are frequently supplemented with screen captures to further illustrate the instructions given.

✔ Note *The screen captures depicted in this manual may not exactly match the windows displayed on your screen.*

Additional Comments

Throughout the manual, text and procedures are occasionally accompanied by special notes. These additional comment types and their meanings are described below.

TIP *Information presented as tips provide helpful advice or shortcuts for completing a task.*

✔ Note *The Note format presents information pertaining to the text or procedure being outlined.*

! CAUTION *Caution notes advise you that the consequence(s) of an action may be irreversible and/or result in lost data.*

▲ WARNING *Warnings alert you to situations where physical harm to person or damage to hardware is possible.*

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2

Chapter 2

Process Tab

*The initial view presented upon opening Affymetrix® LIMS Manager is the **Process** tab. The **Process** tab shows you the data in the system, where it is found and allows you to view environmental property information regarding the data.*

*This chapter orients you to the layout of the **Process** tab window and describes in detail the functions and tasks accomplished here.*

Process Tab Window

The **Process** tab window is divided into three panes **(Figure 2.1)**. The first pane on the left side displays a tree that identifies the active server, process database and data types (**Samples**, **Projects** and **Probe Arrays**). The data type subfolders contain the **Sample Name** , **Project Name** , or **Probe Array Name** files for expression data. The tree stops at this level.

The second pane in the upper right corner takes the **Sample Name** or the **Project Name**, selected in the first pane, copies it as the top node and lists the associated experiment(s) underneath. The first time you click an experiment in this pane, the information is read and a '+' is displayed next to the experiment name. Click the '+' to display processes completed with inputs and outputs, or associated .dat files. Alternatively, double-click an experiment in this pane and the information is read and processes or associated files are displayed. Experiment information in this pane is displayed in either a **Process view** or a **File view**.

The third pane in the lower right corner displays either a Property Information or Local Task status view, depending on the item selected. Property Information lists environment details pertaining to the selected item. This information is defined by the template used during the **Sample Registration** process completed in Affymetrix® Microarray Suite.

The Local Task status view displays the status of processes that may be occurring in the database, such as **Export**, **Import**, **Delete**, **Archive** and **Create**. This view allows you to monitor these jobs while concurrently working on additional tasks within the LIMS system.

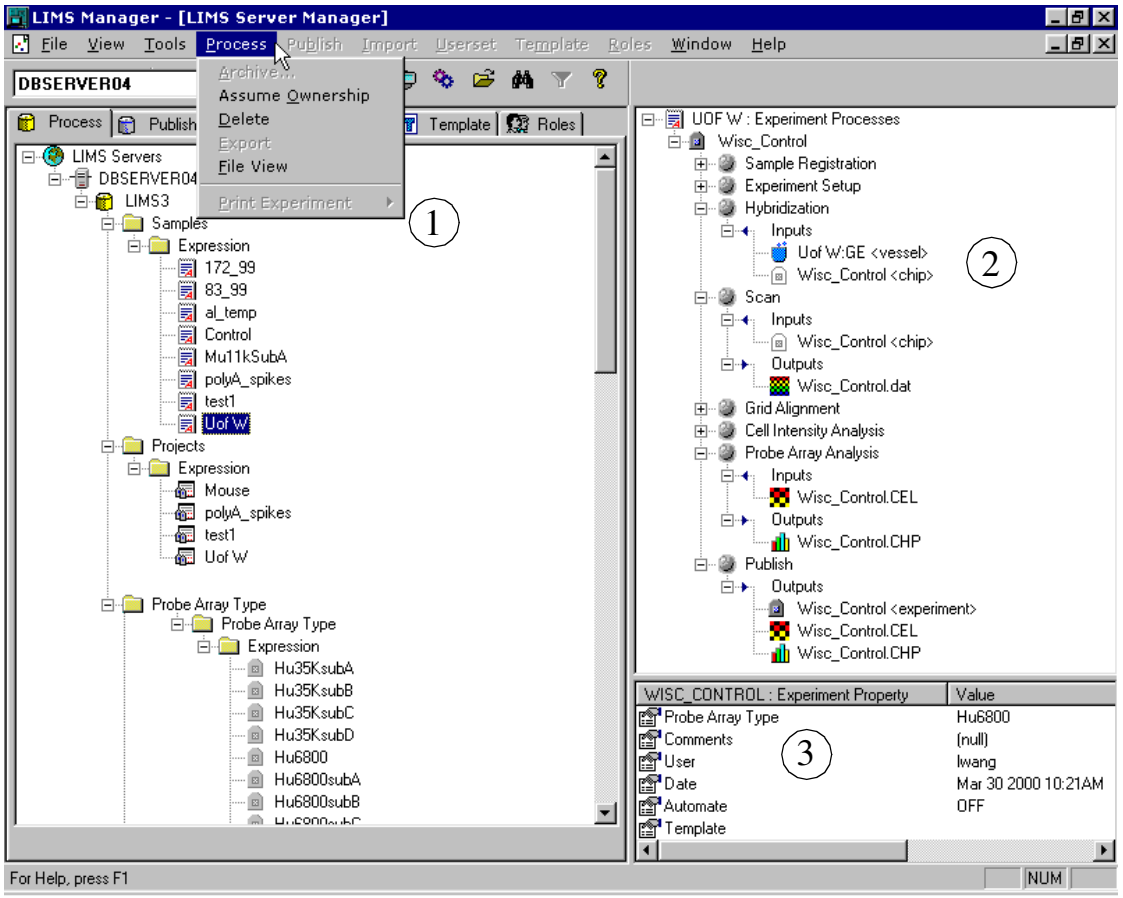


Figure 2.1
Process tab: Process View (2) of selected sample (1) with environmental property information displayed(3)

Process Tab Functions

The primary functions of the **Process** tab include archiving, unarchiving, deleting, exporting, assuming ownership and printing data. These commands are found on the menu bar under **Process**.

The primary data types in the **Process** tab are sample, project, experiment and file. Each data type has associated functions whose commands are found under **Process** on the menu bar, or accessed by right-clicking the data type and selecting from the shortcut menu that appears **(Figure 2.2)**.

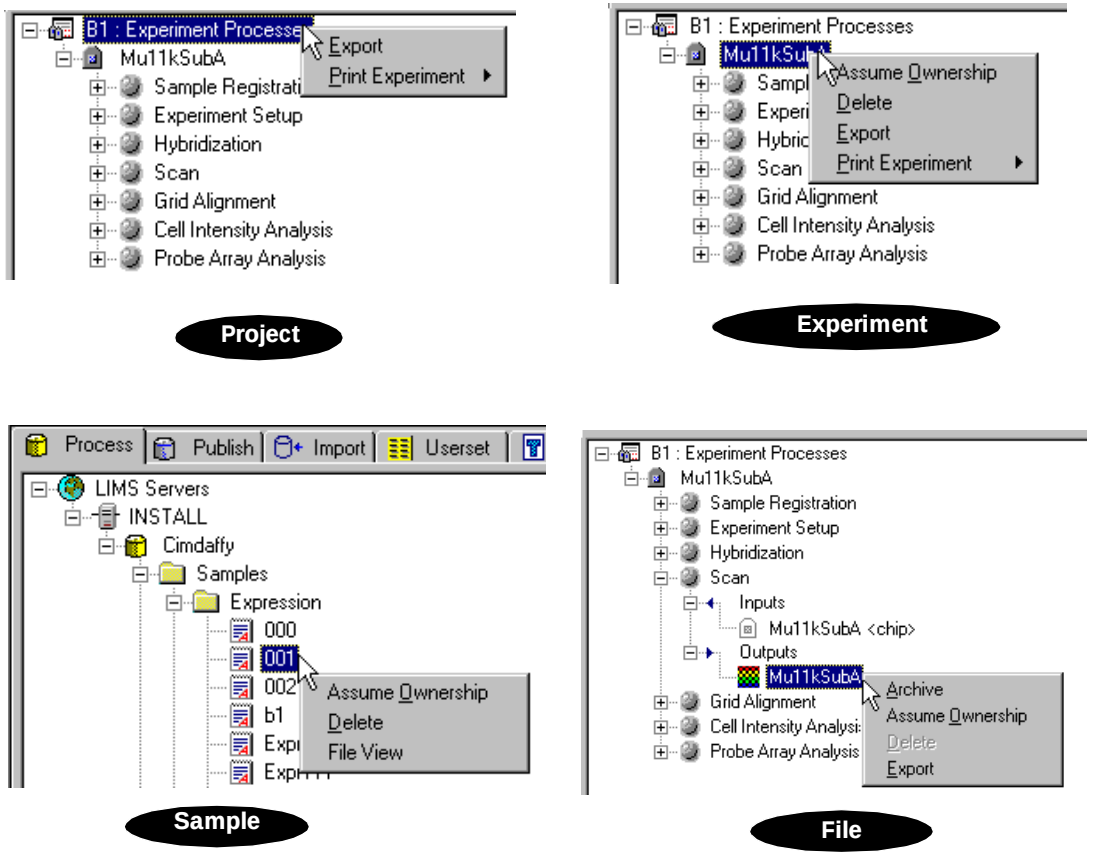


Figure 2.2
Shortcut menus for data types

Data Archive

Archiving data moves specified files and stores them in an external location. Although archived files no longer exist in the process database, their representative icon remains in the tree and appears gray to alert you that this data is available through the **Unarchive** process.

It is not possible in the current version of LIMS to archive experiments. You may only archive specific data files (.dat, .cel and .chp).

Archiving Data Files

1. On the menu bar select **Process** → **File View**, if necessary.
2. In the upper right pane, click to select the file to be archived.

   Selecting a parent file also includes all related children files in the archive process.
3. On the menu bar select **Process** → **Archive**.

   Alternatively, right-click the file to archive and select **Archive** from the shortcut menu that appears.

   ⇒ The Select Archive File Path window appears **(Figure 2.3)**.

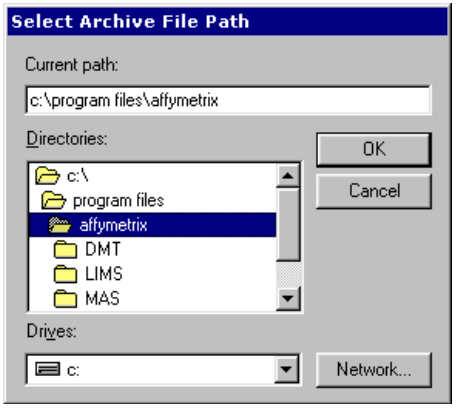


Figure 2.3
Select Archive File Path window

4. Select a **Drive** from the drop-down list and browse to find desired directory.

5. Click **OK**.

   ⇒ The **Archive** Local Task status is displayed in the lower right pane.

   Double-click **Archive** at any time to view additional information pertaining to the archive status, or right-click **Archive** and select **View Task Log** from the shortcut menu that appears.

TIP

Use the Find function to generate a list of files associated with a specific project. Then SHIFT-select and archive these files in one quick step. This only works with .dat, .cel and .chp files in the process database.

Data Unarchive

The icon(s) for data that have been archived lose their color and appear gray. The **Unarchive** command recalls the archived data and restores it to the process database.

Unarchiving Data Files

1. Click to select the file to unarchive.

   Selecting a parent file also includes all related children files in the unarchive process.

   If the archived file cannot be located a **File Location** dialog appears. Use this dialog box to define the location of the desired files.

2. On the menu bar select **Process** → **Unarchive**, or right-click the file and select **Unarchive** from the shortcut menu.

✔ Note

The Process window does not automatically refresh upon completion of the Archive or Unarchive task. Therefore, if you unarchive a data file the icon remains gray even though the task was completed successfully. To refresh the view select View → Refresh from the menu bar.

Assume Ownership

Change the **User** attribute of data to enable the reassignment of data when necessary for security or management purposes. Ownership of samples, experiments or analyses may be assumed when the **Take Ownership Process Data** option is defined for the user in the **Roles** tab.

Assuming Ownership

1. Click to select the appropriate sample, experiment or analyses.
2. From the menu bar select **Process** → **Assume Ownership**.
   ⇒ Your user name appears as **User** in the properties window in the lower right pane.

OR

1. Right-click the appropriate sample, experiment or analyses.
2. Select **Assume Ownership** from the shortcut menu.
   ⇒ Your user name appears as **User** in the properties window in the lower right pane.

Delete Process Data

You may delete samples, experiments, .cel, .chp analyses and usersets. Deleting samples deletes all associated experiments and analyses. Deleting experiments deletes all associated analyses.

! CAUTION *The Delete option permanently removes data from the database. There is no restore function to recover deleted data.*

Deleting Process Data

1. Click to select the item to delete.
2. From the menu bar select **Process** → **Delete**.
   ⇒ A warning / confirmation window appears **(Figure 2.4)**.

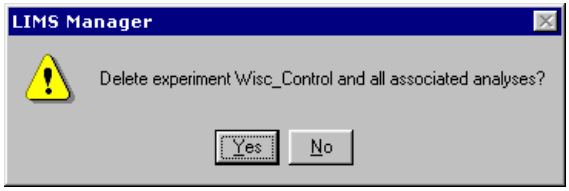


Figure 2.4
Delete warning / confirmation window

3. Click **Yes** to continue.

   ⇒ The **Delete** Local Task status is displayed in the lower right pane.

   Double-click **Delete** at any time to view additional information pertaining to the delete status, or right-click **Delete** and select **View Task Log** from the shortcut menu that appears.

OR

1. Right-click an item to delete.
2. Select **Delete** from the shortcut menu that appears.

   ⇒ A warning / confirmation window appears **(Figure 2.4)**.

3. Click **Yes** to continue.

   ⇒ The **Delete** Local Task status is displayed in the lower right pane.

   Double-click **Delete** at any time to view additional information pertaining to the delete status, or right-click **Delete** and select **View Task Log** from the shortcut menu that appears.

✔ Note

Deleting process data is different from deleting publish data (see Publish Data, on page 57). Deleting published data removes only the data that has been published into a publish database. However, the data source in the process database remains available.

Delete Probe Array Type

Remove an unused or unwanted probe array type from the process database from the left hand pane in the **Process** tab window.

Deleting a Probe Array Type from the Process Database

1. Under the **Probe Array Type** folder in the left hand pane, click to expand the **Expression** folder.
2. Click to select the probe array type of interest.
3. On the menu bar select **Process** → **Delete**, or right-click the probe array type of interest and select **Delete** from the shortcut menu that appears.
   ⇒ A warning / confirmation window appears **(Figure 2.5)**.

Figure 2.5
Delete warning / confirmation window

4. Click **Yes** to delete the probe array type from the process database.
   ⇒ The probe array type is removed and no longer appears listed in the left hand pane.

✔ Note

When a probe array type is deleted the associated usersets are also removed. Data created with these usersets remains, but is not accessible.

Export

The **Export** command allows you to copy all data including sample, experiment, .dat, .cel and .chp files and send them to an external location for storage.

Exporting Data

1. In the left pane, click to select the sample of interest.
2. On the menu bar select **Process** → **File View**, if necessary.

   You may use **Process View** if exporting the entire sample or experiment and related files.
3. In the upper right pane, click to select the data to export.

   Selecting an object takes that object and all associated data with it. For example, selecting a sample takes the sample, experiment and any related .dat, .cel and .chp files.

✔ Note

The sample and experiment data are exported to an Affymetrix® Microarray Suite v4.x .exp file.

4. On the menu bar, select **Tools** → **File Path**, or click the button on the toolbar.

   ⇒ The Select Export File Path window appears **(Figure 2.6)**.

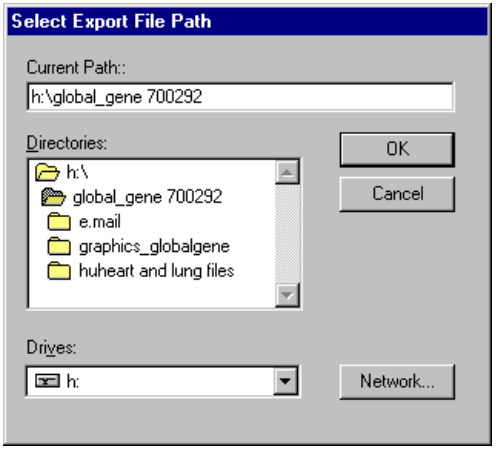


Figure 2.6
Select Export File Path window

5. Select a **Drive** from the drop-down list and browse to find desired export destination directory, then click **OK**.
6. On the menu bar select **Process** → **Export**, or right-click the file and select **Export** from the shortcut menu that appears.
7. Click **OK**.

   ⇒ The **Export** Local Task status is displayed in the lower right pane.

   Double-click **Export** at any time to view additional information pertaining to the **Export** status, or right-click **Export** and select **View Task Log** from the shortcut menu that appears.

Views in Process Tab Window

The upper right pane of the **Process** tab window displays either a **File View** or a **Process View** of the selected sample or data file. The **Process View** identifies the stages completed by the experiment displayed as gray bullets, and stages that are pending are displayed as green bullets. The **File View** displays the experiment and all related files. For samples of both views, see **Figure 2.7**.

Changing Views

1. Click to select a sample in the left pane.
2. From the menu bar select **Process** → **Process View** (or **File View**, as appropriate).

OR

1. Right-click a sample in the pane on the left side of the window.
2. From the shortcut menu that appears, select **Process View** or **File View** as appropriate.

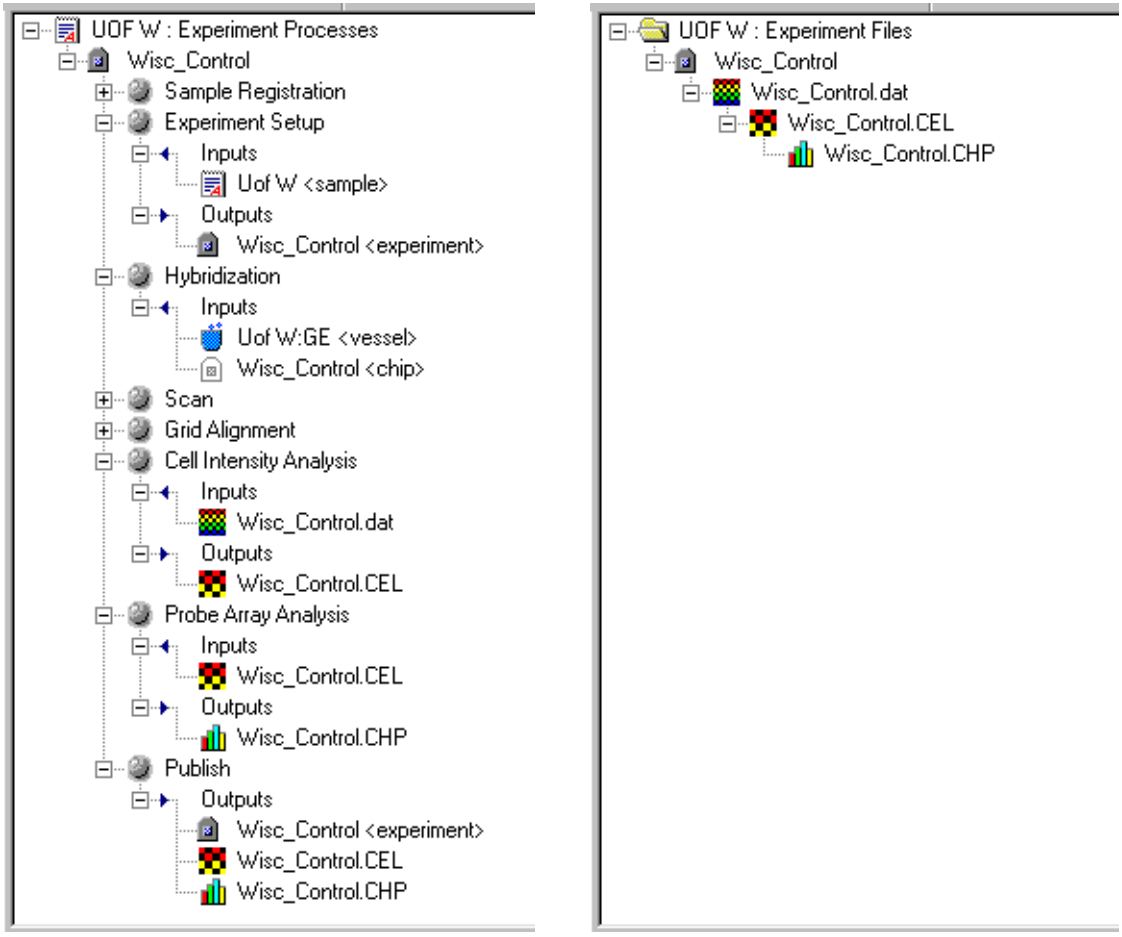


Figure 2.7
Process tab: Process View (left) and File View (right)

Print an Experiment

The **Print Experiment** command allows you to obtain a printout of experimental information. Two print options are available (described below), and samples of each are provided in *Appendix A* on page 119.

Printing an Experiment

1. From the upper right pane in the **Process** tab window, click to select an experiment to print.
2. From the menu bar click **Process**.
3. Select **Print Experiment** → **Diagram Only** or **Diagram & Properties**.
   - **Diagram Only** option displays the experiment process and lists the inputs and outputs for each stage.
   - **Diagram & Properties** option displays the experiment processes, input and outputs and provides property information relevant to each stage.

   ⇒ The experiment information is printed on the default printer.

OR

1. From the upper right pane in the **Process** tab window, right-click the experiment to print.
2. Select **Print** from the shortcut menu.
3. Select **Print Experiment** → **Diagram Only** or **Diagram & Properties**.
   - **Diagram Only** option displays the experiment process and lists the inputs and outputs for each stage.
   - **Diagram & Properties** option displays the experiment processes, input and outputs and provides property information relevant to each stage.

   ⇒ The experiment information is printed on the default printer.

Register a LIMS Server

Registering a LIMS Server means to add a server and make it available to LIMS Manager.

Registering a Server

1. From the menu bar select **Tools** → **Register LIMS Server**, or click the button on the toolbar.

   ⇒ The Register LIMS Server window appears **(Figure 2.8)**.

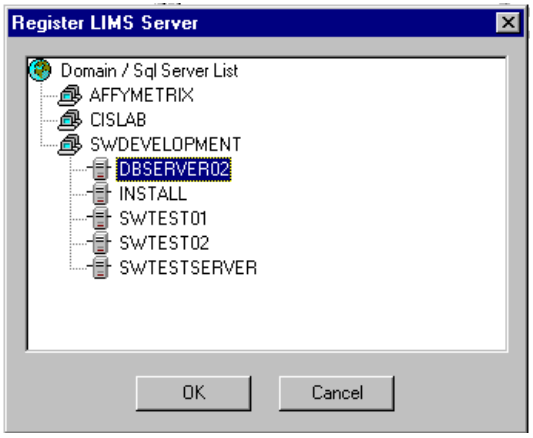


Figure 2.8
Register LIMS Server dialog box

2. Search the tree and select the desired server to register.
3. Click **OK**.

   ⇒ The selected server is added to the drop-down list on the toolbar and appears listed in the left pane of the **Process** tab **(Figure 2.1)**.

✔ Note *The newly registered server becomes the active server.*

   ⇒ If the server selected is not LIMS aware, an error message is displayed **(Figure 2.9)**.

Figure 2.9
Register LIMS Server error message

Note

An error message indicates that there is no LIMS system installed, or that there is an installation error. For further information, please refer to the 'Affymetrix® LIMS Installation and Administration Guide.'

Unregister a LIMS Server

Right-click to select the server to remove and select **Unregister LIMS Server** from the shortcut menu that appears.

Server Events

The **Server Events** option displays a log allowing you to view events occurring on the active LIMS server.

To view the **Server Events** log:
Select **Tools** → **Server Events**, or click the button on the toolbar.

Server Tasks

Use the **Server Tasks** option to view a task window that displays the publishing queue. Review the task list at any time to monitor all publishing occurring on the active server **(Figure 2.10)**.

To view **Server Tasks**:
Select **Tools** → **Server Tasks** or click the button on the toolbar.

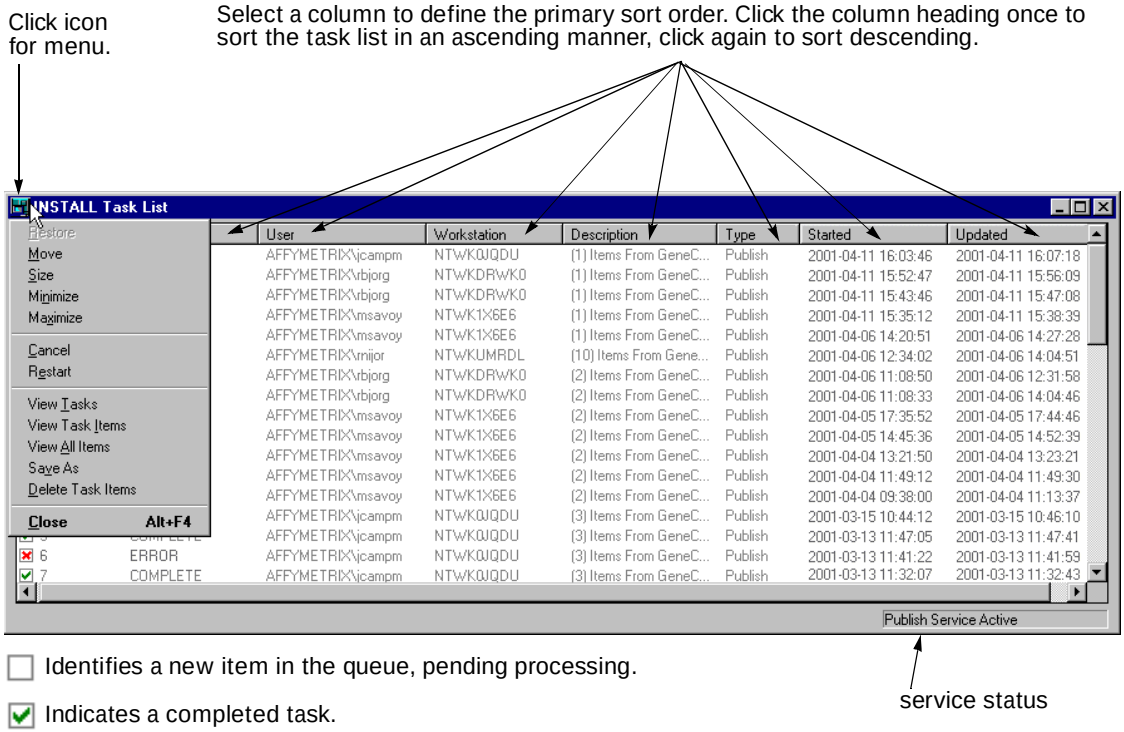


Figure 2.10
Server Tasks window

Task List Commands

Further action may be taken on items in the Task List window. Access the command menu for the task list either by clicking the icon in the upper left corner of the window **(Figure 2.10)**, or by right-clicking a task **(Figure 2.11)**.

Viewing Tasks

The Task List window displays the status of each task on the server when **View Tasks** is selected **(Figure 2.11)**.

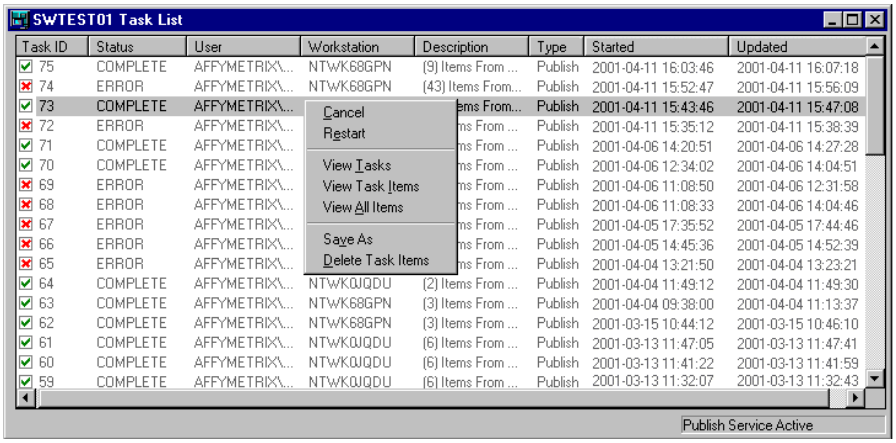


Figure 2.11
Right-click task for shortcut menu

Viewing Task Items

The Task List window displays all items for a specified task when **View Task Items** is selected **(Figure 2.12)**.

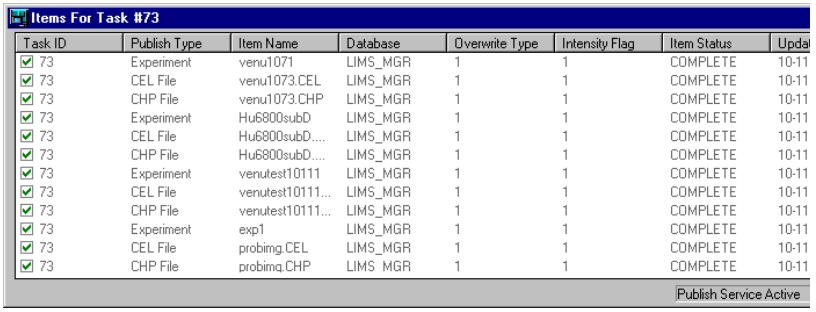


Figure 2.12
View Task Items window

Viewing All Items

All items for all tasks are displayed in the Task List window when **View All Items** is selected.

Saving the Task List

The **Save As** command allows you to save displayed items from the Task List window as a .txt file.

1. Click the icon in the upper left corner of the Task List window and select **Save As** from the drop-down menu.
   Alternatively, right-click a task in the list and select **Save As** from the shortcut menu that appears.
   ⇒ The Save As dialog box appears **(Figure 2.13)**.

Figure 2.13
Save As dialog box

2. From the **Save in** drop-down list, browse to the desired destination.
3. Name the file and click **Save**.
   ⇒ The task list is saved as a text file in the defined destination.

Deleting Task Items

The **Delete Task Items** command removes all listed task items.

1. Click to select a task.
2. Right-click the task and select **Delete Task Items** from the shortcut menu that appears.
   ⇒ A warning / confirmation window appears **(Figure 2.14)**.

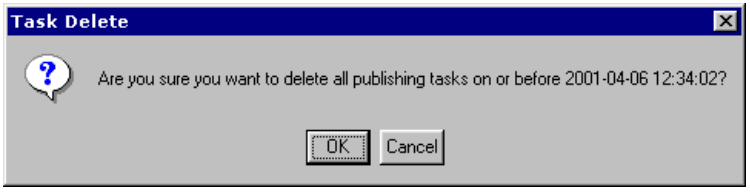


Figure 2.14
Task Delete warning / confirmation window

3. Click **Yes** to delete all tasks on and before the date and time indicated.
   ⇒ Items are deleted and Task List window is empty.

Cancelling an Active Publish Task

Right-click a pending task and select **Cancel** from the shortcut menu to stop the publish process.

Restarting a Cancelled Publish Task

Right-click a task that has been cancelled or stopped due to error and select **Restart** to reactivate the publish process.

Find Function

Use the **Find** feature to query **Samples**, **Experiments** or analyses within the process database for **Export**, **Archive**, **Assume Ownership** or **Delete** functions. When preforming one of these functions after a **Find** command, only the selected objects are affected by the action and do not include any related children objects.

✔ Note — *The Find function only searches the process database.*

Finding a Sample, Experiment or File

1. From the menu bar select **Tools** → **Find**, or click the button on the Toolbar.
   ⇒ The Find window appears **(Figure 2.15)**.

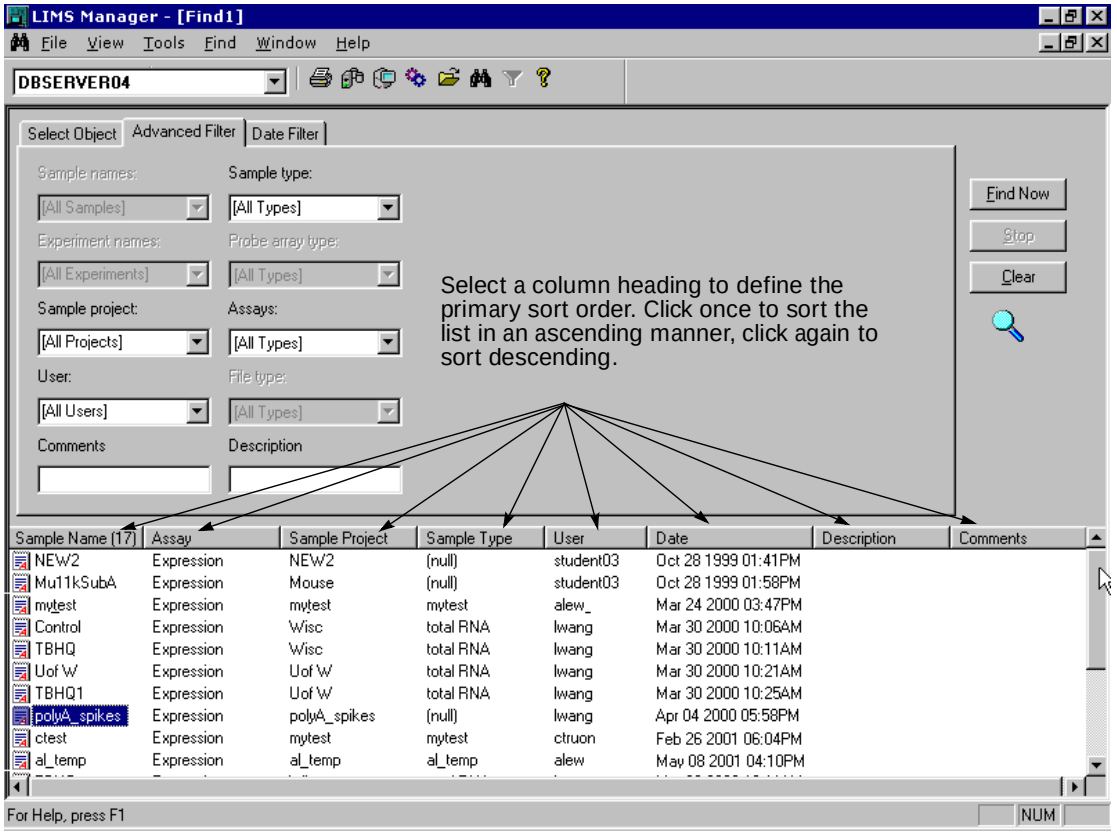


Figure 2.15
Find window with Advanced Filter tab displayed

✔ Note

All three tabs work in union. For Example, if sample is selected as the Object Type in the Select Object tab, when you switch to the Advanced Filter tab, only those boxes that pertain to finding a sample will be active.

Multiple Find windows are allowed.

2. Click either the **Select Object**, **Advanced Filter** or **Data Filter** tab and make selections from the drop-down lists, or type in requested information.

   Further refine your search by selecting additional tabs.

3. Click **Find Now**.

   ⇒ Matching results are displayed at the bottom of the window.

4. Click to select the sample, experiment or file of interest.

   The commands available for the selected object are found under **Find** on the menu bar, or right-click the object to access these commands from the shortcut menu **(Figure 2.17)**.

   To select multiple contiguous objects to act upon: click an object in the list, then SHIFT-click another item anywhere either above or below the first selected. All objects between the two selections are selected.

   To select multiple non-contiguous objects to act upon: click an object in the list, then CTRL-click another item anywhere in the list. Repeat as necessary for additional items.

Follow the procedure(s) for the **Export**, **Archive/Unarchive**, **Delete** and **Assume Ownership** commands outlined earlier in this chapter. There are two differences when performing these procedures after a **Find** task; ❶ the commands are found under **Find** on the menu bar, and ❷ the **Export**, **Assume Ownership** and **Archive/Unarchive** procedures only affect the specific file selected and do not include any associated data.

Sample Filter

The **Filter** function is used to reduce the number of samples displayed in a tree of samples. The **Filter** icon becomes active in the **Process** tab and the **Import** tab when you click a node under a **Samples** folder and remains active from session to session until the parameters are changed.

Using the Sample Filter

1. Click the **Samples** folder.

   ⇒ The tree expands displaying samples and the **Filter** icon on the toolbar becomes active.

2. Click the **Filter** icon .

   ⇒ The Sample Filter dialog box appears **(Figure 2.16)**.

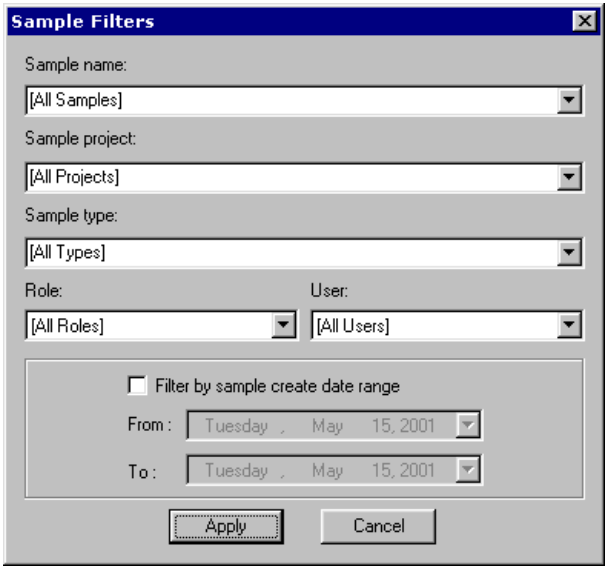


Figure 2.16
Sample Filter dialog box

3. From the drop-down boxes, define filter parameters.

   The **Role** and **User** filter options are mutually exclusive. You may select one or the other, but not both.

4. Click **Apply**.

   ⇒ The Samples are filtered and the sample list is adjusted accordingly.

✔ Note

The filter parameters remain active from session to session. You must reset the parameters when a different display is desired.

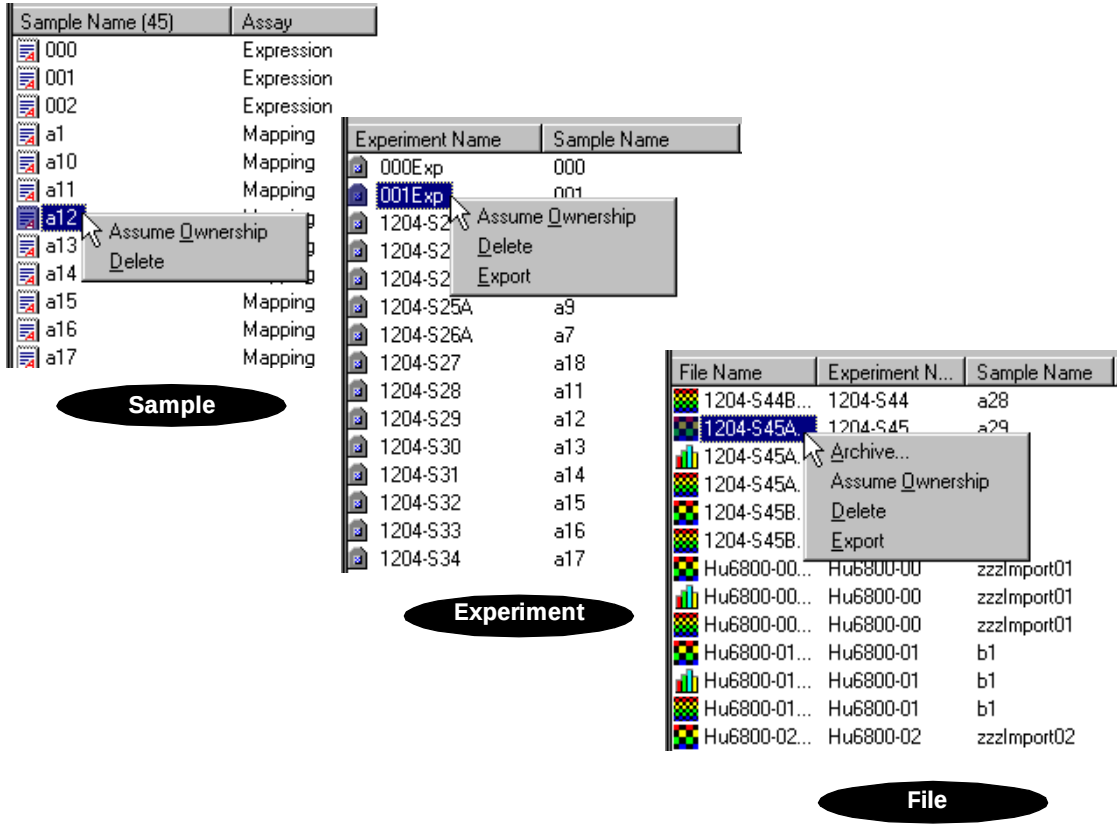


Figure 2.17
Right-click objects for shortcut menus after a Find procedure

3

Chapter 3

Publish Tab

*The **Publish** tab allows you to create new publish databases and delete published data from a database. All publish databases are password-protected and can only be accessed using the password defined during the creation of the database.*

*This chapter orients you to the layout of the **Publish** tab and describes in detail the functions and tasks accomplished here.*

Publish Tab Window

There are three panes in the **Publish** tab window **(Figure 3.1)**. The first pane on the left side displays a tree showing the active LIMS server, all publish databases residing on the server, all supported probe array types and their contents.

The second pane becomes active and is filled with a create database dialog when a **Create Database** command is initiated.

The third pane in the lower right corner is the Local Task status view that displays the status of processes that may be occurring in the database, such as **Export**, **Import**, **Delete**, **Archive** and **Create**. This view allows you to monitor these jobs while concurrently working on additional tasks within the LIMS system.

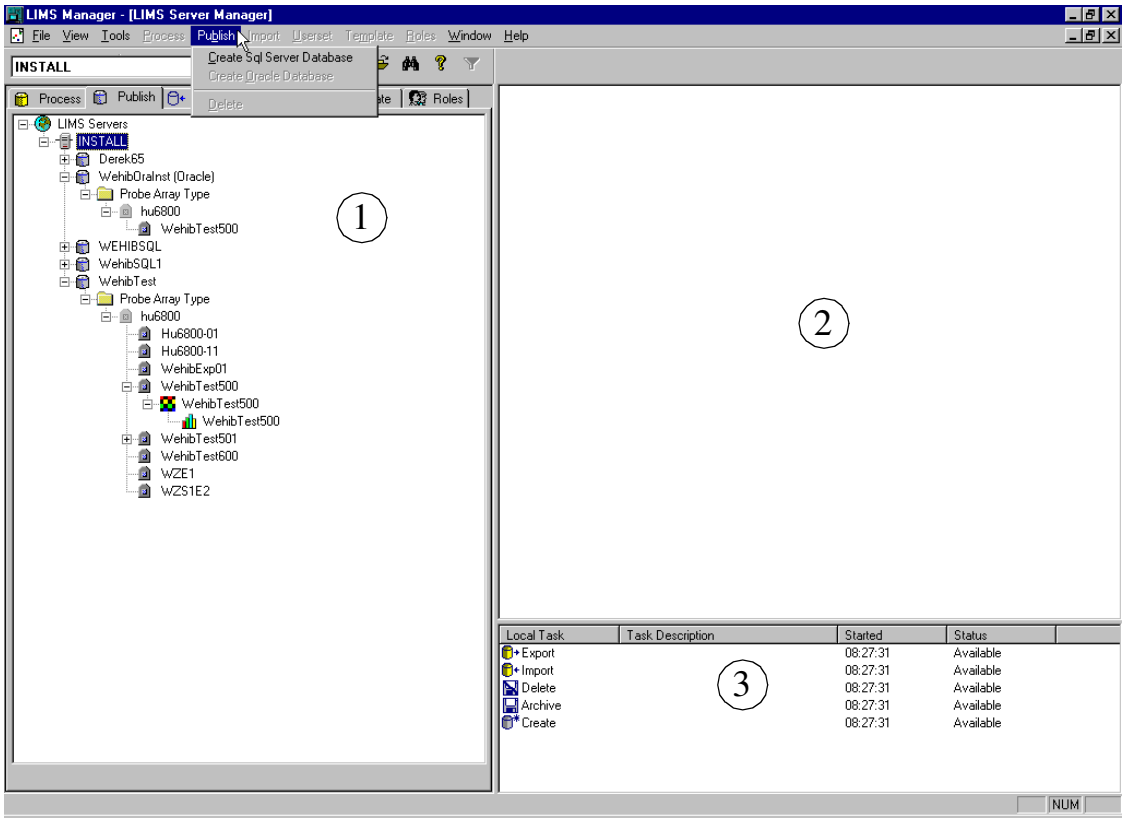


Figure 3.1
The three panes of the Publish tab window

Publish Databases

A new security feature in LIMS Manager v3.0 is password protection for publish databases. Passwords are defined during the creation of the database and can be changed on the server using the LIMS Sync utility. For more information see *Affymetrix LIMS Installation and Administration Guide*.

Accessing Publish Databases

1. From the **Publish** tab, click the database you want to access.
   ⇒ A Publish Database Login window appears.
2. Enter the database **Password** and click **Login**.

✔ Note *Passwords are case-sensitive.*

⇒ The publish database tree expands, displaying the **Probe Array Type** folder **(Figure 3.2)**.

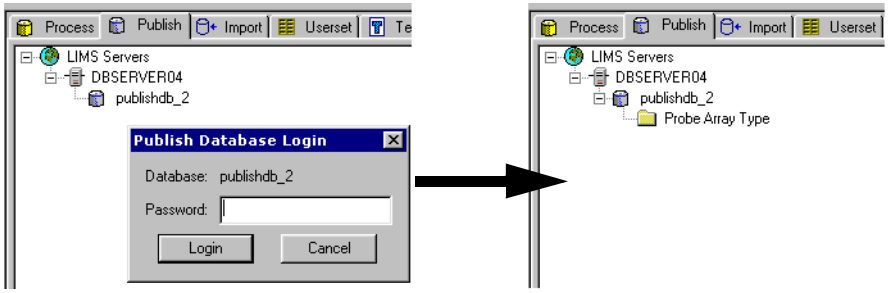


Figure 3.2
Publish Database Login window

Deleting

The **Delete** function allows you to delete data or a probe array type from a publish database.

Probe Array Type

Probe array types that are no longer used may be removed from the publish database. When a probe array type is deleted all published data associated with it, from the parent down, are also deleted.

Deleting a Probe Array Type

1. Click the **Probe Array Type** folder under the publish database of interest.
2. Click to select the probe array type to delete.
3. From the menu bar select **Publish** → **Delete**
   ⇒ A warning window appears **(Figure 3.3)**.

Figure 3.3
Probe array delete warning / confirmation window

4. Click **Yes** to delete the selected probe array type.
   ⇒ The probe array type is removed from the publish database and all associated data is deleted.

OR

1. Right-click the probe array type to delete.
2. Select **Delete** from the shortcut menu that appears.
   ⇒ A warning / confirmation window appears **(Figure 3.3)**.

3. Click **Yes** to delete the selected probe array type.

   ⇒ The probe array type is removed from the publish database and all associated data is deleted.

Publish Data

Deleting publish data removes the specified experiments or analyses from the publish database. When deleting a published data file, all associated files below are also removed.

! CAUTION

Deleting publish data permanently removes data from the database. Deleted data can be restored by repeating the publish procedure in Affymetrix ® Microarray Suite only if the information still resides on a process database.

Deleting Published Data

1. From the drop-down list on the toolbar, select the server where the publish database resides.
2. In the first pane on the left side of the window, select the database of interest and expand the tree.
3. Click to select the data to delete.

   You may either select a single analysis file or an experiment.
4. On the menu bar select **Publish** → **Delete**.

   ⇒ A warning / confirmation window appears **(Figure 3.4)**.

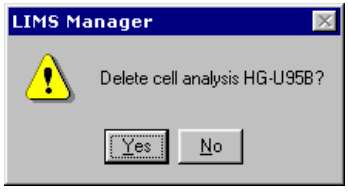


Figure 3.4
Analysis delete warning / confirmation window

5. Click **Yes** to continue.

   ⇒ The **Delete** task proceeds.
   An information window appears asking you to please wait while published file(s) are deleted. In the lower right pane the status is displayed.

   To view more information pertaining to the delete task, double-click **Delete** in the lower right pane, or right-click **Delete** in the lower right pane and select **View Task Log** from the shortcut menu **(Figure 3.6)**.

OR

1. From the drop-down list on the toolbar, select the server where the publish database resides.
2. In first pane on the left side of the window, select the database of interest and expand the tree.
3. Right-click the data to delete and select **Delete** from the shortcut menu **(Figure 3.5)**.

Figure 3.5
Right-click for Delete shortcut

   ⇒ A warning window appears **(Figure 3.4)**.

4. Click **Yes** to continue.

   ⇒ The **Delete** task proceeds.
   An information window appears asking you to please wait while published file(s) are deleted. In the lower right pane the status is displayed.

   To view more information pertaining to the delete task, double-click **Delete** in the lower right pane, or right-click **Delete** in the lower right pane and select **View Task Log** from the shortcut menu **(Figure 3.6)**.

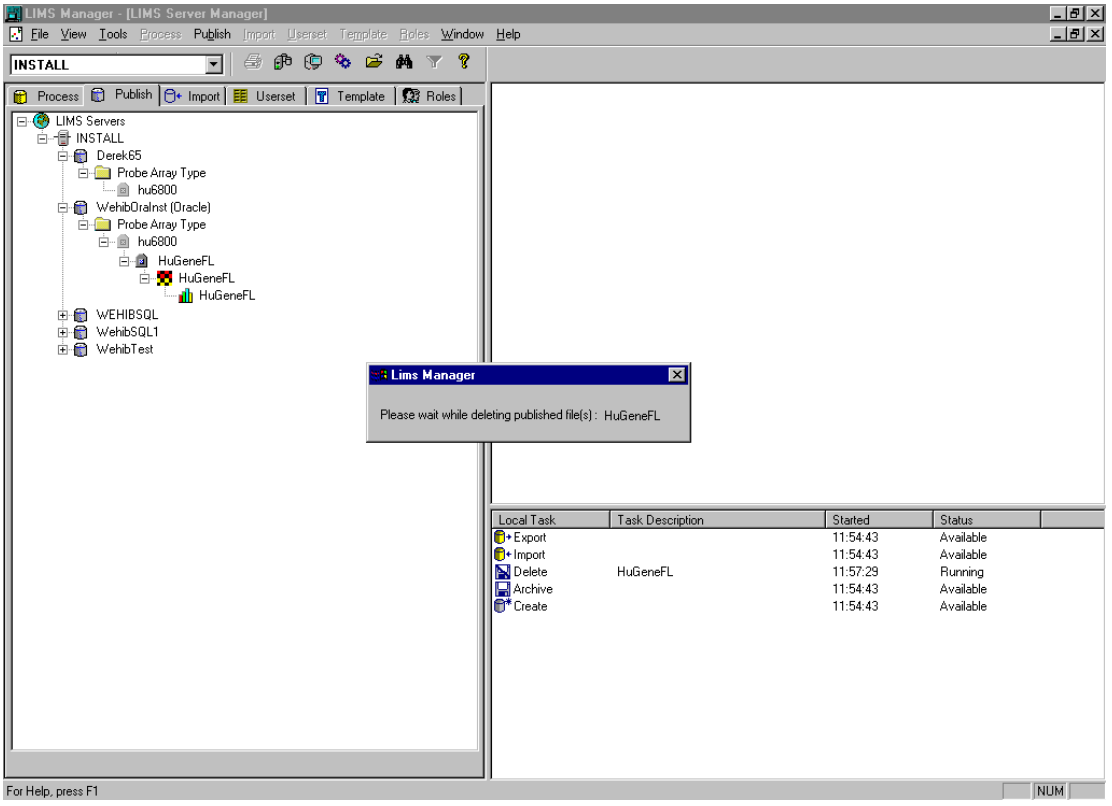


Figure 3.6
Active Delete publish data task

Creating Publish Databases

Create new publish databases at any time from the **Publish** tab of Affymetrix® LIMS Manager. In addition to creating the new database, the system also creates the necessary ODBC DSNs for publishing data. Several key pieces of information are required to create a publish database. This information includes:

- Server on which to create the database
- Username and password with appropriate permissions for creating databases on the selected server
- Size of database to create
- Proper drive and path for the database files

The server name selected on the **Create Publish Database** pages is represented by an ODBC data source name description. This ODBC DSN specifies the location of an administration database that is used to create the actual publish database. This DSN is normally created during the installation process of the Affymetrix® LIMS system.

Database Size Considerations

When creating a Microsoft® SQL Server publish database, the initial size of the database can be between 128 MB and 1024 MB. This size corresponds to approximately the following storage capabilities (based on a probe array with 270 x 270 cells, 1800 probe sets per probe array):

- 8 MB per experiment (includes experiment information, cell file and chip file)
- 8 MB per library file
- 128 MB database = 4 library files and 12 experiments
- 1024 MB database = 16 library files and 110 experiments

Creating an Oracle® publish database has only 2 size options, **Small** and **Large**. The small database takes approximately 6 GB of space and the large is almost 12 GB. These publish databases have enough room to publish approximately 500 and 1000 experiments respectively.

The size of a Microsoft® SQL Server database can easily be increased once the database is created. For information on increasing the size of a SQL Server publish database, see *Affymetrix® LIMS Installation and Administration Guide*.

Microsoft® SQL Server Publish Database

Affymetrix® LIMS Manager 3.0 features increased security with a password-protected publish database. Publish databases can only be accessed with the password defined at the time the publish database was created.

Creating a Microsoft® SQL Server Database

1. From the drop-down list on the toolbar, select the server where the publish database will reside.
2. Click to select the server icon in the left pane of the **Publish** tab.
3. On the menu bar select **Publish** → **Create SQL Database**, or right-click the server icon in the left pane and select **Create SQL Database**.

   ⇒ The Create SQL Database dialog box appears in the upper right pane **(Figure 3.7)**.

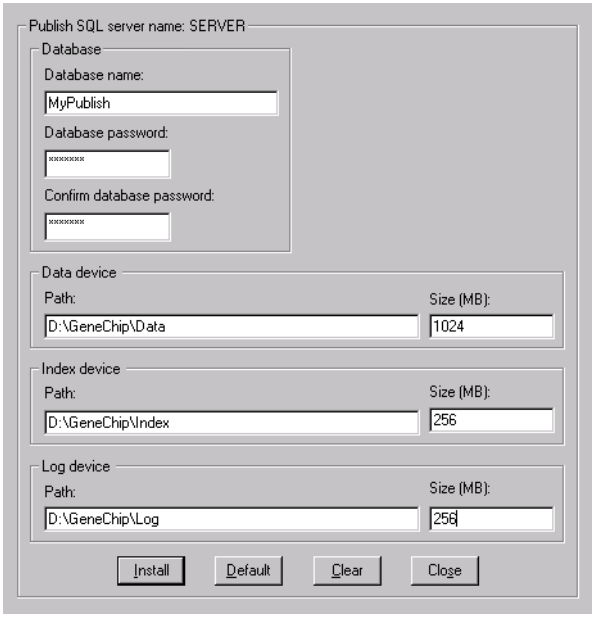


Figure 3.7
Create SQL Database dialog box

4. Enter the following information in the **Database** section:
   - **Database name**: <name for the new publish database>
   - **Database password**: <password of your choice>
   - **Confirm database password**: <re-enter password to confirm>

✔ Note

The publish database name is limited to 22 characters in length.

5. Enter the following information in the **Data device**, **Index device** and **Log device** sections:
   - **Path**: Use the complete drive description, including drive letter, colon and backslash (E:\Affymetrix DBDevices).

✔ Note

The drive letter specifies the drive on the actual publish database server. If the publish database is being created on a remote server, make sure the selected drive letter is available on that server.

   - **Size (MB)**: The size depends on the number of experiments that will be published to the database and the amount of available space on the drive selected. Microsoft® SQL Server databases are relatively easy to expand after creation; therefore, creating a smaller database and expanding it as necessary is recommended.

6. Click **Install**.

   ⇒ It takes several minutes to create the database and allocate the amount of drive space requested (2 -15 minutes or more, depending on the speed of the server and drive).

Once created, the database is available for publishing without further configuration. If the newly created database does not appear in the **Select Publish Database(s)** drop-down list, verify that the database and the ODBC DSN were created properly.

Oracle® Publish Database

✔ Note

The Oracle® publish databases are much larger than the default Microsoft® SQL Server databases. Verify that there is adequate space on the server before creating an Oracle database. The Small Oracle publish database requires 6 GB and the Large database requires 12 GB. These sizes correspond to publishing approximately 500 and 1000 experiments respectively.

Creating an Oracle® Publish Database

1. From the drop-down list on the toolbar, select the server where the publish database will reside.
2. Click to select the server icon in the left pane of the **Publish** tab.
3. On the menu bar select **Publish** → **Create Oracle Database**, or right-click the server icon and select **Create Oracle Database** from the shortcut menu.

   ⇒ The Create Oracle Database dialog box appears in the upper right pane **(Figure 3.8)**.

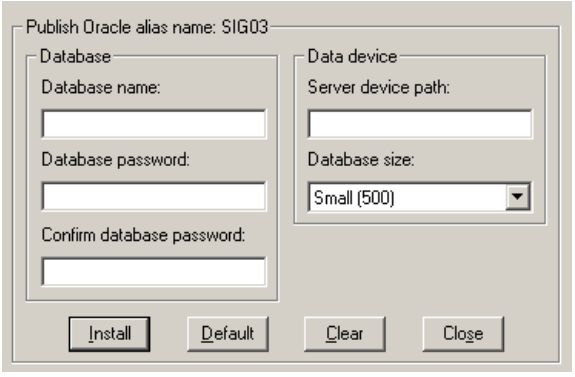


Figure 3.8
Create Oracle Database dialog box

4. In the **Database** section enter the following information:
   - **Database name**: <name for the new publish database>
   - **Database password**: <password of your choice>
   - **Confirm database password**: <re-enter password to confirm>

✔ Note

The publish database name is limited to 22 characters in length.

5. In the **Data Device** section enter the following information:
   - **Server Device Path**: This is the complete path for the database files. Use the complete drive description for Windows 2000. For example: E:\Affymetrix DBdevices\ Be sure to include the trailing slash.

✔ Note

The datafile path directory used specifies the file location on the actual publish database server. If the publish database is being created on a remote server, make sure the path specified is available on that server.

   - **Database Size**: from the drop-down list. The **Small** database requires approximately 6 GB of drive space and the **Large** requires approximately 12 GB.

6. Click **Install**.

   ⇒ It takes several minutes to create the database and allocate the amount of drive space requested (15 - 30 minutes or more, depending on the speed of the server and drive).

   Once created, the database is available for publishing without further configuration. If the newly created database does not appear in the **Select Publish Database(s)** drop-down list, verify that the database and the ODBC DSN were created properly.


LIMS

Chapter 4

Import Tab

*Data created in Affymetrix® Microarray Suite and stored on a local hard drive is moved, or copied, to a process database on a LIMS server with LIMS Manager via the **Import** tab. The additional tasks of editing and updating data are also accomplished from the **Import** tab.*

*This chapter orients you to the layout of the **Import** tab and describes in detail the tasks accomplished here.*

Import Tab Window

The window of the **Import** tab is divided into four panes **(Figure 4.1)**. The first pane displays all registered servers and process databases and lists the samples associated with expression assays.

The second pane in the upper right corner is tabbed with a separate file type on each of the three tabs. The tabs display the corresponding files found at the defined import file path.

In the upper center of the **Import** tab window is the **Data to Import** pane, a staging area where you identify the sample and associate the files of interest with the sample.

The fourth pane found in the lower right corner displays either a Property Information or Local Task status view. Property Information lists environment details pertaining to the selected item. This information is primarily obtained from the **Sample Registration** process and includes information such as **Sample Project**, **Sample Type**, **Initial Stage**, **Description**, **Comments**, **Date**, **User** and **Template**.

The Local Task status view displays the status of processes that may be occurring in the database, such as **Export**, **Import**, **Delete**, **Archive** and **Create**. This view allows you to monitor these jobs while concurrently working on additional tasks within the LIMS system.

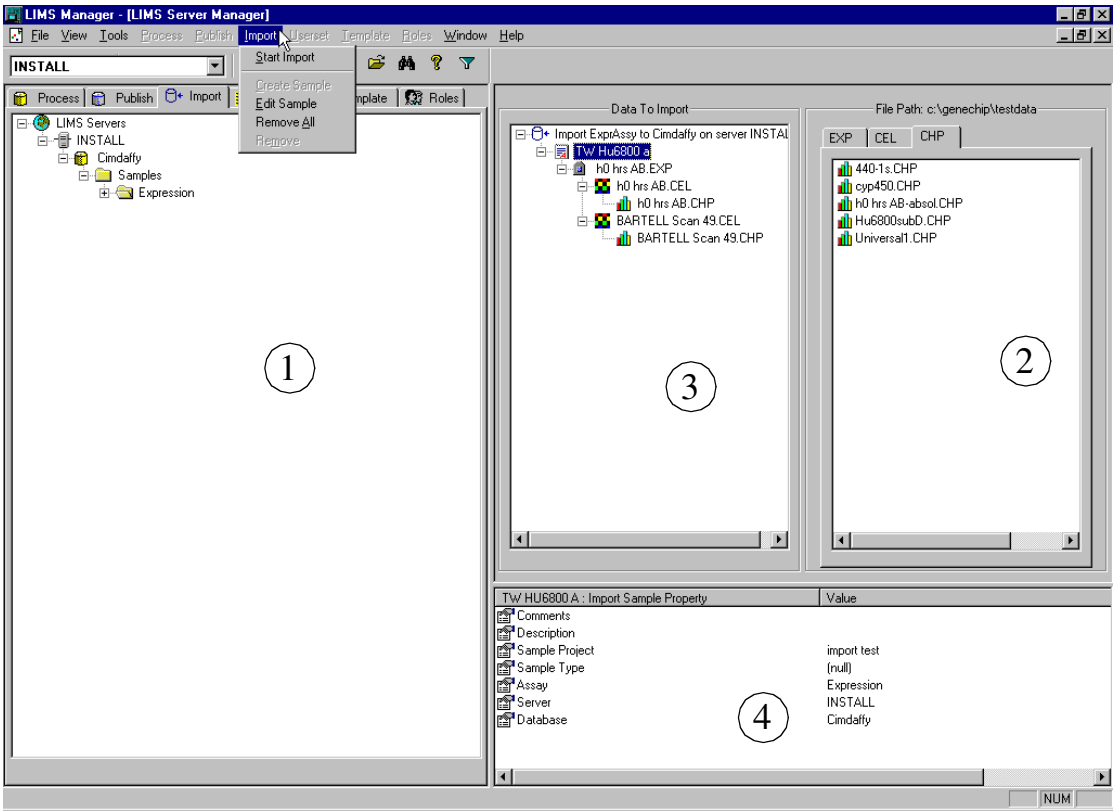


Figure 4.1
The four panes of the Import tab window

Entering and Updating Data

Only the **Import** tab requires your input to enter or update data. The following rules apply for all user input data fields:

Table 4.1
Rules for Data Input

Data Input	Rule
Character length	≤ 64 characters
Invalid Characters	\ / : * ? " < > | ' ~ ´, { } [ ]
Required Data fields	Required fields are indicated by blue titles and may not be left blank
Data fields	Names may not duplicate existing names

Table 4.2
Valid Field Lengths

Editing Samples Attributes	Length
Sample Project	64
Sample Type	64
Description	64
Comments	64
Sample Name	64

Importing Data

The **Import** function imports or copies data files created in Affymetrix® Microarray Suite stored on a local hard drive and moves them to a process database on a LIMS server. It is possible to import data to multiple LIMS Servers. Importing data is a three-step process consisting of selecting a file path, identifying a sample and associating files with the sample.

Selecting an Import File Path

1. On the menu bar select **Tools** → **File Path**, or click the button on the toolbar.
2. Select a **Drive** from the drop-down list and browse to find the desired files.
3. Click **OK**.
   ⇒ The file path defined appears above the upper right pane, and the data files at that location are listed under the **EXP**, **CEL** and **CHP** tabs **(Figure 4.2)**.

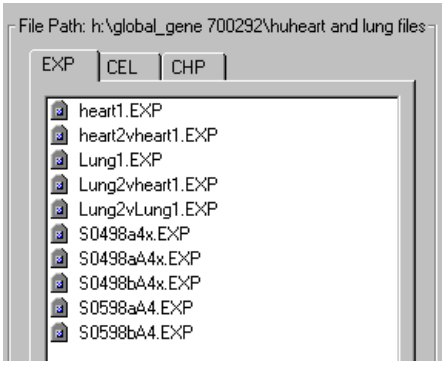


Figure 4.2
File Path location and data type tabs

✔ Note

The default file path is the same path assigned to Affymetrix® Microarray Suite experimental data.

Identifying a Sample

LIMS offers the ability of tracking both the sample and projects associated with an array (experiment). Affymetrix® Microarray Suite starts with the array but does not make project or sample associations. Thus, after selecting a file path, the next step requires you to rebuild this association. This is accomplished by providing a project and sample for each imported array. You do this by creating a new sample or importing data into an existing sample.

Creating a New Sample

The **Create Sample** option, found on the **Import** tab, captures sample information and is available for all assay types. **Create Sample** differs from the **Register Sample** option, available in Affymetrix® Microarray Suite that captures the sample information defined by the template used.

1. In the left pane, click the **Expression** folder.
2. On the menu bar select **Import** → **Create Sample**, or right-click the folder and select **Create Sample** from the shortcut menu.

   ⇒ The Create Sample dialog box appears **(Figure 4.3)**.

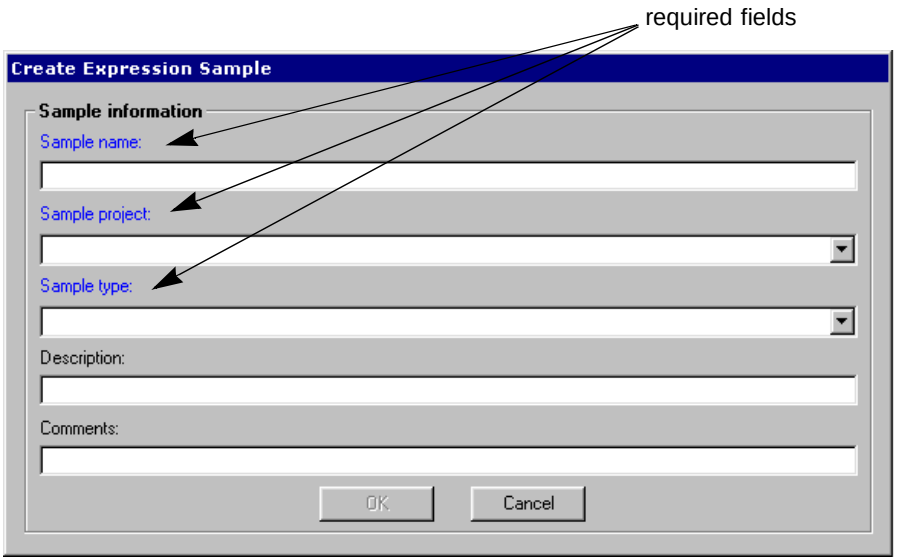


Figure 4.3
Create Sample dialog box

3. Enter the **Sample name**
4. Enter the **Sample project** and **Sample type**, or select from the drop-down lists.
5. Enter **Descriptions** and **Comments**, if desired.
6. Click **OK.**

   ⇒ The sample created appears in the center, **Data to Import** pane.

✔ Note

Once a sample is created, all sample information may be edited except the Sample Name. You may only edit new samples and not existing ones. See "Edit Sample" on page 75.

Selecting an Existing Sample

The second method of identifying a sample is to select an existing sample from the process database tree.

1. In the first pane, expand the **Expression** folder and locate the sample of interest.
2. Click and drag the sample from the first pane and drop into the **Data to Import** pane.

   ⇒ The sample and all associated files appear in the staging area with red check marks indicating that these files already exist in the database **(Figure 4.4)**.

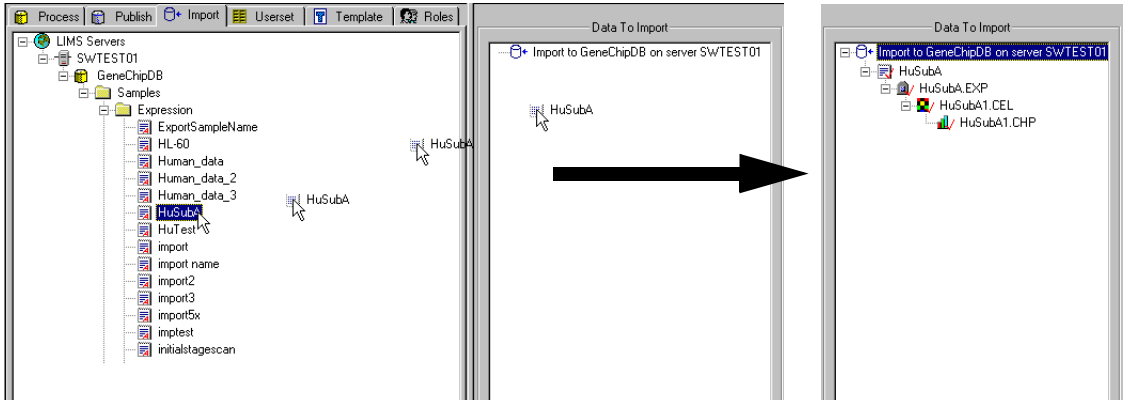


Figure 4.4
Selecting an existing sample for data import

Associating Files

The third and final step of the import data task is to associate files with a sample. Drag and drop an .exp file, and the .cel and .chp files with the same prefix are automatically associated.

Additional files with different prefixes may also be added. This is done in a hierarchical manner. First match the .exp file(s) to the sample. Then match the .cel file(s) to the .exp, and finally the .chp to the .cel.

✔ Note

The filenames of imported files need to conform to the naming conventions within LIMS (see page 69). You may need to rename files to ensure that the filenames conform.

Associating .exp with Sample

The **EXP** tab displays all files located at the designated path that contain the .exp extension. The import process also migrates the .dat file associated with the .exp file via a common filename. Importing an .exp file that does not have an associated .dat file within the designated folder results in an error message. These .dat files without associated .exp files are not available for import.

1. Click and drag the .exp file from the upper right pane and drop on top of the sample you wish to associate it with in the **Data to Import** pane.

   ⇒ The .exp file appears on the branch below the sample name with .cel and .chp files containing the same prefix **(Figure 4.5)**.

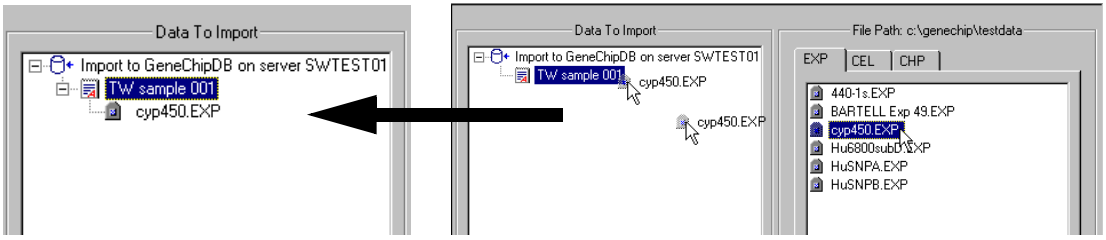


Figure 4.5
Associating .exp file with a sample

2. Repeat step 1 to associate additional .exp files with the sample.

3. If other .cel or .chp files with different prefixes are to be included, continue with the following steps.

Note

You can only associate files from probe array types installed in the LIMS database. If a particular probe array type is not installed, an error message appears when you try to associate files from that probe array type.

Associating .cel with .exp

1. Select the **CEL** tab.
2. Click and drag the .cel file from the upper right pane and drop on top of the .exp file you wish to associate it with in the **Data to Import** pane.
   ⇒ The .cel file appears in the branch below the .exp file in the **Data to Import** pane **(Figure 4.6)**.

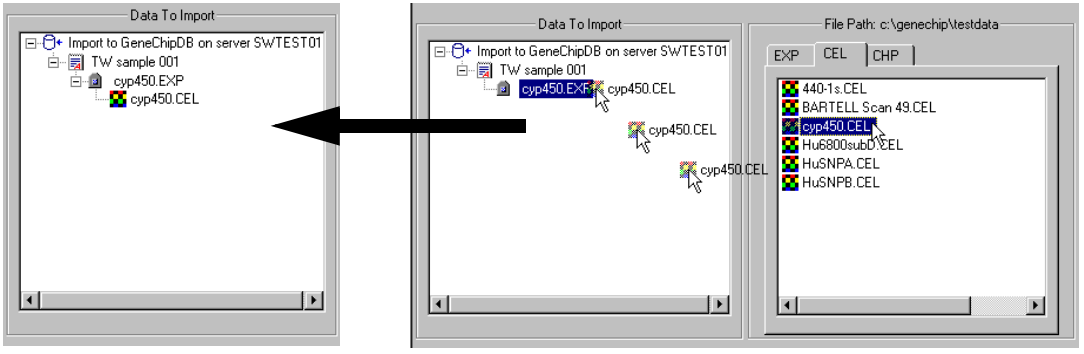


Figure 4.6
Associating a .cel file with an .exp

3. Repeat step 2 for additional .cel files.

TIP

To avoid having to associate a .cel and .chp file with each .exp file imported into the process database, simply import only the .exp file. Then recreate the .cel and .chp files using Affymetrix® Microarray Suite in LIMS mode. This minimizes potential error from mistakenly dragging a .chp file onto the wrong .cel file. Contact Affymetrix Technical Support for help on batch analysis methods in Affymetrix® Microarray Suite, or refer to Affymetrix® Microarray Suite User's Guide.

Associating .chp with .cel

1. Select the **CHP** tab.
2. Click and drag the .chp file from the upper right pane and drop on top of the .cel file you wish to associate it with in the **Data to Import** pane.

   ⇒ The .chp file appears in the branch below the .cel file in the **Data to Import** pane.
3. Repeat step 2 for additional files to associate.

Start Import

From the menu bar select **Import** → **Start Import,** or right-click the sample and select **Start Import** from the shortcut menu.

⇒ The import task proceeds and the status is displayed in the lower right pane.

Double-click **Import** to view more information pertaining to the import task, or right-click **Import** in the lower right pane and select **View Task Log** from the shortcut menu.

Edit Sample

A sample can only be edited in LIMS Manager before it has been imported into a process database. After a sample has been imported, or created via Microarray Suite, it can no longer be edited.

1. Click to select a sample to edit in either the **Data to Import** pane that has not been imported.
2. On the menu bar select **Import** → **Edit Sample**, or right-click the sample and select **Edit Sample** from the shortcut menu.
3. Make changes as necessary. You may not alter the **Sample Name.**
4. Click **OK.**

Remove and Remove All

To correct errors that occur as you build the sample to import, use the **Remove** or **Remove All** command.

1. In the **Data to Import** pane, click to select the file to remove.

   Select a node without children and the **Remove** command is active.

   Select a parent node and the **Remove All** command is active and erases the parent file and all associated children files from the **Data to Import** pane.

2. On the menu bar select **Import** → **Remove** or **Remove All** as appropriate, or right-click the file to remove and select from the shortcut menu.

   ⇒ The file(s) disappear from the **Data to Import** pane.

Sample Filter

The **Filter** function is used to reduce the number of samples displayed in a tree of samples. The **Filter** icon becomes active in the **Process** tab and the **Import** tab when you click a node under a **Samples** folder and remains active from session to session until the parameters are changed.

Using the Sample Filter

1. Click the **Samples** folder.

   ⇒ The tree expands displaying samples and the **Filter** icon on the toolbar becomes active.

2. Click the **Filter** icon  .

   ⇒ The Sample Filter dialog box appears **(Figure 4.7)**.

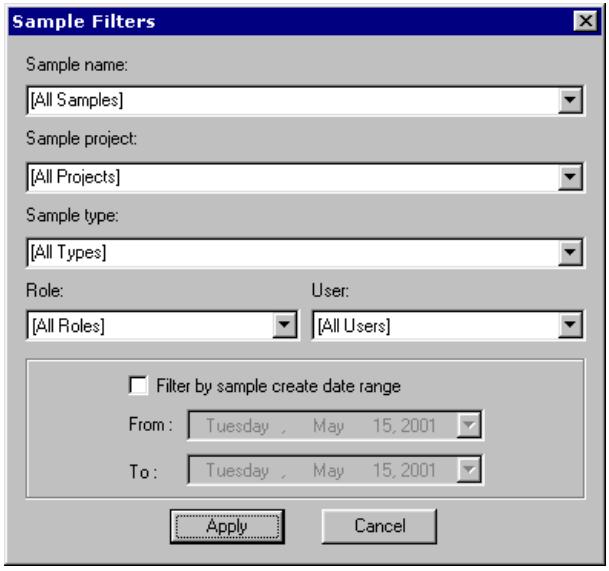


Figure 4.7
Sample Filter dialog box

3. From the drop-down boxes, define filter parameters.

   The **Role** and **User** filter options are mutually exclusive. You may select one or the other, but not both.

4. Click **Apply**.

   ⇒ The Samples are filtered and the sample list is adjusted accordingly.

✔ Note

The filter parameters remain active from session to session. You must reset the parameters when a different display is desired.

5

Chapter 5

Userset Tab

The userset is a predefined set of parameters used when running an expression analysis in Affymetrix® Microarray Suite. Creating and modifying a userset is accomplished from this tab in Affymetrix® LIMS Manager.

*This chapter orients you to the layout of the **Userset** tab window and describes in detail the functions and tasks accomplished here.*

Userset Tab Window

The window of the **Userset** tab is divided into three panes **(Figure 5.1)**. The first pane displays the active servers and process databases, and lists defined usersets and probe array types associated with the expression assay.

The second pane in the upper right corner is the userset definition area where existing usersets are reviewed or edited and where new usersets are created.

The third pane found in the lower right corner displays the Local Task status view that displays the status of processes that may be occurring in the database, such as **Export**, **Import**, **Delete**, **Archive** and **Create**. This view allows you to monitor these jobs while concurrently working on additional tasks within the LIMS system.

You only have access to this tab if the appropriate privileges are defined for you in the **Roles** tab.

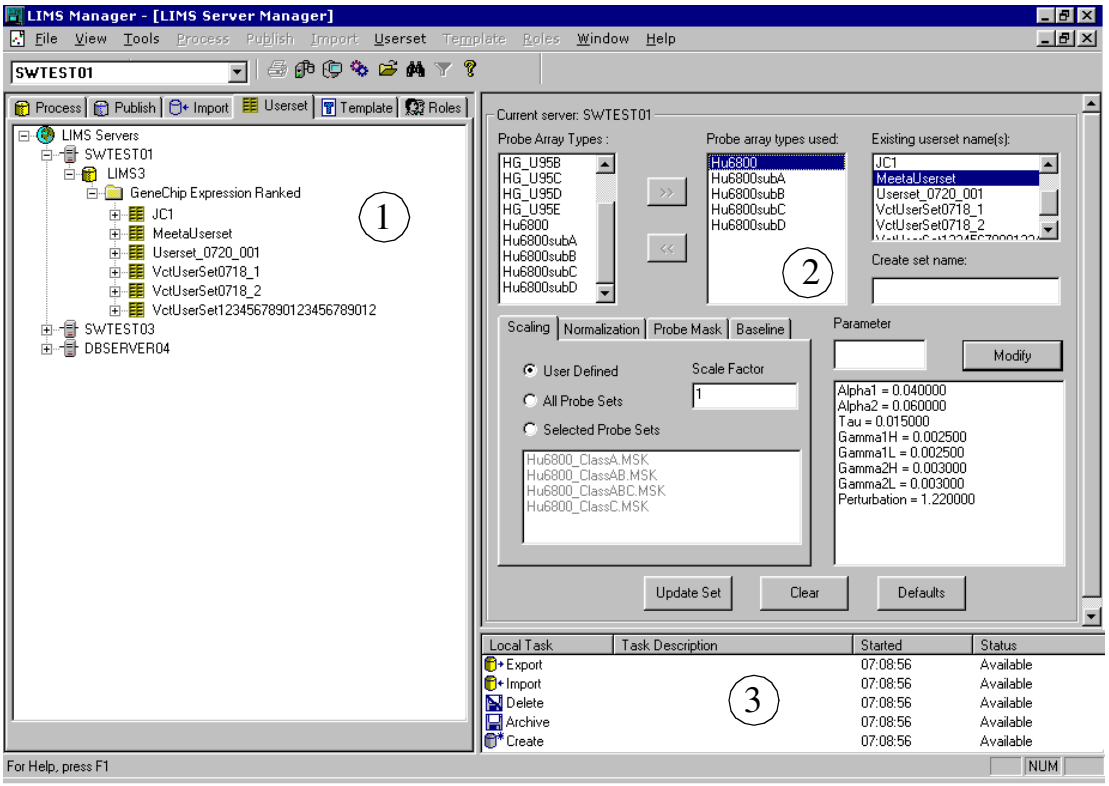


Figure 5.1
The three panes of the Userset tab window

Userset Definition

The algorithm involved in expression probe array analysis has approximately 18 user-defined parameters that are set before an analysis is run. Rather than requiring you to adjust these parameters for each analysis, a predefined userset**,** created by an administrator or other authorized user, frees you to simply select a userset and run the analysis. The function of the userset is to create defined parameters to be used when running an expression analysis.

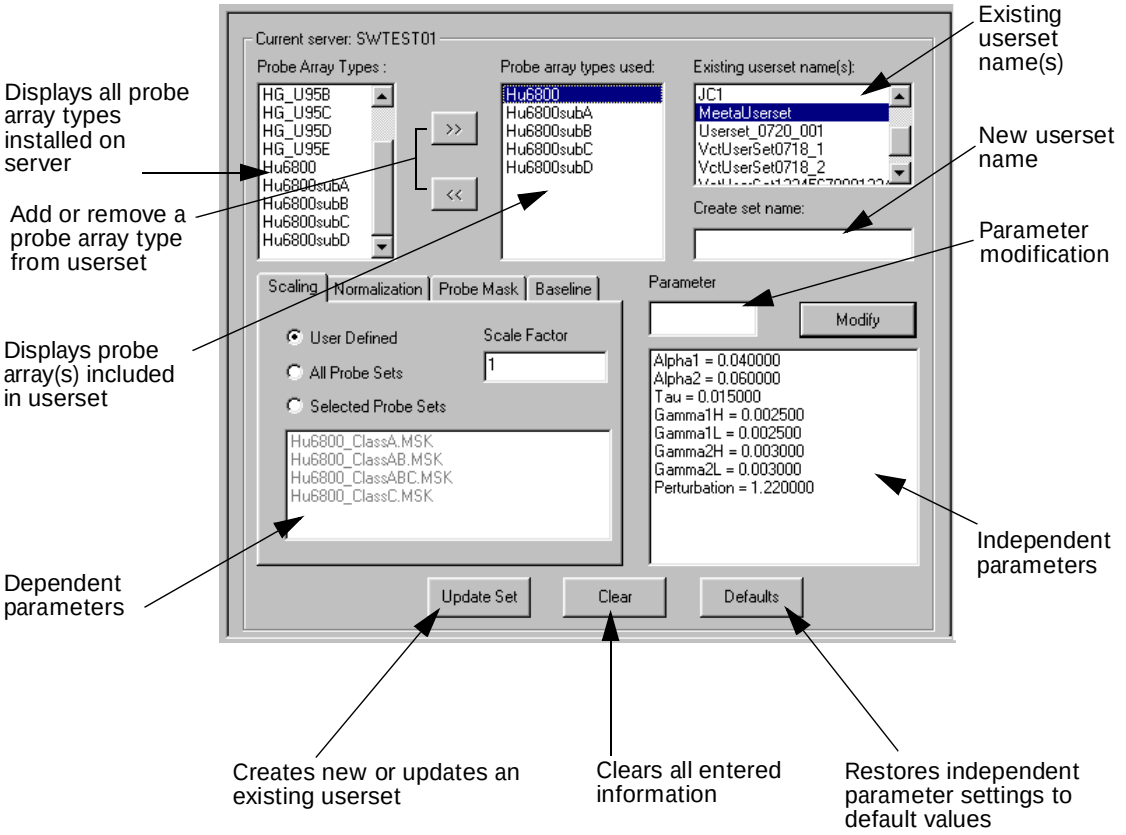


Figure 5.2
Userset definition pane

Creating a Userset

The userset is created in Affymetrix® LIMS Manager and used by Microarray Suite when analyzing a probe array. The procedure outlined below creates the basic shell of a new userset, giving it a name and defining probe array types.

Creating a Userset

1. Type a unique userset name in the **Create set name** box.
2. From the **Probe Array Types** list box, select a probe array type and click **>>** to move to the **Probe array types used** list box **(Figure 5.3)**.

   Repeat this step to add as many probe array types as desired.

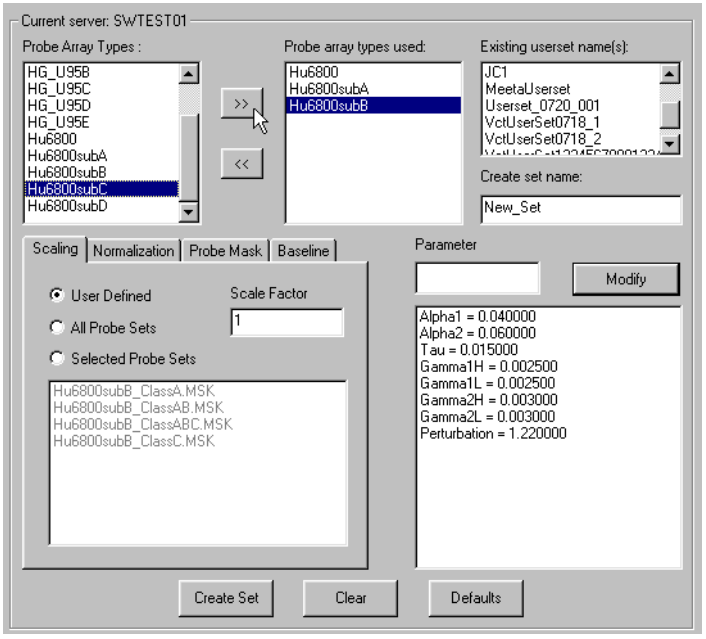


Figure 5.3
Creating a new userset

3. Click **Create Set**.

   ⇒ The name of the new userset appears in the **Existing userset name(s)** list box in the upper right corner and in the left hand pane.

4. Proceed to *Modifying a Userset*.

Modifying a Userset

The 18 user-defined parameter settings are used by the algorithm when running an expression analysis. An existing userset is modified by defining these parameter values.

A userset may also be modified by removing a probe array type. See page 88 for more information.

Define Parameter Values

An independent parameter is a static setting that is not influenced by probe array selection. A dependent parameter is a setting that is specific to the particular probe array type selected. This section outlines how to modify these settings.

TIP *For a detailed explanation of parameters, refer to the Affymetrix® Microarray Suite User's Guide.*

Defining Independent Parameters

1. From the independent parameters list box **(Figure 5.4)** click to select a parameter of interest.

   ⇒ The selected parameter name and current value are displayed in the box above.

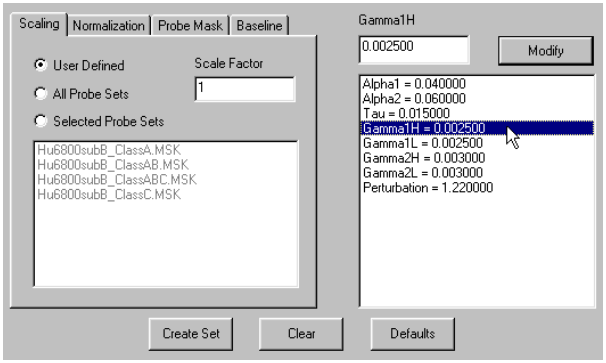


Figure 5.4
Selecting Independent Parameters

2. Type a value in the box above to edit.
3. Click **Modify**.

   New values do not take effect until **Update Set** or **Create Set** is clicked.
4. Repeat for additional values.

   Click **Defaults** to reset independent and dependent parameter values.
5. Click **Update Set**.

Defining Dependent Parameter Values

1. From the **Probe array types used** list box, click to select a probe array type **(Figure 5.5)**.
   ⇒ The selected probe array information appears in the dependent parameter box.
2. Select a method for how the data will be analyzed by clicking the appropriate tab; **Scaling**, **Normalization**, **Probe Mask** or **Baseline**.

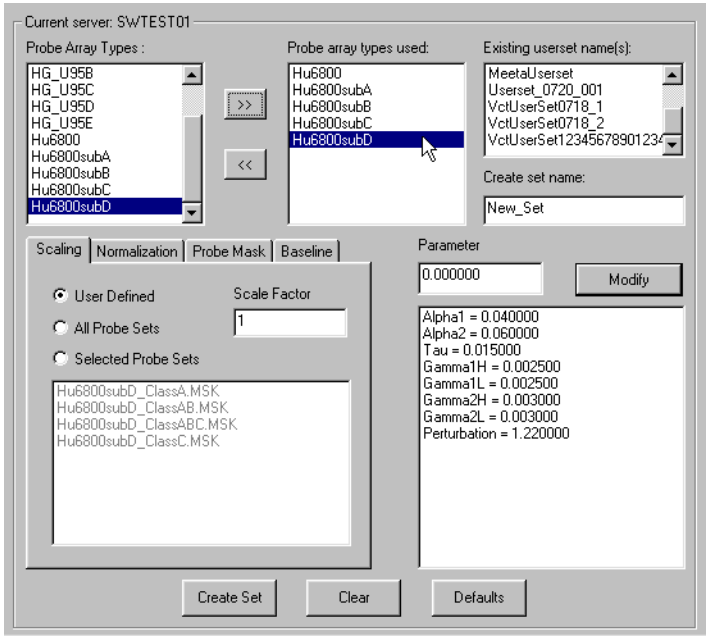


Figure 5.5
Defining parameter values

3. Click **Update Set**.
4. If necessary, repeat for additional probe arrays listed.

Delete a Probe Array Type from a Userset

You may remove a probe array type from an existing userset in one of two ways.

Removing a Probe Array Type Via the Userset Definition Pane

1. Click to select the probe array type to delete in the **Probe array type used** list box in the userset definition pane.
2. Click **<<**.

   ⇒ The probe array type is removed from the **Probe array type used** list box and no longer appears under the userset in the left hand pane.

Removing a Probe Array Type Via the Left Hand Pane

1. In the left hand pane click (+) to expand the userset of interest **(Figure 5.6)**.

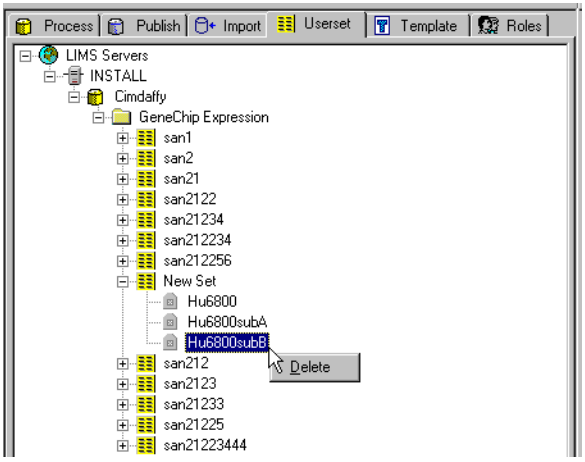


Figure 5.6
Right-click for Delete short cut

2. Click to select the probe array type to delete.

3. From the menu bar select **Userset** → **Delete**, or right-click the probe array type to delete and select **Delete** from the shortcut menu **(Figure 5.6)**.
   ⇒ A warning / confirmation window appears.

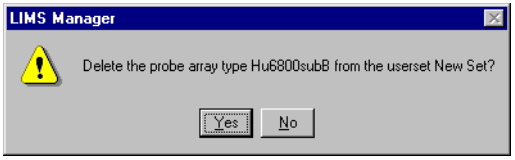


Figure 5.7
Delete probe array warning / confirmation window

4. Click **Yes** to delete.
   ⇒ The probe array type is removed from the userset.

Delete a Userset

Use the delete command to remove a userset that is no longer needed. Deleted usersets are removed in LIMS Manager and are unavailable to Microarray Suite users.

Deleting a Userset

1. In the left hand pane, click to select the userset to delete.

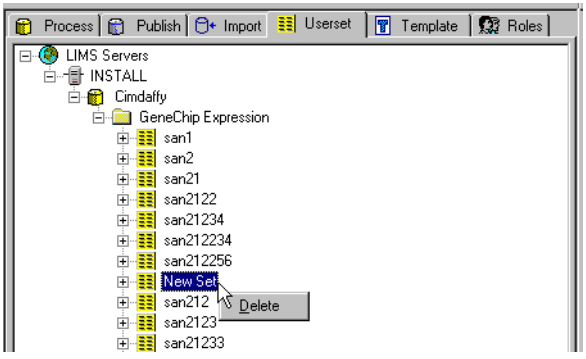


Figure 5.8
Right-click for Delete shortcut menu

2. From the menu bar select **Userset** → **Delete**, or right-click the userset to delete and select **Delete** from the shortcut menu **(Figure 5.8)**.

   ⇒ A warning / confirmation window appears **(Figure 5.9)**.

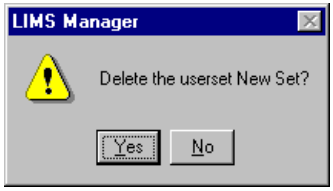


Figure 5.9
Delete warning / confirmation window

3. Click **Yes** to delete userset.

   ⇒ The userset is deleted and removed from both the userset list in the left hand pane and the **Existing userset name(s)** list box in the upper right corner.

6

Chapter 6

Template Tab

A template is a form created by the administrator, or other authorized user in Affymetrix® LIMS Manager, and is used to define the attributes and values for both the experiment and sample registration process. The registration process is a function of Affymetrix® Microarray Suite.

*This chapter orients you to the layout of the **Template** tab window and describes in detail the functions and tasks accomplished here.*

Template Tab Window

The window of the **Template** tab is divided into three panes **(Figure 6.1)**. The first pane displays the active server, the process database and the **Experiment** and **Sample** templates that reside there.

The second pane in the upper right corner is the template attributes area. This pane displays the attributes and values of the template selected in the first pane.

The third pane found in the lower right corner displays the Local Task status view that displays the status of processes that may be occurring in the database, such as **Export**, **Import**, **Delete**, **Archive** and **Create**. This view allows you to monitor these jobs while concurrently working on additional tasks within the LIMS system.

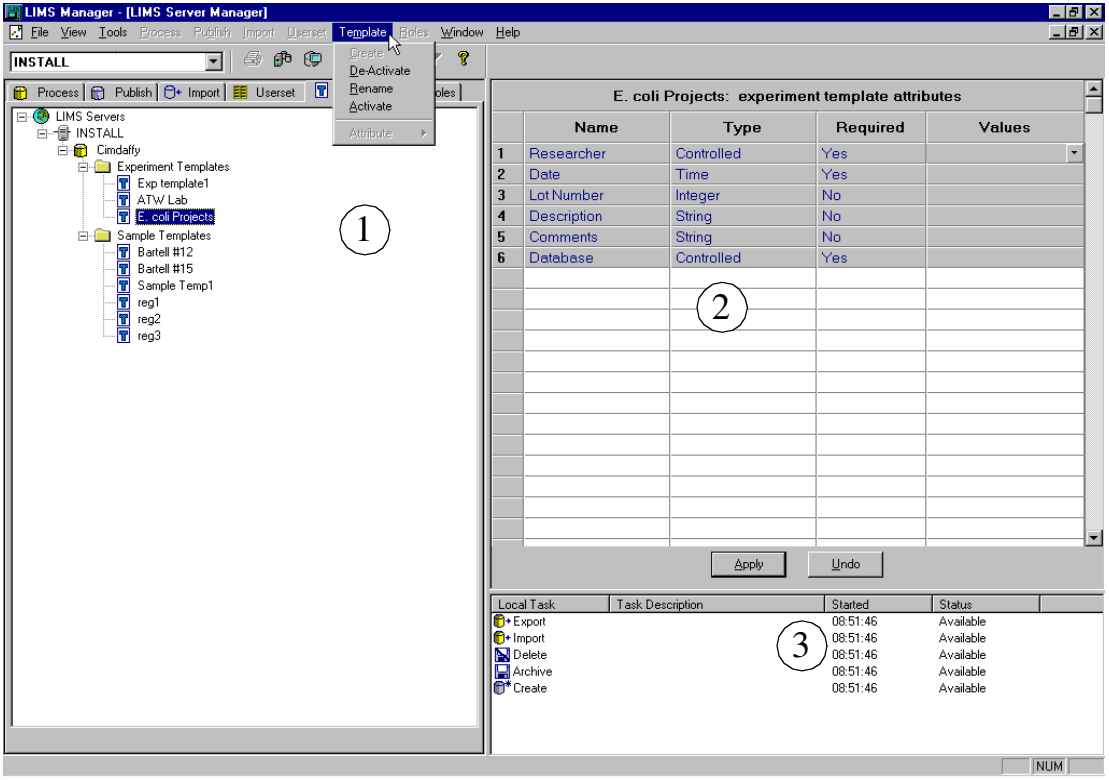


Figure 6.1
The three panes of the template tab window

Templates

Creating a New Template

1. Click to select either the **Experiment Templates** or **Sample Templates** folder.
2. From the menu bar select **Templates** → **Create**, or right-click the templates folder and select **Create** from the shortcut menu that appears **(Figure 6.2)**.

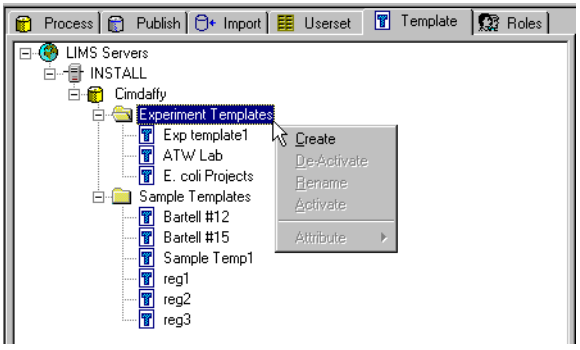


Figure 6.2
Right-click for short cut menu

⇒ The Create Template name dialog box appears **(Figure 6.3)**.

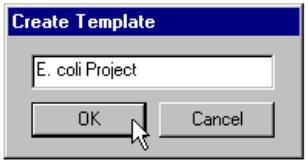


Figure 6.3
Create Template name dialog box

3. Type a unique name for the template type in the box and click **OK**.

   ⇒ The new name appears under the appropriate template folder in the left hand pane, and the upper right hand pane displays the blank template **(Figure 6.4)**.

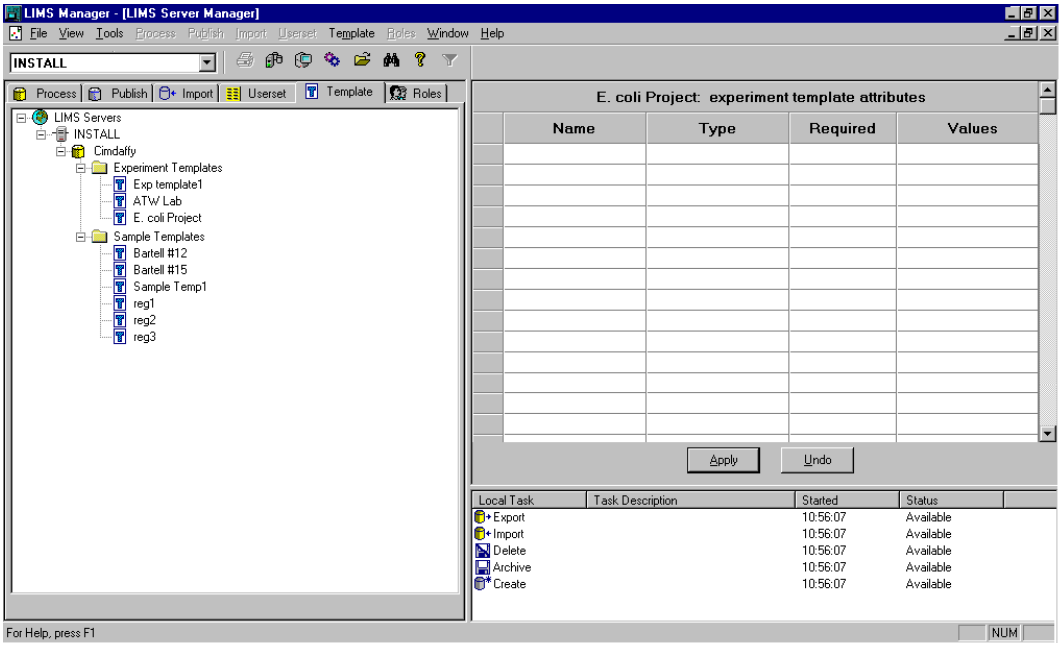


Figure 6.4
New Template appears in List

4. Proceed to *Defining or Editing Attributes and Values*.

Defining or Editing Attributes and Values

The process of defining attributes for a new template, or editing an attribute(s) for an existing template is virtually identical. The procedure below is written as if working with a blank template, however it can also be used for the purpose of editing attributes.

Defining Attributes and Values

1. Click to select a template name in the first pane.
   ⇒ The template appears in the second pane.
2. Double-click a cell under the **Name** column.
   ⇒ The mouse pointer becomes an I-beam, and the other cells in the row are blocked **(Figure 6.5)**.

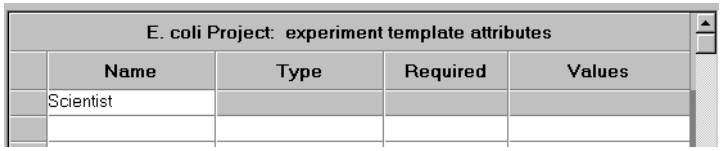


Figure 6.5
Creating an attribute: Naming

3. Type an attribute name and press ENTER.
   ⇒ The attribute name is inserted, and a number appears in the left column.
4. Click the cell under the **Type** column, then click the button that appears.
5. Define the data type for the attribute by selecting from the drop-down list.
   - **Integer**: whole number
   - **Float**: floating point number
   - **String**: limited to 255 characters
   - **Date**: date
   - **Time**: time
   - **Controlled**: limits user response to options listed

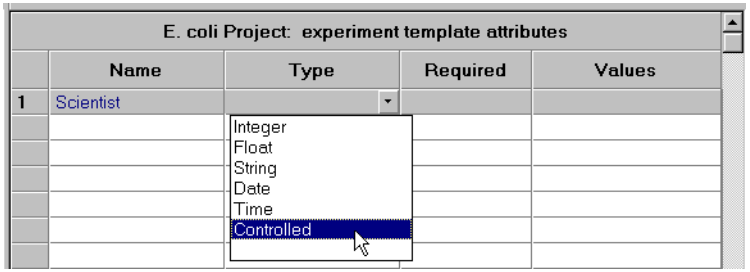


Figure 6.6
Creating an attribute: defining data type

⇒ The data type is defined and appears in the cell **(Figure 6.6)**.

6. Click the cell under the **Required** column, then click the ▾ button that appears **(Figure 6.7)**.

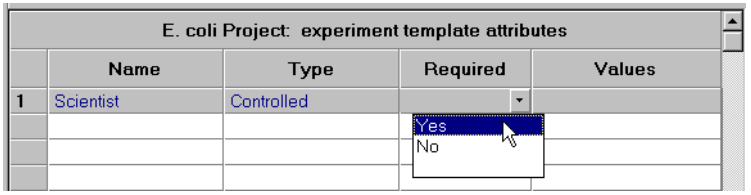


Figure 6.7
Creating an attribute: defining if required

7. Select **Yes** if the information is required or **No** if it is not.

   A **Yes** selection requires the Microarray Suite user to enter a value before the sample or experiment can be registered.

   ⇒ The response entered appears in the cell.

8. If the data type you selected was controlled, double-click the cell under the **Values** column, otherwise go to step 11.

   ⇒ A Controlled Values Edit List dialog box appears **(Figure 6.8)**.

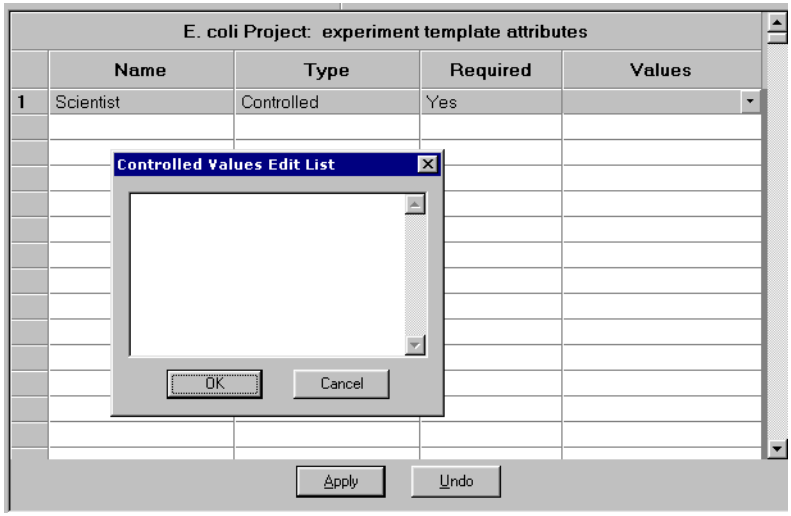


Figure 6.8
Creating an attribute: double-click for Controlled Values Edit List dialog box

9. Define a controlled value by typing the desired value options in the box. Press ENTER after each option **(Figure 6.9)**.

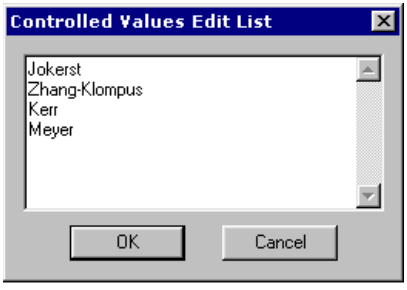


Figure 6.9
Controlled Values Edit List dialog box

10. Click **OK** when finished.

    ⇒ Values appear in drop-down list box under the **Values** column **(Figure 6.10)**.

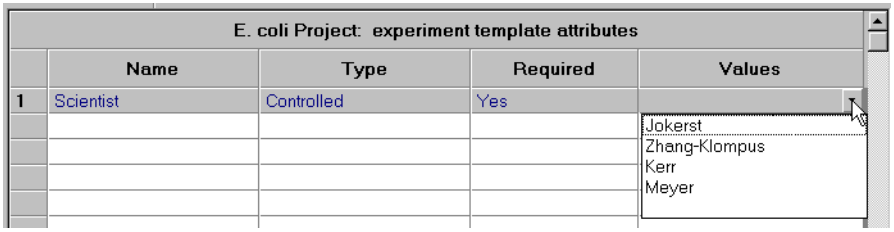


Figure 6.10
Defined controlled values

11. Click **Apply**.

    The defined attributes do not take effect until you click **Apply**.

    ⇒ A warning message appears if this is an update to an existing template **(Figure 6.11)**.

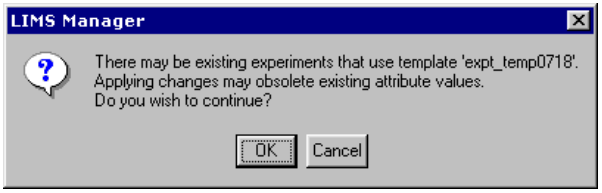


Figure 6.11
Update warning message

12. Click **OK** to continue.
13. Repeat above steps to add additional attributes to the template.
14. Click **Apply**.

    ⇒ The attributes are applied to the template.

TIP

Save time creating and defining attributes in a new template by copying the desired attribute(s) from existing templates and pasting them into a new template. *See page 105.*

Deactivating and Activating

Templates are used in Affymetrix® Microarray Suite during the experiment or sample registration process. Deactivating a template in Affymetrix® LIMS Manager removes it from use in Microarray Suite.

Deactivating a Template

1. Click to select the template to deactivate from the left hand pane.
2. From the menu bar, select **Template** → **Deactivate**, or right-click the template to deactivate and select **Deactivate** from the shortcut menu that appears.
   ⇒ A warning window appears **(Figure 6.12)**.

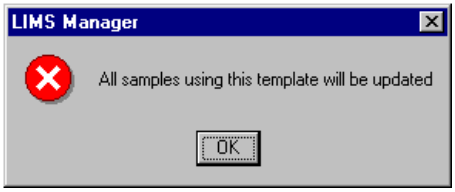


Figure 6.12
Deactivate warning window

3. Click **OK** to deactivate.
   ⇒ The template icon remains in the tree, but appears gray to indicate an inactive template **(Figure 6.13)**.

✔ Note — *Deactivated templates do not appear in Microarray Suite.*

Activating a Template

1. Click to select the template to activate from the left hand pane.
2. From the menu bar, select **Template** → **Activate**, or right-click the template to activate and select **Activate** from the shortcut menu that appears.
   ⇒ The template is activated and the icon is restored to full color **(Figure 6.13)**.

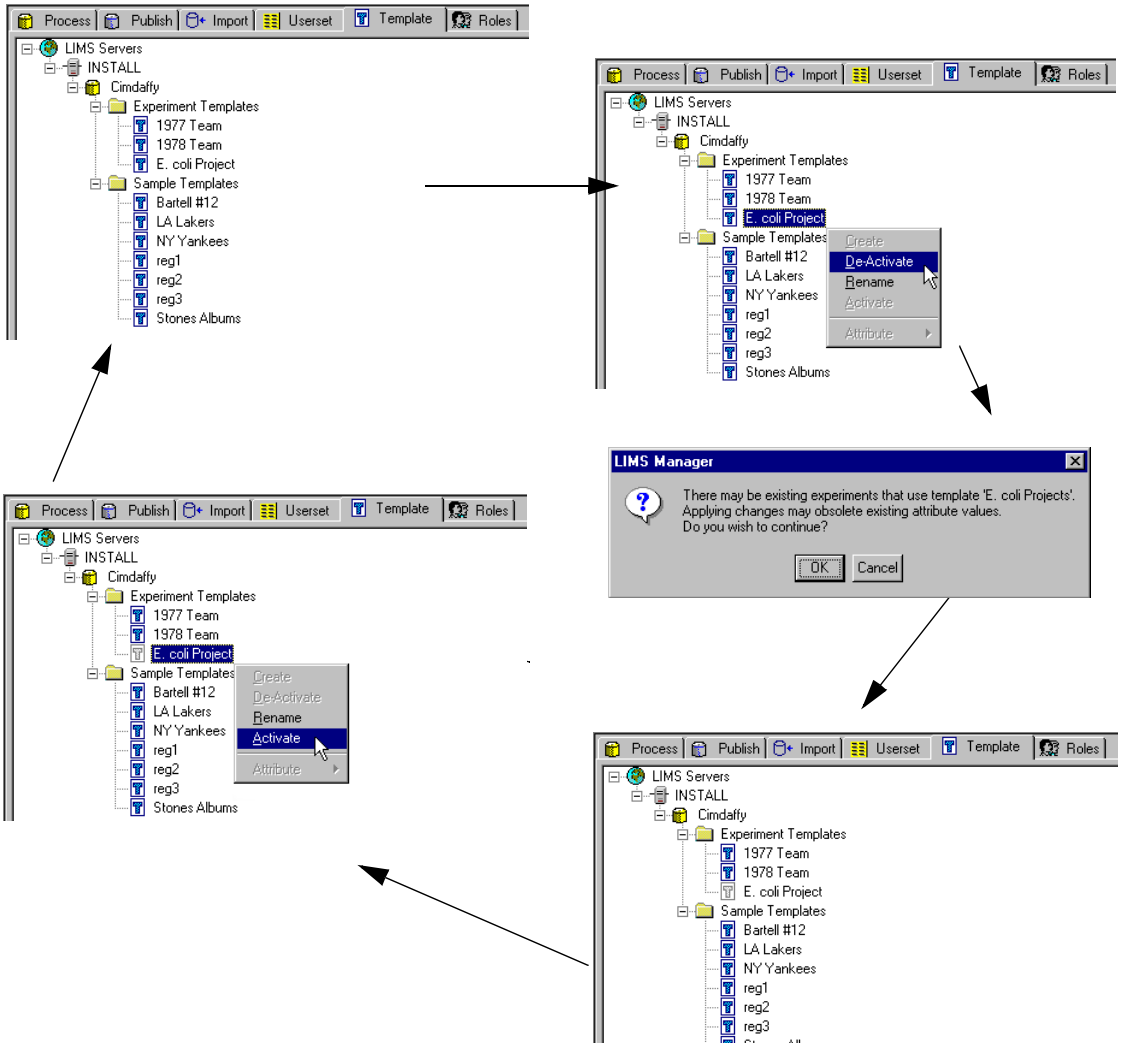


Figure 6.13
Deactivating and Activating Templates

Renaming

Renaming a Template

1. Click to select the template to rename from the left hand pane.
2. From the menu bar, select **Template** → **Rename**, or right-click the template to rename and select **Rename** from the shortcut menu that appears.
3. Type a unique template name in the box, and press ENTER.

Note *You may not duplicate an existing template name for a particular template type.*

Working with Attributes

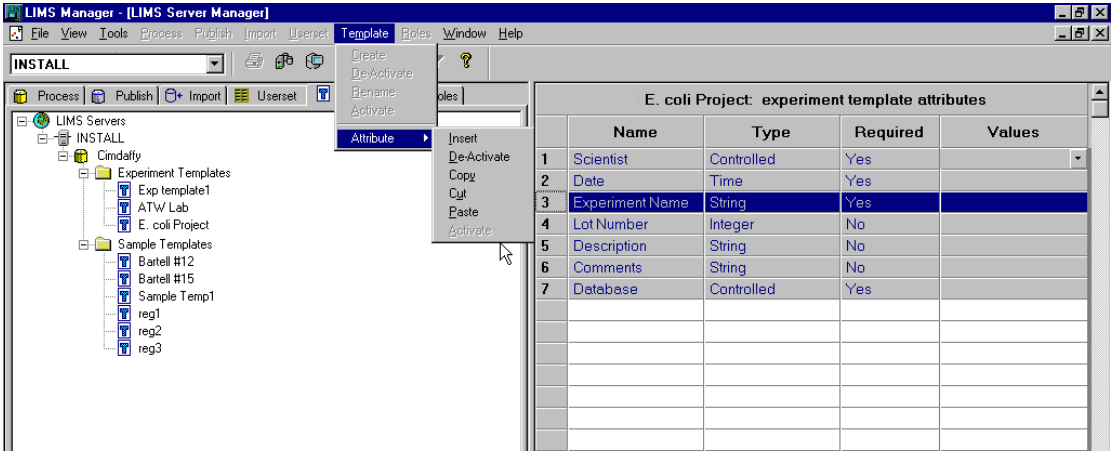


Figure 6.14
Templates menus and commands

Multi selecting

To select multiple contiguous attributes to act upon: click an attribute number in the left column, then SHIFT-click another number anywhere either above or below the first selected. All attributes between the two selections are selected.

To select multiple non-contiguous attributes to act upon: click an attribute number in the left column, then CTRL-click another number anywhere in the list. Repeat as necessary for additional attributes.

Inserting

Inserting an Attribute

1. Select the attribute below the insertion point and click the attribute number in the left column.
2. From the menu bar, select **Template** → **Attribute** → **Insert**, or click the attribute number to select the row then right-click and select **Insert** from the shortcut menu that appears.

   ⇒ A blank row is inserted in the template.
3. Define the attribute.

   For further information, refer to the section *Defining or Editing Attributes and Values* on page 97.
4. Click **Apply**.

Deactivating

Deactivating an Attribute

1. Click the attribute number in the left column.
2. From the menu bar, select **Template** → **Attribute** → **Deactivate**, or click the attribute number to select the row then right-click and select **Deactivate** from the shortcut menu that appears.

   ⇒ The attribute appears grayed-out, but remains in the attribute list.
3. Click **Apply**.

   ⇒ A warning message appears **(Figure 6.15)**.

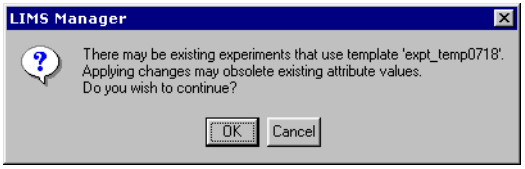


Figure 6.15
Warning message

4. Click **OK** to deactivate the attribute.
   ⇒ The attribute becomes inactive.

✔ Note

In Microarray Suite, deactivated attributes appear for the samples and experiments that have already been saved using the attribute, but cannot be modified. Deactivated attributes are not shown for new samples and experiments.

Activating

Activating an Attribute

1. Click the attribute number in the left column.
2. From the menu bar, select **Templates** → **Attribute** → **Activate**, or click the attribute number to select the row then right-click and select **Activate** from the shortcut menu that appears.
   ⇒ The attribute no longer appears gray.
3. Click **Apply**.
   ⇒ The attribute becomes active.

Copying

Copying an Attribute

1. Click the attribute number in the left column.
2. From the menu bar, select **Template** → **Attribute** → **Copy**, or click the attribute number to select the row then right-click and select **Copy** from the shortcut menu that appears.
   ⇒ The information is copied to the clipboard and is available for a paste action.

Cutting

Cutting an Attribute

1. Click the attribute number in the left column.
2. From the menu bar, select **Template** → **Attribute** → **Cut**, or click the attribute number to select the row then right-click and select **Cut** from the shortcut menu that appears.

   ⇒ The information is removed from the template, copied to the clipboard and is available for a paste action.

Pasting

Pasting an Attribute

1. Click the attribute number in the left column.
2. From the menu bar, select **Template** → **Attribute** → **Paste**, or click the attribute number to select the row then right-click and select **Paste** from the shortcut menu that appears.

   ⇒ The information on the clipboard is pasted on the template as the last item in the list.
3. Click **Apply**.

7

Chapter 7

Roles Tab

A role is a defined set of access privileges created by the administrator to control access to data by users. Creating and defining roles provides the system administrator with a security feature that allows granting various levels of access to different users, or different groups of users.

*This chapter orients you to the layout of the **Roles** tab window and describes in detail the functions and tasks accomplished here.*

Roles Tab Window

The window of the **Roles** tab is divided into three panes **(Figure 7.1)**. The first pane on the left side identifies the server(s) and all the roles that have been created on that server. The branch immediately under the server lists the role names, and is known as the Role Definitions branch **(Figure 7.3)**. **LIMS Administrator** and the **LIMS User** are default roles and cannot be deleted. The LIMS Administrator has the ability to add additional roles.

The process database name for the server is listed below the Role Definitions branch in the first pane. The branch below the process database name lists all role names that have been added to the process database. This is the User Definitions branch and is where users are added and membership to roles is made **(Figure 7.3)**. Double-click a role name to expand the branch and view individual user names listed.

The default view for the second pane in the upper right corner lists the domains that reside on the network. Click a role name in the Role Definitions branch of the first pane and the corresponding template defining the rights and privileges of the role replaces the default view in this pane **(Figure 7.2)**.

The third pane in the lower right corner is the Local Task status view that displays the status of processes that may be occurring in the database, such as **Export**, **Import**, **Delete**, **Archive** and **Create**. This view allows you to monitor these jobs while concurrently working on additional tasks within the LIMS system.

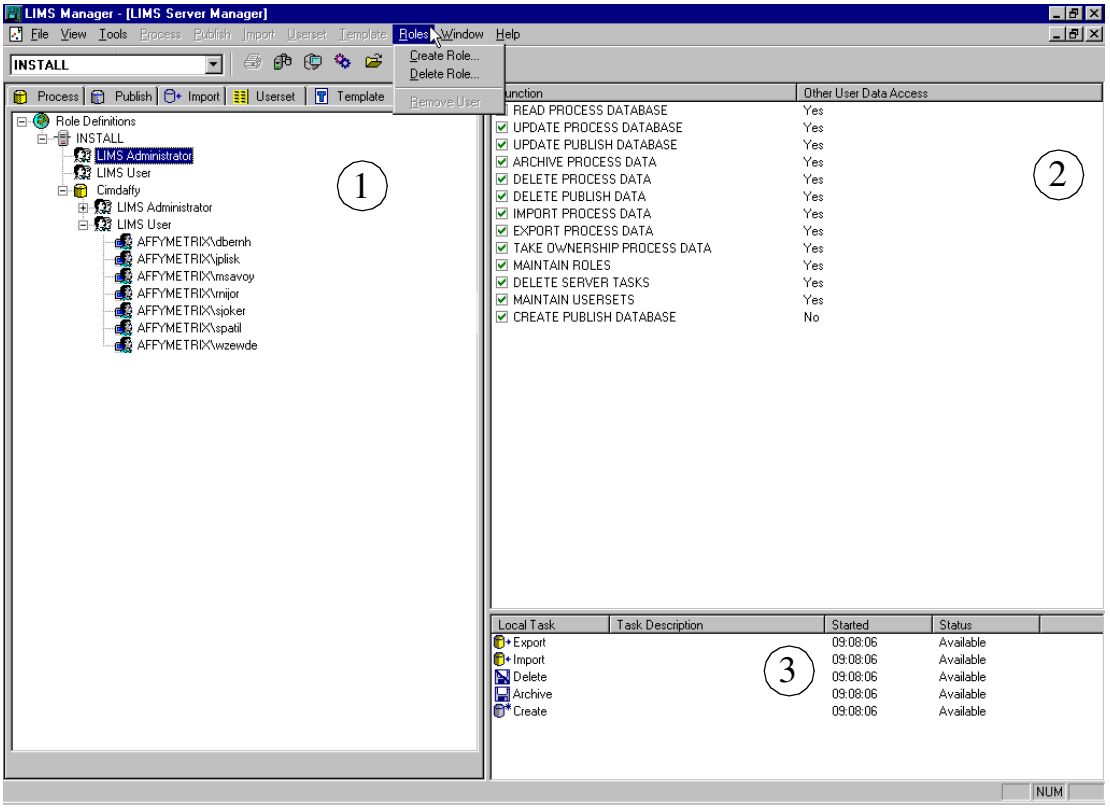


Figure 7.1
The three panes in the Roles tab window

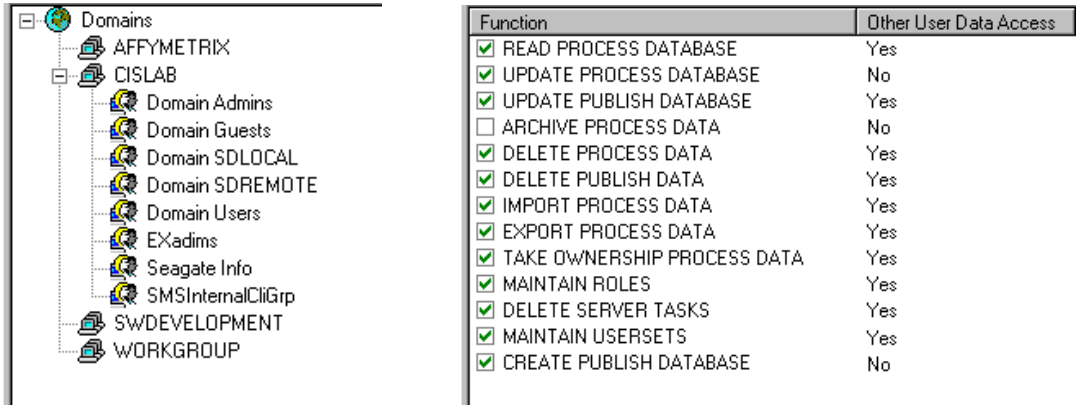


Figure 7.2
Default View and Template View of the second pane of the Roles tab window

Creating a Role

A role provides a user with a set of access privileges. All LIMS users are assigned to a role. Click a role in the Role Definitions branch of the first pane **(Figure 7.3)** and see a template of information about that role appear in the second pane listing role functions. Every role has identical functions associated with it that are static. It is the privileges given to the user to access that function that are modified.

Creating a role is a three-fold process: naming the new role, defining the functions associated with the role, i.e., what the user can and cannot do, and defining role membership.

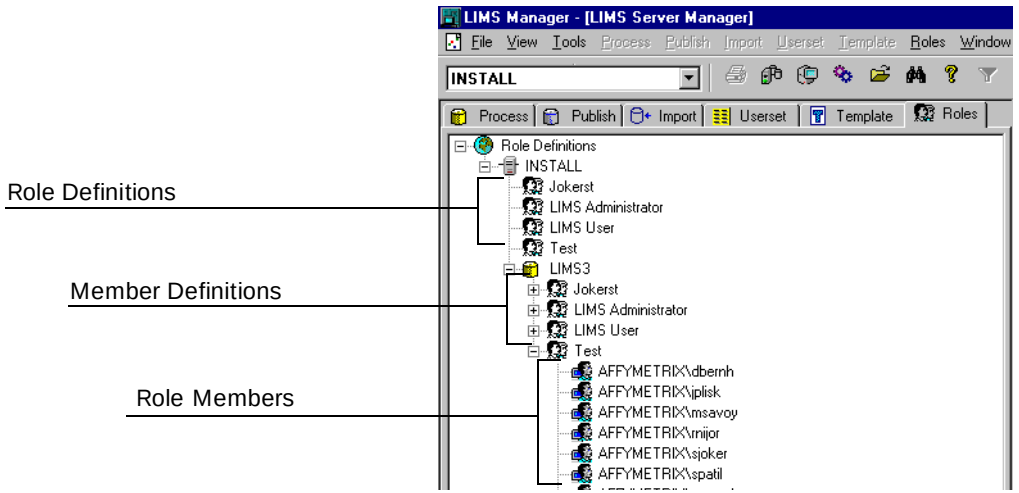


Figure 7.3
Branches identified in the Roles tab

Creating a New Role

1. Click an existing role in the Role Definitions branch in the first pane.
2. On the menu bar select **Roles** → **Create Role**, or right-click an existing role and select **Create Role** from the shortcut menu that appears.
   ⇒ The Create Role dialog box appears **(Figure 7.4)**.

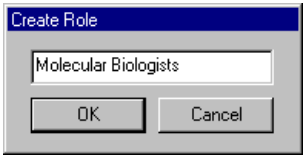


Figure 7.4
The Create Role dialog box

3. Type a role name in box and click **OK**.
   ⇒ The new role appears in the Role Definitions branch in the first pane.

✔ Note *A role name cannot be left blank or duplicate an existing name.*

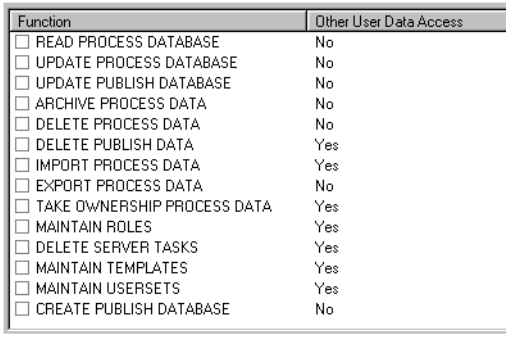
4. Click and drag a role name from the Role Definitions branch and drop it on top of the process database name in the User Definitions branch below.

   ⇒ The new role appears in the User Definitions branch.

Defining Privileges

1. Click the role name in the Role Definitions branch in the first pane.

   ⇒ The corresponding template defining the rights and privileges of the role appear in the second pane **(Figure 7.5)**.



Function	Other User Data Access
☐ READ PROCESS DATABASE	No
☐ UPDATE PROCESS DATABASE	No
☐ UPDATE PUBLISH DATABASE	No
☐ ARCHIVE PROCESS DATA	No
☐ DELETE PROCESS DATA	No
☐ DELETE PUBLISH DATA	Yes
☐ IMPORT PROCESS DATA	Yes
☐ EXPORT PROCESS DATA	No
☐ TAKE OWNERSHIP PROCESS DATA	Yes
☐ MAINTAIN ROLES	Yes
☐ DELETE SERVER TASKS	Yes
☐ MAINTAIN TEMPLATES	Yes
☐ MAINTAIN USERSETS	Yes
☐ CREATE PUBLISH DATABASE	No

Figure 7.5
Default privilege settings

The first column of boxes refers to the rights a role member is given with regards to their own data. The second column is the **Function** or privilege. The third column refers to the rights the role member is given with regards to **Other User Data Access**. **Table 7.1** defines the various privilege functions.

2. Click to select the functions users will have with their own data.

   ⇒ The selected functions appear with a check mark in the box.

3. In the third column, click to toggle **Yes/No** to define the functions a user will have with **Other User Data Access**.

Other User Data Access is always **Yes** and cannot be toggled for the following functions: **Take Ownership**, **Maintain Roles**, **Import Process Data** and **Delete Publish Data**.

✔ Note *The LIMS Administrator role cannot be modified.*

Table 7.1
Role Privileges

Function	Description
Read Process Database	Allows a user to browse sample, experiment and analyses in formation in the process database.
Update Process Database	Allows a user to modify sample and experiment properties information in the process database.
Update Publish Database	Allows a user to overwrite experiment and analyses information in the publish database.
Archive Process Data	Allows a user to move and restore data files from and to the LIMS server.
Delete Process Data	Allows a user to delete sample, experiment, analyses, userset and probe array type information from the process database.
Delete Publish Data	Allows a user to delete experiment and analyses information from any publish database.
Import Process Data	Allows a user to migrate Affymetrix® Microarray Suite datafiles into the process database.
Export Process Data	Allows a user to copy sample, experiment, and analyses files from the LIMS server to a defined location.
Take Ownership of Process Data	Allows a user to assume ownership of a sample, experiment and analyses information with the ability to overwrite a file with new contents (i.e., reanalyzing with different parameters).
Maintain Roles	Allows a user to manage role, role membership and set privileges.
Delete Server Tasks	Allows a user to delete publish tasks on or before a given date.
Maintain Templates	Allows a user to manage templates and their attributes.
Maintain Usersets	Allows a user to manage Expression Analysis parameter sets.
Create Publish Database	Allows a user to create a publish database.

Defining Membership

Adding a User

1. Click to expand the domain name tree in the upper right pane.
   ⇒ The tree expands displaying the user groups residing on the domain.
2. Traverse the tree to find the desired user name.
3. Click and drag the user name and drop it on top of the role in the User Definitions branch in the first pane.
   ⇒ The user is added to the role, and the role name expands to display membership **(Figure 7.6)**.

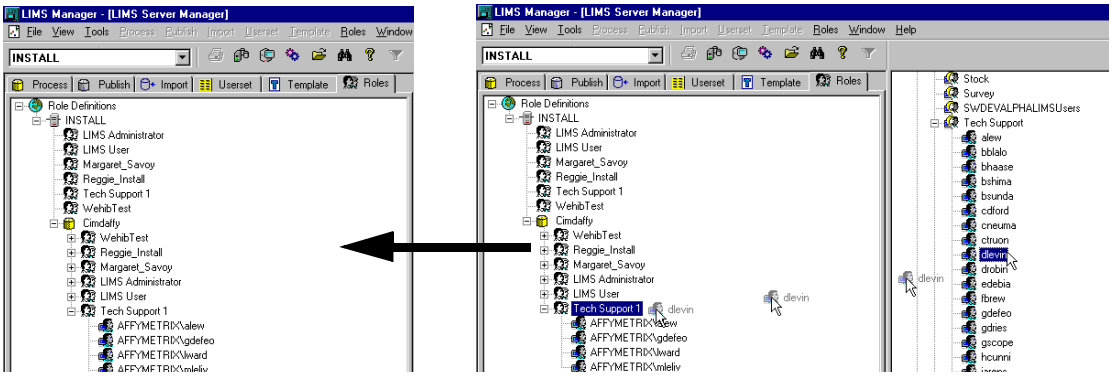


Figure 7.6
Adding a Member

✔ Note

Click and drag the icon to collectively add an entire user group to a role.

Removing a User

1. Click to expand the role in the User Definitions branch of the first pane.
2. Click to select the user to delete.
3. On the menu bar select **Roles** → **Remove User**, or right-click the user name and select **Remove User** from the shortcut menu.
   ⇒ The user name is removed from role membership.

Deleting Roles

✔ Note

LIMS User and LIMS Administrator are default roles and cannot be deleted.

Deleting a Role

1. Click to select the role to delete.
2. On the menu bar select **Roles** → **Delete Role**, or right-click the role to delete and select **Delete Role** from the shortcut menu.

   ⇒ A warning window appears **(Figure 7.7)**.

Figure 7.7
LIMS warning window

3. Click **Yes** to delete.

   ⇒ The role is deleted and disappears from both the Role Definitions and the User Definitions branches in the left pane.

A

Appendix A

Print Samples

The following are samples of two types of print output available in LIMS Manager.

Diagram Only

AFFYMETRIX

ProcessView Report of Experiment:Wisc_Control (Diagram Only) 5/15/01 12:33:37

Sample Name	:	UOF W	Date	:	Mar 30 2000 10:21AM	Server	: DBSERVER04
Sample Project	:	Uof W	Stage	:	Hybridization	Database	: LIMS3
Sample Type	:	total RNA	Template	:		User	: lwang
Comments	:						
Description	:						

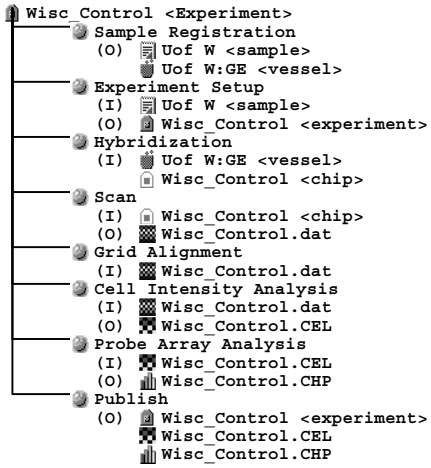


Figure A.1
Print Diagram Only

Diagram & Properties

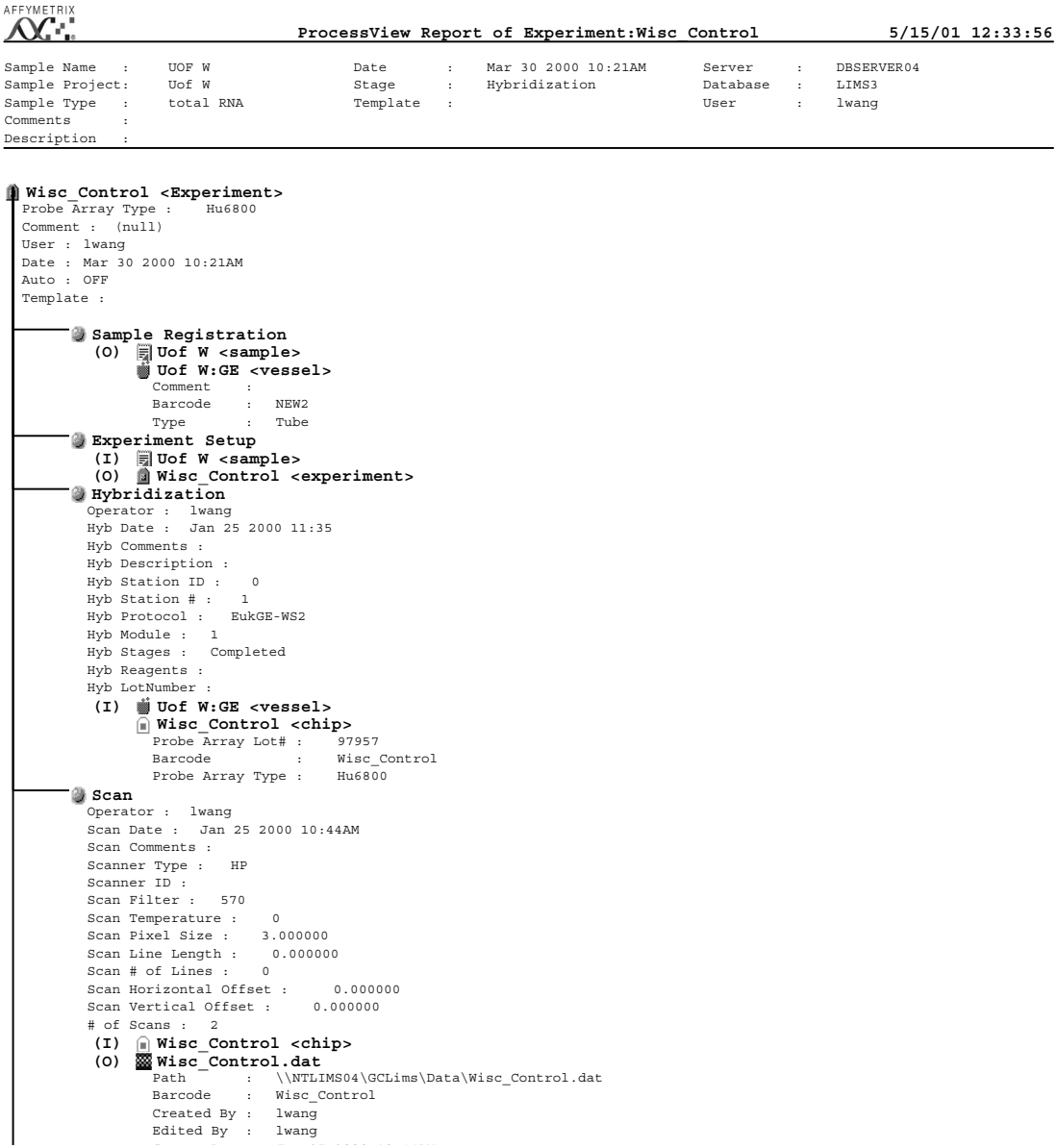


Figure A.2
Print Diagram and Properties (page 1 of 4, only)

B

Appendix B

FAQs

This appendix lists frequently asked questions (FAQs) regarding Affymetrix® LIMS Manager. If after reviewing these questions you still need assistance, please contact Affymetrix Technical Support.

LIMS FAQs

Q: I want to view information about other expression samples. I try to select another sample by clicking its icon but the software refuses to switch to a different sample. What should I do?

A: Throughout the program, click the text representing the sample or experiment name rather than the icon.

Q: How can I change the "export to" or "import from" location?

A: On the menubar, click the icon that depicts a folder opening (see page 18). If you are in the **Process**, **Publish**, or **Find** tabs, this will select a target location for exported files. If you are in the **Import** tab, this will select a location to import files.

Q: How do I use the **Find** command to search the Publish database?

A: The **Find** command only works with the Process database.

Q: Using the **Find** command, I know some of my samples (projects or experiments) are in the process database. However, the results continually produce an empty set. Why does this happen?

A: In the **Find** window, the **Select Object** tab, the **Advanced Filter** tab, and the **Data Filter** tab are additive. Thus if you select experiments with the text string "*xxxAssay*" using the **Select Object** tab and then limit the search to *Project X* using

the **Advanced Filter** tab, then the **Find** command is looking for experiments with the text string "xxxx" that are members of Project X.

Q: I want to delete (assume ownership, export, or archive) multiple files (experiments or samples) at one time. However I cannot select multiple files at one time within the process database. How can I accomplish this?

A: You can SHIFT-select or control-select multiple files, samples, or experiments at one time within the **Find** window. The majority of the functions available within the **Process** tab are also available within the **Find** window.

Q: I want to archive a sample but the software won't let me choose that function. How do I archive a sample?

A: Currently, archiving can be performed on experiments and files, but not samples. A list of available functions within the **Find** window is listed below:

Files: archive, assume ownership, delete, and export

Experiments: assume ownership, delete, export and rename

Samples: assume ownership, delete, and rename

Q: How do I get out of the **Find** window and back to the process database?

A: Simply close **Find** window or go to the Windows menu and select "LIMS server manager."

Q: Can I view property information about files in the publish database?

A: No, this information is not available. But you are able to view property information about files in the process database from either the **Publish** or the **Process** tabs.

Q: I can't find my .dat file under the LIMS **Import** tab. I have confirmed that the .dat file exists on the local drive and that I have the import location mapped correctly. Why doesn't LIMS let me import my .dat file?

A: LIMS will import .exp files and the associated .dat files with the same filename. Make certain that an .exp file that contains the exact same filename is contained within the same folder as your .dat file. As a last resort, open your .dat file in

Affymetrix® Microarray Suite. If an .exp file does not exist for that .dat, Affymetrix® Microarray Suite will automatically create one.

Q: When I try to open a Sample folder, only a few samples are displayed and I know that there should be more in the database. What happened to the samples?

A: The Sample filter remains active during successive sessions. Reset Sample Filter parameters. See *Sample Filter*, on page 47.

Index