ABI PRISM[®] Genotyper[®] 2.5 Software

User's Manual



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Introduction to Genotyper Software Version 2.5

New Features The latest release of the ABI PRISM[®] Genotyper[®] Software, version 2.5, has two new features:

 The ability to import ABI PRISM[®] GeneScan[®] Analysis data from a BioLIMS[®] 2.0 database.

See Chapter 13 for more information.

 The ability to import and process GeneScan sample files containing a 5th dye.

See Chapter 14 for more information.

IMPORTANT Genotyper v. 2.5 runs only on a Power Macintosh[®] computer.

Note The user interface for importing dye colors and raw data has been changed in this version (v. 2.5) of Genotyper Software. This change is described in Chapter 14.

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1

Introducing Genotyper

Chapter Overview

Introduction	This chapter describes ABI PRISM [®] Genotyper [®] 2.5, the components of the ABI PRISM Genotyping Software System, and requirements for installing and starting Genotyper.	
In This Chapter This chapter contains the following topics:		
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Introducing Genotyper 1-1

Overview of ABI PRISM Genotyper 2.5

Definition Genotyper is a software application that enables you to analyze and interpret nucleic acid fragment size and quantitation data by converting it into user defined results.

You can transfer these results to:

- GenBase for storage
- GenoPedigree for display on pedigrees
- Other databases for storage, spreadsheets for statistical analysis or linkage analysis.

1-2 Introducing Genotyper

How You Can Use You can use Genotyper, as well as the other components of the ABI Genotyper PRISM Genotyping Software System, to automate and assist you with many different genetic research projects including:

Microsatellite Analysis

- Fluorescent genotyping for genetic linkage studies
- Paternity identification
- Forensic identification of samples
- Determination of loss of heterozygosity
- Microsatellite instability
- Trisomy analysis

AFLP Analysis

- Gene Mapping using amplified fragment polymorphisms (AFLP)
- Quantitative expression of gene products

Gene Expression Profiling

- Differential display
- Quantitative expression of gene products

Mutation Detection

- Single strand conformation polymorphisms (SSCP)
- Heteroduplex mobility assays (HMA)
- Mismatch cleavage

Mutation Screening

- Oligonucleotide ligation assays (OLA)
- Allele-specific PCR
- Gene dosage PCR
- RNAse protection assays

For more information on ABI PRISM Genotyping Software System components, see "Overview of the ABI PRISM Genotyping Software System" on page 1-5.

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How Genotyper The following figure shows how Genotyper analyzes data imported from Works ABI PRISM GeneScan® and BioLIMS®:

GeneScan Results Data

- Dye color
- · Sample fragment size and quantitative data
- Sample information and comments

Import GeneScan Sample files or BioLIMS data



1-4 Introducing Genotyper

Overview of the ABI PRISM Genotyping Software System

Definition Genotyper[®], GeneScan, GenBase[™], and GenoPedigree[™] are four stand-alone software applications that when used together make up the ABI PRISM Genotyping Software System.

System Components programs through GenBase.

Relationship of The diagram below illustrates how the ABI PRISM Genotyping Software System integrates Genotyper with GenoPedigree and linkage analysis



Introducing Genotyper 1-5

Component	The following table describes the components of the ABI PRISM
Descriptions	Genotyping Software System.

Components of the ABI PRISM Genotyping Software System:

Component	Description
ABI PRISM GeneScan	Analyzes nucleic acid fragment data collected by an ABI PRISM instrument and sizes and quantifies detected fragments, putting the results in GeneScan files.
ABI PRISM Genotyper	Analyzes data from GeneScan files or BioLIMS, labeling fragment data and creating tables specific to your genotyping studies.
ABI PRISM GenoPedigree	An interactive pedigree diagram editor that reads and writes its own documents containing pedigree, layout, and style information.
ABI PRISM GenBase	A database application that stores data for genotypes, pedigrees, markers, traits (diseases), and other relevant information. You can import data from or export data to GenBase from Genotyper, and GenoPedigree.

1-6 Introducing Genotyper

RelatedThe following table describes publications that you can refer to forPublicationsdetailed information about ABI PRISM Genotyping Software System component applications.

Publication List:

Publication	Description	
I	Hard-copy Publications	
ABI PRISM Genotyper User's Manual	Explains how to use features of Genotyper to analyze data from GeneScan files and BioLIMS, and produce results data specific to your Genotyping application.	
ABI PRISM Genotyper Applications Tutorials	Contains tutorial information for using Genotyper and Genotyping Software System components to perform typical genotyping applications.	
ABI PRISM GenoPedigree User's Manual	Explains how to use GenoPedigree to display, generate, and analyze, import and export pedigree diagrams and data.	
ABI PRISM GenBase User's Manual	Explains how to use a database application that stores data for genotypes, pedigrees, markers, traits (diseases), and other relevant information. You can import data from or export data to GenBase from Genotyper and GenoPedigree.	
ABI PRISM GeneScan User's Manual	Explains how to use GeneScan Analysis software to size and quantify nucleic acid fragments detected on an ABI PRISM instrument.	
CD-ROM Publications		
ABI PRISM Genotyper User's Manual	Allows you to use online navigation tools to search for information contained in the Genotyper User's Manual, and access user documentation for other Genotyping System Software components.	
ABI PRISM Genotyper Applications Tutorials	Allows you to use online navigation tools to search for information contained in the Genotyper Applications Tutorials, and access user documentation for other Genotyping System Software components.	
ABI PRISM GenBase User's Manual	Allows you to use online navigation tools to search for information contained in the GenBase User's Manual, and access user documentation for other Genotyping System Software components.	

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Publication List: (continued)

Publication	Description
ABI PRISM GenoPedigree User's Manual	Allows you to use online navigation tools to search for information contained in the GenoPedigree User's Manual, and access user documentation for other Genotyping System
	Software components.

Web Site Information on the software and user manuals of the ABI PRISM® Information Genotyping Software System can be accessed from the Applied Biosystems:

www.appliedbiosystems.com/techsupport

1-8 Introducing Genotyper

Installing and Starting Genotyper

Registering Your Copy of Genotyper	When you register your copy of Genotyper you become eligible for telephone and field service support from Applied Biosystems for 100 days from the date of shipment. To register, fill out the registration card included in this package and return it to Applied Biosystems.
	For Applied Biosystems technical support telephone and address information, see "Technical Support" on page 1-16.
	Registration also allows you to purchase upgrades to the software at a lower price than it would cost you to purchase a new upgraded package.
	IMPORTANT These privileges are available only if you have returned your registration card.
Compatibility With Previous Versions	Genotyper 2.5 can read files created by Genotyper 1.0, 1.1, 1.1.1, and 2.0.
	Previous versions of Genotyper cannot read files created by Genotyper 2.5.
	The commands Add Rows to Tables and Add Rows to Link are supported in Genotyper 2.5 for compatibility with Genotyper 1.X macros. However, there are many new table features in Genotyper 2.0 that require the new versions of these commands. In particular, tables written with Add Rows to Table will need to be rewritten with Setup Table and Append to Table. The older commands may be removed in future versions.
	For more information on using the new table features, see "Working with Tables" on page 8-1.

Introducing Genotyper 1-9

Hardware and
SoftwareThis table describes the components your computer system requires to
run Genotyper 2.5.

Requirements

Genotyper hardware and software requirements:

Svstem	Description		
Component	Recommended	Minimum Requirement	
Computer	A Power Macintosh G3 computer with a 233 MHz or faster processor	A PowerPC Macintosh	
Monitor	A seventeen inch monitor	A 640 x 480 pixels size monitor	
	Note Color monitors are useful, but not required.		
Operating System	Macintosh Operating System 8.0 or later	Macintosh Operating System 7.5.3 with 32 MB of RAM.	
Memory Allocated to Genotyper	15 MB of RAM (without virtual memory 16.5). This allows you to import GeneScan files from approximately one Gel file.	5 MB of RAM (without virtual memory 6.5). This allows you to import only a lim- ited number of GeneScan files at one time.	
	Note Genotyper performance increases when you allocate more memory to the program. Performance decreases, as you import more GeneScan files. Actual results will vary depending on your type of computer system and the kinds of Genotyper tasks you are performing.		
Disk Drive	If you intend to use Genotyper with GenBase, note that the GenBase data file is a single, large disk file, and performance depends on having sufficient unfragmented space on your hard drive. GenBase requires at least 5 MB of free space to launch successfully.		

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Setting Memory Allocation

Because the sizes of the GeneScan data you import can vary, you may need to allocate more memory to Genotyper. You can estimate that each additional megabyte of memory allocated to Genotyper allows you to import approximately 12 GeneScan files when raw data is imported or 20 GeneScan files if raw data is not imported (actual sizes may vary).

Step Action 1 Quit Genotyper. 2 Click the Genotyper application icon to select it. 3 Choose the Get Info command from the Finder's File menu. The Get Info dialog box appears. Genotyper®2.5 Info E Genotyper®2.5 Kind: application program Size: 3.5 MB on disk (3,712,867 bytes) Where: Sandra's: GT Software 2.5: Created: Fri, Nov 20, 1998, 5:00 PM Modified: Wed, Dec 2, 1998, 12:37 PM Yersion: Genotyper® 2.5 Comments Memory Requirements. Suggested Size: 5000 К Minimum Size: 4000 K Preferred Size: 15000 K Locked Note: Memory requirements will increase by 2,985K if virtual memory is turned off. Enter a new value for the Preferred size 4 Note In some versions of the Macintosh System, the Preferred size value is referred to as the Current size. 5 Click the close box in the upper left corner.

To change the memory allocation to Genotyper:

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How to Install Genotyper

How to Install Genotyper comes on a single CD-ROM disc containing the:

- Genotyper Program file
- Tutorials & Examples files
- Genotyper User Manual in Portable Document Format (pdf)

IMPORTANT Do not work off of the CD-ROM disc.

To install Genotyper for the first time:

Step	Action
1	Insert the Genotyper CD into your computer CD-ROM drive.
2	Double-click the Genotyper Installer icon.
3	Choose the hard-drive on which you want the program to be installed.
4	Follow the prompts on the installer to install the program.
5	Eject the Genotyper CD.

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How to Start Genotyper	To start	Genotyper:
	Step	Action
	1	Double click the Genotyper icon in the Finder.
		The first time you start Genotyper, the Registration dialog box appears.
		Product Registration Your Name:
		Please enter the registration code for this product:
	2	Enter your name, your organization, and your registration code.
		Note The first time you use the application, you are asked to enter the registration code on your registration card. Genotyper then verifies the code.
		IMPORTANT Keep your registration code in a place where you can easily retrieve it. If you need to re-install the software at any time, you will be prompted for the registration code once again.
3		Click OK.
		The Genotyper start-up screen appears briefly.
		Image: Sector of the sector
		You are now ready to use Genotyper.

Introducing Genotyper 1-13

Using the Macintosh

Knowledge For the purposes of this manual, it is assumed that you have used a Macintosh computer. If you are not familiar with the terms or procedures Assumptions in the following table, refer to the Macintosh System Software User's Guide for more information.

The table below describes Macintosh procedures that you should be familiar with to use Genotyper.

Macintosh procedures:

Procedure	Description
Using the mouse	Clicking and double-clicking, selecting, and dragging.
Choosing commands	Using pull-down and pop-up menus, dialog boxes, radio buttons and checkboxes.
Working with windows	Opening and closing, re-sizing and repositioning, scrolling, understanding the active window.
Using the Macintosh hierarchical file system	Finding files and creating folders.

Performance and When using Genotyper, you will often be working with many files, and Maintenance accessing the hard disk often, so it is essential that you follow Guidelines guidelines to minimize the occurrence of errors during operation of the computer.

Follow these general guidelines for optimal performance:

- Install only one Macintosh System per hard disk. ٠
- Back up all programs and files regularly. ۲
- ۲ Use discretion when adding software programs, especially control panel and System extension (INIT) files.

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Macintosh Terms Used in This Manual

TermDefinitionDialog BoxesAppear when you need to make a decision or enter information. All other action on the monitor screen is suspended until you close the dialog box by clicking a button such as Cancel, OK, or Done.MenusProvide access to various functions you can perform with the software. A triangle after a menu item indicates that a submenu appears. When you click that choice and hold the mouse button down, a submenu appears. These menus allow you to choose dialog box entries from specific lists of items.Pop-up menusDisplay a triangle and are found in dialog boxes. When you click a pop-up menu and hold the mouse button down, a submenu appears. These menus allow you to choose dialog box entries from specific lists of items.WindowsDisplay information, and in some cases allow you to edit or enter additional information. The top border of an active window always has six horizontal lines and usually has a close box in the upper left corner. If many windows are open, click one window to make it active. When a window is active, you can click the top border, hold the mouse button down, and drag the window to another location on the screen. When you are finished working with a window, click the close box to remove the window from the screen, or click another window.Entry fieldsRectangular areas in which you can enter information. Click in an entry field to display a cursor, and use the keyboard to enter the information.Check boxesSmall circles that appear in front of choices. When you click a radio button with the cursor, a black dot appears in it, indicating that you have selected the option. You can usually select multiple checkboxes.Radio ButtonsSmall circles that appear in front of choices		
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	Buttons	Rectangles with rounded corners that allow you to accept or cancel the contents of a dialog box or perform functions (such as printing) within the dialog box. A button with a heavy outline is the default button that applies if you press the Return key.

Definitions The following terms are used in this manual:

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Technical Support

Contacting Technical Support

You can contact Applied Biosystems for technical support by telephone or fax, by e-mail, or through the Internet. You can order Applied Biosystems user documents, MSDSs, certificates of analysis, and other related documents 24 hours a day. In addition, you can download documents in PDF format from the Applied Biosystems Web site (please see the section "To Obtain Documents on Demand" following the telephone information below).

To Contact Technical Support by E-Mail

To Contact Contact technical support by e-mail for help in the following product cal Support areas:

Product Area	E-mail address
Genetic Analysis (DNA Sequencing)	galab@appliedbiosystems.com
Sequence Detection Systems and PCR	pcrlab@appliedbiosystems.com
Protein Sequencing, Peptide and DNA Synthesis	corelab@appliedbiosystems.com
Biochromatography, PerSeptive DNA, PNA and Peptide Synthesis systems, CytoFluor [®] , FMAT [™] , Voyager [™] , and Mariner [™] Mass Spectrometers	tsupport@appliedbiosystems.com
Applied Biosystems/MDS Sciex	api3-support@sciex.com
Chemiluminescence (Tropix)	tropix@appliedbiosystems.com

Hours for Telephone Technical Support

Hours for In the United States and Canada, technical support is available at the following times:

Product	Hours
Chemiluminescence	8:30 a.m. to 5:30 p.m. Eastern Time
Framingham support	8:00 a.m. to 6:00 p.m. Eastern Time
All Other Products	5:30 a.m. to 5:00 p.m. Pacific Time

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by Telephone or

To Contact In North America

Technical Support To contact Applied Biosystems Technical Support, use the telephone or Fax fax numbers given below. (To open a service call for other support needs, or in case of an emergency, dial **1-800-831-6844** and press **1**.)

Product or Product Area	Telephone Dial	Fax Dial
ABI PRISM [®] 3700 DNA Analyzer	1-800-831-6844, then press 8	1-650-638-5981
DNA Synthesis	1-800-831-6844, then press 21	1-650-638-5981
Fluorescent DNA Sequencing	1-800-831-6844 , then press 22	1-650-638-5981
Fluorescent Fragment Analysis (includes GeneScan [®] applications)	1-800-831-6844, then press 23	1-650-638-5981
Integrated Thermal Cyclers (ABI PRISM®877 and Catalyst 800 instruments)	1-800-831-6844, then press 24	1-650-638-5981
ABI PRISM [®] 3100 Genetic Analyzer	1-800-831-6844 , then press 26	1-650-638-5981
BioInformatics (includes BioLIMS [™] , BioMerge [™] , and SQL GT [™] applications)	1-800-831-6844, then press 25	1-505-982-7690
Peptide Synthesis (433 and 43X Systems)	1-800-831-6844, then press 31	1-650-638-5981
Protein Sequencing (Procise [®] Protein Sequencing Systems)	1-800-831-6844, then press 32	1-650-638-5981
PCR and Sequence Detection	1-800-762-4001, then press 1 for PCR, 2 for the 7700 or 5700, 6 for the 6700 or dial 1-800-831-6844, then press 5	1-240-453-4613

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Product or Product Area	Telephone Dial	Fax Dial
Voyager™ MALDI-TOF Biospectrometry and Mariner™ ESI-TOF Mass Spectrometry Workstations	1-800-899-5858, then press 13	1-508-383-7855
Biochromatography (BioCAD [®] Workstations and Poros [®] Perfusion Chromatography Products)	1-800-899-5858, then press 14	1-508-383-7855
Expedite™ Nucleic acid Synthesis Systems	1-800-899-5858 , then press 15	1-508-383-7855
Peptide Synthesis (Pioneer™ and 9050 Plus Peptide Synthesizers)	1-800-899-5858, then press 15	1-508-383-7855
PNA Custom and Synthesis	1-800-899-5858, then press 15	1-508-383-7855
FMAT [™] 8100 HTS System and Cytofluor [®] 4000 Fluorescence Plate Reader	1-800-899-5858, then press 16	1-508-383-7855
Chemiluminescence (Tropix)	1-800-542-2369 (U.S. only), or 1-781-271-0045	1-781-275-8581
Applied Biosystems/MDS Sciex	1-800-952-4716	1-650-638-6223

Outside North America

Region	Telephone Dial	Fax Dial
Africa	and the Middle East	
Africa (English Speaking) and West Asia (Fairlands, South Africa)	27 11 478 0411	27 11 478 0349
South Africa (Johannesburg)	27 11 478 0411	27 11 478 0349
Middle Eastern Countries and North Africa (Monza, Italia)	39 (0)39 8389 481	39 (0)39 8389 493

Region	Telephone Dial	Fax Dial
Eastern Asia, China, Oceania		
Australia (Scoresby, Victoria)	61 3 9730 8600	61 3 9730 8799
China (Beijing)	86 10 64106608	86 10 64106617
Hong Kong	852 2756 6928	852 2756 6968
Korea (Seoul)	82 2 593 6470/6471	82 2 593 6472
Malaysia (Petaling Jaya)	60 3 758 8268	60 3 754 9043
Singapore	65 896 2168	65 896 2147
Taiwan (Taipei Hsien)	886 2 2358 2838	886 2 2358 2839
Thailand (Bangkok)	66 2 719 6405	66 2 319 9788
	Europe	
Austria (Wien)	43 (0)1 867 35 75 0	43 (0)1 867 35 75 11
Belgium	32 (0)2 712 5555	32 (0)2 712 5516
Czech Republic and Slovakia (Praha)	420 2 61 222 164	420 2 61 222 168
Denmark (Naerum)	45 45 58 60 00	45 45 58 60 01
Finland (Espoo)	358 (0)9 251 24 250	358 (0)9 251 24 243
France (Paris)	33 (0)1 69 59 85 85	33 (0)1 69 59 85 00
Germany (Weiterstadt)	49 (0) 6150 101 0	49 (0) 6150 101 101
Hungary (Budapest)	36 (0)1 270 8398	36 (0)1 270 8288
Italy (Milano)	39 (0)39 83891	39 (0)39 838 9492
Norway (Oslo)	47 23 12 06 05	47 23 12 05 75
Poland, Lithuania, Latvia, and Estonia (Warszawa)	48 (22) 866 40 10	48 (22) 866 40 20
Portugal (Lisboa)	351 (0)22 605 33 14	351 (0)22 605 33 15
Russia (Moskva)	7 095 935 8888	7 095 564 8787
South East Europe (Zagreb, Croatia)	385 1 34 91 927	385 1 34 91 840
Spain (Tres Cantos)	34 (0)91 806 1210	34 (0)91 806 1206
Sweden (Stockholm)	46 (0)8 619 4400	46 (0)8 619 4401
Switzerland (Rotkreuz)	41 (0)41 799 7777	41 (0)41 790 0676
The Netherlands (Nieuwerkerk a/d IJssel)	31 (0)180 331400	31 (0)180 331409

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Region	Telephone Dial	Fax Dial	
United Kingdom (Warrington, Cheshire)	44 (0)1925 825650	44 (0)1925 282502	
All other countries not listed (Warrington, UK)	44 (0)1925 282481	44 (0)1925 282509	
Japan			
Japan (Hacchobori, Chuo-Ku, Tokyo)	81 3 5566 6230	81 3 5566 6507	
Latin America			
Del.A. Obregon, Mexico	305-670-4350	305-670-4349	

Technical Support Through the Internet

To Reach We strongly encourage you to visit our Web site for answers to frequently asked questions and for more information about our products. You can also order technical documents or an index of available documents and have them faxed or e-mailed to you through our site. The Applied Biosystems Web site address is

http://www.appliedbiosystems.com/techsupp

To submit technical questions from North America or Europe:

Step	Action
1	Access the Applied Biosystems Technical Support Web site.
2	Under the Troubleshooting heading, click Support Request Forms , then select the relevant support region for the product area of interest.
3	Enter the requested information and your question in the displayed form, then click Ask Us RIGHT NOW (blue button with yellow text).
4	Enter the required information in the next form (if you have not already done so), then click Ask Us RIGHT NOW .
	You will receive an e-mail reply to your question from one of our technical experts within 24 to 48 hours.

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Demand Web site.

To Obtain Free, 24-hour access to Applied Biosystems technical documents, including MSDSs, is available by fax or e-mail or by download from our

To order documents	Then
by index number	a. Access the Applied Biosystems Technical Support Web site at http://www.appliedbiosystems.com/techsupp
	 b. Click the Index link for the document type you want, then find the document you want and record the index number.
	c. Use the index number when requesting documents following the procedures below.
by phone for fax delivery	 a. From the U.S. or Canada, call 1-800-487-6809, or from outside the U.S. and Canada, call 1-858-712-0317.
	 Follow the voice instructions to order the documents you want.
	Note There is a limit of five documents per request.
through the Internet for fax or e-mail	a. Access the Applied Biosystems Technical Support Web site at http://www.appliedbiosystems.com/techsupp
delivery	 b. Under Resource Libraries, click the type of document you want.
	 Enter or select the requested information in the displayed form, then click Search.
	 d. In the displayed search results, select a check box for the method of delivery for each document that matches your criteria, then click Deliver Selected Documents Now (or click the PDF icon for the document to download it immediately).
	 Fill in the information form (if you have not previously done so), then click Deliver Selected Documents Now to submit your order.
	Note There is a limit of five documents per request for fax delivery but no limit on the number of documents you can order for e-mail delivery.

Planning Genotyper Applications



Chapter Overview

This chapter discusses techniques for collecting and preparing sample data that will help you improve the overall quality of the GeneScan data you import into Genotyper. It also discusses how to plan for use of Genotyper features in your genotyping application.This chapter contains the following topics:See Page		
Completing a GeneScan Sample Sheet	2-3	
Planning for Automation	2-6	
Planning for Linking to GenBase	2-9	
	This chapter discusses techniques for collecting and prepar data that will help you improve the overall quality of the Gen you import into Genotyper. It also discusses how to plan for Genotyper features in your genotyping application. This chapter contains the following topics: Topic Preparing Sample Data for Genotyper Completing a GeneScan Sample Sheet Planning for Automation Planning for Linking to GenBase	

Planning Genotyper Applications 2-1

Preparing Sample Data for Genotyper

Introduction	Genotyper analyzes the results of fragment analysis data collected by an ABI PRISM instrument, and generated by GeneScan.		
	Perfecting techniques for preparing fragment samples, collecting sample data, and using GeneScan to size and quantify fragments will simplify automation of many Genotyper tasks, and minimize editing tasks required to achieve quality genotyping results.		
Preparing Fragment Samples	The source of your fragment samples often affects peak resolution in Genotyper plot displays.		
	When preparing fragment samples for eventual sizing and quantitation by GeneScan, adjust pooling conditions to dilute the amplified products that consistently yield off-scale data. You can obtain optimal results with peak heights of ~1000 fluorescent units.		
	For more information on optimizing sample preparations for GeneScan analysis, see the <i>GeneScan Chemistry Guide</i> .		
Optimizing Data Collection	Optimizing run conditions on your ABI PRISM instrument will ensure a higher quality of fragment data.		
	 Make sure gel run parameters are consistent from run-to-run. 		
	• Choose the right Matrix for the right type of gel and run parameters.		
	For more information on optimizing run conditions, see the user's manual for the ABI PRISM instrument that you are using.		

2-2 Planning Genotyper Applications

Completing a GeneScan Sample Sheet

Introduction You must completely fill out a GeneScan Sample Sheet before running samples on your ABI PRISM instrument (Figure 2-1).

> For detailed information on how to correctly fill out a GeneScan Sample Sheet, see the instrument user's manual for the ABI PRISM instrument that you are using or the GeneScan Analysis User's Manual.

GeneScan Sample instrument. Sheet

Example of a Sample Sheets identify the lane number and contents of each sample that you run when electrophoresing samples on an ABI PRISM



Figure 2-1 Example of a GeneScan Sample Sheet

Planning Genotyper Applications 2-3

Uses Sample Sheet Information

How Genotyper Sample Sheet information from GeneScan is essential for associating the nature of sample fragments with individual dye/lanes and tables in Genotyper. For example, Figure 2-2 shows how Genotyper incorporates information entered in the Sample Info and File Name fields of a GeneScan Sample Sheet into Genotyper tables.

GeneScan Sample Sheet

*	Used	File Name	Sample Name	Dye	Std	Sample Info	Comment	A	P	ł
1		1347-12 PGF		в		S001		Ē	ic.	j
				6		S001			ΪC	j
				Y		S001			ΪĒ	j
				R	٠	GS-350			ĴΕ	j
2	\boxtimes	1347-13 PGM		В		S002			iс	j
	1			6		S002			ÍΕ	j
				Y		S002			ΪC	j
				R	\$	GS-350			ΪĒ	j
3	\boxtimes	1347-01 Father		в		S003			İΕ	j
				6	[S003			IC.	j
				Y		S003			ĬС	j
				R	\$	GS-350			ΪĒ	j
4	\boxtimes	1347-03 Daughter		В		S004			ÍС	i
				6	[S004			ÍΕ	j
				Y	(S004			IC.	j
				R	ŵ	GS-350			ΪC	j
5	\boxtimes	1347-04 Son		В		\$005				j
				6		S005			ΪĒ	j
				Y	[S005			ίC	j
				R	*	GS-350			ÍΕ	j
6	\boxtimes	1347-06 Son		В		S006			IC.	j
				6		S006			ΪĒ	j
				Y	[S006			ÎΞ	j
			1	R	4	GS-350	[Ē	ÍΠ	i
5					_			_	15	5

untitled

Genotyper table			Table - unti	itled 📰			D
	File Name	Lane & Dye	Sample Info	Category	Peak 1	Peak 1	Peak 2 🗄
	011347-12 PGF	1B	S001	D12S83	a 10 1	100.82	a 109 📃
	011347-12 PGF	1B	S001	D7S517	a255	254.88	~
	011347-12 PGF	16	S001	D 13S 171	a 183	182.74	a 193 🖸
	011347-12 PGF	16	S001	D2S391	a 148	148.24	a 152 🏼 🏛
	011347-12 PGF	19	S001	D1S220	a232	232.49	a234 8
	011347-12 PGF	19	S001	D3S1266	a289	289.08	a291 🖗
	021347-13 PGM	2B	S002	D12S83	a101	100.93	a 105 🖧
	021347-13 PGM	2B	S002	D79517	a249	249.11	a251
	021347-13 PGM	26	S002	D13S171	a179	178.86	a 193
	021347-13 PGM	26	S002	D2S391	a 146	146.18	
	021347-13 PGM	29	S002	D1S220	a234	234.39	a244
	021347-13 PGM	29	S002	D3S1266	a291	290.94	a297
	031347-01 Father	3B	S003	D 12S83	a 10 1	100.81	a 105
	031347-01 Father	3B	\$003	D7S517	a249	249.21	a255
	031347-01 Father	36	S003	D 13S 171	a 179	178.86	a 193
	031347-01 Father	36	S003	D2S391	a 146	146.18	a 152
	031347-01 Father	37	S003	D1S220	a234	234.39	
	031347-01 Father	37	S003	D3S1266	a289	289.01	a291 🖓
	<u>م</u>			000000000000000000000000000000000000000			

Figure 2-2 GeneScan Sample Sheet data used in Genotyper tables

2-4 Planning Genotyper Applications

Sample Subfield Example	When you fill in the Sample Info field of the GeneScan Sample Sheet, you can edit the Sample Info field and create Sample subfields. You can use Sample subfields for Genotyper table entries when you create tables.			
	Example			
	SampleInfo: 1001 Mother! Smith 1, lan-00			
	vertical bars separate			
Plan for the Find Command	You can increase the utility of the Find command in Genotyper by carefully planning the format of the information you put into the Sample Info field of the GeneScan Sample Sheet.			
	Example			
	If you have 12 samples, numbered 1, 2, 3,, 12, and you enter these numbers into the Sample Info field, then, when you search for all dye/lanes containing a "1" in the Sample Info field, not only will you select sample 1, you will also get samples 10, 11, and 12.			
	A better plan would be to number the samples 01, 02, 03, and so on, so that a search for the text "01" would select only the desired dye/lanes.			
	In addition, you can place key words in the Sample Comments field that distinguish samples from each other. For example, enter "ladder" for those lanes or capillaries containing allelic ladders.			

Planning Genotyper Applications 2-5

Planning for Automation

Introduction In Genotyper, you can automate many of the repetitive genotyping tasks, simplifying such analysis procedures as importing GeneScan data, labeling peaks, filtering peak labels, and working with plot and table information.

Planning for automation involves choosing the appropriate Genotyper automation feature and the appropriate genotyping tasks to automate for each project.

Ways to Automate

To automate different genotyping tasks:

Genotyping Task	Automation Method	See
Importing Sample files	Running the Set Import Macro	"Importing GeneScan Files" on page 3-13
	Creating a Macro	"Creating Macros from the Step List" on page 4-12
	Using a Template	"Using and Creating Templates" on page 4-16
Defining categories	Defining Categories	"Defining Categories for Labeling" on page 6-4
	Creating a Macro	"Creating Macros from the Step List" on page 4-12
	Using a Template	"Using and Creating Templates" on page 4-16
Selecting Dye/lanes	Using the Find Command	"Searching and Sorting Through Lists" on page 5-9
	Creating a Macro	"Creating Macros from the Step List" on page 4-12
	Using a Template	"Using and Creating Templates" on page 4-16

2-6 Planning Genotyper Applications

To automate different genotyping tasks: (continued)

Genotyping Task	Automation Method	See
Labeling peaks	Automatic Peak Labeling	"Automatic Peak Labeling" on page 6-26
	Defining Categories	"Defining Categories for Labeling" on page 6-4
	Creating a Macro	"Creating Macros from the Step List" on page 4-12
	Using a Template	"Using and Creating Templates" on page 4-16
Filtering labels	Automatic Label filtering	"Filtering Labels" on page 6-29
	Defining Categories	"Defining Categories for Labeling" on page 6-4
	Creating a Macro	"Creating Macros from the Step List" on page 4-12
	Using a Template	"Using and Creating Templates" on page 4-16
Generating plots	Defining Categories	"Defining Categories for Labeling" on page 6-4
	Creating a Macro	"Creating Macros from the Step List" on page 4-12
	Using a Template	"Using and Creating Templates" on page 4-16

Planning Genotyper Applications 2-7

To automate different genotyping tasks: (continued)

Genotyping Task	Automation Method	See
Generating tables	Defining Categories	"Defining Categories for Labeling" on page 6-4
	Creating a Macro	"Creating Macros from the Step List" on page 4-12
	Using a Template	"Using and Creating Templates" on page 4-16
Exporting genotyping data	Using a Template	"Using and Creating Templates" on page 4-16
	Creating a Macro	"Creating Macros from the Step List" on page 4-12
	Setting Linked Program Preferences	"Planning for Linking to GenBase" on page 2-9

2-8 Planning Genotyper Applications

Planning for Linking to GenBase

Introduction One of the components of the ABI PRISM Genotyping Software System, GenBase, is a genotype and phenotype database. It can store relevant sample, or disease information, phenotype information as well as Genotyper results data.

If you are planning to link to the GenBase database application after performing genotyping tasks, you must first install GenBase, and prepare the database for data exchanges.

 Preparing
 The following table shows which topics to refer to in the ABI PRISM

 GenBase for
 GenBase User's Manual for instructions.

For instructions on	See
Installing GenBase	"Chapter 1, Introduction"
Planning for the kinds of Tables you are going to use when Linking to GenBase	"Chapter 2, Preparing the Database"
Preparing the database for data exchange with Genotyper	"Chapter 2, Preparing the Database"

3

Getting Started

Chapter Overview

Introduction	This chapter discusses how to work with Genotyp produce results meaningful to your particular rese covers some of the basic Genotyper procedures genotyping applications.	per Documents to earch activities. It required for all			
In This Chapter	This chapter contains the following topics:				
	Торіс	See Page			
	Choosing a Genotyping Application	3-2			
	Opening Genotyper Documents	3-8			
	Starting from the Main Window	3-9			
	Viewing Genotyper Document Windows.	3-11			
	Importing GeneScan Files	3-13			
	Editing Document Lists	3-16			
	Editing Document Windows	3-18			
	Locking and Unlocking Documents	3-19			
	Printing Genotyper Document Windows	3-20			

Getting Started 3-1

Choosing a Genotyping Application

Introduction The first step in using Genotyper is to decide what kind of genotyping application you want to run. Choosing a genotyping application is the first step in planning your Genotyper project. The features of Genotyper that you use, and how you use them depend on what kind of genotyping application you choose to run.

Genotyping Applications

Kinds of Genotyper enables you to organize your analyzed fragment data into tables. Tables can provide an interpretation of peak data meaningful to your particular genotyping studies. You can print Genotyper tables or export them to databases or other software applications for further analysis.

For this application	Genotyper can produce	For details see
Linkage Mapping	A table of alleles that you can export to a mapping application or a database.	"Linkage Mapping" on page 3-4
Gene Expression Profiling	A comparative analysis table containing normalized data.	"Gene Expression Profiling" on page 3-6
AFLP	A comparative analysis table of polymorphic peaks that shows the presence or absence of peaks.	"Web Site Information" on page 1-8
Paternity Testing	A table of alleles that have been checked for Mendelian inheritance.	"Checking for Mendelian Inheritance" on page 8-37
Forensics/Human Identification	A genotype table to discriminate between individuals.	The ABI PRISM Genotyper 2.0 Applications Tutorials
SSCP	A table of alleles identifying mutants and wild types.	The ABI PRISM Genotyper 2.0 Applications Tutorials

Kinds of tables Genotyper can produce for some genotyping applications:

3-2 Getting Started

Kinds of tables Genotyper can produce for some genotyping applications: *(continued)*

For this application	Genotyper can produce	For details see
Loss of Heterozygosity	A table of peak height ratios that identifies loss of heterozygosity in DNA samples from tumor cells and normal cells.	"Using Analyze and Calculate in Table Commands–An LOH Example" on page 8-26

Getting Started 3-3

Linkage Mapping Linkage mapping applications identify polymorphic fragments by size.

Steps for using Genotyper for linkage mapping applications and where to find related task information for performing each step follow.

To import and analyze data:

Step	Action	See
1	Allocate enough memory for the number of GeneScan files that you are going to import.	"Setting Memory Allocation" on page 1-11
2	Import GeneScan data.	"Importing GeneScan Files" on page 3-13
3	Are you using a Template?	"Using and Creating
	Yes, go to step 5.	page 4-16
	No, go to next step.	
4	Define categories.	"Defining Categories for Labeling" on page 6-4
5	Select dye lanes.	"Working with Dye/lane Lists" on page 5-1
6	Label peaks.	"Approaches to Labeling" on page 6-2
7	Filter labels.	"Filtering Labels" on page 6-29
8	Make a table.	"Setting Up a Table" on page 8-2

3-4 Getting Started

To review analyzed data:

Step	Action	See	
1	View plot data.	"Viewing Plots of Imported Dye/Lanes" on page 7-2	
2	Check for overflows.	"Removing Labels" on page 6-42	
	Are there more than two alleles?		
	Yes, manually remove unwanted labels.		
	No, go to next step.		
3	Update table.	"Updating Tables" on page 8-35	

To export data:

Step	Action	See
1	Export data:	
	♦ To GenBase	 "Importing and Exporting Results Data" on page 10-4
	 To a spreadsheet or linked programs 	 "Linking to Programs and Files" on page 11-1
	♦ To a file	 "Exporting Tables" on page 8-46
2	Print results.	"Printing Genotyper Document Windows" on page 3-20

Getting Started 3-5

Gene Expression Profiling Gene expression applications analyze the quantities of nucleic acid fragments in analyzed samples in terms of peak heights and peak areas.

Steps for comparing peak quantities and where to find related task information for performing each step.

To quantify sample fragments:

Step	Action	See
1	Allocate enough memory for number of GeneScan files you are going to import.	"Setting Memory Allocation" on page 1-11
2	Import GeneScan data.	"Importing GeneScan Files" on page 3-13.
3	Are you using a Template? <u>Yes</u> , skip Defining categories. <u>No</u> , go to next step.	"Using and Creating Templates" on page 4-16
4	Define categories.	"Defining Categories for Labeling" on page 6-4
5	Select dye/lanes in the Dye/lane list.	"Working with Dye/lane Lists" on page 5-1
6	Label peaks.	"Approaches to Labeling" on page 6-2
7	Filter labels.	"Filtering Labels" on page 6-29

To compare sample quantities:

Step	Action	See
1	Normalize labels by control peaks	"Labeling Normalized Peaks—an Example" on page 6-45
2	View plot data	"Viewing Plots of Imported Dye/Lanes" on page 7-2
3	Generate a table	"Setting Up a Table" on page 8-2

3-6 Getting Started

To compare sample quantities: (continued)

Step	Action	See
4	Normalize Labels	
	 Using scale factors 	 "Using Scale Factors for Quantitative Applications" on page 5-15
	 Using Normalize Peaks command 	 "Labeling Normalized Peaks—an Example" on page 6-45
	 Using Calculate in Table command 	 "Calculating Results from Table Data" on page 8-19

To export results data:

Step	Action	See
1	Export data	
	 To a third-party application 	 "Linking to Programs and Files" on page 11-1
	♦ To a file	 "Exporting Tables" on page 8-46
2	Print results	"Printing Genotyper Document Windows" on page 3-20

Opening Genotyper Documents

Definition In Genotyper, you perform all tasks in a Genotyper Document. All Genotyper Documents show different representations of size and quantity data for associated GeneScan files and results of all analysis tasks performed in Genotyper.

You can view the different parts of a Genotyper Document by opening document windows from the Main window.

How to OpenThe steps for opening Genotyper Documents differ depending on
whether you are opening an existing Genotyper Document, or creating
a new one.

To open a Genotyper document:

If you	Then
Are working with an existing Genotyper Document or	a. Choose Openfrom the File menu.
a template file	b. Locate and select the document you want to open.
	c. Click Open.
Do not have an existing Genotyper Document	Choose New from the File menu.

Starting from the Main Window

Definition The Main window displays all parts of a Genotyper Document. You perform all Genotyper tasks from the Main window, or from Document windows you can open within the Main window that let you view GeneScan file data, and results data in different formats.

The Main Window When you open a new Genotyper Document, a blank Main window appears. Once you import GeneScan data and create all the parts of a Genotyper Document, the Main window will look like the figure below.



Figure 3-1 The Main Window

Parts of the Main
WindowThe following table describes the parts of the Main Window in Figure 3-
1 on page 3-9.

Item	Name	Description	
1	Dye/lane list	Shows specific dye/lanes available for analysis.	
2	Upper Graphical Area	Shows electropherogram plots.	
3	Lower Graphical Area	Shows peak labels.	
4	Category list	Shows criteria for a group of peaks selected on the basis of parameters you define using the category features. For example, dye color, size, or height.	
5	Table Area	Shows tabular data for created tables.	
6	Macro list	Lists the names of the macros that you have created and can run.	
7	Window selection buttons	Open windows for a particular Genotyper document, and provides access to GenBase and GenoPedigree data. Main window Dye/lane List window Plot window Category window Table window GenoPedigree GenBase	
8	Step list	Contains the list of steps for the current Step Log or the macro selected in the Macro list.	

3-10 Getting Started

Viewing Genotyper Document Windows.

Introduction	From the Main window, you can open windows that allow you to view parts of a Genotyper Document related to specific kinds of data.
Opening Document Windows	Document windows display the different parts of a Genotyper Document.
Windows	Example
	If you want to view details of plot data, you can open up the Plot window.

To use the selection buttons to open Document windows:

To see the	Click	And Genotyper displays
Dye/lane window		Dye/lanes - untitled SampleInfo: S002 Sample Comment: 011347-12 POF 1 Blue 011347-12 POF 1 Blue 011347-12 POF 1 Blue 011347-12 POF 1 Blue 011347-12 POF 1 Green 011347-12 POF 1 Green 011347-12 POF 1 Green 011347-12 POF 1 Green 011347-12 POF 1 Vellow 011347-12 POF 1 Red 011347-12 POF 1 Red 011347-12 POF 1 Red 021347-13 POH 2 Blue S002 021347-13 POH 2 Blue S002 021347-13 POH 2 Green S002 021347-13 POH 2 Green S002 021347-13 POH 2 Vellow S002 021347-13 POH 2 Net S002 021347-13 POH 2 Net S002
Category window		Categories - untitled

Getting Started 3-11



To use the selection buttons to open Document windows: (continued)

Saving Documents You can save a Genotyper Document as a file. Although the different types of document windows for a document are not saved individually, all of the data for the document is saved in one file regardless of which windows are open at the time you save the document.

3-12 Getting Started

Importing GeneScan Files

Introduction	Importing GeneScan files supplies peak data for all Genotyper tasks. A
	GeneScan file can be a Sample file (GeneScan version 2.0 or later), or
	a Results file (GeneScan 1.x versions).

IMPORTANT You cannot import GeneScan Gel files.

Process When you import a GeneScan file in Genotyper, Genotyper extracts Sample file information and generates one Dye/lane list entry for each dye color of each lane. Each Dye/lane list entry contains size, quantity, and sample information for all fragments labeled with a single dye color and electrophoresed in a single lane.

For more information on how Genotyper generates dye/lanes from imported GeneScan data see, "Where Dye/lanes Come From" on page 5-2.

Ways to ImportYou can either import GeneScan data all at once or in batches. ThereGeneScan Filesare advantages and disadvantages to both approaches.

The advantages and disadvantages of importing GeneScan data all at once or in batches:

Way to Import	Advantages	Disadvantages
All GeneScan data at once. Useful when you are importing data from a few gels or	More convenient. You can see all results after performing the command just once.	 Requires that you allocate more memory to Genotyper for more than 36 lanes.
approximately 36 lanes or capillaries.		 Inefficient processing will slow down the operation.
In batches. Useful when you are importing data from many gels or more than 36 lanes or capillaries.	 More GeneScan data can be processed more efficiently. Does not require as much memory allocated to Genotyper. 	You cannot see all dye/lanes at one time.

Getting Started 3-13

Storing GeneScanWhen setting up and running gels, the number of gels you run and the
number of lanes in each gel determines the number of GeneScan
sample files in a project.

Example

Number of Gels x Number of lanes = Number of GeneScan sample files

Note You usually do not need to refer to Gel files once Sample files have been generated from them.

You can optimize the performance of the ABI PRISM Genotyping Software System if you store all GeneScan sample files in one location, for example one shared disk on a file server, and process all data from that storage location. If you move GeneScan sample files around, then GenBase will not be able to locate them if you want to refer to them at a later time.

How to Import GeneScan Files

To import GeneScan files:

Step	Action	
1	Choose Edit: Set Preferences	
	The Set Preferences dialog box opens.	
	Set Preferences	
	Options for exporting tables: Field delimiter: Tab Comma Space None Line delimiter:	
	When quitting Genotyper: Save linked document	
	✓ Quit linked program Imnort colors:	
	🗹 Blue 🗹 Green 🗹 Yellow	
	🗌 Red 📄 Orange 📄 Import Raw	
	Other options: Double-clicking runs macros & steps	
	BioLIMS Cancel OK	

3-14 Getting Started
To import GeneScan files: (continued)

	Step	Action	
	2	Select the appropriate checkboxes for import options.	
		If you select	Then Genotyper imports
		Import raw data	Unprocessed collection data, as well as data processed by GeneScan.
			Note Not selecting the Import raw data checkbox will improve system performance when importing large numbers of GeneScan files.
		Import colors	Imports only sample fragment data labelled with the dye color you select.
	3	Choose Import (The Import Generation 021347-13 PGM 031347-01 Fathe 041347-03 Daug 051347-04 Son 061347-06 Son 071347-08 Daug 081347-09 Son 091347-10 Son	GeneScan Filesfrom the Flle menu. eScan Files dialog box appears.
	4	Locate and select want to import.	ct the GeneScan Sample file, or Results file that you
	5	Click Import. If you want to im the folder, then of Genotyper reme	port all GeneScan files in a folder, select one file in click Import All. mbers the last folder from which you imported files.
Importing Project	You can	import all files i	n a GeneScan Project by selecting the project

Files file and clicking import.

Import All does not include Project files. If you want to import from more than one project file, you must select each project file one at a time.

Getting Started 3-15

Editing Document Lists

Introduction	Genotyper supplies a number of general editing tools that you can use
	to modify items in Genotyper Document Dye/lane lists, Category lists,
	or Macro lists.

Making a List A vertical bar to the left of a list indicates that list is active. This means Active that all the edit commands apply only to this list.

To make a list active, press the tab key repeatedly until the thin vertical bar appears to the left side of the list you want to make active.

B ♥ ● 011347-12 PGF 1 Blue S001	Vertio	cal bar			
011347-12 PGF 1 Green S001	B Y G B	 011347-12 PGF 011347-12 PGF 011347-12 PGF 	1 Blue 1 Blue 1 Green	\$001 \$001 \$001	

Selecting Items in To edit entries for any list item in Genotyper, you must first select the a List items you are going to edit.

To select items in a list:

If you are selecting	Then
A single item	 Click on the item in the list.
	The item is highlighted, indicating that it is selected.
A range of continuous	 Click on an item in the list.
items	 Hold down the shift key and click on the last item in the range.
	All the items in the range are highlighted.
Discontinuous items in a	 Click on an item in the list.
list	 Hold down the command key and click on another item.
	 Repeat the previous step for each item you want to select.
	Only the items selected are highlighted.

Getting Started 3-17

Editing Document Windows

Using the Cut, Copy, and Paste Commands	The Cut, Copy, and Paste commands available from the Edit menu allow you to transfer the same type of information from one window to another. For example, if you copy an item in a Macro list in one window and paste it into a Macro list in another window, all of the macro data will be transferred. However if you paste the same information onto another application, only the text is transferred; no data is transferred.
	IMPORTANT Copying or pasting many dye/lanes from one document to another requires a lot of memory. Therefore, we recommend that you copy or paste only a few dye/lanes at a time.
Using the Clipboard	Items you copy from Genotyper Document windows will appear on the Clipboard.
	To view the Clipboard, choose Show Clipboard in the Edit menu.
	Note The Clipboard stores only the last item (or group of items) copied.
Copying Windows	You can use the Copy Window command to copy a picture of the Main window or the Plot window.
	To copy a window, choose Copy Window in the Edit menu.
	A picture of everything in the active window (except the title bar) is copied to the Clipboard. You can now paste this image into a paint or draw program to edit it.

Locking and Unlocking Documents

Introduction	After you have created a set of categories, or macros, you can lock them to prevent accidental modification. Categories, macros, and steps that are locked cannot be edited or cleared until they are unlocked.
How to Lock Documents	Choose Lock from the File menu. Padlock icons appear next to the locked panes and in the File menu Lock is checked.
How To Unlock Documents	Choose Unlock from the File menu. The padlock icons disappear and in the File menu Unlock is checked.

Printing Genotyper Document Windows

Introduction You can print any active Genotyper window in a Genotyper Document.

How to Print a **Document Window**

To print the Genotyper Document Window:

Step	Action
1	Select the Genotyper Document Window that you want to print.
2	Choose Page setupfrom the File menu. Your printer's Page Setup dialog box appears.
	LaserWriter Page Setup 7.0 OK Paper: ● US Letter ○ A4 Letter ○ US Legal ○ B5 Letter ○ Tabloid ▼ Cancel Reduce or □00% Printer Effects: Enlarge: ○ Font Substitution? Options Orientation ○ Text Smoothing? ○ Image: ○ Custom Paper Size ○ Custom Paper Size ○
3	Select the appropriate checkboxes and options.
4	
4	
5	Choose Printfrom the File menu. The Print dialog box appears.
	Printing title: Untitled-1 Print pane:

3-20 Getting Started

To print the Genotyper Document Window: (continued)

Step	Action
6	Enter a printing title.
	If you are printing when the Main window is active, the Print dialog box prompts you to specify which part of the document that you want to print.
7	Select the appropriate radio button.
8	Click OK.
	The Print dialog box appears.
9	Click Print to begin printing.
	Note To print multiple dye/lane plots, choose Show Plot Window before printing.

Automating Genotyping Procedures



Chapter Overview

Introduction	Genotyper can automatically perform all calculations, comp analyses, and peak labeling activities once you specify app settings and issue the appropriate sequence of commands Genotyper macros, and templates, you can automate the s analysis parameters, and issuing of commands to perform particular analysis procedure, or all of the procedures for a genotyping application.	oarative propriate Using setting of either a n entire
In This Chapter	This chapter contains the following topics:	
	Торіс	See Page
	Approaches to Automating Procedures	4-2
	Running Macros	4-4
	Recording Steps in the Step List	4-7
	Editing the Step List	4-10
	Creating Macros from the Step List	4-12
	Using and Creating Templates	4-16
	Using AppleScript Scripts	4-18

Automating Genotyping Procedures 4-1

Approaches to Automating Procedures

Introduction Genotyper uses templates, macros, and Apple Scripts to automate procedures for an application.

The macros and templates supplied with Genotyper automate procedures presumed necessary to complete particular genotyping applications. They serve as examples of actual procedures you might want to perform in your application. You must modify them for use with your particular Genotyper application.

Definitions

Definitions of terms used:

Definition
Templates are ready-to-use Genotyper applications. A Genotyper template contains the Category list and macros necessary for automatic analysis of particular applications.
A macro is a sequence of commands or steps that you can run to perform a particular analysis procedure.
AppleScript is a programming language that you use to create Scripts, lists of Genotyper commands for your computer to perform.

4-2 Automating Genotyping Procedures

Automation Genotyper supplies customizable templates for automating complete Options genotyping applications, and macros for automating individual procedures.

Options for automating genotyping applications and procedures:

If you want to automate a Genotyping	And	Then See Topic
Application	You know that a template for a similar application exists,	"How to Create Templates" on page 4-17.
Procedure within an	You know that a macro exists for that procedure,	"How to Run Macros" on page 4-5.
application	You know that a macro does not exist for that procedure,	"How to Create a New Macro" on page 4-12.

Automating Genotyping Procedures 4-3

Running Macros

Introduction	Running a macro executes a pre-defined set of Genotyper commands and functions that automates a procedure. Genotyper provides several macros that can serve as examples of the kinds of macros you can run to automate analysis tasks.
	In addition to running supplied macros, you can create your own macros from the Step list, save them and run them.
	For more information on creating your own macros, see "Recording Steps in the Step List" on page 4-7.
Supplied Macros	Genotyper supplies a number of sample macros on the Tutorials disk that you can select and run to perform Genotyper procedures.
Tips for Running Macros	You can set preferences so that you can run macros by double-clicking a macro after selecting it. Choose Set Preferences from the Edit menu, and select the Double-clicking runs macros & steps checkbox.

4-4 Automating Genotyping Procedures

How to Show the The Macro window shows macros that are stored in the active Macro Window Genotyper Document or Template.

To show the Macro window:

Step	Action	-
1	Open the Main window	
2	From the Views menu, select Show Macro window.	
	The Macro window appears.	
	Macros - LDK Inheritance check.b6	
	Current Step Log	

Macros

How to $Run\quad \mbox{You can run any macro that is displayed in the Macro list.}$

To run a macro:

Step	Action
1	From the Macro List, select a macro.
2	Choose Run Macro from the Macro menu.
	All of the steps in the selected macro are run automatically.
	Note You can assign a command key combination when a macro is created to run the macro. If a command key is assigned, simply press \Re -[assigned key] to run the macro.

Automating Genotyping Procedures 4-5

Importing GeneScan Data

How to Run a You can use the Set Import Macro command to specify a macro that Macro After you want to run immediately after you have imported GeneScan data into Genotyper.

To use the Set Import command:

Step	Action
1	Choose Set Import Macro from the Macro menu.
	The Set Import Macro dialog appears.
	Run this macro automatically after importing a results file: Cancel OK
2	Type in the name of the macro that you want to run immediately after you import GeneScan data.
3	Select the checkbox to run the macro automatically, and click OK.
	The name of the macro selected to run automatically appears in the Import GeneScan data dialog box.

4-6 Automating Genotyping Procedures

Recording Steps in the Step List

Definition The Step list records many of the Genotyper commands after you issue them. You can create macros from the steps you record in the Step list.

Location of Step The Step list appears in the Step window, located in the lower window right-hand corner of the Main window.

	untitled	٩	1
B Y 011347-12 PGF 1 G B 011347-12 PGF 1 011347-12 PGF 1 011347-12 PGF 1 0 01347-13 PGH 2 2	Vellow S001 Red Red Blue S002		
	80 200 220 240 260 280 300 320 340 360 380	■ 約474	
• Everything All peaks from	scan 0 to 32000 in R/B/G/V	\$ \$	
Lane Dye Sample Info	Category Peak 1 Peak 2 Overflow	Ŷ	
1 B S001	Everything 50.11 97.00 Overflow Everything 50.11 97.00 Overflow		
1 G S001	Everything 145.10 147.17 Overflow	₽	
Current Step Log	Label category peaks with the size in bp Show the plot window Update table Show the table window		Step window

Automating Genotyping Procedures 4-7

How to Show the The Step window shows the current list of recorded steps, or the steps Step Window that make up a macro.

To display the Step window:

Step	Action	
1	Open the Main Window.	
2	Select a macro in the Macro list of the Macro window.	
3	From the Views menu, select Show Step window.	
	The Step window showing the steps for the currently selected macro, appears.	
	Clear all categories Select all color lanes Label category peaks with the size in bp Remove labels from peaks whose height is less than 32% of the highest peak in a category's range; then remove labels from peaks whose height is less than 32% of the highest peak in a category's range; then labels from peaks followed by a higher, labeled peak within 0.00 to 3.00 bp Set up table with one category and one lane per row, containing file name, lane & dye, sample info, category. 1 label per peak for 2 peaks per category. the text "Overflow" if number of labels > 2	

Displaying	When you select Current Step Log in the Macro list of the Macro
Commands issued	window, and show the Step window, Genotyper displays commands you
in Documents	have issued since you last cleared the Step Log.

4-8 Automating Genotyping Procedures

How to Record Genotyper records most tasks you perform or commands you issue as Steps a step in the Step list.

To record steps in the Step list:

Step	Action
1	Pull down the Macro menu and verify that Record Steps is checked, If it's not checked, click it to activate it.
2	Actions you perform in Genotyper, such as marking, labeling, and filtering are recorded as steps in the Step list. 1st action taken Label astegory peaks with the size in bp 2nd action Peak in a category 's range; then remove labels from peaks proceeded

How to Turn Off If you are not making a macro, and do not want to fill up the Step list, Step Recording you can turn off step recording.

To turn off the recording of steps:

Step	Action
1	Pull down the Macro menu.
2	Click Record Steps to deactivate it.

Editing the Step List

- **Introduction** You can edit the contents of your current Step list before or after creating a macro.
- How to Edit a Step You can edit steps in the Step list, and change the parameters set when you performed the step. You can only edit steps in the Step list that involve making selections from a dialog box.

To edit steps in the Step list:

Step	Action
1	Select a step from the Step list.
2	Choose Edit Stepfrom the Macro menu.
	The dialog box for that step appears.
	This figure shows an example of the dialog box that appears if you edit the step for a Label Peakscommand.
	Label peaks within marked categories with: The size in bp The peak height The peak height The peak drea The peak area The scan number The text: The category's name The peak source The peak modulation score Cancel OK
3	Change any of the parameter settings in the dialog box that appears.
4	Click Replace.
	The step with edited parameter settings replaces the original step.
	Note You cannot change a step to a completely different type of step.

Pasting from the the Step list. Step List

Copying and You can Cut, Copy and Paste steps to change the sequence of steps in

To copy and paste steps in the Step list:

Step	Action
1	Select a step in the Step list.
2	Choose Copy from the Edit menu.
3	Click on the step that precedes the place you want the copied step to be inserted.
4	Choose Paste from the Edit menu.
	The step is pasted in the place you selected in the Step list.

How to Run a Step If you want to find out what genotyping task a step performs, you can run that step from the Step list.

To run a step in the Step list:

Step	Action
1	Select a step in the Step list.
2	Choose Run Step from the Macro menu.
	This runs the step you selected, and repeats that step in the Step list.
	Note If you have set preferences appropriately, you can double- click on a step to run it.

Creating Macros from the Step List

Introduction If a macro does not already exist for a particular genotyping procedure that you plan on running repeatedly, you can create a macro that performs all of the steps in the procedure, and run it each time you want to repeat that procedure for a different set of GeneScan data.

How to Clear the Before you record steps for a macro, you will want to clear the Step list Step List of steps that have been previously recorded.

To clear the Step list:

Step	Action
1	Make sure that you have selected the Current Step Log in the Macro window.
2	Choose Clear Step Log from the Macro menu.
_	

How to Create a Once you have cleared the Step list of all previously recorded steps, you can create a new macro for a genotyping procedure by performing all of the steps in the procedure once. Genotyper records each of the steps in the Step list.

Note You can select more than one macro at a time from the Macro list to Cut, Copy, and Paste. If more than one macro is selected, nothing appears in the Step list.

To create a new macro:

Step	Action	
1	Pull down the Macro menu and verify that Record Steps is checked, If it's not checked, click it to activate it.	
2	Perform all of the steps in the genotyping procedure for which you want to create a macro.	
	Check the Step list to make sure that each step has been recorded.	

4-12 Automating Genotyping Procedures

To create a new macro: (continued)

Step	Action		
3	Choose Save Step Logfrom the Macro menu.		
	The New Macro name dialog box appears		
	New macro name		
	Macro		
	🗌 Use command key (%) number 🛛		
	Cancel OK		
4	Enter the name of the new Macro in the text box.		
5	Click the checkbox and enter the key you want to press with the command key to run this Macro from the keyboard.		
6	Click OK.		
7	The new Macro appears in the Macro list.		
	Current Step Log ☆ Keyboard Macrol 第1 command for this ↓ New macro		

How to Change a Macro Name

How to Change a You can change the name of any macro.

IMPORTANT If any other macros refer to the macro whose name was changed, you must edit those other macros to use the new name.

To change the name of a macro:

Step	Action	
1	Select a macro from the Macro list.	
2	Choose Change Macro Namefrom the Macro menu.	
	The New macro name dialog box appears with the name of the macro in the text box.	
3	Enter the new macro name.	
4	Click OK.	
	The new macro name should now appear in the Macro list. The comment step at the beginning of a macro does not change when you change the name of the macro.	

4-14 Automating Genotyping Procedures

Macro

How to Add a You can add a comment about any macro in the Macro list, and make Comment to a the comment appear in the macro.

To add a comment to a macro:

Step	Action	
1	Choose Add Commentfrom the Macro menu.	
	The Add Comment dialog box appears.	
	Add comment to macro:	
	Cancel OK	
2	Type in a comment that you want to append to the macro.	
3	Click OK.	
	The comment appears in the Current Step Log.	
4	To make the comment appear in a macro, you can cut and paste it into the macro.	

Automating Genotyping Procedures 4-15

Using and Creating Templates

Definition	Genotyper provides a number of templates that automate all genotyping and analysis tasks for specific applications. Each template is designed for a specific Genotyper application and uses sample GeneScan data to demonstrate how to use it.	
Supplied Templates	Genotyper supplies templates containing procedure examples for different kinds of Genotyper applications. The template name describes the kind of application it automates.	

4-16 Automating Genotyping Procedures

How to Create To create a template, you modify any existing template for your specific Templates application.

To create a template for your specific application:

Step	Action	
1	Make a copy of a supplied template that describes the kind of application that you are running.	
2	In the copy, delete the Category list.	
3	Make a new Category list specific for your application.	
4	Choose Save As	
5	Name the new template.	

Saving Templates Saving a template as a stationary pad prevents it from being changed as Stationery Pads accidentally. A stationary pad can be opened and used, but any changes made can only be saved as a separate document.

To save a template as a stationary pad:

Action	
Click on a template icon in the Finder to select it.	
TCR Template	
Choose Get Info from the File menu.	
The Template info window appears.	
Click the Stationary pad checkbox at the bottom of the info window.	
Click the Close box in the upper left-hand corner of the window. The Template is now saved as a stationary pad. The bottom right corner is folded.	

Automating Genotyping Procedures 4-17

Using AppleScript Scripts

Introduction	You can use the AppleScript programming language to create Scripts that can combine the capabilities of Genotyper with related analysis applications. Using Scripts, you can give your computer a list of things you want it to do, and let the computer do everything on your list.		
System Requirements	You can use Apple Scripts on Power Macintosh computers that use system software version 7.5.3 or later.		
How to Create Scripts	ow to Create ScriptsLike all programs that can be customized with Scripts, Genotyper an AppleScript dictionary. Use the AppleScript editor provided wit system software to create Scripts for automating Genotyper procedures.To create Scripts for your specific application:		
	Step Action		
	1	Turn on the Script Editor's recorder and perform a set of Genotyper procedures.	
		AppleScript keeps a list of what you do while the recorder is turned on.	
	2	Turn the recorder off. You can see the recorded Script.	
	3 When you run the Script, your computer repeats your actions automatically.		

See the AppleScript documentation supplied with your Apple system software, for instructions about how to use AppleScript Scripts.

4-18 Automating Genotyping Procedures

Working with Dye/lane Lists

5

Chapter Overview

In

Introduction Dye/lanes contain sample information for electrophoresed nu fragments. They provide the source data for all Genotyper progenotyper Documents contain a list of all dye/lanes related document. This chapter discusses how you can view, search the information contained in Dye/lane lists to perform particul genotyping analysis tasks.		nucleic acid rocedures. to that h, and use ular
This Chapter This chapter contains the following topics:		
	Торіс	See Page
	Where Dye/lanes Come From	5-2
Viewing Dye/lane Lists		5-4

Viewing Dye/lane Lists5-4Searching and Sorting Through Lists5-9Editing List Contents5-14Using Scale Factors for Quantitative Applications5-15

Working with Dye/lane Lists 5-1

Where Dye/lanes Come From

Introduction Dye/lane lists contain entries that correspond to imported GeneScan files. You use information contained in Dye/lanes for all Genotyping comparison and analysis tasks.

Phases of the Genotyper generates from one to four dye/lanes for each lane of each GeneScan file you import. The following diagram shows three phases in the process of generating Dye/lane list entries from electrophoresed dye-labeled nucleic acid fragments (Figure 5-1).





5-2 Working with Dye/lane Lists

What Happens in What happens in each phase of the dye/lane generation process.

Phase	Process
1	Nucleic acid fragments are labeled with one to four different dye colors (blue, green, yellow, red), and electrophoresed in a single lane (lane 2) of a gel based automated DNA sequencer.
2	GeneScan extracts fragment information from lanes or capillaries and generates one GeneScan file per lane or capillary. Each GeneScan file contains size and quantity information for each dye/labeled fragment.
3	When you import a GeneScan file in Genotyper, Genotyper extracts file information, and generates one dye/lane list entry for each dye color. Each dye/lane list entry contains size, quantity, and sample information for all fragments labeled with a single dye color and electrophoresed in a single lane.

Working with Dye/lane Lists 5-3

Viewing Dye/lane Lists

Definition The Dye/lane list is a list of all dye/lanes in the GeneScan data that you have imported into Genotyper. Dye/lanes are added to the list as you import them from GeneScan.

Settings in the Dye/lane sorting dialog box determines the sort order of the list. For more information on sorting dye/lane lists see "Searching and Sorting Through Lists" on page 5-9.

Setting Viewing
PreferencesYou can set preferences for the information that appears in the Dye/lane
list when you view it. Preference settings apply to all open Genotyper
Documents, not just the active document, and are saved in the
Genotyper Preferences file.

Step Action 1 Choose Set Preferences...in the Edit menu. The Set Preferences dialog box appears. Set Preferences • Options for exporting tables: Field delimiter: 💿 Tab 🔘 Comma 🔘 Space 🔘 None • Additional windows to be opened with main window: 🗌 Dye/lane 🛛 🗌 Plot 🔲 Macro 🔲 Statistics 🗌 Category 👘 🔲 Table 🔲 Step • Information to be shown in dye/lane list: 🗹 File name 🛛 🗹 Dve color 🖓 Sample Info • Automatic options for linked program & document: When opening Genotyper: 🔲 Open linked program 🔲 Open linked document When quitting Genotyper: 🔲 Save linked documents 🗹 Quit linked program • Import colors: 🗹 Yellow 🗹 Blue 🗹 Green 🔲 Red 🔲 Orange 🔲 Import Raw • Other ontions: Double-clicking runs macros & steps BioLIMS... Cancel 0K

To set Dye/lane list viewing preferences:

5-4 Working with Dye/lane Lists

To set Dye/lane list viewing preferences: (continued)

Step	Action		
2	Under the bullet "Information to be shown in dye/lane list:", select the checkboxes for what you want to view in the Dye/Lane list.		
	If you click	Then the Dye/Lane list displays	
	File Name	The name of the associated GeneScan file.	
	Dye color	The dye color of sample fragment labels.	
	Sample Info	Contents of Sample Info field of the GeneScan Sample Sheet.	
	Lane number	The lane number, or injection number for ABI PRISM 310 samples, in which sample fragments were electrophoresed.	
	Scale factor	Normalization factor that you can apply to dye/lane peaks.	
	Sample Comment	Comments entered in the GeneScan Sample Sheet.	

Window

Viewing the
Dye/LanesThe Dye/lanes window displays the Dye/lanes list, and also contains
associated Sample Information and Sample Comments from GeneScan files.

To view the Dye/Lanes window:

Step	Action
1	From the Main Window, click the Dye/lane window icon. The Dye/lanes window appears.
	Dye/lanes - untitled SampleInfo: U-1 Sample Comment:
	TCR Results 2 Blue U-1 TCR Results 2 Green U-1 TCR Results 2 Red 6S-1000 TCR Results 3 Blue U-2 TCR Results 3 Green U-2 TCR Results 3 Green U-2 TCR Results 3 Red 6S-1000 TCR Results 4 Blue U-3 TCR Results 4 Green U-3 TCR Results 4 Blue U-3 TCR Results 5 Blue U-4 TCR Results 5 Blue U-4 TCR Results 5 Blue U-4 TCR Results 5 Red GS-1000 TCR Results 5 Blue U-4 TCR Results 5 Blue U-4 TCR Results 5 Blue U-5.1 TCR Results 6 Green U-5.1 TCR Results 6 Green U-5.1 TCR Results 6 Red GS-1000 TCR Results 7 Rue U-5.2 TCR Results 7 Rue U-5.2
2	Click on the dye/lane of interest, for example, the first one. This displays Sample Information, and Sample Comments for the selected Dye/lane, and allows you to edit these items. These fields contain the same information that was entered in the Sample Sheet for associated GeneScan files. ! WARNING ! Information in the Dye/lanes window is not saved back into the original GeneScan files. The edited data in the Sample Info and Sample Comment fields applies only to the current Genotyper Document.

5-6 Working with Dye/lane Lists

Clearing the List Imported GeneScan data are appended to the Dye/lanes list. Therefore, if you are beginning a new Genotyping session, you might want to clear existing GeneScan data from the list

To clear the Dye/lane list:

Step	Action
1	Choose Clear Dye/Lane List in the Analysis menu.
	The Dye/Lane list is cleared.
	Note If you want to undo this command, choose Undo in the Edit menu. The Undo command must be the next command.

Selecting Dye Using the Dye Selection buttons you can select those lanes that have Colors sample fragments labeled with the dye color you select.

To display Dye/lanes by the color of the dye-label on fragments in the lane:

Step	Action		
1	If the Main window is Window from the Vie	s not already displaye ws menu.	ed, choose Show Main
	The Main Window ap	opears.	
	Selection	B V 031347-01 Father 031347-01 Father 041347-03 Daughter 041347-03 Daughter 041347-03 Daughter 041347-03 Daughter 041347-03 Daughter 041347-03 Daughter 041347-03 Daughter	LDK Inheritance check.b6 3 Green SUU3 3 Vellow SOU3 4 Blue SOU4 4 Green SOU4 4 Units SOU4 1 Vellow SOU4 1 Vellow SOU4 1 Vellow SOU4 1 Vellow SOU4
			Ś.
		D 12583 Hil peaks fi 1 (X) Highest 2 (X) Highest 1 (X) Highest 2 (X) Highest 1 (X) Highest	Form 98.00 to 113.00 bp in blue peak from 100.70 to 101.70 bp in b peak from 102.20 to 103.20 bp in b peak from 102.20 to 103.20 bp in b ye Sample Info Category Peak 1 S001 D12883 1 3
		031347-01 Father 38	S003 D12S83 1 3

Working with Dye/lane Lists 5-7

To display Dye/lanes by the color of the dye-label on fragments in the lane: *(continued)*

Step	Action
2	Click one of the four Dye Selection buttons to select only dye/lanes labeled with the selected dye colors; B (blue), G (green), Y (yellow), R (Red).
	To add to your selection, hold down the Shift key and click another Dye Selection button.

5-8 Working with Dye/lane Lists

Searching and Sorting Through Lists

Introduction For many Genotyper applications, particularly ones in which you import a large number of GeneScan files, you will often want to locate dye/lanes for particular GeneScan Sample files, or Results files. Genotyper offers several search and sorting features that make it easy for you to locate the particular dye/lane or GeneScan file.

How to SortYou can sort the Dye/lanes by various items. You can choose a differentDye/lanessorting order for each Genotyper Document.

To change the sort order of the Dye/lane list:

Step	Action
1	If the Main window is not already displayed, choose Show Main Window from the Views menu.
	The Main Window appears.
2	Choose the Dye/lane sortingcommand in the Views menu.
	The Dye/lane Sorting dialog box appears.
	Dye/Lane Sorting
	Sort dye/lane list in following order:
	Precedence Item Sort order
	1. File name 🔻 🖲 Ascending 🔾 Descending
	2. Lane number ▼
	3. Dye color ▼
	4. Sample Info ▼ ® Ascending ⊃ Descending
	5. Bacending Descending
	Cancel OK
3	sort next to the precedence number in which you want Genotyper to
	to sort them.
	Example
	If you choose File name after Precedence 1, and Lane number after precedence 2, Genotyper first sorts the list by File name, then sorts that list by lane number.

Working with Dye/lane Lists 5-9

To change the sort order of the Dye/lane list: (continued)

Step	Action
4	Click the radio button for how you want items in the list sorted, either in ascending order or descending order.
	Dye colors are sorted in the following ascending order: blue, green, yellow and red.
	Note If you use the Overlapped dyes, separate lanes option, the dye/lanes must be sorted by File name first and then Lane number.
5	Click OK to apply the sorting order to the active Genotyper Document.
	Click Cancel to cancel the sorting selections you have made.

Search Criteria

How to Specify You can specify search criteria for finding one or more dye/lanes in the Dye/lane list. For example, you might specify all colors with the text "001101" in Sample Information. Find commands are recorded and can be used as steps in a Genotyper macro.

To specify a search criteria:

Step	Action
1	Choose Find(光-F) in the Edit menu.
	The Find dialog box appears.
	Find
	● Find the following text: ○ Find non-blank text
	Look in the table In column 1 only
	Look in the dye/lane list In selected dye/lanes only
	☑ In Sample Info □ In Sample Comment
	Look in the category list In category name In category comment
	 In category groups In non-member categories
	In member categories
	Find all occurrences at once Add to current selection
	☑ Ignore upper/lower case differences Look at dyes: ☑ Blue ☑ Green ☑ Yellow ☑ Red ☑ Orange
	Cancel
2	Click the Find the following text radio button.
3	Type in the text you want to locate.

5-10 Working with Dye/lane Lists
To specify a search criteria: (continued)

Step	Action
4	Click the Look in the dye/lane list radio button.
5	Select the checkboxes for how and where you want Genotyper to search for the text string that you have typed (see "How to Search for Dye/lanes" on page 5-12). Example
	If you entered the text "001101" and selected the checkbox for In Sample Comment, Genotyper would search for the specified text in the Sample Comment fields of all dye/lanes.
6	Click OK.

Working with Dye/lane Lists 5-11

How to Search for
Dye/lanesOnce you have defined search criteria (see page 5-10), choose how
you want to search for dye/lanes in the list. The following table shows you how you can search for dye/lanes.

If you are	Then
Searching for all occurrences at once	Click the Find all occurrences at once checkbox.
	All dye/lanes with the designated text are selected.
Adding dye/lanes to the current selection	Click the Add to current selection checkbox.
	Dye/lanes already selected remain selected. Dye/lanes located by this command are also selected.
Restricting the search to currently selected dye/lanes	Click the In selected dye/lanes only checkbox.
	This is useful for narrowing a selection by repeated use of the Find command.
Searching for the next occurrence of a selection	Choose Find Next (\mathbb{H} -G) from the Edit menu.
	The Find Next command repeats the last Find command, using the same options that were used in the last Find command.
Searching for text strings without regard to case	Choose Ignore upper/lower case differences.
	The Find Next command locates all occurrences of the text string you have entered, ignoring the case of any letters you have entered.

GeneScan Data

How to Locate You can locate GeneScan data associated with a specific dye/lane.

To locate GeneScan data:

1 Se	ect a single dye/lane.		
2 Ch	Choose Locate GeneScan File in the File menu.		
The dye	e folder with the GeneScan sample file associated with that /lane is opened and the file is selected in the Finder.		
No app	te If the file is located on an unmounted disk, a dialog box bears and asks you to insert the disk that the file is on.		
IMI froi imp Co ma	PORTANT This feature works only if the dye/lanes are imported m GeneScan sample files. It will not work if the dye/lanes are ported from a BioLIMS database. You will need to open the llection Browser to locate the GeneScan sample file in BioLIMS nually.		

Editing List Contents

Introduction If you want to change the information about any item in the Dye/lane list, you can edit related sample information in the Dye/lane window. These changes will affect only the Genotyper Document. The original GeneScan file remains unchanged.

> Note You can make changes to only one dye/lane item at a time. If more than one dye/lane is selected or if none is selected, Sample information and Sample comments are grayed out.

How to Edit You can edit the sample information in the Sample Info field of the Information

Sample Dye/lanes window. To edit the Sample Info field:

Step	Action	
1	Open the Dye/lanes window.	
2	Select the item in the Dye/lanes list that you want to edit.	
	You can use the arrow keys on the keyboard to scroll up and down the items in the list.	
3	Use the Tab key until the cursor goes to the Sample Info text box, or click in the box.	
4	Type in any changes you want to make to the Sample Information.	

How to Edit You can edit the Sample Comments in the Sample Comment field of the Sample Comments Dye/lanes window.

To edit the Sample Comment field:

Step	Action
1	Open the Dye/lanes window.
2	Select the item in the Dye/lanes list that you want to edit.
	You can use the arrow keys on the keyboard to scroll up and down the items in the list.
3	Use the Tab key until the cursor goes to the Sample Comments field.
4	Type in any changes you want to make to the Sample Comments.
4	Type in any changes you want to make to the Sample Comments.

5-14 Working with Dye/lane Lists

Using Scale Factors for Quantitative Applications

Definition	You can use dye/lane scale factors to normalize the height or area of peaks.		
Why Use Scale Factors	 You can use scale factors for quantitative applications in which you are labeling peaks by height or area, and defining minimum and maximum peak heights in categories. 		
	By using scale factors you can normalize peak heights which helps correct for variations in starting quantities of nucleic acid samples, or variations in amount of samples initially loaded.		
How to See Scale Factors	When visible, scale factors appear next to each dye/lane in the Dye/lane list. To show Scale Factors in the Dye/lane list:		
	Step Action		
	1	Choose Set Preferencesin the Edit menu.	
		The Set Preferences dialog box appears.	
	2	Under the bullet "Information to be shown in dye/lane list:", select the Scale factor checkbox.	
		Scale factors now appear next to each dye/lane in the dye/lane list. The default scale factor is one.	

How to CalculateTo calculate scale factors, determine parameters for the calculation,
and then scale dye/lanes based on those parameters.

To calculate scale factors:

Step	Action		
	Determine parameters for calculation		
1	In the Dye/lane list, select the dye/lane to which you want to scale other dye/lane peaks.		
2	Choose Calculate Scale Factors from the Analysis menu.		
	The Calculate Scale Factors dialog box appears.		
	Calculate Scale Factors		
	Set scale factor for selected dye/lanes to		
3	Select the radio button corresponding to how you want to scale peaks.		
4	Optionally, you can restrict the calculation of scale factors to a particular range of peak sizes by typing in the peak sizes in the text boxes provided.		
5	Click the Normalize button to set the scale factor of the first selected dye/lane peaks to 1.0.		
	IMPORTANT Record the number that fills in the divided by field after you click Normalize to first selected dye/lane. You will use it when you scale dye/lanes to defined parameters.		
6	Click OK.		
	Scale dye/lanes to defined parameters		
1	In the Dye/lane list, select all the dye/lanes that you want to scale to the parameters you just determined.		

5-16 Working with Dye/lane Lists

To calculate scale factors: (continued)

	Step	Action	
	2	Choose Calculate Scale Factors from the Analysis menu.	
		The Calculate Scale Factors dialog box appears (see figure in step 2 of "How to Sort Dye/lanes" on page 5-9).	
	3	In the Calculate Scale Factors dialog box, enter the same parameters that you entered when determining parameters for calculation, including the number in the divided by field.	
		IMPORTANT Do not click normalize to first selected dye/lane again.	
	4	Click OK.	
Normalizing to the First Dye/lane	If you are normalizing all dye/lanes to the first one in your selection, you do not have to perform the four steps listed under "Scale dye/lanes to defined parameters". Instead, select all dye/lanes and perform the first six steps listed under "Determine parameters for calculation".		
How to Reset Scale Factors to One	The default Scale Factor is one. To reset Scale Factors to one, choose the Clear All Scale Factors command from the Analysis menu.		
Applying Scale Factors to Other Peaks	Once you have calculated scale factors for all peaks, you can apply the scale factors you have defined to any peaks in the Dye/lane list, not just the range you originally used to calculate the factor.		

Defining Categories and Labeling

Chapter Overview

Introduction You can label the fragment peaks that appear in plot displays with information such as fragment size, quantity, scan numbers, or customized text. Peak labels appear in the lower pane of the Main window. You can label peaks with more than one kind of label.

In This Chapter This chapter contains the following topics:

Торіс	See Page
Approaches to Labeling	6-2
Defining Categories for Labeling	6-4
Using Exclusive Peak Labeling–An Example	6-10
Creating Category Groups—an Example	6-13
Making Category Members	6-17
Sorting and Editing Categories	6-22
Offsetting Categories	6-24
Automatic Peak Labeling	6-26
Filtering Labels	6-29
Manually Putting Labels On Peaks	6-33
Customizing Text in Labels	6-35
Customizing the Color of Labels	6-38
Removing Labels	6-42
Labeling Normalized Peaks—an Example	6-45
Making Categories from Labels	6-49

Approaches to Labeling

Example of aFigure 6-1 shows an example of a dye/lane fragment peak labeled withLabeled Fragmentthe size of the fragment in base pairs. Fragment size is one kind of labelPeakyou can assign to peak data.



Figure 6-1 Example of a fragment peak labeled with the size in base pairs

Why Label Fragment Peaks

Why Label By labeling fragment peaks, you can:

- Visualize size and quantity information for analyzed sample fragments.
- Discover which samples contain fragments in related categories.
- Identify relationships between sample fragments.
- Make decisions about how to configure comparison and analysis tables.
- Make decisions about which samples to export to tables in GenBase.

Ways to Label Genotyper provides you with two ways to label fragment peaks: Fragments automatically and manually.

The two ways you can label fragment peaks and where you can find detailed instructions for each labeling method.

Labeling MethodDescriptionSee PageAutomaticSimultaneously labels all peaks within selected dye/lanes with specified criteria.6-26ManualPlaces defined labels on individual peaks in plot displays when you click a peak.6-33NoteWhen two or more electropherogram plots are superimposed, click-labeling is disabled6-33			
AutomaticSimultaneously labels all peaks within selected dye/lanes with specified criteria.6-26ManualPlaces defined labels on individual peaks in plot displays when you click a peak.6-33NoteWhen two or more electropherogram plots are superimposed, click-labeling is disabled6-33	abeling lethod	Description	See Page
Manual Places defined labels on individual peaks in plot displays when you click a peak. 6-33 Note When two or more electropherogram plots are superimposed, click-labeling is disabled 6-33	utomatic	Simultaneously labels all peaks within selected dye/lanes with specified criteria.	6-26
cher labeling le disabled.	lanual	Places defined labels on individual peaks in plot displays when you click a peak. Note When two or more electropherogram plots are superimposed, click-labeling is disabled.	6-33

Filtering

Automatic Label Genotyper's automated labeling process screens out peaks resulting from PCR-related artifact fragments detected during electrophoresis. You define the stringency of this filtering process by setting filter parameters that will remove labels from artifact peaks.

> For more information on filtering labels, see "Filtering Labels" on page 6-29.

Defining Categories for Labeling

Definition Categories define which peaks in selected dye/lanes Genotyper will label, and how those peaks will be labeled. You can also use defined categories to specify the contents of tables.

Genotyper uses category information to label appropriate peaks as described in "Automatic Peak Labeling" on page 6-26.

The CategoriesThe Categories window shows a list of all defined categories for selectWindowdye/lanes in the current Dye/lane list, as well as an abbreviated version
of the Add Category dialog box.



Adding Categories	You can add categories that will define how peaks will be labeled when	
you automatically label peaks of interest.		

To add categories:

Step	Action		
1	Choose Add Categoryfrom the Category menu.		
	The Add Category dialog box appears.		
	Display Category Group Category Peak information Range Colors Peak Peak Figure 6-2 Add Category	Add Category Add Category	
2	Enter the range limits in base pairs for fragments that you want label.		
	If you want to	Then	
	Automatically fill in range limits	Select a rectangular area in the plot area, and choose the Add Category command.	
	Specify starting and ending coordinates in the range	Use the pop-up menu to select to. Type in the starting and ending sizes in the range. For example, 120 to 140.	
	Specify a center coordinate and range	Use the pop-up menu to select \pm . Enter a tolerance For example 120 \pm 1.5.	

To add categories: (continued)

Step	Action			
3	Click a radio button to specify which peaks to label within this category:			
	If you want to label	Then click		
	All peaks	All peaks.		
	The highest peak	Highest Peak.		
	The highest "n" peaks (where "n" is an integer)	Highest "n" Peaks, and type an integer for "n".		
	Left most peak in a range	Left Peak.		
	Right most peak in a range	Right Peak.		
4	Click the dye color checkbox	es for the colors you want labeled.		
5	Optionally, define height requirements for peaks you want to label:			
	If you want to define	Then click		
	With (scaled) height of at least, and type a number for the minimum peak height.			
	A maximum height for labeled peaks With (scaled) height of at most, ar type a number for the maximum p height.			
	actor is 1.0, then the scaled height of a k height. If a different scale factor has he then the scaled height of a peak is ded by the Dye/lane's scale factor.			
6	Enter a name for the Category. For example, Alpha.			
7	Optionally, choose a display color for the Category. The entry in the Category list for this Category will appear in this color. Labels for the Category can optionally be displayed in this color.			
8	Optionally, enter a descriptive comment about the Category. The comment will appear in the Category window after the name.			
9	Click OK. The name of the category ap Everything All peaks from scan 0 Alpha Al All peaks from 138.00 A2 All peaks from 140.00	to 140.00 bp in blue to 142.00 bp in blue		

Exclusive Peak
LabelingThe Exclusive checkbox in the Add Category dialog box is a priority
labeling feature. When you select the Exclusive checkbox, any existing
labels on a peak, besides those defined by the "Exclusive" category, are
removed.

For more details on using exclusive peak labeling see, "Using Exclusive Peak Labeling–An Example" on page 6-10.

Adding Multiple Categories Categories Categories command. This can be useful if you are performing applications such as microsatellite repeats where you want to label a large number of peaks that differ by multiples of 2 base pairs.

There are three stages to this process:

- Defining categories
- Choosing optional parameters
- Naming the categories

To define categories:

Step	Action		
1	Choose Add Multiple Categoriesfrom the Category menu.		
	The Add Multiple Categories dialog box appears.		
	Add Multiple Categories		
	Starting size 100.00 Category tolerance ± 0.50 Category spacing 2.00 Number of categories 16 Image: Comparison of the system		
	Cancel		

To define categories: (continued)

/

Step	Action
2	In the Starting size field, enter the starting size for fragments that you want to include in the first category.
3	In the Category width \pm field, enter the range of fragment sizes that you want to be included in the category.
	For example, $100 \pm .50$ labels fragments that are between 99.5 to 100.5 base pairs in length as a single category.
4	In the Category spacing field, enter the number of base pairs between each category.
	For example, if you enter 2, then the second category will begin for all fragments that are between 101.5 and 102.5 base pairs.
5	In the Number of Categories field, enter the number of categories that you want to create.
6	Select the dye color check boxes for the dye colors that you want included in the categories.

To choose optional parameters:

Step	Action
1	Select the Group Name checkbox and type a name to include all categories under a single group name.
2	Select the checkbox for "with (scaled) height of at least", and enter a number if you want to limit the categories to only those peaks that generate a signal intensity of at least a particular height.
3	Select the checkbox for "with (scaled) height of at most", and enter a number if you want to limit the categories to only those peaks that generate signal intensity of at most a particular height.
4	Select the checkbox for Exclusive, if you want to clear any existing labels on peaks.

To name the category:

Step	Action
1	In the Prefix field, type a 1 to 15 character alpha numeric prefix for the category names.

To name the category: (continued)

Step	Action
2	In the First number field, enter the number to follow the prefix for the first category name.
3	In the Number increment, enter the number by which you want to increment each successive category number.
4	Click OK.

Example of Category Naming

Example of How Genotyper names categories based on parameters you enter:

If you define	Then categories are named
Prefix: AB	AB10, AB13, AB16,
First number: 10	
Number increment: 3	

Using Exclusive Peak Labeling-An Example

Introduction	The Exc check be peaks in with the	lusive option is a priority labeling feature. When the Exclusive ox is marked in the Add Category window, all other labels at the "Exclusive" category are cleared and the peak(s) is labeled desired information.
	In gener allows y	al, category ranges should not overlap, but the Exclusive option ou to use overlapping categories in special cases.
Example Application	In this example, the peaks of a marker occur between 106 and 122 bp. Two particular alleles, named A1 and A2, are known to occur around 116 bp and 118 bp. If either of these alleles are present, we would like them to be labeled by name, but if any others are present, we would like them to labeled with the text, "Unknown."	
	In the fir Exclusiv see how	st part of the example, we will see what happens when the e option is not used. In the second part of the example, we will the Exclusive option allows us to obtain the desired results.
Labeling without the Exclusive Option	Labeling without the Exclusive OptionIn the first part of this example, we will see what happens when we la peaks in the example application without using the Exclusive option.OptionTo label peaks without the Exclusive option:	
	Step	Action

Step	Action		
1	Assume categories have been created so that the Category list looks like the list below (note there are no exclusive peak labels).		
	 MFD11 A1 Highest peak from 115.50 to 116.50 bp in blue A2 Highest peak from 117.50 to 118.50 bp in blue Unknown All peaks from 105.00 to 122.00 bp in blue 		
2	Assume peaks have been labeled with the category name checkbox selected and all others de-selected.		

To label peaks without the Exclusive option: (continued)



Result of
Specifying
OverlappingNote that the peaks at 116 bp and 118 bp each have two labels. This is
one of the undesirable consequences of specifying overlapping
category ranges.Category Ranges

How to UseFor this example, you can use the "A1" or "A2" labels exclusively forExclusive Labelingthese peaks, by using the Exclusive option.

To label peaks using the Exclusive option:

Step	Action		
1	Assume that you have defined Categories like those shown below.		
	MFD11 Unknown All peaks from 105.00 to 122.00 bp in blue A1 (X) Highest peak from 115.50 to 116.50 bp in blue A2 (X) Highest peak from 117.50 to 118.50 bp in blue		
2	Label peaks.		
3	View the resulting plot (shown below); known peaks are labeled correctly A1 and A2, others are labeled "Unknown".		
	Filter Stutter Peaks		
1	Choose Filter Labels from the Analysis menu.		
2	Click OK, to use the default filtering parameters. The plot area now shows the two known alleles, and a third, spurious peak labeled "Unknown."		
	106 108 110 112 114 116 118 120 122		

Creating Category Groups—an Example

Introduction	Categor alleles v	y groups may be useful when you want to identify individual vithin the range of a marker category.
	IMPORT. comman	ANT If Category groups in the same dye color overlap, some ds may not perform as expected
	In this e groups t of categ	xample, you will make two sets of categories and specify the hey are associated with. You will also collapse one of those sets ories into a single entry in the Category list.
	Note T relevance	hese categories are only for illustration and have no biological e.
Create a Category GroupCategory groups organize groups of similarly defined category a single name.To create two sets of categories and specifying the groups of they are associated:		y groups organize groups of similarly defined categories under name.
		e two sets of categories and specifying the groups with which associated:
Step Action		Action
	1	Choose Add Categoryfrom the Category menu.
		The Add Category dialog box appears (see figure in step 1 of "Adding Categories" on page 6-5).
	2	Name the first Category "A1."
	3	Click Member of group checkbox and enter "Alpha".
	4	Click the All Peaks radio button.
	5	Enter 138 and 140 for the "Size" range limits.
	6	Click the blue checkbox and de-select the checkboxes for the other colors.
	7	Click OK.

To create two sets of categories and specifying the groups with which they are associated: $(\ensuremath{\textit{continued}})$

Step	Action		
8	Repeat steps 2-7 using the following values:		
	A2; Alpha; All peaks, 140-142; blue		
	♦ A3; Alpha; All peaks, 146-148; blue		
	♦ B1; Beta; All peaks, 121-123; blue		
	◆ B2; Beta; All peaks, 123-125; blue		
	◆ B3; Beta; All peaks, 129-131; blue		
	You have created two groups: Alpha and Beta, with three Categories in each group.		
9	Choose Show Categories Window from the Views menu.		
	The Categories window shows the two marked Category groups		
	you created.		
	Categories - GT2.5 template for UM		
	Category G Group		
	0.00 to 🗢 9999.00 💿 All 🔾 Highest 📿 Highest 2		
	Min height 1 🔒 🗍 🗍 🗍 🗍 🗍 🗍 🗍 🗍 🗍 🗍 🗍 🗍		
	□ Max height 9999 □ Exclusive ☑ B □ G □ Y □ R □ O		
	Everything All peaks from scan 0 to 32000 in R/B/G/Y/0		
	A1 All peaks from 138.00 to 140.00 bp in blue A2 All peaks from 140.00 to 142.00 bp in blue		
	A3 All peaks from 146.00 to 148.00 bp in blue		
	B1 All peaks from 121.00 to 123.00 bp in blue		
	B3 All peaks from 129.00 to 131.00 bp in blue		

Unmark a Group Using Category groups allows you to conveniently mark or unmark all of Categories entries in that group at the same time, rather than marking or unmarking each one individually.

> For more information on marking and unmarking Categories, see "Marking or Unmarking Categories" on page 6-26.

To unmark the alpha category group:

Step	Action			
1	Select "Alpha" in the Categories window.			
2	Choose Unmark (z-U) from the Edit menu.			
	All three Categories in the Alpha group are now unmarked.			
	🗆 📃 Categories – GT2.5 template for VM 📃 🗉 🗄			
	Alpha 🕒 Group			
	138.00 to \$ 148.00 • All • Highest • Highest 2			
	☐ Min height 1 ☐ Max height 9999			
	Everything All peaks from scan 0 to 32000 in R/B/6/V/0			
	R1 All peaks from 138.00 to 140.00 bp in blue R2 All peaks from 140.00 to 142.00 bp in blue R3 All peaks from 146.00 to 148.00 bp in blue			
	Beta B1 All peaks from 121.00 to 123.00 bp in blue B2 All peaks from 123.00 to 125.00 bp in blue			
	B3 All peaks from 129.00 to 131.00 bp in blue			
	Note If all Categories in a group are marked, the group will have a bullet next to its name. If some Categories in a group are marked			
	and some unmarked, the group name will have a dash (-) next to its name.			

Collapse a Group Collapsing a group of categories can make viewing of the Category list of Categories easier, by reducing the members of a group to a single entry in the Categories list.

To collapse the beta category to a single entry in the categories list:

Step	Action		
1	Select the category named Beta in the Categories window.		
2	Choose Collapse Categories (z-]) from the Views menu.		
	Categories - GT2.5 template for UM Beta Group 121.00 to < 131.00 All Highest Highest 2 Min height Leftmost Rightmost Max height Beta Go Y Max height Beta Go Y Max height Beta Go Y Beta Go Y Add Everything All peaks from scan 0 to 32000 in R/B/G/Y/0 Edd R1 All peaks from 138.00 to 140.00 bp in blue Edd Edd R2 All peaks from 140.00 to 142.00 bp in blue Edd Edd R3 R11 peaks from 146.00 to 148.00 bp in blue Edd Edd		

Making Category Members

"A"

Introduction	You can make members of categories that represent a distribution of peak height ranges within a particular category. This allows you to categorize marker data based on a distribution of fragment quantities for applications such as AFLP.
	For complete details for running AFLP applications look for information soon to be available on the Applied Biosystems web site.
Example of Category Members	Figure 6-3 shows an example of the distribution of peak heights or fragment quantities for five category members (B,C,H,D,A). For example, the peak shown here belongs to category member "B".
	"B" "C" "H" "D"

Figure 6-3 Example of peak height distribution for category members

Category Members

How to Make In order to use this command you have to have already created a table. The table must have columns defined for categories and peak height.

> **Note** The following steps refer to an AFLP example soon to be available on the Applied Biosystems web site.

To make category members:

Step	Action		
1	Choose Show Table window from the Views menu.		
	This displays a table with rows of peak height and category data such as that shown in this figure.		
	Lane & Dye Sample Info Category Height		
	25B P2 A01 1908 =		
	28B 10 A01 1613		
	27B 9 R01 1531		
	22B 7 A01 1352 00		
	23B 8 A01 1202 R		
	16B 1 R01 1069 🔂		
	19B 4 R01 1021		
2	Choose Make Category Membersfrom the Category menu The Make Category Members dialog box appears.		
3	Choose the category column from the Look in table column for group names pop-up menu.		
	The domes chosen dategories as groups.		
4	Choose the peak height column from the Look in table column for scaled heights pop-up menu.		

To make category members: (continued)

Step	Action			
5	For each marked category group, Genotyper calculates the distribution of peak heights (for the group) by looking at the appropriate rows in the table. Type in the percentile of this distribution that you want to use for the "reference height." For example, if you want the largest height to be the reference height, type in "100" for the percentile.			
6	Select from one to five checkboxes for the number of members you want to add to each marked category, and type in a name, and a range that is a percentage of the defined reference height.			
7	Click OK. For each box that you checked, Genotyper adds a member, that has a height range that is a certain percentage of the referenced height that you calculated.			
8	Choose Show Categories Window from the Views menu. The Categories window appears and displays new members for each category with varying scaled height ranges as shown in this figure.			
	Categories - Category member examp			
	129.55 ± \$ 0.50 ○ All @ Highest ○ Highest 2			
	☑ Min height 22			
	Maxheight 54 Mexcusive M D 0 0 V Add			
	BIO (A) Bit (A) Highest peak at 103.62 ± 0.50 bp in blue with scaled ht 10 to 187 B B All (X) Highest peak at 103.62 ± 0.50 bp in blue with scaled ht 10 to 187 C B B All (X) Highest peak at 103.62 ± 0.50 bp in blue with scaled ht 10 to 187 C B C B All (X) Highest peak at 103.62 ± 0.50 bp in blue with scaled ht 10 to 187 D B B C C B All (X) Highest peak at 103.62 ± 0.50 bp in blue with scaled ht 27 to 101 D D B All All All All B B C All All			
	■ HIJ (X) Highest peak at 129.55 ± 0.50 bp in blue with scaled ht 54 to 16 ● C IAI (X) Highest peak at 129.55 ± 0.50 bp in blue with scaled ht 54 to 63 ● D IAI (X) Highest peak at 129.55 ± 0.50 bp in blue with scaled ht 17 to 22			

Searching for Categories

_

Introduction	You can define search criteria for categories and locate a particular
	category or categories in the list of defined categories.

Search Criteria

How to Specify To specify a search criteria:

Step	Action		
1	Choose Find(光-F) in the Edit menu.		
	The Find dialog box appears.		
	Find the following text.		
	O Look in the table		
	O Look in the dye/lane list □ In selected dye/lanes only		
	🔲 In Sample Info		
	In Sample Comment		
	Look in the Category list In category name In category comment		
	✓ In category groups		
	☑ In non-member categories		
	Find all occurrences at once		
	Add to current selection		
	☑ Ignore upper/lower case differences		
2	Click the Find the following text radio button.		
3	Type in the text you want to locate.		
4	Click the Look in the category list radio button.		
5	Select the checkboxes for where you want Genotyper to search for the text string that you have typed.		
6	Select the checkboxes for how you want Genotyper to search for the text string that you have typed (Table 6-1 on page 6-21).		
7	Click OK.		

How to Search for
CategoriesOnce you have defined search criteria, choose how you want to search
for dye/lanes in the list. The following table shows you how you can search for categories.

e 6-1 Ways to search for categories:
e 6-1 Ways to search for categories

If you are	Then
Searching for all occurrences at once	Click the Find all occurrences at once checkbox.
	All categories with the designated text are selected.
Adding categories to the current selection	Click the Add to current selection checkbox.
	Categories already selected remain selected. Categories located by this command are also selected.
Searching for the next occurrence of a selection	Choose Find Next (\mathfrak{H} -G) from the Edit menu.
	The Find Next command repeats the last Find command, using the same options that were used in the last Find command.
Searching for text strings without regard to case	Click Ignore upper/lower case differences.
	The Find Next command locates all occurrences of the text string you have entered, ignoring the case of any letters you have entered.
Restricting the search to categories defined for particular dye colors only	Click the checkboxes for the particular dye colors you want to search.

Sorting and Editing Categories

Introduction Once you create a number of different categories, you can easily sort the category list, edit existing categories, and create new categories from existing ones.

Sorting the You can change the sort order of the Category list.

Categories List

To sort the category list:

Step	Action		
1	Choose Category Sortingfrom the Views menu.		
	The Category Sorting dialog box appears.		
	Category Sorting		
	Sort category list in following order:		
	Precedence Item Sort order		
	1. Name 👻 @ Ascending 🔾 Descending		
	2. ▼ ® Ascending ○ Descending		
	3. 🗨 🖲 Ascending 🔿 Descending		
	4. 🗨 🖲 Ascending 🔿 Descending		
	Cancel OK		
2	Choose the precedence of sorting the items (name, size/scan,		
	minimum height, comment, or dye color) by clicking and holding		
	down the pop-up menus.		
3	Choose the sort order of these items in ascending or descending		
	order by clicking the appropriate radio buttons.		
	The "Everything" category always appears first in the Category list.		
	Exclusive categories are sorted after non-exclusive categories,		
	within their groups.		

How to Edit
CategoryOnce you have added a category, you can edit the parameters for that
category at any time.

Parameters

To edit category parameters:

Step	Action
1	Select a category in the Category list.
2	Choose Edit Categoryfrom the Category menu.
	The Edit Category dialog box appears. This dialog is identical to the Add Category dialog box, except for the title (see figure in step 1 of "Adding Categories" on page 6-5).
3	Modify parameter settings.
	Note You cannot edit a member of a group to be a member of another group. A group contains categories, each of which applies to the same set of dye colors.
4	Click Replace.
	The parameters you changed will replace the previous settings for this category.

Offsetting Categories

Introduction	You can use either the Offset Category, or the Calculate an Offset command to temporarily shift the size range of a category.	
How to Offset Categories	To use	the Offset Category command:
	Step	Action
	1	Select one or more categories from the Category list in the Main window.
	2	Choose Offset Categories from the Category menu.
		The Offset Categories dialog box appears.
		Offset selected categories by 0.00 Cancel
	3	Enter a number, positive or negative, for how many base pairs you want to offset the current size range defined for a given category.
	4	Click OK.
		For the selected category in the Category list, the number you entered appears in parentheses next the size range. For example, if you entered -0.2 , (-0.2) appears next to the size range, and the start and end point of the size range is decreased by -0.2 base pairs.

When to CalculateThe Calculate Offset command automates the Offset Category
command. Use the Calculate Offset command if you have run the same
samples in the same lanes of two or more different gels or capillaries.
Calculating an offset can help eliminate run-to-run variability of
fragment size values in categories.

The Calculate Offset command is particularly useful for genotyping applications that make use of allelic ladders.

an Offset

How to Calculate To use the Calculate Offset command:

Ston	Action	
1	For GeneScan data from each gel, establish a standard set of category values for peak data.	
2	Import all GeneScan data that you are using in your application.	
3	Select one or more categories from the Category list in the Main window.	
4	Choose Calculate Offset from the Category menu. The Calculate Offset dialog box appears. Calculate Category Offset Offset selected categories by the difference between 0.00 and the size of the first labeled peak, in the first selected dye/lane, in the range of category Cancel OK	
5	Enter the number for the size in base pairs of your reference peak.	
6	From the pop-up menu, select the category from which you want to calculate the offset.	
7	Click OK.	

Automatic Peak Labeling

Introduction	Automatic peak labeling allows you to label peaks in selected dye/lanes using criteria defined in marked categories, and the Label Peaks dialog box.			
	Note F labels of all previo	Repeated use of the Label Peakscommand will produce duplicate the same type at a peak. Use the Clear All labels command to remove susly added labels.		
Peak Label Limit	No more than 500 peaks should be labeled in any one dye/lane. If more than 500 peaks are labeled, then some commands (such as Filter Labels) may not be available.			
Marking or Unmarking Categories	When you add a category to the Category list, it is marked. Marked categories are used for automatic labeling of peaks. Unmarked categories are ignored. To mark or unmark Categories:			
	Step	Action		
	1	Select one or more Categories from the Category list.		
	2	Choose Mark $(\mathbb{H}-M)$ or Unmark $(\mathbb{H}-U)$ from the Edit menu, or double-click a single category to toggle between a marked and unmarked state.		

A bullet appears to the left of categories, indicating the categories are marked.

How to Label To automatically label peaks:

Peaks

Automatically

Step	Action			
1	Mark categories that define how you want peaks labeled.			
2	Select the dye/lane or dye/lanes that contain the peaks you want to automatically label.			
3	Choose Label Peaksfrom the Analysis menu.			
4	Click the appropriate checkboxes for what you want to appear on labels:			
	If you want to label Peaks with	Then click		
	Fragment size in base pairs	the size in bp.		
	Note Size can be rounded to nearest integer.			
	Height in units defined by GeneScan	the peak height.		
	Note Height can divided by Dye/lane scale factor.			
	Area in units defined by GeneScan	the peak area.		
	Note Area can be divided by Dye/lane scale factor.			
	Number of scans required to detect the peak	the scan number.		
	A pre-defined text description	the text, and type in a peak label.		
	A text box that you can annotate after putting a blank label on a peak	the requested text.		
	Note For click labeling only.			
	Either Manual or Auto depending how the peak was labeled	label/peak source.		
	A score for each peak that indicates how well the peak image resolves with respect to the background	the peak modulation score.		
5	Click OK.			
6	To view the peak labels, click the Plot window Plot data window.	w icon, and show the		

When to Round When setting parameters for how you want to automatically label peaks, select the round integers checkbox only if you are labeling large sized fragments where the numbers to the right of the decimal point can be ignored.

IMPORTANT Do not round size labels to the nearest integer if you are performing a microsatellite application. You will not obtain satisfactory results.

Changing Existing
LabelsThe Change Labels command enables you to change labels within
marked categories on currently selected dye/lanes. If you are running a
genotyping application that uses genetic marker allele designations,
you can change existing labels, by renaming allele labels from size in
base pairs to a category or allele name.

To change existing labels:

Step	Action		
1	Choose Change Labelsfrom the Analysis menu.		
	The Change labels dialog box appears.		
	Change labels of peaks within marked categories to:		
	🗖 the size in bp		
	rounded to integer		
	🗆 the peak height		
	divided by scale factor		
	🗖 the peak area		
	divided by scale factor		
	the scan number		
	the text:		
	🖂 the category's name		
	🔲 label/peak source		
	the peak modulation score		
	Cancel OK		
2	Click the checkboxes for what you want to now appear on peaks with existing labels.		
3	Click OK.		
Filtering Labels

Definition Genotyper may label some peaks that, for various reasons, you may not want to be labeled. You can use Genotyper's filtering feature to remove these unwanted labels.

How to Filter Note When viewing by scan, only the first option in the Filter labels dialog box Labels is available. The other options are intended to be used only when viewing by size.

To filter labels:

Step	Action
1	Choose Filter Labelsfrom the Analysis menu.
	The Filter Labels dialog box appears.
	Filter Labels
	□ Remove labels from peaks in the size range 0.00 to 100.00
	Remove labels from peaks whose height is less than 32 % of the highest peak in a category's range
	⊠ Remove labels from peaks preceeded by higher, labelled peak within 0.00 to 1.60 bp □ (Higher by at least 5 %)
	⊠ Remove labels from peaks followed by higher, labelled peak within 0.00 to 3.00 bp □ (Higher by at least 5 %)
	Cancel OK
	Generally, the default settings in the Filter Labels dialog box remove most of the "stutter" bands and noise from electropherograms. These filtering parameters are designed for dinucleotide microsatellite data repeats.
	Note The filtering operations listed in the dialog box are performed one at a time, in the order they are listed. You can isolate the effect of each filtering operation by performing only one operation at a time.
2	You can change settings to remove labels from peaks that do not represent significant fragment data (see figure in step 1).

Kinds of Peaks You Figure 6-4 shows the kinds of peaks for which you can filter labels and Can Filter remove them from plot displays.



Figure 6-4 Kinds of peaks you can filter

Description of each of the numbered peaks in Figure 6-4:

Peak Number	Description
1	Spurious peaks at known locations.
2	Small peaks.
3	Small peaks on the shoulders of stutter peaks ("+A" peaks).
4	Stutter peaks.

Spurious Peak Labels

How to Remove Spurious peaks are often large thin peaks that appear on the far left of plot displays. They can result from primers, excessive salt in samples, or from pooling samples during PCR preparation.

To remove spurious peak labels at known locations:

Step	Action
1	In the Filter Labels dialog box, click the first checkbox and enter the size range of the spurious peaks that occur in selected electropherograms plots.
2	De-select the other checkboxes.
3	Click OK.

How to Remove Small peaks close to the baseline are referred to as *background noise*, Labels from Small and can result from spectral overlap or other GeneScan matrix file Peaks problems.

To remove small peaks:

Step	Action
1	In the Filter Labels dialog box, click the second checkbox and type in a percentage of the height of the highest peak, for which peaks that are less than this percentage will be removed.
2	De-select the other check boxes.
3	Click OK.

How to Remove One of the most common errors in automated genotyping results from Labels from Small the tendency of Taq DNA Polymerase to add an additional (non-Peaks on Peaks templated) nucleotide, usually an A, to the end of the extending strand. This results in the production of PCR fragments one nucleotide longer than the true allele product which display as small peaks on allele peaks in Genotyper. These "+A" peaks can display on either the left or right side of the true allele peak, usually 1 nucleotide in length.

> **IMPORTANT** When the peak height of the "true" allele product and that of the +A allele are similar, Genotyper may recognize the +A bands as the true allele, resulting in a genotyping error of about 3-5%.

To remove small peaks on the shoulders of allele peaks:

Step	Action
1	In the Filter Labels dialog box, click the third checkbox from the top, and enter the peak range, for peaks you want removed.
2	De-select the other check boxes.
3	Click OK.

In addition to using the Filter Labels command, you can define categories so that only the left or right peak in a pair of peaks is labeled, and the peak that results from the +A artifact remains unlabeled.

How to Remove
Stutter PeaksStutter peaks can occur when genotyping microsatellite samples, and
can be caused by slippage of the polymerase enzyme during PCR.

To remove stutter peaks:

Step	Action
1	In the Filter Labels dialog box, click the fourth checkbox and enter the peak range of peaks to include in the filtering process.
2	Click the Higher by at least checkbox, and type the percentage height that a preceding peak must be to removed.
3	De-select the other checkboxes.
4	Click OK.

Manually Putting Labels On Peaks

Introduction You can label individual peaks in plot displays by locating the peak or peaks of interest, and then clicking on the peak. When you click on the peak a second time, the label is removed.

You can label peaks with more than one label, for example, size and height. Peak labels appear in the lower pane of the Main window.

How to Manually To label fragment peaks manually, define what you want to appear in Label Fragment the label and then click on the peaks that you want to label.

To manually label peaks:

Step	Action
1	Choose Set Click Options from the Analysis menu.
	The Set Click Options dialog box appears.
	Set Click Options Set Clicked peaks with:
	□ rounded to integer
	divided by scale factor
	the peak area
	the scan number
	the text: Found
	🗋 label/peak source
	the peak modulation score
	Cancel OK

To manually label peaks: (continued)

Step	Action	
2	Click the appropriate check boxes for what labels:	you want to appear on
	If you want to label Peaks with	Then click
	Fragment size in base pairs	the size in bp.
	Height in units defined by GeneScan	the peak height.
	Height divided by scale factor	divided by scale factor.
	Area in units defined by GeneScan	the peak area.
	Area divided by scale factor	divided by scale factor.
	Number of scans required to detect the peak	the scan number.
	A Pre-defined text description	the text, and type in a peak label.
	A text box that you can annotate with different text each time you click a peak	the requested text.
	Either Manual or Auto depending how the peak was labeled	label/peak source.
	A score for each peak that indicates how well separated the peak is from background.	the peak modulation score.
3	Click OK.	
4	Select a dye/lane that contains peaks you	vant to label.
5	Move the cursor in the electropherogram pathe vertical line jumps to the peak that you	art of the Plot area until want to label.
6	Click the peak with the mouse button.	
	A label for that peak appears in the lower p	ane of the plot area.

Customizing Text in Labels

Introduction	Once you have assigned labels to peaks, you can customize the text in the labels.
	Note Text and color customizations you make to labels apply only to the labels in the active (frontmost window) Genotyper Document. However, each document can have its own independent customization.
How to Show Labels that Have Been Manually	You can show labels that have been manually removed to provide an audit trail of adjustments to labels that have been automatically assigned to peaks.
Removed	For more information on removing labels from peaks, see "Removing Labels" on page 6-42.
	For more information on automatically labeling peaks, see "Automatic Peak Labeling" on page 6-26.

To display labels that have been manually removed:

Step	Action
1	Choose Plot Options in the Views menu, then choose the Label Optionssubmenu.
	The Label Options dialog box appears.
	Box 1 Show labels that were manually removed Box 2 Add prefix to label for data type: Category Size Size sz Height ht Text tx Scan sc Add prefix to label if changed manually: Rdded RM Removed RM © Draw labels in black & white
	© Use same colors for labels and dyes ○ Use same colors for labels and category names ○ Color labels by data type Category: ▼ Size: ▼ Height: ▼ Text: ▼ Scan: ▼ Area: ▼ Cancel OK
	Figure 6-5 Label Options dialog box

To display labels that have been manually removed: (continued)



How to Add Data Type Prefixes If you want to identify the data type of a peak label, you can add a prefix to labels that identify the type of the label. Data Types and associated default prefixes include:

- Category (ct)
- Size (sz)
- ♦ Height (ht)
- Text (tx)
- ♦ Scan (sc)
- ♦ Area (ar)

To add data type prefixes to labels:

Step	Action
1	Click Box 2 in Label Options dialog box (see Figure 6-5 on page 6-35).
2	Enter the prefixes you want or use the default prefixes.
3	Click OK.
	The labels are assigned prefixes for data type. This figure shows an example of labels with size prefixes (sz).
	60 70 80 90 100 110 120 130 140 150 160 170 180 190 200

Prefix to Manually removed manually. Changed Labels

How to Add a You can add a prefix to labels to mark labels that were either added or

To add a prefix to labels that were added or removed manually:

Step	Action
1	Click Box 3 in the Label Options dialog box (see Figure 6-5 on page 6-35).
2	Enter the prefixes you want or use the default prefixes.
3	Click OK. The prefix "AM" appears on the labels that were added manually; the prefix "RM" appears on the labels that were removed manually.

Customizing the Color of Labels

Introduction To distinguish between different types of labels you can customize the color of the labels.

How to Draw If you are planning to print results data, or display labels on a black and Labels in Black white monitor, you may want to draw labels in black and white.

and White

To draw labels in black and white:

Step	Action
1	Select Plot Options in the Views menu and choose Label Options
	The Label Options dialog box appears (see Figure 6-5 on page 6-35).
2	Select the Draw labels in black and white radio button in the Label Options dialog box.
3	Click OK.
-	

How to Use the You can make peak labels the same color as their associated peaks. Same Colors for For example, blue electropherograms will have all blue labels and green Labels and Dyes electropherograms will have all green labels.

To color labels the same as associated peaks:

Step	Action
1	Select Plot Options in the Views menu and choose Label Options
	The Label Options dialog box appears (see Figure 6-5 on page 6-35).
2	Select the Use same colors for labels and dyes radio button.
3	Click OK.

How to Use the The Add Category dialog box (Figure 6-2 on page 6-5) allows you to Same Colors for associate a color with a category for display purposes. The name of the Labels and category in the Category list will appear in this color. This option allows Category Names you to display labels that have the same color as a particular category.

To color labels the same as associated categories:

Step	Action
1	Select Plot Options in the Views menu and choose Label Options
	The Label Options dialog box appears (see Figure 6-5 on page 6-35).
2	Select the Use same colors for labels and category names button.
3	Click OK.

Data Type

How to Choose You can color labels according to the type of data that the label Color Labels by describes. Data types include:

> ٠ Category

- Peak Size ۲
- Peak Height ۲
- Label Text ۲
- Scan number ۲
- Peak Area ۲

To color labels according to data type:

Step	Action
1	Select Plot Options in the Views menu and choose Label Options
	The Label Options dialog box appears (see Figure 6-5 on page 6-35).
2	Select the Color labels by data type radio button.
3	Click OK.
4	Click and hold down the pull-down menu for color selection by data type.
5	Select a color.
6	Repeat step 5 for each data type label you want to color.
	The data types appear in the selected colors in the Plot window.

How to Select a Custom Color for a Data Type Label

How to Select a To select a custom color for a data type:

Step	Action
1	Select Plot Options in the Views menu and choose Label Options
	The Label Options dialog box appears (see Figure 6-5 on page 6-35).
2	Select Color labels by data type radio button.
3	Click OK.
4	Click and hold down the pull-down menu for color selection by data type.
5	Select the last color in the list (the one with the ellipsis ()).
	O Draw labe Image: Constraint of the state of the
6	Place the cursor on the color wheel and click on the color of your choice.
7	Click OK.
8	Repeat steps 5-7 for each data type color you want to change.

Removing Labels

Introduction	During a labels fr	a genotyping session, you will often want to remove fragment om peaks.
Ways to Remove Labels	You can remove locating removed	remove all labels from peaks, select specific kinds of labels and those labels automatically, or remove individual labels by them in plot displays and clicking on the labels you want d.
Removing All Labels	If you wa or not),	ant to remove all peak labels in all dye/lanes (whether selected choose Clear All Labels from the Analysis menu.
How to Remove Specific Labels	You can To remo	specify the range of peaks for which labels will be removed. ve labels within a specified size range:
	Step	Action
	1	Select the dye/lanes from which you wish to remove labels.
	2	Choose Remove Labelsfrom the Analysis menu.
		The Remove Labels dialog box appears. Remove Labels in size range List of ranges 100.00 to 110.00 110.00 215.00 ± 5.00 280.00 100 100.00 to 282.00 100 100 100 100.00 to 282 100 <t< th=""></t<>
	3	Type in the range in base pairs, then click Insert (\mathbb{H} -I).
		The size range appears in the list of ranges.
		Note You can also specify the size range by choosing " \pm " from the pop-up menu, for example, 105 \pm 10.
	4	Repeat Step 2 for each range you want to include.

To remove labels within a specified size range: (continued)

Step	Action
5	Click OK.
	Labels in the specified ranges in all currently selected dye/lanes are cleared.

How to Correct To correct size range errors in the Remove Labels dialog box (see step Errors in the Size 2 of "How to Remove Specific Labels" on page 6-42):

Step	Action
1	Select the range from the range list.
2	Type in the new range.
3	Click Replace Range (#-R).
4	Click OK.

Removing a Range To remove a range from the range list in the Remove Labels dialog box From the Range (see step 2 on page 6-42):

List

Step	Action	
1	Select the range from the range list.	
2	Click Delete (ಱ-D).	
3	Click OK.	

Removing Removing common labels is useful for genotyping applications such as Common Labels AFLP where you have many labeled peaks of which you are only interested in labels that represent a polymorphism.

To remove common labels:

Step	Action	
1	Select two or more dye/lanes.	
	Note If only one dye/lane is selected, all labels for that dye/lane will be cleared.	

To remove common labels: (continued)

Step	Action
2	Choose Clear Common Labelsfrom the Analysis menu.
	The Clear common labels dialog box appears.
	Clear Common Labels
	Clear labels at labeled peaks common to all selected dye/lanes
	Do not clear labels if ratio of scaled heights of peaks exceeds
	1.8 Cancel OK
2	Enter the telerance in base points
3	Enter the tolerance in base pairs.
	Two peaks are considered to be at the same location if their peaks are within the specified tolerance.
4	If you do not want to clear labels when the peaks in different dye/lanes have a significant height difference, select the checkbox.
5	Click OK.
	Labels are cleared at those peaks that are labeled in <i>all</i> of the currently-selected dye/lanes. For example, if a peak at a particular location is labeled in five out of six lanes, none of the labels will be cleared; only if labels are present for six out of six lanes will they all be cleared.

Labeling Normalized Peaks—an Example

Introduction In quantitative applications, where relative peak height is important, you can normalize peak heights relative to the height of a control peak.

This example shows you how to perform the three procedures required for labeling normalized peaks:

- Defining a control peak
- Normalizing peaks to the control peak
- Labeling normalized peaks

Define a Control The first procedure in labeling normalized peaks is to define a control Peak peak.

To define a control peak:

Step	Action
1	Select a dye/lane.
2	In the Plot pane, select a range that includes the control peak.
3	Choose Add Category() from the Analysis menu.
	The Add Category window appears.
4	Click the Highest peak radio button.
5	Name the Category Control Peak.
	Add Category Name Control Peak Member of group

To define a control peak: (continued)

S	tep	Action
	6	Click OK.

Peak

Normalize Peaks
to the ControlOnce you define a control peak, normalize the heights of other peaks to
the height of your control peak, which serves as a reference.

To normalize peaks to the control peak:

Step	Action	
1	In the plot pane, select a range that contains a peak to be normalized.	
2	Choose Add Category	
3	Name the peak "Peak 1".	
4	Click the Highest Peak radio button.	
	Add Category Name Peak 1 Member of group Comment All peaks Highest peak Highest 2 peaks Left peak Size 103.30 to \$119.89 with dye color(s) Ø blue green _ yellow with (scaled) height of at least 1 with (scaled) height of at most 9999 Exclusive (clears previous labels at same peak) Cancel	
5	Click OK.	
6	Repeat this procedure for another peak to be normalized.	
	The Category list should now look like this figure.	
	Control peak Highest peak from 83.30 to 94.87 bp in blue Peak1 Highest peak from 103.34 to 119.89 bp in blue Peak2 Highest peak from 123.65 to 138.45 bp in blue	

Label Normalized
PeaksOnce you have defined a control peak and the other peaks to be
normalized, you can label them.

To label peaks:

Step	Action	
1	Choose Label Peaksfrom the Analysis menu.	
	The Label Peaks dialog box appears.	
	Label peaks within marked categories with: the size in bp rounded to integer the peak height divided by scale factor the peak area divided by scale factor the scan number the text: the category's name label/peak source	
	☐ label/peak source ☐ the peak modulation score	
	Cancel OK	
2	Click the peak height and/or peak area check box.	
3	Click OK.	
4	Choose Normalize Labels from the Analysis menu.	
	The Normalize Labels dialog box appears.	
	Normalize Labels	
	Divide area & height labels in the ranges of categories named	
	by area or height of first labeled peak in the range of the category	
	located in 💿 in the same lane O in lane number 1	
	Cancel OK	

To label peaks: (continued)

Step	Action	
5	From the upper set of pop-up menus, choose the Categories to be normalized, for example, Control peak, Peak1, and Peak2.	
6	From the middle pop-up menu, choose the name of the Category you defined as a control, for example Control Peak.	
7	Click the "in the same lane" radio button.	
8	Click OK. The plot pane of the Main window now displays peaks with normalized labels.	

Making Categories from Labels

Introduction	For genotyping applications that require making categories from one distinct set of peaks, you can make categories from defined labels. For certain kinds of applications, this process of defining Categories will be easier than defining them as described in "Defining Categories for Labeling" on page 6-4.
When to Make Categories from	Genotyping applications for which making categories from labels may be useful include:
Labels	♦ AFLP applications
	Allelic ladders
	For most microsatellite genotyping applications, you will not want to make categories from labels. Usually you want to define categories while looking at the distribution of several allele peaks, not just one.
	For more information on defining categories while viewing allele distributions, see "Editing Categories in Histograms" on page 9-22.
How to Make Categories from	For select dye/lanes, you can make a separate category for each labeled peak according to what you have specified for each peak label.

Labels To make categories from labels:

Step	Action
1	Import GeneScan data, for either allelic ladders or AFLP studies.
2	Select dye/lanes for which you want to make categories from labeled peak data.
3	Label peaks for which you want to create categories.

To make categories from labels: (continued)

Step	Action	
4	Choose Make from Labels from the Category menu.	
	The Make from Labels dialog box appears.	
	Make Categories from Labels	
	Category tolerance ± 0.50	
	Skip overlapping categories	
	Name	
	Prefix A	
	Number increment	
	With member name member name	
	For dye color(s): 🔲 blue 🔄 green 🗹 yellow	
	🔲 red 🔛 orange	
	Exclusive (clears previous labels at same peak) with (cooled) height of at least	
	with (scaled) height of at most 9999	
	Cancel	
5	Type in the Category tolerance.	
6	Select checkboxes for either including, or skipping overlapping	
	Name esterarios that will be greated	
'	Name categories that will be created.	
	For information on how Genotyper names categories see "Example of Category Naming" on page 6-9.	

To make categories from labels: (continued)

Step	Action		
8	Optionally, select "with" and make created categories a group, or members of a group:		
	If you want to make each category	Then click	And
	A group to which you can add member categories	member	type in the name of the first member of the group.
	A member of a group	group name	type in the name of the group.
9	The remaining category definition checkboxes have the same meaning as those described for the "Add Category dialog box" on page 6-5.		
10	When you are satisfied with a click OK.	ll your choices for	defining categories,
	Genotyper makes a category	for each peak tha	it has a label.

Working with Plot Data

7

Chapter Overview

Introduction Genotyper Documents display dye/lane data as electropherograplots. This chapter explains how to make use of the many option Genotyper offers for viewing, interpreting, and customizing plot of within a Genotyper Document.		ogram ptions plot displays
In This Chapter	This chapter contains the following topics:	
	Торіс	See Page
	Viewing Plots of Imported Dye/Lanes	7-2
	Viewing and Interpreting Peak Data	7-7
	Zooming In and Out	7-11
	Customizing Plot Areas	7-14
	Viewing Table Data in Plots	7-22
	Comparing Plot Data to Reference Plots	7-24

Working with Plot Data 7-1

Viewing Plots of Imported Dye/Lanes

Introduction Genotyper generates plot data from imported dye/lanes in the form of electropherograms (see Figure 7-1).



Figure 7-1 Example of an electropherogram

Electropherograms are peak representations of the size and quantity data from dye-labeled nucleic acid fragments that have been electrophoresed on an ABI PRISM instrument and analyzed in GeneScan.

7-2 Working with Plot Data



The Plot Window The Plot window provides an expanded full screen view of the plot area, allowing you to view each selected dye/lane as an individual electropherogram.



Figure 7-2 The Plot window

Note In the Main window, labels are shown only if one dye/lane is selected. If more than one dye/lane is selected, choose Show Plot Window to view all the labels.

Parts of the Plot Window

Parts of the Plot Parts of the Plot window:

Item	Name	Description
1	Peak Description Area	Displays information about scan line number, size, height, area, and category for peaks the cursor is on.
2	Upper Pane	A reference area where you can display one or more "reference" plots.
3	Lower Pane	Plot area where you can display one or more plots. You can scroll this area and visually compare these plots to those in the Upper Pane.

How to View Plots of a Single Dye/lane

You can view electropherogram plots of any imported dye/lane that appears in the Dye/lane list.

To view plot data of imported dye/lanes:



7-4 Working with Plot Data

Dye/lanes

How to View Plots You can view an electropherogram plot showing all detected peaks for of Multiple multiple dye/lanes.

> Note If you have selected many dye/lanes to be shown, a light gray background, instead of the electropherogram plots, will appear briefly in the plot area. This means Genotyper is processing the electropherograms in the background and will draw them when they are ready. You may continue to run other Genotyper commands or change the dye/lane selections during this time.

To show plot data for multiple dye/lanes.

Step	Action	
1	In the Dye/lane list, locate the dye/lane or dye/lanes for which you want to display plot data.	
2	Select the dye/lanes in the Dye/lane list. An electropherogram plot appears showing overlapping peaks for each selected dye/lane in the Plot Area. The highest peak fills the available area. The vertical scale disappears because each dye/lane plot is scaled independently to occupy the full height available.	
	GT2.5 template for UM	
	B Y 021347-13 PGH 2 Blue S002 C 021347-13 PGH 2 Green S002 021347-13 PGH 2 Vellow S002 031347-01 Father 3 Blue S003 60 80 100 120 140 160 180 200 220 240 250 300 320 340 360 380 60 80 100 120 140 160 180 200 220 240 250 300 320 340 360 380	

Working with Plot Data 7-5

To show plot data for multiple dye/lanes. (continued)



Viewing and Interpreting Peak Data

Introduction Peak data in electropherograms can show you size and quantity data for imported GeneScan files. Following are some key terms for interpreting peak data.

Definitions of terms:

Term	Definition
Peak Height	A representation of the quantity of sample for a given fragment. The height of a peak is determined by the intensity of signal at the highest point that fluoresces for each dye-labeled fragment.
Scan Number	For automated gel data collection software, the laser samples data each time it scans across the gel. Each sampling is stored as a data point. The scan number describes the location of the data point.
Base Pairs	A unit of fragment size. The number of base pairs indicates the estimated length of a nucleic acid fragment, relative to the size standard.

How to View You can view the following data for peaks resulting from GeneScan GeneScan Peak analysis of electrophoresed sample fragments:

- Data

 Scan number
 - Peak size
 - Peak height
 - Peak area
 - Genotyper Category

To view peak data for imported GeneScan files:

Step	Action
1	Select dye/lanes of interest, and view plot data.

Working with Plot Data 7-7

To view peak data for imported GeneScan files: (continued)

Step	Action
2	Use the mouse to move the cross hairs along the plot.
	The vertical line "jumps" from peak to peak. Information about each peak appears above the horizontal scale.
	Peak information Peak: Scan 1824 Size 120.94 Height 915 Brea 9486 Category: HFD11 70 80 90 100 110 120 130 140 150 160 170 180 190 200 Vertical line 440

How to View Relative Peak Size and Quantity

How to View The horizontal and vertical scales for plot data can inform you of the ive Peak Size approximate size and quantity of fragment peaks.

To view approximate size and quantity values for peak data:

If you want to know	Then read
The relative quantity of a dye/lane fragment	The vertical scale. It displays fragment quantity in terms of peak height.
	Vertical scale
	Pesk: Scan 1824 Size 120 94 Height 915 Ares 9466 Category: IPD11
The relative length of a dye/lane fragment in base pairs	The Default horizontal scale at the top is fragment length in base pairs.
Relative time required for a dye/lane fragment to be detected	The Default horizontal scale at the top is fragment length in base pairs. You can change this scale to Scan number.

7-8 Working with Plot Data

How to Change the Size and Quantity Scale

How to Change the You can change the scale Genotyper uses for the horizontal axis.

To change the peak sizing scale:

Step	Action	
1	Select dye/lanes of interest, and view plot data.	
2	From the Views menu, choose how you want to display size and quantity information for peak data.	
	If you choose	Then the horizontal scale displays
	Display by Size	Base pairs.
	Display by Scan	Number of scans required to detect sample fragment data.
	Note If you did not use GeneScan to call fragment sizes, or if no sized peaks were found in a dye/lane, then you will not be able to view the electropherogram when you choose DIsplay by Size. The text No Size Data will appear in the Plot area. To view the electropherogram choose Display by Scan.	

How to Compare For qualitative comparisons of fragment quantities in select dye/lanes, Peak Heights you can compare peak heights in a plot view.

To compare peak heights of select dye/lanes:

Step	Action
1	Select dye/lanes of interest, and view plot data.
2	Use the mouse to move the "cross hairs" to the vertical scale area.
	A horizontal line appears across the length of the plot. You can use this line as a "straight edge" to compare relative peak heights.
	"Straight edge" "Cross hairs"
	1000 1200 1300 1400 1500 1700 1800 1900 2200 2300 2400

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Peak Heights

How to Adjust You can adjust the signal height of peaks by choosing a scaling factor for each of the four dye colors. Dye scaling affects only the appearance of the electropherogram plots. All other data, such as the values appearing in the cursor information line above the plot, remain unchanged.

> Step Action Select dye/lanes of interest, and view plot data. 1 2 Choose Plot Options from the Views menu. 3 Drag the arrow pointer to the submenu, and choose Dye Scaling... The Dye Scaling dialog box appears. Set Dye Scaling Blue 1.00 Green 1.00 Yellow 1.00 Red 1.00 Cancel 0K Signal heights for each color are multiplied by the indicated factor before being plotted. The vertical scale reflects the adjusted heights. 4 Choose the peak colors that you want to scale, and type in a number for the percent by which you want to scale the peak height. Example If you want all the blue peaks to display at half of their current height, type in .50. Click OK. 5

To adjust the height of dye-colored peaks:

Zooming In and Out

Introduction	Zooming in and out of a plot view, allows you to view particular peaks closer up by zooming in, or see a wider range of peaks by zooming out.
How to Zoom in on the Plot Area	For a closer view of particular peaks, or a group of peaks, you can zoom in on the Plot Area.

To zoom in on the entire Plot Area:

Step	Action
1	Select dye/lanes of interest, and view plot data.
2	Choose Zoom In from the Zoom submenu in the Views menu.
	You can now view the middle 50% of the plot.

How to Zoom in on For a closer view of a group of peaks, you can zoom in on a particular a Selected Range region, or range of the Plot Area.

To zoom in on a selected range of the Plot Area:

Step	Action
1	Select dye/lanes of interest, and view the Plot Area.
2	Drag the cross hairs across the region you want to zoom in on.
	The vertical bar becomes a dotted rectangle that indicates the lower and upper limits of the area you selected.
	Lower limit Upper limit
	60 70 80 90 100 110 120 130 140 150 160 170 180 190 200

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To zoom in on a selected range of the Plot Area: (continued)

Step	Action
3	Choose Zoom In (Selected Range) in the Views menu.
	The range you selected is magnified to fill the Plot Area.
	160 165 170 175 180 185 190 195 200 -1000 -500
	Note Only the left and right boundaries of the selection rectangle apply to the Zoom In (Selected range) command. The top and bottom boundaries are not used.

How to Zoom Out For a view of a wider range of peaks in the Plot Area, you can zoom out.

To partially zoom out for a broader view of the plot:

Step	Action
1	Select dye/lanes of interest, and view plot data.
2	Choose Zoom Out $(\mathbb{H}^{-} -)$ from the Zoom submenu in the Views menu. You can now view about 50% more of the plot.
	1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 -

to Full Range range.

How to Zoom Out To view all of the peaks in select dye/lanes you can zoom out to full

To zoom out:

Step	Action
1	Select dye/lanes of interest, and view plot data.

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To zoom out: (continued)



How to Zoom to a Specific Range The table below shows you how to zoom to ranges that you specify.

If you want to zoom to	Then				
A specific size range of fragments	a. Choose Zoom tofrom the Zoom submenu.				
	b. The Set Plot dialog box appears.				
	 c. Enter the plot range (from sizeto size). 				
	d. Click OK.				
The range of one or more Categories	a. Select one or more categories in the Categories list.				
	b. Choose Zoom to Category in the Zoom submenu.				
	c. You can now view the range that includes the range of the selected categories.				
The range of the next marked, unselected Category	a. Choose Zoom to Next Category in the Zoom submenu.				
	b. The next marked Category in the plot is selected automatically.				

Working with Plot Data 7-13

Customizing Plot Areas

Introduction By default, the upper graphical pane in the Main window is the electropherogram view area; the lower graphical pane is reserved for peak labels. However, you can customize the settings to make these areas serve different purposes. Likewise, you can customize the upper and lower panes of the Plot window.

Note You can set the Plot Options for the Plot window only when the Plot window is displayed.

The Main Window The upper pane and lower pane of the Main window plot area. Plot Area



Figure 7-3 Location of upper and lower panes in the Main window



The Plot Window The upper pane and lower pane of the Plot window. Panes



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How to Customize You can customize the plot display in the upper and lower panes of either the Main window (Figure 7-3) or the Plot window (Figure 7-4).

To customize plot displays:

Step	Action					
1	Choose the kind c	of plot display that you want to customize.				
	If you want to customize	Then				
	The Main window					
	Upper pane Select Upper Pane, Main window from the Plot Options sub-menu of the Views menu.					
	Lower pane	Select Lower Pane, Main window from the Plot Options sub-menu of the Views menu.				
		The Plot window				
	Upper pane	Select Upper Pane, Plot window from the Plot Options sub-menu of the Views menu.				
	Lower pane	Select Lower Pane, Plot window from the Plot Options sub-menu of the Views menu.				

To customize plot displays: (continued)

Step	Action						
2	Select the checkboxes for the kind of plot that you want to view.						
	If you click Then the plot displays						
	Analyzed signal	Peaks that have been baselined and analyzed by GeneScan.					
	Raw signal	Peaks from fragments that have not been baselined or analyzed by GeneScan.					
	Grayscale signal bands	A display that looks like autoradiography signals, but is derived from the electropherogram.					
	Labels	Size and quantity labels on peaks.					
	Use colors for different dyes	Electropherograms in color; if unchecked, electropherograms will be drawn in black.					
	Use fixed y-scale	Draws all plots to a specified vertical scale.					
	Category boundaries	Boundaries around peaks in a category. Note Not recommended for Main window displays or overlapped displays.					
		1					

Adding More Detail to the Plots

Adding More You can add more details to your plot displays.

To add more detail to customized plot displays:

Step	Action						
1	From the Plot Options dialog box, click More Choices.						
	This displays a dialog box that offers you more choices of what you can display for the plot area you have chosen to customize.						
	Display the following in upper page of main window						
	Marked or unmarked dye/lanes Marked dye/lanes only Dye/lanes for Table rows Selected table rows						
	Sample Info text Text from table row Separate dye/lanes Overlapped dye/lanes Overlapped dyes separate lanes Overlapped dyes separate lanes						
	Image: Second secon						
	□ Show vertical cursor Plot height: default						
	Reset to Default Fewer Choices Cancel						

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To add more detail to customized plot displays: (continued)

Step	Action							
2	Choose the radio buttons for the kind of plot you want to view.							
	If you click Then the plot area displays							
	Marked or unmarked dye/lanes	Electropherogram plots for all selected dye/lanes. This is the default.						
	Marked dye/lanes only	Only plots for dye/lanes that are both selected, and marked.						
	Unmarked dye/lanes	Only plots for dye/lanes that are both selected, but not marked.						
	Dye/lanes for Table rows	Plots for all rows in the associated table.						
	Selected table rows	Plots for table rows you select.						
	Overlapped dye/lanes	Plots for each selected dye/lane on top of each other in the pane.						
	Separate dye/lanes	Plots for each selected dye/lane separate from one another.						
	Overlapped dyes, separate lanes	All dye colors in a lane superimposed on each other, but each lane appears separately from the others.						

Step	Action							
3	Select the checkboxes for kind of data to include in each plot							
	If you click Then the plot area displays							
	Sample Info text	Text for associated Sample Info field.						
	Analyzed Signal	Plots of peaks that have been baselined and analyzed by GeneScan.						
	Raw Signal	Fluorescent signal before GeneScan analysis.						
	Horizontal scale A horizontal scale.							
	Vertical scale	A vertical scale.						
	Peaks (without signal) a vertical line for each peak.							
	Grayscale signal bands	Bands similar to a Autoradiograph.						
	Labels	Any labels put on peaks.						
	Show horizontal cursor	A horizontal cursor.						
	Show vertical cursor	A vertical cursor.						
	Use common vertical scale	All plots are drawn to the same vertical scale. When this box is unchecked (the default), each plot fills the amount of vertical space available.						
	Use fixed y-scale	All plots drawn to the specified vertical space.						
		Note When selected, then Use common vertical scale is disabled.						
	Use colors for different dyes All dye colors in a lane superimpose on each other, but each lane appear separately from the others.							

To add more detail to customized plot displays: (continued)

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To add more detail to customized plot displays: (continued)

Step	Action										
4	In the Plot height pop-up menu, you can adjust the height of plots that display in the Plot Area.										
	If you choose Then the Plot Area										
	small Fits more plots in the window.										
	default Shows a medium-sized plot.										
	large Shows more detail in the plot.										
5	Click OK to accept yo	our selections.									

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Viewing Table Data in Plots

Introduction	You can	view information from	tables in plot displays.						
	For more information about working with Tables, see "Parts of the Plot Window" on page 7-4.								
Plot Data Associated with Dye/lanes	Genotyper generates all plots from data in dye/lanes. Do not delete dye/lanes that contain data shown in your table or you will not be able to view plots of rows that contain that data.								
How to Show Table Data in Plots	When you display plot data for select dye/lanes, you can include information from related tables in the plot display.								
	To show table row text in plot displays: Step Action								
	1	Open the Genotyper Document that contains the table informatio you want to display in the Plot window.							
	2	Open the Plot window from the Main window.							
	3	Open the Table window.							
	4	Select the rows in the table for which you want to display corresponding plots.NoteA row is considered selected if any cell in the table is							
	5	Choose the Plot Options from the Views menu							
	6	Select the Plot window, lower pane plot option							
	_	The Plot window, lower page dialog box appears							
	7	Click the More Choices button. The More Choices dialog box appears. See figure in step 1 of "Adding More Detail to the Plots" on page 7-18.							
	8	Choose one of the radio buttons after "Dye/lanes for":							
		If you choose	Then the Plot window displays						
		Table rows	Plots for all rows in the table.						
		Selected table rows	Plots for table rows you select.						
	9	Select the Text from tab row text in the correspon	le row checkbox if you want to display the nding plot display.						

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To show table row text in plot displays: (continued)

Step	Action
10	Click OK.
	The Plot Window displays plots and associated information for selected table rows.

Automatic When you select a row in a table, the plot automatically scrolls to the Scrolling corresponding peak data in the plot display.

Working with Plot Data 7-23

Comparing Plot Data to Reference Plots

Introduction You can designate selected dye/lanes as reference plots, and display one or more of these reference plots in the upper pane of the Plot window (Figure 7-2 on page 7-3).

> Once you have set up a reference plot, you can display plots for one or more dye/lanes in the lower pane of the Plot window and compare their plots to the reference plots in the upper pane.

Setting Up You can compare plot information from the reference pane to scrollable Reference Plots plot data in a lower pane.

> <u>____</u>

To set up reference plots:

Step	Action
1	In the Dye/lane list, locate the dye/lane or dye/lanes for which you want to display reference plots.
2	Choose the Mark Command from the Edit menu, or double-click the dye/lanes, marking them with a bullet.
	The bullet signifies that plots for those dye/lanes are reference plots.
3	Select the dye/lanes you marked as reference plots, and any dye/lanes that you want to compare to the reference plots.
4	Click the Plot window icon to display an expanded view of the Plot window (Figure 7-2 on page 7-3).
	The upper pane of the Plot window displays reference plots, and the lower pane displays plots for the dye/lanes that you want to compare to the reference plots. You can scroll plot data in the lower pane.
	Note The upper pane does not scroll, so you will probably only want one or two dye/lanes displayed in this pane.

8

Working with Tables

Chapter Overview

Introduction	Putting your results data into a table allows you to o manner meaningful to your genotyping application. data for comparison analysis, as well as export resu	rganize it in a You can use tabular Jlts to a database.						
In This Chapter	This chapter contains the following topics:							
	Торіс	See Page						
	Setting Up a Table	8-2						
	Arranging Columns of Labeled Peak Data	8-7						
	Specifying Columns for Number of Labels in a Row	8-9						
	Specifying Warning Columns for Edited Tables	8-11						
	Specifying Modulation Warning Columns	8-13						
	Specifying Low-signal Warning Columns	8-15						
	Specifying Saturation Warning Columns	8-17						
	Calculating Results from Table Data	8-19						
	Analyzing Data in Tables	8-23						
	Using Analyze and Calculate in Table Commands–An LOH Example	8-28						
	Editing Table Cells and Column Headings	8-28						
	Sorting the Rows in a Table	8-30						
	Searching for Table Entries	8-33						
	Updating Tables	8-35						
	Deriving a Second Table from an Existing Table	8-36						
	Checking for Mendelian Inheritance	8-37						
	Formatting Tables for Export	8-45						
	Exporting Tables	8-46						

Setting Up a Table

Sources of Table Table contents are generated from labeled fragment peaks within select Data dye/lanes. Before setting up a table make sure that the appropriate dye/lane peaks are labeled with the kind of information that you want to present in your table.

For more information on how to label fragment peaks in dye/lanes, see Chapter 6, "Defining Categories and Labeling".

Choosing a Table The following table shows examples of tables you can create for to Create different genotyping applications.

For this genotyping application	You can	crea	te thi	is ki	ind	of	tabl	ə		
Linkage Mapping										
Ennage mapping	-		Table - un	titled 3			•			
	File None	Lane & Dye	Sample Inf	o Catego	ony Peo	ak 1	Peak 2 0v	er f l d 吕		
	011347-12 PGF	1B	S001	D12583	3 1		4	=		
	021347-13 PGH	2B	S002	D12583	3 1		3	**		
	031347-01 Father	3B	S003	D12583	3 1		3	00		
	041347-03 Daughter	4B	S004	D12583	3 1		3	H		
	051347-04 Son	6B	5005	D12883	3 3		4	8		
	071347-08 Doughter	7B	\$007	D12583	3 3		4	4		
	081347-09 Son	8B	S008	D12583	3 1		2	E		
	091347-10 Son	9B	S009	D12583	3 1		2			
	101347-11 Son	108	S0 10	D12883	3 1		4			
	111347-16 Son	1 1B	S011	D12583	3 2		3			
	121347-02 Nother	128	5012	012583	3 2		4			
	141347-15 HGH	148	5013	012583	3 4		5			
	011347-12 P0F	16	5001	D 13S 17	71 2		4			
	021347-13 PGH	26	S002	D 13S 17	71 1		4			
	031347-01 Father	36	\$003	D 13S 17	71 1		4			
	041347-03 Daughter	40	S004	D 13S 17	71 1		2	\$		
Gene Expression										
	Sample Info	Marker I	Allele 1-ht	Allele	2-ht	Allel	e 3-ht Nu	ber of Alleles	Trisony Asses	snent
Profiling	Tri21 C 021S11	D21S11	650	800		760	3		Triplozygous	frisony
rioning	Trisony 18 D21S11	D21S11	173	176			2		Normal	
	Tri21 C1 D21S11	D21S11 :	243	309		257	3		Triplozygous	Trisony
	Tri21 C2 D21S11	D21S11 ·	433	714			2		Diplozygous Tr	risony
	Control 2 D21S11	D21S11	516	515			2		Nornal	
	Control 3 D21S11	D21S11	1551	1572			2		Nornal	
	Control 4 D21S11	D21S11	1314	1392			2		Nornal	
	Control A D21S11	D21S11	741	909			2		Nornal	
1 (
LOSS OF	Sample Info Cotecor	u Peak 1	Bilele1-bt	Peak 2	Bilete	2-ht	Bilele Both	Ht Bation T/N	LOH Assessment	Overflog
	1N Narker	1 90.43	576	96.45	517		1.114		CONT NODED DIRENT	00011100
Heterozvaositv	1 T Marker	1 90.43	492	96.45	559		0.880	0.790	Normal	
, , , , , , , , , , , , , , , , , , , ,	2 N Marker	1 90.43	488	1	1		488.000			
	2 T Marker	1 90.37	814	1	1		814.000	1.668	LOH	
	4 N Marker	1 88.37	597	92.34	535		1.116	0.000		
	4 I Hanken	1 88.34	997	92.92	414		2,560	0.968	nornal	
	16 T Marker	1 88 34	365	100.44	136		2.509	1.045	Noreal	
	19 N Marker	1 88.37	864	1	1		864.000			
	19 T Marker	1 88.37	675	1	1		675.000	0.781	Normal	
	20 N Marker	1 88.37	546	96.37	461		1.184	-		
	20 T Marker	1 88.37	557	96.37	236		2.350	1.993	LOH	
	44 T Marker	1 96.37	1227	1	li –		1227.000	0.808	Normal	
	55 N Nacker	1 96.46	1521	1	1		1521.000	0.000	- Contract	
	55 T Harker	1 96.37	1356	1	1		1356.000	0.892	Normal	
	68 N Marker	1 88.38	746	1	1		746.000			
	1	• laa aa		ı.				10 705	h	

Limit

Column Number There is a limit of 128 columns in a table.

8-2 Working with Tables

How to Determine
Row ContentsGenotyper generates row contents from dye/lanes in the Dye/lane list
and categories in the Category list.

To determine row contents in your table:

Step	Action		
1	Mark those Categories in the C peak data that you want to inclu	ategory list that ude in the table.	t define the kind of
2	From the table menu, choose Set Up Table		
	The Set up Table dialog box ap	pears.	
	Set	up Table	
	Contents per row: 💿 Category & dy	je∕lane ⊖Sample	
	Include data in columns:	🗌 Name of gel 1	file
	🗌 Name of GeneScan file	🖂 Text if > N lat	oels Options
	🖂 Lane number	🗌 Text if < N lat	oels Options
	🖂 Dye letter	🗌 User commer —	nt Options
	Lane and dye	Marker name	e & individual ID
	Sample info Options	Pedigree (data
	Name of category Options	Innerit	ance check
		Edited-table	warning Options
		Low-signal u	varning Options
	Size-calling method	Saturation w	arning Options
	Size standard file name	— 🗌 Minimum mo	dulation
	🗆 Dye/lane scale factor	🗌 Modulation u	varning Options
	Lane Dye Sample Info Category	Peak 1 Peak 2 Ou	verflow
		• • •	4
	Uncheck All		Cancel OK
	Figure 8-1 The Set up Table of	dialog box	
3	In the Contents per row field, cl	ick one of the tw	wo radio buttons.
	If you want each row to corr	respond to	Then Click
	Marked categories and selec	ted dye/lanes	Category & dye/lane.
	Sample Information entered in	n the Sample	Sample.

Column Contents

How to Determine You can select the column contents for the rows in your table from a list of checkboxes in The Set Up Table dialog box ("The Set up Table dialog box" on page 8-3). The order in which you select the checkboxes determines the order in which the column contents will appear from left to right in your table.

> Step Action 1 From the Table menu, choose Set Up Table.... The Set Up Table dialog box appears (Figure 8-1 on page 8-3). As shown at the bottom of the dialog box, the checkboxes selected beneath the "Include Data in Columns" heading are the current settings for column headings. 2 Click OK to accept the current selections for the column contents, or click the Uncheck All button to clear all the selections. Checkboxes that you can select for column headings depend on the kind of contents per row you defined. The text of unavailable checkboxes appears in gray. Note To change the column heading text, see "Editing Table Cells and Column Headings" on page 8-28.

To determine column contents for each table row:

To determine column contents for each table row: (continued)

Step	Action	
3	Select checkboxes under the Include Data in Columns heading:	
	If you want to define a column for	Then click
	Name of an imported GeneScan file	Name of GeneScan file.
	The lane number of a dye/ lane	Lane number.
	The color of the dye for the dye/lane in a row	Dye letter.
	The lane number and dye color of the dye/lane containing peak data	Lane and dye.
	Contents of Sample Info field	Sample info.
	Contents of Sample comment field in Sample Sheet, and Dye/lane window	Sample comment.
	The name of a selected category	Name of category.
	Labeled Peak data	Labels.
	The number of labels on peaks in the category, dye/lane, or sample	Number of labels.
	GeneScan size-calling method	Size-calling method.
	GeneScan size standard	Size standard file name.
	Scale factors, if defined	Dye/lane scale factor.
	The name of associated Gel files	Gel file name.
	Text, when more than a specified number of labels are detected in a category, dye/lane, or sample	Text if > N labels.
	Text, when less than a specified number of labels are detected in a category, dye/lane, or sample	Text if < N labels.
	Your own comments	User comment.
	Data for, and results of inheritance check	Marker name & Individual ID.
	A warning when labels are edited	Edited-label warning.
	A warning when cell contents edited	Edited-table warning.
	A warning for low dye/lane signal	Low-signal warning.
	A warning for intensity of signal	Saturation warning.
	Lowest modulation score value	Minimum modulation.
	A warning for low modulation scores	Modulation warning.

To determine column contents for each table row: (continued)

Step	Action
4	Click OK when you have defined all the columns that you want to include in your table.

How to Append Once you have created a table, you can append rows to the table. Rows to a Table

To append rows to a table:

Step	Action
1	If it is not already open, open the Genotyper Document that contains the table to which you want to append rows.
2	Select those dye/lanes that have sample information that you want to add to the table.
	IMPORTANT Genotyper puts all information from dye/lanes into the existing format of rows in the current table. All rows in a table must have the same number of columns and the same column headings.
3	From the Table menu, choose Append to Table.
	A row containing sample information from select dye/lanes is added to the bottom of the table.

Re-importing If you have made a table and deleted or cleared all dye/lanes, select a Dye/lanes table cell, then choose Re-import Dye/lane from the File menu.

Arranging Columns of Labeled Peak Data

Introduction For each row in a table, you can order columns of labeled peak data according to the kind and number of labels defined by selected categories.

How to Arrange the Order of Peak Label Columns

To specify the order of peak columns that contain peak data labels:

To specify the order of peak columns that contain peak data

Step	Action	
3	Select the radio button for how you want to a columns containing peak label data:	rrange the order of
	If you want to put columns of	Then click
	Labeled data from the same peaks next to each other (for example: size, height, size height)	labels from same peak are next to each other.
	The same type of labeled peak data next to each other (for example: size, size, height, height)	labels of same type are next to each other.
4	Modify columns based on kinds of peak labe	els in select categories:
	If you want to	Then Select
	Duplicate labels, when only one is found in a category Note When working with homozygote STRs, you assume that any single peak is a result of a homozygotic state.	If only one labeled peak in category, and duplicate the label(s).
	Display a text message when no labeled peaks are found in a category	If category has no labeled peaks, click Put this text in all cells, type a text message.
	Display a pre-defined category comment in all label cells of a row when no labeled peaks are found in a category	Select If category has no labeled peaks, click Put Category comment in all cells.
	Display a text message when no labeled peaks are found in cells defined as columns for peak label data	If some label cells are empty, put this text in empty cells, type in a text. message.
5	Click OK to accept all of your selections.	

8-8 Working with Tables

/

Specifying Columns for Number of Labels in a Row

Introduction You can specify that columns with specified text appear when the number of labels for a particular row is greater than or less than a specified number.

How to Specify In the Set Up Table dialog box, you can specify that columns with Columns for Label customized text are appended to all rows where more or less labels are Detection detected than the number that you specify.

To specify columns for labels in a row:

Step	Action	
1	In the Dye/lane list, select the dye/lanes whose labels you want to put into a table.	
2	Make sure that you mark the Categories that define the kind of labeling you want to include in the table.	
3	From the Table menu, choose Set Up Table.	
	The Set Up Table dialog box appears ("The S on page 8-3).	Set up Table dialog box"
4	Choose what kind of column and text you want to display for the number of labels detected for a specific set of peak labeled data:	
	If you want to display text when the number of labels is	Then click
	More than a specific number	Text if > N labels.
	Less than a specific number	Text if < N labels.
5	Click the Options button. The Label detection dialog box appears.	
	N 2 Text Overflow Cancel OK	
6	For N, type in the number of labels for which message if more or less than that number a specified row.	n you want to display a re detected in a

To specify columns for labels in a row: (continued)

Step	Action
7	Type in the warning text that you want to appear in the column appended to the end of affected rows.
8	Click OK to accept all of your selections.

Specifying Warning Columns for Edited Tables

Introduction You can select checkboxes in the Set Up Table dialog box (Figure 8-1 on page 8-3) that specify that columns with specified text will appear to warn you when any row in a table, or any peak label in a row has been edited.

How to Specify
Warnings for
Edited LabelsWhen setting up a table, you can specify that Genotyper append a
column containing warning text when a peak label has been manually
edited in a category and dye/lane before the table was made.

Step	Action
1	In the Dye/lane list, select the dye/lanes whose labels you want to put into a table.
2	Make sure that you mark the Categories that define the kind of labeling you want to include in the table.
3	From the Table menu, choose Set Up Table The Set Up Table dialog box appears ("The Set up Table dialog box" on page 8-3).
4	Select the Edited-label warning checkbox.
5	Click the Options button. The Edited-label warning dialog box appears.
6	Type in the warning text that you want to appear in the column.
7	Click OK to accept all selections.

To specify warnings for edited labels:

How to Specify When setting up a table, you can specify that Genotyper append a Warnings for column containing warning text to the end of any row that contains cells Edited Tables that have been edited after initial creation of the table.

To specify warnings for rows containing edited table cells:

Step	Action	
1	In the Dye/Lane list, select the dye/lanes whose labels you want to put into a table.	
2	Make sure that you mark the categories that define the kind of labeling you want to include in the table.	
3	From the Table menu, choose Set Up Table	
	The Set Up Table dialog box appears ("The Set up Table dialog box" on page 8-3).	
4	Select the Edited-table warning checkbox.	
5	Click the Options button. The Edited-table dialog box appears.	
6	Type in the warning text that you want to appear in the column.	
7	Click OK.	

8-12 Working with Tables

Specifying Modulation Warning Columns

Introduction	When setting up a table, you can specify that Genotyper append a column containing warning text in any row that contains peaks that have a modulation score lower than what you specify to be adequate for your application.
What is Modulation	Modulation refers to the degree to which peak data resolves with respect to its immediate background.
Modulation Scores	Modulation scores measure the quality of peak resolution. The following figure shows an example of peaks labeled with modulation scores. Note the correlation between modulation scores and the degree of separation of individual peaks from neighboring valleys. Higher scores show a greater degree of separation from the background.



Figure 8-2 Peak modulation scores

How to Specify a Modulation Warning

To specify warnings when peaks do not meet specified modulation scores:

Step Action 1 In the Dye/Lane list, select the dye/lanes whose labels you want to put into a table. Make sure that you mark the categories that define the kind of 2 labeling you want to include in the table. 3 From the Table menu, choose Set Up Table... The Set Up Table dialog box appears (Figure 8-1 on page 8-3). 4 Select the Modulation warning checkbox. 5 Click the Options button. A dialog box appears. If modulation score (for any labeled peak in category) is < 15 insert text for warning: Warning (Cancel) ОК Type in the modulation score for the minimum acceptable degree of 6 peak modulation for your Genotyper application. 7 Type in the warning text that you want to appear in the column, if peaks are found that are less than the modulation score you have specified. 8 Click OK to accept all your selections.

8-14 Working with Tables

Specifying Low-signal Warning Columns

Introduction	When setting up a table, you can specify that Genotyper append a column containing warning text to the end of any row that contains peaks that have a fluorescent signal lower than what you specify to be adequate for your application.
What Causes a Low-Signal	A weak fluorescent signal is often caused by problems during sample preparation; in particular problems with PCR, or errors during loading of samples on your ABI PRISM instrument.
Low Signal Example	Figure 8-3 shows an example of a Genotyper plot display showing the vertical axis maximum set at 150 for peak heights. The peaks in the display are labeled with peak heights. If you create a table using the default value for low signal warning of less than 200, Genotyper will append a column containing warning text to the end of the row containing these peak labels.
	230 240 250 260 270 280 290 300 150 100 50 133 145 143 151

Figure 8-3 Low signals in Genotyper

ন্দ

Warning Column

How to Specify a To specify warnings when peaks data has been generated from a signal defined as low:

Step	Action
1	In the Dye/Lane list, select the dye/lanes whose labels you want to put into a table.
2	Make sure that you mark the categories that define the kind of labeling you want to include in the table.
3	From the Table menu, choose Set Up Table
	The Set Up Table dialog box appears (Figure 8-1 on page 8-3).
4	Select the Low-signal warning checkbox.
5	Click the Options button. A dialog box appears.
6	Type in the minimum amount of signal data acceptable before issuing a low signal warning for the associated labeled peak data.
7	Type in the warning text that you want to appear in the column, if peak data has been generated from fluorescent signals less than the amount you specified in the previous step.
8	Click OK to accept all of your selections.

8-16 Working with Tables

Specifying Saturation Warning Columns

Introduction When setting up a table, you can specify that Genotyper append a column containing warning text to the end of any row that contains peaks that have a fluorescent signal higher than what you specify to be adequate for your application; a saturation warning.

What Causes Saturation When you import raw data from GeneScan files, you may also import saturated signals. Saturated signals result when the fluorescent signal from an excess of PCR product exceeds the detection limit of your ABI PRISM instrument. Consequently, if left undetected, Genotyper will count resulting artifact peaks, such as primer peaks, as actual sample peaks. By identifying peaks caused by saturated signals, you can prevent erroneous peak identification.

SaturationFigure 8-4 shows an example of imported dye/lanes displaying peaksExamplewith saturated signals.

ſ	untitled		J
	15≢s1 copy 15 Blue 15≢s1 copy 15 Green 15≢s1 copy 15 Vellow 15≢s1 copy 15 Red	4 4 5	Û
	60 80 100 120 140 160 180 200 220 240 260 280 300 320 340 360	Ŷ	
	• Everything All peaks from scan 0 to 32000 in R/B/G/Y	₹-	
		· · ·	
	۵ <u>.</u>	₹ \$	
	Current Step Log 슈	↔ Ţ	₹ •

Figure 8-4 Saturated signals in Genotyper

Warning Column

How to Specify a Saturation How to specify warnings when peaks data has been generated from a saturated signal:

Step	Action
1	In the Dye/Lane list, select the dye/lanes whose labels you want to put into a table.
2	Make sure that you mark the categories that define the kind of labeling you want to include in the table.
3	From the Table menu, choose Set Up Table
	The Set Up Table dialog box appears (Figure 8-1 on page 8-3).
4	Select the Saturation warning checkbox.
5	Click the Options button.
	The Saturated signal dialog box appears.
6	Type in the maximum amount of raw signal data acceptable before issuing a saturated signal warning for the associated labeled peak data.
7	Type in the warning text that you want to appear in the column, if peak data has been generated from fluorescent signals greater than the amount you specified in the previous step.
8	Click OK to accept all of your selections.

8-18 Working with Tables

Calculating Results from Table Data

Introduction	You can use the Calculate in Table command to perform numerical calculations of table cell contents. You can review results of calculations in a results column you define when setting up the table.
	For an example of how the Calculate in Table command is used for a genotyping application, see "Using Analyze and Calculate in Table Commands–An LOH Example" on page 8-26.
Setting Up Results Columns	Genotyper puts results of table data calculations in a column you specify. The column for the results must already exist. So, if you plan to calculate results from table data, create some extra columns for your results when setting up columns.
	For more information on setting up table columns, see "Setting Up a Table" on page 8-2.
Reading the Text Box	The key to using the Calculate in Table command is to read the text box at the bottom of the dialog box as you enter parameters. The text box explains the calculation and what the result will be. It is easier to read the text box then it is to review settings in the dialog box.

Kinds of Table 8-1 shows the kinds of calculations you can perform after Calculations specifying values in The Calculate in Table...dialog box. "Fields you can use" refers to those fields shown in the table in "How to Calculate Results From Table Data" on page 8-21.

Kind of Calculation	Description	Fields you can use	
Sum of	Sum of values defined. Useful for many quantitative applications	A,B,C,D	
Difference (A - B)	A minus B. Useful for applications such as HMA where the difference in mobility for a given fragment determines the degree of similarity or difference.	А, В	
Absolute difference A -B	Absolute value of A minus B	A,B	
Ratio (A/B)	A divided by B. Useful for Loss of heterozygosity applications.	A,B	
Average of	Average of values chosen	A,B,C,D	
Product of	Product of values chosen.	A,B,C,D	
Member for category (A) and size/scan (B)	Treat the text in column A as the name of a category group; look through the members of that group and see which one involves size or scan value in column B. The result is the name of the category member.	A, B (must be column value only).	
Difference squared (A -B) * (A - B) of	Square of the difference between value of A and value of B.	А, В	
Square root (A) of	Square root of the value of A.	A	

Table 8-1Kinds of Calculations you can perform on table data

8-20 Working with Tables

Results From data. Table Data

How to Calculate Use the Calculate in Table... command to calculate results from table

To calculate results from table data:

Step	Action
1	Open the Table window from the Main window.
2	Choose Calculate in Tablefrom the Table menu.
	The Calculate in Table dialog box appears.
	Calculate in Table
	Evaluate () for every row () for groups of 2 rows
	sum of
	R ⊕ the constant ⊕ the value in column 5. Peak 1
	1.000000
	B the constant (a) the value in column (6. Peak 2)
	1.000000 🗌 of row 2 🗌 of the group
	C
	1.000000 🗌 of row 3 🗌 of the group
	D the constant (a) the value in column (
	1.000000 🗌 of row 4 🗌 🗆 of the group
	and put the result in column 7. Sum 🔻
	of row 1 of the group
	Evaluate for each row the sum of (the value in column 5) and (the value in column 6), and put the results in column 7
3	Choose the radio button for the rows that you want to include in
	your calculation.
	Note If you choose "for every row". Genotyper counts row 1 as
	the title row, and row 2 is the first row in the table that contains data.
	However, Groups do not count the title row, and row 1 is the first
	row that contains data.

To calculate results from table data: (continued)

Step	Action	
4	From the first pop-up menu, choose the kind of calculation that you want to perform.	
	✓ sum of difference (A - B) of absolute difference A - B of ratio (A ÷ B) of average of product of member for category (A) and size/scan (B) difference squared (A - B) * (A - B) of square root (A) of	
5	In fields A-D, choose the table data on which you want to perform the calculation. Type in constants, or choose the column number from the pop-up menus.	
	For example, if your table has data for peaks in columns 5 and 6, and you want to calculate the sums of the those two peaks, choose column 5 in field A, and column 6 in field B.	
6	In the field "and put the result in column", choose the column and optionally the row or group, where you want to put the calculated result.	
7	Review the text box at the bottom of the dialog box which explains the calculation you've specified. If this is what you intend to do, click OK.	
8	Check the Table window to verify that results have been calculated in the table.	
	For example, if you specified that results from the calculation described in step 5 be placed in column 7 of your table, the resulting table will look like.	
	Table - untitled	
	Lane Dye Sample Info Category Peak 1 Peak 2 Sum	
	1 1 1 1 1 1 1 1 1 1	
	1 Y S001 Everything 50.23 228.58 278.810	
	1 R Everything 50.00 75.00 125.000	
	2 6 S002 Everything 50.54 96.98 147.520 00 2 6 S002 Everything 51.35 60.31 111.660 00	
	2 Y \$002 Everything 50.26 57.53 107.790	
	<u> </u>	

8-22 Working with Tables

Analyzing Data in Tables

Introduction	Genotyper provides some of the functionality found in spreadsheet applications such as Excel. For example, you can select rows in tables, and perform comparison analysis of cell contents. You can review results of analysis algorithms in a results column you define when setting up the table.
Reading the Text Box	The key to using the Analyze Tablecommand is to read the text box at the bottom of the dialog box as you enter conditional parameters in the Analyze Table dialog box (Figure on page 8-24). The Text Box provides a verbal explanation of the calculation and its results. It is often easier to read the text box then to review settings in the dialog box.
	Example Text Box
	For every row, examine columns 3-5; if exactly 2 of these cells in the row are not empty, and if the values in at least 2 cells are greater than 1, then put "Normal" in column 2.
Error Message in Text Box	If the word ERROR appears in the text box, there is a logical inconsistency in the conditional parameters that have been entered. For example, if you specify that Genotyper analyze the cell contents of <i>two</i> columns in a row, but also specify that <i>three</i> of these cells not be empty, Genotyper will issue an error message in the text box.
Examples of Applications	Examples of applications for which you can use the Analyze Table command include:
	◆ Trisomy
	DMD Analysis
	 Loss of Heterozygosity
	Gene Quantitation

How to Analyze Use the Analyze Table command to specify conditions for logical Data in Tables comparisons of table cell contents. If the analysis conditions you specify are met, Genotyper writes a message you specify into a results column.

To analyze data in tables:

01	A
Step	ACUON
1	Choose Analyze Table from the Table menu.
	The Analyze Table dialog box appears.
	Analyze Table
	For every row
	Examine column(s) 3. Allele 1-ht V to 5. Allele 3-ht V
	When exactly v 2 cell(s) is/are not empty
	⊠ and
	at least ▼ is/aregreater than 1
	and
	at most V 1 is/are greater than or equal to V
	75 % of the row maximum ▼
	then end put output
	in/to column 2. Marker 👻
	For every row, examine columns 3-5; if exactly 2 of these cells in the row are not empty, and if the values in at least 2 cells are greater than 1, then put "Normal" in column 2
2	Choose the radio button for the rows that you want to include in
	your analysis.
	Note Groups do not count the title row, and row 1 of the group is
	the first row that contains data.
3	In the Examine column(s) pop-up menus, choose the range of
	columns that you want to include in your analysis.
4	In the When pop-up menu, choose the comparison conditions for
	the columns you are analyzing.
	Note "at least zero", means for every cell.
5	Optionally select the "and" checkboxes if you want to add conditions
	to your analysis. Choose relational operators from the pop-up menus, and type in peak size criteria.

8-24 Working with Tables
To analyze data in tables: (continued)

Step	Action
6	In the "then" field, type in the message text that you either want to "put" or "append" in a select column if the conditions you have specified are met.
7	Review the text box at the bottom of the dialog box which explains the conditions you've specified. If this is what you intend to do, click OK.
8	Check the Table Window to verify that the results of your analysis have been added to your table.

Clearing Columns You can clear entire columns by specifying that if at least zero cells are not empty then clear the column. At least zero, means for every cell.

Example Text Box

For every cell examine column 5. Whether or not the cell is empty, put (blank) in column 4.

In other words, clear column 4.

Using Analyze and Calculate in Table Commands–An LOH Example

What is LOH?	Loss of Heterozygosity (LOH) is the loss of polymorphic DNA markers in tumors compared with normal cells, and often indicates somatic deletion of tumor suppressor genes. LOH detection has application to a wide range of cancers involving tumor suppressor genes.
Genotyper Commands Used to Detect LOH	You can use the Calculate in Table and Analyze Table commands to assess the presence or absence of LOH for labeled DNA fragment data from patient samples.

Example LOH Figure 8-5 shows a table that was created using the Calculate in Table Table Command. Allele peaks were identified, labeled, filtered, and a table was created with columns for allele size and height.

Sample Info	Category	Peak 1	Allele1-ht	Peak 2	Allele 2-ht	Allele Ratio	Ht Ration T/N	LOH Assessment	Overflow
1N	Marker 1	90.43	576	96.45	517	1.114			
1 T	Marker 1	90.43	492	96.45	559	0.880	0.790	Normal	
2 N	Marker 1	90.43	488	1	1	488.000			
2 T	Marker 1	90.37	814	1	1	814.000	1.668	LOH	
4 N	Marker 1	88.37	597	92.34	535	1.116			
4 T	Marker 1	88.34	447	92.42	414	1.080	0.968	Normal	
16 N	Marker 1	88.34	506	100.44	197	2.569			
16 T	Marker 1	88.34	365	100.44	136	2.684	1.045	Normal	
19 N	Marker 1	88.37	864	1	1	864.000			
19 T	Marker 1	88.37	675	1	1	675.000	0.781	Normal	
20 N	Marker 1	88.37	546	96.37	461	1.184			
20 T	Marker 1	88.37	557	96.37	236	2.360	1.993	LOH	
44 N	Marker 1	96.37	1227	1	1	1227.000			
44 T	Marker 1	96.37	991	1	1	991.000	0.808	Normal	
55 N	Marker 1	96.46	1521	1	1	1521.000			
55 T	Marker 1	96.37	1356	1	1	1356.000	0.892	Normal	
68 N	Marker 1	88.38	746	1	1	746.000			
68 T	Marker 1	88.38	549	1	1	549.000	0.736	Normal	
79 N	Marker 1	88.37	683	96.37	593	1.152			
79 T	Marker 1	87.37	208	95.39	185	1.124	0.976	Normal	
80 N	Marker 1	90.36	803	1	1	803.000			
80 T	Marker 1	92.71	244	1	1	244.000	0.304	LOH	

Figure 8-5 Example of table created to assess LOH presence

Command 🖕

Using the To create the table shown in Figure 8-5, we used the Calculate in Table Calculate in Table Command to calculate:

- A ratio of allele 1 to allele 2 for each sample.
- The ratio of the tumor signal to that of the normal signal (T1/T2 over ۲ N1/N2). This value is called the *Allelic Imbalance* or AI.

8-26 Working with Tables

Using the Analyze To create the table shown in Figure 8-5, we used the Analyze Table in Table Command Command to calculate the ratios in Ht Ratio T/N column for presence or absence of LOH. For example, if the ratio is less than 0.67 or more than 1.35, then LOH is entered into a column named Assessment, otherwise Normal is entered in the same column.

Working with Tables 8-27

Editing Table Cells and Column Headings

Introduction	Once you have created a table, you can edit the contents of some of the cells in each row, or change the names of any of the column headings. However, all rows in a table must have the same column headings.			
	IMPORTANT Changes you make to the contents of table cells affect only the table you are editing. For example, if you edit the peak label information in a table cell, the corresponding information in other parts of the Genotyper Document such as dye/lanes or plot displays remains unaffected.			
Marking Rows as Edited	When setting up a table, you can select a checkbox in the Set Up Table dialog box (Figure 8-1 on page 8-3), that enables Genotyper to notify you of any row in a table that has been edited. After any cell in a row is edited, Genotyper enters a text string that you specify in a column at the end of the row.			
	For more information on setting up table features such as this, see "Specifying Warning Columns for Edited Tables" on page 8-11.			
Kinds of Cell Data	There are the three kinds of data you can manually edit in table cells.			
You Can Edit	They are:			
	Column headings			
	Peak label information			
	♦ User comments			

Cells

How to Edit Table To edit cells in a table:

Step	Action
1	Open the Genotyper Document that contains the table that you want to edit.
2	Optionally, open the Table window from the Main window.
3	Select the table cell that you want to edit.
4	Choose Edit Cell from the Edit menu.
5	Type in your changes.
	When you save the Genotyper Document, the changes will be saved in the table.

Recording Steps If you are making a macro, the Step list records edits of individual cells For Editing Table as "selected cells". If you run the macro, the macro will change Cells whatever you have selected to include the text you enter.

Column Headings

How To Edit To edit column headings in tables:

Step	Action
1	Open the Genotyper Document that contains the table that you want to edit.
2	Optionally, open the Table window from the Main window.
3	Select the table cell that you want to edit.
4	Choose Edit Cell from the Edit menu.
5	Type in your changes.
	When you save the Genotyper Document, the changes will be saved in the table.

Column Headings

Recording Steps If you are making a macro, the Step list records edits of column heading For Editing cells as applying to a specific column number of the first row.

Working with Tables 8-29

Sorting the Rows in a Table

Introduction	Rows in tables are initially not sorted; they appear in the order in which they were added to a table. However, you can sort the rows on command.
The Concept of Precedence	The concept of precedence is important when sorting rows in a table. The precedence for a column number establishes a priority when sorting rows.
	Example
	If you choose the Category column as a precedence 1, and Sample Info as a precedence 2, and the sort type is alphabetical, rows will first be sorted in alphabetical order according to category name, and then, within categories, sort them in alphabetical order according to entries in the Sample Info column.

How to Sort Rows

To sort rows in multiple columns of a table:

Step Action 1 To view the Table window more easily, choose Show Table Window from the Views menu. The Table window appears. Table - 5 Loci Template 📃 File Name Lane & Dye Sample Info Category Label(s) Tutorial Results 29 Mother MFD 15 154.86 Tutorial Results 2Y MFD26 113.43 Mother Mother Tutorial Results MFD3 129.10 131.11 OVERFLO 29 Tutorial Results 27 Mother MFD45 87.91 89.74 181.11 MFD59 176.98 Tutorial Results Mother Tutorial Results 57 Child MFD 15 113.43 Tutorial Results 57 Child 1 MFD26 Tutorial Results 5Y Child 1 MFD3 134.79 142.54 Tutorial Results 5Y 89.75 MFD45 91.59 Child 1 Futorial Results 5Y Child 1 MFD59 179.09 181.05 Tutorial Results 6Y Child 2 MFD 15 150.80 113.46 Tutorial Results 6Y Child 2 MFD26 Tutorial Results Child 2 МFDЗ 129.07 142.51 6 Tutorial Results 6Y Child 2 MFD45 85.92 89.77 177.01 Tutorial Results 67 Child 2 MFD59 186.82 Tutorial Results 74 Child 3 MFD 15 150.80 Tutorial Results 7Y Child 3 MFD26 113.38 Tutorial Results 7Y Child 3 MFD3 129.07 130.97 \$<u></u> 2 Choose Sort Table ... from the Analysis menu. The Sort Table dialog box appears. Sort Table Sort table rows in the following order: Precedence Column Sort type Sort order () Numerical Ascending 1 1. Lane • Alphabetical O Descending () Numerical Ascending 2 • Alphabetical ○ Descending O Numerical Ascending 3 • Alphabetical O Descending Cancel OK 3 Under Column number, you can choose from 1 to 3 different columns to sort, by choosing the appropriate pop-up menu.

Working with Tables 8-31

To sort rows in multiple columns of a table: (continued)

Step	Action
4	Under Sort Type, choose the radio button for how you want each column to be sorted, in Alphabetical, or Numerical order.
5	Under Sort Order, choose either ascending or descending order.

Searching for Table Entries

Introduction	You can	use the Find command to locate one or more entries in a tak	ole.
How to Find a Table Entry	You can	search for table entries by alphanumeric text string.	
	Step	Action	
	1	Make the table active to make it easier to view the results of this command.	
		Tab until the vertical bar is on the left of the table. If the table is no active, the selection will be outlined, not highlighted. Or, open the Table window.	ot
	2	Choose Find(\#-F) in the Edit menu.	
		The Find dialog box appears.	
		Find	
		● Find the following text:	
		Look in the table In column 1 Only	
		Look in the dye/lane list In selected dye/lanes only	
		🔲 In Sample Info	
		Look in the category list In category name	
		In category comment	
		 In category groups In non-member categories 	
		In member categories	
		Add to current selection	
		☑ Ignore upper/lower case differences Look at dyes: ☑ Blue ☑ Green ☑ Yellow ☑ Red ☑ Orange	
		Cancel OK	
	3	In the Text box, enter the alphanumeric text you want to find.	
	4	Click the Look In the table radio button.	

To locate a table entry using the Find command: (continued)

Step	Action					
5	Select checkboxes to specify how you want to search for table entries:					
	If you want to	Then click				
	Restrict the search to a particular column	Look in column, and enter the number of the column where you want to search.				
	Find all entries in the table with the designated text	Find all occurrences at once.				
	Select additional table cells located by the command	Add to current selection.				
	Ignore case differences in text searches	Ignore upper/lower case differences.				
6	Click OK.					

How to Find the You can use the Find Next command to repeat the last Find command Next Occurrence using the same options as the last Find command. The Find Next command is equivalent to the most recently used Find command, but eliminates the need to click the OK button in the Find dialog box.

Choose Find Next (\mathbb{H} -G) from the Edit menu.

The next occurrence of the text is selected.

8-34 Working with Tables

Updating Tables

Introduction	on If you have created a table, and made changes to peak labels, you update the corresponding information in your table.					
	IMPORTA label data the table, should us	ANT The Update Table command should only be used to update a in the table. If you change any other information that can appear in such as the sample information or the name of a category, then you se the Clear Table command and start over with a new table.				
How To Update Tables	Update t Genotyp	ables after making changes to information in other parts of your er Document.				
	To update table contents:					
	Step Action					

Step	Action
1	Select dye/lanes that have labels that have been changed.
2	Choose Update Table from the Table menu.
	Table cells that contain data that has been changed are automatically updated to match the labels.

Deriving a Second Table from an Existing Table

Introduction You can create Derived tables by copying the contents of a table and saving it as a Derived table. You can compare the contents of the Derived table to the original table, and export the Derived table.

How to Derive You can derive a second table from an existing table. A Derived table is not linked to dye/lanes or categories like the table from which it was derived.

To derive a second table:

Step	Action
1	Open the Genotyper Document that contains the table for which you want to derive a copy.
2	Open the Table window from the Main window.
3	Choose Show Derived table from the Views menu.
	A blank Derived table window appears.
4	Choose Derive table from the Analysis menu.
5	Choose the Copy Table submenu.
	The table in the Table window is copied to the Derived table window.

Checking for Mendelian Inheritance

Introduction	Performing a Mendelian inheritance check on Genotyper table data verifies that alleles from members of a family follow Mendelian inheritance.
Example Applications	Examples of applications for which performing a Mendelian inheritance check can help you verify genotyping results include:
	Microsatellite analysis
	Disease gene mapping
	Forensic research
	 Paternity testing
Why Perform a Mendelian Inheritance Check	Mendelian inheritance checks can help you identify samples which do <i>not</i> follow expected patterns of Mendelian inheritance. Consequently, you can investigate where possible errors occurred in sample handling during your genotyping experiment, as well as verify non-paternity in paternity testing.
Using GenBase to Access Pedigree Data	To perform an inheritance check you must be able to access pedigree data from GenBase. GenBase can store actual pedigree structures that show family member relationships. For example, each individual in a family study has an ID assigned.
	GenoPedigree can export pedigree information to GenBase. GenBase places this information in its pedigree table. You can then access this pedigree data from Genotyper.
	For information on how to access GenBase from Genotyper, see "Communicating with GenBase" on page 10-1.

Working with Tables 8-37

Start with a Table Figure 8-6 shows an example of the kind of table you must first create before you can perform a Mendelian inheritance check in Genotyper.

	Table -	· LDK Inherit	tance che	ck.b6 🔳			J
File Name	Lane & Dye	Sample Info	Category	Peak 1	Peak 2	Overflow	Ε
011347-12 PGF	1B	S001	D12S83	1	4		Ξ
021347-13 PGM	2B	S002	D12S83	1	3		Ξ
031347-01 Father	3B	S003	D12S83	1	3		1
041347-03 Daughter	4B	S004	D12S83	1	3		I
051347-04 Son	5B	S005	D 12S83	3	4		0
061347-06 Son	6B	S006	D12S83	3	4		2
071347-08 Daughter	7B	S007	D12S83	3	4		4
081347-09 Son	8B	S008	D12S83	1	2		
091347-10 Son	9B	S009	D12S83	1	2		
101347-11 Son	10B	S010	D12S83	1	4		
111347-16 Son	1 1B	S011	D12S83	2	3		
121347-02 Mother	12B	S012	D12S83	2	4		
131347-14 MGF	13B	S013	D12S83	2	3		
141347-15 MGM	14B	S014	D12S83	4	5		
011347-12 PGF	16	S001	D13S171	2	4		
021347-13 PGM	26	S002	D13S171	1	4		
031347-01 Father	36	S003	D13S171	1	4		
041347-03 Daughter	4G	S004	D13S171	1	2		
051347-04 Son	56	S005	D13S171	2	4		
061347-06 Son	6G	S006	D13S171	2	4		
071347-08 Daughter	76	S007	D13S171	1	2		
081347-09 Son	8G	S008	D13S171	2	4		
091347-10 Son	96	S009	D13S171	2	4		
101347-11 Son	106	S010	D13S171	2	4		
111347-16 Son	116	S011	D13S171	2	4		
121347-02 Mother	126	S012	D 13S 171	2	2		1
¢		-				\$	Ę

Figure 8-6 Example of table created for Mendelian inheritance check

The table in Figure 8-6 contains rows for categories and samples. The numbers in the peak 1 and peak 2 columns are the allele names.

For detailed instructions on how to create the table shown in Figure 8-6, see Part 2 of the Microsatellite tutorial, in the ABI PRISM Genotyper Applications Tutorials. The steps used to create the table in that part of the tutorial are the same as you would use to set up a table for most kinds of Mendelian inheritance checks.

8-38 Working with Tables

Sorting the Table For ease of viewing, you can sort the table using the Sort table command. Sorting by markers, you can group all the family members and identify presence or absence of alleles in particular family members.

Typically, you would sort the table by category name first, and then by Sample Information. For more information on how to sort tables, see "Sorting the Rows in a Table" on page 8-30.

Working with Tables 8-39

How to Add Once you have set up a table such as that shown in Figure 8-6, you Columns for must add additional columns to the table before performing the Inheritance inheritance check.

Checking

To add columns to your table:

Step	Action							
1	Clear t	he table	э.					
2	Select t original	the Set ι table sh	ıp Tab Iown ii	le con n Figu	nmar Ire 8-	nd, this c ∙6.	displays	the settings for the
3	Select of and Inh table.	checkbo eritance	xes for check	r Mark k. This	ker na add	ame & ir s seven	ndividual columns	I ID, Pedigree data, s to the original
4	rflow Horker 012883 012883 0138171 0138171 0138171 0138171 0138171 0138171 0138171 0138171 0138171 0138171 0138171 0138171 0138171 0138171 0138171 0138171 0138171 0138171	Individual 10 1947-12 1947-13 1947-03 1947-04 1947-04 1947-06 1947-06 1947-06 1947-06 1947-10 1947-10 1947-10 1947-17 1947-10 1947-17 1947-10 1947-10 1947-10 1947-01 1947-03 1947-04 1947-04 1947-06 1947-10 1947-06 1947-10 1947-06 1947-10 1947-06 1947-10 1947-06 1947-10 1947-06 1947-10 1947-06 1947-10 1947-06 1947-07 1947-06 1947-07 1947-06 1947-07	hother 10 1347-13 1347-02 1	Fother 10 1347-12 1347-01 1347	extended and the second	Parent Check ok Tother? ok ok ok ok ok ok ok ok ok ok ok ok ok	Sibling Check Sibling? Sibling? Sibling? Sibling? Sibling? Sibling? Sibling? Sibling? Ok	e inheritance check
	This ap table.	pends ro	ows to	the ta	able,	adding t	he allelio	c information to the
5	Sort tab	ole by ca	itegory	y nam	e an	d file nai	me.	

How to Import

t	То	import	pediaree	data froi	n GenBase:
-					

_					-1-		
P	e	di	gr	ee	D	ata	

Step	Action
1	Choose Import Inheritance Data from GenBase. This imports the pedigree data from GenBase.
2	A dialog box appears and prompts you for the structure ID that specifies the particular set of pedigree data to use.
	The ID's are imported and placed in columns right next to the appropriate family member sample data.

Working with Tables 8-41

Inheritance

How to Check for Genotyper uses the pedigree IDs to check and see if siblings have inherited Mendelian alleles according to Mendelian principles.

To check Mendelian inheritance in tables:

Step	Action								
1	Choose Check Inheritancefrom the Table menu.								
	The Check Inheritance dialog box appears.								
	Check Inheritance in Table								
	Alleles are in columns 5. Peak 1 V 6. Peak 2 V								
	© Compare allele values, with tolerance 0.50 ○ Compare allele text								
	Marker is sex-linked								
	Check: • Hil rows () Selected rows								
	Check passed: Ok Siblings inconsistent: Sibling?								
	Mother mismatch: Mother? Male has extra X: Extra X?								
	Father mismatch: Father? Sex identifiers:								
	Both mismatch: Both? Male M								
	At least one parent wrong: Parents? Female F								
	Cancel OK								
2	Soloot the columns that contain allele information from the Alleles								
2	are in columns pop-up menus.								
3	Click the radio button for how you want to compare alleles:								
	If you want to compare Then click								
	Allele values Compare allele values, with tolerance, and type in a tolerance.								
	Allele text Compare allele text.								
	Note Select Marker is sex-linked checkbox if you know you are working with sex-linked alleles.								

8-42 Working with Tables

To check Mendelian inheritance in tables: (continued)

	Step	Action						
	4	Click the radio button for the rows you want to check:						
		Action Click the radio button for the rows you want to check: If you want to check Then click All rows in the table All rows. Only rows you have selected in the table Selected rows In the Text Options text boxes, type in messages that you want t appear when certain conditions are met after the inheritance check Click OK. Genotyper performs an inheritance check on family member data in the table. OK should appear in the column next to siblings that have inheri alleles from parents according to Mendelian principles. You can export the table to GenBase send results to GenBase f storage and possibly later retrieval. table cells that contain family members that have been lable ble mismatches, you can select the table cell for that individuals allelic ion. This allows a graphical depiction of the potential mismatical depiction of the potential mismatical depiction of the potential mismatical						
		All rows in the table	All rows.					
		Only rows you have selected in the table	Selected rows.					
	5	In the Text Options text boxes, type in messages that you want to appear when certain conditions are met after the inheritance che						
	6	Click OK. Genotyper performs an inheritance check on family member data in the table.						
		OK should appear in the column next to siblings that have inherited alleles from parents according to Mendelian principles.						
	7	You can export the table to GenBase send results to GenBase for storage and possibly later retrieval.						
Evaluating Results	For any as poss and disp informat	table cells that contain family members that ible mismatches, you can select the table cel play the associated plot view for that individua ion. This allows a graphical depiction of the p	have been labeled I for that individual als allelic potential mismatch.					
Parents Inconsistent Check	This che The che	eck verifies that an individual is the child of the identified parent.						
	♦ Hav	e one allele in common with each known par	ent for each locus.					
	♦ Not	have any alleles not found in the parents.						

Siblings Inconsistent Check This check verifies that the set of individuals identified as siblings are in fact siblings. This check does not depend on the parents. If the check fails, then all purported siblings are labeled with the warning text. This check verifies that: No more than four alleles per locus are allowed among the siblings. A single allele cannot be paired with more than two other alleles for

- a locus.
 If one sibling is homozygous, no more than three alleles for that locus are allowed.
- If two siblings are homozygous for different alleles, no more than two alleles for that locus are allowed.

8-44 Working with Tables

Formatting Tables for Export

Introduction	Some third party applications require that you re-format tables before
	exporting them from Genotyper. To format tables so that they are
	compatible, you can use the Flip Table command and flip tables before
	exporting them.

Tables for Export

How to Format To flip and format tables for export:

Step	Action
1	Choose Derive Table from the Analysis menu.
2	Choose the Flip Table submenu.
	The table in the Table window is flipped, copied and placed in the derived table.
	See Figure 8-7 for an example of how the Flip Table command reformats a table.

Flipped Table

Example of Figure 8-7 shows an example of a table before and after flipping

		Table -	flip table (examp 🗏			I
Lane	Dye	Sample Info	Category	Peak 1	Peak 2	Overflow	
1	В	001 Mother	Everything	76.71	78.54	Overflow	Ξ
1	R	GS2500	Everything	94.00	109.00	Overflow	~
2	в	001 Father	Everything	82.27	84.16	Overflow	D
2	R	GS2500	Everything	94.00	109.00	Overflow	⊞
							Ρī

	Derived Ta	ble - flip ta	able examp		
Lane	1	1	2	2	
Dye	В	R	В	R	≡
Sample Info	001 Mother	GS2500	001 Father	GS2500	₿
Category	Everything	Everything	Everything	Everything	\square
Peak 1	76.71	94.00	82.27	94.00	⊞
Peak 2	78.54	109.00	84.16	109.00	00
Overflow	Overflow	Overflow	Overflow	Overflow	ዔ
¢ 🔳					D)

Figure 8-7 Table before (top) and after (bottom) using Flip Table command

Exporting Tables

Introduction You can export the contents of tables to databases, linked programs, and other Genotyper System applications.

How to Export The following table explains where you can find information for how to Tables export tables to different target applications.

To Export Tables to	See
GenBase	"Exporting Tables to GenBase" on page 10-10.
GenoPedigree	The ABI PRISM GenoPedigree User's Manual.
Linked Programs	"Exporting and Copying Tables" on page 11-8.
Files	"Exporting and Copying Tables" on page 11-8.

How to Export There is a different command to export derived tables, than there is to Derived Tables export tables.

IMPORTANT You can only export derived tables as text files.

To export derived tables:

Step	Action
1	Use the Derive Table command to copy the table you want to export.
	For instructions on how to use the Derive Table command, see "How to Derive Tables" on page 8-36.
2	Choose Export Derived Table from the Analysis menu.
	A file selection dialog box appears.
3	Choose the folder location for where you want to export the table.
4	In the Export Table as field, type in the name of the exported table.

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Working with Statistical Data



Chapter Overview

Introduction	This chapter discusses how you can generate and view statistical data and histograms for peak data in Genotyper Documents. This chapter contains the following topics:		
In This Chapter			
	Торіс	See Page	
	Generating Statistical Data	9-2	
	Choosing the Source of Data	9-4	
	Choosing a Value Type	9-9	
	Determining the Bin Size	9-13	
	Viewing Statistics	9-15	
	Viewing Histograms	9-17	
	Setting Histogram Viewing Options	9-20	
	Editing Categories in Histograms	9-22	

Generating Statistical Data

- Introduction Genotyper generates statistical data from select parts of the active Genotyper Document. You can display generated statistical data in tables or histograms.
- Kinds of Statistical The following table describes the kinds of statistical data Genotyper can Data calculate for Genotyper Document contents.

Kind of Statistic	Description
Source	Within a Genotyper Document, the source of data from which statistics are generated.
Value Type	The kind of data for which Genotyper generates statistics. Possible Value Types are size in base pairs, scan number, peak height, peak area, and label text.
Number of Data Points	The total number of counts.
Minimum	The minimum value for a range of quantities you define by the Value Type you specify.
Maximum	The maximum value for a range of quantities you define by the Value Type you specify.
Mean	The average value for a set of values defined by the Value Type you specify.
Median	The center value of a series of quantities you define by the Value Type you specify.
Standard Deviation	The standard deviation from the mean of a set of values defined by the Value Type you specify.
Bin	The range of Value Types over which Genotyper calculates a count and frequency.
Count	The number of Value Types found within a Bin.
Frequency	The number of Value Types found within a Bin divided by the total number of data points.

Information appearing in the Statistics window:

Setting StatisticsGenotyper generates statistical data and histograms based on settings
you make in the Set Statistics Options dialog box.

To set statistics options, and where you can find instructions for each step:

Step	Action	See Page
1	"Choosing the Source of Data"	9-4
2	"Choosing a Value Type"	9-9
3	"Determining the Bin Size"	9-13

Choosing the Source of Data

Introduction You can specify the source of data in a Genotyper Document for which Genotyper generates statistics. There are two sources of data:

- Labeled peaks
- Tables

IMPORTANT For labeled peak sources, calculated statistics do not depend on the particular type or contents of a label, only whether or not a peak has a label.

 Labeled Peak Data
 Calculate statistics for a range of labeled peaks you select in plot

 from Plot
 displays.

 Selections
 To colouidto statistics from plot coloctions of data.

To calculate statistics from plot selections of data:

Step	Action
1	In the Dye/lane list, select the dye/lane or dye/lanes for which you want to calculate and display statistical data.
	An electropherogram plot showing peaks for each analyzed nucleic acid fragment in the sample appears in the Plot Area.
2	Click the Plot window icon, to open the Plot window.
	IMPORTANT Peaks in the Plot window must be labeled to include them in statistical calculations. If they are not labeled, label them.

To calculate statistics from plot selections of data: (continued)

Step	Action		
3	From the Analysis menu, choose Set Statistics Options.		
	The Set Statistics Options dialog box	appears.	
	Set Statistics Opti	ions	
	Source	-Value	
	Plot selection Range of (first) selected category	© Size in bp O Scan number	
	○ Fixed range 0.00 to 100.00 ○ Table selection	○ Peak height ☐ divided by scale factor	
	Table column(s)	O Peak area	
	to _▼ ○ Value in table column _▼	O Label text	
	when name of first selected category/group is in table column	O Cell value O Cell text	
	Bin size 0.50 Starting bin: @ Deter	mined automatically	
		Cancel OK	
	Figure 9-1 Set Statistics Options dia	alog box	
4	In the Source field, select the Plot sel	ection radio button.	
5	Use the mouse and select a rectangu electropherogram plot.	lar range in the	
6	See "Choosing a Value Type" on page selecting the appropriate Value Type r Statistics Options dialog box.	9-9, for instructions on adio button in the Set	

Labeled Peak Data You can calculate statistics for the range of peaks defined by a selected from Categories category.

To choose categories as the source of peak data:

Step	Action
1	In the Dye/lane list, select the dye/lane or dye/lanes for which you want to calculate and display statistical data.
	An electropherogram plot showing peaks for each analyzed nucleic acid fragment in the sample appears in the Plot Area.
2	Select the category from the Category list which defines the range of peaks for which you want to generate statistical data.

To choose categories as the source of peak data: (continued)

Step	Action
3	From the Analysis menu, choose Set Statistics Options.
	The Set Statistics Options dialog box appears (see Figure 9-1 on page 9-5).
4	In the Source field, select the Range of (first) selected category radio button.
5	See "Choosing a Value Type" on page 9-9, for instructions on selecting the appropriate Value Type radio button in the Set Statistics Options dialog box.

Labeled Peak You can specify a range of fragment sizes in base pairs. Genotyper Fragment Size generates statistical data for all peaks in the selected dye/lane of your active Genotyper Document that are within the fragment size range you specify.

To specify a range of fragment sizes as the source of peak data:

Step	Action
1	In the Dye/Lane list, select the dye/lane or dye/lanes for which you want to calculate and display statistical data.
	An electropherogram plot showing peaks for each analyzed nucleic acid fragment in the sample appears in the Plot Area.
2	From the Analysis menu, choose Set Statistics Options.
	The Set Statistics Options dialog box appears (see Figure 9-1 on page 9-5).
3	In the Source field, select the Fixed Range radio button.
4	Type in the size range in base pairs for fragments that you want to specify as the source of peak data.
5	See "Choosing a Value Type" on page 9-9, for instructions on selecting the appropriate Value Type radio button in the Set Statistics Options dialog box.

Table Cell Contents from Selection

Table Cell You can calculate statistics for the contents of selected table cells.

To choose the contents of table cells as the source of data:

Step	Action
1	Select the cell or cells in the table for which you want to generate statistics.
2	From the Analysis menu, choose Set Statistics Options. The Set Statistics Options dialog box appears (see Figure 9-1 on page 9-5).
3	In the Source field, select the Table Selection radio button.
4	See "Choosing a Value Type" on page 9-9, for instructions on selecting the appropriate Value Type radio button in the Set Statistics Options dialog box.

Table Cell Contents from Column Selection

Step	Action
1	From the Analysis menu, choose Set Statistics Options.
	The Set Statistics Options dialog box appears (see Figure 9-1 on page 9-5).
2	In the Source field, select the range of Table columns for inclusion as source data.
3	From the table column pop-up menus select the columns that define the beginning and ending range or conditions for source peak data.
4	See "Choosing a Value Type" on page 9-9, for instructions on selecting the appropriate Value Type radio button in the Set Statistics Options dialog box.

To specify a range of table columns as the source of peak data:

Table Cell Contents from Category and Column Selection

 Table Cell
 You can specify categories in table columns as a source of data.

To specify a category in a table column as the source of data:

Step	Action
1	Select the cell or cells in the table for which you want to generate statistics.
2	From the Analysis menu, choose Set Statistics Options.
	The Set Statistics Options dialog box appears (see Figure 9-1 on page 9-5).
3	In the Source field, select when name of first selected category/group is in table column.
4	From the table column pop-up menus select table column containing the category or group that you want to define as the source of your data.
5	See "Choosing a Value Type" on page 9-9, for instructions on selecting the appropriate Value Type radio button in the Set Statistics Options dialog box.

Choosing a Value Type

Introduction	The Value Type is the kind of data for which Genotyper generates
	statistics. Possible Value Types are size in base pairs, scan number,
	peak height, peak area, and label text.

Size in Base Pairs When you choose "Size in Base Pairs" as a Value Type, Genotyper generates statistics based on the size of fragments associated with your source peak data.

To choose the Size in Base Pairs as a Value Type:

Step	Action
1	If it is not already open, open the Set Statistics Options dialog box by choosing Set Statistics Options from the Analysis menu. See Figure 9-1 on page 9-5.
2	If you have not already done so, choose a source of peak data. See "Choosing the Source of Data" on page 9-4.
3	In the Value field, select the Size in bp radio button.
4	See "Determining the Bin Size" on page 9-13, for instructions on selecting the appropriate range of fragment sizes, for which Genotyper calculates a count, frequency of occurrence, as well as related statistics.

Scan Number When you choose Scan number as a Value Type, Genotyper generates statistics based on the number of scans used by your ABI PRISM instrument to detect the fragments associated with your source peak data.

To choose the Scan number as a Value Type:

Step	Action
1	If it is not already open, open the Set Statistics Options dialog box by choosing Set Statistics Options from the Analysis menu. See Figure 9-1 on page 9-5.
2	If you have not already done so, choose a source of peak data.
	See "Choosing the Source of Data" on page 9-4.
3	In the Value field, select the Scan Number radio button.

To choose the Scan number as a Value Type: (continued)

Step	Action
4	See "Determining the Bin Size" on page 9-13, for instructions on selecting the appropriate range of Scan numbers, for which Genotyper calculates a count, frequency of occurrence, as well as related statistics.

Peak Height When you choose Peak height as a Value Type, Genotyper generates statistics based on the height of a select source of peak data.

To choose peak height as a Value Type:

Step	Action
1	If it is not already open, open the Set Statistics Options dialog box by choosing Set Statistics Options from the Analysis menu. See Figure 9-1 on page 9-5.
2	If you have not already done so, choose a source for peak data.
	See "Choosing the Source of Data" on page 9-4.
3	In the Value field, select the Peak height radio button.
4	Optionally, select the checkbox for divided by scale factor.
5	See "Determining the Bin Size" on page 9-13, for instructions on selecting the appropriate range of peak data, for which Genotyper calculates a count, frequency of occurrence, as well as related statistics.

Peak Area When you choose Peak area as a Value Type, Genotyper generates statistics based on the area of specified source peaks.

To choose peak area as a Value Type:

Step	Action
1	If it is not already open, open the Set Statistics Options dialog box by choosing Set Statistics Options from the Analysis menu. See Figure 9-1 on page 9-5.
2	If you have not already done so, choose a source of peak data.
	See "Choosing the Source of Data" on page 9-4.
3	In the Value field, select the Peak area radio button.
4	Optionally, select the checkbox for divided by scale factor.

9-10 Working with Statistical Data

To choose peak area as a Value Type: (continued)

Step	Action
5	See "Determining the Bin Size" on page 9-13, for instructions on selecting the appropriate range of peak data for which Genotyper calculates a count, frequency of occurrence, as well as related statistics.

Labeled Text When you choose Labeled text as a Value Type, Genotyper calculates statistics based on the number of text labels within a specified range of source peak data.

To choose Labeled text as a Value Type:

Step	Action
1	If it is not already open, open the Set Statistics Options dialog box by choosing Set Statistics Options from the Analysis menu. See Figure 9-1 on page 9-5.
2	If you have not already done so, choose a source of peak data.
	See "Choosing the Source of Data" on page 9-4.
3	In the Value field, select the Label text radio button.
	Note For the Labeled text Value Type, Genotyper only calculates the Number of Data Points, count, and frequency of text labels located within a specified range.

Cell Value When you choose Cell value as a Value Type, Genotyper generates statistics based on the numerical value in table cells.

To choose Cell value as a Value Type:

Step	Action
1	If it is not already open, open the Set Statistics Options dialog box by choosing Set Statistics Options from the Analysis menu. See Figure 9-1 on page 9-5.
2	If you have not already done so, choose a source of data.
	See "Choosing the Source of Data" on page 9-4.
3	In the Value field, select the Cell value radio button.

To choose Cell value as a Value Type: (continued)

Step	Action
4	See "Determining the Bin Size" on page 9-13, for instructions on selecting the appropriate range of peak data for which Genotyper calculates a count, frequency of occurrence, as well as related statistics.

Cell Text When you choose Cell text as a Value Type, Genotyper generates statistics based on the text in table cells.

To choose Cell text as a Value Type:

Step	Action
1	If it is not already open, open the Set Statistics Options dialog box by choosing Set Statistics Options from the Analysis menu. See Figure 9-1 on page 9-5.
2	If you have not already done so, choose a source of data. See "Choosing the Source of Data" on page 9-4.
3	In the Value field, select the Cell Text radio button. Note For the Cell Text Value Type, Genotyper only calculates the Number of Data Points, count, and frequency of Cell text labels located within a specified range.

9-12 Working with Statistical Data

Determining the Bin Size

Definition	Definition The Bin size defines an interval within which Genotyper calculates a count and frequency of each occurrence of labeled peak data that matches criteria defined by the Source and Value Type. Results of th calculations are displayed in the Statistics Window, and Histogram window.			
Guidelines for Bin Size Selection	Selection If you choose too small of a number for your Bin size, you will have a large number of bins making it difficult to view a histogram representation of the statistical data.			
	There is window.	a limit of 5000 bins that can be displayed in the Statistics		
How to Define the Bin Size	You defi	ne the Bin size in the Set Statistics Options dialog box.		
	Step	Action		
	1	If it is not already open, open the Set Statistics Options dialog box by choosing Set Statistics Options from the Analysis menu. See Figure 9-1 on page 9-5.		
	2	If you have not already done so, choose a source of peak data. See "Choosing the Source of Data" on page 9-4.		
	3	If you have not already done so, choose a Value Type. See "Choosing a Value Type" on page 9-9.		
	4	In the Bin size field, type in an interval within which you want to calculate the count and frequency of occurrences of the specified Value Type.		
	5	Determine the starting bin.		
		See "How to Determine the Starting Bin" on page 9-14.		

the Starting Bin

How to Determine The Starting bin determines the initial value of the Bin size. You can either determine the Starting bin automatically, or specify a starting value.

To define the Starting bin:

Step	Action				
1	If it is not already open, open the Set Statistics Options dialog box by choosing Set Statistics Options from the Analysis menu. See Figure 9-1 on page 9-5.				
2	If you have not already done so, choose a source of peak data.				
	See "Choosing the Source of Data" on page 9-4.				
3	If you have not already done so, choose a Value Type.				
	See "Choosing a Value Type" on page 9-9.				
4	In the Bin size field, type in an interval within which you want to calculate the count and frequency of occurrences of labeled peak data.				
5	In the Starting bin field, determine the Starting bin:				
	If you want to	Then click			
	Use the first bin containing one or more counts	Determine automatically.			
	Define the Starting bin size	At value, and type in the Starting bin.			
6	When you are satisfied with all the settings in the Set Statistics Options dialog box, click OK.				

9-14 Working with Statistical Data
Viewing Statistics

Introduction	Once you have set statistics options, you can show statistics for the
	kinds of data you have selected.

The Statistics The Statistics window displays the statistics of selected data. Window

🔲 Statistics - Category member examp 📃			
Sourc Value typ Number of data point Minimu Maximu Maximu Medi Media	≥ : col 4 when "A01" in ≥ : cell value 5 : 12 h : 808.00 h : 1908.00 h : 1231.83 h : 1059.00	Locate in Table	
Standard deviatio	n : 328.60		Ř
Bin	Count	Frequency	
800.00 - 850.00	1	0.083	✤
850.00 - 900.00	1	0.083	
900.00 - 950.00	0	0.000	
950.00 - 1000.00	0	0.000	-
1000.00 - 1050.00	3	0.250	-
1050.00 - 1100.00	1	0.083	-
1100.00 - 1150.00	0	0.000	-
1150.00 - 1200.00	0	0.000	-
1200.00 - 1250.00	- 1250.00 1 0.083		
1250.00 - 1300.00	0	0.000	-
1300.00 - 1350.00	0	0.000	-
1350.00 - 1400.00	2	0.167	-
1400.00 - 1450.00	0	0.000	-
1450.00 - 1500.00	0	0.000	-₽-
			2



Working with Statistical Data 9-15

How to View Peak Once you have set statistics options, you can show the Statistics Statistics window at any time.

To view the Statistics window:

	-
Step	Action
1	Complete the Set Statistics Options dialog box (Figure 9-1 on page 9-5).
2	Select the data from the appropriate part of the Genotyper document that corresponds to the source you selected in Set Statistics Options dialog box.
3	Choose Show Statistics window from the Views menu. The Statistics window appears (Figure 9-2 on page 9-15). To see statistics from a different source of data, or of a different Value Type, or of a different Bin size, make changes in the Set Statistics Options dialog box.

How to Locate You can use the Locate in Table button to find data in a table that Bins in Tables corresponds to bins in the Statistics window. The Locate in Table button is enabled when you are using table columns (not table selection) as the source of data for statistics.

To locate bins in tables:

Step	Action
1	Open the Table window.
2	Select one or more cells in contiguous rows in the Statistics window (Figure 9-2 on page 9-15).
3	Click the Locate in Table button.
	Cells in the table that correspond to selected bins are highlighted.

Viewing Histograms

Introduction	Histograms show a graphical representation of data shown in the
	Statistics window.

The Histogram The Histogram window displays a histogram of data based on settings Window you have made in the Set Statistics Options dialog box.



Figure 9-3 The Histogram window

completed the Set Statistics Options dialog box.

How to View the You can show the Histogram window at any time once you have Histogram Window

To view the Histogram window:

Step	Action
1	Complete the Set Statistics Options dialog box (Figure 9-1 on page 9-5).
2	Select the data from the appropriate part of the Genotyper document that corresponds to the source you selected in Set Statistics Options dialog box.

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To view the Histogram window: (continued)

Step	Action
3	Choose Show Histogram window from the Views menu.
	The Histogram window appears (Figure 9-3). The bars in the Histogram window represent the defined bin sizes. Putting your cursor on a bar displays Statistical information for that bin at the bottom of the Histogram window.
	To see a different kind of histogram, make changes in the Set Statistics Options dialog box.

Statistics

Displaying Bin The bars in the Histogram window show statistics for defined Bin sizes. To display Statistical information for that bin at the bottom of the Histogram window, use the mouse to select a range in the Histogram window. Bin statistics for the range you selected display at the bottom of the window (Figure 9-4).



Figure 9-4 Bin statistics for a selected range

Viewing Histograms with Small Bin Sizes

Viewing If the text "WARNING - "Bin sizes too small to display" appears at the bottom of the Histogram window, this means that the width of one or more bins is too narrow to be displayed on your computer screen.

To view histograms with small bins sizes, do one of the following:

- Choose Set Statistics Options from the Analysis menu, and increase the Bin size to a value adequate for viewing.
- Zoom in on the region of the histogram that you want to view.
- Increase the size of the histogram window.

Working with Statistical Data 9-19

Setting Histogram Viewing Options

Introduction You can set options for viewing histograms which allows you to associate histogram data with corresponding data in plot displays and tables.

How to Set Plot Zooming Options You can associate data in histograms with corresponding Plot displays, so that when you zoom to a region of peaks in the Plot window, the histogram view zooms to the corresponding region of data. Plots views also zoom to corresponding regions of peak data when you zoom to the region in the histogram.

To set display options for histograms:

Step	Action	
1	View the Histogram for peak data you want to associate with corresponding plot display.	
2	Choose Set Histogram Options from the Analysis menu.	
	The Set Histogram Options dialog box appears.	
	Set Histogram Options	
	🗌 Zoom histogram with plot	
	Treat table values as: Size in bp	
	⊖ Scan number ⊖ Peak height	
	⊖ Peak area	
	Cancel OK	
3	Select Zoom histogram with plot.	
4	Open the Plot window, and select a region of the electropherogram.	
5	Choose Zoom to a selected range (\Re -R).	
	The Histogram window zooms to the region in the histogram that contains the corresponding peak data.	

9-20 Working with Statistical Data

Table Data

Viewing If you want to view histograms of data from tables, you need define the Histograms of value type of the data in the table.

> For example, if your table contains peak sizes and peak heights, and you have chosen to make a histogram of the peak heights by selecting table columns, then select the Peak height radio button in the Set Histogram Options dialog box(Figure).

For more information on choosing a source of data for histograms see"Choosing the Source of Data" on page 9-4.

Step	Action		
1	View the Histogram for the table you defined as a source of peak data. Choose Set Histogram Options from the Analysis menu.		
2			
	The Set Histogram Options dialog box appears.		
	Set Histogram Options		
	🗌 Zoom histogram with plot		
	Treat table values as: Size in bp 		
	O Scan number		
3	In the "Treat table values as:" field, click the value type of the data in your table. Click OK.		
4			
	The Histogram window should now display the same type of peak data as the associated table.		

To set display options for histograms:

Working with Statistical Data 9-21

Editing Categories in Histograms

Introduction The Histogram window provides a graphical display of peak size ranges. When viewing the Histogram window you can define new categories or edit existing ones.

How to Define the You can define the range of peak sizes in the Histogram window to Range for a New include in a new category.

Category

To define the range for a new category:

Step	Action	
1	View the appropriate histogram by showing the Histogram window.	
2	Place the cursor on the part of the histogram that displays peak sizes for the start point of the range of peak sizes that you want to include in your new category.	
3	Drag the mouse across the histogram display drawing a box around the range of peak sizes that you want to include in your new category.	
	Histogram - untitled	
	Category 🔽 📕	
	Member Locate in Table	
	5- ₽	
	4-	
	Count: 7 Value: 100.40 - 101.30 Category: D12S83: a101	
4	Choose Add Categoryfrom the Category menu.	
	The Add Category dialog box appears. A size range of from/to will be defined by the Add Category dialog box. If you instead hold down the Shift key when choosing Add Category, the range will be \pm a fixed number centered on the weighted average of bins in the	
	selected range (or a center value if no bins have been selected).	

9-22 Working with Statistical Data

To define the range for a new category: (continued)

	Step	Action	
5 Type in the name of the new category.		Type in the name of the new category.	
		The name of the newly defined category is added to the Category pop-up menu of the Histogram window.	

Category Size Ranges

How to View You can edit existing categories from the Histogram window, redefining the range of peak sizes included in the category.

To view category size ranges in histograms:



How to Change Category Size Ranges

You can change the size range of categories from the Histogram window.

To change the category size ranges in histograms:



Another Category

How to Select After you have adjusted the size range of one category, you can select another category from the Histogram window, and modify its size range as well. There are four different ways that you can select another category:

- Select another category from the Category pop-up menu. The handles move to the dashed box of the selected category.
- Click within the dashed box representing the size range of a ٠ category. The category name of your selection changes in the Category pop-up menu.
- Make your selection from the Category list.
- Press \mathbb{H} -J, the Zoom to next category command.

Communicating with **10** GenBase

Chapter Overview

Introduction	This chapter discusses how you can expand your genoty efforts by communicating with GenBase, a database of g results data. Once you establish a link to GenBase, you ca relevant to your research into your Genotyper Documents your results data to GenBase for storage or later retrieval also provides you access to data exported from GenoPeo other linkage analysis applications.	chapter discusses how you can expand your genotyping research is by communicating with GenBase, a database of genotyping ts data. Once you establish a link to GenBase, you can import data ant to your research into your Genotyper Documents, or export results data to GenBase for storage or later retrieval. GenBase provides you access to data exported from GenoPedigree and r linkage analysis applications.	
In This Chapter	This chapter contains the following topics:		
	Торіс	See Page	

Linking to GenBase	10-2
Importing and Exporting Results Data	10-4
Importing Tables from GenBase	10-6
Exporting Tables to GenBase	10-10
Importing and Exporting Categories	10-15
Importing and Exporting GenoPedigree Data	10-16

Linking to GenBase

What is GenBase	 GenBase is a database application that enables you to create large databases of genotyping results data without reformatting. In GenBase, you can manipulate genotyping results data and other information related to Genotyper Documents, GeneScan files, or GenoPedigree drawings. For detailed information about interacting with GenBase to perform any of the procedures discussed in this Chapter, refer to the ABI PRISM GenBase User's Manual. 		
Why Link to GenBase	By linking to GenBase, you can exchange Genotyper results data with relevant research data stored in GenBase tables.		
	Some reasons why you might want to communicate with GenBase include:		
	 Importing or exporting genotypes or genotyping data such as sample, patient, pedigree information. 		
	 Accessing genetic disease research information such as penetrance data and patient sample information relevant to your applications. 		
	 Improving error checking by maintaining an audit trail of previous genotyping activities. 		
	By linking to GenBase, you can retrieve information about sample types, gel conditions, or patient related information such as pedigree data, patient ID from previous genotyping applications and compare it to your most recent data.		
	 Creating a repository of allelic bin settings. 		
	• Calculating frequency of markers used in previous studies similar to your application.		
	 Performing Mendelian inheritance checks. 		

How to Link to GenBase After you link to GenBase, you can import or export results data from Genotyper. You only need to perform the following steps for linking to GenBase once. After you have established a link, the next time you start Genotyper, you only have to click the GenBase icon from the Main Window to access the database.

Step Action 1 Install GenBase on the same computer as Genotyper. 2 Select Links from the File menu. 3 Select Choose GenBase. An application selection dialog box appears. ____ SR4400/200 💱 GenBase 2.0.1 😫 👹 GenBase 2.0.1 Eject Desktop Cancel Select Highlight the version of GenBase to which you want to connect. 4 5 Click Select and Genotyper is connected to GenBase. Once you've established a link to GenBase, each time you want to access the database, click the GenBase icon on the Main window.

To link to GenBase from Genotyper:

Importing and Exporting Results Data

Introduction GenBase stores all results data in a Genotype Record. Once you have linked to GenBase from Genotyper, you can import information from the Genotype Record or export Genotyper results data to the Genotype Record. Using GenBase commands, you can manipulate the exported Genotyper data.

IMPORTANT Once you begin communicating with GenBase, do not attempt to switch to another GenBase data file while Genotyper is still running. Quit both programs first, before switching GenBase to a different data file. If you save a Genotyper document that contains dye/lanes or a table, do not attempt to use this file with a different GenBase data file other than the one originally used with the document, even if you quit both programs first.

The GenotypeThe Genotype Record window in GenBase shows all of the fields in a
RecordRecordGenotype Record.



Figure 10-1 The Genotype Record

For a detailed description of fields in the Genotype Record, see the *ABI PRISM GenBase User's Manual*.

10-4 Communicating with GenBase

Kinds of Results Genotyper can exchange results data for tables and categories with Data You Can GenBase. The following table shows which pages to refer to for Exchange instructions on how to either import or export the specified results data.

Kinds of results data Genotyper and GenBase exchange:

If you want to	See Page
Import tables	10-6
Export tables	10-10
Import categories	10-15
Export categories	10-15

Importing Tables from GenBase

- Introduction GenBase organizes all genotyping results data into function-specific tables. For example, data for populations, samples, and allele definitions are organized in separate tables. You can import data from GenBase tables into Genotyper for modification or inclusion in Genotyper tables.
- Kinds of GenBase GenBase tables are stored in the Genotyper Record. This table shows Tables the kind of GenBase tables that contain data appropriate for import and use in Genotyper.

Kinds of GenBase tables:

GenBase Table Name	Description
Category Members	Stores category definitions from Genotyper.
Genotypes	Stores genotyping results from Genotyper.
Individuals	Keeps track of information on every individual in your study and provides convenient cross-references for sorting and searching through patient populations.
Markers	Defines markers. You can specify map locations (for a particular map) and alternate names (for a particular Alternate Marker Name Set).
Pedigrees	Provides information that is imported from GenoPedigree. Can be set up manually if you don't have GenoPedigree.
Pedigree Structures	List of names of hypotheses for pedigree relationships.
Samples	Assigns IDs to your nucleic acid samples, and provides cross-references to individuals and their samples.

10-6 Communicating with GenBase

How to Specify the Before you import data from a GenBase table into Genotyper, use the Format Set Up Table... command in Genotyper to specify formats for imported GenBase data.

To import GenBase tables into Genotyper:

Step	Action	
1	Link to GenBase.	
2	Select Clear Table from the Analy	vsis menu.
3	Select Set Up Table from the Tab	le menu.
	The Set Up Table dialog box app	ears.
	Set u	n Table
	Contents per row: © Category & dye	/lane () Sample
	Include data in columns:	□ Name of gel file
	🗌 Name of GeneScan file	🛛 Text if > N labels Options
	🖂 Lane number	🗌 Text if < N labels Options
	🖂 Dye letter	User comment Options
	🗌 Lane and dye	🗌 Marker name & individual ID
	🛛 Sample info 🛛 Options	Pedigree data
	Sample comment Options	Inheritance check
	Name of category Options	Edited-label warning Options
	🛛 Labels Options	Edited-table warning Options
	Number of labels	Low-signal warning Options
	Size-calling method	Saturation warning Options
	Size standard file name	Minimum modulation
	U Dye/lane scale factor	Modulation warning Options
	Lane Dye Sample Info Category F	Peak 1 Peak 2 Overflow
		\$
	Uncheck All	Cancel OK
	<u>k</u>	

To import GenBase tables into Genotyper: (continued)

Step	Action				
4	Select the following checkboxes:				
	◆ Sample Info				
	 Name of category 				
	♦ Labels				
	The following fields are optional:				
	◆ Name of GeneScan file				
	♦ Lane number				
	◆ Dye letter				
	♦ Lane and dye				
	♦ Text if >N labels				
	 Edited-label warning 				
	 Edited-table warning 				
	Note Other fields are not available for import.				
5	Click OK.				

How to ImportYou can import data from GenBase tables, and further analyze it with
Genotyper commands.

To import GenBase tables into Genotyper:

Step	Action
1	Link to GenBase.
2	Open the Genotypes Summary Table in GenBase.
3	Select and show records that you want to import, and append to your Genotyper table.
4	In Genotyper, set up the kind of table to which you want to append rows of Genotype Records.
	For more information on setting up tables in Genotyper, see "Setting Up a Table" on page 8-2.
5	From the Table menu, choose Append from GenBase.
	A dialog box appears telling you how many records, or rows Genotyper will append to your table.

10-8 Communicating with GenBase

To import GenBase tables into Genotyper: (continued)

Step	Action
6	Click OK and Genotyper imports select records and appends them as rows to your table.
	Note If you plan to edit the table data in Genotyper and then export the table to GenBase, you must use the Re-import Dye/lane command to import the associated dye/lanes into the Dye/lane list before exporting the table.
	For more information on using the Re-import Dye/lane command, see "Re-importing Dye/lanes" on page 8-6.

Exporting Tables to GenBase

Introduction	GenBase organizes all genotyping results data into function specific tables. For example, data for populations, samples, and allele definitions are organized in separate tables. You can export data from Genotyper tables for inclusion in specific GenBase tables.			
	IMPORTANT The label data must be set up correctly in the table for the Export to GenBasecommand to give satisfactory results. If the table is not set up correctly in Genotyper, then the data in GenBase may end up in the wrong format.			
How to Specify the Format	 Before you export data from a Genotyper table into GenBase, use the Set Up Table command in Genotyper to specify formats for exported GenBase data. To specify format of tables for export to GenBase: 			
	Step	Action		
	1	Link to GenBase.		
	2	2 Select Clear Table from the Analysis menu.		
	3	Select Set Up Table from the Table menu.		
	The Set Up Table dialog box appears.			
	Set up Table			
	Contents per row: Category & dye/lane Sample			
		Include data in columns: 🗌 Name of gel file		
		□ Natrie of Genesican Trie □ Text if < N labels □ Options		
		☑ Dye letter ☑ User comment Options		
		🗌 🗌 Lane and dye 🗌 Marker name & individual ID		
		Sample info Options Pedigree data		
		□ sample comment uptions □ Inneritance cneck		
		□ Labels Options □ Edited-table warning Options		
		Number of labels Low-signal warning Options		
		Size-calling method Saturation warning Options		
		Usize standard file name Uminimum modulation		
	Lane Uye Sample into Category Yeak 1 Yeak 2 Uvertiow			
		Uncheck All OK		

10-10 Communicating with GenBase

To specify format of tables for export to GenBase: (continued)

Step	Action		
4	Select the following checkboxes:		
	Sample Info		
	Name of category		
	◆ Labels		
	The following fields are optional, and will only be sent if checked:		
	 Size-calling method 		
	◆ Text if >N labels		
	 Low-signal warning 		
	Saturation warning		
	Minimum modulation		
	Modulation warning		
	The following fields are sent automatically and do not need to be checked:		
	◆ Name of GeneScan file		
	◆ Lane number		
	♦ Dye letter		
	◆ Name of Gel file		
	◆ Edited-label warning		
	Edited-table warning		
	Note Other fields are not available for export.		

To specify format of tables for export to GenBase: (continued)

Step	Action		
5	Choose the kind of label data that you want to send to GenBase:		
	If your labeled peaks have	Then	
	Size labels only	Choose one label per peak in the labels options of the Set Up Tablecommand.	
	Sizes and allele names	Choose two labels per peak in the labels options of the Set Up Tablecommand.	
		Note Category member names correspond to allele names.	
	Note If you choose sizes and allele names, make sure that end labeled peak has two labels. For a description of how to set up categories to insure that all peaks are labeled with either the con allele name or with the name "Unknown" to indicate a new allele been detected, see "Using Exclusive Peak Labeling–An Example on page 6-10.		
6	Click OK.		

How to Export You can export data from Genotyper to specific GenBase tables stored Tables in the Genotype Record.

IMPORTANT The Export to GenBase command sends data from the dye/lanes as well as the table. If associated dye/lanes have been deleted or are not present in dye/lane list, do not export the table to GenBase.

To export Genotyper tables to GenBase:

Step	Action			
1	Establish a link to GenBase.			
2	Open the Genotyper Document that contains the data that you want to export.			
	Note If a document does not already exist, import the GeneScan files that contain the sample data that you want to export.			

10-12 Communicating with GenBase

To export Genotyper tables to GenBase: (continued)

Step	Action		
3			
	If the Genotyper Document	Then	
	Contains a Table that you want to export	Go to step 7.	
	Does not contain a Table you want to export	Choose Set Up Table from the Table menu, and specify the format for the table you want to export.	
	For more information on setting Up a Table" on page 8-2.	up tables in Genotyper, see "Setting	
4	Select the dye/lanes from the D in the Table.	ye/lane list that you want to include	
5	Select the category that specific include from select dye/lanes.	es the kind of peak data you want to	
	Select Append to Table from the Table menu, and the selected dye/lane peak information appears in the Table view of the Main Window.		
	tu	t1 table	
	B Y TutoriaIts=001 1 Blue 001 fb TutoriaIts=001 1 Red 652500 TutoriaIts=001 2 Blue 001 fb TutoriaIts=001 2 Blue 001 fb	ther ☆ 日 ither ☆ 日 ither ☆ ↓ ↓ ↓ ↓ ↓ ↓ ↓ ↓ ↓ ↓ ↓ ↓ ↓ ↓ ↓ ↓ ↓ ↓	
	70 80 90 100 110 120 130 14		
		<u> </u>	
	• Everything All peaks from scan 0 t	o 32000 in R/B/G/Y 규	
	Lane Dye Sample Info Category 1 8 001 Hother Everything 1 R 052500 Everything 2 B 001 Father Everything	Peak 1 Peak 2 Overflow 1 1 -	
	Current Step Log 🔐 Set up table w number, dy peaks per c 	rith one category and one lane per row, containing lane (e, sample info, table item type 7, 1 label per peak for 2 lategory, the text "Overflow" if number of labels > 2 ato table	

To export Genotyper tables to GenBase: (continued)

Step	Action
7	Select Export to GenBase from the Table menu.

How to Update If you have appended rows to a Genotyper table from a GenBase table, Tables in GenBase and then edited the contents of that table either by editing cells or by clicking on labels and updating the table, you may want to update the corresponding table in GenBase with your edited table.

To update tables in GenBase with table data edited in Genotyper, choose Update Table in GenBase from the Table menu.

Note Remember that the associated dye/lanes must be present in the Dye/lane list in order for you to update the table in GenBase.

10-14 Communicating with GenBase

Importing and Exporting Categories

Introduction	Once you have linked to GenBase, You can import marker data and categories from GenBase, and Export Genotyper categories to GenBase.
	IMPORTANT You can only export members of category groups to GenBase. The first time you attempt to export a non-member category, Genotyper issues an alert. reminding you that such categories will not be sent to GenBase.
A Comparison of Markers and Categories	GenBase stores categories and markers. Although it is not uncommon to use the terms interchangeably, GenBase allows you to make a distinction between the two terms and assign multiple categories to each marker.
How to Import Categories	To import Genotyper categories from GenBase:
0	Step Action

Step	Action
1	Link to GenBase.
2	Open the Category Members table in GenBase, and make sure that only those categories that you want to import are currently shown in the table.
3	Choose Import Categories from Database, from the Category menu. Note Categories are imported from GenBase and appear in the
	Category list of your active Genotyper Document.

How to Export To export Genotyper categories to GenBase:

Categories

Step	Action
1	Mark the categories to export from the Category list in the Main window.
2	Select Export Marked Category to Database from the Category menu.

Importing and Exporting GenoPedigree Data

Introduction Establishing a link to GenBase provides a means of exchanging results data between Genotyper and GenoPedigree, the pedigree drawing software application.

Through GenBase, you can import pedigree drawings, marker and allele data into Genotyper from GenoPedigree, and export table and category information from Genotyper to GenoPedigree.

For detailed instructions on how to import and export GenoPedigree data, see the ABI PRISM GenoPedigree User's Manual.

How to Link to
GenoPedigreeYou can link to GenoPedigree from the Genotyper Main window, if you
have installed the pedigree drawing program on the same system as
Genotyper.DataGenotyper.

StepAction1Select Links from the File menu.2Select Choose GenoPedigree.An application selection dialog box appears.3Highlight the version of GenoPedigree to which you want to connect.4Click Select and Genotyper is connected to GenoPedigree.Once you've established a link to GenoPedigree, each time you want to access the database, click the GenoPedigree icon on the Main window.

To link to GenoPedigree from Genotyper:

10-16 Communicating with GenBase

Linking to Programs

Chapter Overview

Introduction	This chapter discusses how you can expand your genotyping research efforts by linking Genotyper to third-party programs or files and transferring results data.	
In This Chapter	This chapter contains the following topics:	
	Торіс	See Page
	Planning to Link to Programs and Documents	11-2
	Choosing Linked Programs and Documents	11-5
	Running a Macro or Script in a Linked Program	11-7
	Exporting and Copying Tables	11-8

Linking to Programs and Files 11-1

Planning to Link to Programs and Documents

Introduction If you are planning to link to third-party programs or spreadsheet applications, after performing genotyping tasks, you need to set up Genotyper so that you can generate results data that is compatible with the program you are planning to use.

How to Set Preferences for Linking to Programs You can set preferences for opening a linked program or document when you start Genotyper. These linking preferences apply to all open Genotyper Documents, not just the active document. Genotyper remembers all links you have established when you quit Genotyper.

Note Preference settings are saved in the Genotyper preferences file in the System Preferences folder.

To set preferences for linked programs:

Step	Action		
1	Choose Set Preferencesin the Edit menu.		
	The Set Preferences dialog box appears.		
	Set Preferences		
	 Options for exporting tables: Field delimiter: Tab Comma Space None Line delimiter: CR CR/LF LF Additional windows to be opened with main window: Dye/lane Plot Macro Statistics Category Table Step Information to be shown in dye/lane list: File name Dye color Sample Info 		
	• Automatic options for linked program & document: When opening Genotyper: Open linked program Open linked document When quitting Genotyper: Save linked documents		
	Import colors: Import colors: Blue Red Orange Import Raw Other options: Double-clicking runs macros & steps BioLIMS Cancel		

11-2 Linking to Programs and Files

To set preferences for linked programs: (continued)

Step	Action	
2	Under the bullet "Automatic options for linked program & document:", select the checkboxes for how you want to link to third- party programs and documents when opening and quitting Genotyper.	
	Note These preference settings do not apply to GenBase or GenoPedigree.	
3	Click OK.	

Linking to Programs and Files 11-3

Preferences for Exporting a Table to a File

How to Set You can export Genotyper tables to a file. Some programs or documents that read this file require the data to be in a specific format; for example, fields must be delimited by tabs or commas. These format options are available in the Set Preferences dialog box.

> Note Preference settings are saved in the Genotyper preferences file in the System Preferences folder.

To set preferences for exporting tables to files:



11-4 Linking to Programs and Files

Choosing Linked Programs and Documents

Introduction	You can link Genotyper to spreadsheet programs or data base programs that have Apple Event capabilities and use the Apple Event table suite. You may want to link to third-party programs if you have specialized applications that require different analysis procedures than those offered by GenBase or GenoPedigree.		
Example Programs	Some e transfer	xamples of third-party programs you might want to link to and your results data include:	
Microsoft Excel			
	ris FileMaker Pro		
How to Choose a Linked Program	a To choose a program to link to from Genotyper:		
	Step	Action	
	1	From the File menu, point to Links and click on Choose Linked Program	
		The Directory dialog box appears.	
	2	Locate and select the program to be linked.	
	L		

How to Choose a You can choose a document in the linked program after you have Linked Document chosen the linked program. If you do not choose a specified linked document, Genotyper will use the untitled default document, if any, opened by the linked program.

Step	Action
1	From the File menu, point to Links and click on Choose Linked Document
	The Directory dialog box appears.
2	Locate and select the document to be linked.

Linking to Programs and Files 11-5

Opening a Linked Program If you have configured the Set Preferences dialog box to open the linked program automatically, and if the linked program was already opened by Genotyper, then you do not need to use the Open Linked Program command.

To open a linked program:

Step	Action
1	Choose Open Linked Program in the File menu.
	The linked program opens.

IMPORTANT If a program is already opened, but was not opened using the Open Linked Program command in Genotyper, you still need to choose Open Linked Program.

Opening a Linked Document

To open a linked document:

Step	Action
1	Choose Open Linked Document in the File menu.
	A specific document in the linked program opens.

11-6 Linking to Programs and Files

Running a Macro or Script in a Linked Program

Introduction	You can run a macro or script from Genotyper that you created in a
	linked program.

Macro/Script in a

How to Run a To run a macro/script in a linked program:

Linked Program

Step	Action
1	Create and name a macro/script in the linked program.
2	In Genotyper, choose Run Linked Macro/Scriptin the Macro menu.
3	Enter the name of the macro that was defined in the linked program.
4	Click OK.
	The macro runs in the linked program.

Programs 🖕

Examples of The following are examples of how you can define macros in different Macros in Linked kinds of linked programs:

- FileMaker Pro users enter the name of the FileMaker Pro script.
- Microsoft Excel users enter the following: ٠ [name of Macro Sheet]![name of macro]()

Example

Macro1!Record()

IMPORTANT The macro will not work for Excel programs without the pair of parentheses at the end.

Exporting and Copying Tables

Introduction You can export a Genotyper table to a plain text file so that you can read it using a word processing or spreadsheet application. You can open this file in Simple Text to view it.

> **IMPORTANT** Once a table is exported to a file it cannot be imported back into Genotyper. If you want to continue working with the table, save your work as a Genotyper Document by using the Save command. This will save the dye/lanes, categories, or labels, and will allow you to continue your work at a later time.

How to Export a To export a table to a file:

Table

Step	Action
1	Choose Export Tablefrom the Edit menu.
	The standard Macintosh Directory dialog box appears.
2	Enter the name of the file in the text box.
3	Designate where you want to place that file (for example, desktop or in another folder).
4	Click Save.

How to Copy As an alternative to making a table in a linked spreadsheet document, Tables you can copy a table to a spreadsheet document.

To copy tables to spreadsheets:

Step	Action
1	Select a contiguous portion of the Genotyper table.
2	Choose Copy in the Edit menu.
3	Select the spreadsheet program.
4	Choose Paste in the Edit menu.

11-8 Linking to Programs and Files
Menu and Command 12 Reference

Chapter Overview

Introduction	This chapter provides a reference for the names, locations, and definitions of all menus and commands available in Genotyper 2.5.	
In This Chapter This chapter contains the following topics:		
	Торіс	See Page
	Genotyper Menus	12-2
	The File Menu	12-3
	The Edit Menu	12-5
	The Analysis Menu	12-7
	The Category Menu	12-9
	The Table Menu	12-11
	The Views Menu	12-13
	The Macro Menu	12-16

Genotyper Menus

Introduction	You can access all Genotyper commands and options from pull-down
	menus listed on the menu bar.

- The Menu Bar The menu bar displays across the top of your computer screen after you start the Genotyper application.
 - ᡩ File Edit Analysis Category Table Views Macro

Menu Items Menus you can access from the menu bar:

Menu	Description
The File menu	Lists commands for working with Genotyper Documents and GeneScan files.
The Edit menu	Lists commands for editing Genotyper Documents and table contents.
The Analysis menu	Lists commands for labeling fragment peak data, and determining statistical data for fragment peaks.
The Category menu	Lists commands for defining categories.
The Table menu	Lists commands for setting up Tables and working with tabular data.
The Views menu	Lists commands for opening windows for Genotyper Document windows in the Main window, and for customizing viewing of these windows.
The Macro menu	Lists commands for creating and running macros for automating Genotyper procedures and applications.

12-2 Menu and Command Reference

The File Menu

Definition	The File menu contains commands for working with Genotyper Documents.			
Menu Options	The figure below shows the list of commands you can access from the File menu.			
	File			
	New Onen	%°N ≌∩		
	Close	ww.		
	Save	жs		
	Save As			
	Import Locate GeneScan File Re-Import Dye/lane	► ₩D		
	Locate in GenBase	≋В		
	Links		Open GenoPedigree	
	Lock	-	Chaosa ConoRedignee	
	V ONIUCK		Choose GenBase	
	Page Setup Print	ж₽	Onen Linked Program	
	Ouit	900.	Open Linked Document	
	Quit	~ v	Choose Linked Program Choose Linked Document	
			Clear Links	

Commands

Commands in the File menu:

Command	Description
New	Opens a new, untitled Genotyper document.
Open	Opens a previously saved Genotyper document.
Close	Closes the active window.
Save	Saves the active Genotyper document.
Save As	Saves the Genotyper document under a new name.
From GeneScan File	Brings up a dialog box which allows you to import a GeneScan file or multiple GeneScan files.

Commands in the File menu: (continued)

Command	Description
From BioLIMS	Opens BioLIMS Collection Browser if a database connection has been established.
Locate GeneScan File	When you select an entry in the Dye/lanes list, and then choose this command, the Finder locates the original GeneScan file for that selection and opens its folder.
Re-Import Dye/lane	Re-imports dye/lanes if you have made a table and deleted or cleared all dye/lanes.
Locate in GenBase	Finds specified text in a GenBase database if you are linked to it.
Links	Sub-menu with several choices for linking.
Open GenoPedigree	Provides access to the GenoPedigree program.
Open GenBase	Provides access to GenBase.
Choose GenoPedigree	Provides link to GenoPedigree program.
Choose GenBase	Provides link to GenBase database.
Choose GenBase File	Provides link to files in GenBase.
Open Linked Program	Opens an application program that is linked to Genotyper.
Open Linked Document	Opens a document that is linked to Genotyper.
Choose Linked Program	Brings up a dialog box which allows you to choose a linked program.
Choose Linked Document	Brings up a dialog box which allows you to choose a linked document.

12-4 Menu and Command Reference

The Edit Menu

Definition	The Edit menu contains commands for editing Genotyper documents.		
Menu Options	The figure below shows the list of commands you can access from the Edit Menu.		
	Edit Can't Undo %Z Cut %X Copy %C Paste %V Clear Select All %A		
	Select Copy Window Edit Cell %E Find %F Find Next %G Mark %M Unmark %U	Blue Green Yellow Red Orange	
	Show Clipboard		

Commands

S Commands in the Edit menu:

Command	Description
Can't Undo	Undoes the last command (whenever possible).
Cut	Cuts the selection and places it on the Clipboard.
Сору	Copies the selection to the Clipboard.
Paste	Pastes the selection at the cursor location.
Clear	Clears the currently selected entries in the Dye/lane list, Categories list, Macro list, or Step list.
Select All	Selects every entry in the selected list or table.
Select	
♦ Blue	 Selects all entries in the Dye/lane list that have a blue dye color.
♦ Green	 Selects all entries in the Dye/lane list that have a green dye color.
◆ Yellow	 Selects all entries in the Dye/lane list that have a yellow dye color.

Commands i	n the	Edit r	nenu:	(continued)
------------	-------	--------	-------	-------------

Command	Description
◆ Red	 Selects all entries in the Dye/lane list that have a red dye color.
♦ Orange	 Selects all entries in the Dye/lane list that have an orange dye color.
Copy Window	Copies the active window to the clipboard.
Edit cell	Allows you to change the contents of individual cells in tables.
Find	Shows a dialog box which allows you to locate and select an alphanumeric text in the Dye/lane list, Category list, or the table.
Find Next	Allows you to locate and select the next case of a previously defined alphanumeric text, without the need to repeatedly use the Find dialog box.
Mark	Places a bullet (•) in front of the Categories list or Dye/lane list item. When a dye/lane is not marked, the plot corresponding to that item appears in the upper Plot window. When a category is marked, it is used by labeling and table commands.
Unmark	Removes a bullet (•) from the Category or Dye/lane list item. When a dye/lane is not marked, the plot corresponding to that item no longer appears in the upper Plot window. When a category is not marked, it is not used by labeling and table commands.
Set Preferences	Shows a dialog box which allows you to set options for exporting tables, define additional windows to be opened with the main window, define information to be shown in the Dye/lane list, and set automatic options for a linked program or document.
Show Clipboard	Shows items that have been cut, or copied, and still reside in the clipboard.

12-6 Menu and Command Reference

The Analysis Menu

Definition	The Analysis menu contains commands for labeling fragment peak
	data, and determining statistical data for fragment peaks.

Menu Options The figure below shows the list of commands you can access from the Analysis Menu.



Commands

Commands in the Analysis menu:

Command	Description
Set Click Options	Shows a dialog box in which you can set parameters for manual labeling of peaks (for example, labeling by size, height, scan number, or area).
Set Statistics Options	Shows a dialog box in which you can set parameters for what displays in the Statistics window. Settings include: calculate statistics for peak size, scan number, bin size.
Set Histogram Options	Shows a dialog box in which you can set parameters for how the histogram window interacts with other parts of a Genotyper Document.

Commands in the Analysis menu: (continued)

Command	Description
Label Peaks	Shows a dialog box which allows you to label peaks for selected dye/lanes that have been defined by marked category parameters.
Change Labels	Shows a dialog box which, for selected lanes in the Dye/lane list, allows you to change the labels at currently labeled peaks.
Normalize Labels	Shows a dialog box which allows you to normalize data in several peak labels to data in a specific (control) label.
Filter Labels	Removes unwanted labels from peaks.
Remove Labels	Shows a dialog box which allows you to remove labels from specified peak locations of selected dye/lanes in the dye/lane list.
Clear Common Labels	In currently-selected set of dye/lanes, remove labels for peaks that (within tolerance) are at the same location and are labeled in each of the dye/lanes; shows a dialog box to set the tolerance.
Calculate Scale Factors	Normalizes the height or area of peaks.
Derive Table	Enables you to derive a second table from an existing table. A derived table is not linked to dye/lanes or categories like the table from which it was derived.
Copy Table	Copies the table in the Table window to the Derived table window.
Flip Table	Flips the table in the Table window, copies it and places it in the derived table window.
Export Derived Table	Exports derived tables as text files.
Clear Category list	Clears all entries in the Category list.
Clear All Labels	Removes all labels from all peaks (whether selected or not) in the Plot window.
Clear Table	Removes all rows and columns from the table.
Clear Dye/Lane list	Removes all entries from the Dye/lane list.
Clear All Scale Factors	Resets all scale factors from dye/lanes in the Dye/lane list to 1.0.

12-8 Menu and Command Reference

The Category Menu

Definition	The Category menu contains commands for defining categories.	
Menu Options	Ienu Options This figure shows the list of commands you can access from the Category menu.	
	Category Add Category %L Add Multiple Categories Edit Category	
	Offset Categories Calculate Offset	
	Енрогt Marked Categories to Database Import Categories from Database	

Commands

Commands in the Category menu:

Make from Labels... Make Category Members.

(1
Command	Description
Add Category	Shows a dialog box which allows you to set category parameters for new categories.
Add Multiple Categories	Shows a dialog box which allows you to create multiple categories at once.
Edit Category	Shows a dialog box which allows you to change the parameters of the selected category.
Offset Categories	Allows you to adjust the size range for peak labeling for selected categories.
Calculate Offset	Automatically adjusts the size range for peak labeling for selected categories.
Export Marked Categories to Database	Exports marked Genotyper categories to GenBase.
Import Categories from Database	Imports Genotyper categories from GenBase.
Make from Labels	Shows a dialog box that allows you to create categories from labels.

Commands in the Category menu: (continued)

Command	Description
Make Category Members	Shows a dialog box that allows you to create member categories for specialized applications.

12-10 Menu and Command Reference

The Table Menu

Definition	The Table menu contains commands for setting up Tables and working
	with tabular data.

Menu Options This figure shows the list of commands you can access from the Table menu.

Table
Set up Table
Append to Table
Update Table
Sort Table
Analyze Table
Calculate in Table
Check Inheritance
Export to File
Export to GenBase
Export to GenoPedigree
Update to GenBase
Export to Link
Append from GenBase
Import Inheritance Data from GenBase
Add Rows to Table
Add Rows to Link

Commands

Commands in the Table menu:

Command	Description
Set up Table	Shows a dialog box which allows you to define the contents and order of rows and column headings for tables.
Append to Table	Adds rows to an existing table.
Update Table	If you have created a table, and made changes to peak labels, updates the corresponding information in your table.
Sort Table	Shows a dialog box which allows you to sort the rows of a table in a Genotyper document.
Analyze Table	Allows you to specify conditions for logical comparisons of table cell contents.
Calculate in Table	Allows you to perform numerical calculations of table cell contents.

Commands in the Table menu: (continued)

Command	Description
Check Inheritance	Shows a dialog box that allows you to check Mendelian inheritance in the table.
Export to File	Exports table contents to a text file.
Export to GenBase	Exports select tables to GenBase.
Update to GenBase	Updates GenBase tables with information from select Genotyper tables.
Export to Link	Exports table contents to a linked program (other than GenBase or GenoPedigree).
Append from GenBase	Allows you to append rows to Genotyper tables from GenBase tables.
Import IDs from GenBase	Imports data from GenBase for inheritance checking.
Add Rows to Table	For compatibility with Genotyper versions 1.x only.
Add Rows to Link	For compatibility with Genotyper versions 1.x only.

12-12 Menu and Command Reference

The Views Menu

Definition	The Views menu contains commands for opening windows for	
	Genotyper Document windows in the Main window, and for customizing	
	viewing of these windows.	

Menu Options This figure shows the list of commands you can access from the Views Menu.



Commands

Commands in the Views menu:

Command	Description
Display by Size	Changes the horizontal scale in the plot areas to base pairs.
Display by Scan	Changes the horizontal scale in the plot areas to scan line.
Expand Categories	Displays all categories in a selected category group in the Category list.
Collapse Categories	Displays only the category group name of a selected category in the Category list.

Commands in the Views menu: (continued)

Command	Description
Show Main Window	Shows all parts of a Genotyper Document in one window, the Main window.
Show Dye/lanes Window	Opens an additional, larger window that shows only the Dye/lane list.
Show Plot Window	Opens an additional, larger window that shows only the plots and peak labels. The window expands vertically to fill the computer screen.
Show Categories Window	Opens an additional, larger window that shows only the Category list.
Show Table Window	Opens an additional, larger window that shows only the table.
Show Macro Window	Opens an additional, larger window that shows only the Macro list.
Show Step Window	Opens an additional, larger window that shows only the Step list.
Show Statistics Window	Opens window displaying statistics of selected peaks (number of labeled peaks, minimum, maximum, median, standard deviation, count, and bin).
Show Histogram Window	Opens window displaying histogram representation of statistics of selected peaks.
Show Derived Table Window	Opens window displaying Derived table, if one exists.
Dye/Lane Sorting	Brings up a dialog box which allows you to sort the Dye/lane list by file names, lanes, dye color, sample information, or sample comments in ascending or descending order.
Category Sorting	Brings up a dialog box which allows you to sort category names, category starting size or scan number, and category dye color in ascending or descending order.
Plot Options	
Label Options	Brings up a dialog box which allows you to modify and use colors and prefixes in labels.
Dye Scaling	Brings up a dialog box which allows you to modify signal heights.

12-14 Menu and Command Reference

Commands in the Views menu: (continued)

Command	Description
Main Window, Upper Pane	Displays the Plot Options dialog box, allowing you to change the display options in the upper pane of the Main window.
Main Window, Lower Pane	Displays the Plot Options dialog box, allowing you to change the display options in the lower pane of the Main window.
Plot Window, Upper Pane	When the Plot window is open, displays the Plot Options dialog box, allowing you to change the display options in the upper pane of the Plot window.
Plot Window, Lower Pane	When the Plot window is open, displays the Plot Options dialog box, allowing you to change the display options in the lower pane of the Plot window.
Zoom	
Zoom In	Zoom in by a factor of two.
Zoom In (Selected Range)	Expands the selected portion of an electropherogram to fill the full plot area.
Zoom Out	Shows a somewhat larger section of the electropherogram.
Zoom Out (Full Range)	Shows the complete electropherogram.
Zoom To	Brings up a dialog box which allows you to specify a zoom range.
Zoom To Category	Zooms to a range that includes the ranges of currently-selected categories.
Zoom To Next Category	Zoom to the range of the next marked category following the currently-selected category.

The Macro Menu

- **Definition** The Macro menu contains commands for creating and running macros for automating Genotyper procedures and applications.
- Menu Options This figure shows the list of commands you can access from the Macro menu.

Macro	
✓Record Steps Save Step Log	
Run Macro	
Change Macro Name	
Duplicate Macro	
Run Linked Macro/Script.	
Edit Step	
Run Step	
Add Comment	
Set Import Macro	
Clear Step Log	

Commands

Commands in the Macro menu:

Command	Description
Record Steps	When this menu item is checked, your steps (commands) will be added to the Current Step Log.
Save Step Log	Creates a macro from the current step log and brings up a dialog box which allows you to name the macro and choose a keyboard command to run it.
Run Macro	Runs the selected macro.
Change Macro Name	Brings up a dialog box which allows you to change the name of the selected macro and change the keyboard command which runs it.
Duplicate Macro	Makes a copy of the selected macro. This is useful if you have a macro that you want to modify slightly, but you do not want to lose the original macro.

12-16 Menu and Command Reference

Commands in the Macro menu: (continued)

Command	Description
Run Linked Macro/Script	Sends a DoScript Apple event to the linked program.
Edit Step	Brings up a dialog box which allows you to adjust the values used by the step command. This works only for steps created using a dialog box.
Run Step	Runs the selected step.
Add Comment	Brings up a dialog box which allows you to add comments at the end of the Current Step log.
Set Import Macro	Automatically runs a selected macro immediately after import of GeneScan files.
Clear Step Log	Removes all steps in the Current Step log.

Importing Data from a **13** BioLIMS Database

Chapter Overview

New Feature of Genotyper V. 2.5	Genotyper Software version 2.5 has the ability to read ABI I GeneScan [®] Analysis data from a BioLIMS [®] 2.0 database.	Prism®
	 You can now import data from both GeneScan sample i BioLIMS at the same time into a single document. 	files and
	 Data imported from BioLIMS can be exported to a Gen database after being processed in Genotyper. 	Base
	Note Genotyper v. 2.5 has read-only access to BioLIMS. Hence, results cannot be written back to the BioLIMS database. Instead th stored in individual Genotyper documents, exported as text files, or GenBase [™] database.	, Genotyper ney can be or stored in a
In This Chapter	This chapter describes how to access the BioLIMS [®] database, how to set the preferences, and how to open or process fragment data that is located in the BioLIMS database.	
	Appendix F, "Troubleshooting the BioLIMS database, a Analysis Software Version 3.1 User's Manual (P/N 4306157	;ee ; GeneScan ').
	Торіс	See Page
	Configuring the Macintosh Computer for BioLIMS Database Access	13-2
	Setting Up Access to the BioLIMS Database	13-9
	Importing GeneScan Data From BioLIMS	13-11
	About Server Names	13-15
	Using the Collection Browser Window	13-18

Configuring the Macintosh Computer for BioLIMS Database Access

Sybase or Oracle? This section provides instructions on how to configure the client Macintosh computer (that runs the Genotyper software) for database access.

The BioLIMS database resides on either a Sybase SQL Server or an Oracle Server.

To configure for the	See
Sybase SQL Server	"Configuring for Sybase SQL Server Connection" on page 13-2.
Oracle Server	"Configuring for Oracle Server Connection" on page 13-5.

Sybase SQL **Server Connection**

Configuring for Follow the steps below to configure a Macintosh computer for connection to the Sybase® SQL server.

> **IMPORTANT** The BioLIMS client software for Sybase® must be installed on your Macintosh computer.

IMPORTANT Any time the name, port number, IP address, or host and domain name of the BioLIMS database server is changed, you will need to repeat this procedure.

To configure for Sybase SQL Server connection:

Step	Action
1	Find the interfaces file in the BioLIMS 2.0:BioLIMS Extras:Sybase folder.
	V 🗋 BioLIMS 2.0
	▽ 🗅 Sybase
	▶ 🗅 bin
	▷ □ charsets
	🗋 interfaces
	D locales
2	Open the file with SimpleText or a similar text editing application.

To configure for Sybase SQL Server connection: (continued)

	Step	Action
I	3	Find the lines:
		SYBASE
		query MacTCP mac_ether neuron.apldbio.com 2500
		and edit them as follows:
		 Replace SYBASE by an alias name for the database server (see "About Server Names" on page 13-15).
		 Replace neuron.apldbio.com with the IP address or host and domain name of the server machine.
		 2500 is the default port number for the Sybase database. If necessary, replace 2500 with the port number recommended by your BioLIMS database administrator.
		 Insert a tab space before the start of the second line if there is no tab space already present.
		You can find this information in the interfaces file on the Sybase Server, or your BioLIMS database administrator can provide the information.
	4	If you have access to more than one server, duplicate the two lines and edit them for the other server(s).
		For example, for two servers, one called SYBASE and one called SERVER2, the interfaces file might look like this:
		SYBASE query MacTCP mac_ether neuron.apldbio.com 2500
		SERVER2 query MacTCP mac_ether 192.135.191.128 2025
Ī	5	Save and close the interfaces file.

To configure for Sybase SQL Server connection: (continued)

Step	Action
6	Open the SybaseConfig control panel. This control panel is found in the Control Panels folder in the System folder.
	SybaseConfig Default Server (DSQUERY) SYBASE Network Driver: MacTCP Default Language (LANG) Sybase Interfaces File Help
7	The first time the SybaseConfig control panel is opened, a file browser opens automatically. If a file browser does not open immediately, click the Interfaces Files button to open one.
	Sybase ▼ Charsets interfaces locales ↓ect Desktop ↓ Open Cancel Where is the interfaces file?
8	Use the file browser to locate and open the interfaces file edited in the steps above.
9	Set the Default Language pop-up menu to us_english.
10	Close the SybaseConfig control panel.

Connection

Configuring for Use the program Easy Config to configure your Macintosh computer for Oracle Server connection to the Oracle Server.

> **IMPORTANT** The BioLIMS client software for Oracle must be installed on your Macintosh computer.

IMPORTANT Any time the name, port number, IP address, or host and domain name of the BioLIMS database server is changed, you will need to repeat this procedure.

Note At installation, Easy Config is placed into the BioLIMS 2.0:BioLIMS Extras:Oracle:Applications:Networking folder.

To configure your computer for the Oracle Server connection:



Importing Data from a BioLIMS Database 13-5

To configure your computer for the Oracle Server connection: (continued)

Step	Action
3	Click New.
	The Protocol dialog box appears.
	Protocol What networking protocol do you want to use with this alias?
4	Select TCP/IP and click OK.
	The TCP/IP dialog box appears.
	ТСР/ІР
	Alias Name:
	Server Name: (0r IP address, eg. 129.25.51.36)
	Oracle SID: ORCL (Identifies the Oracle database)
	Cancel OK

To configure your computer for the Oracle Server connection: (continued)

Step	Action
5	Enter text in the fields as follows:
	 Alias Name: Enter an alias name for the database server. (See "About Server Names" on page 13-15.)
	 Server Name: Enter the server name. This may be an IP address or host (and domain name) of the server machine.
	Note This field does not scroll horizontally for display even though it accepts characters typed past the end of the field. If the server name is longer than 20 characters, you may want to enter the end characters first and go back or just use the IP address.
	 Oracle SID: Enter the value of the ORACLE_SID environment variable.
	You can find this information in the tnsnames.ora file on the Oracle Server, or your BioLIMS database administrator can provide you with the information.
6	Click OK to close the TCP/IP dialog box.
7	From the File menu, choose Save Configuration.
8	From the File menu, choose Quit to exit the Easy Config program.
9	Find the application Set Oracle Home.
	Set Oracle Home The application is contained in your BioLIMS 2.0:BioLIMS Extras:Oracle:Applications folder.
	V Discuttors
	About BioLIMS 2.0
	About Sample2DB 2.0 BioLIMS Manager
	BioLIMS Manager SQL Log
	r internet 2.6 ▼ im Oracle
	Applications Networking
	Set Oracle Home
	intervies the second s
	Cine Messages

To configure your computer for the Oracle Server connection: (continued)



Setting Up Access to the BioLIMS Database

Introduction The following procedure describes how to access the BioLIMS database by completing the Set Preferences dialog box.

> Before you can work with the Genotyper software, you must establish a connection to the BioLIMS database. This connection is made through the BioLIMS Access button in the Set Preferences dialog box.

Using the

Preferences Box To set up your preferences:

Step	Action
1	Launch Genotyper v 2.5.
2	Choose Set Preferences under Edit in the main menu.
	The Set Preferences dialog box appears.
	·····
	Set Preferences
	Options for exporting tables:
	Field delimiter: 💿 Tab 🔾 Comma 🔾 Space 🔾 None
	Line delimiter:
	 Additional windows to be opened with main window:
	Dye/lane Plot Macro Statistics
	🔄 Category 🔄 Table 🔄 Step
	• Information to be shown in dye/lane list:
	✓ File name
	M Lane number 🔄 scale lactor 🔄 sample comment
	Automatic options for linked program & document: When exempting Construer: When exempting Construer:
	Open linked document
	When quitting Genotyner: Save linked documents
	Quit linked program
	• Import colors:
	🗹 Blue 🗹 Green 🗹 Yellow
	🗌 Red 👘 Orange 📄 Import Raw
	• Other options:
	Double-clicking runs macros & steps
	BioLIMS Cancel OK

To set up your preferences: (continued)

Step	Action
3	Click the BioLIMS button if you wish to open a connection to the database and save the preferences you have made in the session manager.
	The BioLIMS Preferences dialog box opens.
	Password: eeeeee Save Password Database: biolims2_d25 Server: SYBASE Alias: Untitled
	Open Open Cancel Save
	Enter the requested information and click Open to open a connection.
	Note User entry fields appear gray and will not accept any input if you have already accessed files in BioLIMS through the Choose Channel to Open box (see step 3 on page 13-12). In this case click on the Close button to close the database connection. Now you can re-enter the information into these fields.
4	Click Save to save the information you entered.
5	Click OK in the Set Preferences dialog box.

Importing GeneScan Data From BioLIMS

Introduction After the client Macintosh has been configured for BioLIMS access, you can access files stored in BioLIMS from the File menu of Genotyper v. 2.5.

Accessing Files in BioLIMS

To access files stored in BioLIMS:

Siep	Action
1	Launch Genotyper v. 2.5.
2	From the File menu, point to Import and click on From BioLIMS Database.
	File Edit Analysis Category Table Views Macro Help
	New %N Open %O
	Close %W
	Save %S Save As
	Import From GeneScan File #1
	Locate GeneScan File From BioLIMS Database Re-Import Dye/Iane %D
	Locate in GenBase %B Links
	Lock ✓ Unlock
	Page Setup
	HEINUM APPL

To access files stored in BioLIMS: (continued)

Step	Action		
3	Enter the following information requested by the session manager in the Choose Channel to Open box.		
	 Your user name for the database. 		
	 Your password for your database account. 		
	 The name of the database on the server. (You may have access to more than one database on the server.) 		
	Note For Oracle, this entry is the schema owner and not the database name.		
	 The server name. This is an alias to the database server which is contained in the interfaces file (Sybase) or in the tnsnames.ora file (Oracle). 		
	IMPORTANT All of these text boxes are case sensitive.		
	Choose Channel to Open		
Username			
	Password 📃 🔲 Save Password		
	Database		
	Server		
	Alias Untitled		
	🗌 Open on Launch 🔄 Make Default		
	Cancel Open		
	Click the sheet has labeled Caus Descurred if you want to		
4	Click the check box labeled Save Password if you want to:		
 Save your password so that you do not have to enter i time you open the connection. 			
	 Run AppleScripts that do not contain password information. 		
	☑ Save Password		

To access files stored in BioLIMS: (continued)

Step	Action		
5	If you want the database to open automatically when you launch the Genotyper software, click the check box labeled Open on Launch. Open on Launch		
	Note You must also click the check box labeled Save Password if you want the database to open automatically.		
6	If you intend to use more than one database or user account, enter an alias for this BioLIMS session information. You can use an alias to connect to the database if no database connection is open.		
	Once you enter an alias, click Open to connect to the database.		
7	If you have more than one alias, click the Make Default check box to choose which one appears when you first open the Edit Session dialog box.		
	Note The default alias is the database that opens if you choose File:Import:From BioLIMS Database.		
	Note If both the Make Default and the Save Password boxes are checked, no dialog box will appear when a connection to the server is requested. Since all the information required of the user has been saved, the software will connect to the database automatically.		
8	Use the pop-up menu to add, change, or remove aliases.		

To access files stored in BioLIMS: (continued)

Step	Action			
9	9 Click Open and take one of the following actions:			
	If the login was	Then		
	successful	the Collection Browser window opens. For more information see page 13-19.		
	unsuccessful	an alert dialog box appears.		
		Login to database failed.		
		The database responded with this error message when logging on. Please check that your logon information is correct before you attempt to logon again.		
Check that:	Check that:			
		 All the login information was entered correctly and in the correct case. 		
		 The interfaces file is correctly configured for a Sybase database (page 13-2). 		
		 The tnsnames.ora file is correctly configured for an Oracle database (page 13-5). 		
		 If the connection is still not open, consult Appendix F, "Troubleshooting the BioLIMS Database", in the GeneScan Analysis Software Version 3.1 User's Manual (P/N 4306157). 		

About Server Names

Sybase or Oracle?	The BioLIMS Session Manager decides whether you are connected to
	Sybase SQL Server or to an Oracle Server database by looking at the
name in the Server field in the Session Manager dialog box.	

How Names Are The table below summarizes how names are recognized. Recognized

If the Session Manager sees a Server		
name	It assumes a …	Example
all in uppercase letters	Sybase SQL Server database connection	MOZART
suffixed by ":s" or ":S"	Sybase SQL Server database connection	Offenbach:S
containing any lowercase letters	Oracle Server database	Oramozart
suffixed by ":o" or ":O"	Oracle Server database	SIBELIUS:O

Sybase SQL Example 1 Server Examples If the interfe

If the interfaces file contains this:

MOZART query MacTCP mac_ether mozart.apldbio.com 2500

Note Insert a tab space before the start of the second line if none already exists.

MOZART is recognized as a Sybase SQL Server because the server name is in all uppercase letters.

The Session Manager would look like this:

Username	jane	
Password	•••••• 🗌 Save Pa	assword
Database	biolims2	
Server	MOZART	

Example 2

If the interfaces file contains this:

Offenbach query MacTCP mac_ether mozart.apldbio.com 2500

the Session Manager would look like this:

Username [jane	
Password [•••••	🗌 Save Password
Database [biolims2	
Server	Offenbach :S	

For Offenbach to be recognized as a Sybase SQL Server, the name in the Server field is suffixed with ":S".

Oracle Server	Example 1
Examples	If the tnsnames.ora file contains this:
	Oramozart=(DESCRIPTION= (ADDRESS= (PROTOCOL=TCP)(host=mozart)(port=1521)) (CONNECT_DATA=(SID=WG733)))
	Oramozart is recognized as an Oracle Server because the server name begins with "O".
	The Session Manager would look like this:
	Username j _{ane} Password •••••• 🗌 Save Password
	Database jane

Note The database entry field should contain the name of the schema owner which may be the same as the username.

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Server Oramozart

Example 2

If the tnsnames.ora file contains this:

the Session Manager would look like this:

Username jane	
Password •••••	🗌 Save Password
Database jane	
Server SIBELIUS:0	

For SIBELIUS to be recognized as a Oracle Server, the name in the Server field is suffixed with ":O".

Note The database entry field should contain the name of the schema owner which may be the same as the username.

Using the Collection Browser Window

Applications That Use the Collection	The Collection Browser window is common to the following BioLIMS-aware applications.		
Browser Window	◆ AutoAssembler [™] DNA Sequence Assembly Software.		
	♦ GeneScan [®] Analysis Software.		
	 Factura[™] Feature Identification Software. 		
	 Sample2DB Software. 		
	 Sequencing Analysis Software. 		
	♦ Genotyper [®] Software v. 2.5.		
Ways to Search the Database	Using the Collection Browser window from within Genotyper software, you can search the BioLIMS database for specific collections and fragments.		

The following table lists ways you can search:

Search by	See page
Up to 5 collection-specific criteria	13-21
Up to 14 fragment-specific criteria	13-22

In This Section This subsection includes the following topics.

For this topic	See page
Displaying the Collection Browser Window	13-19
Collection Browser Window Example	13-19
Parts of the Collection Browser Window	13-20
Collection Search Criteria	13-21
Fragment Search Criteria	13-22
Searching the BioLIMS Database	13-26
Displaying the Collection Browser Window

Displaying the To display the Collection Browser window:

If you want to	Then	Result
add a fragment to a Genotyper document to view or analyze	choose Import from the File menu and From BioLIMS Database from the submenu.	The Collection Browser window opens if a database connection has been opened.
		For more information, see "Collection Browser Window Example" on page 13-19.

Collection Browser The following is an example of the Collection Browser window. Window Example

	Criteria pop-up menu		Se	arch button
Collection search criteria pop-up menus and text boxes	Select oriteria to find Collections Collection Creator contains t Collection Name contains t Collection Type is Creation Date any t	Collection Browser		Search
Fragment search criteria pop-up menus and text boxes Split bar	Modification Date any Sequence-Frag Name contains Sample Creator contains Sample Name contains			
Search results	Name Name S00259-373XL/64wSQ/53L(Cust) G00260-373XL/64wSQ/52L(Cust)	Modified May 29 1998 10:41:11 AM May 29 1998 10:36:28 AM	Type project project	Creator
Status line	 ◀ Ⅲ 2 collections found 		Select	Cancel

Importing Data from a BioLIMS Database 13-19

Window

Parts of the
Collection BrowserThe table below describes the parts of the Collection Browser window
that were labeled in the figure above.

Description of the Collection Browser window:

Item	Description
Criteria pop-up menu	Use this pop-up menu to specify the search criteria visible on the Collection Browser window.
	Note If you only intend to use a subset of criteria, setting only that subset visible helps to reduce clutter in the window. The search results are the same whether a criterion is invisible or blank and visible.
Search button	Click this button to query the BioLIMS database.
	Note All collections in the database will be displayed if you click on Search without first specifying any search criteria.
	Note You can also press the Return key to begin a search.
Collection search criteria pop-up menus	Use these pop-up menus and text boxes to define the collection criteria of the search.
and text boxes	IMPORTANT Only those fragments that match each and every criterion you specify are returned. That is, search criteria are combined using the logical AND operation.
	For more information, see "Collection Search Criteria" on page 13-21.
Fragment search criteria pop-up menu	Use these pop-up menus and text boxes to define the fragment criteria of the search.
and text boxes	IMPORTANT A collection is returned if one or more of the fragments contained in it fulfill all of the specified fragment criteria.
	Note Only fragments meeting search criteria will be displayed in the Collection Browser window.
	For more information, see "Fragment Search Criteria" on page 13-22.

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Description of the Collection Browser window: (continued)

Item	Description
Split bar	Drag this bar to alter the relative amount of space allocated to the top and bottom portions of the Collection Browser window.
Search results	After a successful query, found sample files are listed in this area as Name, Modification date, type, and Creator.
Status line	Search results, error messages, and other important information is reported here.
	For example, the Status Line lists how many collections were returned in a search.

Collection Search The table below shows the collection search criteria. The collections Criteria returned by the Collection Browser window must match all of the collection criteria and contain at least one fragment that matches all of the fragment criteria.

Allowed Collection Search Criteria:

Criterion	Pop-up Menu Choices	Allowed Text	Description
Collection Creator	♦ is♦ starts with	up to 255 characters	Name of the creator/owner of the collection
	 ends with 		
	 contains 		
Collection	♦ is	up to 31	Name of the
Name	 starts with 	characters	collection.
	 ends with 		
	♦ contains		
Collection Type	♦ any	NA	Collection type.
	♦ run		Default is any
	 project 		menu item.
	♦ other		

Importing Data from a BioLIMS Database 13-21

Allowed Collection Search C	Criteria:	(continued)
-----------------------------	-----------	-------------

Criterion	Pop-up Menu Choices	Allowed Text	Description
Creation Date	anyisbefore	date — set with arrow buttons using the format mm/dd/yy	Date the collection was created.
	◆ after◆ between		
Modification Date	 any is before after between 	date — set with arrow buttons using the format mm/dd/yy	Date the collection was last modified.

Fragment Search The table below shows the fragment search criteria. The collections Criteria returned by the Collection Browser window must contain at least one fragment that matches all of the specified fragment criteria.

Fragment Search Criteria:

Criterion	Pop-up Menu Choices	Allowed Text	Description
Sequence-Frag Name	 is starts with ends with contains 	up to 31characters including letters, numbers, and punctuation	Name of the fragment. This is the file name entered in the Sample
		Cannot use colons (:).	Sheet.
Sample Creator	 is starts with ends with contains 	up to 255 characters including letters, numbers, and punctuation	Name of the person responsible for the run.

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Criterion	Pop-up Menu Choices	Allowed Text	Description
Sample Name	 is starts with ends with contains 	up to 255 characters including letters, numbers, and punctuation	Sample name from the Sample Sheet.
Instrument Name	 is starts with ends with contains 	up to 255 characters including letters, numbers, and punctuation	Set in the General Settings Preferences of the Data Collection software.
Instrumentation	 any gel capillary 	NA	Whether the sample was run on a gel or capillary instrument.
Start Collect Date	 any is before after between 	date— set with arrow buttons using format mm/dd/yy	Date data collection began.
End Collect Date	 any is before after between 	date — set with arrow buttons using format mm/dd/yy	Date data collection ended.
Gel Path	 is starts with ends with contains 	up to 255 characters including letters, numbers, and punctuation	The full path name to the original gel file, e.g., Hard Disk:Data: GelRuns:L28t.

Fragment Search Criteria: (continued)

Importing Data from a BioLIMS Database 13-23

Fragment Sea	rch Criteria:	(continued)
--------------	---------------	-------------

Criterion	Pop-up Menu Choices	Allowed Text	Description
Sample Info	 is starts with ends with contains 	up to 255 characters including letters, numbers, and punctuation	Sample information from the Sample Sheet.
Sample Comment	 is starts with ends with contains 	up to 255 characters including letters, numbers, and punctuation	Comment from the Sample Sheet.
Size Data	 is present is not present does not 	NA	Is present means that one or more dyes contain sizing information.
	apply		Is not present means none of the dye sample contain sizing information.
Size Calling	 done not done does not apply 	NA	Done means sample file has completed size calling indicated by a size curve.
			Not done indicated by a missing size curve.
% Matched Peaks	 any equal to less than greater than between 	0—100	Percentage based on size standard matched peaks divided by size standard defined peaks.

13-24 Importing Data from a BioLIMS Database

Fragment Search Criteria: (continued)

Criterion	Pop-up Menu Choices	Allowed Text	Description
Offscale Data	 present does not apply 	NA	Present means the analyzed range contains off-scale dye sample peaks.

Importing Data from a BioLIMS Database 13-25

Searching the
BioLIMS DatabaseFollow these steps to use the Collection Browser window to search the
BioLIMS database for specific collections and fragments.

To search the BioLIMS database:

Step	Action
1	Note From the Select Criteria pop-up menu, select the criteria by which you want to search
	Note To list all of the items in the BioLIMS database, perform the search with no criteria specified. For large databases, this process may be slow.
	Collection Browser

	Co	llectio	on Browser	<u> </u>
Select crit	teria Collection Creator	h Frag	gments	Search
Collection Sequence-	 Vai Collection Name Collection Type Creation Date Fra 			
Name I IIII	 Sequence-Frag Name Sample Creator Sample Name Instrument Name Instrument Name End Collect Date Gel Path Sample Info Sample Comment Size Data Size Calling Matched Peaks Offscale Data 	odified	Type Cr	reator
ady			Select	Cancel 🛷
2	To use the pop-up mer	าน:		
	Choose menu items		To define the search by	See page
	above the horizontal li	ine	Collection Search Criteria	13-21
	below the horizontal li	ne	Fragment Search	13-22

13-26 Importing Data from a BioLIMS Database

To search the BioLIMS database: (continued)

Step	Action
•	

The following is an example of the Collection Browser window showing all five collection search criteria and all 14 fragment search criteria.

	Colle	ection Browser		
Select criteria 🗦	to find Collections wit	th Fragments		Search
Collection Creator Collection Name	contains 🗘			
Collection Type Creation Date	is any 🔹	any 文		
Modification Date	any 🗘			
Sequence-Frag Name Sample Creator	contains 💠			
Sample Name Instrument Name	contains 🗘			
Instrumentation Start Collect Date End Collect Date	is any 🗘 any 🗘	any ᅌ		
Gel Path Sample Info	contains 🗘			
Size Data Size Calling	is present has completed			
% Matched Peaks Offscale Data	any 🗘			*
Name	М	odified	Sample Name	Type
Ready			Select	► Cancel
Use the p	op-up menus a	nd text fields t	o define your	search quer
Refer to " Search C criteria.	Collection Sear riteria" on page	ch Criteria" on 13-22, for det	page 13-21, a alls about the	and "Fragme search
When you are satisfied with the search, click Search.				
The resul	ts of the search	appear in the	lower portion	of the windo
Note must mat fragment	Collections retu ch all of the coll that matches al	rned by the Co lection criteria	ollection Brow and contain a ent criteria.	ser window t least one

Importing Data from a BioLIMS Database 13-27

To search the BioLIMS database: (continued)



13-28 Importing Data from a BioLIMS Database

To search the BioLIMS database: (continued)

Step	Action	
5	Select one or more fragments. If you wish to selec fragment file, refer to the procedure below.	t more than one
	If	Then
	The fragment files you wish to select are listed in sequence	Hold the shift key and click on the file
	Collection Browser	names.
	Instrumentation is gel +	
	Name Modified Sample Name Modified St. ANE RUN 2ND 4/18 Aug 06 1998 09:58:30 AM	
	₩0 0.1 ⊆ Sample File Sep 09 1998 05:15:40 PM ₩0 02_Sample File Aug 06 1998 09:54:25 AM ₩0 03_S5mple File Aug 06 1998 09:54:27 AM	
	Image: Source of the state of the	
	Ot - sampler file Aug 06 1596 055-055-054 AV Coll Ba.Sample File Aug 06 1598 0574-056 AM O 05_Sample File Aug 06 1598 0574-056 AM O 05_Sample File Aug 06 1598 0574-056 AM	
	10_Sample File Aug 06 1998 09 :54 :40 AM	
	Collection 96 LAME KOM 2/10 4/18 contains 95 Select Cancel	
	The fragment files you wish to select are not listed in sequence	Hold the command key (ℋ) and click
	Collection Browser	on the file
	Instrumentation is gel 3	names.
	Name Modified Sample Name ▼ 96 LANE RUN 2ND 4/18 Aug 06 1998 09:58:30 AM1 ▲	
	Image: Sep 09 1998 05:15:40 PM Image: Sep 09 1998 05:15:40 PM Image: Sep 09 1998 05:15:40 PM Image: Sep 09 1998 05:425 AM Image: Sep 09 1998 05:427 AM Image: Sep 09 1998 05:427 AM Image: Sep 09 1998 05:427 AM Image: Sep 09 1998 05:428 AM	
	Orizontip/File Aug 06 1598 03:54:30 AM Cold-Sample File Aug 06 1598 03:54:32 AM Ob_Sample File Aug 06 1598 03:54:32 AM	
	OTSample File Aug 06 1998 09:54:34 Al1 W 05.Sample File Aug 06 1998 09:54:35 Al1 D 05.Sample File Aug 06 1998 09:54:33 Al1	
	Collection '96 LANE RUN 2ND 4/18' contains 95 Select Cancel	
^	Click Select in the Collection Browser window or n	ross Boturn on

Importing Data from a BioLIMS Database 13-29

Importing and Processing a 5th Dye

Chapter Overview

New Feature of Genotyper V. 2.5	Genotyper Software version 2.5 has the ability to read and process GeneScan sample files containing a 5th dye. Further, Genotyper processed data with a 5th fluorescent dye can be exported to a GenBase database.				
	Note	Reagent kits containing a 5th dye may be available at a fut	ture date.		
In This Chapter	This c Gene	hapter describes how to import, view, analyze, and ex Scan data containing a 5th fluorescent dye.	(port		
	Торі	C	See Page		
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	View	ing Data	14-4		
	Anal	yzing and Exporting Data	14-7		

Importing and Processing a 5th Dye 14-1

Importing 5th Dye Data

Procedure for Data containing a 5th dye can be imported, just like data on any of the Importing 5th Dye other four dyes, from either GeneScan sample files or a BioLIMS Data database.

> You must first choose the dyes you wish to import from the Set Preferences dialog box. You can access this dialog box from the Edit pull-down menu.

To import 5th dye data:

Step	Action			
1	Select Set Preferences from the Edit pull-down menu of Genotyper Software v. 2.5.			
	The Set Preferences dialog box appears.			
2	Choose the dyes by clicking their respective boxes under Import colors in the Set Preferences dialog box.			
	Note The 5th dye is designated Orange.			
	Set Preferences			
	• Options for exporting tables:			
	Field delimiter: 🖲 Tab 🔾 Comma 🔾 Space 🔾 None			
	Line delimiter: 💿 CR 🔘 CR/LF 🔘 LF			
	 Additional windows to be opened with main window: 			
	Dye/lane Plot Macro Statistics			
	🗌 Category 🔲 Table 🔤 Step			
	• Information to be shown in dye/lane list:			
	I lano numbor □ Scalo factor □ Sample Info			
	Lane number State factor Sample comment			
	• Automatic options for inneed program & document. When opening Genotyper: 🔲 Open linked program			
	Open linked document			
	When guitting Genotyper: 🔲 Save linked documents			
	☑ Quit linked program			
	• Import colors:			
	☑ Blue ☑ Green ☑ Yellow			
	Ked M Orange I Import Raw			
	• Other options: Jun uye			
	BioLIMS Cancel OK			

14-2 Importing and Processing a 5th Dye

To import 5th dye data: (continued)

Step	Action			
3	Click OK.			
	The Set Preferences box goes away and you are returned to the Main window.			
4	From the File menu, point to Import and click on either From GeneScan or From BioLIMS Database.			
	File Edit Analysis Category Table Views Macro Help			
	New %N Open %O			
	Close #W			
	Save as			
	Import From GeneScan File %I			
	Re-Import Dye/Iane %D			
	Locate in GenBase %B Links			
	Lock Vunlock			
	Page Setup Print %P			
	Quit %Q			

Viewing Data

Two Methods to View Data

Two Methods to There are two ways to view dye data in the Main window.

- Use the Menu bar or
- Use the Dye buttons on the Main window.

Using the Menu Bar

To use the menu bar to view dye data:

Step	Action						
1	From the Edit men view.	u, point	to Sele	ct and clic	ck on the	e dye you	wish to
	Edit						
	Cut Cut Copy Paste Clear Select All	#X ₩C ₩V ₩A					
	Select Copy Window Edit Cell	жЕ	Blue Green Yellow				
	Find Find Next	₩F ≋G	Red Orange				
	Mark Unmark	₩M ℋU					
	Set Preferences Show Clipboard						
	Data for that dye a window.	ire grap	hically o	displayed	as peal	ks in the n	nain

14-4 Importing and Processing a 5th Dye

To use the menu bar to view dye data: (continued)

Step	Action		
2	To display data for more than one dye in the same window,		
	Step	Action	
	1	From the Edit menu, point to Select and hold down the shift key.	
		A + symbol appears to the left of each dye in the menu window. This indicates that data from more than one dye can be selected for viewing.	
		Edit Undo Click Label %Z Cut %X Copy %C Paste %V Clear %E Select + Blue Edit Cell %E Find %E Find %E Find %E	
	2	With the shift key held down, click on a dye. The data for the first dye selected is graphically displayed in the Main Window.	
	3	Repeat step 2 to add more dyes to the same Main window.	
		Data from the each dye selected is graphically displayed in the same window as the first dye.	

Using the Dye Buttons

To use the dye buttons to view data:

lick the dye buttons on the Main window to display the dat ach dye.	a for
Image: state	
'e 50 100 150 200 250 300 350	1000 500
Everything All peaks from scan 0 to 32000 in R/B/G/V/0	•
Image: Current Step Log Image: Select green lanes	4
Everything All peaks from scan 0 to 32000 in R/B/	3/V/0

14-6 Importing and Processing a 5th Dye

To use the dye buttons to view data: (continued)

Step	Action
2	To display data from more than one dye in the same window, hold down the shift key and click on the buttons of the dyes you want to view.
	Data for the dyes you selected will be displayed in the same window.
	untitled 2
	B Y 071347-08 Daughter 7 Blue \$007 G R 071347-08 Daughter 7 Green \$007 0 071347-08 Daughter 7 Yellow \$007 0 071347-08 Daughter 7 Orange Y
	50 100 150 200 250 300 350
	Everything All peaks from scan 0 to 32000 in R/B/G/V/0
	Current Step Log And select green lanes And select yellow lanes

Analyzing and Exporting Data

Analyzing Data	Data containing a 5th dye can be analyzed just like the other four dyes.
Exporting Data	The final results from the Genotyper table can be exported either:
	♦ To a GenBase database
	♦ As text files.

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Printed in the USA, 01/2001 Part Number 904648D

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