Genotyper® 3.5 NT Software

User's Manual

PE Biosystems

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About Genotyper Software

1

Chapter Overview

Introduction This chapter describes ABI PRISM™ Genotyper® 3.5 NT software, the components of the ABI PRISM Genotyping Software System, and requirements for installing and starting the Genotyping software.

In This Chapter This chapter contains the following topics:

Topic	See Page
Overview of ABI Prism Genotyping Software	1-2
Registering the Genotyper Software	1-5
Hardware and Software Requirements	1-6
Converting Macintosh Computer Sample Files	1-7
Installing and Starting the Genotyper Software	1-10
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Overview of ABI PRISM Genotyping Software

Definition

The Genotyper software is an 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 databases for storage, spreadsheets for statistical analysis, or linkage analysis software.

New Features

The Genotyper 3.5 NT software has two new features.

Feature	Description
The ability to read ABI PRISM® GeneScan® Analysis Software data from a BioLIMS™ 2.0 database	You can now import data from GeneScan sample files and from the BioLIMS database at the same time in a single document. **Note** Genotyper 3.5 NT software has read-only access to the BioLIMS database. Hence, Genotyper results cannot be written back to the BioLIMS database. Instead, they can be stored in individual Genotyper Documents or exported as text files.
The ability to read and process GeneScan Analysis Software sample files containing a 5th dye.	Data containing a 5th dye can be analyzed just like the other four dyes. The final results from the Genotyper table can be exported as text files.

How You Can Use the Genotyper Software

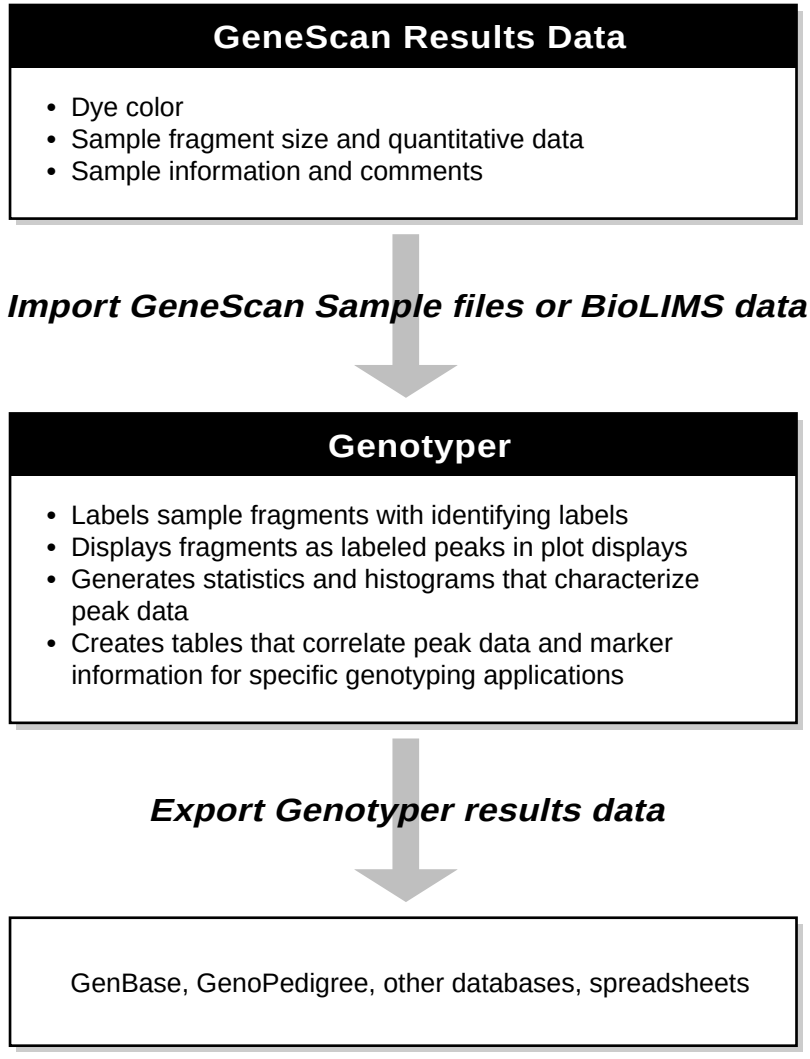
The following table lists some genetic research projects that the Genotyper software, as well as the other components of the ABI PRISM Genotyping Software System, can automate and assist.

For more information on ABI PRISM Genotyping Software System components, see“Registering the Genotyper Software” on page 1-5.

Research project	Activities
Microsatelite 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.

How the Genotyper Software Works

The following figure shows how the Genotyper software analyzes imported ABI PRISM® GeneScan Analysis Software sample files.



Registering the Genotyper Software

Why Register

When you register your copy of the Genotyper software you become eligible for the following:

- Telephone and field service support from PE Biosystems for 100 days from the date of shipment.
- Purchase upgrades to the software at a lower price than it would cost you to purchase a new upgraded package.

How to Register

To register, fill out the registration card included in this package and return it to PE Biosystems.

For PE Biosystems technical support telephone and address information, see “How To Get Help” on page 1-19.

IMPORTANT These privileges are available only if you have returned your registration card.

Hardware and Software Requirements

Compatibility With Previous Versions

The Genotyper 3.5 NT software can read files created by Genotyper 1.x and 2.x on the Macintosh® computer. You need to use the AppleScript® software provided with the Genotyper software installer CD-ROM to convert the Macintosh computer files to Windows format.

Files created with Genotyper 3.5 NT software can be read with the Genotyper software 2.5 Macintosh version only. You need to copy the files from the Windows computer to the Macintosh computer, run the Win-to-Mac AppleScript and then open the files using the Genotyper software (see “Converting Macintosh Computer Sample Files” on page 1-7).

Genotyper (Macintosh) template macros containing the Add rows to Table and Add rows to Link will not work with Genotyper software since these features are not available in this version. Similarly, Macintosh macros containing steps related to the GenBase™ Genotyping Software and the GenoPedigree® software will not work using Genotyper 3.5 NT software.

Hardware and Software Requirements

The following table describes the components your computer system requires to run Genotyper 3.5 NT software.

System Component	Minimum Requirement	Recommended
Computer	Dell®	
Monitor	A 640 x 480 pixels size monitor **Note** Color monitors are useful, but not required.	A seventeen inch monitor
Operating System	Windows NT v 4.0	

Converting Macintosh Computer Sample Files

About Converting Files

When you insert the Genotyper 3.5 NT software CD-ROM into a Macintosh® computer's CD-ROM drive, a folder appears that contains two applications. Use these applications to change sample files created on the Macintosh computer to files that can be read by an NT-based computer, and to change files that were created on an NT-based computer so that they can be read by a Macintosh computer.

The AppleScripts can connect Genotyper documents or templates in addition to sample files. The Genotyper documents will have an *.GTA* extension.

Converting Macintosh Files to Windows Files

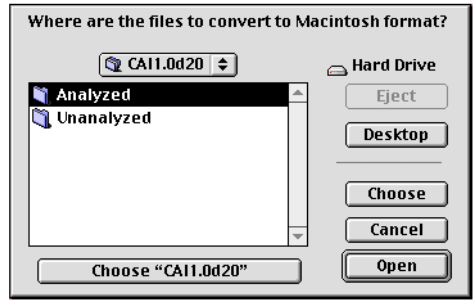
To convert Macintosh computer sample files for use on the NT-based computer.

Step	Action
1	Double-click the Sample File Mac to Win icon to start the application. The following dialog box appears.
2	Click the Run button and the following directory dialog box appears.

Step	Action
3	Navigate to the folder that contains the GeneScan sample files or Genotyper templates that you want to convert and click the Choose button. If there are no problems, the program will perform the task and automatically quit. When you open the folder, the sample files will have the extension *.GTA*.

Converting Windows Files to Macintosh Files

To convert NT-based computer sample files and templates, for use on the Macintosh computer:

Step	Action
1	Double-click the Sample File Win to Mac icon to start the application. The following directory dialog box appears. 

Step	Action
2	Navigate to the folder that contains the sample files or templates that you want to convert and click the Choose button. If there are no problems, the program will perform the task and automatically quit. When you open the folder, you can double-click the sample files or templates to open them using the Genotyper software on a Macintosh computer.

Installing and Starting the Genotyper Software

CD-ROM Contents

IMPORTANT Do not work off of the CD-ROM.

The Genotyper software comes on a CD-ROM. The contents of the CD-ROM are as follows:

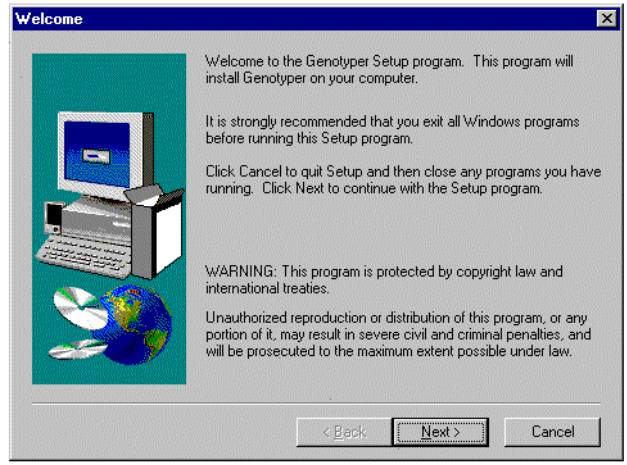
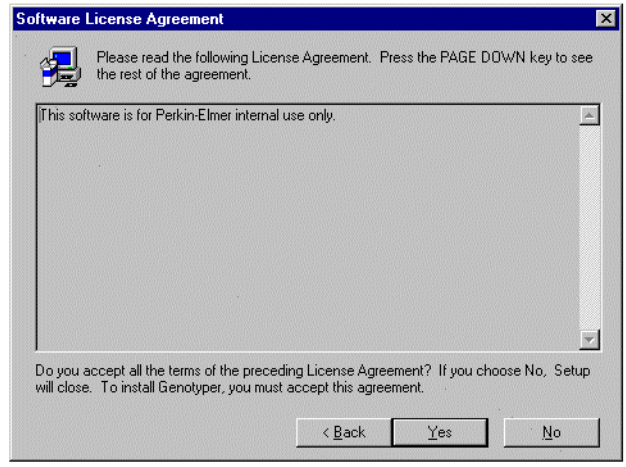
Contents	Includes
Genotyper program installer	♦ LMS v 2 templates. ♦ Electronic (pdf) version of the user's manual and the tutorial. ♦ A Macintosh partition containing the AppleScripts.
Tutorials and Examples	

Installing and Starting the Genotyper Software

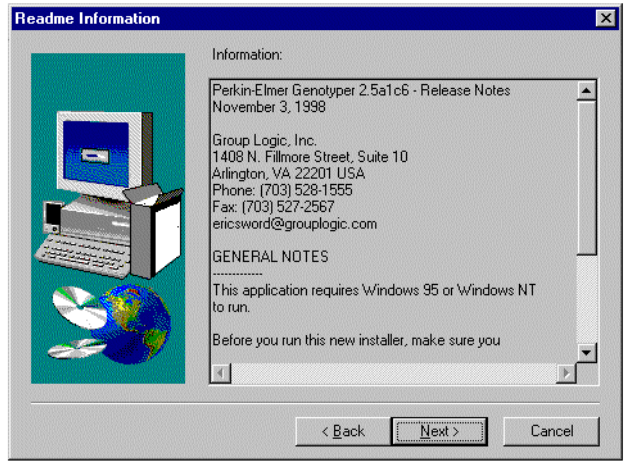
To install and start the Genotyper software:

Step	Action
	Installing the Genotyper Software
1	Insert the Genotyper 3.5 NT software CD-ROM into the computers CD-ROM drive.
2	Double-click the Genotyper software installer icon.

To install and start the Genotyper software: *(continued)*

Step	Action
3	When the Welcome window appears, click Next. 
4	The Software License Agreement window appears.  This window contains important information that you should read. Use the scroll bar to page down to see the rest of the license agreement. After you have read the license agreement, click Yes.

To install and start the Genotyper software: *(continued)*

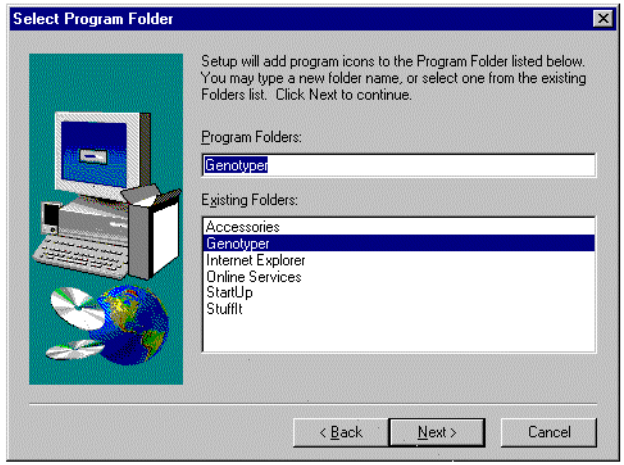
Step	Action
5	The Readme Information window appears. Click Next. 

To install and start the Genotyper software: *(continued)*

Step	Action
6	The Choose Destination Location window appears. Take the following action: **If...** / **Then...** you want to choose a new destination directory — click Browse. you want to accept the directory that appears in the Destination Directory box — click Next.

To install and start the Genotyper software: *(continued)*

<table>
<tr><th>Step</th><th>Action</th></tr>
<tr><td>7</td><td>The Select Program Folder window appears. Click Next.

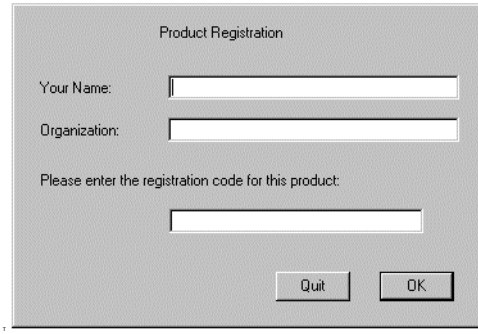
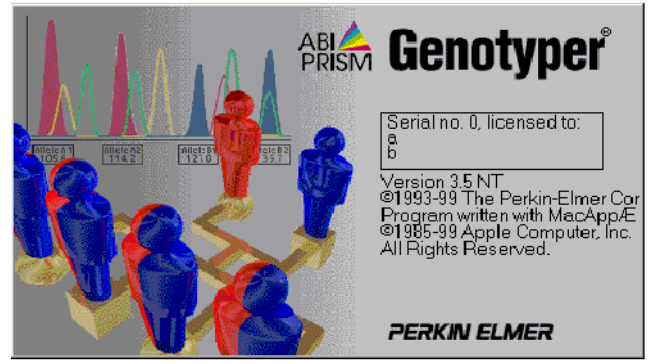
 

A progress bar appears and the Genotyper software is installed in the destination directory you choose.</td></tr>
<tr><td colspan="2">Starting the Genotyper Software</td></tr>
<tr><td>1</td><td>Take the following action:

<table>
<tr><th>You can either...</th><th>Result</th></tr>
<tr><td>double-click the Genotyper icon.

</td><td rowspan="2">The first time you start the Genotyper software, the Product Registration dialog box appears (see below).</td></tr>
<tr><td>click Start, point to Programs, point to Genotyper, and point to Genotyper program.</td></tr>
</table>
</td></tr>
</table>

To install and start the Genotyper software: *(continued)*

Step	Action
	
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 found on your registration card. The Genotyper software then verifies the code. 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.  You are now ready to use the Genotyper software.

Technical Support

To Reach Us On the Web

PE Biosystems' web site address is http://www.perkin-elmer.com/ab

We strongly encourage you to visit our web site for answers to frequently asked questions, and to learn more about our products. You can also order technical documents and/or an index of available documents and have them faxed to you through our site (see the "Fax-on-Demand" section below).

Hours for Telephone Technical Support

In the United States and Canada, technical support is available at the following times.

Product	Hours
Chemiluminescence	9:00 a.m. to 5:00 p.m. Eastern Time
LC/MS	9:00 a.m. to 5:00 p.m. Pacific Time
All Other Products	5:30 a.m. to 5:00 p.m. Pacific Time

See the "Regional Offices Sales and Service" section below for how to contact local service representatives outside of the United States and Canada.

To Reach Us by Telephone or Fax in North America

Call Technical Support at 1-800-831-6844, and select the appropriate option (below) for support on the product of your choice at any time during the call. (To open a service call for other support needs, or in case of an emergency, press 1 after dialing 1-800-831-6844.)

For Support On This Product	Dial 1-800-831-6844, and...
DNA Synthesis	Press: 21 / FAX: 650-638-5981
Fluorescent DNA Sequencing	Press: 22 / FAX: 650-638-5891
Fluorescent Fragment Analysis (includes GeneScan applications)	Press: 23 / FAX: 650-638-5891

<table>
<tr><th>For Support On This Product</th><th>Dial 1-800-831-6844, and...</th></tr>
<tr><td>BioLIMS</td><td><table><tr><th>Press</th><th>FAX</th></tr><tr><td>25</td><td>650-638-5891</td></tr></table></td></tr>
<tr><td>Integrated Thermal Cyclers</td><td><table><tr><th>Press</th><th>FAX</th></tr><tr><td>24</td><td>650-638-5891</td></tr></table></td></tr>
<tr><td>PCR and Sequence Detection</td><td><table><tr><th>Press</th><th>FAX</th></tr><tr><td>5, or call
1-800-762-4001, and press 1 for PCR, or 2 for Sequence Detection</td><td>203-761-2542</td></tr></table></td></tr>
<tr><td>Peptide Synthesis</td><td><table><tr><th>Press</th><th>FAX</th></tr><tr><td>31</td><td>650-638-5981</td></tr></table></td></tr>
<tr><td>Protein Sequencing</td><td><table><tr><th>Press</th><th>FAX</th></tr><tr><td>32</td><td>650-638-5981</td></tr></table></td></tr>
<tr><td>Chemiluminescence</td><td><table><tr><th>Telephone</th><th>FAX</th></tr><tr><td>1-800-542-2369 (U.S. only), or
1-617-271-0045 (Tropix)</td><td>617-275-8581 (Tropix)
9:00 a.m. to 5:00 p.m. ET</td></tr></table></td></tr>
<tr><td>LC/MS</td><td><table><tr><th>Telephone</th><th>FAX</th></tr><tr><td>1-800-952-4716</td><td>650-638-6223
9:00 a.m. to 5:00 p.m. PT</td></tr></table></td></tr>
</table>

Fax-on-Demand

Free 24-hour access to PE Biosystems' technical documents is available by fax.

You can access Fax-on-Demand documents through the internet or by telephone:

If you want to order...	Then...
through the internet	Use http://www.perkin-elmer.com/fod You can search for documents to order using keywords. Up to five documents can be faxed to you by title.
by phone from the United States or Canada	a. Call 1-800-487-6809 from a touch-tone phone. Have your fax number ready. b. Press 1 to order an index of available documents and have it faxed to you. Each document in the index has an ID number. (Use this as your order number in step "d" below.) c. Call 1-800-487-6809 from a touch-tone phone a second time. d. Press 2 to order up to five documents and have them faxed to you.
by phone from outside the United States or Canada	a. Dial your international access code, then 1-650-596-4419, from a touch-tone phone. Have your complete fax number and country code ready (011 precedes the country code). b. Press 1 to order an index of available documents and have it faxed to you. Each document in the index has an ID number. (Use this as your order number in step "d" below.) c. Call 1-650-596-4419 from a touch-tone phone a second time. d. Press 2 to order up to five documents and have them faxed to you.

To Reach Us by E-Mail

Contact technical support by e-mail for help in the following product areas.

For this product area	Use this e-mail address
Chemiluminescence	info@tropix.com
Genetic Analysis	galab@perkin-elmer.com
LC/MS	apisupport@sciex.com
PCR and Sequence Detection	pcrlab@perkin-elmer.com
Protein Sequencing, Peptide and DNA Synthesis	corelab@perkin-elmer.com

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If you are outside the United States and Canada, you should contact your local PE Biosystems' service representative.

The Americas	
United States PE Biosystems 850 Lincoln Centre Drive Foster City, California 94404 Tel: (650) 570-6667 (800) 345-5224 Fax: (650) 572-2743	Canada (Mississauga, Ontario) Tel: (905) 821-8183 (800) 668-6913 Fax: (905) 821-8246
	Latin America (Del.A. Obregon, Mexico) Tel: (305) 670-4350 Fax: (305) 670-4349

Europe	
Austria (Wien) Tel: 01 602 3101 Fax: 01 602 5174	Denmark (Allerød) Tel: 48 100 400 Fax: 48 100 401
Benelux (Nieuwerkerk a/d IJssel, Netherlands) Tel: 31(0) 180 331400 Fax: 31(0) 180 331409	Finland (Espoo) Tel: 09 751 72 700 Fax: 09 751 72 701
Chekia Rep. (Praha) Tel: 2 61 22 21 64 Fax: 2 61 22 21 68	France (Paris) Tel: 33-1 69 59 85 85 Fax: 33-1 69 59 85 00

Europe *(continued)*	
Germany (Weiterstadt) Tel: (0) 6150/ 101 0 Fax: (0) 6150/ 101 101	South Africa (Johannesburg) Tel: 27 11 478 0411 Fax: 27 11 478 0349
Hungary (Budapest) Tel: 36-1-258-8410 Fax: 36-1-256-9802	Spain (Madrid) Tel: (1) 806 1200 Fax: (1) 804 0414
Italy (Milano) Tel: (039) 23831 Fax: (039) 2383490	Sweden (Sundbyberg) Tel: (0)8 619 4400 Fax: (0)8 619 4401
Norway (Oslo) Tel: (0) 22 02 1500 Fax: (0) 22 02 1501	Switzerland (Rotkreuz) Tel: (0) 41 799 7708 Fax: (0) 41 790 0676
Poland (Warszawa) Tel: (48 22) 866 40 10 Fax: (48 22) 866 40 20	United Kingdom (Warrington, Cheshire) Tel: (01925) 825650 Fax: (01925) 282502
Portugal (Lisboa) Tel: (351-1) 386 0997 Fax: (351-1) 386 1000	All Other European Countries, Middle East/West Asia, Africa (Langen, Germany) Tel: 49 6103 708 301 Fax: 49 6103 708 310
Russia (Moskva) Tel: 095 935 8888 Fax: 095 564 8787	

Japan
Japan (Chiba) Tel: (0473) 80 8500 Fax: (0473) 80 8505

Eastern Asia, China, Oceania	
Australia (Scoresby, Victoria) Tel: (03) 9212 8585 Fax: (03) 9212 8502	Malaysia (Kuala Lumpur) Tel: 60 3 758 1118 Fax: 60 3 754 9043
China (Beijing) Tel: 86 10 6238 1156 Fax: 86 10 6238 1162	Singapore Tel: 65 896 2118 Fax: 65 896 2147
Hong Kong Tel: 852 2756 6928 Fax: 852 2756 6968	Taiwan (Taipei Hsisn) Tel: 886 2 698 3505 Fax: 886 2 698 3405
Korea (Seoul) Tel: 822 592 7238 Fax: 822 532 4908	Thailand (Bangkok) Tel: 662 719 6406 Fax: 662 319 9788

Planning Genotyper Applications 2

Chapter Overview

Introduction This chapter discusses techniques for collecting and preparing sample data that will help you improve the overall quality of the GeneScan® Analysis Software files you import into the Genotyper® 3.5 NT software. It also discusses how to plan for use of the Genotyper software features in your genotyping application.

In This Chapter This chapter contains the following topics:

Topic	See page
Preparing Sample Data for the Genotyper Software	2-2
Completing a GeneScan Analysis Software Sample Sheet	2-3
Planning for Automation	2-6

Preparing Sample Data for the Genotyper Software

Introduction

The Genotyper software analyzes the results of fragment analysis data collected by an ABI PRISM® instrument, and generated by the GeneScan Analysis Software.

Perfecting techniques for preparing fragment samples, collecting sample data, and using the GeneScan Analysis Software to size and quantify fragments will simplify automation of many the Genotyper software 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 the Genotyper software plot displays.

When preparing fragment samples for eventual sizing and quantitation by the GeneScan Analysis Software, 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 the GeneScan Analysis Software, see the *GeneScan Chemistry Guide*.

Optimizing Data Collection

Optimizing run conditions on your ABI PRISM instrument will ensure a higher quality of fragment data.

- Making sure gel or capillary run parameters are consistent from run-to-run.
- Choosing the right Matrix for the right type of gel or capillary polymer and run parameters.

For more information on optimizing run conditions, see the user's manual for the ABI PRISM instrument that you are using.

Completing a GeneScan Analysis Software Sample Sheet

Introduction

You must completely fill out a GeneScan Analysis Software Sample Sheet before running samples on your ABI PRISM instrument (see "GeneScan Sample Sheet Example" below.

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

GeneScan Sample Sheet Example

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

BL6b - Sample Sheet

#	Used	File Name	Sample Name	Dye	Std	Sample Info	Comment	A	P
1	☒		1347-02	B		1347-02	Panel 15 FAM	☒	☐
				G		1347-02	Panel 15 TET	☒	☐
				Y		1347-02	Panel 15 HEX	☒	☐
				R	◆	GS-350	Size Standard	☒	☐
2	☒		1347-01	B		1347-01	Panel 15 FAM	☒	☐
				G		1347-01	Panel 15 TET	☒	☐
				Y		1347-01	Panel 15 HEX	☒	☐
				R	◆	GS-350	Size Standard	☒	☐
3	☒		884-15	B		884-15	Panel 15 FAM	☒	☐
				G		884-15	Panel 15 TET	☒	☐
				Y		884-15	Panel 15 HEX	☒	☐
				R	◆	GS-350	Size Standard	☒	☐
4	☒		884-16	B		884-16	Panel 15 FAM	☒	☐
				G		884-16	Panel 15 TET	☒	☐
				Y		884-16	Panel 15 HEX	☒	☐
				R	◆	GS-350	Size Standard	☒	☐
5	☒		1340-01	B		1340-01	Panel 15 FAM	☒	☐
				G		1340-01	Panel 15 TET	☒	☐
				Y		1340-01	Panel 15 HEX	☒	☐
				R	◆	GS-350	Size Standard	☒	☐
6	☒		1340-01	B		1340-01	Panel 15 FAM	☒	☐
				G		1340-02	Panel 15 TET	☒	☐
				Y		1340-02	Panel 15 HEX	☒	☐
				R	◆	GS-350	Size Standard	☒	☐

How the Genotyper Software Uses Sample Sheet Information

Sample Sheet information from the GeneScan Analysis Software is essential for associating the nature of sample fragments with individual dye/lanes and tables in the Genotyper software.

For example, the figure below shows how the Genotyper software incorporates information entered in the Sample Info and the File Name fields of a GeneScan Analysis Software Sample Sheet into the Genotyper software tables.

GeneScan Analysis Software Sample Sheet

BL6b - Sample Sheet

#	Used	File Name	Sample Name	Dye	Std	Sample Info	Comment	A	P
1	☒		1347-02	B		1347-02	Panel 15 FAM	☒	
				G		1347-02	Panel 15 TET	☒	
				Y		1347-02	Panel 15 HEX	☒	
				R	◆	GS-350	Size Standard	☒	
2	☒		1347-01	B		1347-01	Panel 15 FAM	☒	
				G		1347-01	Panel 15 TET	☒	
				Y		1347-01	Panel 15 HEX	☒	
				R	◆	GS-350	Size Standard	☒	
3	☒		884-15	B		884-15	Panel 15 FAM	☒	
				G		884-15	Panel 15 TET	☒	
				Y		884-15	Panel 15 HEX	☒	
				R	◆	GS-350	Size Standard	☒	
4	☒		884-16	B		884-16	Panel 15 FAM	☒	
				G		884-16	Panel 15 TET	☒	
				Y		884-16	Panel 15 HEX	☒	
				R	◆	GS-350	Size Standard	☒	
5	☒		1340-01	B		1340-01	Panel 15 FAM	☒	
				G		1340-01	Panel 15 TET	☒	
				Y		1340-01	Panel 15 HEX	☒	
				R	◆	GS-350	Size Standard	☒	
6	☒		1340-01	B		1340-01	Panel 15 FAM	☒	
				G		1340-02	Panel 15 TET	☒	
				Y		1340-02	Panel 15 HEX	☒	
				R	◆	GS-350	Size Standard	☒	

Genotyper Software table

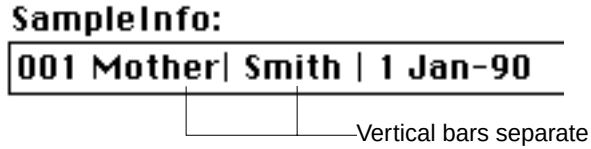
Table - untitled

File Name	Lane & Dye	Sample Info	Category	Peak 1	Peak 1	Peak 2
011347-12 PGF	1B	S001	D12S83	a101	100.82	a109
011347-12 PGF	1B	S001	D7S517	a255	254.88	
011347-12 PGF	1G	S001	D13S171	a183	182.74	a193
011347-12 PGF	1G	S001	D2S391	a148	148.24	a152
011347-12 PGF	1Y	S001	D1S220	a232	232.49	a234
011347-12 PGF	1Y	S001	D3S1266	a289	289.08	a291
021347-13 PGM	2B	S002	D12S83	a101	100.93	a105
021347-13 PGM	2B	S002	D7S517	a249	249.11	a251
021347-13 PGM	2G	S002	D13S171	a179	178.86	a193
021347-13 PGM	2G	S002	D2S391	a146	146.18	
021347-13 PGM	2Y	S002	D1S220	a234	234.39	a244
021347-13 PGM	2Y	S002	D3S1266	a291	290.94	a297
031347-01 Father	3B	S003	D12S83	a101	100.81	a105
031347-01 Father	3B	S003	D7S517	a249	249.21	a255
031347-01 Father	3G	S003	D13S171	a179	178.86	a193
031347-01 Father	3G	S003	D2S391	a146	146.18	a152
031347-01 Father	3Y	S003	D1S220	a234	234.39	
031347-01 Father	3Y	S003	D3S1266	a289	289.01	a291

Sample Subfield Example

When you fill in the Sample Info field of the GeneScan Analysis Software Sample Sheet, you can edit the Sample Info field and create Sample subfields. You can use Sample subfields for the Genotyper software table entries when you create tables.

Example



Plan for the Find Command

You can increase the utility of the Find (Ctrl+F) command in the Genotyper software by carefully planning the format of the information you put into the Sample Info field of the GeneScan Analysis Software Sample Sheet.

Example

One method	
If...	**Then...**
you have 12 samples, numbered 1, 2, 3,..., 12, and you enter these numbers into the Sample Info field	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	
If...	**Then...**
you number the samples 01, 02, 03, and so on	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 for Automation

Introduction

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

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

Ways to Automate

The following table lists how you can automate different genotyping tasks, and where to find detailed information on using a particular automation method.

Genotyping task	Automation method	See topic
Importing Sample files	Running the Set Import Macro	"Importing and Storing GeneScan Sample Files" on page 3-13.
	Creating a Macro	"Creating Macros from the Step List" on page 4-11.
	Using a Template	"Using and Creating Templates" on page 4-14.
Defining categories	Defining Categories	"Defining Categories for Labeling" on page 6-4.
	Creating a Macro	"Creating Macros from the Step List" on page 4-11.
	Using a Template	"Using and Creating Templates" on page 4-14.

Genotyping task	Automation method	See topic
Selecting Dye/lanes	Using the Find Command	“Searching and Sorting Through Lists” on page 5-10.
	Creating a Macro	“Creating Macros from the Step List” on page 4-11.
	Using a Template	“Using and Creating Templates” on page 4-14.
Labeling peaks	Automatic Peak Labeling	“Automatic Peak Labeling” on page 6-28.
	Defining Categories	“Defining Categories for Labeling” on page 6-4.
	Creating a Macro	“Creating Macros from the Step List” on page 4-11.
	Using a Template	“Using and Creating Templates” on page 4-14.
Filtering labels	Automatic Label filtering	“Filtering Labels” on page 6-32.
	Defining Categories	“Defining Categories for Labeling” on page 6-4.
	Creating a Macro	“Creating Macros from the Step List” on page 4-11.
	Using a Template	“Using and Creating Templates” on page 4-14.
Generating plots	Defining Categories	“Defining Categories for Labeling” on page 6-4.
	Creating a Macro	“Creating Macros from the Step List” on page 4-11.
	Using a Template	“Using and Creating Templates” on page 4-14.

Genotyping task	Automation method	See topic
Generating tables	Defining Categories	“Defining Categories for Labeling” on page 6-4.
	Creating a Macro	“Creating Macros from the Step List” on page 4-11.
	Using a Template	“Using and Creating Templates” on page 4-14.
Exporting genotyping data	Using a Template	“Using and Creating Templates” on page 4-14.
	Creating a Macro	“Creating Macros from the Step List” on page 4-11.

3 Getting Started

Chapter Overview

Introduction This chapter discusses how to work with the Genotyper Documents to produce results meaningful to your particular research activities. It covers some of the basic Genotyper® 3.5 NT software procedures required for all genotyping applications.

In This Chapter This chapter contains the following topics:

Topic	See page
Choosing a Genotyping Application	3-2
Opening Genotyper Documents	3-7
Starting from the Main Window	3-8
Viewing and Saving Genotyper Document Windows.	3-10
Importing and Storing GeneScan Sample Files	3-13
Editing Document Lists	3-18
Editing Document Windows	3-19
Locking and Unlocking Documents	3-20
Printing Genotyper Document Windows	3-21

Choosing a Genotyping Application

Introduction

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

Kinds of Genotyping Applications

The Genotyper software 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 the Genotyper software tables or export them to databases or other software applications for further analysis.

Table of Genotyping Applications

Table of genotyping applications:

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 3-3.
Gene Expression Profiling	A comparative analysis table containing normalized data.	“Gene Expression Profiling” on page 3-5.
AFLP	A comparative analysis table of polymorphic peaks that shows the presence or absence of peaks.	http://www.perkin-elmer.com
Forensics/Human Identification	A genotype table to discriminate between individuals.	The *ABI PRISM Genotyper 3.5 NT Software Applications Tutorials*.
SSCP	A table of alleles identifying mutants and wild types.	

Table of 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 8-31.

Linkage Mapping

Linkage mapping applications identify polymorphic fragments by size.

To use the Genotyping software for linkage mapping applications:

Step	Action	See topic
	Importing and Analyzing Data	
1	Importing GeneScan Analysis Software files.	"Importing and Storing GeneScan Sample Files" on page 3-13.
2	Are you using a Template? **If...** / **Then...** yes / go to step 4. no / go to step 3.	"Using and Creating Templates" on page 4-14.
3	Defining categories	"Defining Categories for Labeling" on page 6-4.
4	Selecting dye lanes	"Working with Dye/lane Lists" on page 5-1.
5	Labeling peaks	"Approaches to Labeling" on page 6-2.
6	Filtering labels	"Filtering Labels" on page 6-32.
7	Making a table	"Setting Up a Table" on page 8-2.
	Reviewing Analyzed Data	
1	Viewing plot data	"Viewing Plots of Imported Dye/Lanes" on page 7-2.

To use the Genotyping software for linkage mapping applications: *(continued)*

<table>
<tr><th>Step</th><th>Action</th><th>See topic</th></tr>
<tr><td>2</td><td colspan="2">Checking for overflows

Are there more than two alleles?

<table>
<tr><th>If...</th><th>Then...</th><th>See...</th></tr>
<tr><td>yes</td><td>manually remove unwanted labels.</td><td rowspan="2">“Removing Labels” on page 6-47</td></tr>
<tr><td>no</td><td>go to step 3.</td></tr>
</table></td></tr>
<tr><td>3</td><td>Updating table</td><td>“Updating Tables” on page 8-41.</td></tr>
<tr><td colspan="3">Exporting Data</td></tr>
<tr><td>1</td><td colspan="2">Exporting data

<table>
<tr><th>To export to...</th><th>See...</th></tr>
<tr><td>a file</td><td>“Exporting and Copying Tables” on page 8-44.</td></tr>
</table></td></tr>
<tr><td>2</td><td>Printing results</td><td>“Printing Genotyper Document Windows” on page 3-21.</td></tr>
</table>

Gene Expression Profiling

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

To compare peak quantities:

<table>
<tr><th>Step</th><th>Action</th><th>See topic</th></tr>
<tr><td colspan="3">Quantify Sample Fragments</td></tr>
<tr><td>1</td><td>Importing GeneScan files.</td><td>“Importing and Storing GeneScan Sample Files” on page 3-13.</td></tr>
<tr><td>2</td><td>Are you using a Template?

<table><tr><th>If...</th><th>Then...</th></tr><tr><td>yes</td><td rowspan="2">go to step 3.</td></tr><tr><td>no</td></tr></table></td><td>“Using and Creating Templates” on page 4-14.</td></tr>
<tr><td>3</td><td>Defining categories</td><td>“Defining Categories for Labeling” on page 6-4.</td></tr>
<tr><td>4</td><td>Selecting dye/lanes in the Dye/lane list.</td><td>“Working with Dye/lane Lists” on page 5-1.</td></tr>
<tr><td>5</td><td>Labeling peaks</td><td>“Approaches to Labeling” on page 6-2.</td></tr>
<tr><td>6</td><td>Filtering labels</td><td>“Filtering Labels” on page 6-32.</td></tr>
<tr><td colspan="3">Compare Sample Quantities</td></tr>
<tr><td>1</td><td>Normalizing labels by control peaks</td><td>“Labeling Normalized Peaks—an Example” on page 6-50.</td></tr>
<tr><td>2</td><td>Viewing plot data</td><td>“Viewing Plots of Imported Dye/Lanes” on page 7-2.</td></tr>
<tr><td>3</td><td>Generating a table</td><td>“Setting Up a Table” on page 8-2.</td></tr>
</table>

To compare peak quantities: *(continued)*

<table>
<tr><th>Step</th><th>Action</th><th>See topic</th></tr>
<tr><td>4</td><td colspan="2">Normalizing Labels

<table><tr><th>If...</th><th>Then...</th></tr><tr><td>you are using scale factors</td><td>see “Using Scale Factors for Quantitative Applications” on page 5-15.</td></tr><tr><td>you are using Normalize Peaks command</td><td>see “Labeling Normalized Peaks—an Example” on page 6-50.</td></tr><tr><td>you are using Calculate in Table command</td><td>see “Calculating Results from Table Data” on page 8-22.</td></tr></table></td></tr>
<tr><td colspan="3">Export Results Data</td></tr>
<tr><td>5</td><td colspan="2">Export data

<table><tr><th>If...</th><th>Then...</th></tr><tr><td>you want to export data to a file</td><td>see “Exporting and Copying Tables” on page 8-44.</td></tr></table></td></tr>
<tr><td>6</td><td>Print results</td><td>see “Printing Genotyper Document Windows” on page 3-21.</td></tr>
</table>

Opening Genotyper Documents

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

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

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

The following table lists the steps for opening a Genotyper Document.

If...	Then...
you are working with: ♦ An existing Genotyper Document or, ♦ A template file	a. Choose Open (Ctrl+O) from the File menu. b. Locate and select the document you want to open. c. Click Open.
you do not have an existing Genotyper Document	Choose New (Ctrl+N) from the File menu.

Closing Genotyper Documents

Procedure Choose Close (Ctrl+W) from the Edit menu to close the Genotyper Document.

Starting from the Main Window

Definition

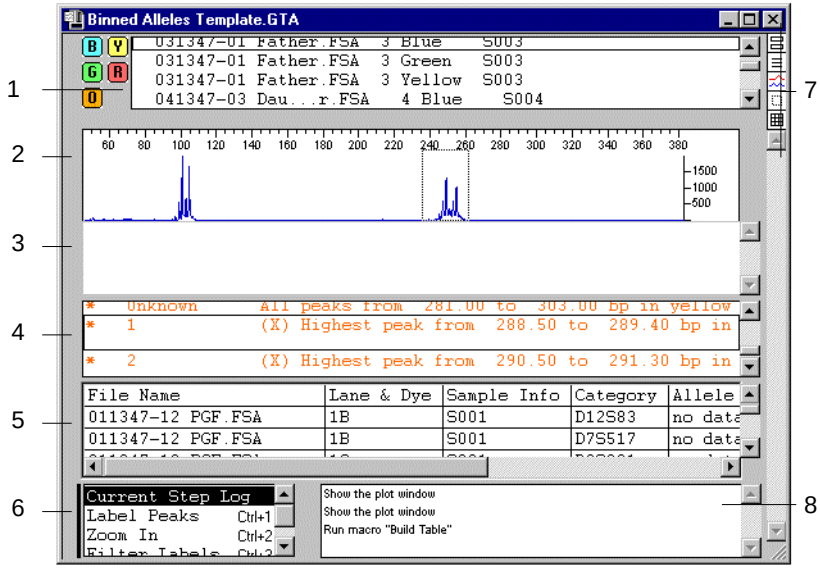
The Main window displays all parts of a Genotyper Document. You perform all Genotyper software tasks from the Main window, or from Document windows you can open within the Main window that let you view GeneScan Analysis Software file data, and results data in different formats.

Displaying the Main Window

Choose Show Main Window from the Views menu. The Main window appears.

Main Window Example

When you open a new Genotyper Document, a blank Main window appears. Once you've imported GeneScan Analysis Software files and created all the parts of a Genotyper Document the Main window looks like the following figure.



Parts of the Main Window

The following table describes the part of the Main Window in the above figure.

Parts of the Main Window:

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.
8	Step list	Contains the list of steps for the current Step Log or the macro selected in the Macro list.

Button	Description
	Main window
	Dye/lane List window
	Plot window
	Category window
	Table window

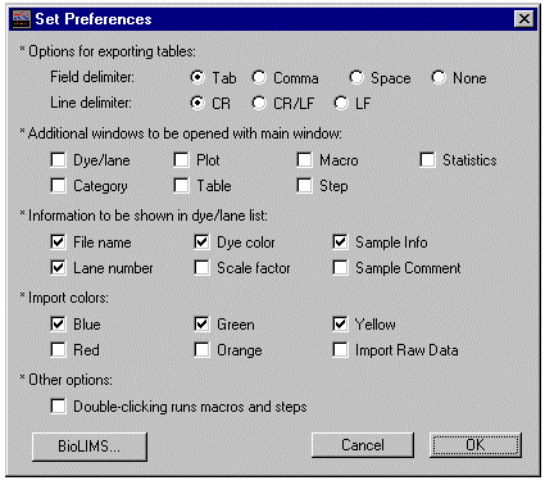
Viewing and Saving Genotyper Document Windows.

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.

Defining Windows to Open with Main Window

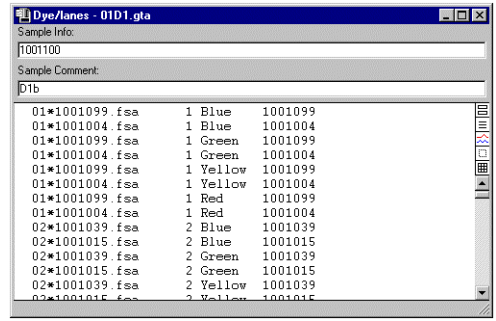
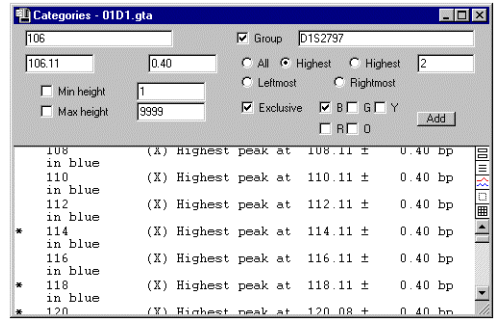
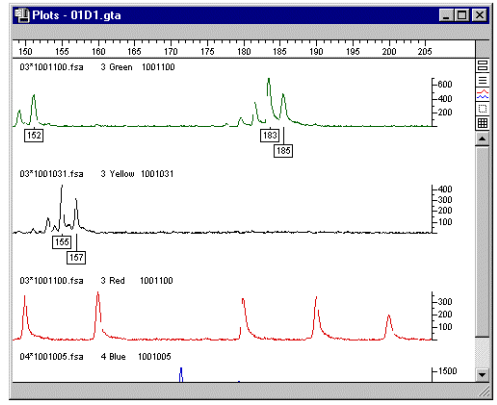
To define additional windows to be opened with the Main window:

Step	Action
1	Choose Set Preferences from the Edit menu. The Set Preferences dialog box appears. 
2	In the Additional windows to be opened with the main window section, choose the checkboxes for the windows that you want opened with the main window.
3	Click OK

Viewing Windows

The following table lists how to use the selection button to open Document windows. Document windows display the different parts of a Genotyper Document.

How to use the selection buttons to open Document windows.

To see the...	Click...	Choose...	And Genotyper displays...
Dye/lane window		Show Dye/Lanes Window from the Views menu.	
Category window		Show Categories Window from the Views menu.	
Plot window		Show Plot Window from the Views menu.	

How to use the selection buttons to open Document windows. *(continued)*

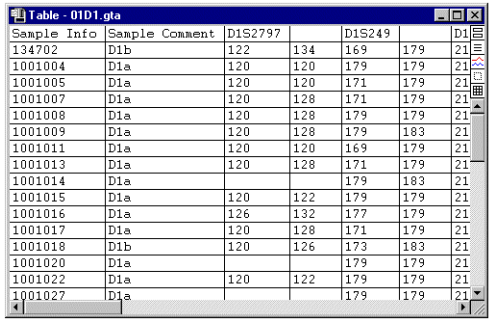
To see the...	Click...	Choose...	And Genotyper displays...
Table window		Show Table Window from the Views menu.	

Table - 01D1.gta

Sample Info	Sample Comment	D1S2797		D1S249		D1
134702	D1b	122	134	169	179	21
1001004	D1a	120	120	179	179	21
1001005	D1a	120	120	171	179	21
1001007	D1a	120	128	171	179	21
1001008	D1a	120	128	179	179	21
1001009	D1a	120	128	179	183	21
1001011	D1a	120	120	169	179	21
1001013	D1a	120	128	171	179	21
1001014	D1a			179	183	21
1001015	D1a	120	122	179	179	21
1001016	D1a	126	132	177	179	21
1001017	D1a	120	128	171	179	21
1001018	D1b	120	126	173	183	21
1001020	D1a			179	179	21
1001022	D1a	120	122	179	179	21
1001027	D1a			179	179	21

Cascading Windows

Choose Cascade from the Window menu. Arranges windows so they are the same size and stacked from back to front, with only the title visible.

Saving a Genotyper Document

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.

To...	Then...
save the active Genotyper Document	choose Save (Ctrl+S) from the File menu.
save the Genotyper Document using a new name	choose Save As from the File menu. The Save As dialog box appears. Enter a file name and click Save.

Importing and Storing GeneScan Sample Files

Introduction

Importing GeneScan Analysis Software files supplies peak data for all Genotyper software tasks.

A GeneScan file can be a:

- Sample file (GeneScan version 2.0 or later), or
- Results file (GeneScan 1.x versions).

IMPORTANT You cannot import GeneScan Gel files.

Process

When you import a GeneScan file in the Genotyper software, 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 files see, “Where Dye/lanes Come From” on page 5-2.

Ways to Import GeneScan Files

You can either import GeneScan files all at once or in batches. There are advantages and disadvantages to both approaches.

Ways to import GeneScan files and advantages and disadvantages.

Way to Import	Advantages	Disadvantages
All GeneScan files at once. Useful when importing data from a few gels or approximately 36 lanes or capillaries.	More convenient. You can see all results after performing the command just once.	♦ Requires more memory. ♦ Inefficient processing will slow down the operation.

Ways to import GeneScan files and advantages and disadvantages.

Way to Import	Advantages	Disadvantages
In batches. Useful when importing data from many gels or more than 36 lanes or capillaries.	♦ More GeneScan files can be processed more efficiently. ♦ Does not require as much memory allocated to Genotyper.	You cannot see all dye/lanes at one time.

Determining the Number of GeneScan Files in Project

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

Example:

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

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

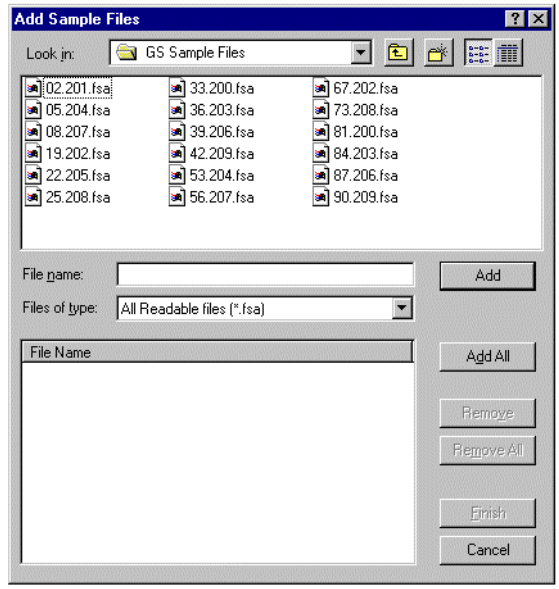
Optimizing Performance

The following table lists how you can optimize the performance of the ABI PRISM Genotyping Software System:

If...	Then...
you store all GeneScan files in one location	you can optimize the performance of the ABI PRISM Genotyping Software System
you move the GeneScan files around	other software applications will not be able to locate them if you want to refer to them at a later time.

Importing GeneScan Files

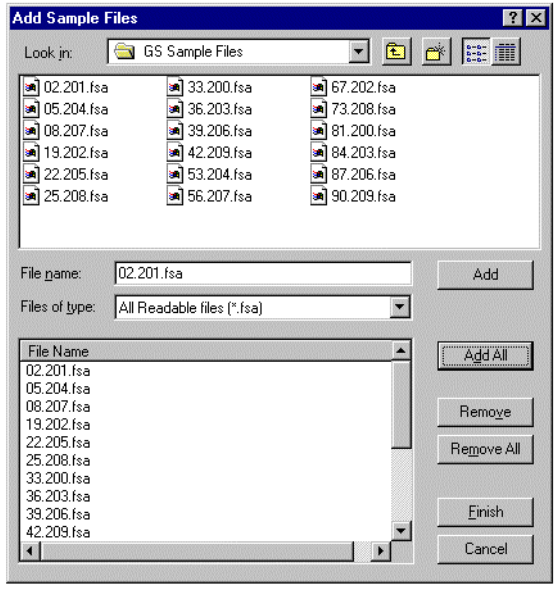
To import GeneScan Analysis Software files:

Step	Action
1	Click Import from the File menu and point to From GeneScan File (Ctrl+I). The Add Samples dialog box appears. 
2	In the upper list box, locate and open the folder that contains the files you want to import.

To import GeneScan Analysis Software files: *(continued)*

<table>
<tr><th>Step</th><th>Action</th></tr>
<tr><td>3</td><td>Add the files that you want to import to the bottom of the dialog box by taking the following action.
<table>
<tr><th>To add…</th><th>Do this...</th></tr>
<tr><td>a single file to the list</td><td>select the file, then either:
♦ Choose Add, or
♦ Double-click the name of the file.</td></tr>
<tr><td>all the files to the list</td><td>choose Add All.</td></tr>
<tr><td>one file and all the files after that file to the list</td><td>click the first file you want to add and go the last file and click-Shift.</td></tr>
<tr><td>some of the files to the list</td><td>either
♦ Add them individually, or
♦ Choose Add All, then use the Remove button to remove the files you do not want in the list.</td></tr>
</table>
</td></tr>
</table>

To import GeneScan Analysis Software files: *(continued)*

Step	Action
4	When all the files you want are in the lower list, click the Finish button to close the dialog box and import the files. The Genotyper software remembers the last folder from which you imported files. 

Editing Document Lists

Introduction

The Genotyper software 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 Active

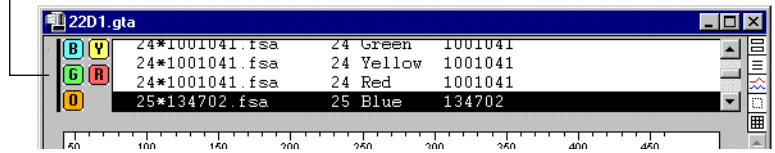
What Indicates a List is Active

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

How to Make a List Active

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.

Vertical bar



Selecting Items in a List

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

The following table shows how to select items in any Genotyper 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.
Discontinuous items in a list	a. Click on an item in the list. b. Hold down the Ctrl+key and click on another item. c. Repeat the step b for each item you want to select. Only the items selected are highlighted.

Editing Document Windows

Table of Editing Commands

To edit document windows, from the Edit menu, choose the following commands:

Use the...	To...
Undo command (Ctrl+Z)	undo the last command (whenever possible). **Note** If you want to undo the last command, then Undo (Ctrl+Z) must be the next command.
Cut (Ctrl+X) Copy (Ctrl+C) Paste (Ctrl+V) commands	transfer the same type of information from one window to another. **For example:** The Cut (Ctrl+X), Copy (Ctrl+C), and Paste (Ctrl+V) commands available from the Edit menu allow you to transfer the same type of information from one window to another. **IMPORTANT** Copying or pasting many dye/lanes from one document to another requires a lot of memory. Therefore, copy or paste only a few dye/lanes at a time.
Copy Window command	copy a picture of the Main window or the Plot window. A picture of everything in the active window (except the title bar) is copied to the Clipboard. **Showing the Clipboard** Choose Clipboard from the Window menu to show the items that have been cut, or copied, and reside in the clipboard. You can now paste this image into a paint or draw program to edit it.
Clear	clear the currently selected entries in the Dye/lane list, Categories list. Macro list, or Step list.
Select All (Ctrl+A)	select every entry in the selected list or table.

Locking and Unlocking Documents

About Locking and Unlocking

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.

Procedure

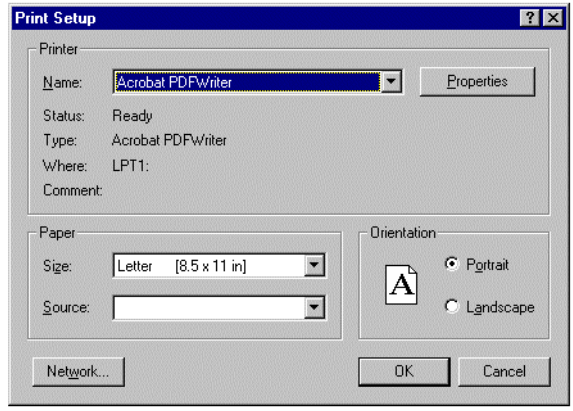
Use the following procedures to lock and unlock documents:

To...	Then choose...
lock documents	Lock from the File menu. Padlock icons appear next to the locked panes and in the File menu Lock is checked.
unlock documents	Unlock from the File menu. The padlock icons disappear and in the File menu Unlock is checked.

Printing Genotyper Document Windows

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

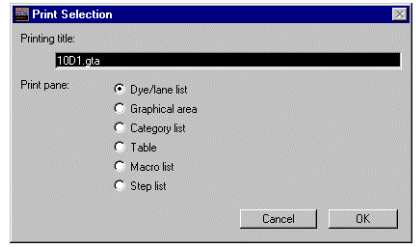
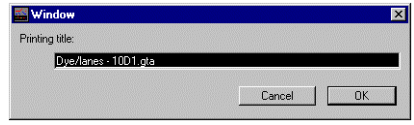
To print the Genotyper Document Window:

Step	Action
1	Select the Genotyper Document Window that you want to print.
2	Choose Print Setup from the File menu. Your printer's Print Setup dialog box appears. The following is an example of the Print Setup dialog box 
3	Select the appropriate checkboxes and options and click OK.
4	Choose Print (Ctrl+P) from the File menu.

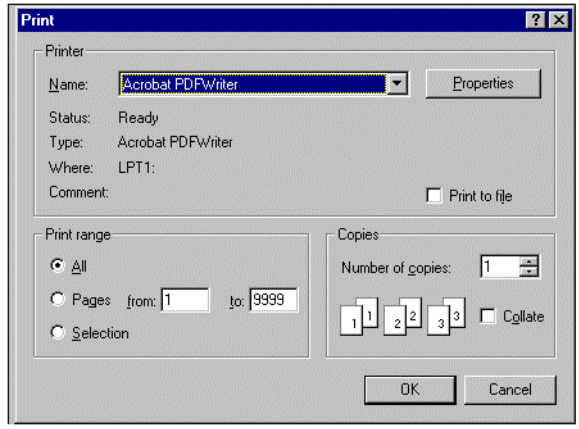
To print the Genotyper Document Window: *(continued)*

Step	Action

Take the following action:

If...	Then...
you are printing from the Main window	this dialog box appears:  ♦ Enter a printing title. ♦ Click the radio button for the pane that you want to print and click OK. The Print dialog box appears.
you are printing from any other window, other than the Main window	this dialog box appears:  Enter a printing title and click OK. The Print dialog box appears.

To print the Genotyper Document Window: *(continued)*

Step	Action
	The following is an example of the Print dialog box. 
5	Click OK to begin printing.

Automating the Genotyper Software 4

Chapter Overview

Introduction

The Genotyper® 3.5 NT software can automatically perform all calculations, comparative analyses, and peak labeling activities once you specify appropriate settings and issue the appropriate sequence of commands.

Using Genotyper macros, and templates, you can automate the setting of analysis parameters, and issuing of commands to perform either a particular analysis procedure, or all of the procedures for an entire genotyping application.

In This Chapter

This chapter contains the following topics:

Topic	See page
Approaches to Automating Procedures	4-2
Running Macros	4-3
Recording Steps in the Step List	4-5
Editing the Step List	4-9
Creating Macros from the Step List	4-11
Using and Creating Templates	4-14

Approaches to Automating Procedures

Introduction

The Genotyper software software uses templates and macros to automate procedures for an application.

The macros and templates supplied with the Genotyper software software 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

The following table lists definitions:

Item	Definition
Template	Templates are ready-to-use Genotyper documents. A Genotyper template contains the Category list and macros necessary for automatic analysis of particular applications.
Macro	A macro is a sequence of commands or steps that you can run to perform a particular analysis procedure.

Automation Options

The Genotyper software software supplies customizable templates for automating complete genotyping applications, and macros for automating individual procedures.

Options for automating genotyping applications and procedures:

If you want to automate a Genotyping...	and...	See...
application	you know that a template for a similar application exists.	“Creating Templates” on page 4-14.
procedure within an application	you know that a macro exists for that procedure.	“How to Run Macros” on page 4-4.
	you know that a macro does not exist for that procedure.	“Creating a New Macro” on page 4-11.

Running Macros

Predefined Macros

Running a macro executes a pre-defined set of Genotyper software commands and functions that automates a procedure. The Genotyper software provides several macros that can serve as examples of the kinds of macros you can run to automate analysis tasks.

About Creating Your Own Macros

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 4-5.

Supplied Macros

The Genotyping software supplies a number of sample macros on the Tutorials disk that you can select and run to perform Genotyper procedures.

Tips For Using Macros

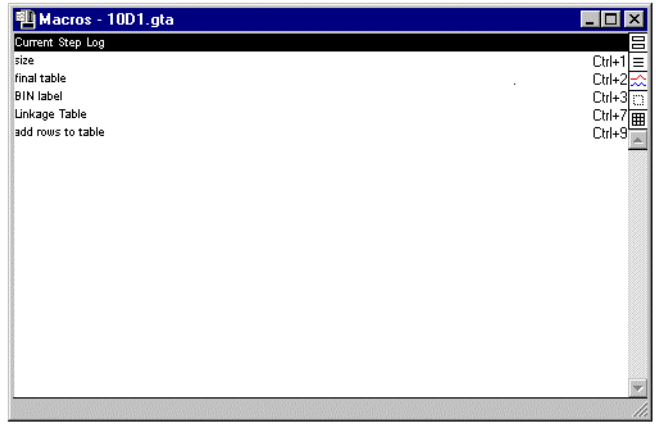
The following table lists two tips for running and creating macros:

Tips for Running Macros
You can run macros by double-clicking a macro after selecting it. This is the default. To set this if it was changed, choose Set Preferences from the Edit menu, and under Other options, select the Double-clicking runs macros and steps checkbox.
Tips for Creating Macros
Select a macro from the list and choose Duplicate Macro from the Macro menu. This makes a copy of the selected macro, which is useful if you have a macro that you want to modify slightly, but do not want to lose the original macro.

Showing the Macro Window

The Macro window shows macros that are stored in the active 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. 

How to Run Macros

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, press Ctrl+[assigned key] to run the macro.

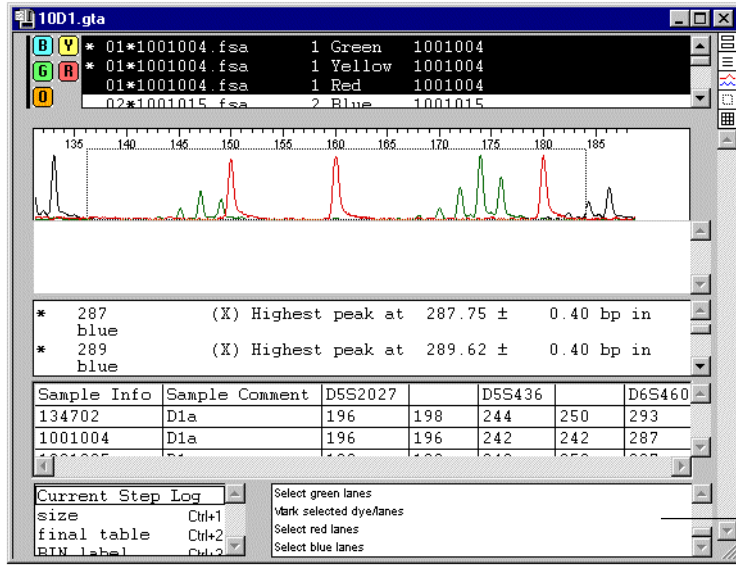
Recording Steps in the Step List

Step List Definition

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

Location of Step Window

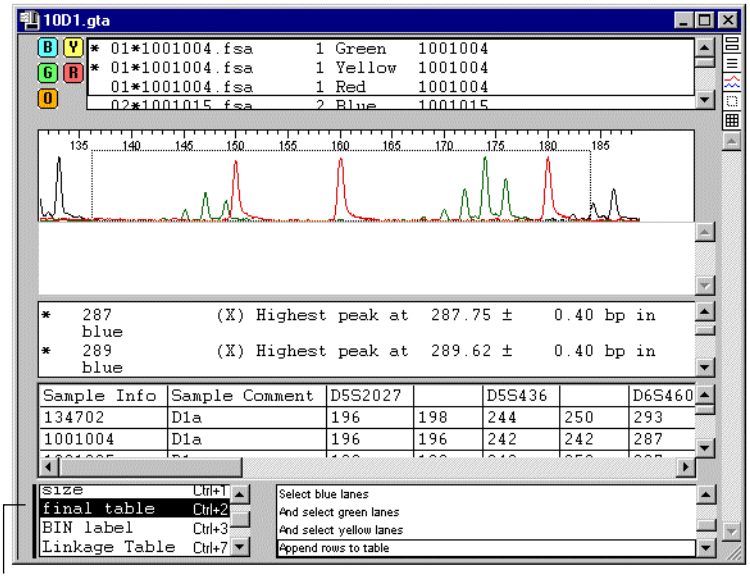
The Step list appears in the Step window, located in the lower right-hand corner of the Main window.



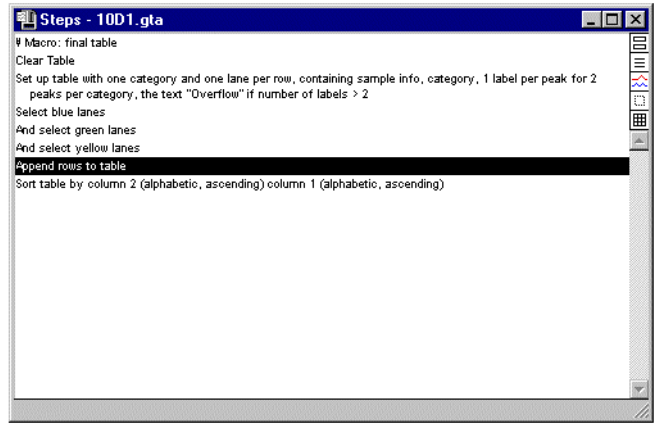
Showing the Step Window

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

To show the Step window:

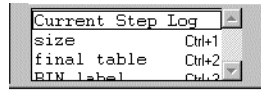
Step	Action
1	Open the Main Window.
2	Select a macro in the Macro list of the Macro window.
	 Select a macro in the Macro list
3	From the Views menu, select Show Step window. The Step window appears. This window shows the steps for the currently selected macro. The following is an example of a Step list in a Step window.

To show the Step window: *(continued)*

Step	Action
	

Displaying Commands issued in Documents

To display commands issued:

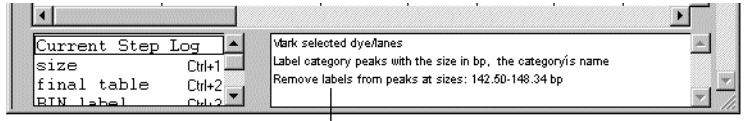
Step	Action
1	Select Current Step Log in the Macro list of the Macro window. 
2	Choose Show Step Window from the View menu. The Genotyper software displays the commands you have issued since you last cleared the Step Log,

Recording Steps in the Step List

The Genotyper software records most tasks you perform or commands you issue as 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 using the Genotyper software, such as marking, labeling, and filtering are recorded as steps in the Step list.



Turning Off Step Recording

If you are not making a macro, and do not want to fill up the Step list, 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

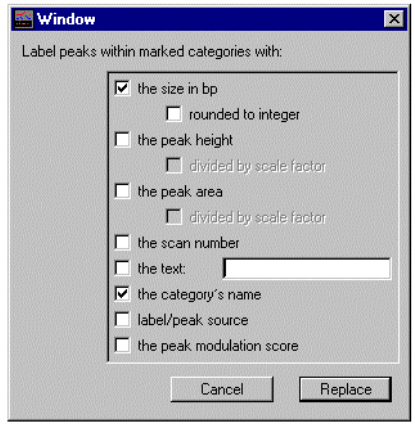
Introduction

You can edit the contents of your current Step list before or after creating a macro.

Editing 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 Step from the Macro menu. The dialog box for that step appears. The following figure is an example of the dialog box that appears if you edit the step for a Label Peaks command. 
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.

Copying and Pasting from the Step List

You can Cut, Copy and Paste steps to change the sequence of steps in the Step list.

To copy and paste steps in the Step list:

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

Running 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 Analysis Software files.

Clearing the Step List

Before you record steps for a macro, you will want to clear the 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.

Creating a New Macro

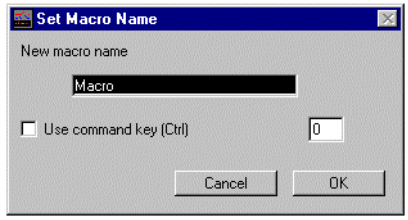
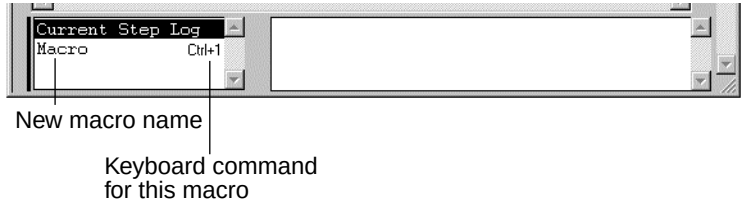
Once you have cleared the Step list of all previously recorded steps, you can create a new macro for a genotyping procedure by performing all of the steps in the procedure once. The Genotyper software records each of the steps in the Step list.

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.

To create a new macro: *(continued)*

Step	Action
3	Choose Save Step Log from the Macro menu. The Set Macro Name dialog box appears. 
4	Enter the name of the new Macro in the text box.
5	Click the checkbox and enter the key in the text that you want to press with the command key to run this Macro from the keyboard.
6	Click OK. The new Macro appears in the Macro list.
	

Changing a Macro Name

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 Name from the Macro menu. The Set Macro Name dialog box appears with the name of the macro in the text box.
3	Enter the new macro name.

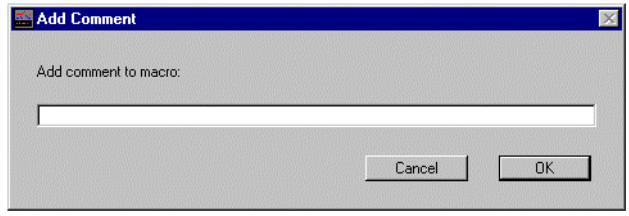
To change the name of a macro: *(continued)*

Step	Action
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.

Adding a Comment to a Macro

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

To add a comment to a macro.

Step	Action
1	Choose Add Comment from the Macro menu. The Add Comment dialog box appears. 
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.

Using and Creating Templates

Definition

The Genotyper software software 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 Analysis Software files to demonstrate how to use it. The template name describes the kind of application it automates.

Creating Templates

To create a template, modify any existing template for your specific application:

Step	Action
1	In the Genotyper Tutorials & Examples (NT) folder, select an existing template that describes the kind of application that you are running.
2	Choose Copy (Ctrl+C) and then Paste (Ctrl+V) from the Edit menu to make a copy of the template.
3	Start the Genotyper software and open the file that you just copied.
4	Delete the Category list by: a. Choosing Show Categories Window (Ctrl+K) from the Views menu. a. Choosing Select All (Ctrl+A) from the Edit menu. b. Choosing Clear from the Edit menu.
5	Make a new Category list specific for your application by:
6	Choose Save As from the File menu. The Save this document as dialog box appears.
7	Name the new template, choose a folder to save the template, and click Save.

Saving Templates as Read-Only Files

Saving a template as a read-only file prevents it from being changed accidentally. A read-only file can be opened and used, but any changes made can only be saved as a separate document.

To save a template as a read-only file:

Step	Action
1	Click the Start button, and then point to Programs.
2	Click Windows NT Explorer and find the template file in the folder you want to save as a read-only file.
3	Click the template file and choose Properties from the File menu. The Properties dialog box appears.
4	In the Attributes section, select the Read-only checkbox and click OK.
5	Click the Close box in the upper left-hand corner of the window. The Template is now saved as a read-only file.

Working with Dye/lane Lists

5

Chapter Overview

Introduction

Dye/lanes contain sample information for electrophoresed nucleic acid fragments. They provide the source data for all the Genotyper® 3.5 NT software procedures. Genotyper Documents contain a list of all dye/lanes related to that document. This chapter discusses how you can view, search, and use the information contained in Dye/lane lists to perform particular genotyping analysis tasks.

In This Chapter

This chapter contains the following topics:

Topic	See page
Where Dye/lanes Come From	5-2
Importing Dye Data	5-4
Viewing Dye/lane Lists	5-5
Searching and Sorting Through Lists	5-10
Editing List Contents	5-14
Using Scale Factors for Quantitative Applications	5-15

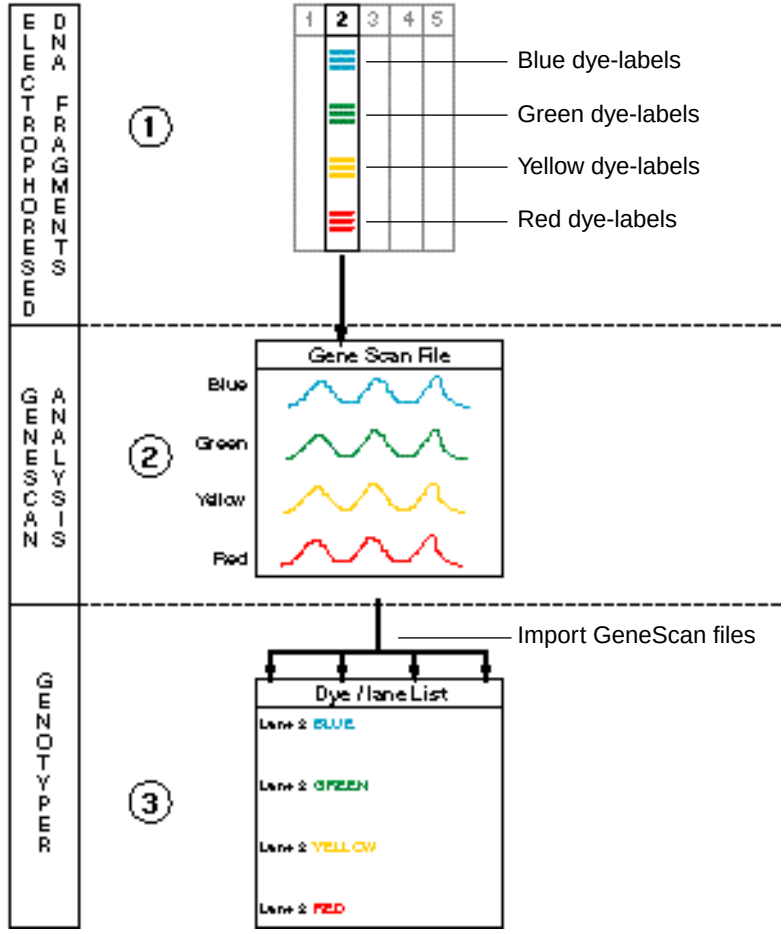
Where Dye/lanes Come From

Introduction

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

Phases of the Process

The Genotyper software 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.



What Happens in Each Phase

The following table lists 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	The GeneScan Analysis Software 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 the Genotyper software, 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.

Importing Dye Data

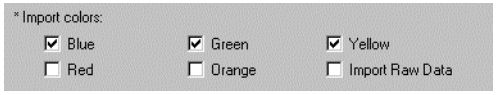
About 5th Dye Data

Genotyper 3.5 NT software can read and process GeneScan Analysis Software data containing a 5th fluorescent dye.

Note Reagent kits containing a 5th dye may be available at a later date.

Procedure

To import dye data:

Step	Action
1	Select Set Preferences from the Edit menu. The Set Preference dialog box appears.
2	Choose the dyes by clicking their respective boxes under Import colors. **Note** The 5th dye is designated Orange. 
3	Click OK. The Set Preferences dialog box goes away and you are returned to the Main window.
4	Take the following action: **To...** / **Then...** import GeneScan data — choose Import from the File menu and From GeneScan from the submenu. import BioLIMS™ data — choose Import from the File menu and From BioLIMS from the submenu.

Viewing Dye/lane Lists

Dye/lane List Definition

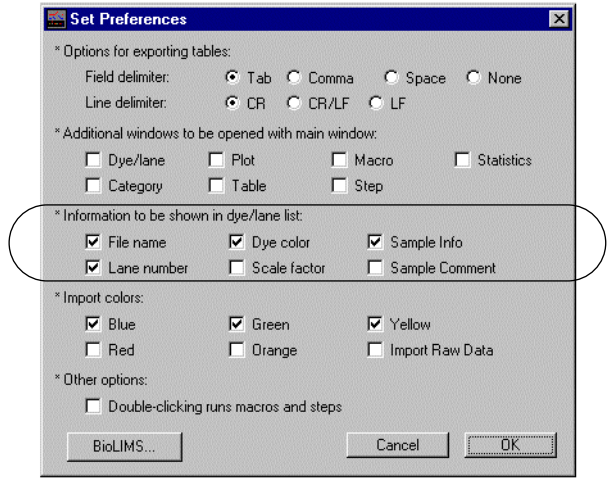
The Dye/lane list is a list of all dye/lanes in the GeneScan Analysis Software files that you have imported into the Genotyper software. Dye/lanes are added to the list as you import them from GeneScan.

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 5-10.

Setting Viewing Preferences

You 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.

To set Dye/lane list viewing preferences:

Step	Action
1	Choose Set Preferences in the Edit menu. The Set Preferences dialog box appears. The circled section below indicates the dye/lane list information. 

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

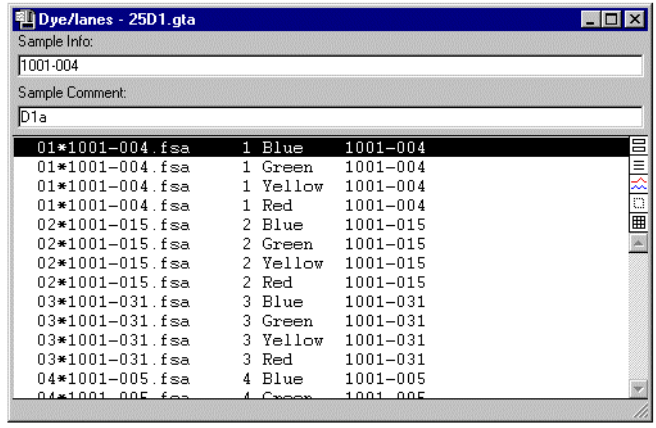
<table>
<tr><th>Step</th><th>Action</th></tr>
<tr><td>2</td><td>Under the bullet “Information to be shown in dye/lane list:”, select the checkboxes for what you want to view in the Dye/Lane list.

<table>
<tr><th>If you click...</th><th>Then the Dye/Lane list displays...</th></tr>
<tr><td>File name</td><td>name of the associated GeneScan file.</td></tr>
<tr><td>Dye color</td><td>dye color of sample fragment labels.</td></tr>
<tr><td>Sample Info</td><td>Contents of Sample Info field of the GeneScan Sample Sheet.</td></tr>
<tr><td>Lane number</td><td>The lane number, or injection number for ABI PRISM 310 samples, in which sample fragments were electrophoresed.</td></tr>
<tr><td>Scale factor</td><td>Normalization factor that you can apply to dye/lane peaks.</td></tr>
<tr><td>Sample Comment</td><td>Comments entered in the GeneScan Sample Sheet.</td></tr>
</table>
</td></tr>
</table>

Viewing the Dye/Lanes Window

The Dye/lanes window displays the Dye/lanes list, and also contains associated Sample Information and Sample Comments from GeneScan Analysis Software files.

To view the Dye/Lanes window:

<table>
<tr><th>Step</th><th>Action</th></tr>
<tr><td>1</td><td>From the Main Window:
<table>
<tr><th>You can either:</th><th>Result</th></tr>
<tr><td>click the Dye/lane window icon.</td><td rowspan="2">The Dye/lanes window appears.</td></tr>
<tr><td>choose Show Dye/lanes Window from the Views menu.</td></tr>
</table>

</td></tr>
<tr><td>2</td><td>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.</td></tr>
</table>

Clearing the List

Why Clear Existing GeneScan Files from List

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

Clearing the Dye/lane List

Choose	Action
Clear Dye/Lane List in the Analysis menu.	The Dye/Lane list is cleared.

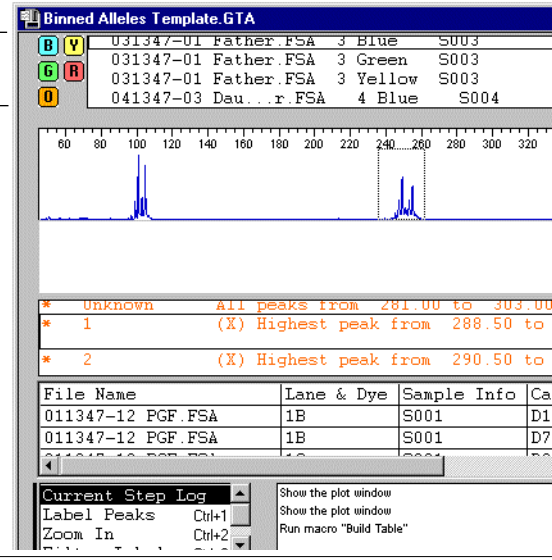
Note If you want to undo this command, choose Undo (Ctrl+Z) in the Edit menu. The Undo command must be the next command.

Selecting Dye Colors

Using the Dye Selection buttons you can select those lanes that have 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 it's not already displayed, show the Main window by choosing Show Main Window from the Views menu. The Main Window appears.



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

<table>
<tr><th>Step</th><th>Action</th></tr>
<tr><td>2</td><td>To select only dye/lanes labeled with the selected dye colors; B (blue), G (green), Y (yellow), R (Red), you can take the following action:

<table>
<tr><th>Either...</th><th>Result</th></tr>
<tr><td>click one of the five Dye Selection buttons, or</td><td rowspan="2">All the entries in the Dye/lane list for the color you chose are selected.</td></tr>
<tr><td>choose Select from the Edit menu and the dye color from the submenu.</td></tr>
</table>
</td></tr>
<tr><td>3</td><td>To add to your selection, hold down the Ctrl+key and click another Dye Selection button.</td></tr>
</table>

Searching and Sorting Through Lists

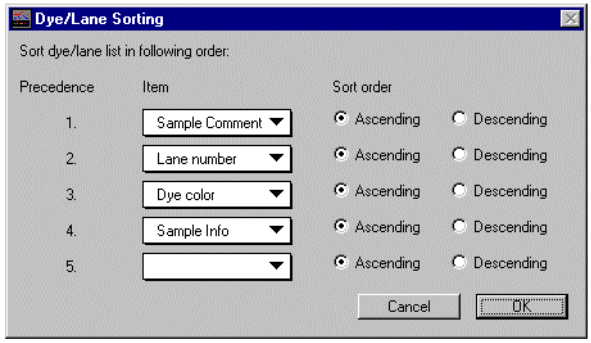
Introduction

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

Sorting Dye/lanes

You can sort the Dye/lanes by various items. You can choose a different sorting order for each Genotyper Document.

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

Step	Action
1	If it is not already displayed, show the Main window by choosing Show Main Window from the Views menu. The Main Window appears.
2	Choose the Dye/lane Sorting command in the Views menu. The Dye/lane Sorting dialog box appears. 

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

<table>
<tr><th>Step</th><th>Action</th></tr>
<tr><td>3</td><td>From the pop-up menus, select items that you want the Genotyper software to sort next to the precedence number in which you want Genotyper to sort them.

The table below provides an example:

<table>
<tr><th>If...</th><th>Then Genotyper...</th></tr>
<tr><td>you choose File name after Precedence 1, and Lane number after precedence 2</td><td>first sorts the list by File name, and then sorts that list by lane number.</td></tr>
</table>
</td></tr>
<tr><td>4</td><td>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
♦ Red
♦ Orange

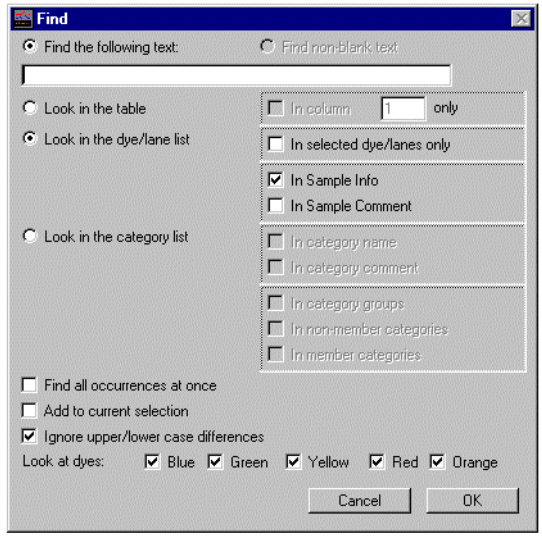
Note If you use the Overlapped dyes, separate lanes option, the dye/lanes must be sorted by File name first and then Lane number.</td></tr>
<tr><td>5</td><td>Take the following action:

<table>
<tr><th>To...</th><th>Click...</th></tr>
<tr><td>apply the sorting order to the active Genotyper Document</td><td>OK.</td></tr>
<tr><td>cancel the sorting selections you have made</td><td>Cancel.</td></tr>
</table>
</td></tr>
</table>

Specifying Search Criteria

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.

To specify search criteria:

Step	Action
1	Choose Find (Ctrl+-F) in the Edit menu. The Find dialog box appears 
2	Click the Find the following text radio button.
3	Type in the text you want to locate.
4	Click the Look in the dye/lane list radio button and select the checkboxes for how and where you want the Genotyper software to search for the text string that you have typed. See “Searching for Dye/lanes” on page 5-13. The following table provides an example: **If...** / **Then Genotyper...** you entered the text “001101” and selected the checkbox for In Sample Comment / would search for the specified text in the Sample Comment fields of all dye/lanes.
5	Click OK.

Searching for Dye/lanes

Once you have defined search criteria (see “Specifying Search Criteria” on page 5-12), choose how you want to search for dye/lanes in the list. The following table shows you how you can search for dye/lane

<table>
<tr><th>If you are...</th><th>Then...</th></tr>
<tr><td>Searching for all occurrences at once</td><td>click the Find all occurrences at once checkbox.

All dye/lanes with the designated text are selected.</td></tr>
<tr><td>Adding dye/lanes to the current selection</td><td>click the Add to current selection checkbox.

<table><tr><th>Dye/lanes...</th><th>Then...</th></tr><tr><td>already selected</td><td>remain selected.</td></tr><tr><td>located by this command</td><td>are also selected.</td></tr></table></td></tr>
<tr><td>Restricting the search to currently selected dye/lanes</td><td>click the In selected dye/lanes only checkbox.

This is useful for narrowing a selection by repeated use of the Find command.</td></tr>
<tr><td>Searching for the next occurrence of a selection</td><td>choose Find Next (Ctrl+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.</td></tr>
<tr><td>Searching for text strings without regard to case</td><td>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.</td></tr>
</table>

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 (see “Viewing the Dye/Lanes Window” on page 5-7). These changes will affect only the Genotyper Document. The original GeneScan Analysis Software 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.

Editing Sample Information

You can edit the Sample Information in the Sample Info field of the Dye/lanes window.

To edit the Sample Info field:

Step	Action
1	Choose Show Dye/lanes Window from the Views menu.
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.

Editing Sample Comments

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

To edit the Sample Comment field:

Step	Action
1	Choose Show Dye/lanes Window from the Views menu.
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.

Using Scale Factors for Quantitative Applications

About Scale Factors

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.

Showing 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 Preferences in the Edit menu. The Set Preferences dialog box appears (see “Setting Viewing Preferences” on page 5-5).
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.

Calculating Scale Factors

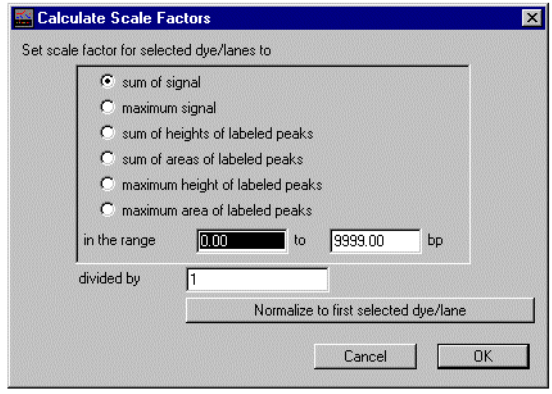
Calculate scale factors by determining parameters for the calculation, and then scaling dye/lanes based on those parameters.

To calculate scale factors:

<table>
<tr><th>Step</th><th>Action</th></tr>
<tr><td colspan="2">Determine parameters for calculation</td></tr>
<tr><td>1</td><td>Open the Dye/lane list:

<table>
<tr><th>You can either...</th><th>Result</th></tr>
<tr><td>click the Dye/lanes button </td><td rowspan="2">The Dye/lanes Window appears.</td></tr>
<tr><td>choose Show Dye/lanes Window from the Views menu</td></tr>
</table></td></tr>
<tr><td>2</td><td>In the Dye/lane list, select the dye/lane to which you want to scale other dye/lane peaks.</td></tr>
<tr><td>3</td><td>Choose Calculate Scale Factors from the Analysis menu.

The Calculate Scale Factors dialog box appears.

 
</td></tr>
<tr><td>4</td><td>Select the radio button corresponding to how you want to scale peaks.</td></tr>
<tr><td>5</td><td>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.</td></tr>
</table>

To calculate scale factors: *(continued)*

Step	Action
6	Click the Normalize to first selected dye/lane 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.
7	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.
2	Choose Calculate Scale Factors from the Analysis menu. The Calculate Scale Factors dialog box appears (see step 3 on page 5-16).
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” on page 5-16.

Resetting Scale Factors to One

To reset Scale Factors to one, choose the Clear All Scale Factors command from the Analysis menu.

The default Scale Factor is one.

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

6

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.

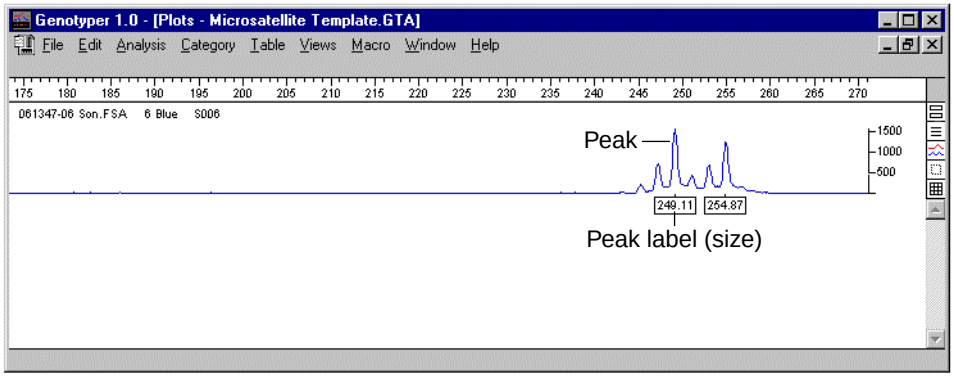
In This Chapter This chapter contains the following topics:

Topic	See page
Approaches to Labeling	6-2
Defining Categories for Labeling	6-4
Using Exclusive Peak Labeling–An Example	6-11
Creating Category Groups—an Example	6-14
Making Category Members	6-18
Searching for Categories	6-22
Sorting and Editing Categories	6-24
Offsetting Categories	6-26
Automatic Peak Labeling	6-28
Filtering Labels	6-32
Manually Placing Labels On Peaks	6-37
Customizing Text in Labels	6-39
Customizing the Color of Labels	6-43
Removing Labels	6-47
Labeling Normalized Peaks—an Example	6-50
Making Categories from Labels	6-55

Approaches to Labeling

Example of a Labeled Fragment Peak

The following figure is an example of a dye/lane fragment peak labeled with the size of the fragment in base pairs. Fragment size is one kind of label you can assign to peak data.



Why Label Fragment Peaks

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.

Ways to Label Fragments

The Genotyper® 3.5 NT software provides you with two ways to label fragment peaks: automatically and manually.

Two ways to label fragment peaks:

Labeling Method	Description	See page
Automatic	Simultaneously labels all peaks within selected dye/lanes with specified criteria.	6-28

Two ways to label fragment peaks: *(continued)*

Labeling Method	Description	See page
Manual	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.	6-37

Automatic Label Filtering

The Genotyper software'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 6-32.

Defining Categories for Labeling

Definition

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

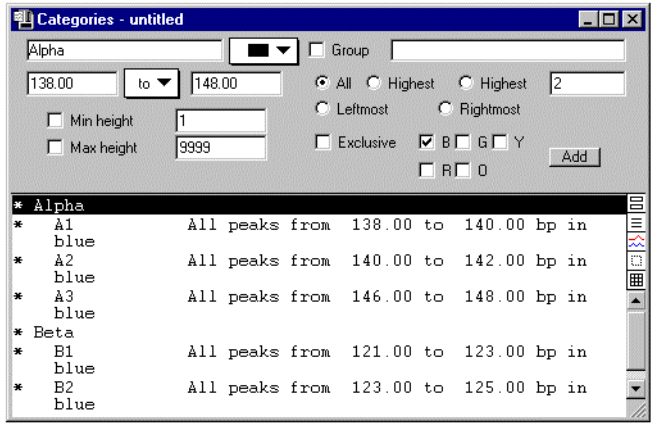
Genotyper uses category information to label appropriate peaks as described in “Automatic Peak Labeling” on page 6-28.

Displaying the Categories Window

You can either....	Result...
click the Categories button.	The Categories window appears.
choose Show Categories Window (Ctrl+K) from the Views menu.	

The Categories Window Example

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



Clearing the Category List

Choose Clear Category List from the Analysis menu. The Category List is cleared.

Note If you want to undo this command, choose Undo from the Edit menu, The Undo command (Ctrl+Z) must be the next command.

Expanding and Collapsing Categories

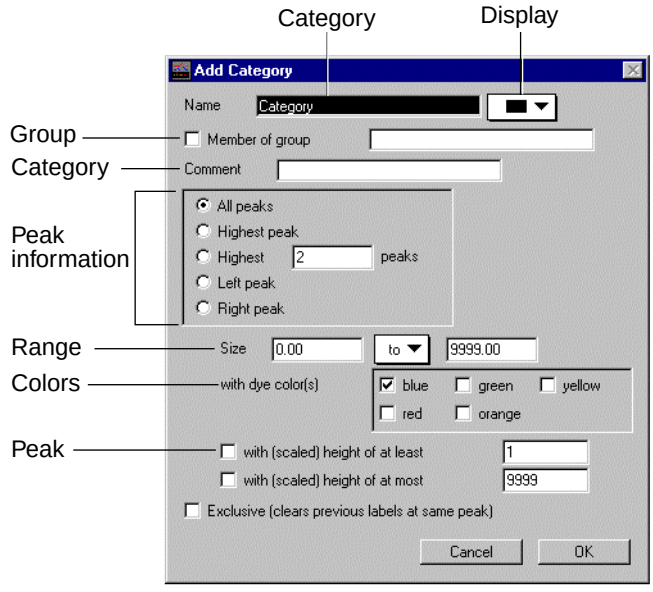
The following table lists how to expand and collapse categories:

To...	Then...
display all categories in a selected category group in the Category list	choose Expand Categories (Ctrl+[) from the Views menu.
display only the category group name of a selected category in the Category list	choose Collapse Categories (Ctrl+]) from the Views menu.

Adding Categories

To add categories:

Step	Action
1	Choose Add Category (Ctrl+L) from the Category menu. The Add Category dialog box appears.



To add categories: *(continued)*

<table>
<tr><th>Step</th><th>Action</th></tr>
<tr><td>2</td><td>Enter the range limits in base pairs for fragments that you want to label.

<table>
<tr><th>If you want to...</th><th>Then...</th></tr>
<tr><td>automatically fill in range limits</td><td>a. Select a rectangular area in the plot area.
b. Choose the Add Category (Ctrl+L) command from the Category menu.</td></tr>
<tr><td>specify starting and ending coordinates in the range</td><td>a. Use the to pop-up menu to select to.
b. Type in the starting and ending sizes in the range. For example, 120 to 140.</td></tr>
<tr><td>specify a center coordinate and range</td><td>a. Use the pop-up menu to select ±.
b. Enter a tolerance For example 120 ± 1.5.</td></tr>
</table>
</td></tr>
<tr><td>3</td><td>Click a radio button to specify which peaks to label within this category:

<table>
<tr><th>If you want to label...</th><th>Then click this radio button...</th></tr>
<tr><td>all peaks</td><td>All peaks.</td></tr>
<tr><td>the highest peak</td><td>Highest peak.</td></tr>
<tr><td>the highest “n” peaks (where “n” is an integer)</td><td>Highest “n” Peaks, and type an integer for “n”.</td></tr>
<tr><td>left most peak in a range</td><td>Left peak.</td></tr>
<tr><td>right most peak in a range</td><td>Right peak.</td></tr>
</table>
</td></tr>
<tr><td>4</td><td>Click the dye color checkboxes for the colors you want labeled.</td></tr>
</table>

To add categories: *(continued)*

<table>
<tr><th>Step</th><th>Action</th></tr>
<tr><td>5</td><td>Optionally, define height requirements for peaks you want to label:

<table>
<tr><th>If you want to define...</th><th>Then select the...</th></tr>
<tr><td>a minimum height for labeled peaks</td><td>with (scaled) height of at least checkbox and type a number for the minimum peak height.</td></tr>
<tr><td>a maximum height for labeled peaks</td><td>with (scaled) height of at most checkbox and type a number for the maximum peak height.</td></tr>
</table>

The following table lists how the scale factor affects the scaled height of a peak.

<table>
<tr><th>If...</th><th>Then the scaled height of a peak is...</th></tr>
<tr><td>the dye/lane scale factor is 1.0</td><td>the same as the peak height.</td></tr>
<tr><td>a different scale factor has been calculated for a dye/lane</td><td>equal to the peak height divided by the Dye/lane's scale factor.</td></tr>
</table>
</td></tr>
<tr><td>6</td><td>Enter a name for the Category.

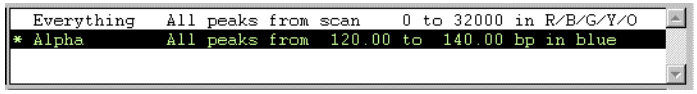
For example, Alpha.</td></tr>
<tr><td>7</td><td>Optionally, choose a display color for the Category from the pop-up menu.

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.</td></tr>
<tr><td>8</td><td>Optionally, enter a descriptive comment about the Category.

The comment will appear in the Category window after the name.</td></tr>
<tr><td>9</td><td>Click OK.

The name of the category appears in the Category list.



</td></tr>
</table>

Exclusive Peak Labeling

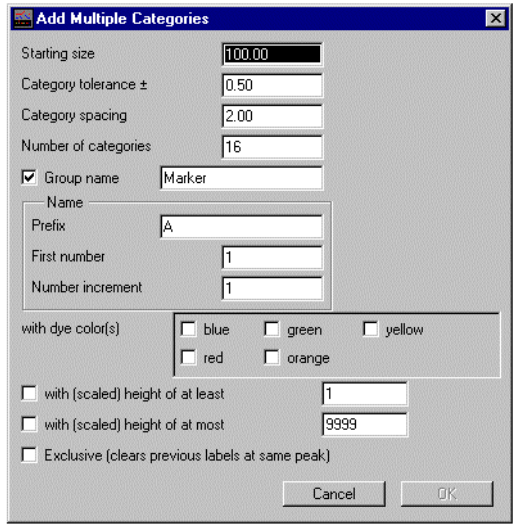
The Exclusive checkbox in the Add Category dialog box is a priority labeling feature. When you select the Exclusive checkbox, any existing labels on a peak, besides those defined by the “Exclusive” category, are removed.

For more details on using exclusive peak labeling see, “Using Exclusive Peak Labeling–An Example” on page 6-11.

Adding Multiple Categories

You can create multiple categories at once by using the Add Multiple 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.

To add multiple categories:

Step	Action
	Defining Categories
1	Choose Add Multiple Categories from the Category menu. The Add Multiple Categories dialog box appears. 
2	In the Starting size field, enter the starting size for fragments that you want to include in the first category.

To add multiple categories: *(continued)*

<table>
<tr><th>Step</th><th>Action</th></tr>
<tr><td>3</td><td>In the Category width ± field, enter the range of fragment sizes that you want to be included in the category.

For example, 100 ± .50 labels fragments that are between 99.5 to 100.5 base pairs in length as a single category.</td></tr>
<tr><td>4</td><td>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.</td></tr>
<tr><td>5</td><td>In the Number of Categories field, enter the number of categories that you want to create.</td></tr>
<tr><td>6</td><td>Select the dye color check boxes for the dye colors that you want included in the categories.</td></tr>
<tr><td colspan="2">Choosing Optional Parameters</td></tr>
<tr><td>1</td><td>Select the Group Name checkbox and type a name to include all categories under a single group name.</td></tr>
<tr><td>2</td><td>You can take the following action:

<table>
<tr><th>If you want to....</th><th>Then select the checkbox labeled...</th></tr>
<tr><td>limit the categories to only those peaks that generate a signal intensity of a least a particular height</td><td>“with (scaled) height of at least”, and enter a number.</td></tr>
<tr><td>limit the categories to only those peaks that generate signal intensity of at most a particular height.</td><td>“with (scaled) height of at most”.</td></tr>
<tr><td>clear any existing labels on peaks</td><td>Exclusive.</td></tr>
</table>
</td></tr>
<tr><td colspan="2">Naming the Categories</td></tr>
<tr><td>1</td><td>In the Prefix field, type a 1 to 15 character alpha numeric prefix for the category names.</td></tr>
<tr><td>2</td><td>In the First number field, enter the number to follow the prefix for the first category name.</td></tr>
<tr><td>3</td><td>In the Number increment, enter the number by which you want to increment each successive category number.</td></tr>
</table>

To add multiple categories: *(continued)*

Step	Action
4	Click OK.

Example of Category Naming

How Genotyper software 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 Exclusive option is a priority labeling feature. When the Exclusive check box is marked in the Add Category window, all other labels at peaks in the Exclusive category are cleared and the peak(s) is labeled with the desired information.

In general, category ranges should not overlap, but the Exclusive option allows you to use overlapping categories in special cases.

Example Application

In this example, the peaks of a marker occur between 105 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.”

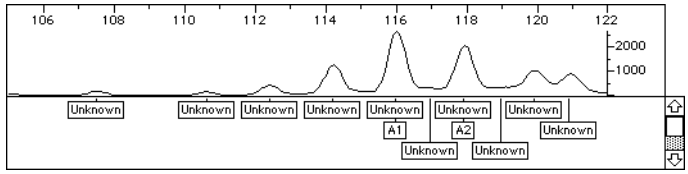
In the first part of the example, we will see what happens when the Exclusive option is not used. In the second part of the example, we will see how the Exclusive option allows us to obtain the desired results.

Labeling without the Exclusive Option

To label peaks *without* the Exclusive option:

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 Highest peak 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.

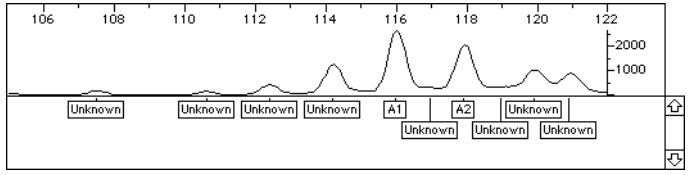
To label peaks *without* the Exclusive option: *(continued)*

Step	Action
3	View the Plot window, which should now look like the plot below.  **Note** The peaks at 116 bp and 118 bp each have two labels. This is one of the undesirable consequences of specifying overlapping category ranges

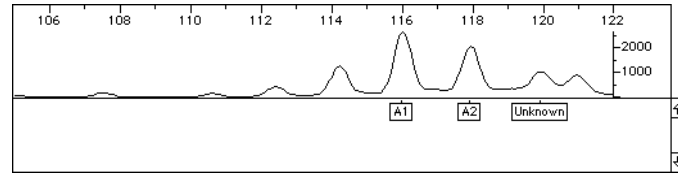
Using Exclusive Labeling

For this example, you can use the “A1” or “A2” labels exclusively for these peaks, by using the Exclusive option.

To label peaks using the Exclusive option:

Step	Action
	Labeling Peaks
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”. 
	Filtering Stutter Peaks
1	Choose Filter Labels from the Analysis menu.

To label peaks using the Exclusive option: *(continued)*

Step	Action
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.” 

Creating Category Groups—an Example

Introduction

Category groups may be useful when you want to identify individual alleles within the range of a marker category.

IMPORTANT If Category groups in the same dye color overlap, some commands may not perform as expected.

About This Example

In this example, you will make two sets of categories and specify the groups they are associated with. You will also collapse one of those sets of categories into a single entry in the Category list.

Note These categories are only for illustration and have no biological relevance.

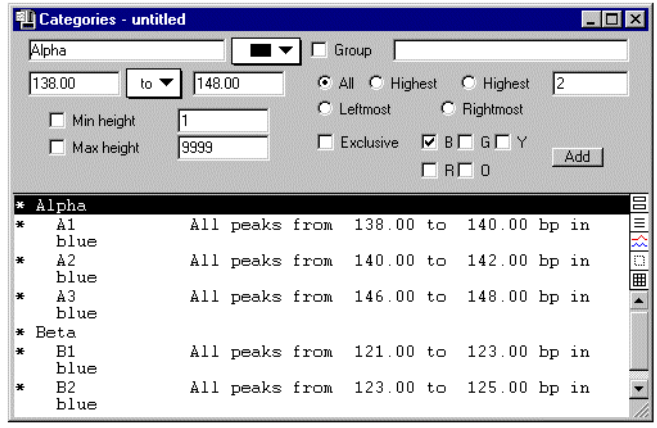
Creating a Category Group

Category groups organize groups of similarly defined categories under a single name.

To create two sets of categories and specifying the groups with which they are associated:

Step	Action
1	Choose Add Category (Ctrl+L) from the Category menu. The Add Category dialog box appears (step 1 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.

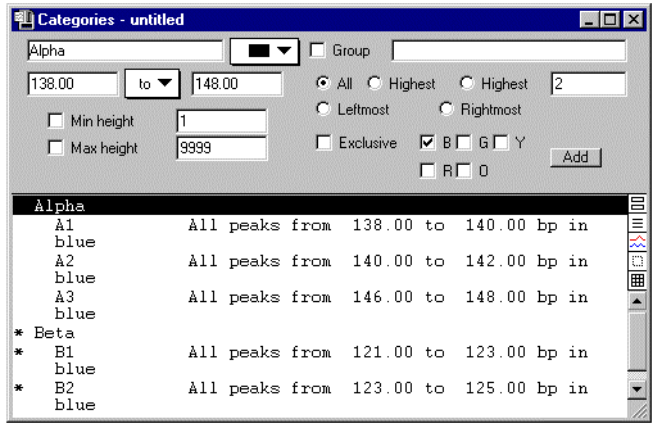
To create two sets of categories and specifying the groups with which they are associated: *(continued)*

Step	Action
8	Repeat step 2 to step 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 (Ctrl+K) from the Views menu. The Categories window shows the two marked Category groups you created. 

Unmarking a Group of Categories

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

To unmark the alpha Category group:

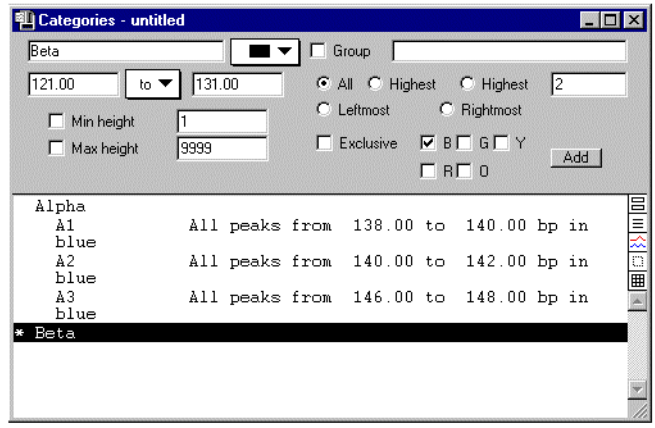
Step	Action
1	Select “Alpha” in the Categories window.
2	Choose Unmark (Ctrl+U) from the Edit menu. All three Categories in the Alpha group are now unmarked. 

If...	Then...
all Categories in a group are marked	the group will have a bullet next to its name.
some Categories in a group are marked, and some unmarked	the group name will have a dash (-) next to its name.

Collapsing a Group of Categories

Collapsing a group of categories can make viewing of the Category list 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 (Ctrl+]) from the Views menu.  The Beta group of categories is collapsed into a single line.

Making Category Members

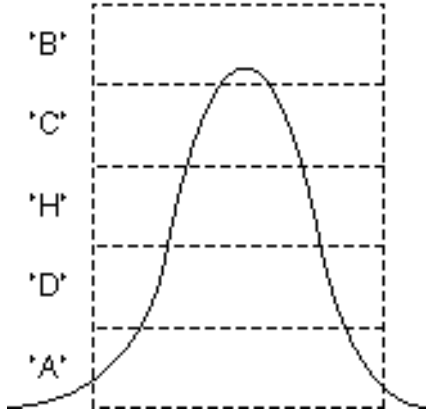
Introduction

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 PE Biosystems web site.

Example of Category Members

The following figure 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”.



Procedure

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.

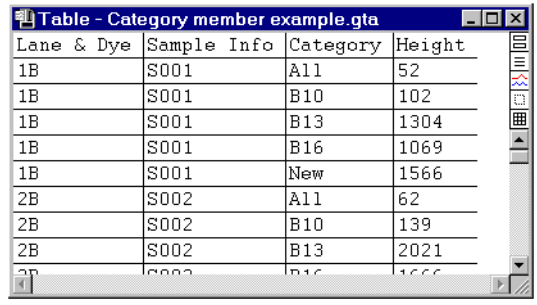
Note The following steps refer to an AFLP example soon to be available on the PE Biosystems web site.

To make category members:

<table>
<tr><th>Step</th><th>Action</th></tr>
<tr><td>1</td><td>Take the following action:

<table>
<tr><th>You can either...</th><th>Result</th></tr>
<tr><td>click the Table button.

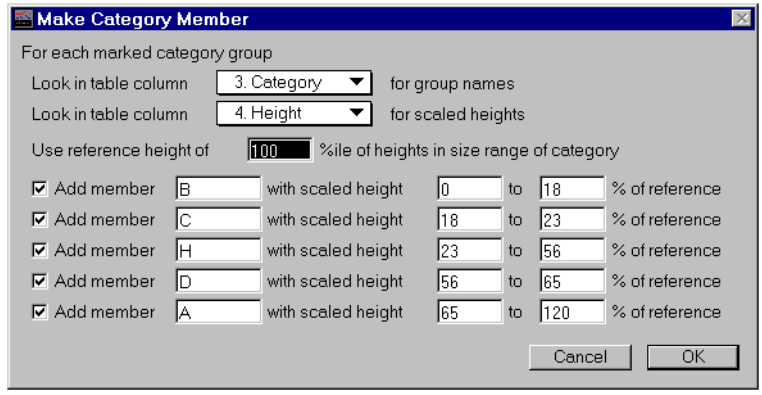
 </td><td rowspan="2">This displays a table with rows of peak height and category data.</td></tr>
<tr><td>choose Show Table Window (Ctrl+T) from the Views menu.</td></tr>
</table>

</td></tr>
<tr><td>2</td><td>Choose Make Category Members from the Category menu

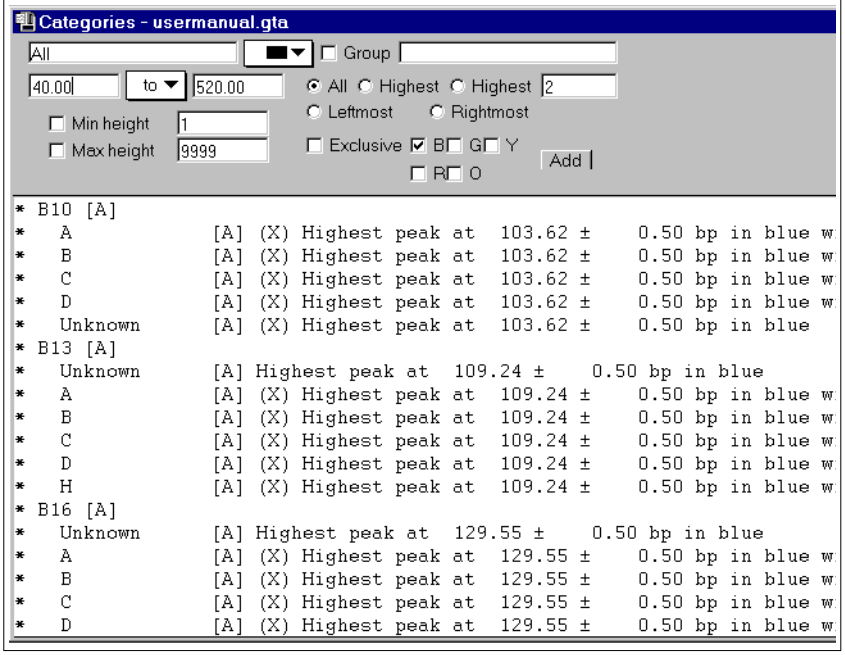
The Make Category Members dialog box appears.</td></tr>
</table>

To make category members: *(continued)*

Step	Action
	
3	Choose Category from the Look in table column for group names pop-up menu. This defines chosen categories as groups.
4	Choose Peak 1 from the Look in table column for scaled heights pop-up menu. For each marked category group, the Genotyper software calculates the distribution of peak heights (for the group) by looking at the appropriate rows in the table.
5	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	a. Select from one to five checkboxes for the number of members you want to add to each marked category. b. 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, the Genotyper software 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 (Ctrl+K) from the Views menu. The Categories window appears and displays new members for each category with varying scaled height ranges.

To make category members: *(continued)*

Step	Action



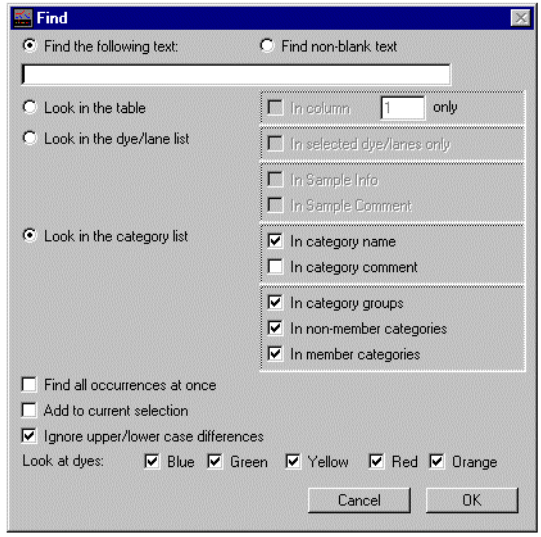
Searching for Categories

About Searching for Categories

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

Specifying Search Criteria

Steps for specifying search criteria:

Step	Action
1	Choose Find...(Ctrl+-F) in the Edit menu. The Find dialog box appears 
2	a. Click the Find the following text radio button. b. Type in the text that you want to locate in the text box.
3	a. Click the Look in the category list radio button. b. Select the checkboxes for where you want the Genotyper software to search for the text string that you have typed.
4	Select the checkboxes for how you want the Genotyper software to search for the text string that you have typed (see “Searching for Categories” on page 6-23).
5	Click OK.

Searching for Categories

Once you have defined search criteria (see “Specifying Search Criteria” on page 6-22), choose how you want to search for dye/lanes in the list.

The following table shows you how you can search for categories:

<table>
<tr><th>If you are...</th><th>Then...</th></tr>
<tr><td>Searching for all occurrences at once</td><td>click the Find all occurrences at once checkbox.

All dye/lanes with the designated text are selected.</td></tr>
<tr><td>Adding dye/lanes to the current selection</td><td>click the Add to current selection checkbox.

<table><tr><th>Dye/lanes...</th><th>Then...</th></tr><tr><td>already selected</td><td>remain selected.</td></tr><tr><td>located by this command</td><td>are also selected.</td></tr></table></td></tr>
<tr><td>Restricting the search to currently selected dye/lanes</td><td>click the In selected dye/lanes only checkbox.

This is useful for narrowing a selection by repeated use of the Find command.</td></tr>
<tr><td>Searching for the next occurrence of a selection</td><td>choose Find Next (Ctrl+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.</td></tr>
<tr><td>Searching for text strings without regard to case</td><td>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.</td></tr>
</table>

Sorting and Editing Categories

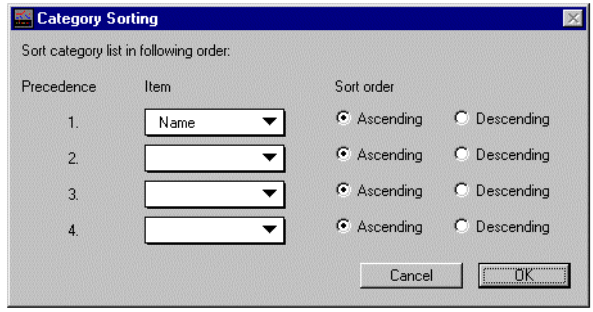
Introduction

Once you've created a number of different categories, you can easily sort the Category list, edit existing categories, and create new categories from existing ones.

Sorting the Categories List

You can change the sort order of the Category list.

To sort the Category list:

Step	Action
1	Choose Category Sorting from the Views menu. The Category Sorting dialog box appears. 
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.

Editing Category Parameters

Once you have added a category, you can edit the parameters for that category at any time.

To edit category parameters:

Step	Action
1	Select a category in the Category list.
2	Choose Edit Category from the Category menu. The Edit Category dialog box appears. This dialog is identical to the Add Category dialog box, except for the title (see step 1 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

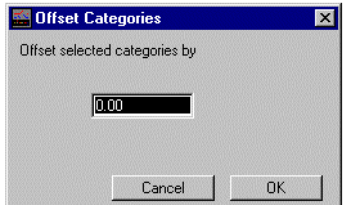
Two Ways to Offset Categories

There are two commands to temporarily shift the size range of a category.

Use this command...	To...
Offset Category command	adjust the size range for peak labeling for selected categories.
Calculate Offset command	automate the Offset Category command.
When to use the Calculate Offset Command	
Use 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.

Using the Offset Category Command

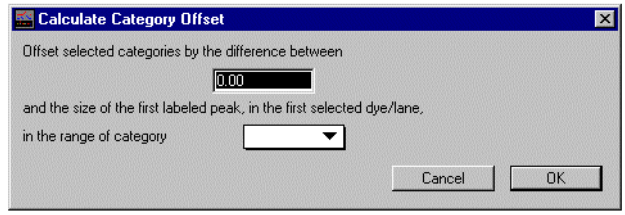
To use the Offset Category command:

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. 
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.

Step	Action
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...** / **Then...** 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.

Using the Calculate Offset Command

To use the Calculate Offset command:

Step	Action
1	Establish a standard set of category values for peak data for the GeneScan® Analysis Software files from each gel.
2	Choose Import from the File menu and From GeneScan File (Ctrl+I) from the submenu to import all the GeneScan files that you are using into 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 Category Offset dialog box appears. 
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

About Automatic Peak Labeling

Automatic peak labeling allows you to label peaks in selected dye/lanes using criteria defined in marked categories, and the Label Peaks dialog box.

Importance of Marking 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.

If You Produce Duplicate Labels

Repeated use of the Label Peaks command will produce duplicate labels of the same type at a peak. Remove all previously added labels by using the Clear All labels command.

Peak Label Limit

No more than 500 peaks should be labeled in any one dye/lane.

If...	Then...
more than 500 peaks are labeled	some commands (such as Filter Labels) may not be available.

Labeling Peaks Automatically

To automatically label peaks:

Step	Action
1	Mark categories that define how you want peaks labeled by taking the following action:

Step	Action
a.	Select one or more Categories from the Category list.
b.	Take the following action:

Either	Result
Choose Mark (Ctrl+M) or Unmark (Ctrl+U) from the Edit menu, or	A bullet appears to the left of categories, indicating the categories are marked.
Double-click a single category to toggle between a marked and unmarked state.	

Step	Action
2	Select the dye/lane or dye/lanes that contain the peaks you want to automatically label.
3	Choose Label Peaks from the Analysis menu. The Label Peaks window appears.
4	Click the appropriate checkboxes for what you want to appear on labels:

Step	Action

If you want to label peaks with...	Then click the...
fragment size in base pairs Size can be rounded to nearest integer. **Note** Only choose the rounded to integer checkbox if you are labeling large sized fragments where the number to the right of the decimal sign 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.	size in bp.
height in units defined by GeneScan Height can divided by Dye/lane scale factor.	peak height.
area in units defined by GeneScan Area can be divided by Dye/lane scale factor.	peak area.
number of scans required to detect the peak	scan number.
a pre-defined text description	text, and type in a peak label.
the category name.	category name.
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	peak modulation score.

5	Click OK.

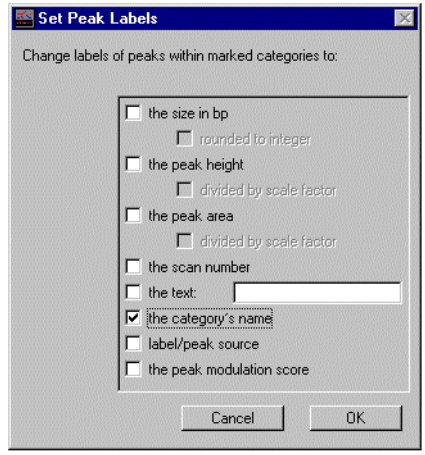
Viewing Labeled Peaks

To view the peak labels, click the Plot window icon ( ) to show the Plot data window.

Changing Existing Labels

The 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 Labels from the Analysis menu. The Change labels dialog box appears. 
2	Click the checkboxes for what you want to now appear on peaks with existing labels.
3	Click OK.

Filtering Labels

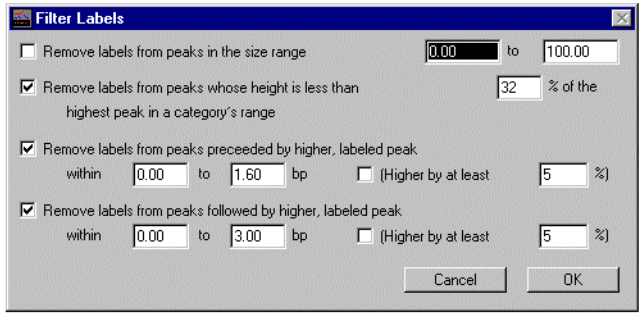
Definition

The Genotyper software 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.

Filtering Unwanted Labels

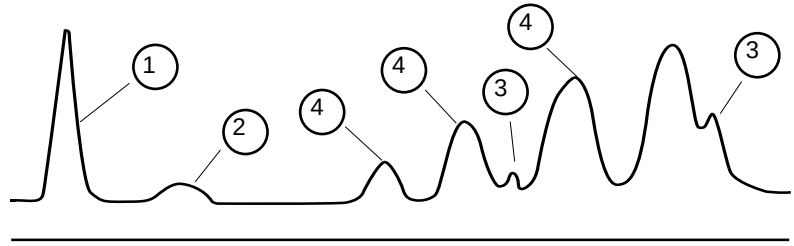
Note When viewing by scan, only the first option in the Filter labels dialog box is available. The other options are intended to be used only when viewing by size.

To filter unwanted labels:

Step	Action
1	Choose Filter Labels from the Analysis menu. The Filter Labels dialog box appears.  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 in the Filter Labels dialog box to remove labels from peaks that don't represent significant fragment data.

Kinds of Peaks You Can Filter

The following figure shows the kinds of peaks for which you can filter labels, and remove them from plot displays.



The following table describes each of the numbered peaks in the above figure:

Peak Number	Description	See...
1	Spurious peaks at known locations.	“Removing Spurious Peak Labels” on page 6-34.
2	Small peaks.	“Removing Labels from Small Peaks” on page 6-34.
3	Small peaks on the shoulders of stutter peaks (“+A” peaks).	“Removing Labels from Small Peaks on Peaks” on page 6-35.
4	Stutter peaks.	“Removing Stutter Peaks” on page 6-36.

Removing Spurious Peak Labels

About Spurious Peaks

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.

Procedure

To remove spurious peak labels at known locations:

Step	Action
1	In the Filter Labels dialog box: a. Click the first checkbox (Remove labels from peaks in the size range). b. Enter the size range of the spurious peaks that occur in selected electropherograms plots.
2	De-select the other checkboxes and click OK.

Removing Labels from Small Peaks

About Small Peaks

Small peaks close to the baseline are referred to as background noise, and can result from spectral overlap or other GeneScan Analysis Software matrix file problems.

Procedure

To remove small peaks:

Step	Action
1	In the Filter Labels dialog box: a. Click the second checkbox (Remove labels from peaks whose height is less than). b. 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 and click OK.

Removing Labels from Small Peaks on Peaks

Why You May Need to Remove Labels From Small Peaks

One of the most common errors in automated genotyping results from the tendency of Taq DNA Polymerase to add an additional (non-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 the Genotyper software. 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, the Genotyper software may recognize the +A bands as the true allele, resulting in a genotyping error of about 3-5%.

Procedure

To remove small peaks on the shoulders of allele peaks:

Step	Action
1	In the Filter Labels dialog box: a. Click the third checkbox (Remove labels from peaks proceeded by higher, labelled peak within) from the top. b. Enter the peak range, for peaks you want removed. **Note** 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.
2	De-select the other check boxes and click OK.

Removing Stutter Peaks

About Stutter Peaks

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

Procedure

To remove stutter peaks:

Step	Action
1	In the Filter Labels dialog box: a. Click the fourth checkbox (Remove labels from peaks followed by higher, labeled peak within) b. 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 and click OK.

Manually Placing Labels On Peaks

Introduction

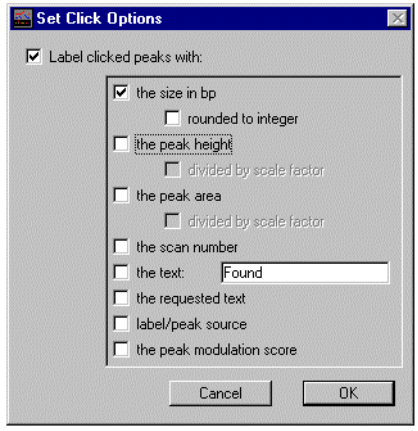
You can label individual peaks in plot displays by locating the peak or peaks of interest, and then clicking on the peak. When you click on the peak a second time, the label is removed.

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.

Manually Labeling Fragment Peaks

Use the Set Click Options dialog box to label fragment peaks manually, define what you want to appear in 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. 
2	Click the appropriate check boxes for what you want to appear on labels:

To manually label peaks: *(continued)*

Step	Action

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 want to label.
5	Move the cursor in the electropherogram part of the Plot area until the vertical line jumps to the peak that you want to label.
6	Click the peak with the mouse button. A label for that peak appears in the lower pane of the plot area.

Customizing Text in Labels

Introduction

Once you've 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.

Showing Labels that Have Been Manually Removed

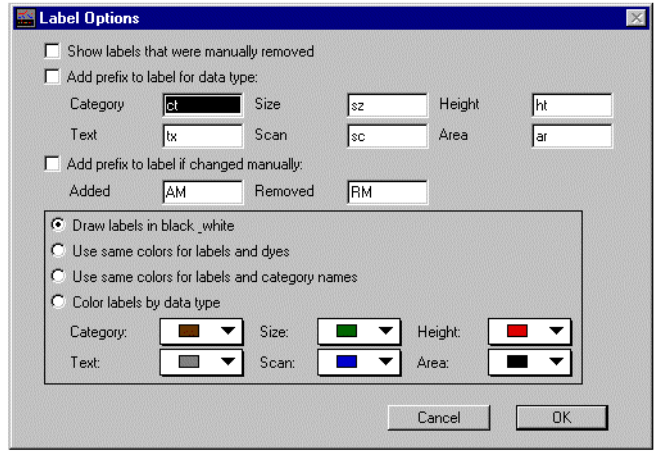
Why You May Want to Show Manually Removed Labels

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.

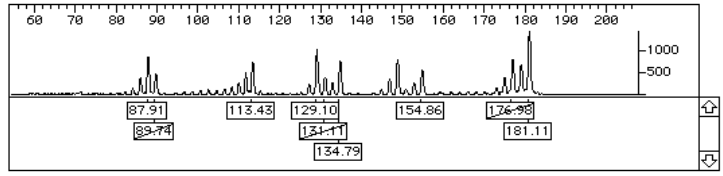
For more information on...	See...
removing labels from peaks	"Removing Labels" on page 6-47.
automatically labeling peaks	"Automatic Peak Labeling" on page 6-28.

Procedure

To show labels that have been manually removed:

Step	Action
1	Choose Plot Options from the Views menu and choose Label Options from the submenu. The Label Options dialog box appears. 

To show labels that have been manually removed: *(continued)*

Step	Action
2	Click the checkbox labeled Show labels that were manually removed. The Labels that have been manually removed are shown with slashes in plot displays. 

Adding Data Type Prefixes

Data Types and Associated Default Prefixes

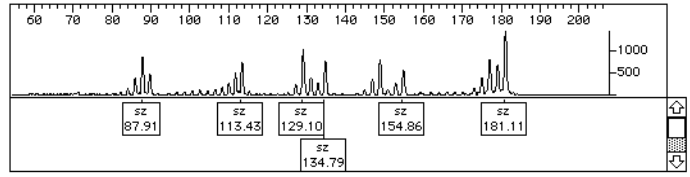
If you want to identify the data type of a peak label, you can add a prefix to labels that identify the type of the label.

The following table lists data types and associated default prefixes include:

Data type	Associated default prefix
Category	ct
Size	sz
Height	ht
Text	tx
Scan	sc
Area	ar

Procedure

To add data type prefixes to labels:

Step	Action
1	Click the Add prefix to label for data type checkbox in the Label Options dialog box.
2	Enter the prefixes you want or use the default prefixes.
3	Click OK. The labels are assigned prefixes for data type. The figure below shows an example of labels with size prefixes (sz). 

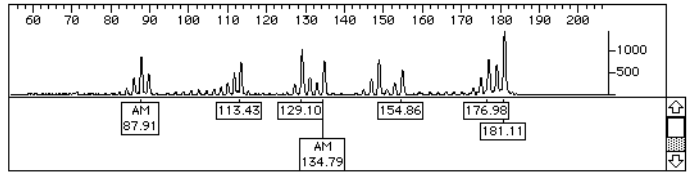
Adding a Prefix to Manually Changed Labels

You can add a prefix to labels to mark labels that were either added or removed manually.

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

Step	Action
1	Click the Add prefix to label if changed manually checkbox in the Label Options dialog box.
2	Enter the prefixes you want or use the default prefixes.

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

Step	Action
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

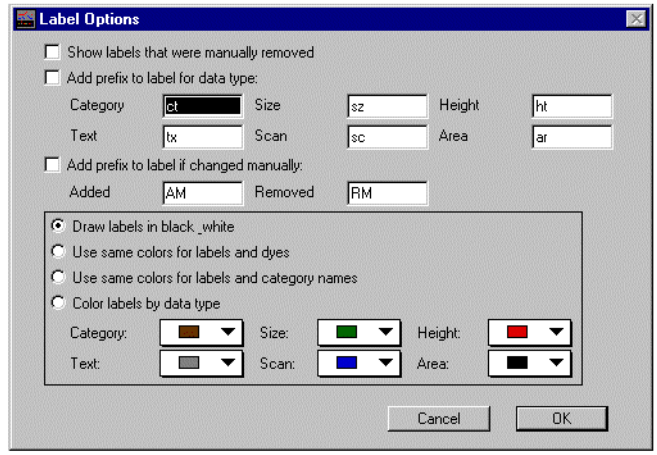
Introduction

To distinguish between different types of labels you can customize the color of the labels using the Label Options dialog box.

Drawing Labels in Black and White

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

To draw labels in black and white:

Step	Action
1	Select Plot Options in the Views menu and choose Label Options from the submenu The Label Options dialog box appears. 
2	Select the Draw labels in black and white radio button in the Label Options dialog box.
3	Click OK.

Using the Same Colors for Labels and Dyes

You can make peak labels the same color as their associated peaks. For example, blue electropherograms will have all blue labels and green 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 from the submenu. The Label Options dialog box appears.
2	Select the Use same colors for labels and dyes radio button.
3	Click OK.

Using the Same Colors for Labels and Category Names

Why Use the Same Colors for Labels and Category Names

The Add Category dialog (see step 1 on page 6-5) allows you to associate a color with a category for display purposes. The name of the category in the Category list will appear in this color. This option allows you to display labels that have the same color as a particular category.

Procedure

To color labels the same as associated categories:

Step	Action
1	Select Plot Options in the Views menu and choose Label Options from the submenu. The Label Options dialog box appears.
2	Select the Use same colors for labels and category names button.
3	Click OK.

Choosing Color Labels by Data Type

About Coloring Labels By Data Type

You can color labels according to the type of data that the label describes.

Data types include:

Category	Scan
Text	Height
Size	Area

Procedure

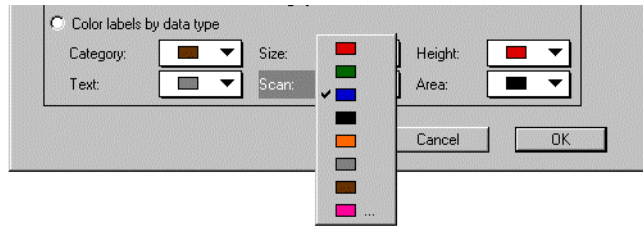
To color labels according to data type:

Step	Action
1	Select Plot Options in the Views menu and choose Label Options from the submenu.
2	Select the Color labels by data type radio button and click OK.
3	Click and hold down the pull-down menu for color selection by data type.
4	Select a color.
5	Repeat step 4 for each data type label you want to color. The data types appear in the selected colors in the Plot window.

Selecting a Custom Color for a Data Type Label

To select a custom color for a data type:

Step	Action
1	Select Plot Options in the Views menu and choose Label Options from the submenu. The Label Options dialog box appears.
2	Select Color labels by data type radio button and click OK.
3	Click and hold down the pull-down menu for color selection by data type.

Step	Action
4	Select the last color in the list, the one with the ellipsis (...).  A color dialog box appears. **Note** Selecting a custom color may temporarily change the highlight color.
5	Click on the color of your choice and click OK.
6	Repeat step 4 to step 5 for each data type color you want to change.

Removing Labels

Introduction

During a genotyping session, you will often want to remove fragment labels from peaks.

Ways to Remove Labels

The three ways to remove labels are by:

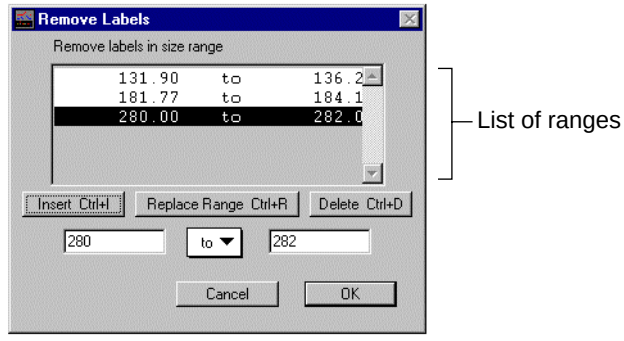
Method	See page
Removing All Labels	6-47
Removing Specific Labels	6-47
Removing Common Labels	6-49

Removing All Labels

If you want to remove all peak labels in all dye/lanes (whether selected or not), choose Clear All Labels from the Analysis menu.

Removing Specific Labels

To remove labels within a specified size range:

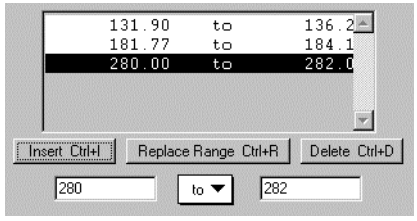
Step	Action
1	Select the dye/lanes from which you wish to remove labels.
2	Choose Remove Labels from the Analysis menu. The Remove Labels dialog box appears 

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

Step	Action
3	Type in the range in base pairs, then click Insert (Ctrl+I). The size range appears in the list of ranges. **Note** You can also specify the size range by choosing "±" from the pop-up menu, for example, 105 ± 10.
4	Repeat step 2 for each range you want to include.
5	Click OK. Labels in the specified ranges in all currently selected dye/lanes are cleared.

Correcting Errors in the Size Range

To correct size range errors in the Remove Labels dialog box:

Step	Action
1	Select the range from the range list. 
2	Type in the new range in the text boxes.
3	Click Replace Range (Ctrl+R).
4	Click OK.

Removing a Range From the Range List

To remove a range from the range list in the Remove Labels dialog box:

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

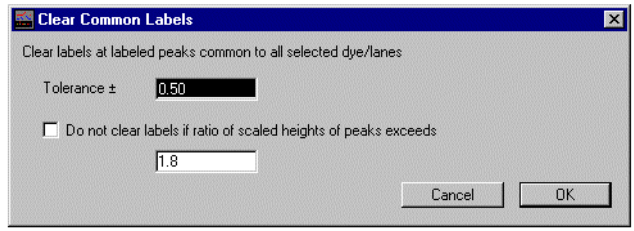
Removing Common Labels

When This Is Useful

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

Procedure

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.
2	Choose Clear Common Labels from the Analysis menu. The Clear Common Labels dialog box appears. 
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 all of the currently-selected dye/lanes. For example:

If...	Then...
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.

About This Example

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.

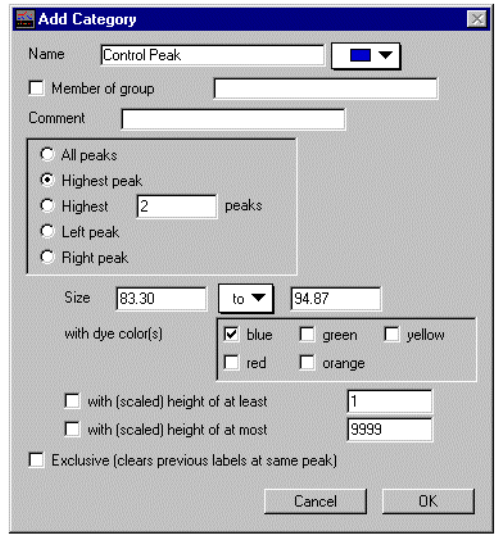
Defining a Control Peak

The first procedure in labeling normalized peaks is to define a control 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 (Ctrl+L) from the Category menu. The Add Category window appears.
4	Click the Highest peak radio button.
5	Name the Category Control Peak. The Add Category dialog box will look like the following figure.

To define a control peak: *(continued)*

Step	Action
	
6	Click OK.

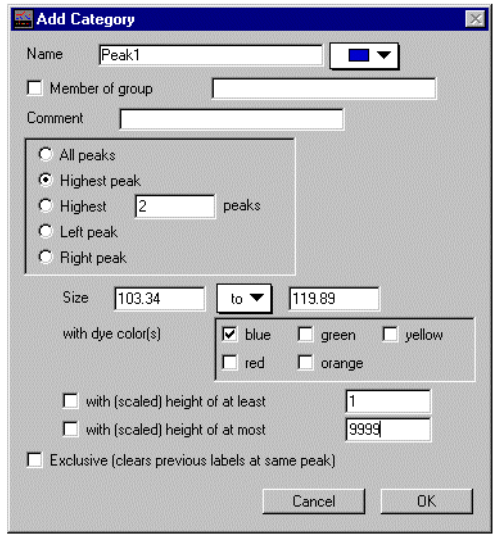
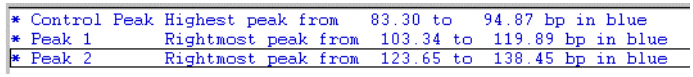
Normalizing Peaks to the Control Peak

Once 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 (Ctrl+L) from the Category menu.
3	Name the peak “Peak 1”.
4	Click the Highest Peak radio button. The Add Category dialog box will look like the following figure.

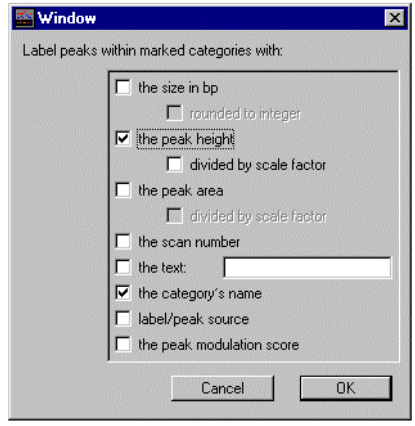
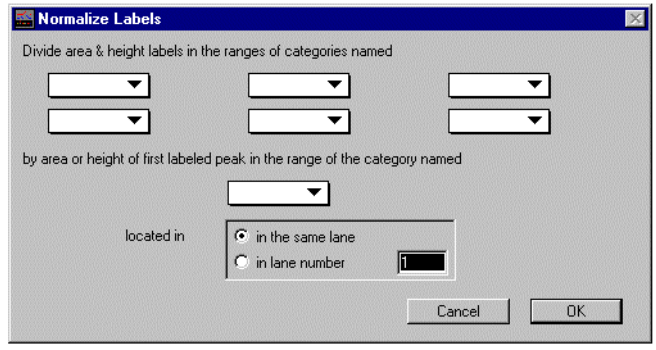
To normalize peaks to the control peak: *(continued)*

Step	Action
	
5	Click OK.
6	Repeat this procedure for another peak to be normalized. The Category list should now look like the following figure. 

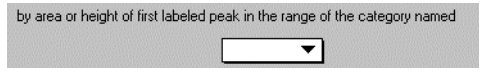
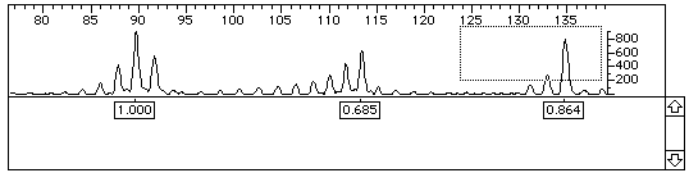
Labeling Normalized Peaks

Once you've defined a control peak, and the other peaks to be normalized, you can label them.

To label the peaks:

Step	Action
1	Choose Label Peaks from the Analysis menu. The Label Peaks dialog box appears. 
2	Click the peak height and/or peak area check box and click OK
3	Choose Normalize Labels from the Analysis menu. The Normalize Labels dialog box appears. 
4	From the upper set of pop-up menus, choose the Categories to be normalized, for example, Control peak, Peak1, and Peak2.

To label the peaks: *(continued)*

Step	Action
5	From the middle pop-up menu, choose the name of the Category you defined as a control, for example Control Peak. 
6	Click the radio button labeled “in the same lane”.
7	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 Labels

Genotyping applications for which making categories from labels may be useful include:

- 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 9-24.

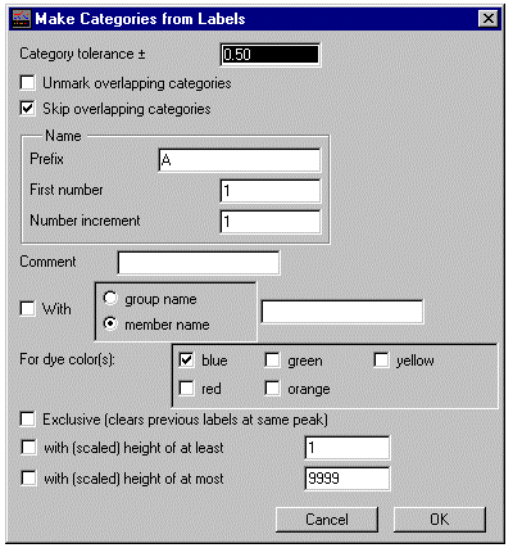
Procedure

For select dye/lanes, you can make a separate category for each labeled peak according to what you have specified for each peak label.

To make categories from labels:

Step	Action
1	Import the GeneScan files, for either allelic ladders or AFLP studies, by choosing Import from the File menu and From GeneScan File (Ctrl+I) from the submenu.
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 Categories from Labels dialog box appears. 
5	Type in the Category tolerance.
6	Select checkboxes for either including, or skipping overlapping categories.
7	Name categories that will be created. For information on how the Genotyper software names categories see “Example of Category Naming” on page 6-10.
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 type in the name...
a group to which you can add member categories	member name	of the first member of the group.
a member of a group	group name	of the group.

To make categories from labels: *(continued)*

<table>
<tr><th>Step</th><th>Action</th></tr>
<tr><td>9</td><td>You can take the following action:
<table>
<tr><th>If you want to....</th><th>Then select the checkbox labeled...</th></tr>
<tr><td>limit the categories to only those peaks that generate a signal intensity of a least a particular height</td><td>“with (scaled) height of at least”, and enter a number.</td></tr>
<tr><td>limit the categories to only those peaks that generate signal intensity of at most a particular height.</td><td>“with (scaled) height of at most”.</td></tr>
<tr><td>clear any existing labels on peaks</td><td>Exclusive.</td></tr>
</table></td></tr>
<tr><td>10</td><td>When you are satisfied with all your choices for defining categories, click OK.

The Genotyper software makes a category for each peak that has a label.</td></tr>
</table>

Working with Plot Data 7

Chapter Overview

Introduction Genotyper Documents display dye/lane data as electropherogram plots. This chapter explains how to make use of the many options the Genotyper® 3.5 NT software offers for viewing, interpreting, and customizing plot displays within a Genotyper Document.

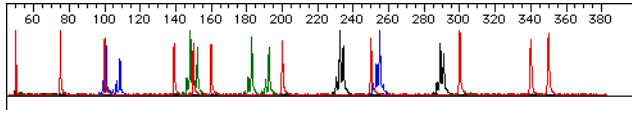
In This Chapter This chapter contains the following topics:

Topic	See page
Viewing Plots of Imported Dye/Lanes	7-2
Viewing and Interpreting Peak Data	7-8
Zooming In and Out	7-13
Customizing Plot Areas	7-17
Viewing Table Data in Plots	7-24
Comparing Plot Data to Reference Plots	7-26

Viewing Plots of Imported Dye/Lanes

Introduction

The Genotyper software generates plot data from imported dye/lanes in the form of electropherograms.



Electropherogram Defined

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 the GeneScan® Analysis Software.

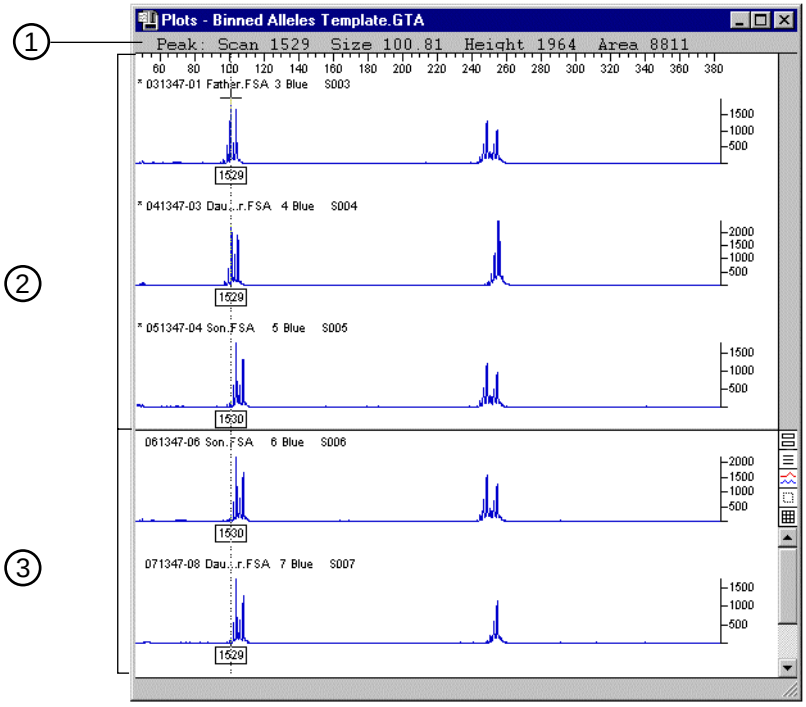
Plot Window

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.

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 (Ctrl+Y) from the Views menu to view all the labels.

Plot Window Example

The following is an example of the Plot window.



Parts of the Plot Window

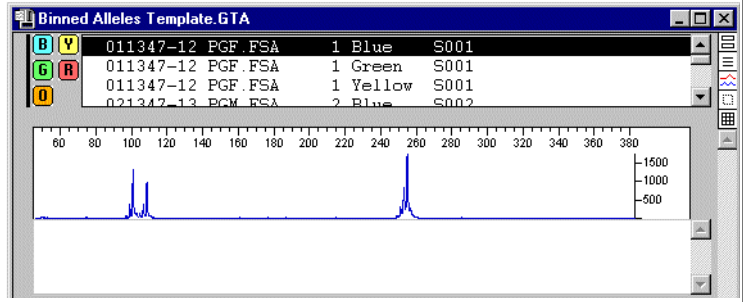
Parts of the Plot window.

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.

Viewing 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:

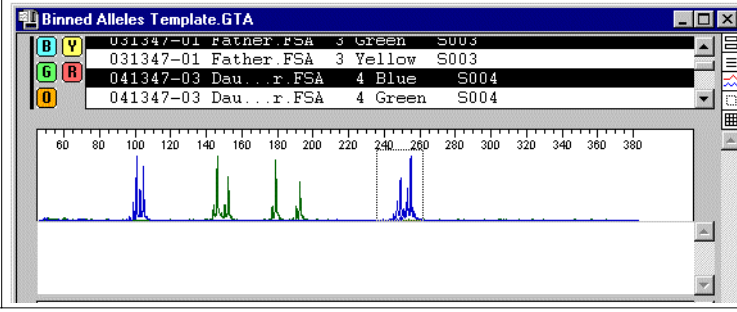
Step	Action
1	In the Dye/lane list, locate the dye/lane for which you want to display plot data.
2	Select the dye/lane in the Dye/Lane list. An electropherogram plot showing peaks for each analyzed nucleic acid fragment in the sample appears in the Plot Area.  The following table describes the vertical and horizontal scale in the above electropherogram. **Scale** / **Description** The vertical scale on the right — Shows the relative peak height. Thedefault horizontal scale at the top — Shows the fragment length.
3	You can take the following action: **You can either....** / **Result** click the Plot window icon ( ). — The Plot window opens, displaying electropherograms for each selected dye/lane. choose Show Plot Window (Ctrl+Y) from the Views menu. For information on the Plot window, see “Plot Window” on page 7-2.

Viewing Plots of Multiple Dye/lanes

You can view an electropherogram plot showing all detected peaks for 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 the Genotyper software 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.

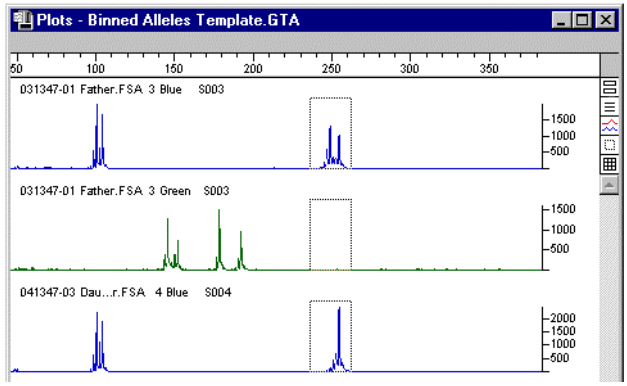
To show plot data for multiple dye/lanes:

Step	Action
1	In the Dye/lane list, click the Ctrl-key and select the dye/lanes for which you want to display plot data. 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. 

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

Step	Action
2	To view each selected dye/lane as an individual electropherogram plot:

You can either....	Result
click the Plot window icon ( ).	The Plot window opens, displaying electropherograms for each selected dye/lane.
choose Show Plot Window (Ctrl+Y) from the Views menu.	



Determining the Order of Plot Display

The following table describes the order of the plot display.

For plots derived from...	Then the order...
the dye/lane list	that the plots are displayed is determined by the dye/lane list order preferences (determined by the Dye/lane Sorting command).
table rows	the plots is determined by the table row order.

Low Memory Warning

If a dark gray background appears in the plot area, the Genotyper software is running low on memory. Save your work as soon as possible, quit from Genotyper, then allocate more memory to Genotyper.

Viewing and Interpreting Peak Data

Introduction

Peak data in electropherograms can show you size and quantity data for imported GeneScan files.

The following are some key terms for interpreting peak data.

Term	Description
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.

GeneScan Peak Data Results

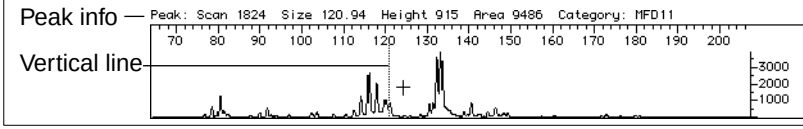
You can view the following data for peaks resulting from GeneScan Analysis Software analysis of electrophoresed sample fragments:

Scan number	Peak height
Peak size	Peak area
Genotyper Category	

Viewing GeneScan Peak Data

To view GeneScan peak data:

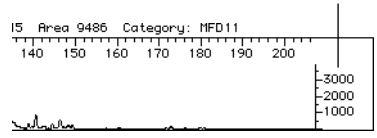
Step	Action
1	Select dye/lanes of interest, and view plot data. **You can either....** / **Result** click the Plot window icon ( ). — The Plot window opens, displaying electropherograms for each selected dye/lane. choose Show Plot Window (Ctrl+Y) from the Views menu.
2	Use the mouse to move the cross hairs along the plot. The vertical line "jumps" from peak to peak. Information about each peak appears above the horizontal scale.



Viewing Relative Peak Size and Quantity

The horizontal and vertical scales for plot data can inform you of the 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...
the relative quantity of a dye/lane fragment	vertical scale (see below). It displays fragment quantity in terms of peak height. Vertical scale 
the relative length of a dye/lane fragment in base pairs	default horizontal scale at the top is fragment length in base pairs.

To view approximate size and quantity values for peak data:

If you want to know...	Then read the...
relative time required for a dye/lane fragment to be detected	default horizontal scale at the top is fragment length in base pairs. You can change this scale to Scan number.

Changing the Size and Quantity Scale

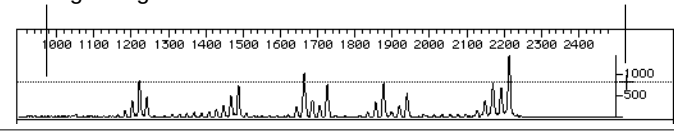
To change the size and quantity scale:

Step	Action
1	Select dye/lanes of interest, and view plot data. **You can either....** / **Result** click the Plot window icon ( ). — The Plot window opens, displaying electropherograms for each selected dye/lane. choose Show Plot Window (Ctrl+Y) from the Views menu.
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** The following table lists the consequences if you did not use the GeneScan Analysis Software. **If...** / **Then...** you did not use the GeneScan Analysis Software 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. To view the electropherogram, choose Display by Scan from the Views menu. The text No Size Data will appear in the Plot area.

Comparing Peak Heights

For qualitative comparisons of fragment quantities in select dye/lanes, 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. **You can either....** / **Result** click the Plot window icon ( ). — The Plot window opens, displaying electropherograms for each selected dye/lane. choose Show Plot Window (Ctrl+Y) from the Views menu.
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” 

Adjusting Peak Heights

About Adjusting Peak Heights

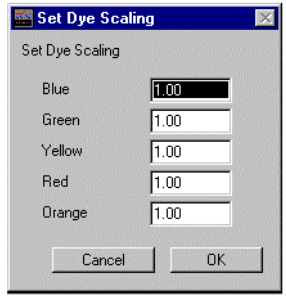
You can adjust the signal height of peaks by choosing a scaling factor for each of the four dye colors. Dye scaling affects only the appearance of the electropherogram plots. All other data, such as the values appearing in the cursor information line above the plot, remain unchanged

Procedure

To adjust the height of dye-colored peaks:

<table>
<tr><th>Step</th><th>Action</th></tr>
<tr><td>1</td><td>Select dye/lanes of interest, and view plot data.
<table>
<tr><th>You can either....</th><th>Result</th></tr>
<tr><td>click the Plot window icon ( ).</td><td rowspan="2">The Plot window opens, displaying electropherograms for each selected dye/lane.</td></tr>
<tr><td>choose Show Plot Window (Ctrl+Y) from the Views menu.</td></tr>
</table></td></tr>
<tr><td>2</td><td>Choose Plot Options from the Views menu and Dye Scaling from the submenu.

The Set Dye Scaling dialog box appears.

Signal heights for each color are multiplied by the indicated factor before being plotted.

The vertical scale reflects the adjusted heights.</td></tr>
<tr><td>3</td><td>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.

For example, if you want all the blue peaks to display at half of their current height, type in .50.</td></tr>
<tr><td>4</td><td>Click OK.</td></tr>
</table>

Zooming In and Out

About Zooming

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.

Zooming 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:

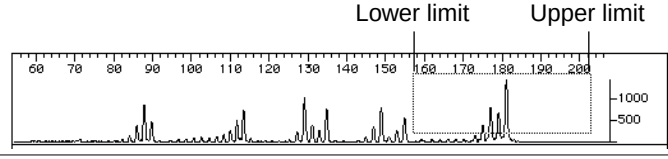
Step	Action
1	Select dye/lanes of interest, and view plot data.
2	

You can either....	Result
choose Zoom from the Views menu and Zoom In from the submenu, or	You can now view the middle 50% of the plot.
press the Ctrl+(equal sign) keys.	

Zooming in on a Selected Range

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

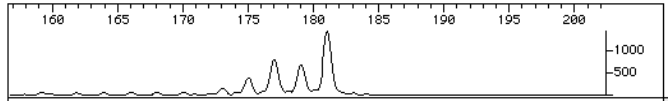
To zoom in on a selected range of the Plot Area:

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. 

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

Step	Action
3	

You can either....	Result
choose Zoom from the Views menu and Zoom In (Selected Range) from the submenu, or	The range you selected is magnified to fill the Plot Area.
press the Ctrl+R keys.	



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.

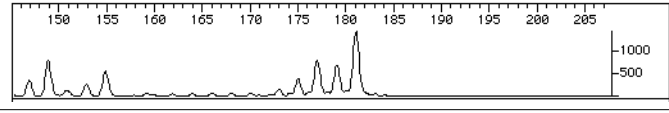
Zooming Out

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

To zoom out for a broader view of the plot:

Step	Action
1	Select dye/lanes of interest, and view plot data.
2	

You can either....	Result
choose Zoom from the Views menu and Zoom Out from the submenu, or	You can now view about 50% more of the plot.
press the Ctrl+(minus sign) keys.	



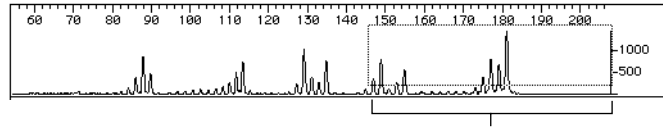
Zooming Out to Full Range

Zoom out to full range to view all of the peaks in select dye/lanes.

To zoom out to view the entire plot:

Step	Action
1	Select dye/lanes of interest, and view plot data.
2	

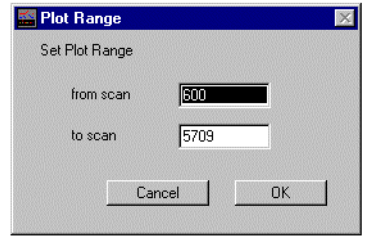
You can either....	Result
choose Zoom from the Views menu and Zoom Out (Full Range) from the submenu, or	You can now view the entire plot. The range you selected is magnified to fill the Plot Area. The dotted rectangle in the plot area indicates the range limits that existed before you zoomed out to full range.
press the Ctrl+H keys.	



Range limits before zooming out

Zooming to a Specific Range

You can specify a range of peaks that you want to view in the Plot Area.The following table lists how to zoom to ranges that you specify.

If you want to zoom to...	Then...
a specific size range of fragments	a. Choose Zoom from the Views menu and Zoom to from the submenu. The Set Plot Range dialog box appears.  b. Enter the plot range (from scan__to scan). c. Click OK.
the range of one or more Categories	a. Select one or more categories in the Categories list. b. Choose Zoom from the Views menu and Zoom To Category from the submenu. You can now view the range that includes the range of the selected categories.
the range of the next marked, unselected Category	Choose Zoom from the Views menu and Zoom To Next Category (Ctrl+J) from the submenu. The next marked Category in the plot is selected automatically.

Customizing Plot Areas

Default Plot Areas

The following lists the default plot areas in the Main window:

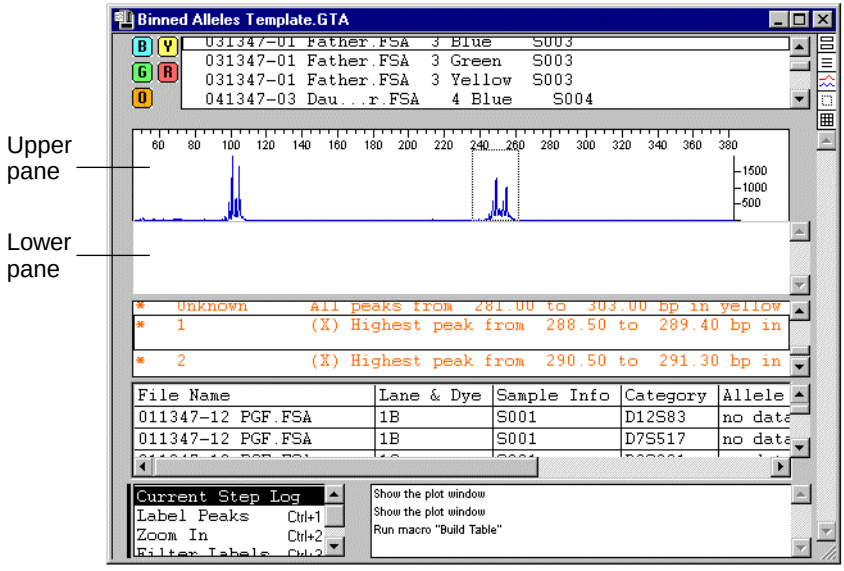
The...	Is the...
upper graphical pane	electropherogram view area.
lower graphical pane	reserved from peak labels.

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.

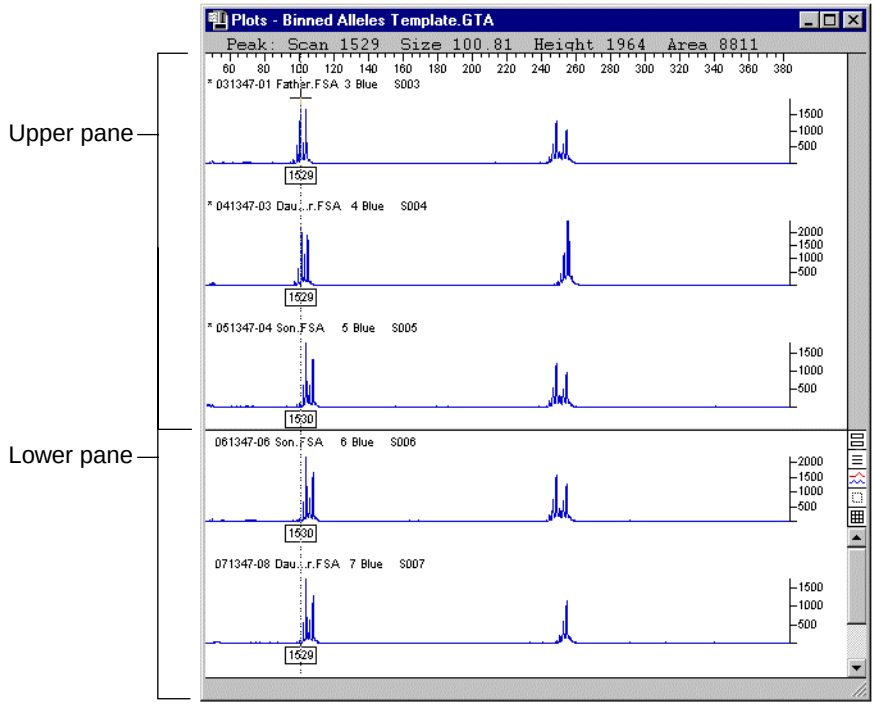
Note You can set the Plot Options for the Plot window only when the Plot window is displayed.

Main Window Plot Area

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



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



Customizing Plot Displays

The following table lists how to customize the plot display in the upper and lower panes of either the:

- Main window (see “Main Window Plot Area” on page 7-17) or the
- Plot window (see “Plot Window Panes” on page 7-18).

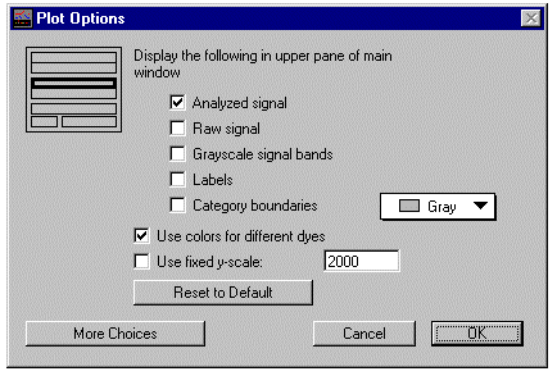
To customize plot displays:

Step	Action
1	Choose the kind of plot display that you want to customize.

If you want to customize...	Then...
The Main window	
Upper pane	select Plot Options from the Views menu and Main Window, Upper Pane from the submenu.
Lower pane	select Plot Options from the Views menu and Main Window, Lower Pane from the submenu.
The Plot window	
Upper pane	select Plot Options from the Views menu and Plot window, Upper Pane from the submenu.
Lower pane	select Plot Options from the Views menu and Plot Window, Lower Pane from the submenu.

2	The Plot Options dialog box appears. The following is an example of the Plot Options dialog box used to customize the upper pane of the main window.

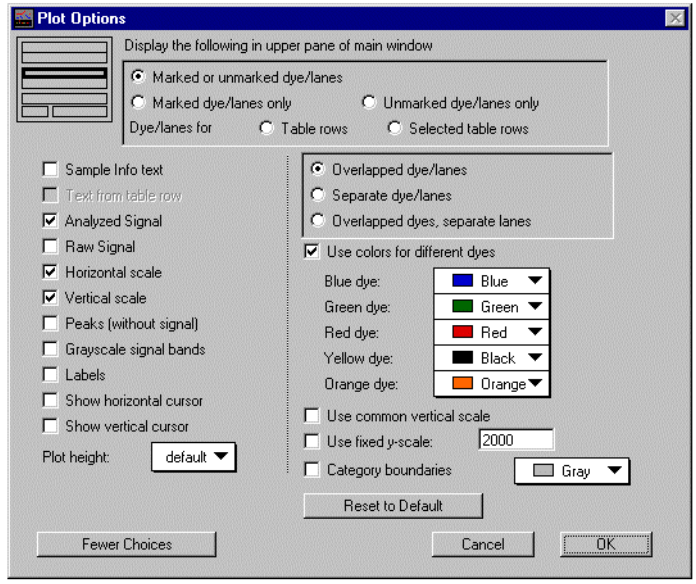
To customize plot displays: *(continued)*

Step	Action
	
3	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 the GeneScan Analysis Software.
Raw signal	peaks from fragments that have not been baselined or analyzed by the GeneScan Analysis Software.
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 the 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. Not recommended for Main window displays or overlapped displays.

Adding More Detail to the Plots

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. 
2	Choose the radio buttons for the kind of plot you want to view.

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

Step	Action

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.

3	Select the checkboxes for kind of data to include in each plot:

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

<table>
<tr><th>Step</th><th>Action</th></tr>
<tr><td></td><td>
<table>
<tr><th>If you click...</th><th>Then the plot area displays...</th></tr>
<tr><td>Sample Info text</td><td>text for associated Sample Info field.</td></tr>
<tr><td>Analyzed Signal</td><td>plots of peaks that have been baselined and analyzed by GeneScan Analysis Software.</td></tr>
<tr><td>Raw Signal</td><td>fluorescent signal before GeneScan analysis.</td></tr>
<tr><td>Horizontal scale</td><td>a horizontal scale.</td></tr>
<tr><td>Vertical scale</td><td>a vertical scale.</td></tr>
<tr><td>Peaks (without signal)</td><td>a vertical line for each peak.</td></tr>
<tr><td>Grayscale signal bands</td><td>bands similar to a Autoradiograph.</td></tr>
<tr><td>Labels</td><td>any labels put on peaks.</td></tr>
<tr><td>Show horizontal cursor</td><td>a horizontal cursor.</td></tr>
<tr><td>Show vertical cursor</td><td>a vertical cursor.</td></tr>
<tr><td>Use common vertical scale</td><td>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.</td></tr>
<tr><td>Use fixed y-scale</td><td>All plots drawn to the specified vertical space.
Note When selected, then Use common vertical scale is disabled.</td></tr>
<tr><td>Use colors for different dyes</td><td>All dye colors in a lane superimposed on each other, but each lane appears separately from the others.</td></tr>
</table>
</td></tr>
<tr><td>4</td><td>In the Plot height pop-up menu, you can adjust the height of plots that display in the Plot Area as follows:
<table>
<tr><th>If you choose...</th><th>Then the Plot Area...</th></tr>
<tr><td>small</td><td>fits more plots in the window.</td></tr>
<tr><td>default</td><td>shows a medium-sized plot.</td></tr>
<tr><td>large</td><td>shows more detail in the plot.</td></tr>
</table>
</td></tr>
<tr><td>5</td><td>Click OK to accept your selections.</td></tr>
</table>

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 7-3.

Plot Data Associated with Dye/lanes

The Genotyper software software 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.

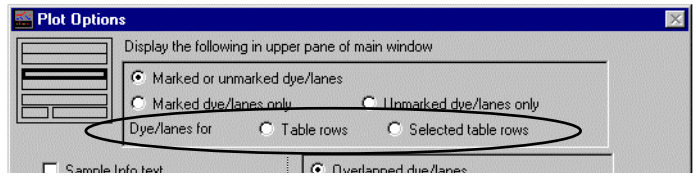
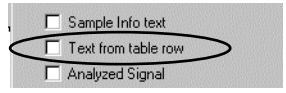
Showing Table Data in Plots

When displaying 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 information you want to display in the Plot window.
2	Open the Plot window from the Main window by either: ♦ Choosing Show Plot Window (Ctrl+Y) from the Views menu, or ♦ Clicking the Plot window icon ( ).
3	Open the Table window by either: ♦ Choosing Show Table Window (Ctrl+T) from the View menu, or ♦ Clicking the Table window icon ( ).
4	Select the rows in the table for which you want to display corresponding plots. **Note** A row is considered selected if any cell in the table is selected.
5	Choose the Plot Options from the Views menu and Plot Window, Lower Pane from the submenu. The Plot Options dialog box appears, with the lower pane selected.
6	Click the More Choices button.

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

Step	Action
7	In the Dye/lanes for box, choose one of the radio buttons:  **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.
8	If you selected the Table rows radio button in step 7, then if you want to display the row text in the corresponding plot display, select the Text from table row checkbox. 
9	Click OK. The Plot Window displays plots and associated information for selected table rows.

Automatic Scrolling

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

Comparing Plot Data to Reference Plots

Process

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 (see “Plot Window” on page 7-2).

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 Reference Plots

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

To set up reference plots:

<table>
<tr><th>Step</th><th>Action</th></tr>
<tr><td>1</td><td>In the Dye/lane list, click the Ctrl-key and select the dye/lanes for which you want to display reference plots.</td></tr>
<tr><td>2</td><td>Take the following action:
<table>
<tr><th>You can either...</th><th>Result</th></tr>
<tr><td>choose the Mark Command (Ctrl+M) from the Edit menu, or</td><td rowspan="2">The lanes that you selected are marked with a bullet.

The bullet signifies that plots for those dye/lanes are reference plots.</td></tr>
<tr><td>double-click the dye/lanes, marking them with a bullet.</td></tr>
</table></td></tr>
<tr><td>3</td><td>Press the Ctrl+key and select the dye/lanes you marked as reference plots, and any dye/lanes that you want to compare to the reference plots.</td></tr>
</table>

To set up reference plots: *(continued)*

<table>
<tr><th>Step</th><th>Action</th></tr>
<tr><td>4</td><td>To display an expanded view of the Plot window:

<table>
<tr><th>You can either....</th><th>Result</th></tr>
<tr><td>click the Plot window icon ( ).</td><td rowspan="2">The Plot window opens, displaying electropherograms for each selected dye/lane.</td></tr>
<tr><td>choose Show Plot Window (Ctrl+Y) from the Views menu.</td></tr>
</table>

The Plot window shows the following:

<table>
<tr><th>The...</th><th>Displays...</th></tr>
<tr><td>upper pane</td><td>reference plots

Note The upper pane does not scroll, so you will probably want one or two dye/lanes displayed in this lane.</td></tr>
<tr><td>lower pane</td><td>plots for the dye/lanes than you want to compare to the reference plots.

You can scroll the plot data in the lower pane.</td></tr>
</table>
</td></tr>
</table>

8 Working with Tables

Chapter Overview

In This Chapter

Putting your results data into a table allows you to organize it in a manner meaningful to your genotyping application. You can use tabular data for comparison analysis, as well as export results to a database.

This chapter contains the following topics:

Topic	See page
Setting Up a Table	8-2
Arranging Columns of Labeled Peak Data	8-8
Specifying Columns for Number of Labels in a Row	8-11
Specifying Warning Columns for Edited Tables	8-13
Specifying Modulation Warning Columns	8-16
Specifying Low-signal Warning Columns	8-18
Specifying Saturation Warning Columns	8-20
Calculating Results from Table Data	8-22
Analyzing Data in Tables	8-27
Using Analyze and Calculate in Table Commands–An LOH Example	8-33
Editing Table Cells and Column Headings	8-33
Sorting the Rows in a Table	8-36
Searching for Table Entries	8-39
Updating Tables	8-41
Deriving a Second Table from an Existing Table	8-42
Formatting Tables for Export	8-43
Exporting and Copying Tables	8-44

Setting Up a Table

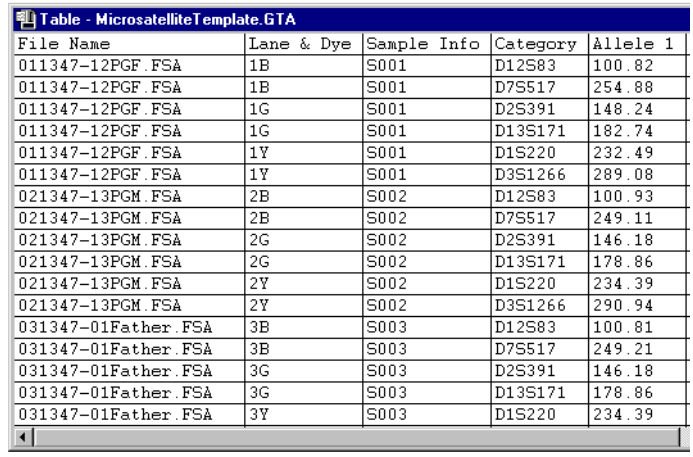
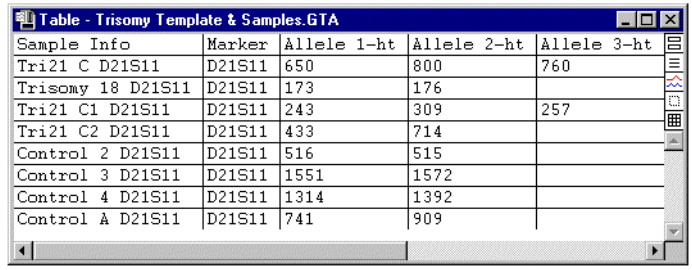
Sources of Table Data

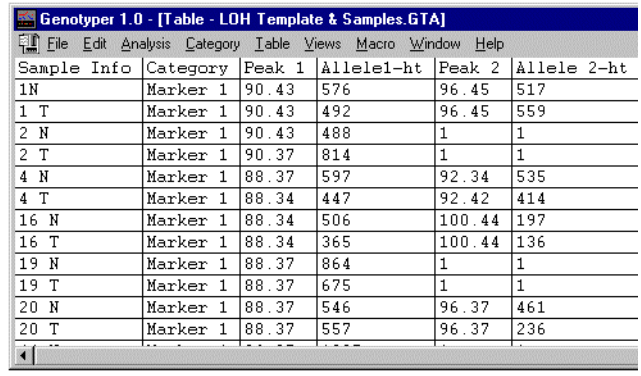
Table contents are generated from labeled fragment peaks within select dye/lanes. Before setting up a table make sure that the appropriate dye/lane peaks are labeled with the kind of information that you want to present in your table.

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

Choosing a Table to Create

The choices of tables you can create for different genotyping applications are as follows:

For this genotyping application...	You can create this kind of table...
Linkage Mapping	
Gene Expression Profiling	

For this genotyping application...	You can create this kind of table...
Loss of Heterozygosity	

Genotyper 1.0 - [Table - LOH Template & Samples.GTA]

File Edit Analysis Category Table Views Macro Window Help

Sample Info	Category	Peak 1	Allele1-ht	Peak 2	Allele 2-ht
1N	Marker 1	90.43	576	96.45	517
1 T	Marker 1	90.43	492	96.45	559
2 N	Marker 1	90.43	488	1	1
2 T	Marker 1	90.37	814	1	1
4 N	Marker 1	88.37	597	92.34	535
4 T	Marker 1	88.34	447	92.42	414
16 N	Marker 1	88.34	506	100.44	197
16 T	Marker 1	88.34	365	100.44	136
19 N	Marker 1	88.37	864	1	1
19 T	Marker 1	88.37	675	1	1
20 N	Marker 1	88.37	546	96.37	461
20 T	Marker 1	88.37	557	96.37	236

Column Number Limit

There is a limit of 128 columns in a table.

Determining Row Contents

The Genotyper® 3.5 NT software generates row contents from dye/lanes in the Dye/lane list and categories in the Category list.

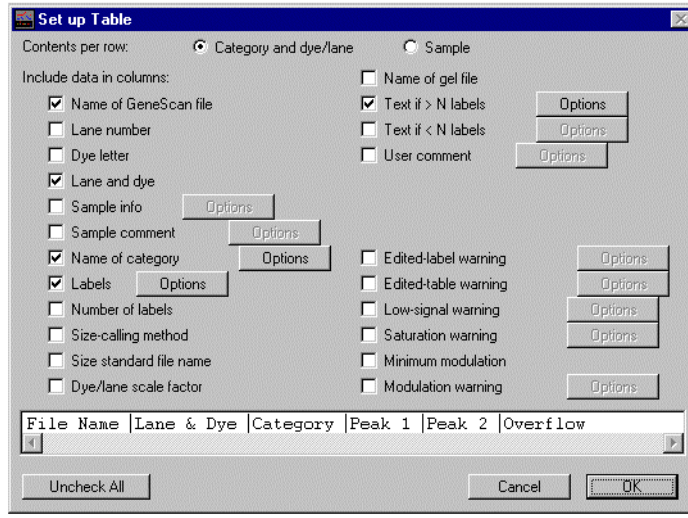
To determine row contents in your table:

Step	Action
1	Select those categories in the Category List that define the kind of peak data that you want to include in the table and take the following action:

You can either...	Result
choose the Mark Command (Ctrl+M) from the Edit menu, or	The lanes that you selected are marked with a bullet.
double-click the dye/lanes, marking them with a bullet.	The bullet signifies that plots for those dye/lanes are reference plots.

Step	Action
2	From the table menu, choose Set Up Table. The Set Up Table dialog box appears.

To determine row contents in your table: *(continued)*

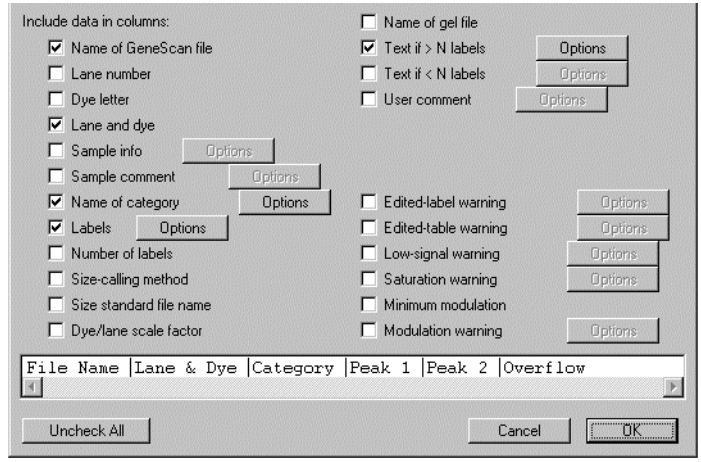
Step	Action
	
3	In the Contents per row field, click one of the two radio buttons: **If you want each row to correspond to...** / **Then click the...** marked categories and selected dye/lanes / Category and dye/lane radio button. sample Information entered in the Sample Info field for a dye/lane entry / Sample radio button.

Determining Column Contents

You can select the column contents for the rows in your table from a list of checkboxes in the Set Up Table dialog box (see step 2 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.

To determine column contents for each table row:

Step	Action
1	From the Table menu, choose Set Up Table. 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	Take the following action: **To...** / **Then click...** accept the current selections for the column contents — OK. clear all selections — Uncheck All. 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 8-33.
3	Select checkboxes under the Include Data in Columns heading.

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

Step	Action

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	Name of Gel file.
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.
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.

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

Appending Rows to a Table

Once you've created a table, you can append rows to the 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	You can take the following action: **To select...** / **Then...** a single dye/lane — click the dye/lane that you want to add to the table. multiple dye/lanes — Ctrl+click those dye/lanes that you want to add to the table. **IMPORTANT** The Genotyper software 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 Dye/lanes

If you have made a table and deleted or cleared all dye/lanes, select a table cell, then choose Re-import Dye/lane (Ctrl+D) 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.

Arranging the Order of Peak Label Columns

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

<table>
<tr><th>Step</th><th>Action</th></tr>
<tr><td colspan="2">Select Source of Peak Labels</td></tr>
<tr><td>1</td><td>Make sure that you mark the categories that define the kind of labeling you want to include in the table.

<table>
<tr><th>You can either...</th><th>Result</th></tr>
<tr><td>choose the Mark Command (Ctrl+M) from the Edit menu, or</td><td rowspan="2">The lanes that you selected are marked with a bullet.

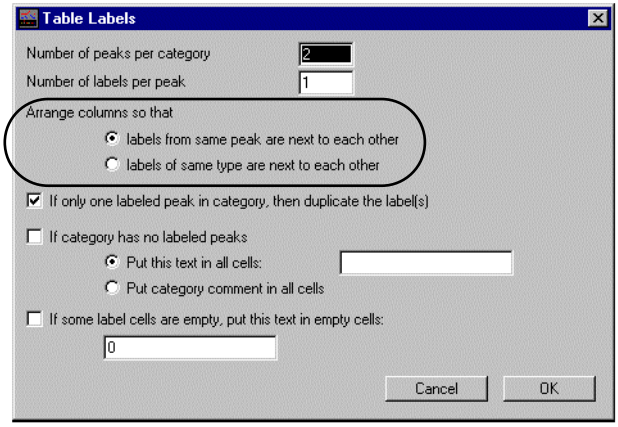
The bullet signifies that plots for those dye/lanes are reference plots.</td></tr>
<tr><td>double-click the dye/lanes, marking them with a bullet.</td></tr>
</table>
</td></tr>
<tr><td>2</td><td>Choose Set Up Table from the Table menu.

The Set Up Table dialog box appears.</td></tr>
<tr><td colspan="2">Arrange Columns of Peak Labels</td></tr>
<tr><td>1</td><td>Select the Labels checkbox.

</td></tr>
<tr><td>2</td><td>Click the Options button.

The Label Options dialog box appears.</td></tr>
</table>

To specify the order of peak columns that contain peak data

Step	Action
	
3	In the Arrange columns so that section, select the radio button for how you want to arrange the order of columns containing peak label data.

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 radio button.
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 radio button.

4	Modify columns based on kinds of peak labels in select categories.

To specify the order of peak columns that contain peak data

Step	Action

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) checkbox.
Display a text message when no labeled peaks are found in a category	a. If category has no labeled peaks checkbox. b. Click Put this text in all cells radio button. c. Type a text message in the text box.
Display a pre-defined category comment in all label cells of a row when no labeled peaks are found in a category	a. If category has no labeled peaks checkbox. b. Click Put Category comment in all cells radio button.
Display a text message when no labeled peaks are found in cells defined as columns for peak label data	a. If some label cells are empty, put this text in empty cells checkbox. b. Type in a text message in the text box.

5	Click OK to accept all of your selections.

Specifying Columns for Number of Labels in a Row

Introduction

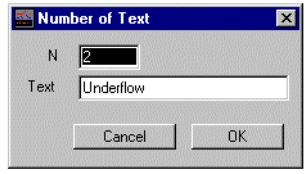
In the Set Up Table dialog box, you can specify that columns with customized text are appended to all rows where more or less labels are detected than the number that you specify.

Specify Columns for Label Detection

To specify columns for labels in a row:

Step	Action
1	In the Dye/lane list, click the Ctrl-key and select the dye/lanes you want to put in a table.
2	Make sure that you mark the Categories that define the kind of labeling you want to include in the table. **You can either...** / **Result** choose the Mark Command (Ctrl+M) from the Edit menu, or / The lanes that you selected are marked with a bullet. double-click the dye/lanes, marking them with a bullet. / The bullet signifies that plots for those dye/lanes are reference plots.
3	From the Table menu, choose Set Up Table. The Set Up Table dialog box appears.
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.

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

Step	Action
5	Click the Options button. The Number of Text dialog box appears. 
6	For N, type in the number of labels for which you want to display a message if more or less than that number are detected in a specified row.
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 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.

Specifying When a Peak Label Has Been Edited

When setting up a table, you can specify that the Genotyper software 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.

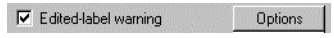
To specify when a peak label has been edited:

<table>
<tr><th>Step</th><th>Action</th></tr>
<tr><td>1</td><td>In the Dye/lane list, click the Ctrl-key and select the dye/lanes you want to put in a table.</td></tr>
<tr><td>2</td><td>Make sure that you mark the Categories that define the kind of labeling you want to include in the table.

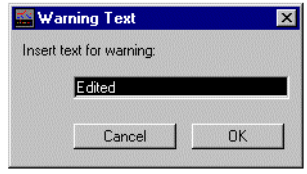
<table>
<tr><th>You can either...</th><th>Result</th></tr>
<tr><td>choose the Mark Command (Ctrl+M) from the Edit menu, or</td><td rowspan="2">The lanes that you selected are marked with a bullet.

The bullet signifies that plots for those dye/lanes are reference plots.</td></tr>
<tr><td>double-click the dye/lanes, marking them with a bullet.</td></tr>
</table>
</td></tr>
<tr><td>3</td><td>From the Table menu, choose Set Up Table.

The Set Up Table dialog box appears.</td></tr>
<tr><td>4</td><td>Select the Edited-label warning checkbox.

 
</td></tr>
<tr><td>5</td><td>Click the Options button.

The Warning Text dialog box appears.

 
</td></tr>
</table>

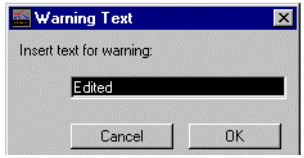
To specify when a peak label has been edited: *(continued)*

Step	Action
6	Type in the warning text that you want to appear in the column.
7	Click OK to accept all selections.

Specifying When a Peak Label in a Row Has Been Edited

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

To specify when a peak label in a row has been edited:

Step	Action
1	In the Dye/lane list, click the Ctrl-key and select the dye/lanes you want to put in a table.
2	Make sure that you mark the categories that define the kind of labeling you want to include in the table. **You can either...** / **Result** choose the Mark Command (Ctrl+M) from the Edit menu, or — The lanes that you selected are marked with a bullet. double-click the dye/lanes, marking them with a bullet. — The bullet signifies that plots for those dye/lanes are reference plots.
3	From the Table menu, choose Set Up Table. The Set Up Table dialog box appears.
4	Select the Edited-table warning checkbox.
5	Click the Options button. The Warning Text dialog box appears. 
6	Type in the warning text that you want to appear in the column.

To specify when a peak label in a row has been edited: *(continued)*

Step	Action
7	Click OK.

Specifying Modulation Warning Columns

Introduction

When setting up a table, you can specify that the Genotyper software 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.

Modulation Definition

Modulation refers to the degree to which peak data resolves with respect to its immediate background.

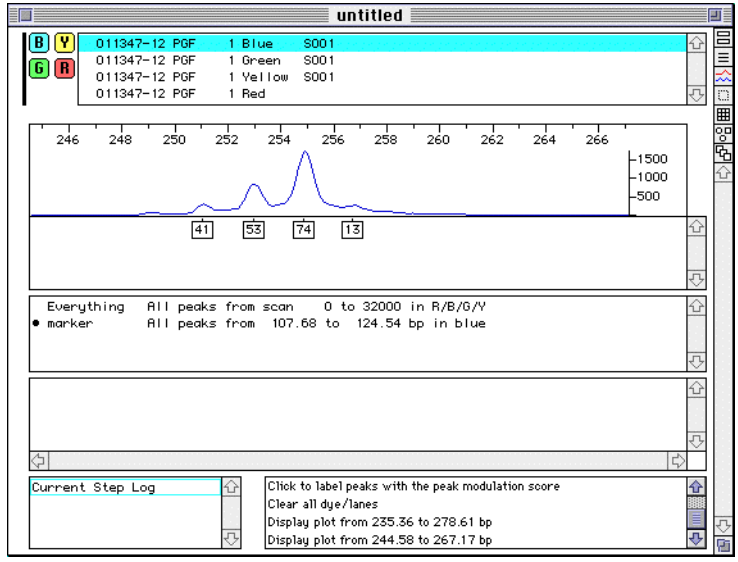
Modulation Scores

What Are Modulation Scores

Modulation scores measure the quality of peak resolution.

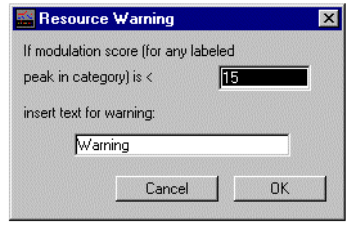
Modulation Score Example

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.



Specifying a Modulation Warning

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

Step	Action
1	In the Dye/lane list, click the Ctrl-key and select the dye/lanes you want to put in a table.
2	Make sure that you mark the categories that define the kind of labeling you want to include in the table. **You can either...** / **Result** choose the Mark Command (Ctrl+M) from the Edit menu, or — The lanes that you selected are marked with a bullet. double-click the dye/lanes, marking them with a bullet. — The bullet signifies that plots for those dye/lanes are reference plots.
3	From the Table menu, choose Set Up Table. The Set Up Table dialog box appears.
4	Select the Modulation warning checkbox.
5	Click the Options button. The Resource Warning dialog box appears. 
6	Type in the modulation score for the minimum acceptable degree of peak modulation for your Genotyper software 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 of your selections.

Specifying Low-signal Warning Columns

Introduction

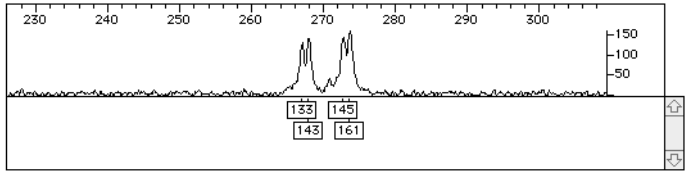
When setting up a table, you can specify that the Genotyper software append a column containing warning text to the end of any row that contains peaks that have a fluorescent signal lower than what you specify to be adequate for your application.

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

The figure below is an example of a Genotyping software plot display showing the vertical axis maximum set at 150 for peak heights. The peaks in the display are labeled with peak heights.

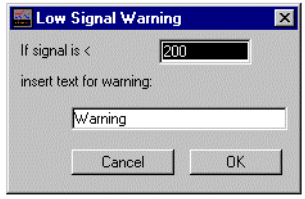


A Low Signal Value Less Than 200

The following table describes where Genotyper appends the column if a table is created using a default low signal warning of less that 200:

If...	Then...
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.

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

Step	Action
1	In the Dye/lane list, click the Ctrl-key and select the dye/lanes you want to put in a table.
2	Make sure that you mark the categories that define the kind of labeling you want to include in the table. **You can either...** / **Result** choose the Mark Command (Ctrl+M) from the Edit menu, or — The lanes that you selected are marked with a bullet. double-click the dye/lanes, marking them with a bullet. — The bullet signifies that plots for those dye/lanes are reference plots.
3	From the Table menu, choose Set Up Table. The Set Up Table dialog box appears.
4	Select the Low-signal warning checkbox.
5	Click the Options button. The Low Signal Warning 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	If peak data has been generated from fluorescent signals less than the amount you specified in the previous step, type in the warning text that you want to appear in the column.
8	Click OK to accept all of your selections.

Specifying Saturation Warning Columns

Introduction

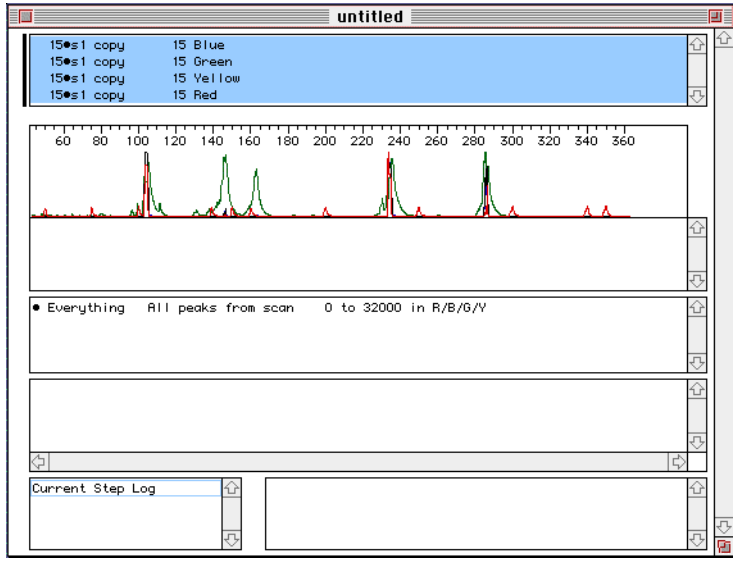
When setting up a table, you can specify that the Genotyper software append a column containing warning text to the end of any row that contains peaks that have a fluorescent signal higher than what you specify to be adequate for your application; a saturation warning.

What Causes Saturation

When you import raw data from GeneScan® Analysis Software 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, the Genotyper software 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.

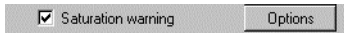
Saturation Example

The following is an example of imported dye/lanes displaying peaks with saturated signals.



Specifying Warnings

To specify warnings when peaks data has been generated from a saturated signal:

Step	Action
1	In the Dye/lane list, click the Ctrl-key and select the dye/lanes you want to put in a table.
2	Make sure that you mark the categories that define the kind of labeling you want to include in the table. **You can either...** / **Result** choose the Mark Command (Ctrl+M) from the Edit menu, or — The lanes that you selected are marked with a bullet. double-click the dye/lanes, marking them with a bullet. — The bullet signifies that plots for those dye/lanes are reference plots.
3	Choose Set Up Table from the Table menu. The Set Up Table dialog box appears.
4	Select the Saturation warning checkbox. 
5	Click the Options button. The Saturated Warning 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	If peak data has been generated from fluorescent signals greater than the amount you specified in the previous step, then type in the warning text that you want to appear in the column.
8	Click OK to accept all of your selections.

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 8-31.

Setting Up Results Columns

The Genotyper software 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 Calculations

The following table lists the kinds of calculations you can perform after specifying values in the Calculate in Table dialog box (see 8-24). The “Fields you can use” column refers to those fields shown in step 2 on page 8-24.

Kinds of calculations you can perform on table data:

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.	A, B

Kinds of calculations you can perform on table data: *(continued)*

Kind of calculation	Description	Fields you can use
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.	A, B
Square root (A) of	Square root of the value of A.	A

Procedure

To calculate results from table data:

<table>
<tr><th>Step</th><th>Action</th></tr>
<tr><td>1</td><td>Open the Table window from the Main window.

<table>
<tr><th>You can either...</th><th>Result</th></tr>
<tr><td>click the Table button.
 </td><td rowspan="2">This displays a table with rows of peak height and category data.</td></tr>
<tr><td>choose Show Table Window (Ctrl+T) from the Views menu.</td></tr>
</table>
</td></tr>
<tr><td>2</td><td>Choose Calculate in Table from the Table menu.

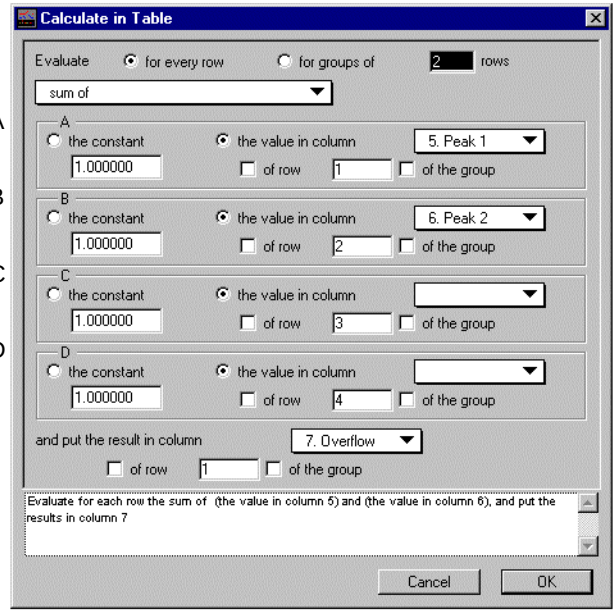
The Calculate in Table dialog box appears.

Field A

Field B

Field C

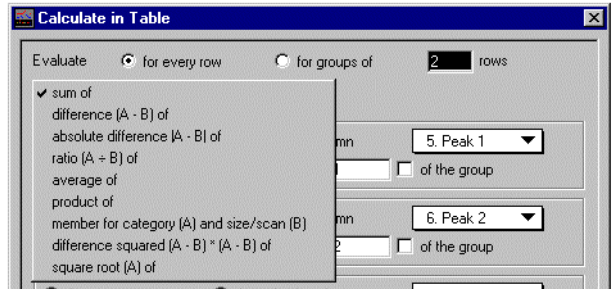
Field D

 
</td></tr>
</table>

To calculate results from table data: *(continued)*

<table>
<tr><th>Step</th><th>Action</th></tr>
<tr><td>3</td><td>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.</td></tr>
<tr><td>4</td><td>From the first pop-up menu, choose the kind of calculation that you want to perform.

 
</td></tr>
<tr><td>5</td><td>a. In fields A-D (see step 2 on page 8-24), choose the table data on which you want to perform the calculation.
b. Type in constants, or choose the column number from the pop-up menus.

For example:

<table>
<tr><th>If...</th><th>Then...</th></tr>
<tr><td>your table has data for peaks in columns 5 and 6, and you want to calculate the sums of the those two peaks</td><td>choose column 5 in field A, and column 6 in field B.</td></tr>
</table></td></tr>
<tr><td>6</td><td>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.

</td></tr>
<tr><td>7</td><td>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.</td></tr>
</table>

To calculate results from table data: *(continued)*

Step	Action
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 the figure below.

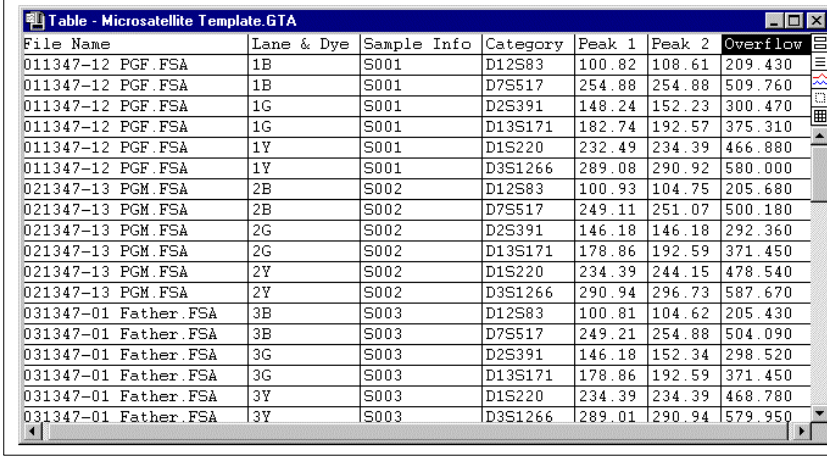


Table - Microsatellite Template.GTA

File Name	Lane & Dye	Sample Info	Category	Peak 1	Peak 2	Overflow
011347-12 PGF.FSA	1B	S001	D12S83	100.82	108.61	209.430
011347-12 PGF.FSA	1B	S001	D7S517	254.88	254.88	509.760
011347-12 PGF.FSA	1G	S001	D2S391	148.24	152.23	300.470
011347-12 PGF.FSA	1G	S001	D13S171	182.74	192.57	375.310
011347-12 PGF.FSA	1Y	S001	D1S220	232.49	234.39	466.880
011347-12 PGF.FSA	1Y	S001	D3S1266	289.08	290.92	580.000
021347-13 PGM.FSA	2B	S002	D12S83	100.93	104.75	205.680
021347-13 PGM.FSA	2B	S002	D7S517	249.11	251.07	500.180
021347-13 PGM.FSA	2G	S002	D2S391	146.18	146.18	292.360
021347-13 PGM.FSA	2G	S002	D13S171	178.86	192.59	371.450
021347-13 PGM.FSA	2Y	S002	D1S220	234.39	244.15	478.540
021347-13 PGM.FSA	2Y	S002	D3S1266	290.94	296.73	587.670
031347-01 Father.FSA	3B	S003	D12S83	100.81	104.62	205.430
031347-01 Father.FSA	3B	S003	D7S517	249.21	254.88	504.090
031347-01 Father.FSA	3G	S003	D2S391	146.18	152.34	298.520
031347-01 Father.FSA	3G	S003	D13S171	178.86	192.59	371.450
031347-01 Father.FSA	3Y	S003	D1S220	234.39	234.39	468.780
031347-01 Father.FSA	3Y	S003	D3S1266	289.01	290.94	579.950

Analyzing Data in Tables

Introduction

The Genotyping software 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.

Key to Using the Analyze Table Command

The key to using the Analyze Table command is to read the text box at the bottom of the dialog box as you enter conditional parameters in the Analyze Table dialog box (see step 1 on page 8-28).

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...	Then...
you specify that the Genotyper software analyze the cell contents of two columns in a row, but also specify that three of these cells not be empty	Genotyper will issue an error message in the text box.

Examples of Applications

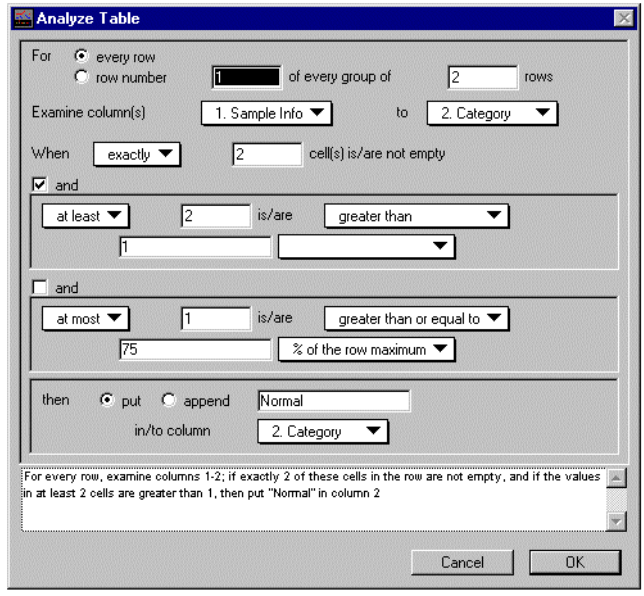
Examples of applications for which you can use the Analyze Table command include:

- Trisomy
- DMD Analysis
- Loss of Heterozygosity
- Gene Quantitation

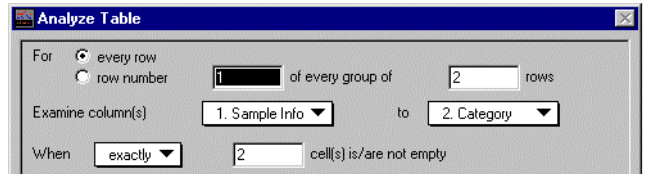
Procedure

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

To analyze data in tables:

Step	Action
1	Choose Analyze Table from the Table menu. The Analyze Table dialog box appears. 

To analyze data in tables: *(continued)*

Step	Action
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.
6	In the "then" field, click the put or append radio button and type in the message text that you either want 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

The following table lists how to clear an entire column:

To clear entire columns...	Result
choose at least from the pop-up menu and enter zero in the text box	This specifies 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?

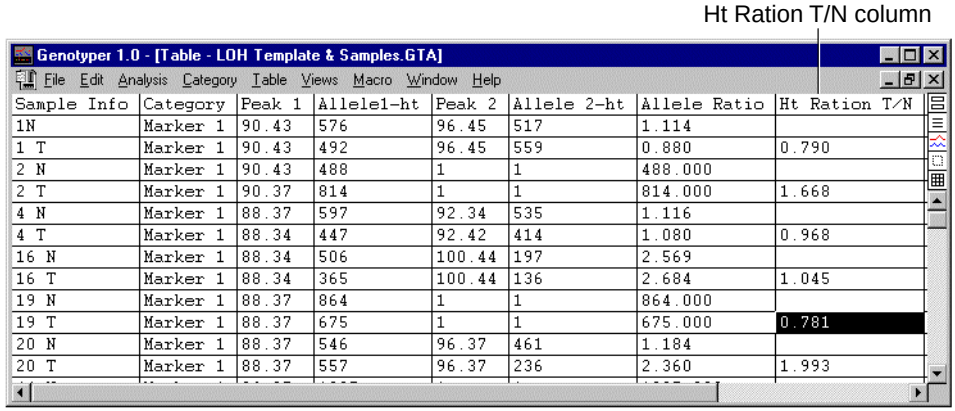
Loss of Heterozygosity (LOH) is the loss of polymorphic DNA markers in tumors compared with normal cells, and often indicates somatic deletion of tumor suppressor genes. LOH detection has application to a wide range of cancers involving tumor suppressor genes.

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 Table

The following figure shows a table that was created using the Calculate in 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
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
2 N	Marker 1	90.43	488	1	1	488.000	
2 T	Marker 1	90.37	814	1	1	814.000	1.668
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
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
19 N	Marker 1	88.37	864	1	1	864.000	
19 T	Marker 1	88.37	675	1	1	675.000	0.781
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

Using the Calculate in Table Command

To create the table shown in “Example LOH Table,” the Calculate in Table Command was used 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 N1/N2). This value is called the *Allelic Imbalance* or AI.

Using the Analyze in Table Command

To create the table shown in “Example LOH Table,” the Analyze Table Command was used to calculate the ratios in Ht Ratio T/N column for presence or absence of LOH.

For example:

If...	Then...	Otherwise...
the ratio is less than 0.67 or more than 1.35	LOH is entered into a column named Assessment	normal is entered in the same column.

Editing Table Cells and Column Headings

Introduction

Once you've 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

To have the Genotyper software notify you of any row in a table has been edited:

Step	Action
1	Choose Set Up Table from the Table menu. The Set Up Table dialog box appears.
2	Select the checkbox labeled Edited-table warning. 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 8-13.

Kinds of Cell Data That is Editable

The following kinds of table cell data is editable:

- Column headings
- Peak label information
- User comments

These are the only three kinds of data you can manually edit in table cells.

Editing Table Cells

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. **You can either...** / **Result** click the Table button. — This displays a table with rows of peak height and category data. choose Show Table Window (Ctrl+T) from the Views menu.
3	Select the table cell that you want to edit.
4	Choose Edit Cell (Ctrl+E) 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 For Editing Table Cells

If you...	Then the...
are making a macro	Step list records edits of individual cells as “selected cells.”
run the macro	macro will change whatever you have selected to include the text you enter.

Editing Column Headings

Steps for how 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.

You can either...	Result
choose the Mark Command (Ctrl+M) from the Edit menu, or	The lanes that you selected are marked with a bullet.
double-click the dye/lanes, marking them with a bullet.	The bullet signifies that plots for those dye/lanes are reference plots.

Step	Action
3	Select the table cell that you want to edit.
4	Choose Edit Cell (Ctrl+E) 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 For Editing Column Headings

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

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

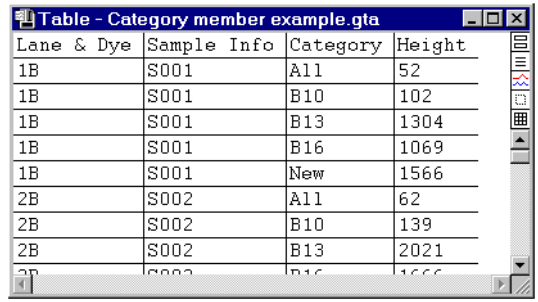
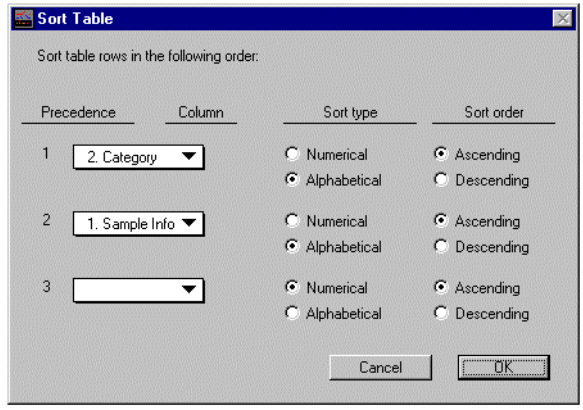
The concept of *precedence* is important when sorting rows in a table. The precedence for a column number establishes a priority when sorting rows.

For example:

If you choose the....	Then the rows will...
♦ Category column as a precedence 1, and ♦ Sample Info as a precedence 2, and ♦ The sort type is alphabetical.	♦ 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.

Sorting Rows

To sort rows in multiple columns of a table:

Step	Action
1	To view the Table window more easily, choose Show Table Window (Ctrl+T) from the Views menu. The Table window appears. 
2	Choose Sort Table from the Analysis menu. The Sort Table dialog box appears. 
3	Under Column, you can choose from 1 to 3 different columns to sort, by choosing the appropriate pop-up menu.

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

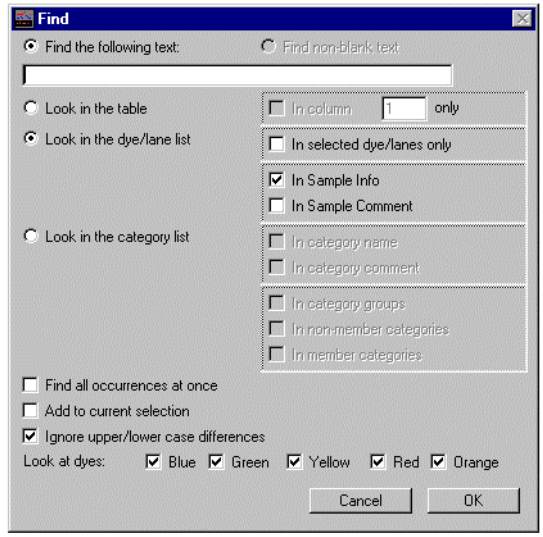
Introduction

You can use the Find command to locate one or more entries in a table.

Finding a Table Entry

You can search for table entries by alphanumeric text string.

To locate a table entry using the Find command:

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. **Note** If the table is not active, the selection will be outlined, not highlighted, or open the Table window.
2	Choose Find (Ctrl+F) in the Edit menu. The Find dialog box appears. 
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 select the...** restrict the search to a particular column → Look in column checkbox, 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 checkbox. select additional table cells located by the command → Add to current selection checkbox. ignore case differences in text searches → Ignore upper/lower case differences checkbox.
6	Click OK.

Finding the Next Occurrence

About the Find Next Command

You can use the Find Next command to repeat the last Find command 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.

Procedure

Action	Result
Choose Find Next (Ctrl+G) from the Edit menu.	The next occurrence of the text is selected.

Updating Tables

Introduction

If you have created a table, and made changes to peak labels, you can update the corresponding information in your table.

Clearing the Table

The Update Table command should only be used to update label data in the table. If you change any other information that can appear in the table, such as the sample information or the name of a category, then you should use the Clear Table command from the Analysis menu, and start over with a new table.

Procedure

Update tables after making changes to information in other parts of your Genotyper Document.

To update table contents:

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

About Derived Tables

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. A Derived table is not linked to dye/lanes or categories like the table from which it was derived.

Procedure

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. **You can either...** / **Result** click the Table button. — This displays a table with rows of peak height and category data. choose Show Table Window (Ctrl+T) from the Views menu.
3	Choose Show Derived Table Window from the Views menu. A blank Derived table window appears.
4	Choose Derive table from the Analysis menu and Copy Table from the submenu. The table in the Table window is copied to the Derived table window.

Clearing the Derived Table

Choose Clear Derived Table from the Analysis menu. The Derived Table window is cleared.

Note If you want to undo this command. choose Undo from the Edit menu. The Undo command (Ctrl+Z) must be the next command.

Formatting Tables for Export

Introduction

Some third party applications require that you re-format tables before exporting them from the Genotyper software.

To format tables so that they are compatible, you can use the Flip Table command and flip tables before exporting them.

Flipping Tables and Formatting for Export

To flip tables and format them for export:

Action	Result
Choose Derive Table from the Analysis menu and Flip Table from the submenu.	The table in the Table window is flipped, copied and placed in the derived table. See “Flipped Table Example” below for an example of how the Flip Table command reformats a table

Flipped Table Example

The following shows an example of a table before and after flipping. The top table is below using the Flip Table command and the bottom table is after using the command.

Before using the Flip Table command

Table - 01D1.gta

Sample Info	Sample Comment	D1S2797		D1S249		D1S
134702	D1b	122	134	169	179	211
1001004	D1a	120	120	179	179	211
1001005	D1a	120	120	171	179	211
1001007	D1a	120	128	171	179	211
1001008	D1a	120	128	179	179	219
1001009	D1a	120	128	179	183	211
1001011	D1a	120	120	169	179	219

After using the Flip Table command

Derived Table - 01D1.gta

Sample Info	134702	1001004	1001005	1001007	1001008	100
Sample Comment	D1b	D1a	D1a	D1a	D1a	D1a
D1S2797	122	120	120	120	120	120
	134	120	120	128	128	128
D1S249	169	179	171	171	179	179
	179	179	179	179	179	183
D1S2800	211	219	219	219	219	211
	211	219	219	219	219	227
D1S234	276	276	272	272	272	272
	280	280	276	276	272	276

Exporting and Copying Tables

About Exporting a Table to a File

A Genotyper software table can be exported to a plain text file and read using:

- Word processing or spreadsheet application.
- Simple Text.

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.

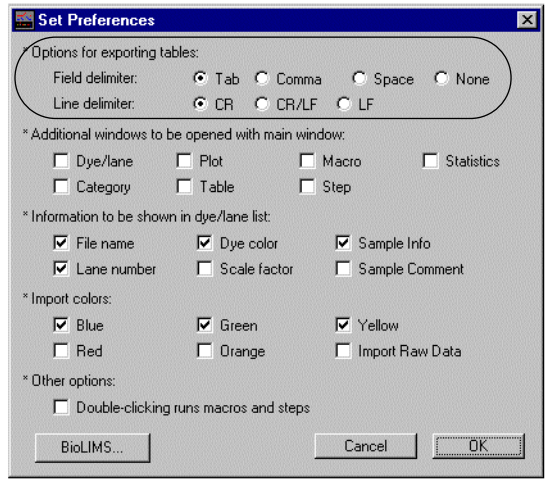
IMPORTANT

Once a table is exported to a file it cannot be imported back into the Genotyper software.The following table lists how to continue working with a table if the table has been exported.

If...	Then...
you want to continue working with the table	save your work as a Genotyper Document by using the Save (Ctrl+S) command. This will save the dye/lanes, categories, or labels, and will allow you to continue your work at a later time.

Setting Preferences for Exporting Tables

To set preferences for exporting tables to files:

Step	Action
1	Choose Set Preferences in the Edit menu. The Set Preferences dialog box appears. 
2	Under the bullet “Options for exporting tables:”, click the appropriate radio buttons for Field delimiting and Line delimiting.
3	Click OK.

Exporting Tables to Text File

To export the contents of a table to a text file:

Step	Action
1	Choose Export to File from the Table menu. An Export Table dialog box appears.
2	Choose the folder location for where you want to export the table.
3	In the File name field, type in the name of the exported table and click Save.

Exporting Derived Tables

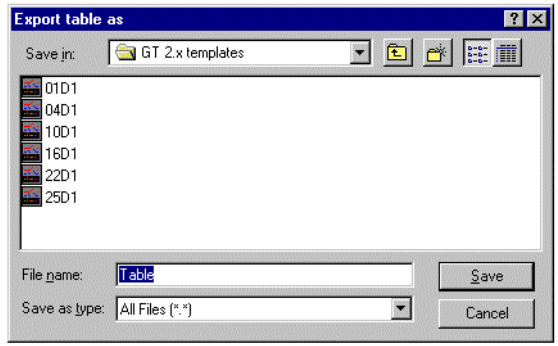
There is a different command to export Derived tables, than there is to export tables.

IMPORTANT You can only export Derived tables as text files.

To export Derived tables:

Step	Action
1	To copy the table you want to export, choose the Derive Table command from the Analysis menu and Copy Table from the submenu. For instructions on how to use the Derive Table command, see “Procedure” on page 8-42.

To export Derived tables:

Step	Action
2	Choose Export Derived Table from the Analysis menu. An Export table as dialog box appears. 
3	Choose the folder location for where you want to export the table.
4	In the File name field, type in the name of the exported table and click Save.

Copying Tables

As an alternative to exporting a table, you can copy a table to a spreadsheet document.

To copy tables to spreadsheets:

Step	Action
1	Select a contiguous portion of the Genotyper software table.
2	Choose Copy (Ctrl+C) in the Edit menu.
3	Select the spreadsheet program.
4	Choose Paste (Ctrl+V) in the Edit menu.

Working with Statistical Data

9

Chapter Overview

Introduction This chapter discusses how you can generate and view statistical data and histograms for peak data in Genotyper Documents.

In This Chapter This chapter contains the following topics:

Topic	See page
Generating Statistical Data	9-2
Choosing the Source of Data	9-4
Choosing a Value Type	9-10
Determining the Bin Size	9-15
Viewing Statistics for Selected Data	9-17
Viewing Histograms	9-19
Setting Histogram Viewing Options	9-22
Editing Categories in Histograms	9-24

Generating Statistical Data

Introduction

The Genotyper® 3.5 NT software generates statistical data from select parts of the active Genotyper Document. You can display generated statistical data in tables or histograms.

Kinds of Statistical Data

The following table describes the kinds of statistical data the Genotyper software can calculate for Genotyper Document contents.

Kind of statistic	Description
Source	Source of data from which statistics are generated, from within a Genotyper Document.
Value Type	Kind of data for which the Genotyper software generates statistics. Possible Value Types are: size in base pairs, scan number, peak height, peak area and, label text.
Number of data points	Total number of counts.
Minimum	Minimum value for a range of quantities you define by the Value Type you specify.
Maximum	Maximum value for a range of quantities you define by the Value Type you specify.
Mean	Average value for a set of values defined by the Value Type you specify.
Median	Center value of a series of quantities you define by the Value Type you specify.
Standard deviation	Standard deviation from the mean of a set of values defined by the Value Type you specify.
Bin	Range of Value Types over which Genotyper calculates a count and frequency.
Count	Number of Value Types found within a Bin.
Frequency	Number of Value Types found within a Bin divided by the total number of data points.

Setting Statistics Options

The Genotyper software generates statistical data and histograms based on settings you make by choosing the Set Statistics Options dialog box from the Analysis menu.

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	9-10
3	Determining the Bin Size	9-15

Choosing the Source of Data

Introduction

You can specify the source of data in a Genotyper Document for which the Genotyper software generates statistics.

Two Sources of Data

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.

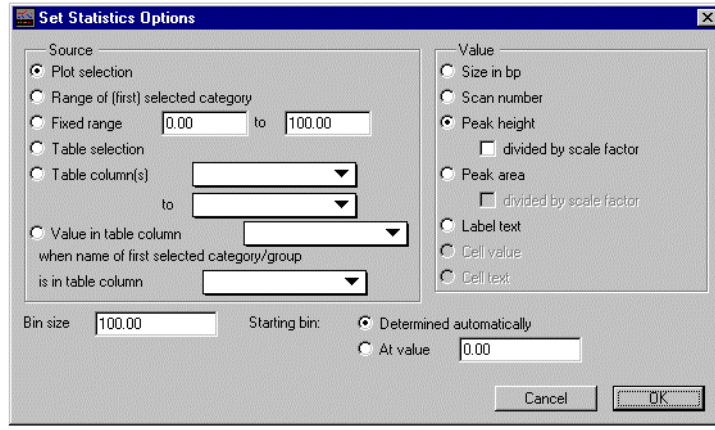
Labeled Peak Data from Plot Selections

Calculate statistics for a range of labeled peaks you select in plot displays.

To calculate statistics from plot selections of data:

Step	Action
1	In the Dye/lane list, click the Ctrl-key and select the dye/lanes for which you want to calculate and display statistical data.
2	Open the Plot window: **You can either....** / **Result** click the Plot window icon ( ). — The Plot window opens, displaying electropherograms for each selected dye/lane. choose Show Plot Window (Ctrl+Y) from the Views menu. An electropherogram plot showing peaks for each analyzed nucleic acid fragment in the sample appears in the Plot Area. **IMPORTANT** Peaks in the Plot window must be labeled to include them in statistical calculations. If they are not labeled, label them by choosing Label Peaks from the Analysis menu.
3	From the Analysis menu, choose Set Statistics Options. The Set Statistics Options dialog box appears.

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

Step	Action
	
4	In the Source field, select the Plot selection radio button.
5	Use the mouse and select a rectangular range in the electropherogram plot.
6	See “Choosing a Value Type” on page 9-10, for instructions on selecting the appropriate Value Type radio button in the Set Statistics Options dialog box.

Labeled Peak Data from Categories

You can calculate statistics for the range of peaks defined by a selected category.

To choose categories as the source of peak data:

Step	Action
1	In the Dye/lane list, click the Ctrl-key and select the dye/lanes for which you want to calculate and display statistical data.

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

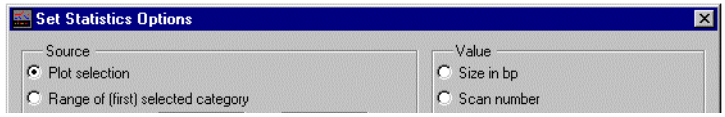
<table>
<tr><th>Step</th><th>Action</th></tr>
<tr><td>2</td><td>Open the Plot window:

<table>
<tr><th>You can either....</th><th>Result</th></tr>
<tr><td>click the Plot window icon ( ).</td><td rowspan="2">The Plot window opens, displaying electropherograms for each selected dye/lane.</td></tr>
<tr><td>choose Show Plot Window (Ctrl+Y) from the Views menu.</td></tr>
</table>

An electropherogram plot showing peaks for each analyzed nucleic acid fragment in the sample appears in the Plot Area.</td></tr>
<tr><td>3</td><td>Select the category from the Category list which defines the range of peaks for which you want to generate statistical data.</td></tr>
<tr><td colspan="2">
<table>
<tr><th>You can either....</th><th>Result...</th></tr>
<tr><td>click the Categories button.

</td><td rowspan="2">The Categories window appears.</td></tr>
<tr><td>choose Show Categories Window (Ctrl+K) from the Views menu.</td></tr>
</table>
</td></tr>
<tr><td>4</td><td>From the Analysis menu, choose Set Statistics Options.

The Set Statistics Options dialog box appears.</td></tr>
<tr><td>5</td><td>In the Source field, select the Range of (first) selected category radio button.

 
</td></tr>
<tr><td>6</td><td>See “Choosing a Value Type” on page 9-10, for instructions on selecting the appropriate Value Type radio button in the Set Statistics Options dialog box.</td></tr>
</table>

Labeled Peak Fragment Size

You can specify a range of fragment sizes in base pairs. The Genotyper software 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:

<table>
<tr><th>Step</th><th>Action</th></tr>
<tr><td>1</td><td>In the Dye/lane list, click the Ctrl-key and select the 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.</td></tr>
<tr><td>2</td><td>Open the Plot window:

<table>
<tr><th>You can either....</th><th>Result</th></tr>
<tr><td>click the Plot window icon ( ).</td><td rowspan="2">The Plot window opens, displaying electropherograms for each selected dye/lane.</td></tr>
<tr><td>choose Show Plot Window (Ctrl+Y) from the Views menu.</td></tr>
</table>

An electropherogram plot showing peaks for each analyzed nucleic acid fragment in the sample appears in the Plot Area.</td></tr>
<tr><td>3</td><td>From the Analysis menu, choose Set Statistics Options.

The Set Statistics Options dialog box appears.</td></tr>
<tr><td>4</td><td>In the Source field, select the Fixed range radio button.

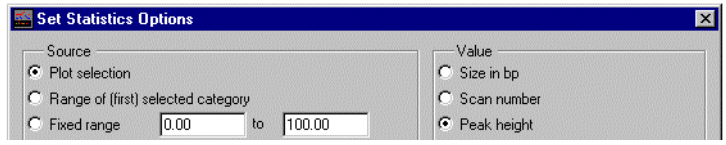
 
</td></tr>
<tr><td>5</td><td>Type in the size range in base pairs for fragments that you want to specify as the source of peak data.</td></tr>
<tr><td>6</td><td>See “Choosing a Value Type” on page 9-10, for instructions on selecting the appropriate Value Type radio button in the Set Statistics Options dialog box.</td></tr>
</table>

Table Cell Contents From Selection

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

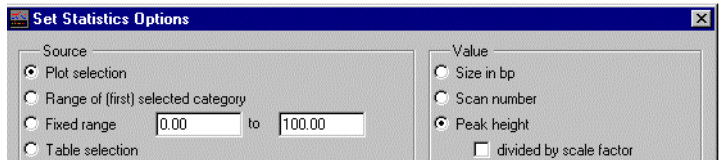
Step	Action
1	In the table list, click the Ctrl-key and select the cell or cells in the table for which you want to generate statistics.
2	From the Analysis menu, choose Set Statistics Options. The Set Statistics Options dialog box appears.
3	In the Source field, select the Table selection radio button. 
4	See “Choosing a Value Type” on page 9-10, for instructions on selecting the appropriate Value Type radio button in the Set Statistics Options dialog box.

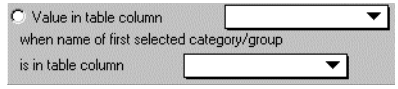
Table Cell Contents from Column Selection

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

Step	Action
1	From the Analysis menu, choose Set Statistics Options. The Set Statistics Options dialog box appears.
2	In the Source field, select the Table column(s) radio button for inclusion as source data.
3	From the Table column(s) 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 9-10, for instructions on selecting the appropriate Value Type radio button in the Set Statistics Options dialog box.

Table Cell Contents from Category and Column Selection

To specify categories in table columns as a source of data:

Step	Action
1	In the table list, click the Ctrl-key and 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.
3	In the Source field, select the Value in table column radio button. 
4	Take the following action: **From the...** / **Select...** first pop-up menu — a table column. second pop-up menu — the table column you want to define as the source of your data.
5	See “Choosing a Value Type” on page 9-10, for instructions on selecting the appropriate Value Type radio button in the Set Statistics Options dialog box.

Choosing a Value Type

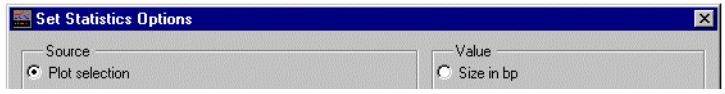
Definition The Value Type is the kind of data for which the Genotyper software generates statistics.

Value Types Possible Value Types are:

Size in Base Pairs	Peak Area
Scan Number	Labeled Text
Peak Height	Cell Value
Cell Text	

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

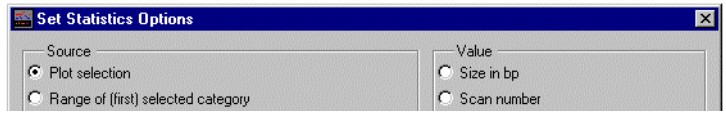
To choose the Size in Base Pairs as a Value Type:

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 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 9-15, 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, the Genotyper software 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 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. 
4	See “Determining the Bin Size” on page 9-15, for instructions on selecting the appropriate range of Scan numbers, for which Genotyper calculates a count, frequency of occurrence, as well as related statistics.

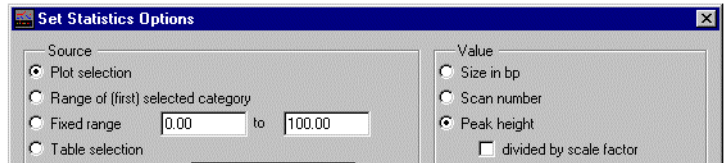
Peak Height

When you choose “Peak Height” as a Value Type, the Genotyper software 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 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.

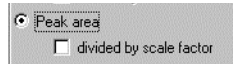
To choose Peak Height as a Value Type: *(continued)*

Step	Action
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 9-15, 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, the Genotyper software generates statistics based on the area of specified source peaks.

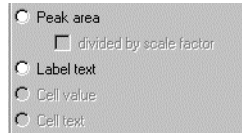
To choose peak area as a Value Type:

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 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.
5	See “Determining the Bin Size” on page 9-15, 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, the Genotyping software calculates statistics based on the number of text labels within a specified range of source peak data.

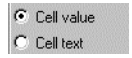
To choose Labeled Text as a Value Type:

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 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, the Genotyper software 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 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. 

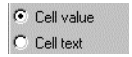
To choose Cell Value as a Value Type: *(continued)*

Step	Action
4	See “Determining the Bin Size” on page 9-15, 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, the Genotyper software 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 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.

Determining the Bin Size

Definition

The Bin size defines an interval within which the Genotyper software calculates a count and frequency of each occurrence of labeled peak data that matches criteria defined by the Source and Value Type. Results of the calculations are displayed by choosing Show Statistics Window, or Show Histogram Window from the Views menu.

Guidelines for Bin Size 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 a limit of 5000 bins that can be displayed in the Statistics window.

How to Define the Bin Size

To define the Bin size:

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 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 9-10.
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 9-16.

How to Determine the Starting Bin

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 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 9-10.
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:
6	When you are satisfied with all the settings in the Set Statistics Options dialog box, click OK.

If you want to...	Then click...
use the first bin containing one or more counts	Determined automatically.
define the Starting bin size	At value, and type in the Starting bin.

Viewing Statistics for Selected Data

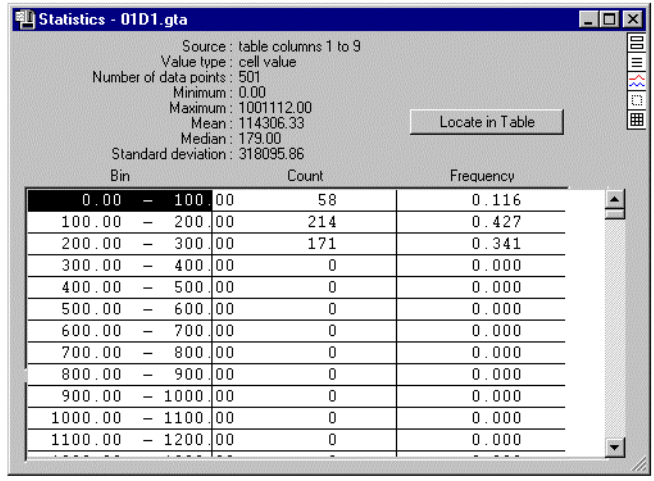
Introduction

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

Viewing Peak Statistics

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

To viewing the Statistics window:

Step	Action
1	Complete the Set Statistics Options dialog box (see 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. 

Viewing Different Statistics

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.

Locating Bins in Tables

Use the Locate in Table button to find data in a table that 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:

<table>
<tr><th>Step</th><th>Action</th></tr>
<tr><td>1</td><td>Open the Table window.
<table>
<tr><th>You can either...</th><th>Result</th></tr>
<tr><td>click the Table button.
 </td><td rowspan="2">This displays a table with rows of peak height and category data.</td></tr>
<tr><td>choose Show Table Window (Ctrl+T) from the Views menu.</td></tr>
</table>
</td></tr>
<tr><td>2</td><td>Select one or more cells in contiguous rows in the Statistics window (see “Viewing Peak Statistics” on page 9-17).</td></tr>
<tr><td>3</td><td>Click the Locate in Table button.
Cells in the table that correspond to selected bins are highlighted.</td></tr>
</table>

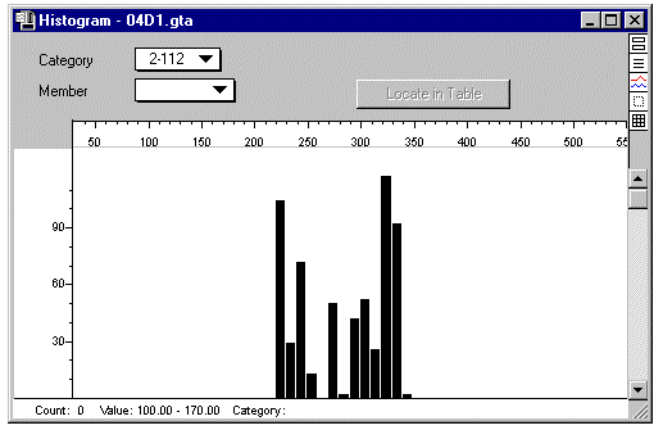
Viewing Histograms

What Histograms Show

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

Histogram Window Example

The Histogram window displays a histogram of data based on settings you have made in the Set Statistics Options dialog box (see page 9-5).



Viewing the Histogram Window

You can show the Histogram window at any time once you have completed the Set Statistics Options dialog box.

To view the Histogram window:

Step	Action
1	Complete the Set Statistics Options dialog box (see 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.

To view the Histogram window: *(continued)*

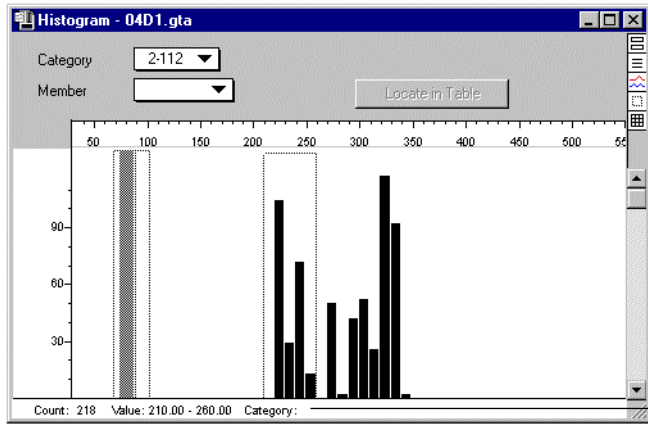
Step	Action
3	Choose Show Histogram window from the Views menu. The Histogram window appears (see “Histogram Window Example”). The bars in the Histogram window represent the defined bin sizes. You can take the following action:

To display...	Then...
statistical information for a bin at the bottom of the Histogram window	put the cursor on a bar.
a different kind of histogram	make changes in the Set Statistics Options dialog box (see page 9-5).

Displaying Bin Statistics

The bars in the Histogram window show statistics for defined Bin sizes.

To...	Then...
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.



Viewing Histograms with Small Bin Sizes

If WARNING Message Appears

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.

Viewing Histograms with Small Bin Sizes

To view histograms with small bins sizes, either:

- 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.

Setting Histogram Viewing Options

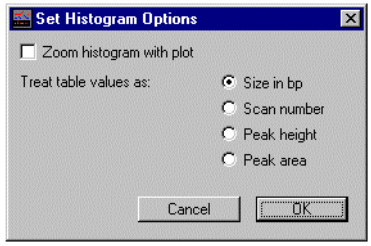
Introduction

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

Setting 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 by: a. Selecting the data from the appropriate part of the Genotyper Document that corresponds to the source you selected in the Set Statistics dialog box. b. Choosing Show Histogram Window from the Views menu.
2	Choose Set Histogram Options from the Analysis menu. The Set Histogram Options dialog box appears. 
3	Select Zoom histogram with plot and click OK.
4	Open the Plot window, and select a region of the electropherogram.
5	Choose Zoom to a selected range (Ctrl+R). The Histogram window zooms to the region in the histogram that contains the corresponding peak data.

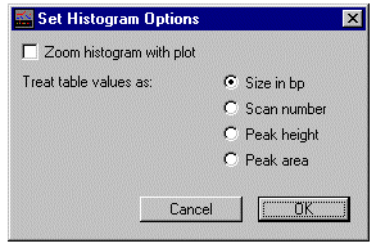
Viewing Histograms of Table Data

Introduction

If...	Then...
you want to view histograms of data from tables	you need to define the Value Type of the data in the table.
For example, if...	**Then**
your table contains peak sizes and peak heights, and you have chosen to make a histogram of the peak heights by selecting table columns	select the Peak height radio button in the Set Histogram Options dialog box (see step 2). For more information on choosing a source of data for histograms see“Choosing the Source of Data” on page 9-4.

Procedure

To set display options for histograms:

Step	Action
1	View the Histogram for the table you defined as a source of peak data.
2	Choose Set Histogram Options from the Analysis menu. The Set Histogram Options dialog box appears. 
3	In the “Treat table values as:” field, click the Value Type of the data in your table.
4	Click OK. The Histogram window should now display the same type of peak data as the associated table.

Editing Categories in Histograms

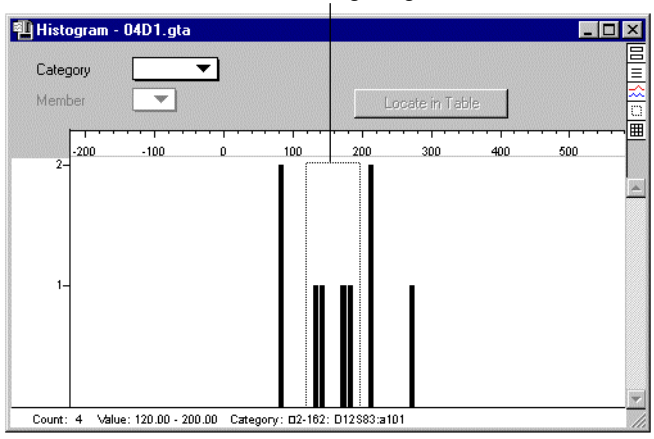
Introduction

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.

Defining the Range for a New Category

You can define the range of peak sizes in the Histogram window to include in a new category.

To define the range for a new category:

Step	Action
1	View the appropriate histogram by choosing Show Histogram Window from the Views menu.
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. Box defining range 

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

Step	Action
4	Choose Add Category (Ctrl+L) from the Category menu. The Add Category dialog box appears. A size range of from/to will be defined by the Add Category dialog box. **Defining a ± a Fixed Number Range** **To define a ± Fixed Number Range...** / **Then...** that will centered on the weighted average of bins in the selected range (or a center value if no bins have been selected) / hold down the Ctrl+key when choosing Add Category from the Category menu.
5	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.

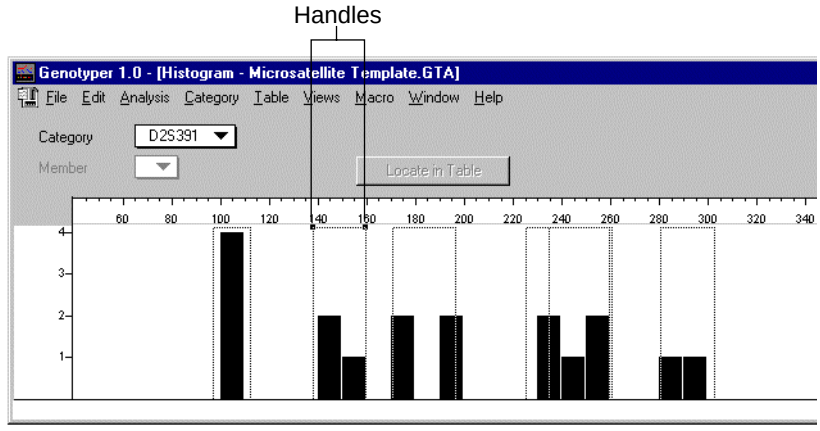
Viewing Category Size Ranges

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:

Step	Action
1	Generate a histogram of peak sizes.
2	Choose a category from the Category pop-up menu. All category groups and non-member categories will have ranges shown with dashed boxes. The selected category will have *handles*.

To view category size ranges in histograms: *(continued)*

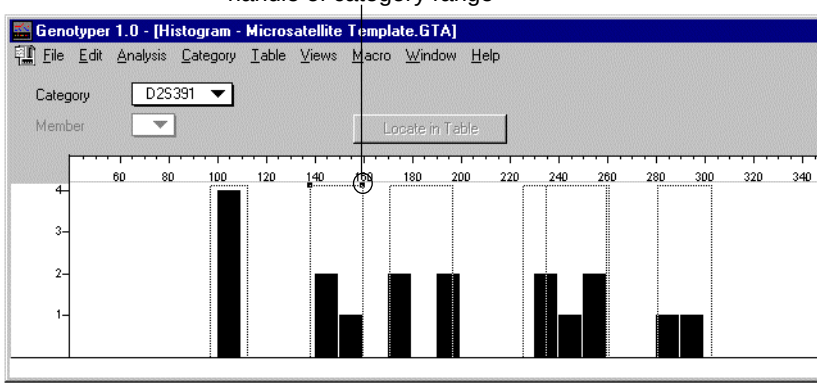
Step	Action
	
3	To view ranges for category members, choose a member in the Member pop-up menu. All members of selected groups will have ranges shown with dashed boxes. Selected members will have handles.

Changing Category Size Ranges

To change the size range categories from the Histogram window:

Step	Action
1	Generate a histogram of peak sizes.
2	Show the Histogram window.
3	Choose a category or a member from the appropriate pop-up menu.
4	Move the cursor to the handle of selected category.

To change the size range categories from the Histogram window: *(continued)*

Step	Action
	Cursor on upper-right handle of category range 
5	Using the mouse, drag the the handle on the box until the size range is modified to your specifications. **Note** The range will be changed to align with bin boundaries. Overlapping categories will not be allowed. **If WARNING Message Appears** **If...** / **Then...** the text "WARNING - Bin sizes too small to display" appears at the bottom of the Histogram window, you will not be able to modify the categories by this method. / use the Set Statistics Options command from the Analysis menu to increase the bin size to an adequate value.

Selecting Another Category

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.

The following table lists the four different ways to select another category:

You can...	Then the...
select another category from the Category pop-up menu.	handles move to the dashed box of the selected category
click within the dashed box representing the size range of a category.	category name of your selection changes in the Category pop-up menu.
make your selection from the Category list.	
press Ctrl+J, the Zoom to next category command.	

Using the BioLIMS 2.0 Database 10

Chapter Overview

Introduction This section 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.

Assumptions The following assumptions are:

- The user already has Oracle 7.3.3 client for Windows NT®-based computer installed and configured on the workstation where Genotyper® 3.5 NT software is going to be installed.
- BioLIMS 2.0 has been installed and that there is a database name (alias), server name, user name, and password.

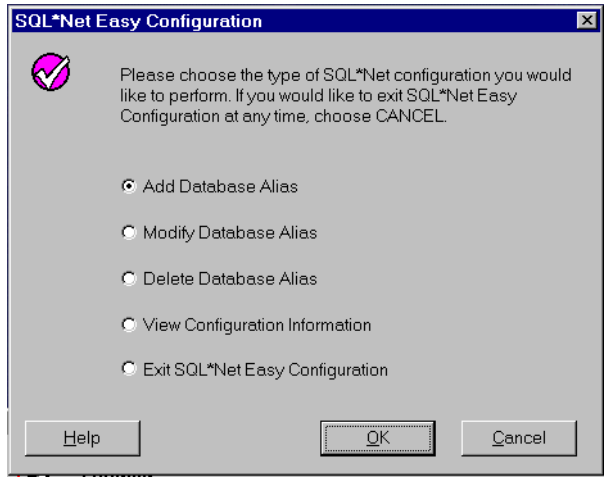
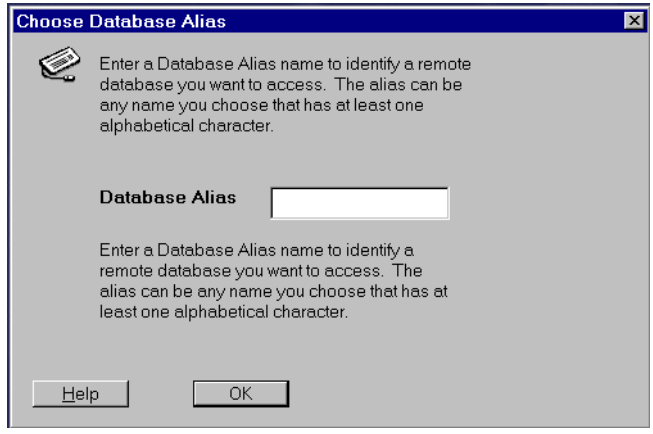
In This Chapter This chapter contains the following topics:

Topic	See Page
Configuring for the BioLIMS Database for Oracle	10-2
Testing the BioLIMS Database Connection	10-5
Configuring Genotyper 3.5 NT for BioLIMS Database Access	10-7
Importing GeneScan Data From the BioLIMS Database	10-10
Using the Collection Browser Window	10-12

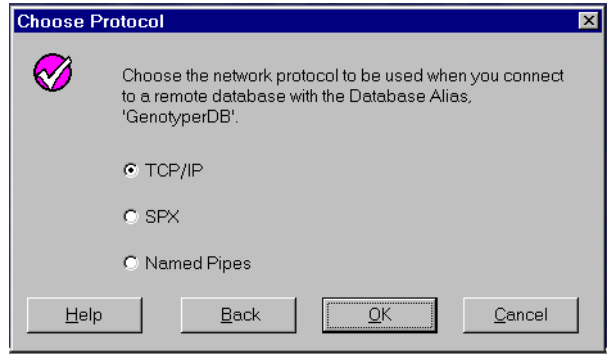
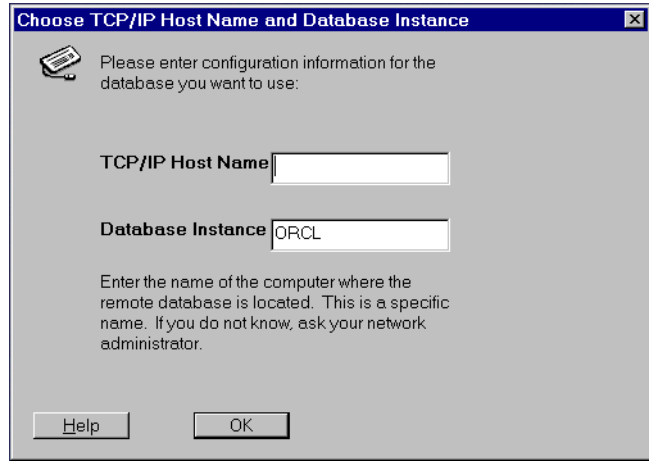
Configuring for the BioLIMS Database for Oracle

Procedure

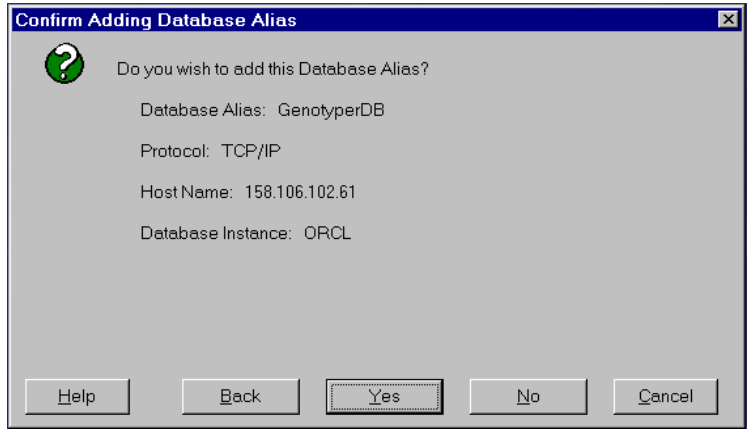
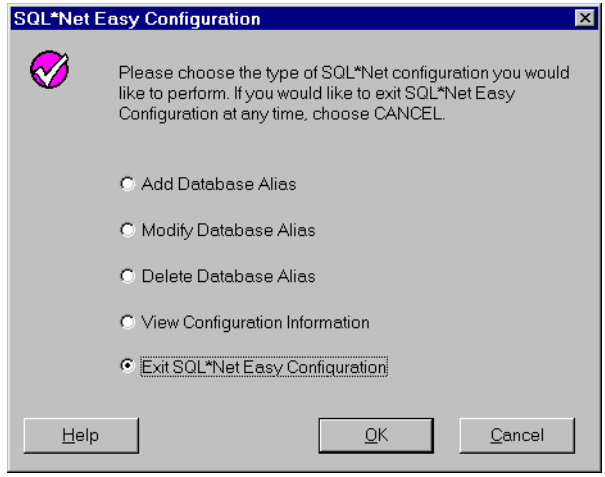
To configure the BioLIMS database for Oracle® WindowsNT:

Step	Action
1	From the Start menu, choose Programs, point to Oracle for WindowsNT, and point to SQL Net Easy Configuration. The following dialog box appears. 
2	Click the Add Database Alias radio button and click OK. The following dialog box appears. 

To configure the BioLIMS database for Oracle® WindowsNT: *(continued)*

Step	Action
3	Enter the database alias name that you have chosen for the BioLIMS database and click OK. The following dialog box appears. 
4	Choose the type of network protocol, TCP/IP in this example, to be used and click OK. The following dialog box appears. 
5	Enter the TCP/IP Host name (IP Address) and the Database Instance name in the Choose TCP/IP Host Name window, and click OK. The following dialog box appears.

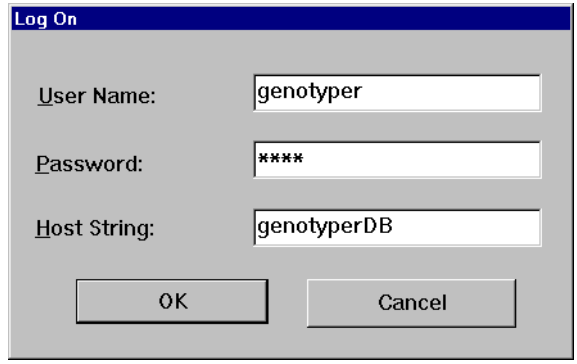
To configure the BioLIMS database for Oracle® WindowsNT: *(continued)*

Step	Action
	
6	The SQL Net Easy Configuration window appears, again. Click the Exit SQL Easy Configuration radio button and click OK. 
7	Click Ok in the next window to exit SQL Net Easy Configuration.

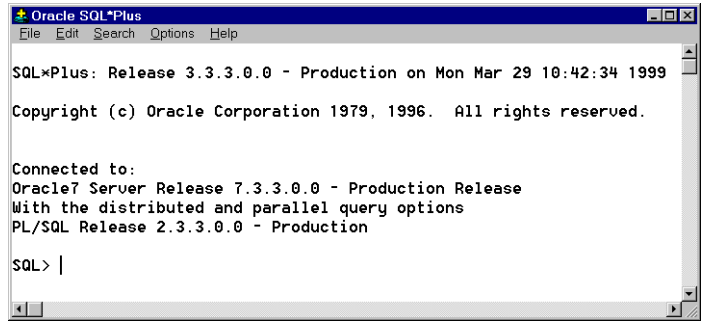
Testing the BioLIMS Database Connection

Procedure

To test the BioLIMS database connection:

Step	Action
1	From the Start menu, choose Programs, point to Oracle for WindowsNT, and point to SQL Plus 3.3. The following dialog box appears. 
2	Enter the following and click OK: ♦ User Name ♦ Password ♦ Host String
3	Take the following action: **If...** / **Then...** the BioLIMS server is configured correctly — the following message appears (see below). the BioLIMS server is not configured correctly — contact Technical Support, see “BioLIMS” on page 1-17.

To test the BioLIMS database connection:

Step	Action
	
4	Choose File/Exit from the SQL*Plus menu to end the test.

Procedure

Note Make sure that all Oracle database files are installed correctly. If files are missing, re-install them using the Oracle client installer CD-ROM.

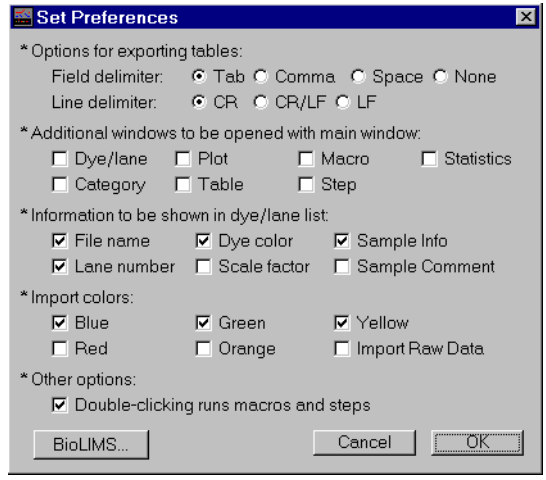
To configure the Genotyper software for BioLIMS database access:

<table>
<tr><th>Step</th><th>Action</th></tr>
<tr><td>1</td><td>Take the following action:

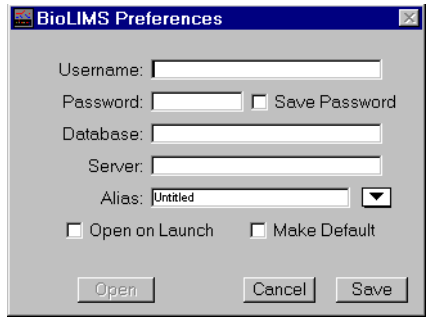
<table>
<tr><th>You can either...</th><th>Result</th></tr>
<tr><td>double-click the Genotyper icon.

</td><td rowspan="2">A blank Main window appears.</td></tr>
<tr><td>click Start, point to Programs, point to Genotyper, and point to Genotyper program.</td></tr>
</table>
</td></tr>
<tr><td>2</td><td>Select Set Preferences from the Edit menu.

The Set Preferences dialog box appears.

 
</td></tr>
</table>

To configure the Genotyper software for BioLIMS database access: *(continued)*

Step	Action
3	Click the BioLIMS button. The BioLIMS Preferences dialog box appears. 
4	Enter the user name, password, database, and server information that you entered in step 2 on page 10-5 and click Open.
5	Click the check box labeled Save Password if you want to save your password so that you do not have to enter it every time you open the connection.
6	If you want the database to open automatically when you launch the Genotyping software, click the check box labeled Open on Launch. **Note** You must also click the check box labeled Save Password if you want the database to open automatically.
7	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.

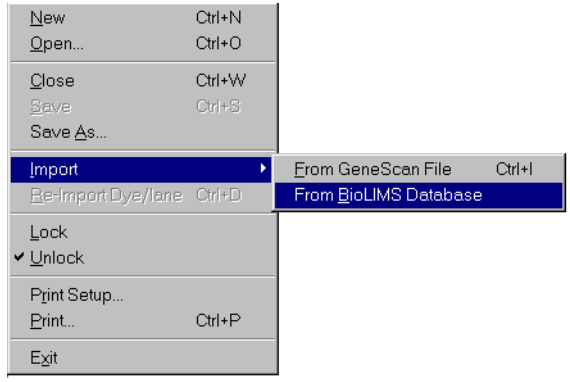
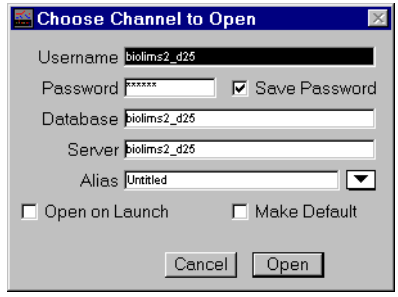
To configure the Genotyper software for BioLIMS database access: *(continued)*

Step	Action
8	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.
9	Use the pop-up menu to add, change, or remove aliases.
10	Click Save to save the information that you just entered.
11	Click OK in the BioLIMS Preferences dialog box.

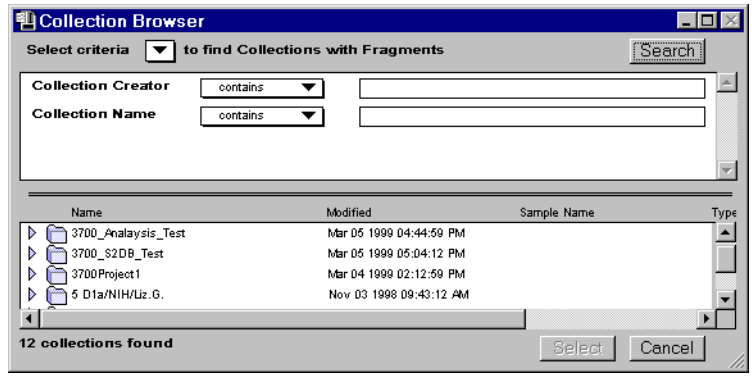
Importing GeneScan Data From the BioLIMS Database

Procedure

To import GeneScan® Analysis Software data from the BioLIMS database:

Step	Action
1	Start Genotyper 3.5 NT, if it is not already open.
2	Choose Import from the File menu and From BioLIMS Database from the submenu.  The following dialog box appears. 
3	Click Open. The Collection Browser window appears (see below).

To import GeneScan® Analysis Software data from the BioLIMS database: *(continued)*

Step	Action
	
4	Select a set of samples to import and click the Select button. For more information, see “Using the Collection Browser Window” on page 10-12.

Using the Collection Browser Window

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	10-15
Up to 14 fragment-specific criteria	10-16

In This Section

This subsection includes the following topics.

For this topic	See page
Displaying the Collection Browser Window	10-12
Collection Browser Window Example	10-13
Parts of the Collection Browser Window	10-13
Collection Search Criteria	10-15
Fragment Search Criteria	10-16

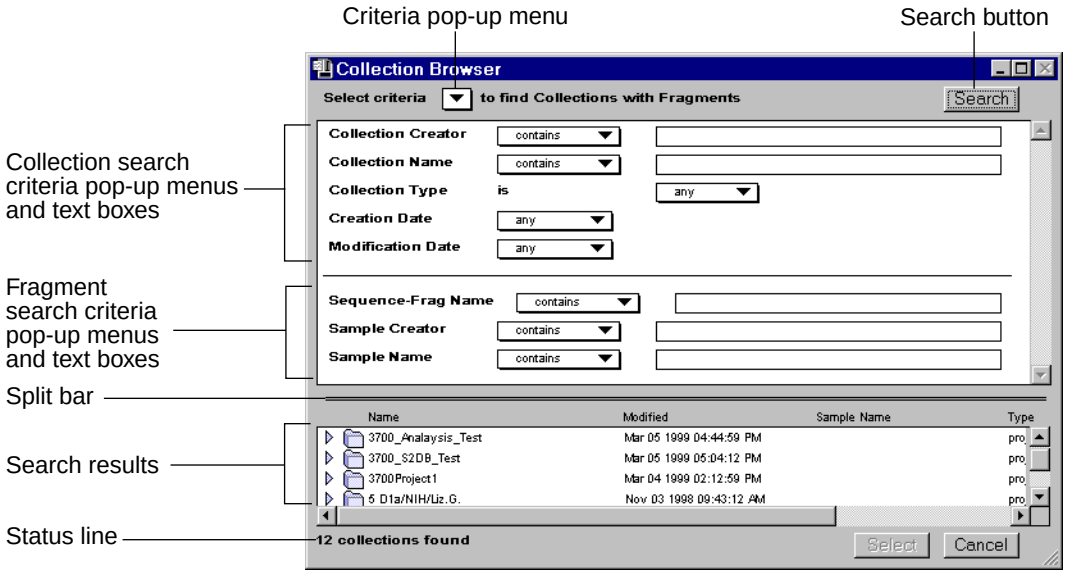
Displaying the Collection Browser Window

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 10-13.

Collection Browser Window Example

The following is an example of the Collection Browser window.



Parts of the Collection Browser Window

The 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.

Description of the Collection Browser window: *(continued)*

Item	Description
Collection search criteria pop-up menus and text boxes	Use these pop-up menus and text boxes to define the collection criteria of the search. **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 1-21.
Fragment search criteria pop-up menu and text boxes	Use these pop-up menus and text boxes to define the fragment criteria of the search. **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 1-22.
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 Criteria

The table below shows the collection search criteria. The collections 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 ♦ ends with ♦ contains	up to 255 characters	Name of the creator/owner of the collection.
Collection Name	♦ is ♦ starts with ♦ ends with ♦ contains	up to 31 characters	Name of the collection.
Collection Type	♦ any ♦ run ♦ project ♦ other	NA	Collection type. Default is any menu item.
Creation Date	♦ any ♦ is ♦ before ♦ after ♦ between	date — set with arrow buttons using the format mm/dd/yy	Date the collection was created.
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 Criteria

The table below shows the fragment search criteria. The collections 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 Cannot use colons (:).	Name of the fragment. This is the file name entered in the Sample 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.
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.

Fragment Search Criteria *(continued)*

Criterion	Pop-up Menu Choices	Allowed Text	Description
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.
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 apply	NA	Is present means that one or more dyes contain sizing information.
			Is not present means none of the dye sample contain sizing information.

Fragment Search Criteria *(continued)*

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

Menu and Command Reference 11

Chapter Overview

Introduction This chapter provides a reference for the names, locations, and definitions of all menus and commands available in the Genotyper® 3.5 NT software.

In This Chapter This chapter contains the following topics:

Topic	See page
About Genotyper Software Menus	11-2
File Menu	11-3
Edit Menu	11-5
Analysis Menu	11-8
Category Menu	11-11
Table Menu	11-12
Views Menu	11-14
Macro Menu	11-19
Window Menu	11-21

About Genotyper Software Menus

Introduction You can access all Genotyper software 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 software.

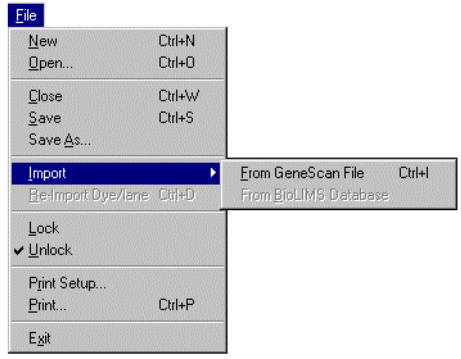
Menu Items Menus you can access from the menu bar:

Menu	This menu lists commands for...	For information, see...
File menu	working with Genotyper Documents and the GeneScan® Analysis Software files.	“File Menu” on page 11-3.
Edit menu	editing Genotyper Documents and table contents.	“Edit Menu” on page 11-5.
Analysis menu	labeling fragment peak data, and determining statistical data for fragment peaks.	“Analysis Menu” on page 11-8.
Category menu	defining categories.	“Category Menu” on page 11-11.
Table menu	setting up Tables and working with tabular data.	“Table Menu” on page 11-12.
Views menu	opening windows for Genotyper Document windows in the Main window, and for customizing viewing of these windows.	“Views Menu” on page 11-14.
Macro menu	creating and running macros for automating Genotyper software procedures and applications.	“Macro Menu” on page 11-19.

File Menu

Definition The File menu contains commands for working with Genotyper Documents.

Menu Options The following figure shows the list of commands you can access from the File menu.



Commands

File menu commands:

Command	Description	For more information, see
New (Ctrl+N)	Opens a new, untitled Genotyper Document.	"Opening Genotyper Documents" on page 3-7.
Open (Ctrl+O)	Opens a previously saved Genotyper Document.	
Close (Ctrl+W)	Closes the active window.	"Closing Genotyper Documents" on page 3-7.
Save (Ctrl+S)	Saves the active Genotyper Document.	"Saving a Genotyper Document" on page 3-12.
Save As...	Saves the Genotyper Document under a new name.	

File menu commands: *(continued)*

<table>
<tr><th>Command</th><th>Description</th><th>For more information, see</th></tr>
<tr><td>Import</td><td colspan="2">Displays the following submenu.

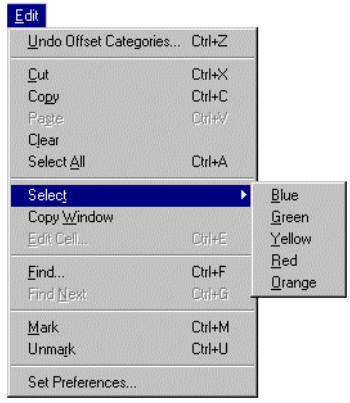
<table>
<tr><th>Submenu</th><th>Description</th><th>See...</th></tr>
<tr><td>From GeneScan File (Ctrl+I)</td><td>displays a dialog box used to import a GeneScan Analysis Software file or multiple GeneScan files.</td><td>“Importing GeneScan Files” on page 3-15.</td></tr>
<tr><td>From BioLIMS Database</td><td>displays a dialog box used to import a or multiple files from the BioLIMS™ database.</td><td>“Importing GeneScan Data From the BioLIMS Database” on page 10-10.</td></tr>
</table></td></tr>
<tr><td>Re-Import Dye/lane

(Ctrl+D)</td><td>Re-imports dye/lanes if you have made a table and deleted or cleared all dye/lanes.</td><td>“Re-importing Dye/lanes” on page 8-7.</td></tr>
</table>

Edit Menu

Definition The Edit menu contains commands for editing Genotyper Documents.

Menu Options The following figure shows the list of commands you can access from the Edit menu



Commands

Edit menu commands:

Command	Description	For more information, see
Undo (Ctrl+Z)	Undoes the last command (whenever possible).	"Editing Document Windows" on page 3-19.
Cut (Ctrl+X)	Cuts the selection and places it on the Clipboard.	
Copy (Ctrl+C)	Copies the selection to the Clipboard.	
Paste (Ctrl+V)	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.	

Edit menu commands: *(continued)*

<table>
<tr><th>Command</th><th>Description</th><th>For more information, see</th></tr>
<tr><td>Select All
(Ctrl+A)</td><td>Selects every entry in the selected list or table.</td><td>“Editing Document Windows” on page 3-19.</td></tr>
<tr><td>Select</td><td colspan="2">The following submenu commands appear:

<table>
<tr><th>Command</th><th>Description</th><th>See...</th></tr>
<tr><td>Blue</td><td>Selects all entries in the Dye/lane list that have a blue dye color.</td><td rowspan="5">step 2 on page 5-9.</td></tr>
<tr><td>Green</td><td>Selects all entries in the Dye/lane list that have a green dye color.</td></tr>
<tr><td>Yellow</td><td>Selects all entries in the Dye/lane list that have a yellow dye color.</td></tr>
<tr><td>Red</td><td>Selects all entries in the Dye/lane list that have a red dye color.</td></tr>
<tr><td>Orange</td><td>Selects all entries in the Dye/lane list that have a orange dye color.</td></tr>
</table></td></tr>
<tr><td>Copy Window</td><td>Copies the active window to the clipboard.</td><td>“Editing Document Windows” on page 3-19.</td></tr>
<tr><td>Edit Cell
(Ctrl+E)</td><td>Allows you to change the contents of individual cells in tables.</td><td>“Editing Table Cells” on page 8-34.</td></tr>
<tr><td>Find...
(Ctrl+F)</td><td>Shows a dialog box which allows you to locate and select an alphanumeric text in the Dye/lane list, Category list, or the table.</td><td>“Finding a Table Entry” on page 8-39.</td></tr>
<tr><td>Find Next
(Ctrl+G)</td><td>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.</td><td>“Finding the Next Occurrence” on page 8-40.</td></tr>
</table>

Edit menu commands: *(continued)*

<table>
<tr><th>Command</th><th>Description</th><th>For more information, see</th></tr>
<tr><td>Mark
(Ctrl+M)</td><td colspan="2">Places a bullet (•) in front of the Categories list or Dye/lane list item.

<table><tr><th>When a...</th><th>Then...</th></tr><tr><td>dye/lane is not marked</td><td>the plot corresponding to that item appears in the upper Plot window.</td></tr><tr><td>category is marked</td><td>it is used by labeling and table commands.</td></tr></table></td></tr>
<tr><td>Unmark
(Ctrl+U)</td><td colspan="2">Removes a bullet (•) from the Category or Dye/lane list item.

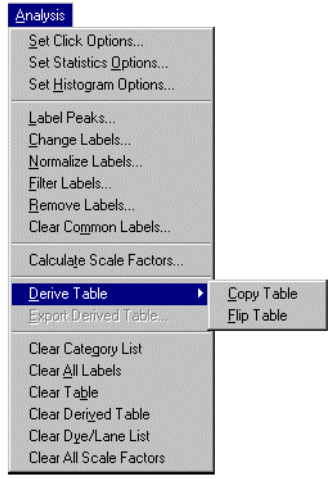
<table><tr><th>When a...</th><th>Then...</th></tr><tr><td>dye/lane is not marked</td><td>the plot corresponding to that item no longer appears in the upper Plot window.</td></tr><tr><td>category is not marked</td><td>it is not used by labeling and table commands.</td></tr></table></td></tr>
<tr><td>Set Preferences</td><td colspan="2">Display a dialog box that allows you to:

<table><tr><th>To...</th><th>See...</th></tr><tr><td>set options for exporting tables.</td><td>“Setting Preferences for Exporting Tables” on page 8-45.</td></tr><tr><td>define additional windows to be opened with the main window.</td><td>“Defining Windows to Open with Main Window” on page 3-10.</td></tr><tr><td>define information to be shown in the Dye/lane list.</td><td>“Setting Viewing Preferences” on page 5-5.</td></tr><tr><td>double-click to run macros and steps.</td><td>“Tips for Running Macros” on page 4-3.</td></tr><tr><td>set BioLIMS preferences.</td><td>Chapter 10, “Using the BioLIMS 2.0 Database.”.</td></tr></table></td></tr>
</table>

Analysis Menu

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

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



Commands

Analysis menu commands:

Command	Description	For information, see...
Set Click Options	Displays a dialog box used to set parameters for manual labeling of peaks. For example, labeling by size, height, scan number, or area.	“Manually Labeling Fragment Peaks” on page 6-37.

Analysis menu commands: *(continued)*

Command	Description	For information, see...
Set Statistics Options	Displays a dialog box used to set parameters for what appears in the Statistics window. Settings include: calculate statistics for peak size, scan number, bin size.	"Setting Statistics Options" on page 9-3.
Set Histogram Options	Displays a dialog box used to set parameters for how the histogram window interacts with other parts of a Genotyper Document.	"Setting Histogram Viewing Options" on page 9-22.
Label Peaks	Displays a dialog box used to label peaks for selected dye/lanes that have have been defined by marked category parameters.	"Labeling Peaks Automatically" on page 6-28.
Change Labels	Displays a dialog box which, for selected lanes in the Dye/lane list, allows you to change the labels at currently labeled peaks.	"Changing Existing Labels" on page 6-31.
Normalize Labels	Displays a dialog box used to normalize data in several peak labels to data in a specific (control) label.	"Labeling Normalized Peaks—an Example" on page 6-50.
Filter Labels	Removes unwanted labels from peaks.	"Filtering Labels" on page 6-32.
Remove Labels	Displays a dialog box used to remove labels from specified peak locations of selected dye/lanes in the dye/lane list.	"Removing Labels" on page 6-47.
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. A dialog box appears that is used to set the tolerance.	"Removing Common Labels" on page 6-49.

Analysis menu commands: *(continued)*

<table>
<tr><th>Command</th><th>Description</th><th>For information, see...</th></tr>
<tr><td>Calculate Scale Factors</td><td>Normalizes the height or area of peaks.</td><td>“Calculating Scale Factors” on page 5-16.</td></tr>
<tr><td>Derive Table</td><td colspan="2">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.

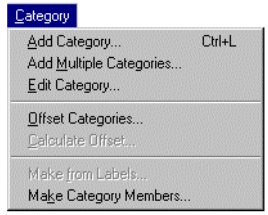
The following submenu commands appear:

<table>
<tr><th>Command</th><th>Description</th><th>See...</th></tr>
<tr><td>Copy Table</td><td>Copies the table in the Table window to the Derived table window.</td><td>“Deriving a Second Table from an Existing Table” on page 8-42.</td></tr>
<tr><td>Flip Table</td><td>Flips the table in the Table window, copies it, and places it in the derived table window.</td><td>“Formatting Tables for Export” on page 8-43.</td></tr>
</table>
</td></tr>
<tr><td>Export Derived Table</td><td>Exports derived tables as text files.</td><td>“Exporting and Copying Tables” on page 8-44.</td></tr>
<tr><td>Clear Category list</td><td>Clears all entries in the Category list.</td><td>“Clearing the Category List” on page 6-5.</td></tr>
<tr><td>Clear All Labels</td><td>Removes all labels from all peaks (whether selected or not) in the Plot window.</td><td>“Removing All Labels” on page 6-47.</td></tr>
<tr><td>Clear Derived Table</td><td>Clears derived table.</td><td>“Clearing the Derived Table” on page 8-42.</td></tr>
<tr><td>Clear Table</td><td>Removes all rows and columns from the table.</td><td>“Clearing the Table” on page 8-41</td></tr>
<tr><td>Clear Dye/Lane list</td><td>Removes all entries from the Dye/lane list.</td><td>“Clearing the List” on page 5-8.</td></tr>
<tr><td>Clear All Scale Factors</td><td>Resets all scale factors from dye/lanes in the Dye/lane list to 1.0.</td><td>“Resetting Scale Factors to One” on page 5-17.</td></tr>
</table>

Category Menu

Definition The Category menu contains commands for defining categories.

Menu Options The following figure shows the list of commands you can access from the Category menu.



Commands Category menu commands:

Command	Description	For information, see...
Add Category (Ctrl+L)	Displays a dialog box used to set category parameters for new categories.	“Adding Categories” on page 6-5.
Add Multiple Categories	Displays a dialog box used to create multiple categories at once.	“Adding Multiple Categories” on page 6-8.
Edit Category	Shows a dialog box used to change the parameters of the selected category.	“Editing Category Parameters” on page 6-25.
Offset Categories	Allows you to adjust the size range for peak labeling for selected categories.	“Using the Offset Category Command” on page 6-26.
Calculate Offset	Automatically adjusts the size range for peak labeling for selected categories.	“Using the Calculate Offset Command” on page 6-27.
Make from Labels	Displays a dialog box used to create categories from labels.	“Making Categories from Labels” on page 6-55.
Make Category Members	Displays a dialog box used to create member categories for specialized applications.	“Making Category Members” on page 6-18.

Table Menu

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

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

Commands

Table menu commands:

Command	Description	For information, see...
Set up Table	Displays a dialog box used to define the contents and order of rows and column headings for tables.	♦ "Determining Row Contents" on page 8-3. ♦ "Determining Column Contents" on page 8-5.
Append to Table	Adds rows to an existing table.	"Appending Rows to a Table" on page 8-7.
Update Table	If you have created a table, and made changes to peak labels, updates the corresponding information in your table.	"Updating Tables" on page 8-41.
Sort Table	Displays a dialog box used to sort the rows of a table in a Genotyper Document.	"Sorting the Rows in a Table" on page 8-36.
Analyze Table	Allows you to specify conditions for logical comparisons of table cell contents.	"Analyzing Data in Tables" on page 8-27.
Calculate in Table	Allows you to perform numerical calculations of table cell contents.	"Calculating Results from Table Data" on page 8-22.

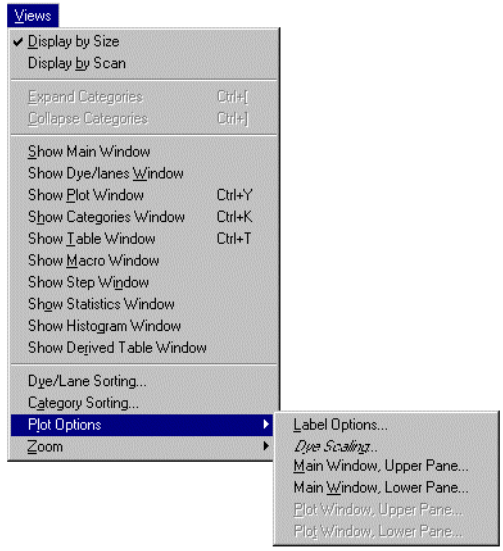
Table menu commands: *(continued)*

Command	Description	For information, see...
Export to File	Exports table contents to a text file.	“Exporting Tables to Text File” on page 8-46.

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 The following figure shows the list of commands you can access from the Views Menu.



Commands

Views menu commands:

Command	Description	For information, see...
Display by Size	Changes the horizontal scale in the plot areas to base pairs.	step 2 on page 7-10.
Display by Scan	Changes the horizontal scale in the plot areas to scan line.	
Expand Categories (Ctrl+[)	Displays all categories in a selected category group in the Category list.	"Expanding and Collapsing Categories" on page 6-5.
Collapse Categories (Ctrl+])	Displays only the category group name of a selected category in the Category list.	
Show Main Window	Shows all parts of a Genotyper Document in one window, the Main window.	"Displaying the Main Window" on page 3-8.
Show Dye/lanes Window	Opens an additional, larger window that shows only the Dye/lane list.	"Show Dye/Lanes Window from the Views menu." on page 3-11.
Show Plot Window (Ctrl+Y)	Opens an additional, larger window that shows only the plots and peak labels. The window expands vertically to fill the computer screen.	"Show Plot Window from the Views menu." on page 3-11.
Show Categories Window (Ctrl+K)	Opens an additional, larger window that shows only the Category list.	"Show Categories Window from the Views menu." on page 3-11.
Show Table Window (Ctrl+T)	Opens an additional, larger window that shows only the table.	"Show Table Window from the Views menu." on page 3-12.
Show Macro Window	Opens an additional, larger window that shows only the Macro list.	"Showing the Macro Window" on page 4-4.
Show Step Window	Opens an additional, larger window that shows only the Step list.	"Showing the Step Window" on page 4-6.

Views menu commands: *(continued)*

Command	Description	For information, see...
Show Statistics Window	Opens window displaying statistics of selected peaks (number of labeled peaks, minimum, maximum, median, standard deviation, count, and bin).	“Viewing Peak Statistics” on page 9-17.
Show Histogram Window	Opens window displaying histogram representation of statistics of selected peaks.	“Viewing the Histogram Window” on page 9-19.
Show Derived Table Window	Opens window displaying Derived table, if one exists.	“Deriving a Second Table from an Existing Table” on page 8-42.
Dye/Lane Sorting	Displays a dialog box used to sort the Dye/lane list by file names, lanes, dye color, sample information, or sample comments in ascending or descending order.	“Searching and Sorting Through Lists” on page 5-10.
Category Sorting	Displays a dialog box used to sort category names, category starting size or scan number, and category dye color in ascending or descending order.	“Sorting and Editing Categories” on page 6-24.

Views menu commands: *(continued)*

<table>
<tr><th>Command</th><th>Description</th><th>For information, see...</th></tr>
<tr><td>Plot Options</td><td colspan="2">A submenu appears with the following options:

<table>
<tr><th>Command</th><th>Description</th><th>See...</th></tr>
<tr><td>Label Options...</td><td>Displays a dialog box used to modify and use colors and prefixes in labels.</td><td>step 1 on page 6-39.</td></tr>
<tr><td>Dye Scaling...</td><td>Displays a dialog box used to modify signal heights.</td><td>“Procedure” on page 7-12.</td></tr>
<tr><td>Main Window, Upper Pane...</td><td>Displays the Plot Options dialog box, used to change the display options in the upper pane of the Main window.</td><td rowspan="4">“Customizing Plot Displays” on page 7-19.</td></tr>
<tr><td>Main Window, Lower Pane...</td><td>Displays the Plot Options dialog boxed, used to change the display options in the lower pane of the Main window.</td></tr>
<tr><td>Plot Window, Upper Pane...</td><td>When the Plot window is open, displays the Plot Options dialog box, used to change the display options in the upper pane of the Plot window.</td></tr>
<tr><td>Plot Window, Lower Pane...</td><td>When the Plot window is open, displays the Plot Options dialog box, used to change the display options in the lower pane of the Plot window.</td></tr>
</table>
</td></tr>
</table>

Views menu commands: *(continued)*

<table>
<tr><th>Command</th><th>Description</th><th>For information, see...</th></tr>
<tr><td>Zoom</td><td colspan="2">A submenu appears with the following options:

<table>
<tr><th>Command</th><th>Description</th><th>See...</th></tr>
<tr><td>Zoom In

(Ctrl+=)</td><td>Zoom in by a factor of two.</td><td>“Zooming in on the Plot Area” on page 7-13.</td></tr>
<tr><td>Zoom In (Selected Range)

(Ctrl+R)</td><td>Expands the selected portion of an electropherogram to fill the full plot area.</td><td>“Zooming in on a Selected Range” on page 7-13.</td></tr>
<tr><td>Zoom Out

(Ctrl+-)</td><td>Displays a somewhat larger section of the electropherogram.</td><td>“Zooming Out” on page 7-14.</td></tr>
<tr><td>Zoom Out (Full Range)

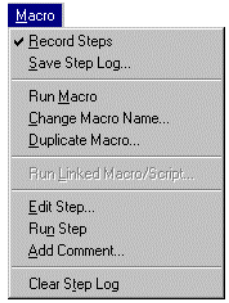
(Ctrl+H)</td><td>Displays the complete electropherogram.</td><td>“Zooming Out to Full Range” on page 7-15.</td></tr>
<tr><td>Zoom To...</td><td>Displays a dialog box used to specify a zoom range.</td><td rowspan="3">“Zooming to a Specific Range” on page 7-16.</td></tr>
<tr><td>Zoom To Category</td><td>Zooms to a range that includes the ranges of currently-selected categories.</td></tr>
<tr><td>Zoom To Next Category

(Ctrl+J)</td><td>Zoom to the range of the next marked category following the currently-selected category.</td></tr>
</table>
</td></tr>
</table>

Macro Menu

Definition The Macro menu contains commands for creating and running macros for automating the Genotyper software procedures and applications.

Menu Options The following figure shows the list of commands you can access from the Macro menu.



Commands

Macro menu commands:

Command	Description	For information, see...
Record Steps	When this menu item is checked, your steps (commands) will be added to the Current Step Log.	"Recording Steps in the Step List" on page 4-8.
Save Step Log	Creates a macro from the current step log and brings up a dialog box that allows you to name the macro and choose a keyboard command to run it.	step 3 on page 4-12.
Run Macro	Runs the selected macro.	"How to Run Macros" on page 4-4.
Change Macro Name	Displays a dialog box used to change the name of the selected macro and change the keyboard command which runs it.	"Changing a Macro Name" on page 4-12.

Macro menu commands: *(continued)*

Command	Description	For information, see...
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.	“Tips For Using Macros” on page 4-3.
Edit Step	Displays a dialog box used to adjust the values used by the step command. This works only for steps created using a dialog box.	“Editing the Step List” on page 4-9.
Run Step	Runs the selected step.	“Running a Step” on page 4-10.
Add Comment	Displays a dialog box used to add comments at the end of the Current Step log.	“Adding a Comment to a Macro” on page 4-13.
Clear Step Log	Removes all steps in the Current Step log.	“Clearing the Step List” on page 4-11.

Window Menu

Definition The Window menu contains commands for.

Menu Options The following figure shows the list of commands you can access from the Window menu.

Commands Window menu commands:

Command	Description	For information, see...
Cascade	Arranges windows so they are the same size and stacked from back to front, with only the title of each visible.	“Cascading Windows” on page 3-12.
Arrange Icons		
1 Clipboard	Shows items that have been cut, or copied, and still reside in the clipboard.	“Editing Document Windows” on page 3-19.
(More Windows)	Lists all currently open Genotyping software windows.	

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A

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