PROGENY

User's Manual
Version 8.0

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Customer Support

Support is available for Support Plan members who purchase Progeny Clinical, Progeny Lab, or Progeny LIMS and that have an annual support agreement and for trial users. Contact Progeny Software, LLC at:

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Table of Contents

Section 1: Progeny Core Database Functionality

Chapter 3: Datasheet Basics 83

Chapter 4: Spreadsheet Basics 103

Section 2: Progeny Clinical

Section 3: Progeny Lab

Section 4: Progeny LIMS

Preface

Welcome to the *Progeny Software User's Manual*. The purpose of the *Progeny Software User's Manual* is to answer your questions and guide you through the procedures necessary to use the Progeny Clinical application, the Progeny Lab application, and the Progeny LIMS application efficiently and effectively.

Using the manual

You will find the *Progeny Software User's Manual* easy to use. You can simply look up the topic that you need in the table of contents or the index. Later, in this Preface, you will find a brief discussion of each chapter to further assist you in locating the information that you need.

Special information about the manual

The *Progeny Software User's Manual* has a dual purpose design. It can be distributed electronically and then printed on an as-needed basis, or it can be viewed online in its fully interactive capacity. If you print the document, for best results, it is recommended that you print it on a duplex printer; however, single-sided printing will also work. If you view the document online, a standard set of bookmarks appears in a frame on the left side of the document window for navigation through the document. For better viewing, decrease the size of the bookmark frame and use the magnification box to increase the magnification of the document to your viewing preference.

If you do print the document using a single-sided printer, you might see a single blank page at the end of some chapters. This blank page has been added solely to ensure that the next chapter begins on an odd-numbered page. This blank page in no way indicates that your book is missing information.

Conventions used in the manual

The *Progeny Software User’s Manual* uses the following conventions:

- Information that can vary in a command—variable information—is indicated by alphanumeric characters enclosed in angle brackets; for example, <Sample ID>. Do not type the angle brackets when you specify the variable information.
- A new term, or term that must be emphasized for clarity of procedures, is *italicized*.
- Page numbering is “online friendly.” Pages are numbered from 1 to x, *starting with the cover* and ending on the last page of the index.

Although numbering begins on the cover page, this number is not visible on the cover page or front matter pages. Page numbers are visible starting with the first page of the table of contents.

- The Progeny application provides multiple ways of accessing the same Progeny functions. If an option is available from the toolbar as well as other areas (for example, the main menu or a context menu), then this manual references the toolbar. Although this manual does not address all the multiple ways of accessing the same function, you can use whatever method best suits your working needs.
- This manual is intended for both print and online viewing.
    - If information appears in blue, it is a hyperlink. Table of Contents and Index entries are also hyperlinks. Click the hyperlink to advance to the referenced information.

Assumptions for the manual

The *Progeny Software User’s Manual* assumes that:

- You are familiar with windows-based applications and basic Windows functions, navigational elements, and icons.

Organization of the manual

In addition to this Preface, the *Progeny Software User’s Manual* contains the following sections and appendices:

- Section 1, “Progeny Core Database Functionality,” on page 29 details the necessary steps for designing and maintaining a Progeny database that are necessary for data storage, data retrieval, and ensuring the integrity of the data in your database.
- Section 2, “Progeny Clinical,” on page 195 details the complete functionality of the Progeny Clinical module, which is pedigree and clinical data management software that you use for family-based studies.

- Section 3, “Progeny Lab,” on page 315 details the complete functionality of the Progeny Lab module, which is software that is designed for the management of whole genome association, targeted genotyping, and linkage studies.
- Section 4, “Progeny LIMS,” on page 475 details the complete functionality of the Progeny LIMS module, which is is software that is designed for managing any type of sample and associated data in a fully customizable multi-level inventory system with the freedom to create any laboratory workflow.
- Chapter A, “System Fields,” on page 551 details the read-only fields that Progeny automatically stores for a record. Each record type (individual, pedigree, sample, and marker) has its own unique system fields.
- Chapter B, “Importing Clinical Data,” on page 559 details the Import module to import external pedigrees, individuals, and samples that *do not already exist* in a Progeny database. You can also use the Import module to import data that updates individuals and samples that already exist in the database.

Section 1

Progeny Core Database Functionality

Section Contents

Chapter 1

Getting Started with Progeny

Progeny software is actually a suite of three individual products—Progeny Clinical, Progeny Lab, and Progeny LIMS—with each product designed for data management in a specific area. Progeny Clinical is designed for the management of clinical data, Progeny Lab is designed for the management of genotype data, and Progeny LIMS is designed for the management of sample data and inventories. Progeny Clinical, Progeny Lab, or Progeny LIMS can be combined in any fashion (including all three products) into a single application that is ideal for *complete* genetic data management. This chapter provides an overview of the Progeny main window and its major navigational elements.

This chapter covers the following topics:

- “Launching Progeny and the Progeny Main Window” on page 33.

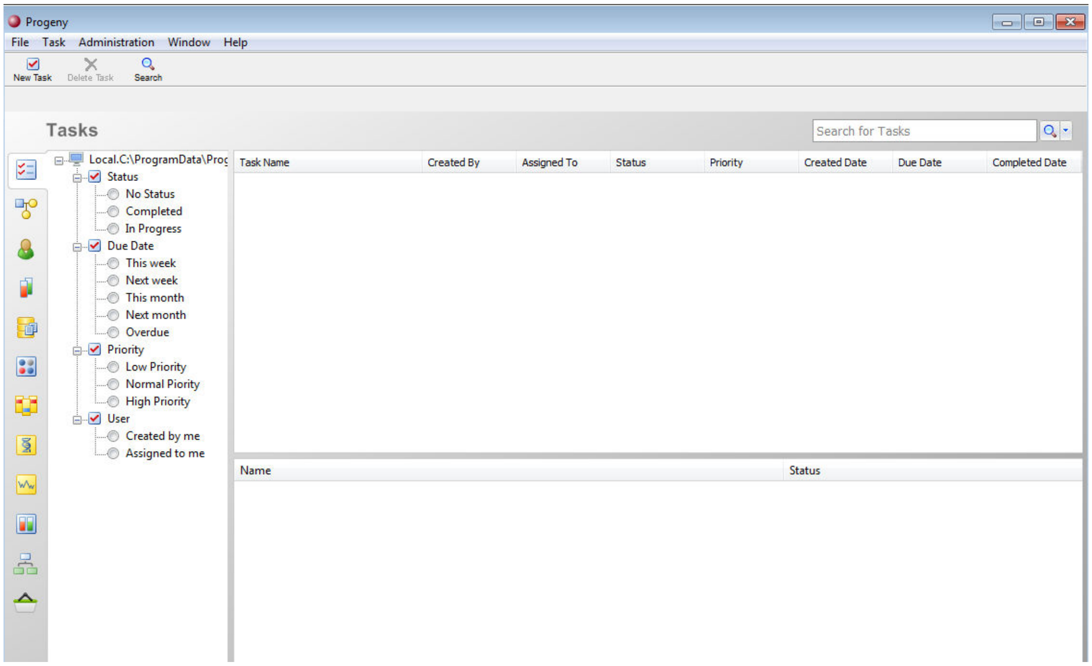
Launching Progeny and the Progeny Main Window

After your administrator installs Progeny, a shortcut icon for the application is placed on your desktop. An option for the application is also available from your Start menu. You can double-click the desktop icon, or you can select the option from your Start menu to open the Login window.

Figure 1-1: Progeny desktop icon

After you login to the application, the Progeny main window opens. The Progeny main window is your starting point for the Progeny application. The Progeny main window has six major components—the panes, the title bar, the main menu, the navigation bar, the toolbar, and the tab bar.

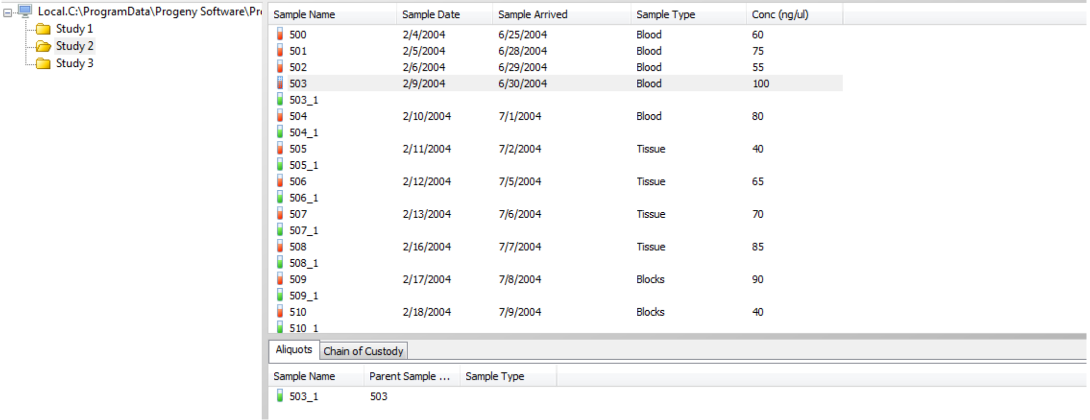
Figure 1-2: Progeny main window



Panes

The Progeny main window has three panes. The left vertical pane displays the folder organization for a particular functional area in a classic Windows Explorer-style structures. You simply click on a folder in the pane to open the folder. As you open folders and sub-folders in this pane, detailed information about the folder's content is displayed in the upper and lower right horizontal right panes. (Information is not displayed in a bottom pane until you select an item in the corresponding upper pane.) You can also right-click on a folder or item in a window pane and open a context menu that contains a limited set of choices for the folder or item. All the context menus offer a limited set of choices based on not only what window is currently open, but also, what folder or item is currently selected. Some of the choices on a context menu are also available from the main menu and/or the toolbar, while other choices are found only on a context menu.

Figure 1-3: Progeny main window panes

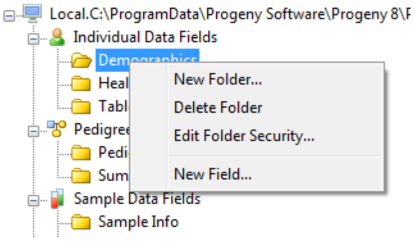


Sample Name	Sample Date	Sample Arrived	Sample Type	Conc (ng/ul)
500	2/4/2004	6/25/2004	Blood	60
501	2/5/2004	6/28/2004	Blood	75
502	2/6/2004	6/29/2004	Blood	55
503	2/9/2004	6/30/2004	Blood	100
503_1				
504	2/10/2004	7/1/2004	Blood	80
504_1				
505	2/11/2004	7/2/2004	Tissue	40
505_1				
506	2/12/2004	7/5/2004	Tissue	65
506_1				
507	2/13/2004	7/6/2004	Tissue	70
507_1				
508	2/16/2004	7/7/2004	Tissue	85
508_1				
509	2/17/2004	7/8/2004	Blocks	90
509_1				
510	2/18/2004	7/9/2004	Blocks	40
510_1				

Sample Name	Parent Sample ...	Sample Type
503_1	503	

To see all of the information that is displayed in the main window, you should always maximize the Progeny main window.

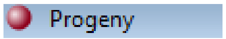
Figure 1-4: Example of a folder context menu



Title bar

The name "Progeny" appears in the title bar at the top of the Progeny main window. (The version number is not displayed in the title bar. The version number is available on the desktop icon and on the Start menu option.)

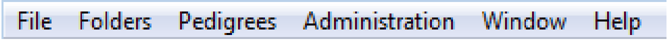
Figure 1-5: Title bar



Main menu

The main menu is set up in a standard Windows menu format with menu commands grouped into menus (File, Folders, Pedigrees, Administration, Window, and Help) across the menu bar. Some of these menu commands are available in other areas of the application.

Figure 1-6: Main menu



Navigation bar

The navigation bar is a vertical bar that is displayed on the left side of the main window. The navigation bar contains buttons that provide quick access to all the features that are available in a Progeny product. Two buttons (Tasks and Fields) are common to all three Progeny products. The other navigation buttons that are displayed depend on the products that your organization has purchased and installed.

When Progeny is installed, the navigation buttons are displayed in a default order on the navigation bar. You can change the order of the buttons on the Navigator bar to better suit your working needs simply by dragging a button to a new location.

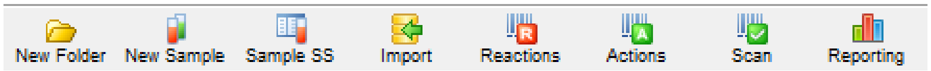
Button	Description
☑	Tasks—The Tasks feature centralizes any task that has been flagged with a reminder in the database in a single location. When you log into Progeny, if any tasks have been flagged with a reminder, then the Tasks main window opens with these tasks displayed on a per user basis. The Tasks button is displayed for all three Progeny products.
⊶	Pedigrees—The Pedigrees button opens the Pedigrees main window. The window has options for creating, organizing and storing pedigrees in the database. The Pedigrees button is displayed only if your organization has purchased and installed Progeny Lab or Progeny Clinical.
👤	Individuals—The Individuals button opens the Individuals main window. The window has options for creating, organizing, and storing people in the database. A person, or individual, can be a standalone individual or part of a pedigree. The Individuals button is displayed only if your organization has purchased and installed Progeny Lab or Progeny Clinical.
📊	Samples button—The Samples button opens the Samples main window. The window has options for creating, organizing and storing data sample information in the database. A person, or individual, can be a standalone individual or part of a pedigree. The Samples button is displayed only if your organization has purchased and installed Progeny Lab or Progeny LIMS.
📊	Inventory button—The Inventory button opens the Inventory main window. The window has options for complete sample inventory tracking in the database, including multi-level inventory and individual sample tracking. The Inventory button is displayed only if your organization has purchased and installed Progeny LIMS.

Button	Description
	Workflows button—The Workflows button opens the Workflows main window. The window has options for creating, organizing and storing workflows in the database. The Workflows button is displayed only if your organization has purchased and installed Progeny LIMS.
	Containers button—The Containers button opens the Containers main window. The window has options for creating, organizing and storing container information in the database. The Containers button is displayed only if your organization has purchased and installed Progeny LIMS.
	Markers button—The Markers button opens the Markers main window. The window has options for creating, organizing and storing marker information in the database. The Markers button is displayed only if your organization has purchased and installed Progeny Lab.
	Genotypes button—The Genotypes button opens the Genotypes main window. The window has options for importing and managing genotype data in the database. The Genotypes button is displayed only if your organization has purchased and installed Progeny Lab.
	Analysis button—The Analysis button opens the Analysis main window. The window has options for managing the exporting of a variety of linkage formats (MLINK, Genehunter, MEGA2, Allegro, and Merlin). The Analysis button is displayed only if your organization has purchased and installed Progeny Lab.
	Fields button—The Fields button opens the Fields main window. The window has options for creating, modifying and deleting folders and fields in the database. The Fields button is displayed for all three Progeny products.
	Orders button—The Orders button opens the Orders main window. The window has options for managing sample order information in the database. The Orders button is displayed only if your organization has purchased and installed Progeny LIMS.

Toolbar

The toolbar is located just below the main menu. The toolbar provides quick access to all the available functions for a selected product feature. The toolbar is dynamically updated based on the window that is open. Many of the commands that are available from the toolbar are also available in other areas of the application, for example, from the main menu or from a context menu, which is a menu that opens when you right-click on a folder or item in a Progeny main window pane.

Figure 1-7: Example of the toolbar when Samples is selected



Tab bar

Datasheets, spreadsheets, lookup tables, tables, and pedigrees open as separate tabs just below the toolbar in the main window. To open a datasheet, spreadsheet, table, or pedigree, simply click the tab for it. You can return to the main window at any time by clicking the Main tab. To close a tab, right-click on the tab and select Close Tab.

Figure 1-8: Tab bar

Chapter 2
Progeny Database Design

At a very high level, database design is the logical design of the base data structures that are used to store the data in the database. Complete and accurate database design is critical for data storage, data retrieval, and ensuring the integrity of the data in your database. This chapter details the procedures for creating, maintaining, and modifying a Progeny database.

This chapter covers the following topics:

Creating a Progeny Database

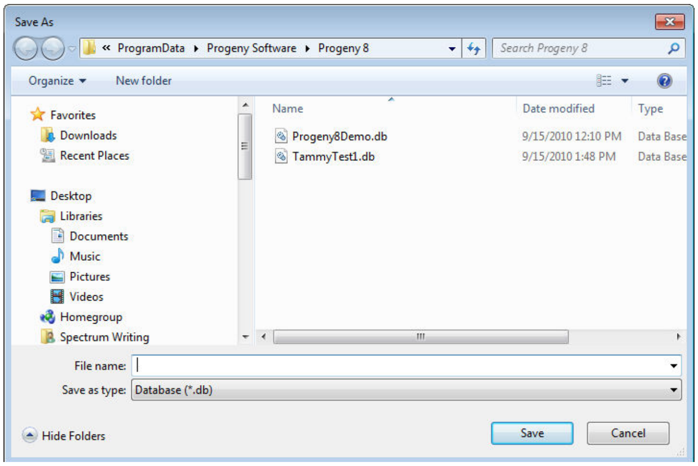
The Progeny application is shipped with a single demo database, Progeny<Version Number>demo.db, for example, Progeny8demo.db. The database contains some data fields with sample data. You can modify this database as needed to create your own Progeny database, you can use this database as a template for creating other Progeny databases, or you can create your own Progeny databases completely "from scratch." The database that ships with Progeny is unique to Progeny. Only databases created in Progeny work in Progeny. You can create as many databases as needed to support your business needs.

To create a Progeny database

1. Launch the Progeny application.
2. On the Login window, click Create.

   The Save As dialog box opens. The Save as Type field is automatically populated with the file type of Database (.db) and you cannot change this value.

Figure 2-1: Save As dialog box



« ProgramData ▸ Progeny Software ▸ Progeny 8

Name	Date modified	Type
Progeny8Demo.db	9/15/2010 12:10 PM	Data Base
TammyTest1.db	9/15/2010 1:48 PM	Data Base

File name:

Save as type: Database (*.db)

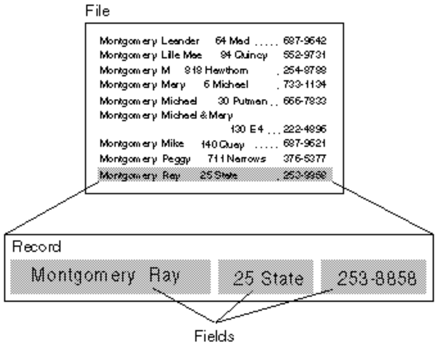
3. Browse to the location in which the database is to be saved, and then in the File name field, enter a name for the database.
4. Click Save.

   You can now add fields to the new database and/or copy fields from the sample database or another database into the new database. See "Adding, Editing, and Deleting Database Fields" on page 51 and "Copying Fields between Databases" on page 75.

Progeny Record-Level Database Fields

A database field is a single piece of information from a record. A *database record* is a set of fields. A *file* is a collection of records.

Figure 2-2: Example of the components of a database

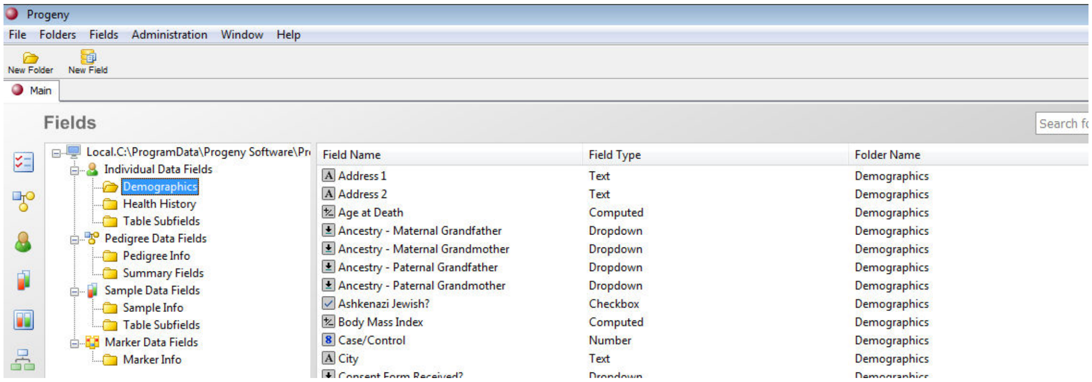


The Fields window displays the record-level fields that are contained in a Progeny database. To open this window, click the Fields button on the Navigation bar.

There are four different types of record-level fields in Progeny:

- Individual database fields—Individual database fields are stored at the individual record level. The demo database that is shipped with Progeny contains individual data fields grouped into Demographics, Health History, and Table Subfields folders. Individual database fields are displayed on the Fields window only if your organization has purchased and installed Progeny Lab or Progeny Clinical.

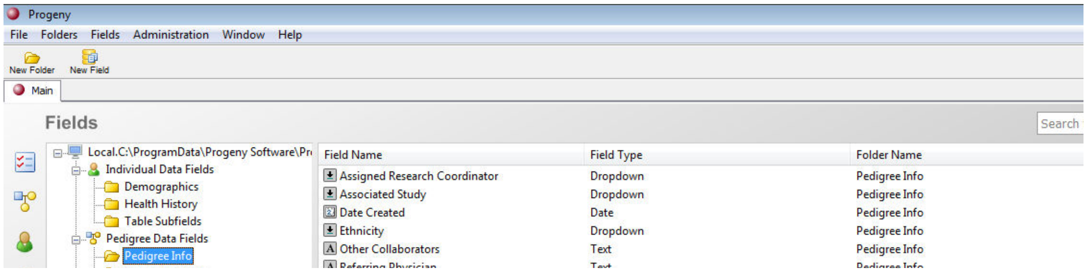
Figure 2-3: Individual database fields in Progeny demo database



Field Name	Field Type	Folder Name
Address 1	Text	Demographics
Address 2	Text	Demographics
Age at Death	Computed	Demographics
Ancestry - Maternal Grandfather	Dropdown	Demographics
Ancestry - Maternal Grandmother	Dropdown	Demographics
Ancestry - Paternal Grandfather	Dropdown	Demographics
Ancestry - Paternal Grandmother	Dropdown	Demographics
Ashkenazi Jewish?	Checkbox	Demographics
Body Mass Index	Computed	Demographics
Case/Control	Number	Demographics
City	Text	Demographics
Consent Form Received?	Dropdown	Demographics

- Pedigree database fields—Pedigree database fields are stored at the pedigree record level. The demo database that is shipped with Progeny contains pedigree data fields grouped into Pedigree Information and Summary Fields folders. Pedigree database fields are displayed on the Fields window only if your organization has purchased and installed Progeny Lab or Progeny Clinical.

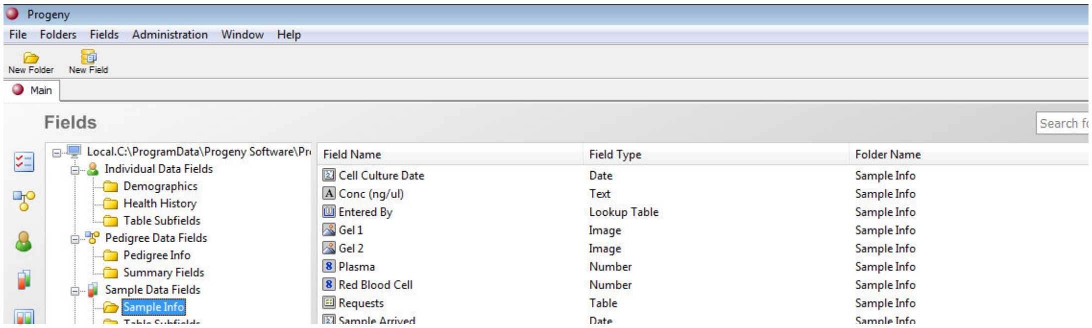
Figure 2-4: Pedigree database fields in Progeny demo database



Field Name	Field Type	Folder Name
Assigned Research Coordinator	Dropdown	Pedigree Info
Associated Study	Dropdown	Pedigree Info
Date Created	Date	Pedigree Info
Ethnicity	Dropdown	Pedigree Info
Other Collaborators	Text	Pedigree Info

- Sample database fields—Sample database fields are stored at the sample record level. The demo database that is shipped with Progeny contains sample data fields grouped into Sample Information and Table Subfields folders. Sample database fields are displayed on the Fields window only if your organization has purchased and installed Progeny Lab or Progeny LIMS.

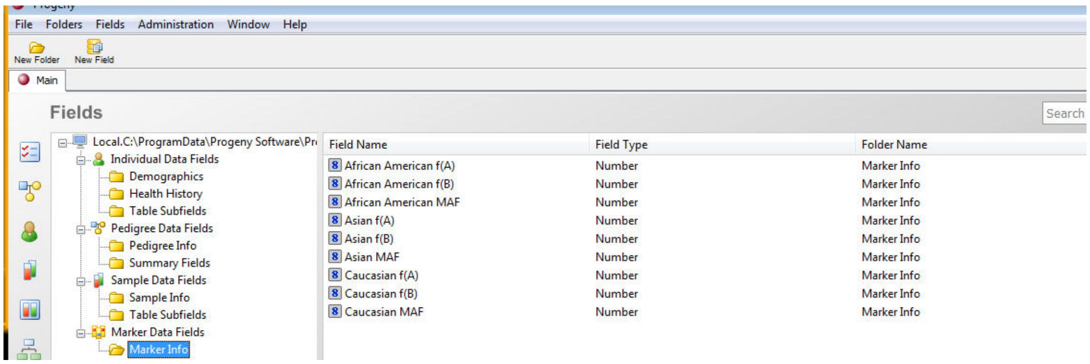
Figure 2-5: Sample database fields in Progeny demo database



Field Name	Field Type	Folder Name
Cell Culture Date	Date	Sample Info
Conc (ng/ul)	Text	Sample Info
Entered By	Lookup Table	Sample Info
Gel 1	Image	Sample Info
Gel 2	Image	Sample Info
Plasma	Number	Sample Info
Red Blood Cell	Number	Sample Info
Requests	Table	Sample Info

- Marker database fields—Marker database fields are stored at the marker record level. The demo database that is shipped with Progeny contains marker data fields grouped into a Marker Information folder. Marker database fields are displayed on the Fields window only if your organization has purchased and installed Progeny Lab.

Figure 2-6: Marker database fields in Progeny demo database



Field Name	Field Type	Folder Name
African American f(A)	Number	Marker Info
African American f(B)	Number	Marker Info
African American MAF	Number	Marker Info
Asian f(A)	Number	Marker Info
Asian f(B)	Number	Marker Info
Asian MAF	Number	Marker Info
Caucasian f(A)	Number	Marker Info
Caucasian f(B)	Number	Marker Info
Caucasian MAF	Number	Marker Info

Database Field Types

When you creating record-level fields in a Progeny database, you must specify the type for the field. The field type determines the type of data that a user can enter into the field (alphanumeric, numeric, date, and so on) or determines how the field functions in the database, for example, is an image displayed in the field when a user selects an image file of an allowed type, does the field link to another field in a different database, and so on. By default, each field type is marked with a unique icon in application. Not all field types are available for all record types. Table 2-1 lists the field types that are available for a record-level field in a Progeny database. It also provides a description of each field and the records for which the field type is applicable.

Table 2-1: Progeny database field types

Field Type	Icon	Description	Individual	Pedigree	Sample	Marker
Text	A	Alphanumeric characters (all digits and printable characters) up to a maximum of 32,000 characters.	X	X	X	X
Date	2	M/D/YY or M/D/YYYY	X	X	X	X
Numeric	8	The digits 0-9. Negative numbers and decimals allowed.	X	X	X	X
Yes/No	✓	Checkbox field that holds a value of either 1 (to indicate Yes) or 0 (to indicate No).	X	X	X	X
Dropdown	↓	Displays a list of pre-defined list of items from which the user can select one item.	X	X	X	X
Image	🖼	Allows for the display of an image in an allowed format in the field. **Note:** Applicable only for fields on an Individual datasheet.	X			
Table	▦	The field is to be included in a table. The field does not have a pre-defined value.	X	X	X	X
Lookup Table	▥	The field is to be included in a table. The fields have pre-defined values.	X	X	X	

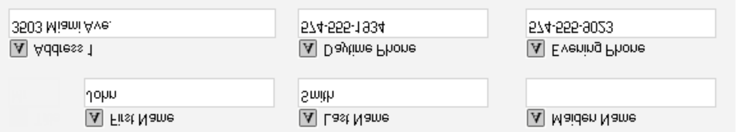
Table 2-1: Progeny database field types (continued)

Field Type	Icon	Description	Individual	Pedigree	Sample	Marker
Computed	±	No data entry is allowed in this field. Instead, a non-editable value is displayed in the field. The value that is displayed is automatically calculated based on the expression, function, or constant assigned to the field or values that are contained in other fields.	X	X	X	X
Summary	Σ	Provides summary information for a given column on a per pedigree basis. The summary can be an average, a total count, a minimum value, a maximum value, or a sum total.	X	X	X	
Table Summary	Σ	A computed field that summarizes the data for a given column in a given table.	X	X	X	
Hyperlink	H	Links to an external document, website, and so on.	X	X	X	X

Text field

A text field is for alphanumeric data (all digits and printable characters). You can enter up to a maximum of 32,000 characters in a text field. A text field is the most generic and least restrictive of all the available field types. Examples of text fields include First Name, Last Name, Address, City, Notes and so on.

Figure 2-7: Text field example



3503 Miami Ave.
☑ Address 1

274-222-1934
☑ Daytime Phone

274-222-9053
☑ Evening Phone

John
☑ First Name

Smith
☑ Last Name

☑ Maiden Name

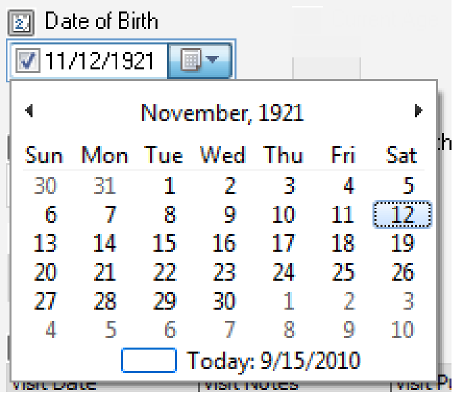
Date field

A date field contains a calendar. You can use the calendar to enter a date in a date field, or you can simply enter the date in the field. The *first* time that you click on a date field, the checkbox for the field is not selected, which means that the field is not editable. To make the field editable, you can do one of the following:

- Press the spacebar on your keyboard.
- Select the checkbox in the date field.
- Use the calendar by clicking on the dropdown arrow in the field, and then scrolling to and clicking on the appropriate date.

A date is stored in the database in a four digit format (M/D/YY) regardless of the date's display when you use the calendar (MM/DD/YYYY) or if you manually entered a four digit year. Dates are displayed in a date field based on the regional settings for the client.

Figure 2-8: Date field example



Date of Birth

☑ 11/12/1921

November, 1921

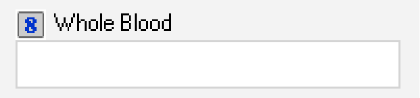
Sun	Mon	Tue	Wed	Thu	Fri	Sat
30	31	1	2	3	4	5
6	7	8	9	10	11	12
13	14	15	16	17	18	19
20	21	22	23	24	25	26
27	28	29	30	1	2	3
4	5	6	7	8	9	10

Today: 9/15/2010

Numeric field

You can enter only the digits 0 through 9 in a numeric field. Decimals and negative numbers are allowed; however, no other characters, either alphabetic or special (such as dashes or commas) are allowed. If you want to sort data based on numeric values, then you must use a numeric field. You cannot sort based on numeric values if the data is entered in a text field.

Figure 2-9: Numeric field example

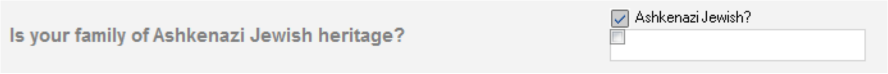


Yes/No field

A Yes/No field is a checkbox field that holds a value of either 1 (to indicate Yes) or 0 (to indicate No). Progeny always stores a value in a database for a checkbox field whether the field is checked. If the field is checked, Progeny stores a value of "1" in the database. If the field is not checked, Progeny stores a value of "0" in the database.

If a checkbox field has never been edited (meaning selected and then cleared) it registers as Null, not No. You must select the checkbox and then clear it for it to register as No. You should use the Yes/No field for fields where you want to track only Yes values. To track both Yes and No values, you should use a Dropdown field. See "Dropdown field."

Figure 2-10: Yes/No field example



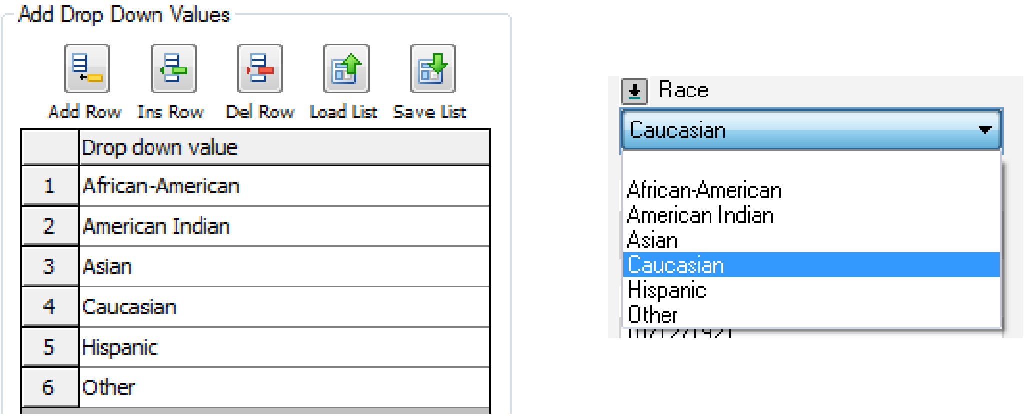
Is your family of Ashkenazi Jewish heritage?

☑ Ashkenazi Jewish?
☐

Dropdown field

A dropdown field displays a pre-defined list of items from which you can make a selection. To open the list, simply click in the field. You can scroll through the list and select one item at a time. The items are mutually exclusive. For example, you might create a dropdown field named "Race," and the available items are African American, American Indian, Asian, and so on. When you are adding/editing a dropdown field, the order in which you enter the items on the Add New Field/Edit Field dialog box is the order in which the items are displayed in the dropdown list. You can use the arrow keys on your keyboard to move up and down the list of available values for the field. If you are selecting from a lengthy dropdown list on a datasheet, you can enter the first few letters of the name of the item that you want to select and the list is dynamically updated with the items that meet your search criteria.

Figure 2-11: Add Dropdown Values pane on the Add New Field/Edit Field dialog box and corresponding Dropdown field



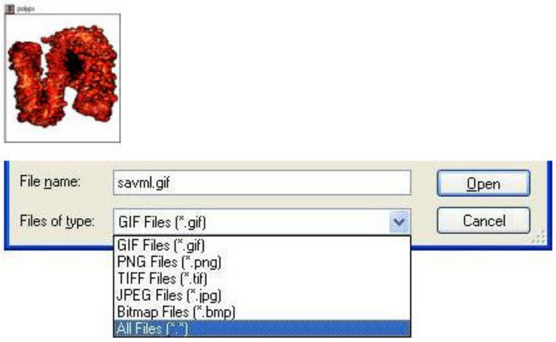
	Drop down value
1	African-American
2	American Indian
3	Asian
4	Caucasian
5	Hispanic
6	Other

Race: Caucasian

Image field

An image field is functional only on Individual datasheets. An image field can display an image file in one of the following formats—.bmp, .gif, .png, .tiff, and .jpg/.jpeg. When you click on an image field, you are prompted to enter the type of image file that you want to display. You then scroll to the appropriate image file and select it. After you select the image file, the image is displayed in the Image field.

Figure 2-12: Image field example



File name: savml.gif

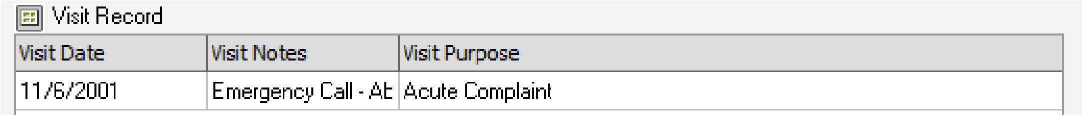
Files of type: GIF Files (*.gif)

- GIF Files (*.gif)
- PNG Files (*.png)
- TIFF Files (*.tif)
- JPEG Files (*.jpg)
- Bitmap Files (*.bmp)
- All Files (*.*)

Table

A table contains fields that are related in some way. The fields can be of the same or different field types. Because table fields are used for data entry, when you add fields to a table, they are added as empty fields. For example, you might add a table called Visit Information that would allow a user to enter data that is related in some way to a patient's visit such as the Visit Date field (a date field), the Visit Type field (a text field), and the Visit Purpose field (a dropdown field).

Figure 2-13: Table field example



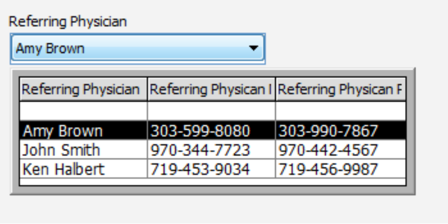
Visit Record

Visit Date	Visit Notes	Visit Purpose
11/6/2001	Emergency Call - Ab	Acute Complaint

Lookup Table

Like a table, a lookup table contains fields that are related in some way. Unlike a table, however, each field contains a pre-defined value. Lookup table fields are used primarily as a reference rather than for data entry. For example, you might create a lookup table called Referring Physician that would allow a user to associate fields that are related in some with the referring physician's name, for example, the physician's phone number and the physician's pager number. To enter data in a lookup table field, simply click in the field to open the table, and select the appropriate value from the table.

Figure 2-14: Lookup table field example



Referring Physician
Amy Brown

Referring Physician	Referring Physican I	Referring Physican F
Amy Brown	303-599-8080	303-990-7867
John Smith	970-344-7723	970-442-4567
Ken Halbert	719-453-9034	719-456-9987

Computed field

You cannot enter data into a computed field. Instead, a computed field contains an *expression* that yields a value that is automatically calculated each time the window that contains the field is opened. For example, a computed field for Current Age is defined as the difference in years between the date that is in the Current Date field and the date that is in the Date of Birth field.

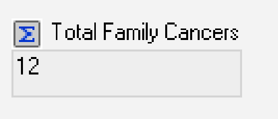
Figure 2-15: Computed field example

Current Age

Summary field

A summary field provides summary information for a given column *on a per pedigree basis*. Summary functions can be carried out on all fields that are *not* contained in tables. (The fields can be contained in lookup tables).

Figure 2-16: Summary field example

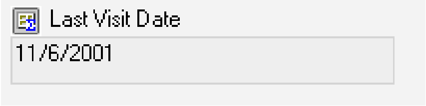


Total Family Cancers
12

Table Summary field

A table summary field is a computed field that summarizes the data for a given column in a given table. For example, you might create a table called Visit Information with a field in it called Visit Date and you want to see what the most recent visit date is for a specific patient. You can create a table summary field called Most Recent Visit Date that displays the most recent visit date for a patient that has five distinct visit date entries in the Visit Record table.

Figure 2-17: Table summary field example



Last Visit Date
11/6/2001

Hyperlink field

A hyperlink field contains a hyperlink to an external file, program or website. Simply click on the link in the field to open the file, program, or website. For example, a hyperlink field named Email could contain an individual's email address. When you click on the email address in the field, an untitled email addressed to the individual opens in the available email client such as Microsoft Outlook. Hyperlink fields are ideal for referencing external documents for an individual. As long as the referenced file has a valid extension and the appropriate program is installed on your computer, you can open the referenced document. For example, if a hyperlink field contains the link C:\My Documents\ConsentLetter.doc and you have Microsoft Word installed on your computer, then you can click the link to open the document.

Figure 2-18: Example of a hyperlink field

Email Address
jfisher@msn.com

Adding, Editing, and Deleting Database Fields

You can add, edit, and delete record-level database fields only from the Fields window. When adding record-level fields in a Progeny database, you must specify the field type. You can also set a default value for the field, add validation rules to the field, and set security for the field. You can also create folders for storing and organizing database fields. You can also delete a database field. When you delete a database field, it deletes not only the field, but also, any data that is stored in the field.

The remainder of this procedure details the high-level steps for adding new database fields to a database, regardless of the data type. If you simply want to copy existing fields from another database into a new database, see "Copying Fields between Databases" on page 75.

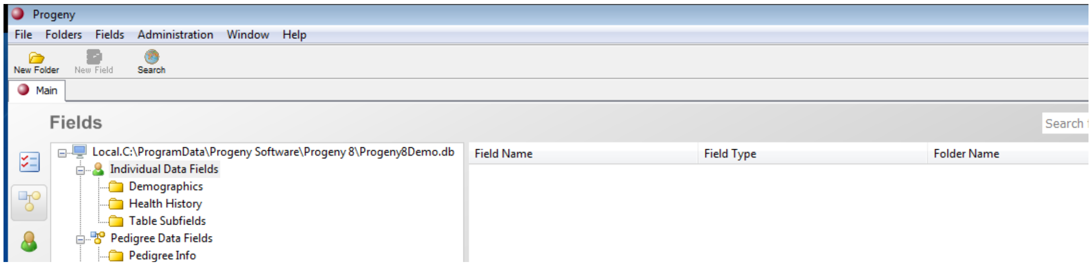
To add a database field

Make sure that you are logged in to the database to which you want to add the fields.

1. On the Progeny main window navigation bar, click the Fields button .

   The Fields window opens.

Figure 2-19: Fields window

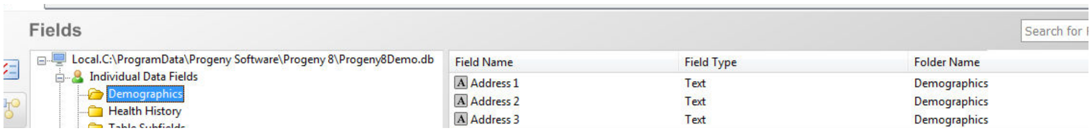


2. Determine the record type for which you are creating the field (Individual, Pedigree, Sample, or Marker), and then in the left pane of the window, open the database folder in which you are adding the field.

   A list of the fields that are already contained in the folder is displayed in the right pane of the Fields window.

For information about organizing database folders in folders, including adding new folders, see "Adding, Editing and Deleting Database Folders" on page 81.

Figure 2-20: Selected records folder with fields displayed in Fields window

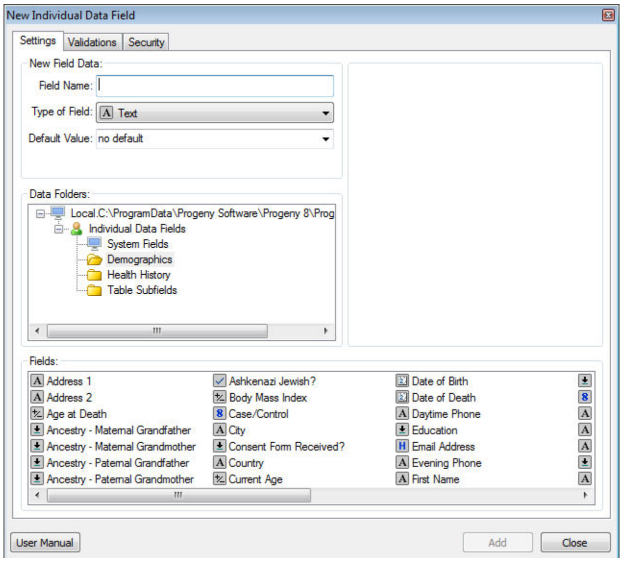


Field Name	Field Type	Folder Name
Address 1	Text	Demographics
Address 2	Text	Demographics
Address 3	Text	Demographics

3. On the Progeny toolbar, click the New Field button New Field .

   The New Data Field dialog box opens. The Settings tab is the active tab for the dialog box. All the fields that are contained in the selected folder are displayed alphabetically in the lower pane of the dialog box.

Figure 2-21: Example of a New Individual Data Field dialog box



Field Name:
Type of Field: Text
Default Value: no default

4. In the Field Name dialog box, enter the name for the new field.

5. On the Type of Field dropdown list, select the type for the new field.

   The field type determines the type of data that a user can enter into the field or it determines how the field functions in the database. Not all field types are available for all record types. (See “Database Field Types” on page 44.) In addition, if you are adding any of the following field types—Table, Lookup Table, Computed, Summary, or Table Summary field—then you must carry out additional steps to add the database field. See:

   - “Adding a Table” on page 55.
   - “Adding a Lookup Table” on page 57.
   - “Adding a Computed Field” on page 62.
   - “Adding a Summary Field” on page 67.
   - “Adding a Table Summary Field” on page 73.

6. Optionally, do one or more of the following:
    - If available, in the Default Value field, enter the default value for the field. A user can always edit this value.
    - Open the Validations tab and set the validation rules for the field. See "Setting Validations for a Database Field" on page 77.
    - Open the Security tab and set the security for the field. See "Setting Database Field Security" on page 140.
7. Click Add.

    A message opens indicating that the new field was added successfully.
8. Click OK.

    The message closes. The Add New Field dialog box remains open. The new field is displayed in the lower pane of the dialog box.

To edit a database field

1. On the navigation bar, click the Fields button .

    The Fields window opens.
2. In the left pane of the window, select the folder that contains the field that you are editing.

    A list of the fields that are contained in the folder is displayed in the right pane of the Fields window.
3. Double-click the field that you are deleting.

    The Edit Field dialog box opens. The dialog box displays all the current information for the field.
4. Edit the information for the field, including the field name, as needed. See:
    - To modify the validation settings, see "Setting Validations for a Database Field" on page 77.
    - To modify the security settings, see "Setting Database Field Security" on page 140.
5. Click Change.

    A message opens asking you if you are sure that you want to change the field.
6. Click Yes.

    The message and Edit Field dialog box close. You return to the Fields window with the fields listed in the right pane.

To delete a database field

You can delete a database field only if no datasheets, spreadsheets, or pedigrees are open. If any of these items are open, right-click on the item’s tab and click Close Tab. You can then continue with deleting database fields.

1. On the navigation bar, click the Fields button .

   The Fields window opens.

2. In the left pane of the window, on the Main tab, select the folder that contains the field that you are deleting.

   A list of the fields that are contained in the folder is displayed in the right pane of the Fields window.

3. Right-click on the field that you are deleting (CTRL-click to select multiple fields), and on the context menu that opens, click Delete Field.

   A message opens asking you if you are sure that you want to delete the selected fields and that the operation will delete the fields and the data.

4. Click OK.

   The message closes and the field (and the data stored in the field) is deleted from the database.

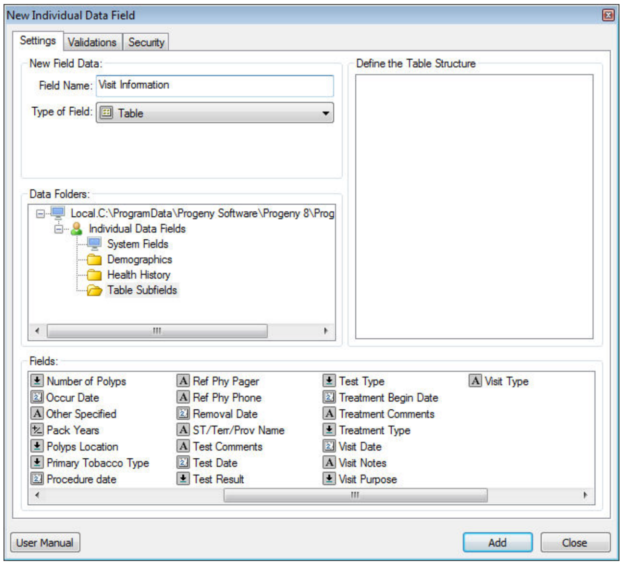
Adding a Table

Before you add a table, you must confirm that the fields that are to be added to the table already exist in the database, otherwise, you must add them. For example, before adding a table called Visit Information, you need to confirm that the fields Visit Date, Visit Type, and Visit Purpose already exist in the database (see "Contextual Search" on page 179), otherwise you must add them.

To add a table

1. On the New Field dialog box, enter the name for the Table field and select Table for the field type.

Figure 2-22: New Data Field dialog box, Adding a Table



Field Name: Visit Information
Type of Field: Table

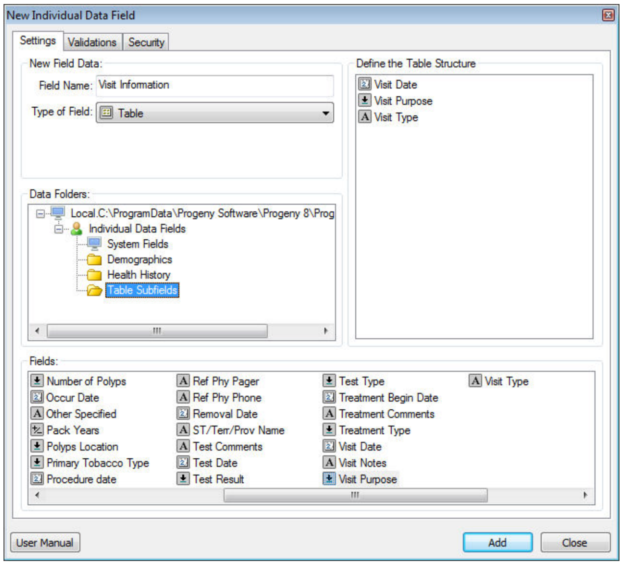
2. In the Data Folders pane, open the data folder that contains the fields that are to be added to the Table.

   The fields that are contained in the data folder are displayed in the Fields pane at the bottom of the Add New Data Field dialog box.

3. Drag each field that are you are adding to the Table from the Fields pane to the Define the Table Structure pane (upper right pane) of the Add New Data Field dialog box.

The order in which the fields are displayed in the Define the Table Structure pane is the order in which the rows are displayed in the table. You can change this order if needed. See "To format a table in a datasheet" on page 94.

Figure 2-23: New Data Field dialog box, Defining the Table structure



Field Name: Visit Information
Type of Field: Table

Define the Table Structure:
- Visit Date
- Visit Purpose
- Visit Type

4. Click Add.

   A message opens indicating that the new field was added successfully.

5. Click OK.

   The message closes.

6. Click Close in the Add New Field dialog box to close the dialog box and return to the Fields window.

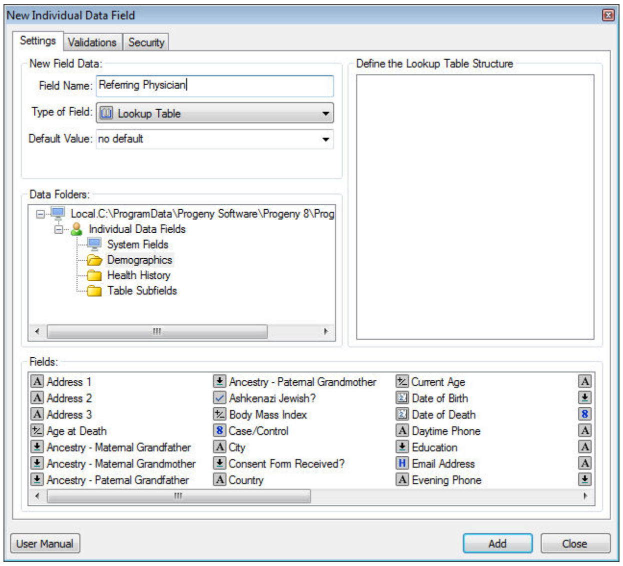
Adding a Lookup Table

Before you add a lookup table, you must confirm that the fields that are to be added to the lookup table already exist in the database, otherwise, you must add them to the database. For example, before adding a lookup table called Referring Physician, you need to confirm that the fields Ref Phy Phone and Ref Phy Pager already exist in the database (see "Contextual Search" on page 179), otherwise you must add them. After you add a lookup table, you can add the data to the fields in the table "from scratch," or you can import data from a text file into the fields.

To add a lookup table

1. On the New Field dialog box, enter the name for the lookup table and select Lookup Table for the field type.

Figure 2-24: New Data Field dialog box, Adding a Lookup Table



New Individual Data Field

Field Name: Referring Physician

Type of Field: Lookup Table

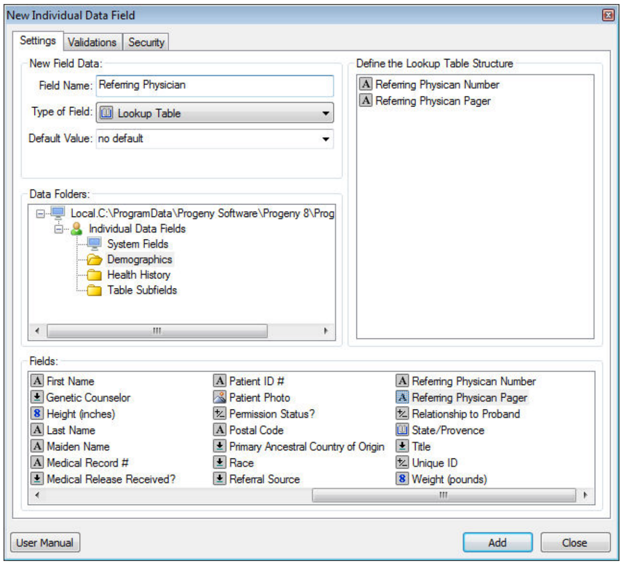
Default Value: no default

2. In the Data Folders pane, open the data folder that contains the fields that are to be added to the lookup table.

   The fields that are contained in the data folder are displayed in the Fields pane at the bottom of the Add New Data Field dialog box.

3. Drag each field that are you are adding to the lookup table from the Fields pane to the Define the Lookup Table Structure pane (upper right pane) of the Add New Data Field dialog box.

Figure 2-25: New Data Field dialog box, Defining the Lookup Table structure



Field Name: Referring Physician
Type of Field: Lookup Table
Default Value: no default

Define the Lookup Table Structure:
- Referring Physican Number
- Referring Physican Pager

Data Folders:
- Local.C:\ProgramData\Progeny Software\Progeny 8\Prog
  - Individual Data Fields
    - System Fields
    - Demographics
    - Health History
    - Table Subfields

Fields:
- First Name
- Genetic Counselor
- Height (inches)
- Last Name
- Maiden Name
- Medical Record #
- Medical Release Received?
- Patient ID #
- Patient Photo
- Permission Status?
- Postal Code
- Primary Ancestral Country of Origin
- Race
- Referral Source
- Referring Physican Number
- Referring Physican Pager
- Relationship to Proband
- State/Provence
- Title
- Unique ID
- Weight (pounds)

4. Continue to any other necessary tasks for the field, or click Add to add the field the database.

After you have added the lookup table, you can add data to the fields, either “from scratch,” or by importing a text file that contains the necessary data. See:

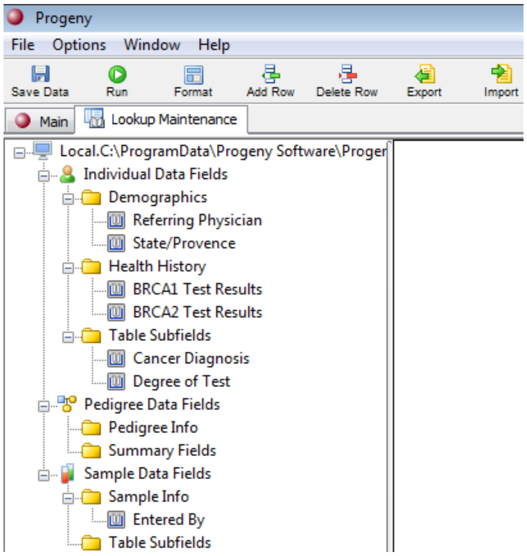
- “To add data “from scratch” to a lookup table” on page 59.
- “To import data into a lookup table” on page 60.

To add data “from scratch” to a lookup table

1. If you have not already done so, on the navigation bar, click the Fields button to open the Fields window.
2. On the main menu, click Fields > Lookup Table Maintenance.

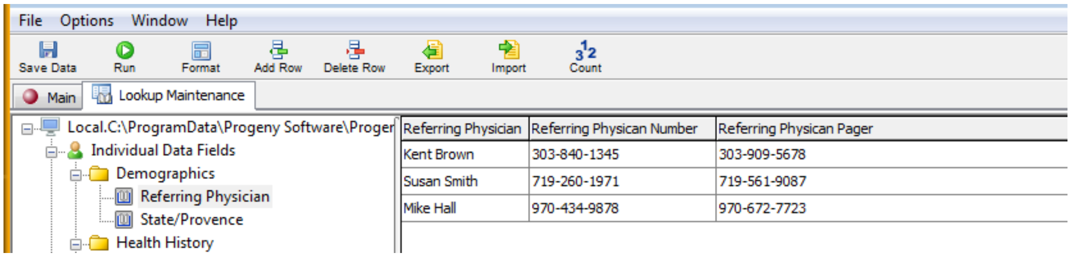
   The Lookup Maintenance tab opens. This tab displays every lookup table (by folder) that currently exists in the selected database.

Figure 2-26: Lookup Maintenance tab



3. In the left pane of the Lookup Maintenance tab, select the lookup table to which you are adding data.
4. On the Lookup Maintenance toolbar, click the Add Row button to enter data into the lookup table.

Figure 2-27: Adding data to a lookup table



Referring Physician	Referring Physican Number	Referring Physican Pager
Kent Brown	303-840-1345	303-909-5678
Susan Smith	719-260-1971	719-561-9087
Mike Hall	970-434-9878	970-672-7723

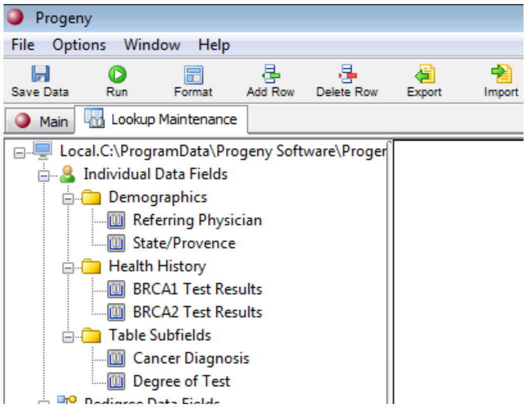
To import data into a lookup table

You can import data into a lookup table from a delimited file. The file can be a comma delimited file, a tab-delimited file, or you can specify another delimiter type.

1. If you have not already done so, on the navigation bar, click the Fields button to open the Fields window.
2. On the main menu, click Fields > Lookup Table Maintenance.

   The Lookup Maintenance tab opens. This tab displays every lookup table (by folder) that currently exists in the selected database.

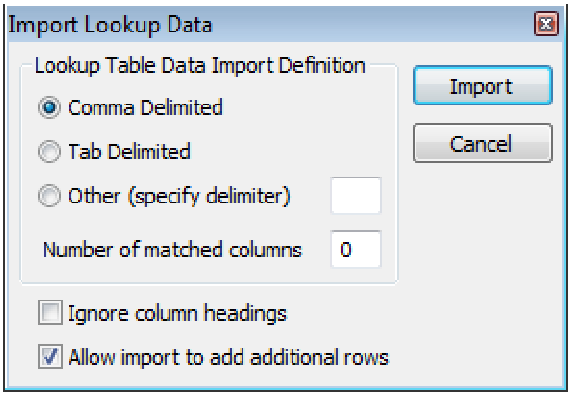
Figure 2-28: Lookup Maintenance tab



3. In the left pane of the Lookup Maintenance tab, select the lookup table into which you are importing the data.
4. On the Lookup Maintenance toolbar, click the Import button .

   The Import Lookup Data dialog box opens. Comma Delimited is selected by default.

Figure 2-29: Import Lookup Data dialog box



● Comma Delimited
○ Tab Delimited
○ Other (specify delimiter)
Number of matched columns 0
☐ Ignore column headings
☑ Allow import to add additional rows

5. Select the type of delimited file that you are importing. (If the file is not comma delimited or tab delimited, then you must specify the delimiter that the file uses.)

6. Specify the values for the following:
    - Number of Matched Columns—Enter the number of columns in the text file that you are importing that match to the number of columns in the lookup table. No data in the matched columns is overwritten. Only data from the matched point forward is overwritten. For example, if your lookup table and import text file have three columns, and you indicate “1” for the number of matched columns, then when the data is imported into the lookup table, the data in Column 1 of the lookup table is not overwritten; however, the data in Columns 2 and 3 of the lookup table is overwritten by the data in Columns 2 and 3 of the import file.

⚠ *The correct value for the number of matched columns is critical to ensuring the integrity of the data in the lookup table.*

    - Ignore column headings—If the file that is being imported contains column headings, select Ignore column headings.
    - Allow import to add additional rows—To allow the imported to add more rows of data to the lookup table during the import process, leave Allow import to add additional rows selected.
7. Click Import.

    The Open File dialog box opens.
8. In the Open File dialog box, browse to select and select the file that you are importing, and then click Open.

    A message opens indicating the Import operation was successful.
9. Click OK.

    The message closes. You return to the Lookup Maintenance tab. The imported information is displayed in the lookup table.

Adding a Computed Field

You cannot enter data into a computed field. Instead, when you add a computed field, you must define an *expression* for the field that yields a non-editable value that is automatically calculated each time the window that contains the field is opened. For example, a computed field for Current Age is defined as the difference in years between the dates in the Current Date field and the Date of Birth field. The expression can use functions, constants, and values in other fields for the calculation of the value. For example, a computed field can display the Body Mass Index (BMI) for an individual by calculating BMI based on the values in the Height and Weight fields. You can also specify the parameters for a computed field so that the field displays data only if another field is null (no data has been entered in the field). A computed field can be displayed in spreadsheets, pedigrees, and data sheets without displaying the fields on which its calculation is based. For example, the Current Age field can be displayed without displaying the Current Date and/or Date of Birth fields.

Computed field expressions

An *expression* is a group of characters or symbols that represent either a quantity/value or an operation. Table 2-2 lists the expressions that are allowed for a computed field.

Table 2-2: Computed field expressions

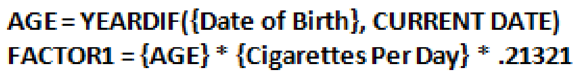
Expression	Description	Example
Operators		
• Addition	• expression + expression	• SUM = {NUM1} + {NUM2}
• Subtraction	• expression - expression	• DIFF = {NUM1} - {NUM2}
• Negation	• - expression	• - (SUM = {NUM1} + {NUM2})
• Multiplication	• expression * expression	• PROD = {NUM1} * {NUM2}
• Division	• expression / expression	• DIV = {NUM1} / {NUM2}
• String concatenation	• expression || expression or • expression + expression	
Note: If an expression has more than one operator, then the order of operations is followed.		
IF THEN ELSE	• IF condition THEN expression1 ELSE expression2 ENDIF Evaluates to expression1 if the condition is true and expression2 if the condition is false. The result is NULL if the condition is NULL or UNKNOWN. You can nest IF conditions.	PASS/FAIL VAR = IF ({NUM1} /500 > 1) THEN 1 ELSE 0 ENDIF
Note: For detailed information about working with NULL fields with IF/THEN expressions, see "NULL values in computed field expressions" on page 64.		

Table 2-2: Computed field expressions (continued)

Expression	Description	Example
System Constants • CURRENTDATE • CURRENT TIME • CURRENT TIMESTAMP • NULL • CURRENT USER	• All CURRENT constants pull their values from the current client settings. • A NULL field has never had data entered into the field.	• AGE = YEARDIF ({Date of Birth}, CURRENT DATE) • DAYS SINCE LAST TREATMENT = DAYS({Treatment Date}, CURRENT_DATE)

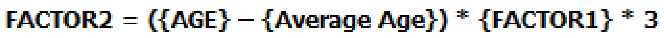
You can include other computed fields, summary fields, and/or system fields when you are defining the expression for a computed field. For example, in Figure 2-30, the Age database is field is a computed field that is used in the calculation of the computed database field named FACTOR1. In Figure 2-31, the Average Age database field is a pedigree Summary field that is used in the calculation of the computed database field named FACTOR2.

Figure 2-30: Including computed fields in the definition of a computed field



AGE = YEARDIF({Date of Birth}, CURRENT DATE)
FACTOR1 = {AGE} * {Cigarettes Per Day} * .21321

Figure 2-31: Including Summary fields in the definition of a computed field



FACTOR2 = ({AGE} – {Average Age}) * {FACTOR1} * 3

An example of including system fields when you are defining the expression for a computed field is the expression {Global ID} + 1000, which is a computed field that would display the value in the system field {Global ID} plus 1000 in the field. (See Appendix A, “System Fields,” on page 551.)

When you are defining the expression for a computed field, all *references to database fields must be enclosed in curly brackets {}*. For example, the sum (SUM) of the two database fields NUM1 and NUM2 is defined as {NUM1} + {NUM2}. To make data entry easier, you can drag a database field from the Fields pane at the bottom of the Add New Field dialog box into its correct location in the expression. The database field is automatically enclosed in curly brackets when you add it to the expression.

NULL values in computed field expressions

A NULL field is a database in which no data has been entered. Any expression that receives a NULL parameter returns NULL, and this is often not an acceptable result. For example, the following expression returns the sum of three numeric fields:

{Field1} + {Field2} + {Field3}

However, if either Field1 or Field2 and/or Field3 is null, the expression returns NULL.

Field Values				
Field1	**Field2**	**Field3**	**Returned Value**	**Acceptable Result?**
1	2	1	4	Yes
1	NULL	1	NULL	No
NULL	NULL	NULL	NULL	No

You can use the IFNULL function to return a value of one of the fields in the expression, or a zero value. For example, if you use the IFNULL function to define the allowed returned value:

IFNULL({Field1}, 0, {Field1}) + IFNULL({Field2}, 0, {Field2}) + IFNULL({Field3}, 0, {Field3})

then:

Field Values				
Field1	**Field2**	**Field3**	**Returned Value**	**Acceptable Result?**
1	2	1	4	Yes
1	NULL	1	2	Yes
NULL	NULL	NULL	0	Yes

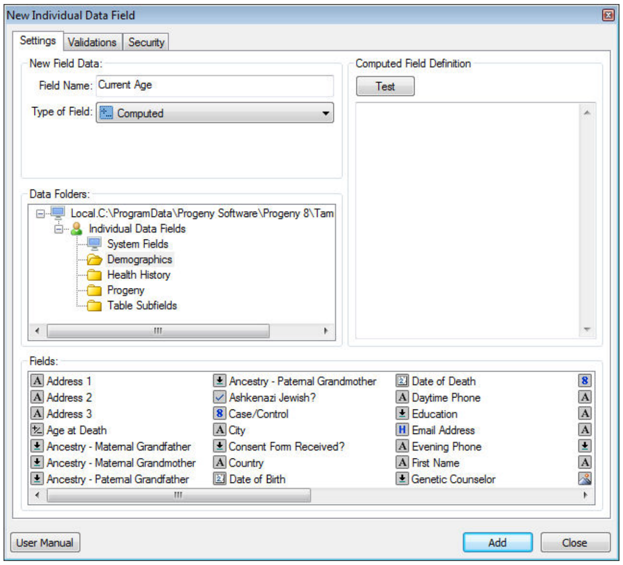
For information about the IFNULL function, go to http://infocenter.sybase.com/help/index.jsp?topic=/com.sybase.help.sqlanywhere.11.0.1/sqlanywhere_en11/help_top_index.htm, and then click Using SQL > SQL functions.

To add a computed field

The following example is simply a high-level example of the typical approach used to define a computed field expression. For a complete list of all the functions that are supported for a computed field expression, go to http://infocenter.sybase.com/help/index.jsp?topic=/com.sybase.help.sqlanywhere.11.0.1/sqlanywhere_en11/help_top_index.htm, and then click Using SQL > SQL functions.

1. On the New Field dialog box, enter the name for the computed field and select Computed for the field type.

Figure 2-32: New Data Field dialog box, Adding a Computed field



Field Name: Current Age
Type of Field: Computed

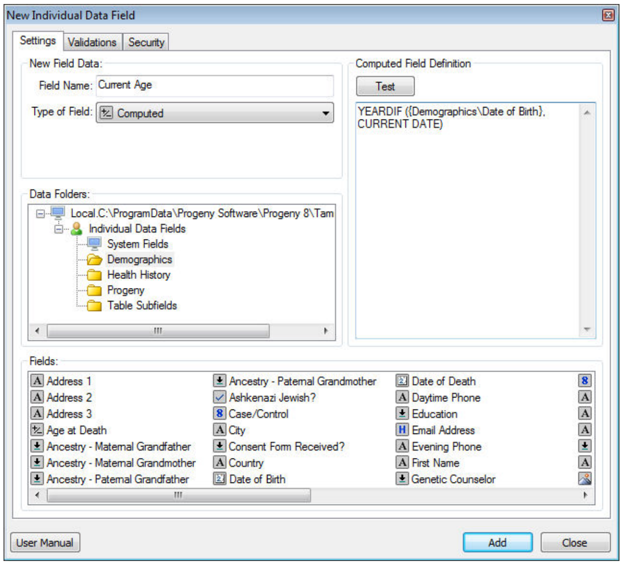
2. In the Computed Field Definition pane, enter the expression for the computed field that results in the difference between the Date of Birth and the Current Date (in years) being displayed in the Current Age field. For example:
   - Enter the YEARDIF function followed by an open left parenthesis: YEARDIF (
   - In the Data Folder pane, open the Demographics folder, and drag and drop the Date of Birth field after the open left parenthesis. The expression now looks like this: YEARDIF ({Demographics\Date of Birth}

Remember, when you drag a database field from the Fields pane at the bottom of the Add New Field dialog box into its correct location in the expression, the database field is automatically enclosed in curly brackets.

- After the right curly bracket, enter the a comma followed by a space and then the system constant CURRENT DATE. Complete the expression with a closing right parenthesis. The complete expression now looks like this:

  YEARDIF ({Demographics\Date of Birth}, CURRENT DATE)

Figure 2-33: New Data Field dialog box, Defining the computed field expression



Field Name: Current Age

Type of Field: Computed

```
YEARDIF ({Demographics\Date of Birth},
CURRENT DATE)
```

3. Click Test.
   - If the definition is acceptable, then a message opens stating that the expression is OK.
   - If the definition is not acceptable, then a message opens indicating that there is an error in the expression.
4. Click OK to close the message.
   - If the expression is acceptable, then continue to any other necessary tasks for the field, or click Add to add the field the database.
   - If the expression has an error, continuing modifying and testing the expression until it is acceptable, then continue to any other necessary tasks for the field, or click Add to add the field the database.

Adding a Summary Field

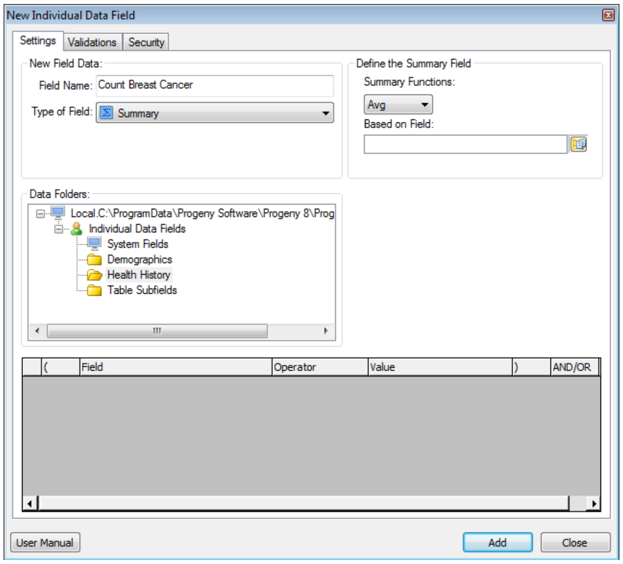
A summary field provides summary information for a given column *on a per pedigree basis*. Summary functions can be carried out on all fields that are *not* contained in tables. (The fields can be contained in lookup tables). When you add a summary field, you must specify the type of summary value (Average, Count, Maximum, Minimum, or Sum) that is to be returned in the field.

To summarize the data for a given column in a given table, see "Adding a Table Summary Field" on page 73.

To add a summary field

1. On the New Field dialog box, enter the name for the summary field and select Summary for the field type.

Figure 2-34: New Data Field dialog box, Adding a Summary field



New Individual Data Field

Field Name: Count Breast Cancer

Type of Field: Summary

Summary Functions: Avg

Based on Field:

2. In the Define the Summary Field pane, do the following:
   - Select the Summary type. All summaries are calculated on a per pedigree basis. Available values are:
     - Avg—Calculate the average value of a field. See "Average" on page 68.
     - Count—Return the total count of items in a field. See "Count" on page 69.
     - Max—Return the maximum value in a field. See "Maximum" on page 70.
     - Min—Return the minimum value in a field. See "Minimum" on page 71.
     - Sum—Return the sum total of a numeric field. See "Sum" on page 72.
   - Select the field in the pedigree that you are summarizing.

3. Define a query to filter the data:
   - In the Data Folders pane, open the folder that contains the field on which to base the query. (If the field is contained in a table, then open the Table Subfields folder.)
   - Drag the query field to the lower pane in the Add New Field dialog box, and then complete the query (Operator, Value, and so on).

See "Database Query Format" on page 173 for detailed information about formatting a database query.

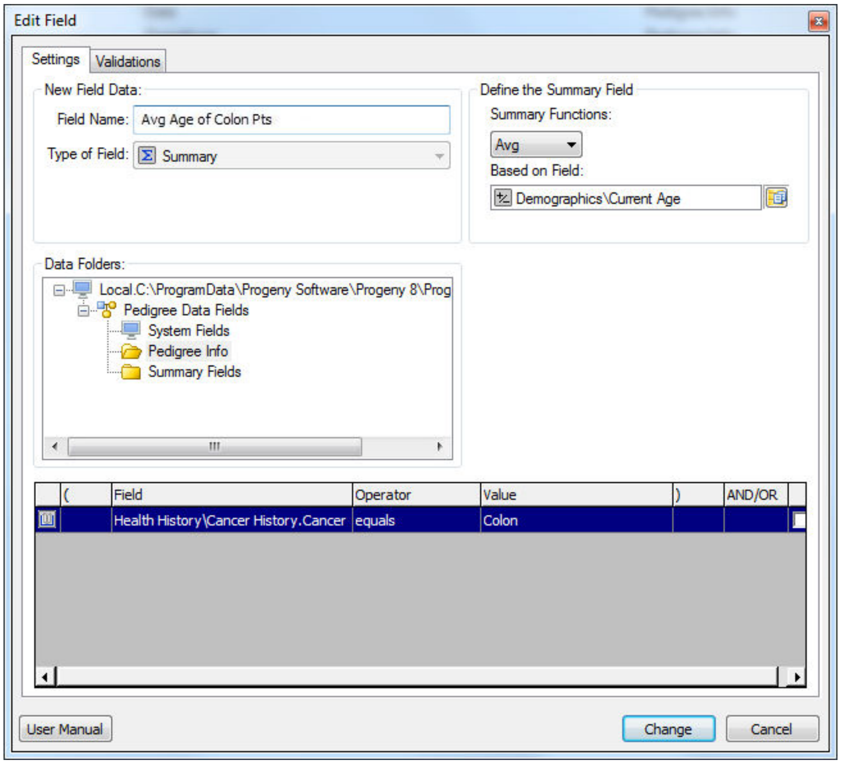
---

4. Continue to any other necessary tasks for the field, or click Add to add the field the database.

Average

The field shown in Figure 2-35 below returns the current average age of all the colon cancer patients in a pedigree. The average is calculated based on the current age of every individual in a pedigree. Summary fields in a spreadsheet display the same value for every individual in the spreadsheet for a given pedigree.

Figure 2-35: Summary field that returns an Average



New Field Data:
Field Name: Avg Age of Colon Pts
Type of Field: Summary

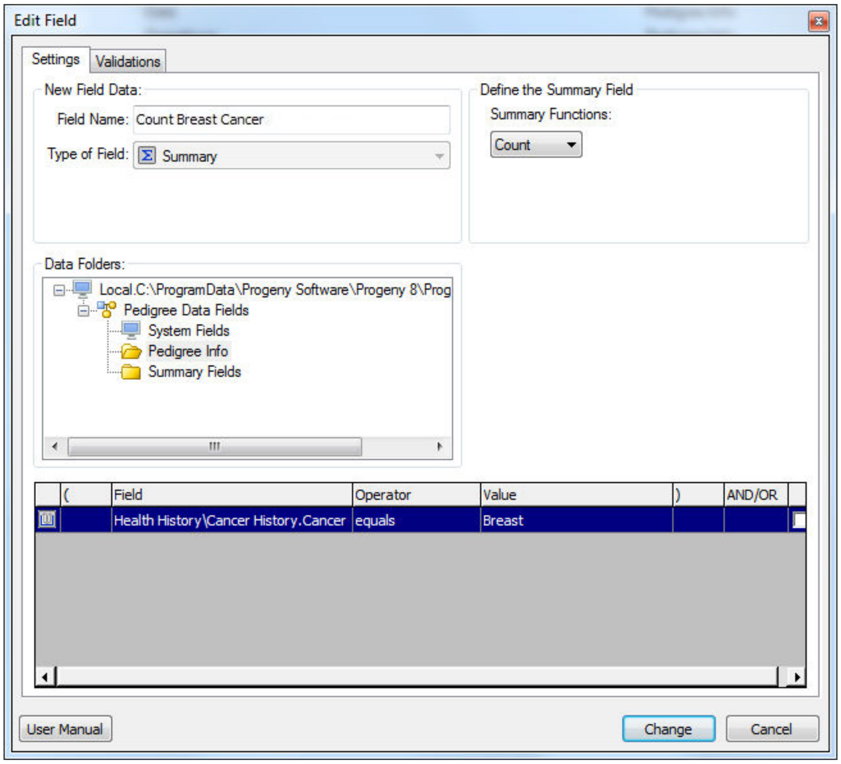
Define the Summary Field
Summary Functions: Avg
Based on Field: Demographics\Current Age

(	Field	Operator	Value	)	AND/OR
	Health History\Cancer History.Cancer	equals	Colon		

Count

The field shown in Figure 2-36 below returns the total count of the number of individuals in the pedigree where the Cancer Diagnosis = Breast.

Figure 2-36: Summary field that returns a Count



Field Name: Count Breast Cancer

Type of Field: Summary

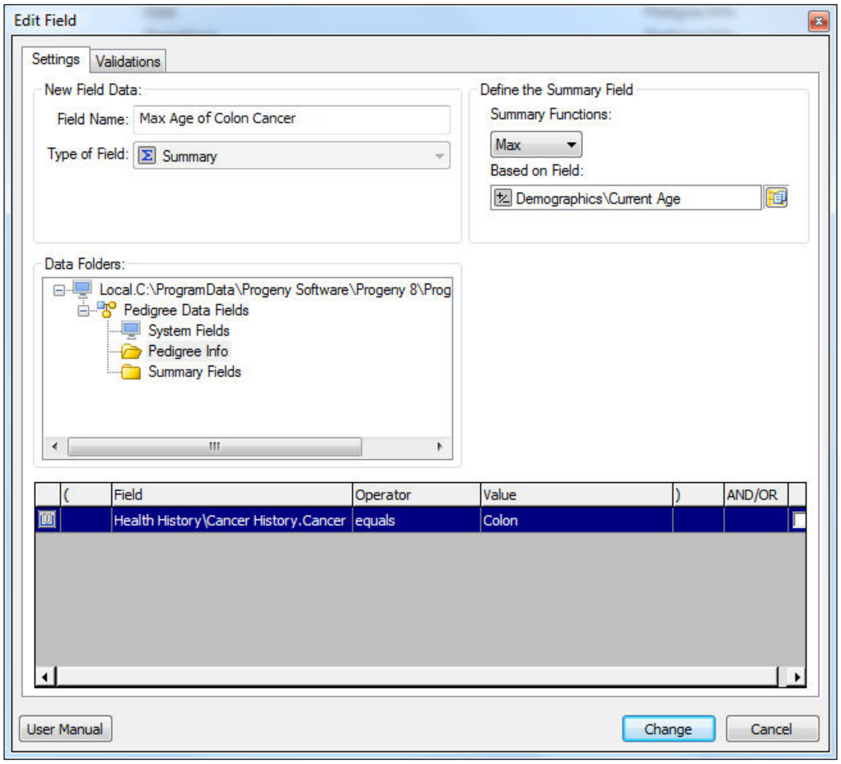
Summary Functions: Count

(	Field	Operator	Value	)	AND/OR
	Health History\Cancer History.Cancer	equals	Breast		

Maximum

The field shown in Figure 2-37 below returns the maximum current age of an individual in the pedigree who has been diagnosed with colon cancer.

Figure 2-37: Summary field that returns a Maximum



New Field Data:

Field Name: Max Age of Colon Cancer

Type of Field: Summary

Define the Summary Field

Summary Functions: Max

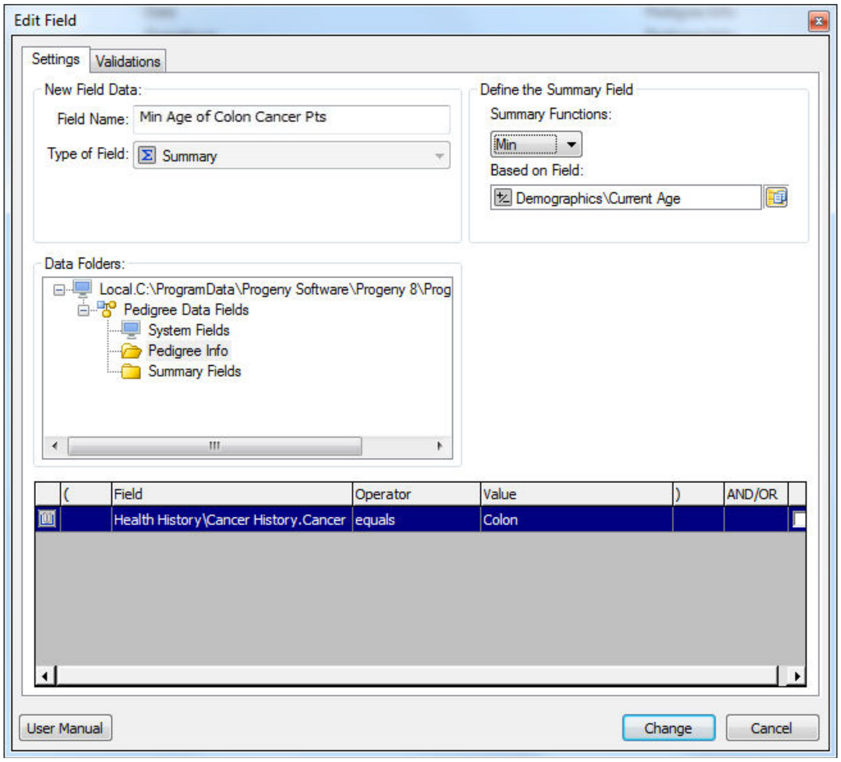
Based on Field: Demographics\Current Age

(	Field	Operator	Value	)	AND/OR
	Health History\Cancer History.Cancer	equals	Colon		

Minimum

The field shown in Figure 2-38 below returns the minimum current age of an individual in the pedigree who has been diagnosed with colon cancer.

Figure 2-38: Summary field that returns a Minimum



Field Name: Min Age of Colon Cancer Pts

Type of Field: Summary

Summary Functions: Min

Based on Field: Demographics\Current Age

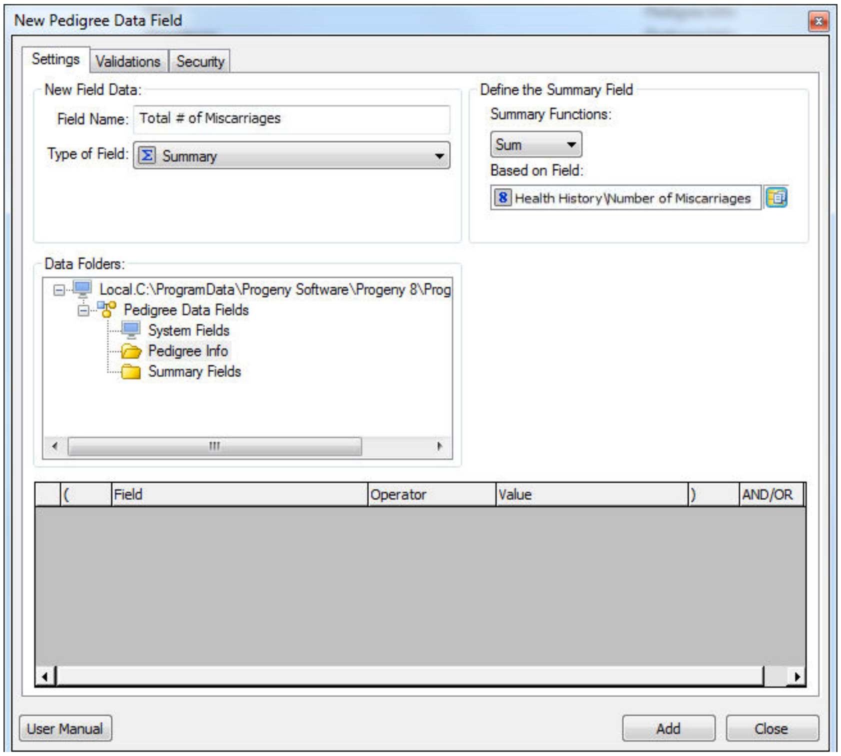
Local.C:\ProgramData\Progeny Software\Progeny 8\Prog
- Pedigree Data Fields
  - System Fields
  - Pedigree Info
  - Summary Fields

(	Field	Operator	Value	)	AND/OR
	Health History\Cancer History.Cancer	equals	Colon		

Sum

The field shown in Figure 2-39 below displays the total number of miscarriages in a given pedigree by adding the values in the numeric field Number of Miscarriages. If there are three individuals each having had two miscarriages, the Total #of Miscarriages field displays the number 6 in the field.

Figure 2-39: Summary field that returns a Sum



New Pedigree Data Field

New Field Data:
Field Name: Total # of Miscarriages
Type of Field: Summary

Define the Summary Field
Summary Functions: Sum
Based on Field: Health History\Number of Miscarriages

Data Folders:
- Local.C:\ProgramData\Progeny Software\Progeny 8\Prog
  - Pedigree Data Fields
    - System Fields
    - Pedigree Info
    - Summary Fields

Adding a Table Summary Field

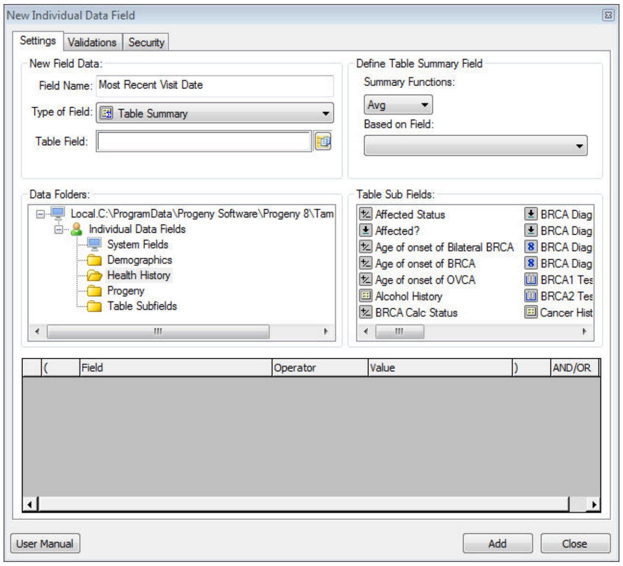
A table summary field is a computed field that summarizes the data for a given column *in a given table.* For example, you might add a table called Visit Record with a field in it called Visit Date and you want to see what the most recent visit date is for a specific patient. You can add a table summary field called Most Recent Visit Date that displays the most recent visit date for a patient who has five distinct visit date entries in the Visit Record table.

To summarize the data for a given column in a given pedigree, see "Adding a Summary Field" on page 67.

To add a table summary field

1. On the New Field dialog box, enter the name for the table summary field and select Table Summary for the field type.

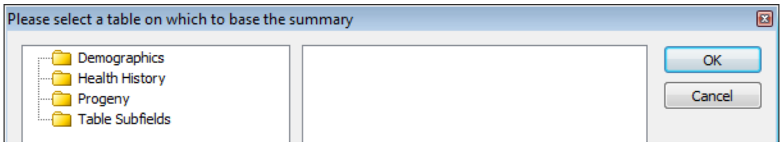
Figure 2-40: New Data Field dialog box, Adding a Table Summary field



Field Name: Most Recent Visit Date
Type of Field: Table Summary
Summary Functions: Avg

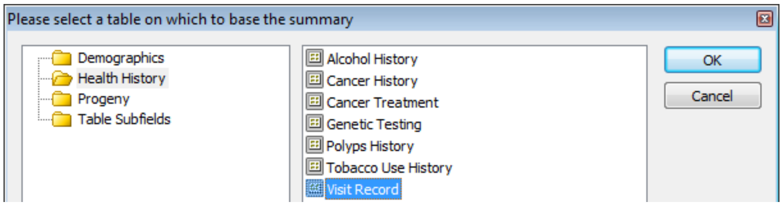
The Select Table dialog box opens.

Figure 2-41: Select Table dialog box



2. Select the table that contains the field on which you are basing the summary, and then click OK.

Figure 2-42: Select Table dialog box



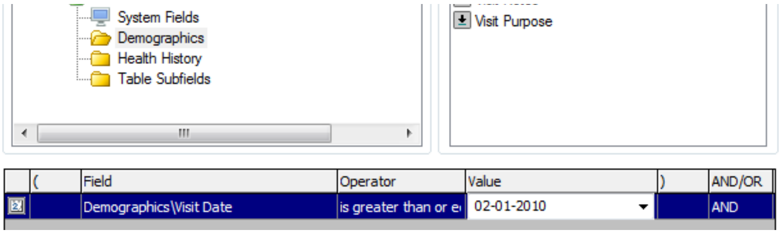
The Select Table dialog box closes. You return to the New Data Field dialog box.

3. In the Define Table Summary field pane, do the following:
   - Select the Summary type. Available values are:
     - Avg—Calculate the average value of a field.
     - Count—Return the total count of items in a field.
     - Max—Return the maximum value in a field.
     - Min—Return the minimum value in a field.
     - Sum—Return the sum total of a numeric field.
   - Select the field in the table that you are summarizing.
4. Optionally, do the following to define a query to further filter the data:
   - Open the Table Subfields folder. All the fields that are contained in the table are displayed in the Table Sub Fields pane.
   - Determine the table field on which to base the query, drag this field from the Table Sub Fields pane to the lower pane in the Add New Field dialog box, and then complete the query (Operator, Value, and so on).

See "Database Query Format" on page 173 for detailed information about the components of a database query.

For example, in Figure 2-43, the query that is displayed filters the data to the most recent visit that occurred on or after February 1, 2010.

Figure 2-43: Adding a Table Summary field, Defining the field



(	Field	Operator	Value	)	AND/OR
	Demographics\Visit Date	is greater than or e	02-01-2010		AND

5. Continue to any other necessary tasks for the field, or click Add to add the field the database.

Copying Fields between Databases

When you are creating a new database, or modifying an existing database, you have the option of adding new fields “from scratch” to the database; however, if an existing database already contains the needed fields, you can simply copy these fields. When you copy fields between databases, if any fields have the same name and are of the same or different type, then a prompt opens asking you if you want to overwrite the original field and all of the data in the field. You can select to overwrite the original field and all its data, or you can leave the original field and its data as-is.

To copy fields between databases

1. Log in to the database *from* which you are copying the fields.
2. On the Progeny main window navigation bar, click the Fields button .

   The Fields window opens.
3. If you are copying all the data fields for all the record types, go to Step 4; otherwise, do one of the following:
   - To copy only selected fields, in the left pane of the Fields window, open the folder that contains the fields that are to copied, and then in the right pane of the main window, select the fields (CTRL-click to select multiple fields).
   - To copy all the fields for a record type, in the left pane of the Fields window, select the record type. For example, to copy all the Individual data fields, then select Individual Data Fields.
4. On the main menu, click Fields > Save Fields as Text, and then select one of the following:
   - Save Selected Fields.
   - Save All < > Data Fields, where < > can be Individual, Pedigree, Sample Data, or Marker Data, for example, Save All Individual Data Fields.
   - Save All Data Fields.

   Select Save All Data Fields only if you are copying all the data fields for all the record types.

   The selected fields are saved to a file and the Open dialog box opens.
5. In the Open dialog box, browse to the location where the copied fields are to be saved, enter a name for the file that contains the copied fields, and then click Open.

   The file as is saved as text file and you cannot change this type.

6. Log out of the database *from* which you are copying the fields, and then log in to the database *into* which you are copying the fields.

7. On the navigation bar, click the Fields button .

   The Fields window opens.

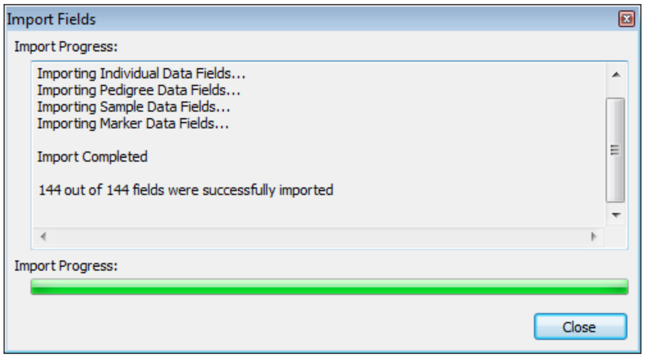
8. On the main menu, click Fields > Load Fields from Text.

   The Open dialog box opens.

9. Browse to and select the text file that you saved, and then click Open.

   If none of the fields in the text file has the same name as any of the fields in the database into which you are importing the fields, then the Import Fields dialog box opens. The dialog box indicates the number and type of fields that were successfully imported into the database; otherwise, for each matching field, a prompt opens that asks you if you want to overwrite the original field and all its data. Click Yes to overwrite the original field and all its data, or click No to leave the original field and all its data as-is. After you have responded to the prompt for each matching field, the Import Fields dialog box opens.

Figure 2-44: Import Fields dialog box



```
Importing Individual Data Fields...
Importing Pedigree Data Fields...
Importing Sample Data Fields...
Importing Marker Data Fields...

Import Completed

144 out of 144 fields were successfully imported
```

10. When the import is complete, click Close to close the Import Fields dialog box.

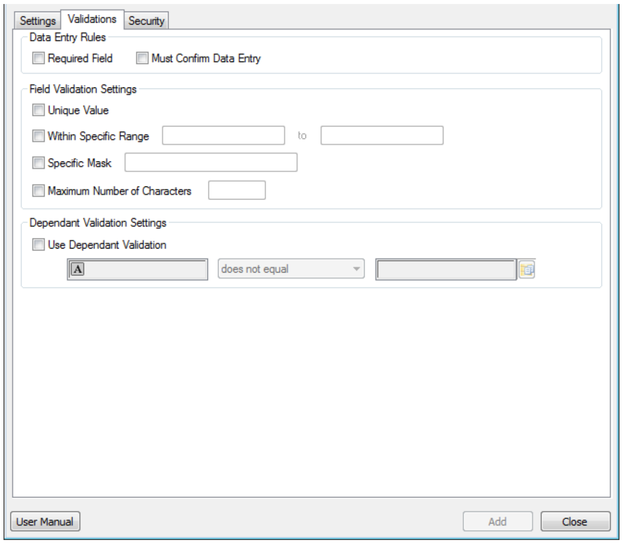
Setting Validations for a Database Field

When you are adding or editing a database field, you have the option of setting validations for the field. Validations guarantees to the Progeny that every data value that is entered into the field is correct and accurate. Three types of field-level validations are available—data entry rules, field validation settings, and dependent validations. If field validation settings and/or dependent validations are violated when you attempt to save data, then validation errors are generated.

To set validations for a database field

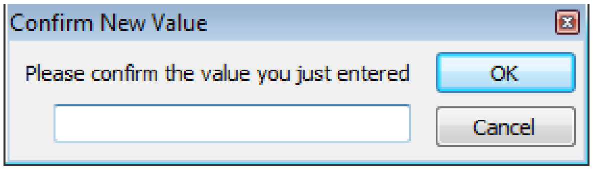
1. If the field is already open in the Add New Field dialog box, then go to Step 3; otherwise, on the navigation bar, click the Fields button to open the Fields window.
2. In the left pane of the Fields window, open the folder that contains the field for which you are setting the validations, and then in the right pane of the window, double-click the field to open the field in the Edit Field dialog box.
3. Open the Validations tab on the Add New Field/Edit Field dialog box.

Figure 2-45: Add Data Field dialog box, Validations tab



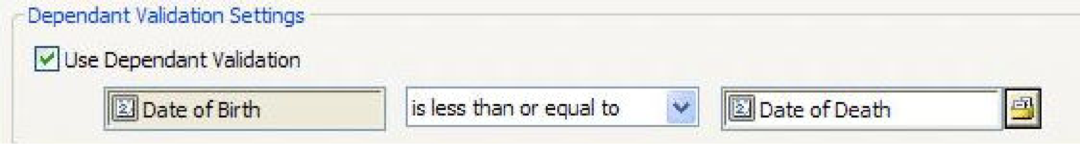
4. Set the validations for the field.
   - Data Entry Rules—These rules are applied only at data entry time. (Data entry in a data sheet, spreadsheet, and the Update Workflow window.)
     - Required Field—You must enter a value in the field before you can the data.
     - Must Confirm Data Entry—You are prompted to re-enter the data in the field before you can save the data. If a field has the Must Confirm Data Entry validation assigned to it, then a Confirm New Value dialog box opens for repeating the entry.

Figure 2-46: Confirm New Value dialog box



   - Field Validation Settings—These settings are applied at the database level and are applied at all times (data entry, imports, and so on).
     - Unique value—You must enter a unique value in the field wherever it is used (pedigree, individual, or sample).
     - Within Specific Range—Indicates the allowed range of values (numbers, dates, and so on) for the field.
     - Specific Mask—Defines how you must enter data into the field maintain consistency and to make your database easier to manage. For example, with the underscore character (_) representing a single character, an input mask of (___)___-____ would require a phone number like this: (574)968-0822.
     - Maximum Number of Characters—Indicates the maximum number of characters that you can enter into the field.
   - Dependent Validation Settings—These settings are applied at the database level and are applied at all times (data entry, imports, and so on).
     - Select Use Dependent Validation, and then specify the relation that the field must have with another field *of the same type*. For example, the following figure, shows how the value in the Date of Birth field must be less than or equal to the value in the Date of Death field.

Figure 2-47: Example of a dependent validation setting


Dependant Validation Settings

☑ Use Dependant Validation

Date of Birth | is less than or equal to | Date of Death

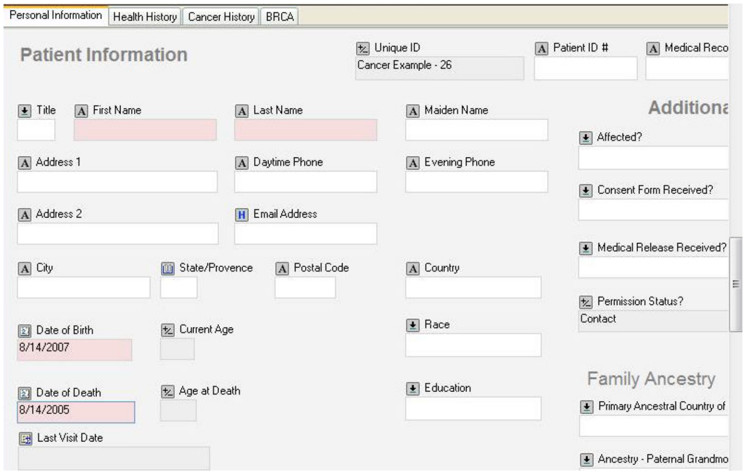
5. Continue to any other necessary tasks for the field, or click Add to add the field the database.

Data validation errors

If field validation settings and/or dependent validations are violated when you attempt to save data, then the fields with the validation errors are filled with red on the affected data sheet and spreadsheet and a Validation Errors dialog box opens. This dialog box lists the of validation errors on a field by field basis. You can double-click on a field that is listed in error to go the field in the open datasheet or spreadsheet.

Data entry rules are not included in the generation of validation errors. Instead, you are prompted with the rules before you save the data.

Figure 2-48: Data validation errors noted on a data sheet



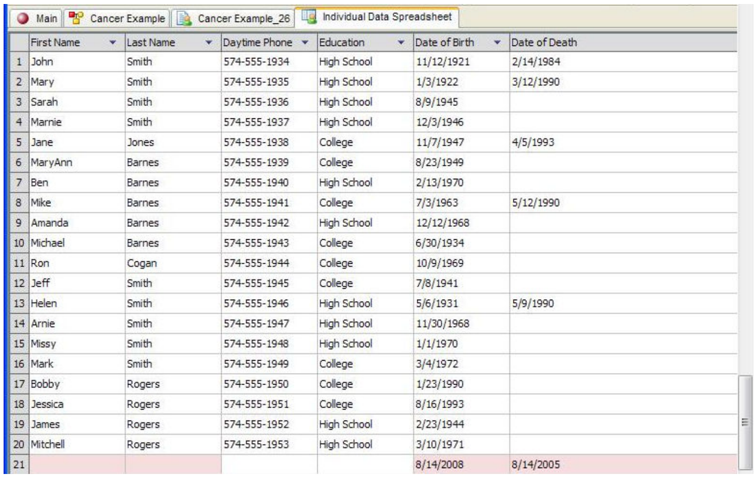
Unique ID: Cancer Example - 26

Date of Birth: 8/14/2007

Date of Death: 8/14/2005

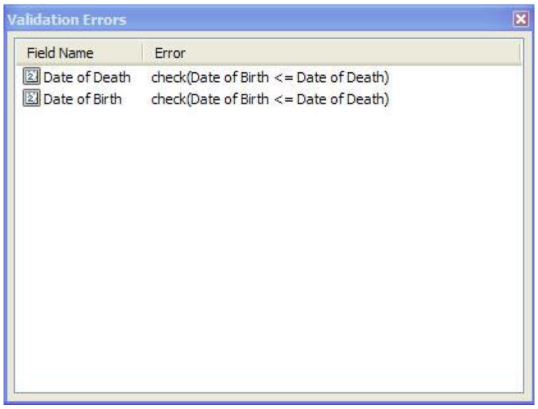
Permission Status?: Contact

Figure 2-49: Data validation errors noted on a spreadsheet



	First Name	Last Name	Daytime Phone	Education	Date of Birth	Date of Death
1	John	Smith	574-555-1934	High School	11/12/1921	2/14/1984
2	Mary	Smith	574-555-1935	High School	1/3/1922	3/12/1990
3	Sarah	Smith	574-555-1936	High School	8/9/1945	
4	Marnie	Smith	574-555-1937	High School	12/3/1946	
5	Jane	Jones	574-555-1938	College	11/7/1947	4/5/1993
6	MaryAnn	Barnes	574-555-1939	College	8/23/1949	
7	Ben	Barnes	574-555-1940	High School	2/13/1970	
8	Mike	Barnes	574-555-1941	College	7/3/1963	5/12/1990
9	Amanda	Barnes	574-555-1942	High School	12/12/1968	
10	Michael	Barnes	574-555-1943	College	6/30/1934	
11	Ron	Cogan	574-555-1944	College	10/9/1969	
12	Jeff	Smith	574-555-1945	College	7/8/1941	
13	Helen	Smith	574-555-1946	High School	5/6/1931	5/9/1990
14	Arnie	Smith	574-555-1947	High School	11/30/1968	
15	Missy	Smith	574-555-1948	High School	1/1/1970	
16	Mark	Smith	574-555-1949	College	3/4/1972	
17	Bobby	Rogers	574-555-1950	College	1/23/1990	
18	Jessica	Rogers	574-555-1951	College	8/16/1993	
19	James	Rogers	574-555-1952	High School	2/23/1944	
20	Mitchell	Rogers	574-555-1953	High School	3/10/1971	
21					8/14/2008	8/14/2005

Figure 2-50: Validation Error dialog box



Field Name	Error
Date of Death	check(Date of Birth <= Date of Death)
Date of Birth	check(Date of Birth <= Date of Death)

You can double-click on a field that is listed in this dialog box to go the field in the open datasheet or spreadsheet.

Adding, Editing and Deleting Database Folders

Folders provide a means of organizing your database fields. You can add as many root folders and sub-folders as needed to support your business needs. After you add a folder, you can set the security for the folder as well as for fields that are in the folder. You can also edit the security for a database folder. The default security settings for a folder are set to Read and Write for All Users. As the Progeny administrator, if you have yet to add any other user classes, then only two default user classes—Clinical and Laboratory—are displayed for a folder; otherwise, all the user classes that you have added are displayed. You can add more classes if needed. You can delete a folder only if the folder is empty (contains no database fields).

For information about adding a user class and setting folder security for a user class, see "Setting Database Folder Security" on page 143.

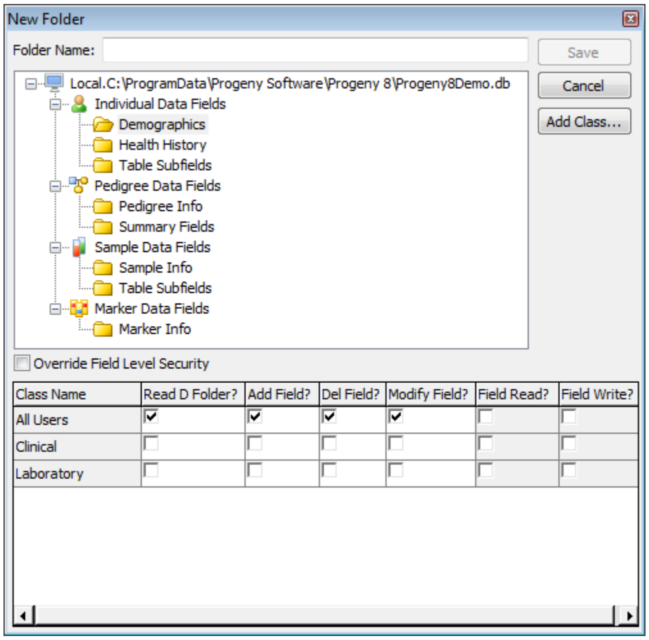
To add a database folder

1. On the navigation bar, click the Fields button to open the Fields window.

2. On the Fields window toolbar, click the New Folder button New Folder.

   The New Folder dialog box opens.

Figure 2-51: New Folder dialog box



Folder Name:

☐ Override Field Level Security

Class Name	Read D Folder?	Add Field?	Del Field?	Modify Field?	Field Read?	Field Write?
All Users	☑	☑	☑	☑	☐	☐
Clinical	☐	☐	☐	☐	☐	☐
Laboratory	☐	☐	☐	☐	☐	☐

3. In the Folder Name field, enter the name for the new folder.

4. Select the location for the new folder. For example, to create a folder at the root level for Individual data, select Individual Data Fields. To create a folder that is a subfolder of Individual Demographic data, under Individual Data Fields, select the Demographics folder.

You can create as many root folders and subfolders as needed to support your business needs.

5. Click Save.

   A message opens indicating that the folder was successfully added.

6. Click OK.

   The message closes. You return to the Fields window. The newly added folder is displayed in the window.

When you create database fields, you typically set the security for the fields on a field by field basis; however, if you want to apply the same security settings for every single field that is contained in the same database folder in a single step, then you can apply the settings at the folder level. See "Setting Database Folder Security" on page 143.

To edit a folder

You can rename a folder, and you can change the security settings for a folder.

- To rename a folder, *triple-click* on the folder in the Fields window to select it, and then modify the name as needed.

Figure 2-52: Example of a folder name selected for modifying

Individual Study

- To modify the security for a folder, see "Setting Database Folder Security" on page 143.

To delete a database folder

You can delete a selected database folder only if the folder is empty (contains no database fields). If you want to delete a database folder that contains fields, you must first delete all of the fields in the folder. (See "To delete a database field" on page 54.)

1. On the navigation bar, click the Fields button to open the Fields window.

2. In the left pane of the Fields window, right-click on the folder that you are deleting, and on the context menu that opens, select Delete Folder.

   A message opens asking you to confirm the deletion of the folder.

3. Click OK to close the message and delete the folder.

Chapter 3
Datasheet Basics

In layman's terms, a *datasheet* is a paper form or document that data that details the properties of a particular product or component. The form contains fields for collecting specific data about the product or component. By analogy, you use datasheets in Progeny to enter and store data for individuals, pedigrees, markers, and samples. Each datasheet contains database fields that store specific data for an individual, a pedigree, a marker set, and or a sample.

This chapter covers the following topics:

- "Datasheet Types" on page 85.
- "Creating and Formatting Datasheets" on page 86.
- "Working with Tables in a Datasheet" on page 93.
- "Saving and Loading Datasheet Formats" on page 99.
- "Printing a Datasheet" on page 101.

This chapter addresses only the basics for all datasheet types. Detailed information about adding the necessary components for creating a specific type of datasheet (for example, creating folders and adding individuals to the folder so that you can create an individual datasheet) are discussed in detail in the appropriate chapter (Progeny Clinical, Progeny Lab, or Progeny LIMS) in this manual.

Datasheet Types

In layman's terms, a *datasheet* is a paper form or document that data that details the properties of a particular product or component. The form contains fields for collecting specific data about the product or component. By analogy, you use datasheets in Progeny to store data for individuals, pedigrees, markers, and samples. After you add the necessary database fields to your Progeny database, you can use these fields to define a datasheet that stores specific information for an individual, a pedigree, a marker, or a sample. You can create five different types of datasheets in Progeny:

- Individual datasheets—You use individual datasheets to enter and store information about individuals in your Progeny database. An Individual datasheet can contain individual database fields, pedigree database fields, and marker database fields.
- Pedigree datasheets—You use pedigree datasheets to enter and store information about pedigrees in your Progeny database. A Pedigree datasheet can contain only pedigree database fields.
- Sample datasheets—You use sample datasheets to enter and store information about samples in your Progeny database. A Sample datasheet can contain all four types of Progeny database fields—individual database fields, pedigree database fields, sample database fields, and marker database fields.
- Marker datasheets—You use marker datasheets to enter and store information about markers in your Progeny database. A Marker datasheet can contain only marker database fields.
- Table datasheets—Table datasheets contain subfields from a table. Each table datasheet can contain table subfields from only a single table. A table datasheets is, in turn, contained in one of the other four types of datasheets—individual, pedigree, sample, or marker.

Creating and Formatting Datasheets

After you have added the necessary field types to your Progeny database, and you have added the necessary components for creating a specific type of datasheet (for example, you have created Individual folders and you have added individuals to a folder in preparation for creating an individual datasheet), you can create the datasheet. When you are creating a datasheet, you have a variety of options for formatting the datasheet, including the following:

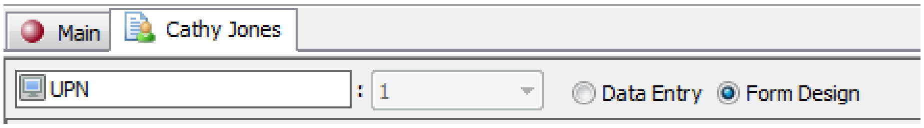
- Adding tabs to the datasheet.
- Positioning and aligning the fields on the datasheet.
- Specifying default settings for the fields on the datasheet.
- Adding static text to the datasheet.
- Creating table datasheets for table fields.

The following procedure assumes that you have already added the required components for creating a specific type of datasheet. (For example, you have created folders and added individuals to the folder so that you can create an individual datasheet.) Detailed procedures for creating the necessary components for adding a specific type of datasheet are discussed in detail in the appropriate chapter (Progeny Clinical, Progeny Lab, or Progeny LIMS) in this manual.

To create and format a datasheet

1. At the top of the blank datasheet, click Form Design.

Figure 3-1: Datasheet toolbar

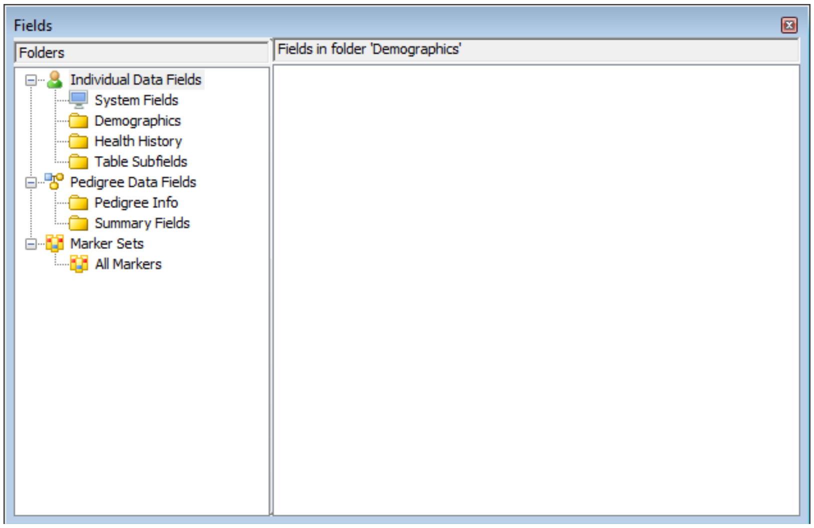


○ Data Entry ● Form Design

2. On the datasheet toolbar, click the Fields button Fields.

   The Fields dialog box opens. This dialog box contains all the fields (grouped by folder) that you can add to the datasheet. It also lists the system fields that you can add to the datasheet. For example, if you are creating an individual datasheet, then the dialog box lists all the individual data fields (grouped by folders), all the pedigree data fields (grouped by folders), and all the marker sets (grouped by folder) that you can add to the datasheet. It also lists all the individual system fields that you can add to the datasheet. See Figure 3-2 on page 87.

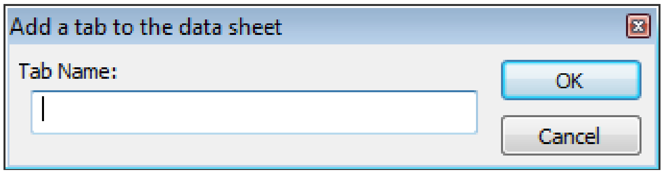
Figure 3-2: Fields dialog box for an Individual datasheet



System fields are read-only fields that Progeny automatically stores in its database for a record. Each record type (individual, pedigree, sample, and marker) has its own unique system fields. You can include system fields on a datasheet if there is information that you want to view at all times, but not edit, for an individual, a pedigree, a sample, or a marker. For a complete list of system fields and the read-only value that is displayed in each field, see Appendix A, "System Fields," on page 551.

3. If the datasheet is to be a single sheet, (that is, no tabs), then continue to Step 4; otherwise, for each tab that you are adding to the datasheet, on the datasheet toolbar, click the Add Tab button Add Tab to open the Add Tab dialog box, enter a name for the new tab, and then click OK.

Figure 3-3: Add Tab dialog box



4. In the left pane of the Fields dialog box, open the folder that contains the field or fields that you are adding to the datasheet.

   The list of fields contained in the folder is displayed in the right pane of the Fields dialog box.

If you need to review the different field types that you can add to a datasheet, see "Adding a Table" on page 55.

5. If applicable, make sure that the correct tab is open and then from the right pane of the Fields dialog box, drag the needed field or fields (CTRL-click to select multiple fields) to the datasheet.

You can add the same field to multiple tabs on the datasheet. The field can be shown in different locations on each tab if needed. When you enter data in a field on one tab, the same data is automatically entered in the field on the other tabs.

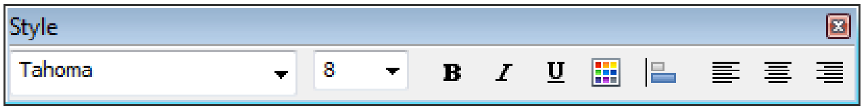
If you added a field in error, or want to remove a field from the datasheet, select the field, and then click the Delete key on your keyboard.

6. Format the fields on your datasheet as necessary. See:
   - "To align multiple fields" below.
   - "To add static text to a datasheet" on page 89.
   - "To set the properties for all the fields on the datasheet" on page 90.
   - "To set the field properties on a field by field basis" on page 91.
   - "Working with Tables in a Datasheet" on page 93.
7. On the datasheet toolbar, click the Save Position button Save Pos .

To align multiple fields

1. CTRL-click to select the fields that you are aligning.
2. On the datasheet toolbar, click the Style button Style to open the Style toolbar.

Figure 3-4: Style toolbar



3. On the Style toolbar, click the Alignment button to open a menu with a variety of options for modifying the field alignment.

Option	Description
Align Left	From top to bottom, vertically aligns the left edges of the selected fields.
Align Right	From top to bottom, vertically aligns the right edges of the selected fields.
Align Top	From left to right, horizontally aligns the top edges of the selected fields.
Align Bottom	From left to right, horizontally aligns the bottom edges of the selected fields.
Size Horz	Sets the width of all the selected fields to same width as the first selected field.
Size Vert	Sets the height of all the selected fields to same height as the first selected field.
Space Horz	Sets the horizontal spacing between all the selected fields to the same as the spacing between the first two selected fields.

Option	Description
Space Vert	Sets the vertical spacing between all the selected fields to same as the spacing between the first two selected fields.

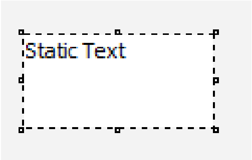
To add static text to a datasheet

Static text is free-standing text that is not tied to any field on a datasheet. You can add static text anywhere on a datasheet.

1. On the datasheet toolbar, click the Add Text button Add Text .

   A blank text box with the phrase “Static Text” is displayed on the worksheet.

Figure 3-5: Blank text box



Static Text

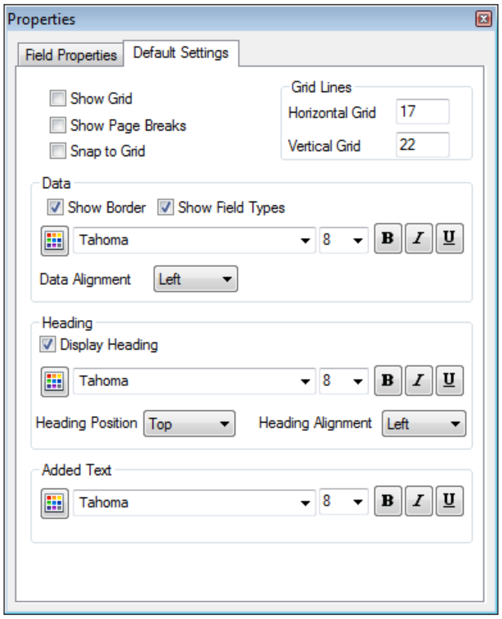
2. Click on the phrase “Static Text” to select it, and then replace the phrase with the appropriate text.
3. Drag the top, side, or corner handles to resize the text box as needed.
4. Click and hold on the center of the text box and drag the text box to the correct location on the datasheet.
5. To change the format for the static text (font size, font color, and so on), see one of the following:
   - “To set the properties for all the fields on the datasheet” on page 90.
   - “To set the field properties on a field by field basis” on page 91.

To set the properties for all the fields on the datasheet

You can set the same default properties for all the fields on the datasheet and all static text in a single step.

1. On the datasheet toolbar, click the Properties button ✓ Properties to open the Properties dialog box.
2. If needed, open the Default Settings tab.

Figure 3-6: Properties dialog box, Default Settings tab



Properties

Field Properties | Default Settings

☐ Show Grid
☐ Show Page Breaks
☐ Snap to Grid

Grid Lines
Horizontal Grid 17
Vertical Grid 22

Data
☑ Show Border ☑ Show Field Types
Tahoma 8 B I U
Data Alignment Left

Heading
☑ Display Heading
Tahoma 8 B I U
Heading Position Top
Heading Alignment Left

Added Text
Tahoma 8 B I U

3. Set the default values as needed.

Option	Description
• Show Grid	• Displays a background grid (a set of intersecting lines used to align objects) on the datasheet.
• Show Page Breaks	• Displays the edges of the print pages in Print Preview mode.
• Snap to Grid	• When moving a field, aligns (or “snaps”) the field to the nearest intersection of lines in the grid, even if the grid is not visible.
Data	• Show Border—Shows the border around all fields. • Show Field Type—Displays the icon for each field at the top left corner of the field. • Data Alignment—The horizontal alignment of the data that is displayed in the fields. Values are Left, Center, and Right.

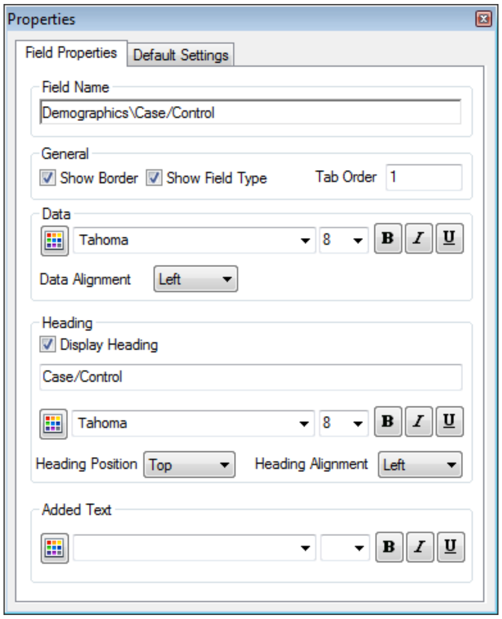
<table>
<tr><th>Option</th><th>Description</th></tr>
<tr><td>Heading</td><td>• Display Heading—Displays the field name as the field heading for each field.
• Heading Position—The location of the field heading relative to the field. Values are Top, Left, Bottom, and Right.
• Heading Alignment—The alignment of the field heading relative to the field. Values are Left (aligned with the left edge of the field), Center (centered relative to the field), and Right (aligned with the right edge of the field.</td></tr>
<tr><td colspan="2"> Use the formatting options to format the font color, font type, font size, and font properties (Bold, Italics, or Underline) for the data that is entered into a field, the field headings, and any static text on the datasheet.</td></tr>
</table>

To set the field properties on a field by field basis

You can set the properties for all fields on the datasheet, including static text fields, on a field by field basis.

1. Select the field for which you are setting the properties.
2. On the datasheet toolbar, click the Properties button ☑ Properties to open the Properties dialog box.
3. If needed, open the Field Properties tab. The database name of the selected field (including the name of its folder) is displayed in the Field Name field and you cannot change this value.

Figure 3-7: Properties dialog box, tab



Field Name: Demographics\Case/Control

General: ☑ Show Border ☑ Show Field Type Tab Order 1

Data: Tahoma 8

Data Alignment: Left

Heading: ☑ Display Heading

Case/Control

Tahoma 8

Heading Position: Top Heading Alignment: Left

Added Text

4. Set the default values as needed.

Option	Description
General	• Show Border—Shows the border around the field. • Show Field Type—Displays the icon for the field at the top left corner of the field. • Tab Order—The order in which a user tabs through the fields on a datasheet. The default tab order is the order in which you added the fields to the datasheet.
Data	• Data Alignment—The horizontal alignment of the data that is displayed in the field. Values are Left, Center, and Right.
Heading	• Display Heading—Displays a user-defined value as the heading for the field. **Note:** Any value that you enter here does not overwrite the database name for the field. It is simply a display value for the field on the datasheet. • Heading Position—The location of the field heading relative to the field. Values are Top, Left, Bottom, and Right. • Heading Alignment—The alignment of the field heading relative to the field. Values are Left (aligned with the left edge of the field), Center (centered relative to the field), and Right (aligned with the right edge of the field.
 Use the formatting options to format the font color, font type, font size, and font properties (Bold, Italics, or Underline) for the data that is entered into the field, the field heading, or any static text on the datasheet.	

Working with Tables in a Datasheet

Data entry for most of the fields in a datasheet is very straight forward and is described for each field type in "Database Field Types" on page 44. The tab order for the fields determines the order in which you move through the fields on the datasheet and enter data in them. A variety of options, however, are available for working with table fields in datasheets, including resizing a table, saving and loading table formats, and entering data either directly into the table or creating table datasheets and entering the data into a table through its table datasheet.

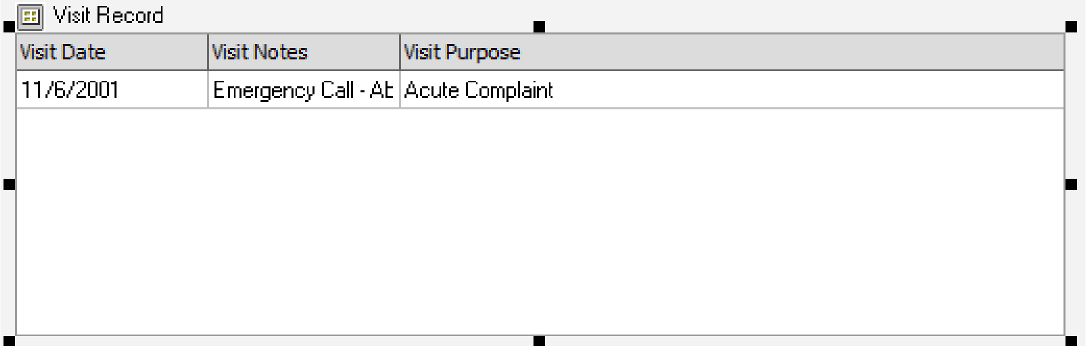
To resize a table

When you add a table field to a datasheet, the table is added with a default size (width and height). You can resize the window if needed.

1. At the top of the datasheet, click Form Design.
2. Click in the table field to select it.

   Resizing handles appear on the table.

Figure 3-8: Selected table in a datasheet



Visit Record

Visit Date	Visit Notes	Visit Purpose
11/6/2001	Emergency Call - At	Acute Complaint

3. Drag the top, side, or corner handles to resize the table as needed.

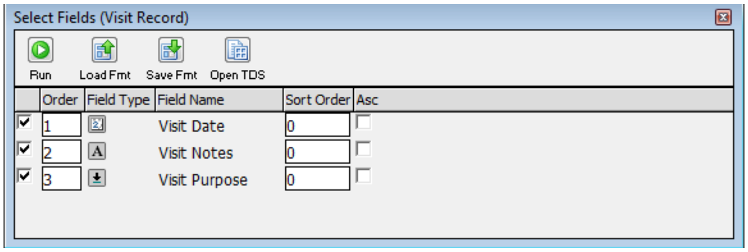
To format a table in a datasheet

When you *first* add a table to a datasheet, the order in which the fields are displayed in the Define the Table Structure pane in the Add New Field dialog box (see "Adding a Table" on page 55) is the order in which the rows are displayed in the table in the datasheet. You change this order if needed, and you can also save the new order as a table format. You can save multiple formats for the same table and load different formats for the same table in different datasheets.

1. In Form Design mode, right-click on the table in the datasheet, and on the context menu that opens, click Show Fields.

   The Select Fields window opens. This window lists all of the fields in the table and their current order in the table.

Figure 3-9: Select Fields table



	Order	Field Type	Field Name	Sort Order	Asc
☑	1		Visit Date	0	☐
☑	2	A	Visit Notes	0	☐
☑	3		Visit Purpose	0	☐

2. In the Order column, enter the new order for the table fields.
3. Optionally, to sort the table display, enter the sort order for the table fields.

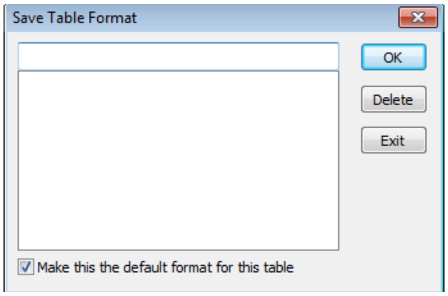
   For example, to sort the data in the Visit Table shown in Figure 3-9 above by the most recent visit date, in the Sort Order column for Visit Date, enter a "1," and then select Asc (which indicates Ascending order). To sort by the oldest visit data, do not select Asc.

4. Click the Run button Run to change the order of the table fields in the datasheet.
5. Optionally, to save this new order of rows as a table format, click the

   Save Format button Save Fmt .

   The Save Table Format dialog box opens.

Figure 3-10: Save Table Format dialog box



☑ Make this the default format for this table

6. Enter a name for the table format, and if you want to make this format the default format for the table, leave Make this the default format for the table selected.

You can create as many formats as needed, but only one format can be the default format.

7. Click OK.

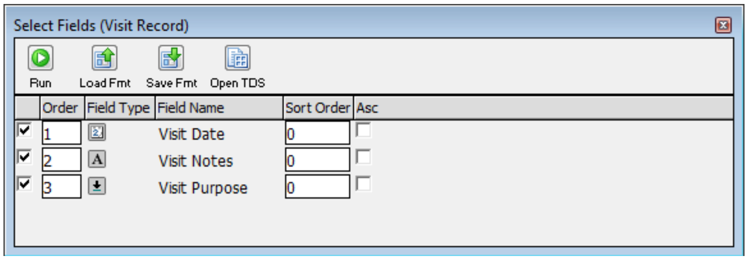
To load a different format for a table in a datasheet

When you add a table field with multiple formats to a datasheet, the table is added in its default format. You can load a different format for the table.

1. In Form Design mode, right-click on the table in the datasheet, and on the context menu that opens, click Show Fields.

   The Select Fields window opens. This window lists all of the fields in the table and their current order in the table.

Figure 3-11: Select Fields table

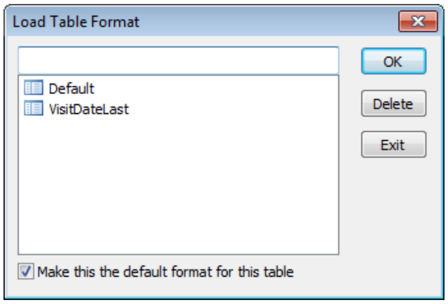


	Order	Field Type	Field Name	Sort Order	Asc
☑	1		Visit Date	0	☐
☑	2	A	Visit Notes	0	☐
☑	3		Visit Purpose	0	☐

2. Click the Load Format button Load Fmt.

   The Load Table Format dialog box opens. This dialog box lists all of the available formats for the table.

Figure 3-12: Load Table Format dialog box



Default
VisitDateLast

☑ Make this the default format for this table

3. Select the format that you want to apply to the table, and then click OK.

   The Load Table Format dialog box closes and you return to the Select Format window.

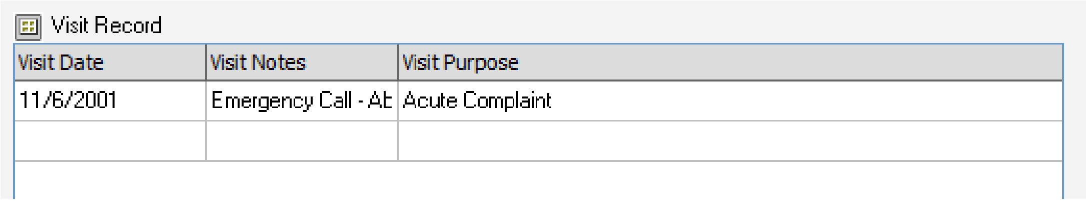
4. Click the Run button Run to apply the selected format to the table.

To enter data directly into a table in a datasheet

1. At the top of the datasheet, click Data Entry.
2. Right-click in the table, and on the context menu that opens, click Add Row.

   A new blank row opens for adding data.

Figure 3-13: Table with a blank row for adding data



Visit Record

Visit Date	Visit Notes	Visit Purpose
11/6/2001	Emergency Call - At	Acute Complaint

3. Click in each table cell of the blank row to add the necessary data.

If a table has a large number of columns, you can create a table datasheet for the table to make data entry easier. See "To create a table datasheet" below.

To create a table datasheet

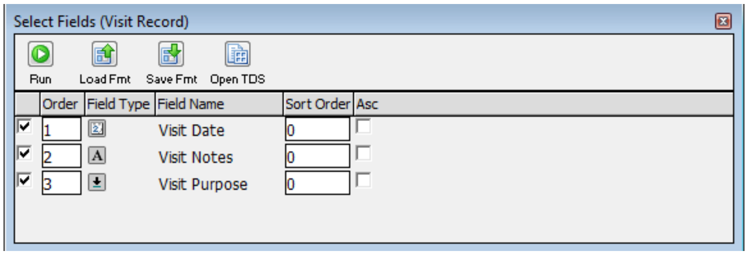
If you have a table in a datasheet that has a large number of fields in which to enter data, then date entry can become quite cumbersome. To make data entry easier for a large table, you can set up a table datasheet for the table. The table datasheet displays all the fields for a table row in a single view. You do not have to scroll through a table row to add data to each field in the row. You can create a table datasheet from both the Form Design mode and the Data Entry mode.

To create a table datasheet while in Form Design mode

1. Right-click on the table, and on the context menu that opens, click Show Fields.

   The Select Fields window opens. This window lists all of the fields in the table and their current order in the table.

Figure 3-14: Select Fields table

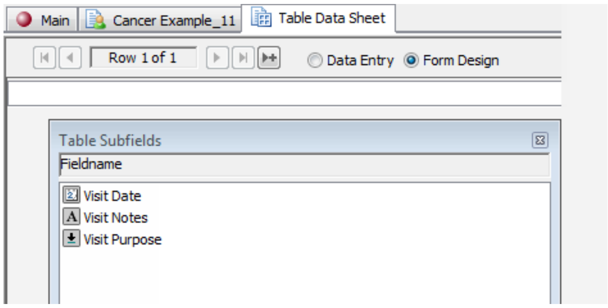


	Order	Field Type	Field Name	Sort Order	Asc
☑	1	▦	Visit Date	0	☐
☑	2	A	Visit Notes	0	☐
☑	3	↓	Visit Purpose	0	☐

2. Click the Open TDS button Open TDS.

   The Table Subfields dialog box opens. This dialog box lists all of the fields in the table.

Figure 3-15: Table Subfields dialog box



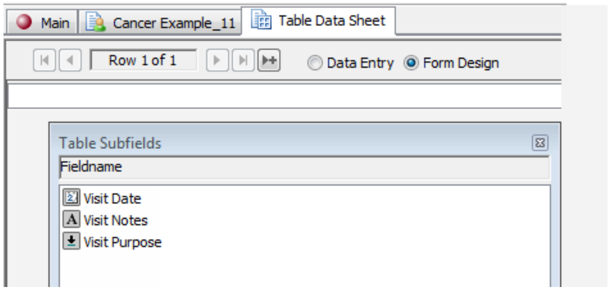
3. Drag the needed field or fields (CTRL-click to select multiple fields) to the datasheet.
4. Optionally, format the fields. See:
   - "To align multiple fields" on page 88.
   - "To add static text to a datasheet" on page 89.
   - "To set the properties for all the fields on the datasheet" on page 90.
   - "To set the field properties on a field by field basis" on page 91.
5. Continue with any other activities as needed for the datasheet, and after the datasheet is saved, you can enter data into the table datasheet. See "To enter data into a table datasheet" on page 98.

To create a table datasheet in Data Entry mode

1. Right-click on the table, and on the context menu that opens, click Open Table Datasheet.

   The Table Subfields dialog box opens. This dialog box lists all of the fields in the table. The mode changes to Form Design.

Figure 3-16: Table Subfields dialog box



2. Drag the needed field or fields (CTRL-click to select multiple fields) to the datasheet.

3. Optionally, format the fields. See:
    - “To align multiple fields” on page 88.
    - “To add static text to a datasheet” on page 89.
    - “To set the properties for all the fields on the datasheet” on page 90.
    - “To set the field properties on a field by field basis” on page 91.

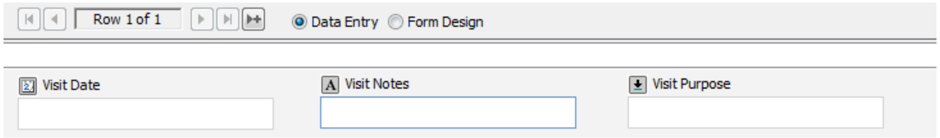
    You now have added the first blank row for the table datasheet, and you can continue immediately with entering data in the table datasheet. Go to Step 2 of “To enter data into a table datasheet” below.

To enter data into a table datasheet

1. In Data Entry mode, right-click on the table, and on the context menu that opens, click Open Data Table Sheet.

    A blank row in the table datasheet opens.

Figure 3-17: Example of a blank row in a table datasheet



2. Enter the data in the table row.
3. Click the Save Data button Save Data.
4. To add a new data row, click the New Row button ▶+.
5. Repeat Step 2 through Step 4 until you have added all of the necessary data for the table.

To move among the different rows in the table datasheet, use the navigation buttons at the top of the datasheet.

Button	Description
⏮	Move to first row in table datasheet.
◀	Move to previous row in table datasheet.
▶	Move to next row in table datasheet.
⏭	Move to last row in table datasheet.

Saving and Loading Datasheet Formats

After you have created a datasheet with a specific format, you can save the format. You can then retrieve this saved format and load it into another datasheet *of the same type.*

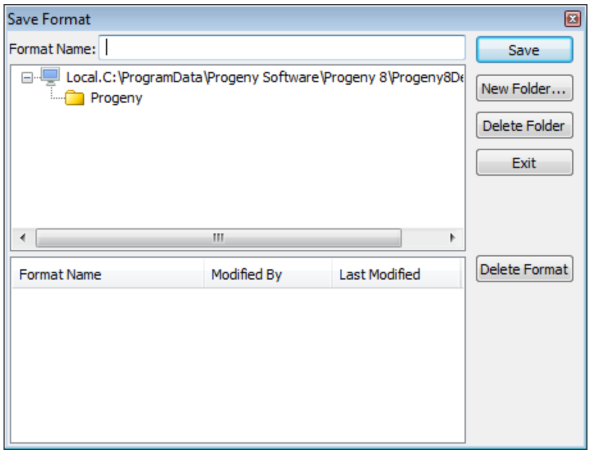
To save a datasheet format

1. Create and format the datasheet as needed. See "Creating and Formatting Datasheets" on page 86.

2. On the datasheet toolbar, click the Save Format button Save Fmt.

   The Save Format dialog box opens. It provides a default folder named Progeny in which to save the datasheet format. (This folder is located in the database that you are currently logged in to and you cannot change this location.)

Figure 3-18: Save Format dialog box



3. Enter a name for the datasheet format, and then do one of the following:
   - Select the Progeny folder.
   - Click New Folder, and on the Format Folder dialog box that opens, do the following:
     - Enter the name of the new folder in which to save to format.
     - Select the location for the new folder. The folder can be stored at the root level (the same level as the Progeny folder), or it can be a sub-folder of the Progeny folder, or of another folder.
     - Click Save.
4. Click Save on the Save Format dialog box.

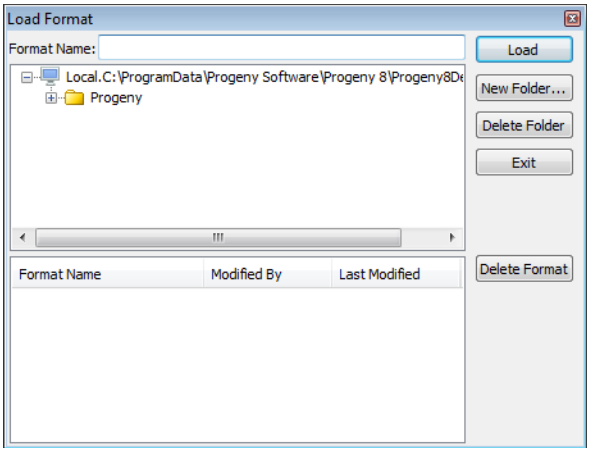
To load a datasheet format

You can a retrieve a saved datasheet format and load it into another datasheet *of the same type*.

1. Open the datasheet into which you are loading a saved format.
2. On the datasheet toolbar, click the Load Format button Load Fmt.

   The Load Format dialog box opens.

Figure 3-19: Load Format dialog box



3. Open the folder that contains the datasheet format that you are loading, select the format, and then click Load.

   The datasheet is refreshed with the loaded format. You can now edit the datasheet, enter data, and so on.

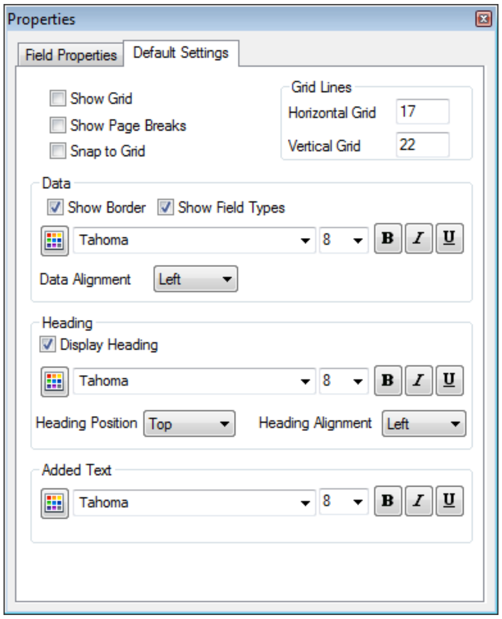
Printing a Datasheet

You can print a datasheet in either portrait or landscape mode. You can always view the page breaks for multiple page datasheets before you print the datasheet.

To print a datasheet

1. Optionally, before you print the datasheet, to view the page breaks on each page, do the following:
    - At the top of the datasheet, click Form Design.
    - On the datasheet toolbar, click the Properties button Properties to open the Properties dialog box.
    - If needed, open the Default Settings tab.
    - Select Show Page Breaks.

Figure 3-20: Properties dialog box, Default Settings tab



Properties

Field Properties | Default Settings

☐ Show Grid
☐ Show Page Breaks
☐ Snap to Grid

Grid Lines
Horizontal Grid 17
Vertical Grid 22

Data
☑ Show Border ☑ Show Field Types
Tahoma 8 B I U
Data Alignment Left

Heading
☑ Display Heading
Tahoma 8 B I U
Heading Position Top
Heading Alignment Left

Added Text
Tahoma 8 B I U

2. Optionally, right-click on the datasheet and on the context menu that opens, click Print Setup to open the Print Setup dialog box and confirm or modify the printing options as needed, including select the printing orientation (Portrait or Landscape).

3. On the datasheet toolbar, click the Print button Print.

Chapter 4

Spreadsheet Basics

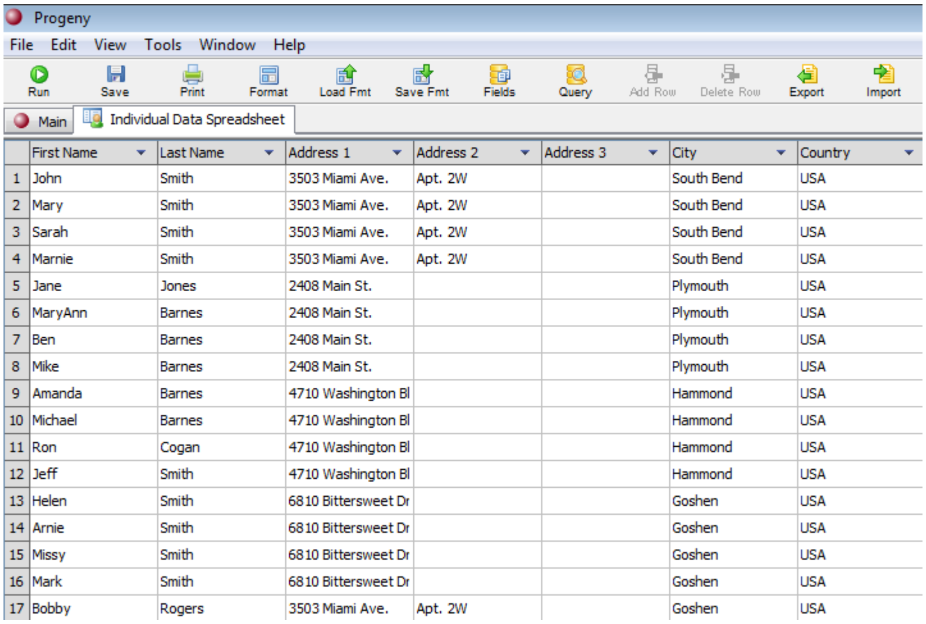
A *spreadsheet* is a table of values that are arranged in rows and columns. In Progeny, you use spreadsheets to organize multiple individuals, pedigrees, samples, or markers by rows and the database fields for entering the corresponding data by columns.

This chapter covers the following topics:

Spreadsheet Types

A *spreadsheet* is a table of values that are arranged in rows and columns. In Progeny, you use spreadsheets to organize your individuals, pedigrees, samples, or markers by rows and the database fields for entering the corresponding data by columns.

Figure 4-1: Example of an individual spreadsheet



	First Name	Last Name	Address 1	Address 2	Address 3	City	Country
1	John	Smith	3503 Miami Ave.	Apt. 2W		South Bend	USA
2	Mary	Smith	3503 Miami Ave.	Apt. 2W		South Bend	USA
3	Sarah	Smith	3503 Miami Ave.	Apt. 2W		South Bend	USA
4	Marnie	Smith	3503 Miami Ave.	Apt. 2W		South Bend	USA
5	Jane	Jones	2408 Main St.			Plymouth	USA
6	MaryAnn	Barnes	2408 Main St.			Plymouth	USA
7	Ben	Barnes	2408 Main St.			Plymouth	USA
8	Mike	Barnes	2408 Main St.			Plymouth	USA
9	Amanda	Barnes	4710 Washington Bl			Hammond	USA
10	Michael	Barnes	4710 Washington Bl			Hammond	USA
11	Ron	Cogan	4710 Washington Bl			Hammond	USA
12	Jeff	Smith	4710 Washington Bl			Hammond	USA
13	Helen	Smith	6810 Bittersweet Dr			Goshen	USA
14	Arnie	Smith	6810 Bittersweet Dr			Goshen	USA
15	Missy	Smith	6810 Bittersweet Dr			Goshen	USA
16	Mark	Smith	6810 Bittersweet Dr			Goshen	USA
17	Bobby	Rogers	3503 Miami Ave.	Apt. 2W		Goshen	USA

Unlike a datasheet, which displays the data for a single individual, pedigree, sample, or marker, a spreadsheet displays the data for *all* individuals, *all* pedigrees, *all* samples or *all* markers in a Progeny database.

You can create four different types of spreadsheets in Progeny:

- Individual spreadsheets—You use Individual spreadsheets to enter and store information about individuals in your Progeny database. An individual spreadsheet can contain individual database fields, pedigree database fields, and marker database fields.
- Pedigree spreadsheets—You use Pedigree datasheets to enter and store information about pedigrees in your Progeny database. A Pedigree datasheet can contain only pedigree database fields, including summary fields.
- Sample spreadsheets—You use Sample spreadsheets to enter and store information about samples in your Progeny database. A Sample datasheet can contain all four types of Progeny database fields—individual database fields, pedigree database fields, sample database fields, and marker database fields.
- Marker spreadsheets—You use Marker spreadsheets to store information about markers in your Progeny database. A Marker datasheet can contain only marker database fields.

Generating a Spreadsheet

Unlike a datasheet, which displays the data for a single individual, pedigree, sample, or marker, a spreadsheet that you generate from the Progeny main window displays the data for *all* individuals, *all* pedigrees, *all* samples or *all* markers in a Progeny database. A spreadsheet that is generated for all individuals, all pedigrees, and so on in a Progeny database is sometimes referred to as a *global* spreadsheet.

You can also generate a spreadsheet just for the individuals who are contained in the same pedigree. See "Generating a Spreadsheet for the Individuals in a Pedigree" on page 262.

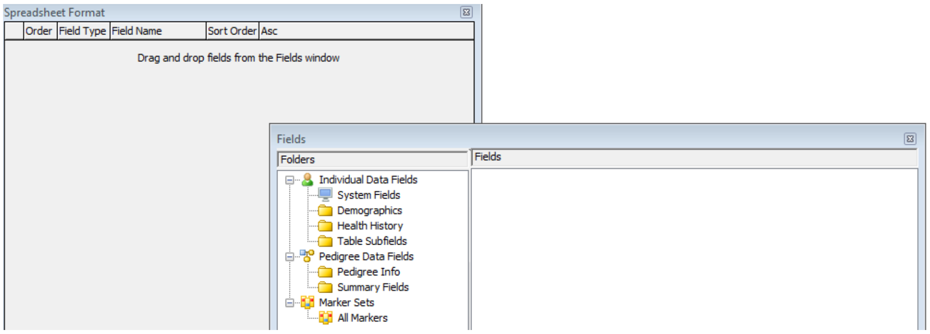
To generate a spreadsheet

The following procedure details the generation of an Individual spreadsheet, but, by analogy, you can apply this procedure to generate spreadsheets for all pedigrees, all samples, and all markers in a Progeny database.

1. On the Progeny main window navigation bar, click the Individuals button to open the Individuals window.
2. On the Individuals window toolbar, click the Individual Spreadsheet button Indiv SS.

   The Fields dialog box opens on top of the Spreadsheet Format window.

Figure 4-2: Fields dialog box and Spreadsheet Format window



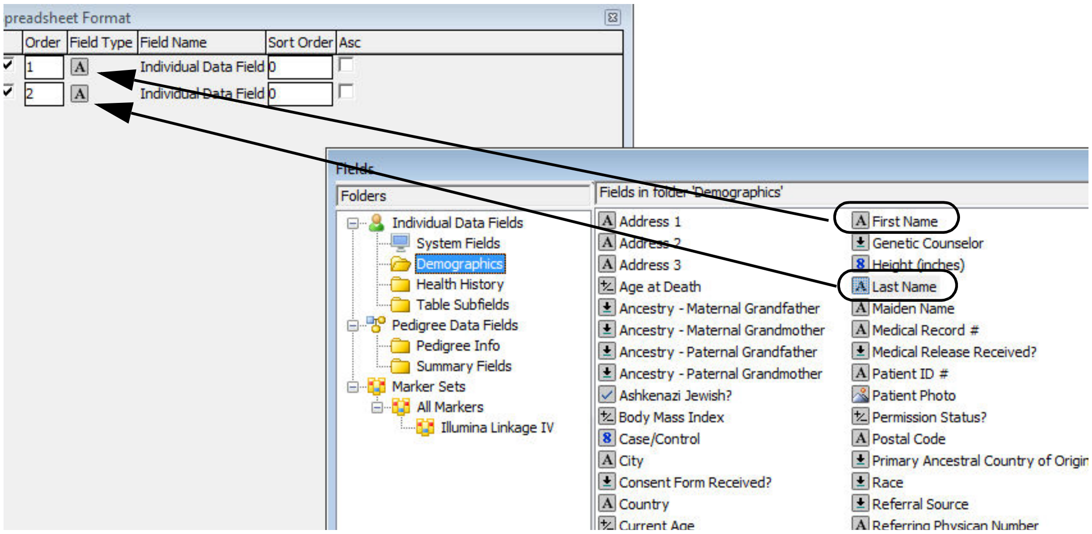
Drag and drop fields from the Fields window

3. Drag the fields (including any system fields) that are to be displayed in the spreadsheet from the Fields dialog box onto the Spreadsheet Format window.

System fields are read-only fields that Progeny automatically stores in its database for a record. Each record type (individual, pedigree, sample, and marker) has its own unique system fields. You can include system fields on a spreadsheet if there is information that you want to view at all times, but not edit, for an individual, a pedigree, a sample, or a marker. For a complete list of system fields and the read-only value that is displayed in each field, see Appendix A, "System Fields," on page 551.

For all fields other than table fields, the order in which you drag the fields is the order in which they appear in columns (from left to right) in the spreadsheet. If you drag a table field to the Spreadsheet Format window, then all of the fields (columns) in the table are added; however, none of the columns is assigned an order. You must assign an order to the table fields for the fields to be displayed in the spreadsheet. (See "Tables in spreadsheets" on page 110.) If you drag a lookup table field to the Spreadsheet Format window, then all of the fields (columns) in the table are added; however, only the lookup table field is assigned an order. None of the table subfields that are associated with the lookup table is assigned an order. You must assign an order to the table subfields for the fields to be displayed in the spreadsheet. (See "Lookup tables in spreadsheets" on page 111.)

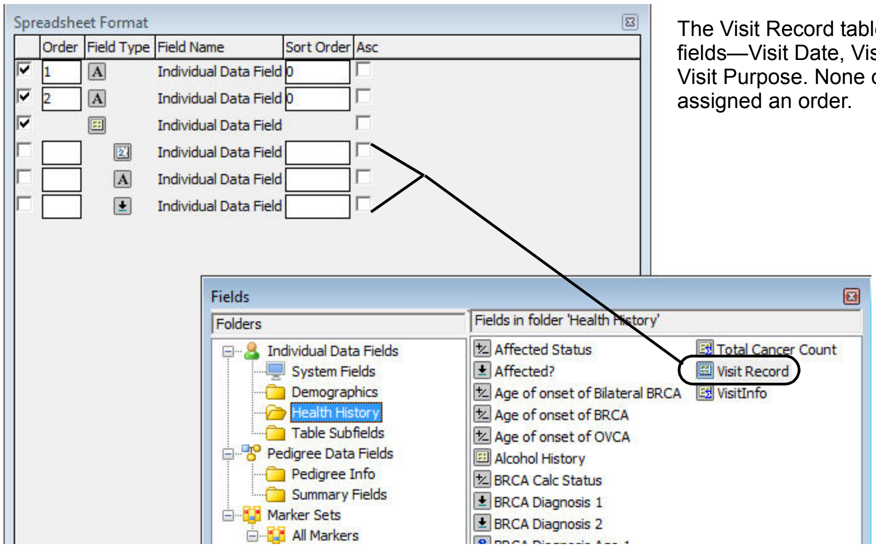
Figure 4-3: Dragging non-table fields to a spreadsheet



preadsheet Format

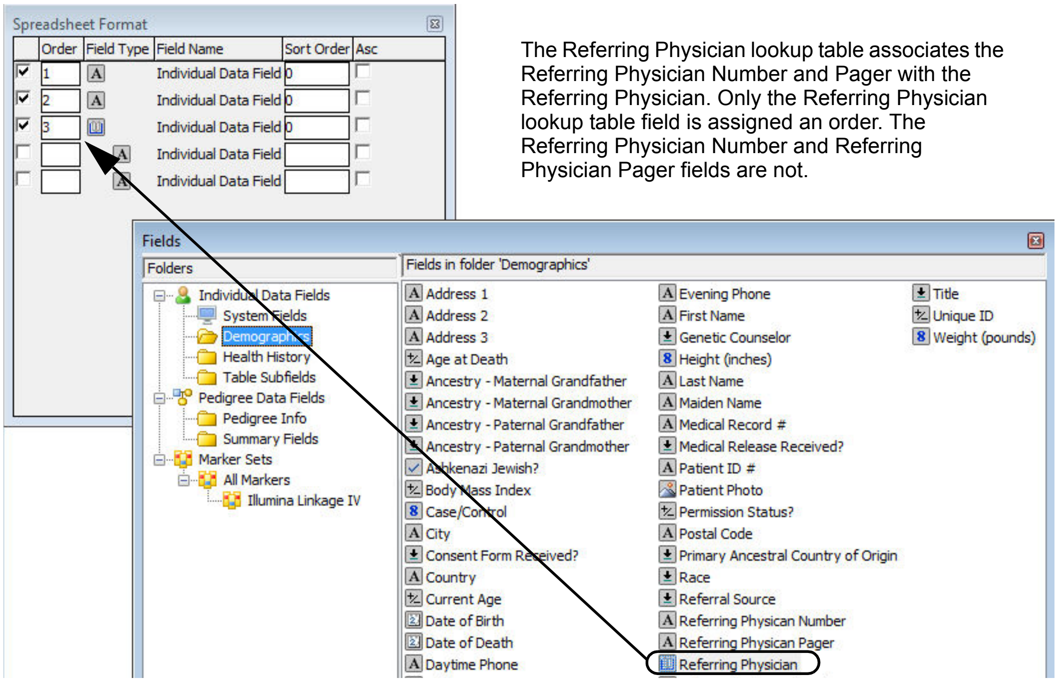
	Order	Field Type	Field Name	Sort Order	Asc
✓	1	A	Individual Data Field	0	☐
✓	2	A	Individual Data Field	0	☐

Figure 4-4: Dragging table fields to a spreadsheet



The Visit Record table has three fields—Visit Date, Visit Notes, and Visit Purpose. None of the fields is assigned an order.

Figure 4-5: Dragging lookup table fields to a spreadsheet



The Referring Physician lookup table associates the Referring Physician Number and Pager with the Referring Physician. Only the Referring Physician lookup table field is assigned an order. The Referring Physician Number and Referring Physician Pager fields are not.

4. If you have added a table to the spreadsheet, in the Order Column on the Spreadsheet Format window, assign an order to the table fields that are to be displayed in the spreadsheet.

5. Optionally, to sort the data in the spreadsheet, enter the sort order for the fields.

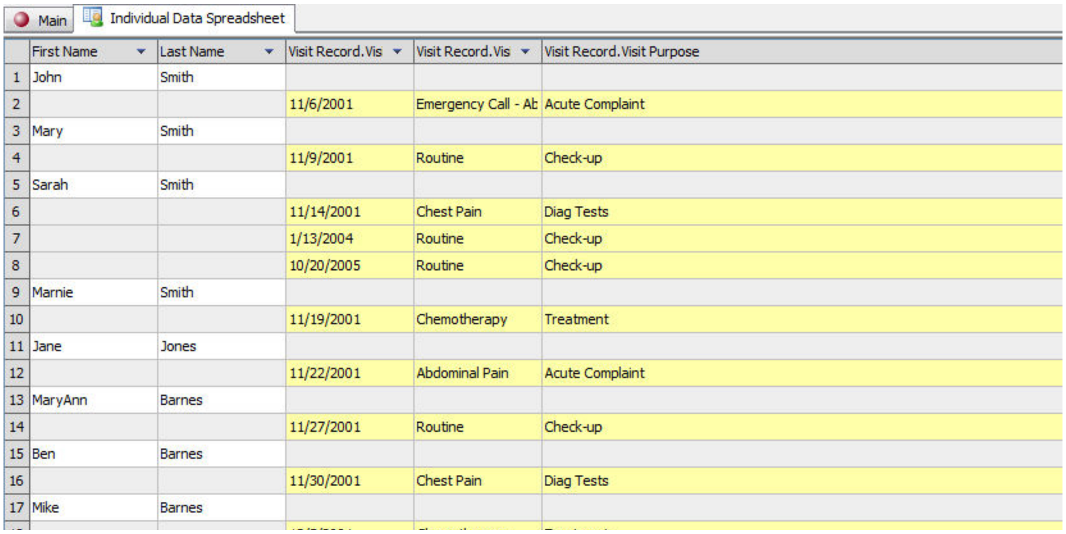
   For example, to sort the data in the spreadsheet shown in Figure 4-4 above by the most recent visit date, in the Sort Order column for the Visit Date field, enter a "1," and then select Asc (which indicates Ascending order). To sort by the oldest visit, do not select Asc.

6. Click the Run button Run to generate the spreadsheet.

7. Click the Save button Save to save the spreadsheet.

For a detailed explanation of how tables are displayed in a spreadsheet, see "Tables in spreadsheets" on page 110 and "Lookup tables in spreadsheets" on page 111.

Figure 4-6: Individual spreadsheet example



	First Name	Last Name	Visit Record.Vis	Visit Record.Vis	Visit Record.Visit Purpose
1	John	Smith			
2			11/6/2001	Emergency Call - Ab	Acute Complaint
3	Mary	Smith			
4			11/9/2001	Routine	Check-up
5	Sarah	Smith			
6			11/14/2001	Chest Pain	Diag Tests
7			1/13/2004	Routine	Check-up
8			10/20/2005	Routine	Check-up
9	Marnie	Smith			
10			11/19/2001	Chemotherapy	Treatment
11	Jane	Jones			
12			11/22/2001	Abdominal Pain	Acute Complaint
13	MaryAnn	Barnes			
14			11/27/2001	Routine	Check-up
15	Ben	Barnes			
16			11/30/2001	Chest Pain	Diag Tests
17	Mike	Barnes			

If you need to adjust the width of a spreadsheet column, place the cursor on the right edge of the column heading. The cursor changes to a double-headed arrow indicating that you can now drag the right edge of the column heading until the column is the width that you want.

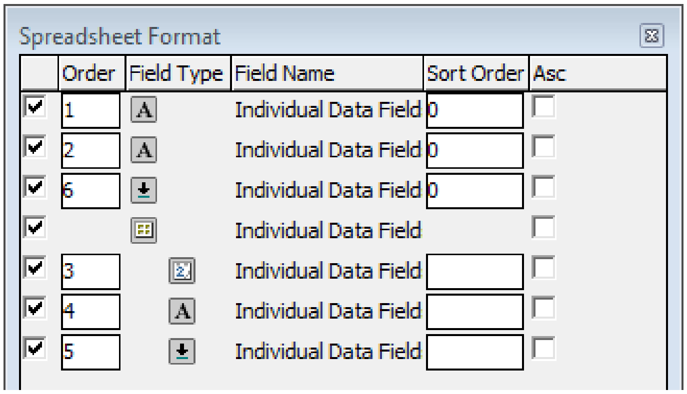
8. Optionally, after the spreadsheet is generated, do one or more of the following:

   - To view the individual datasheet for an individual in the spreadsheet, right-click on the individual in the spreadsheet, and on the context menu that opens, click Open Individual Datasheet.
   - If the individual is a member of a pedigree, to view the pedigree, right-click on the individual in the spreadsheet, and on the context menu that opens, click Open Pedigree. The pedigree opens in the Pedigree Drawing window. See "Drawing and Customizing Pedigrees" on page 267.

Tables in spreadsheets

If you add table fields to a spreadsheet, then all non-table fields are displayed first (from left to right) in the spreadsheet based on the order that you specified in the Spreadsheet format window. Any table fields are always displayed as the right-most columns in the spreadsheet (after all other non-table fields) in the order that you specified on the Spreadsheet format window. For example, in the Spreadsheet Format window shown below, the order of the fields is 1, 2, and 6, and the order of all table subfields is 3, 4, and 5.

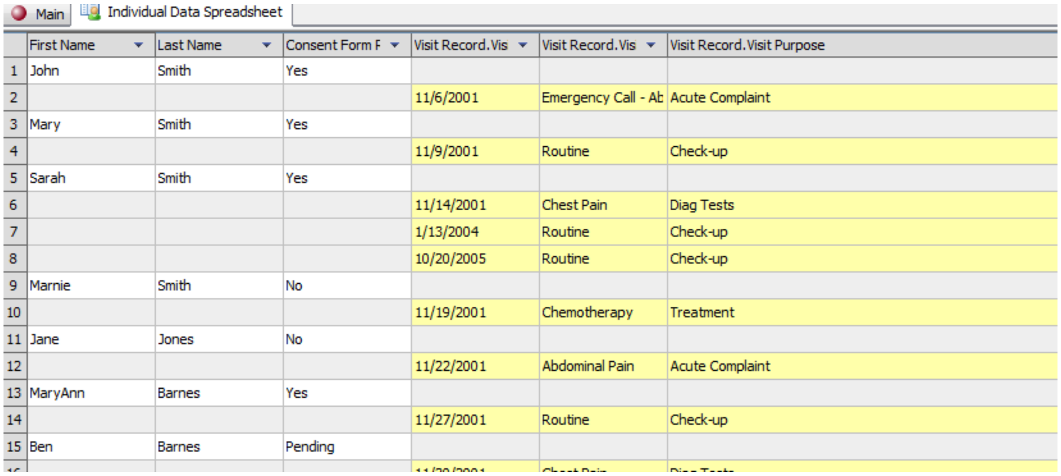
Figure 4-7: Spreadsheet Format window with order specified for spreadsheet columns



	Order	Field Type	Field Name	Sort Order	Asc
☑	1	A	Individual Data Field	0	☐
☑	2	A	Individual Data Field	0	☐
☑	6	⤓	Individual Data Field	0	☐
☑		▦	Individual Data Field		☐
☑	3	▣	Individual Data Field		☐
☑	4	A	Individual Data Field		☐
☑	5	⤓	Individual Data Field		☐

The spreadsheet that is generated from this format is shown in Figure 4-8 below. Note that the first three columns correspond to the non-table fields ordered 1, 2, and 6 and that the last three columns correspond to the table subfields ordered 3, 4, and 5.

Figure 4-8: Spreadsheet generated



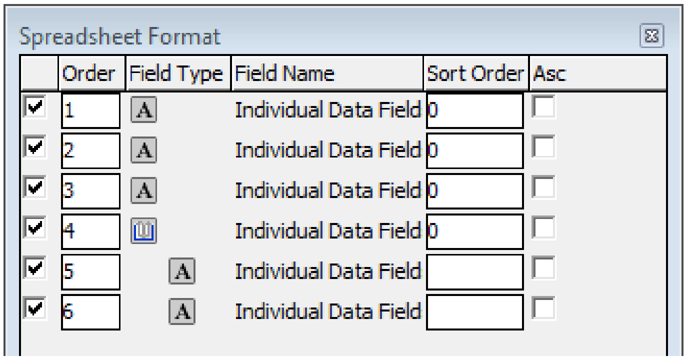
	First Name	Last Name	Consent Form F	Visit Record.Vis	Visit Record.Vis	Visit Record.Visit Purpose
1	John	Smith	Yes			
2				11/6/2001	Emergency Call - Ab	Acute Complaint
3	Mary	Smith	Yes			
4				11/9/2001	Routine	Check-up
5	Sarah	Smith	Yes			
6				11/14/2001	Chest Pain	Diag Tests
7				1/13/2004	Routine	Check-up
8				10/20/2005	Routine	Check-up
9	Marnie	Smith	No			
10				11/19/2001	Chemotherapy	Treatment
11	Jane	Jones	No			
12				11/22/2001	Abdominal Pain	Acute Complaint
13	MaryAnn	Barnes	Yes			
14				11/27/2001	Routine	Check-up
15	Ben	Barnes	Pending			

For each individual, pedigree, sample, or marker in a spreadsheet, a blank gray row indicates a table. Data that has been entered in the table is displayed below the blank gray row and is highlighted in yellow. If no data has been entered in the table for the individual, pedigree, sample, or marker, then only the blank gray row is displayed.

Lookup tables in spreadsheets

If you add a lookup table to a spreadsheet, then all non-table fields and any lookup table fields are always displayed from left to right in the order that you specified on the Spreadsheet format window. For example, in the Spreadsheet Format window shown below, the order of the non-table fields is 1, 2, and 3, and the order of all table fields is 4, 5, and 6.

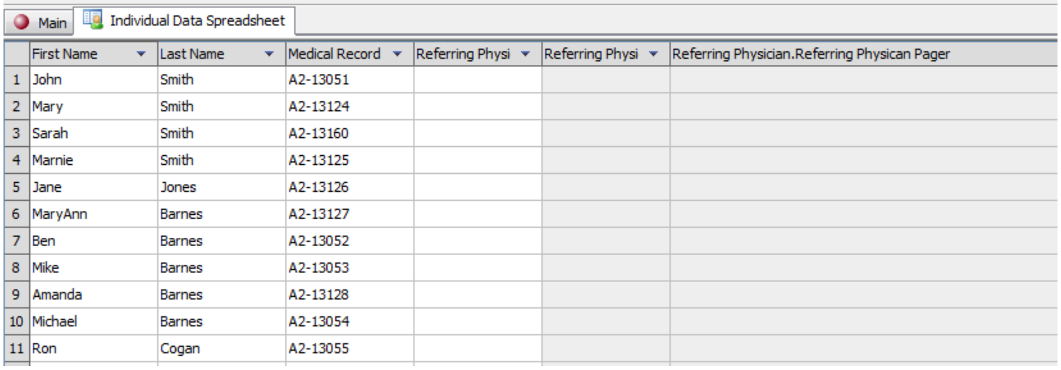
Figure 4-9: Spreadsheet Format window with order specified for spreadsheet columns



	Order	Field Type	Field Name	Sort Order	Asc
☑	1	A	Individual Data Field	0	☐
☑	2	A	Individual Data Field	0	☐
☑	3	A	Individual Data Field	0	☐
☑	4		Individual Data Field	0	☐
☑	5	A	Individual Data Field		☐
☑	6	A	Individual Data Field		☐

The spreadsheet that is generated from this format is shown in Figure 4-10 on page 111. Note that the first three columns correspond to the non-table fields ordered 1, 2, and 3 and that the last three columns correspond to the table fields ordered 4, 5, and 6.

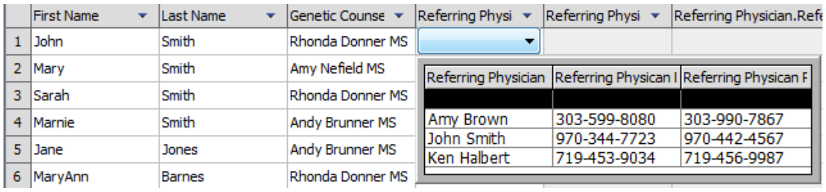
Figure 4-10: Spreadsheet generated



	First Name	Last Name	Medical Record	Referring Physi	Referring Physi	Referring Physician.Referring Physican Pager
1	John	Smith	A2-13051			
2	Mary	Smith	A2-13124			
3	Sarah	Smith	A2-13160			
4	Marnie	Smith	A2-13125			
5	Jane	Jones	A2-13126			
6	MaryAnn	Barnes	A2-13127			
7	Ben	Barnes	A2-13052			
8	Mike	Barnes	A2-13053			
9	Amanda	Barnes	A2-13128			
10	Michael	Barnes	A2-13054			
11	Ron	Cogan	A2-13055			

For each individual, pedigree, or sample in a spreadsheet, a blank row indicates a lookup table. The lookup table field in the row is not highlighted and the table subfields are highlighted in gray. To view the lookup table in a spreadsheet, click on the lookup table field.

Figure 4-11: Viewing data in a lookup table in a spreadsheet



	First Name	Last Name	Genetic Counse	Referring Physi	Referring Physi	Referring Physician.Refe
1	John	Smith	Rhonda Donner MS			
2	Mary	Smith	Amy Nefield MS			
3	Sarah	Smith	Rhonda Donner MS			
4	Marnie	Smith	Andy Brunner MS			
5	Jane	Jones	Andy Brunner MS			
6	MaryAnn	Barnes	Rhonda Donner MS			

Referring Physician	Referring Physican I	Referring Physican F
Amy Brown	303-599-8080	303-990-7867
John Smith	970-344-7723	970-442-4567
Ken Halbert	719-453-9034	719-456-9987

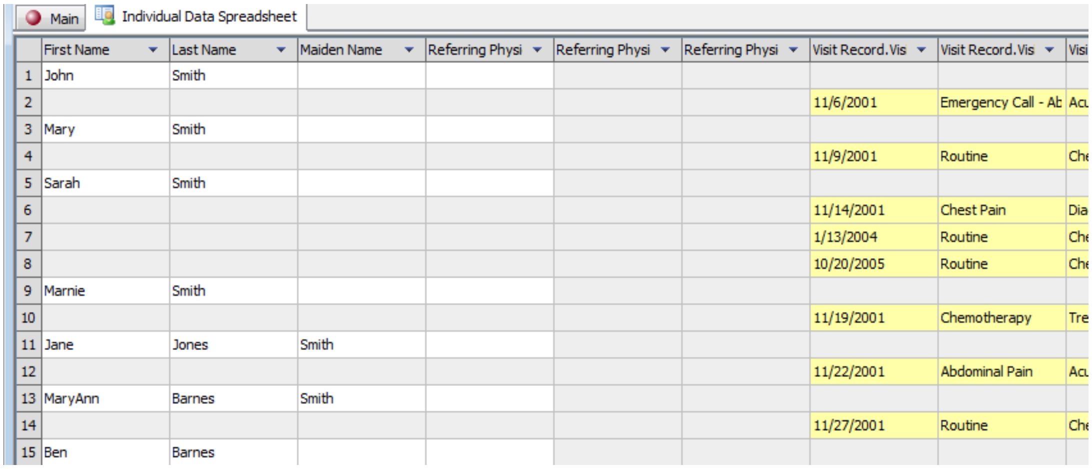
Entering Data into a Spreadsheet

You have a variety of options for entering data into a spreadsheet, including manually entering data, copying and pasting data, finding and replacing data, using the Fill feature, and importing data. Regardless of the method used, after you have completed data entry in a spreadsheet, click the Save button Save on the spreadsheet toolbar to save the data.

To manually enter data into a spreadsheet cell

Data entry for the fields in a spreadsheet is very straight forward. You simply click in the cell and enter the needed data, or select the data from a dropdown list. You can enter data into a spreadsheet cell that has no highlighting or that is highlighted in yellow (a table field). Fields that are highlighted in gray are read-only fields, such as system fields or lookup table subfields, and you cannot enter data directly into these fields. If you want to add more rows to a table, or populate the table subfields for a lookup table, see “To add more rows to a table in a spreadsheet” below or “To add data to a lookup table field in a spreadsheet” on page 113.

Figure 4-12: Data entry fields and read-only fields in a spreadsheet



	First Name	Last Name	Maiden Name	Referring Physi	Referring Physi	Referring Physi	Visit Record.Vis	Visit Record.Vis	Visi
1	John	Smith							
2							11/6/2001	Emergency Call - Ab	Acu
3	Mary	Smith							
4							11/9/2001	Routine	Che
5	Sarah	Smith							
6							11/14/2001	Chest Pain	Dia
7							1/13/2004	Routine	Che
8							10/20/2005	Routine	Che
9	Marnie	Smith							
10							11/19/2001	Chemotherapy	Tre
11	Jane	Jones	Smith						
12							11/22/2001	Abdominal Pain	Acu
13	MaryAnn	Barnes	Smith						
14							11/27/2001	Routine	Che
15	Ben	Barnes							

To move from one field to the next within the same row, press the Tab key on your keyboard. To move back a field within the same row, press and hold the Shift key and then press the Tab key. To move from one row to the next, press the Enter key. (Pressing the Enter key does not delete the data in a spreadsheet cell.)

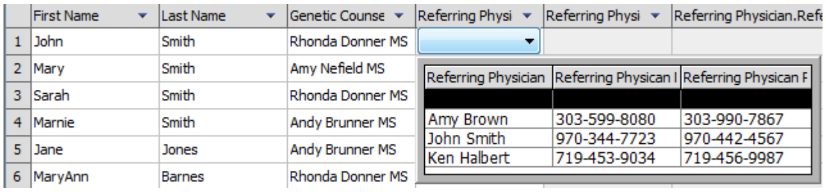
To add more rows to a table in a spreadsheet

1. Select the individual, sample, pedigree, or marker for which you are adding the data, and on the spreadsheet toolbar, click the Add Row button Add Row.
2. Click in each table cell of the blank row to add the necessary data.

To add data to a lookup table field in a spreadsheet

1. Click on the lookup table field and select the appropriate value for the field.

Figure 4-13: Viewing data in a lookup table in a spreadsheet



	First Name	Last Name	Genetic Counse	Referring Physi	Referring Physi	Referring Physician.Refe
1	John	Smith	Rhonda Donner MS			
2	Mary	Smith	Amy Nefield MS			
3	Sarah	Smith	Rhonda Donner MS			
4	Marnie	Smith	Andy Brunner MS			
5	Jane	Jones	Andy Brunner MS			
6	MaryAnn	Barnes	Rhonda Donner MS			

Referring Physician	Referring Physican I	Referring Physican F
Amy Brown	303-599-8080	303-990-7867
John Smith	970-344-7723	970-442-4567
Ken Halbert	719-453-9034	719-456-9987

2. On the spreadsheet toolbar, click the Save button Save .

3. On the spreadsheet toolbar, click the Run button Run to populate the table subfields for the lookup table.

To copy and paste data

You can use standard keyboard commands or menu commands to copy *text* data or *numeric* data from one cell into another. To copy text in a range of cells, click and hold the left mouse button and drag the mouse to select the region that you want to copy. Use standard keyboard commands or menu commands to paste the copied text into other cells.

To find and replace data

The Edit menu contains Find and Replace options that you can to search for data in a spreadsheet, and if needed, replace *text* or *numeric* data with another value.

Figure 4-14: Find dialog box

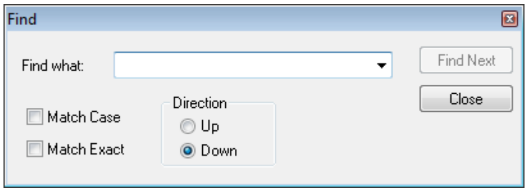
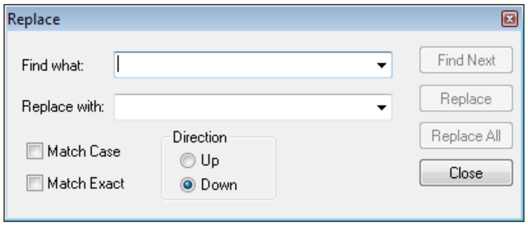


Figure 4-15: Replace dialog box



To use the Fill feature

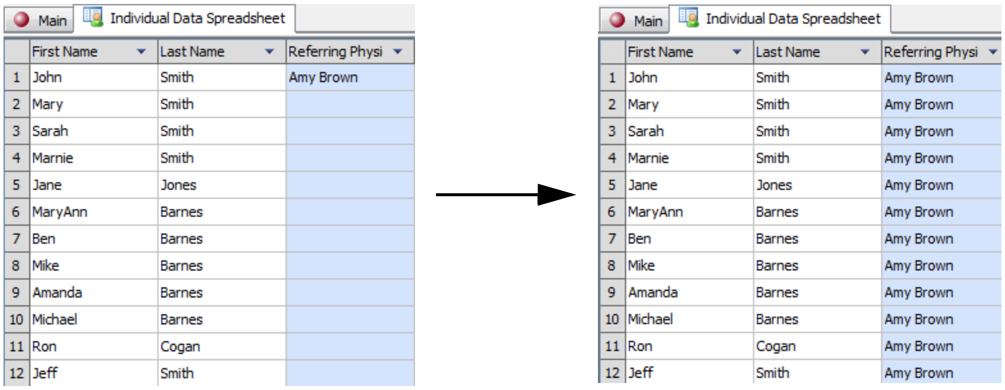
You can use the spreadsheet Fill function to blank cells with data from adjacent cells as long as the cells *are the same field type*. The Fill function is found under the Edit menu and has four options:

- Fill Down—Fills cells that fall below a selected cell.
- Fill Right—Fills cells that all to the right of a selected cell.
- Fill Up—Fills cells that are located above a selected cell.
- Fill Left—Fills cells that are located to the left of a selected cell.

When you are filling blank fields that are dropdown list fields, the filled values are stored only in the spreadsheet and not at the database level. For example, the available values for a filled dropdown list field in the spreadsheet are Yes, No, and Pending and you set all the fields to Pending. The available values for a blank dropdown list field are Received, Due, and N/A, but you fill the fields with Pending. Although Pending is displayed in these filled fields, when you edit any of these fields, the only available values will be Received, Due, and N/A, which are the values stored in the database for the field.

Figure 4-16: Example of Fill Down/Fill Up

To fill in Amy Brown as the Referring Physician for Patients2 through 12, select the column that includes Amy Brown as the Referring Physician for Patient 1 and the blank Referring Physician cells for Patients 2 through 12, and on the Edit menu, click Fill > Fill Down.

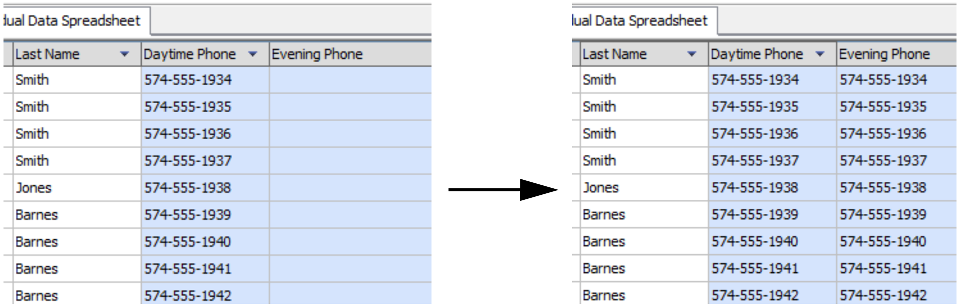


	First Name	Last Name	Referring Physi
1	John	Smith	Amy Brown
2	Mary	Smith	
3	Sarah	Smith	
4	Marnie	Smith	
5	Jane	Jones	
6	MaryAnn	Barnes	
7	Ben	Barnes	
8	Mike	Barnes	
9	Amanda	Barnes	
10	Michael	Barnes	
11	Ron	Cogan	
12	Jeff	Smith	

	First Name	Last Name	Referring Physi
1	John	Smith	Amy Brown
2	Mary	Smith	Amy Brown
3	Sarah	Smith	Amy Brown
4	Marnie	Smith	Amy Brown
5	Jane	Jones	Amy Brown
6	MaryAnn	Barnes	Amy Brown
7	Ben	Barnes	Amy Brown
8	Mike	Barnes	Amy Brown
9	Amanda	Barnes	Amy Brown
10	Michael	Barnes	Amy Brown
11	Ron	Cogan	Amy Brown
12	Jeff	Smith	Amy Brown

Figure 4-17: Example of Fill Right/Fill Left

To fill in the daytime phone as the evening phone number for Patients 1 through 9 select the column that includes the daytime phone number for Patients 1 through 9 and the column that includes the evening phone number for the same patients, and on the Edit menu, click Fill > Fill Right.



Last Name	Daytime Phone	Evening Phone
Smith	574-555-1934	
Smith	574-555-1935	
Smith	574-555-1936	
Smith	574-555-1937	
Jones	574-555-1938	
Barnes	574-555-1939	
Barnes	574-555-1940	
Barnes	574-555-1941	
Barnes	574-555-1942	

Last Name	Daytime Phone	Evening Phone
Smith	574-555-1934	574-555-1934
Smith	574-555-1935	574-555-1935
Smith	574-555-1936	574-555-1936
Smith	574-555-1937	574-555-1937
Jones	574-555-1938	574-555-1938
Barnes	574-555-1939	574-555-1939
Barnes	574-555-1940	574-555-1940
Barnes	574-555-1941	574-555-1941
Barnes	574-555-1942	574-555-1942

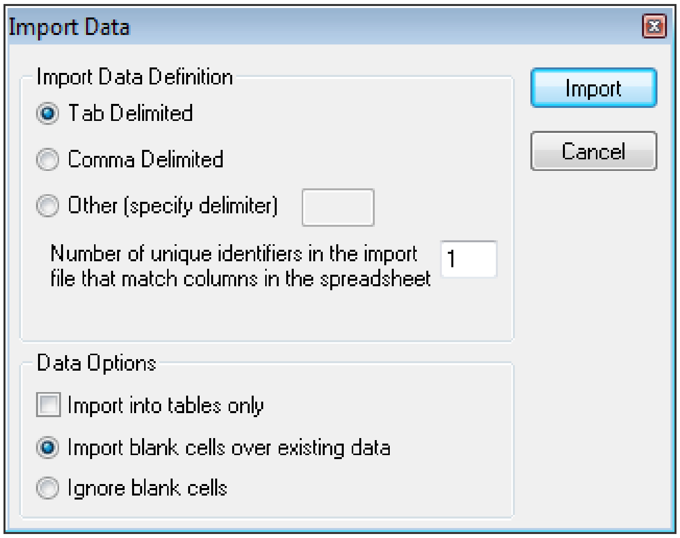
To import data into a spreadsheet

You can import data into a spreadsheet from a delimited file. The file can be a comma delimited text file, a tab delimited text file, or you can specify another delimiter type. You can import flat fields (standard fields) *or* you can import into table rows. If you are importing flat (standard) fields, then the data that is in the spreadsheet and the data that you are importing must be *the same field type*. If you are importing dropdown fields, and the data that is being imported has different values than the data in the spreadsheet, then the imported values are stored only in the spreadsheet and not at the database level. For example, if the available values for a dropdown list in the spreadsheet are Yes, No, and Pending and the available values for the corresponding dropdown list in the import file are Received, Due, and N/A, and you set the value in the import file to Received, then after the import, "Received" will indeed be displayed in the spreadsheet field; however, when you edit the field, the only available values will be Yes, No, and Pending, which are the values stored in the database for the field. If you are importing data into table rows, then the spreadsheet can contain only the table and its subfields. You can import new rows of table data, however, you cannot import into existing rows of table data.

1. On the spreadsheet toolbar, click the Import button Import.

   The Import Data dialog box opens. Tab Delimited is selected by default.

Figure 4-18: Import Data dialog box



Import Data Definition

● Tab Delimited

○ Comma Delimited

○ Other (specify delimiter)

Number of unique identifiers in the import file that match columns in the spreadsheet: 1

Data Options

☐ Import into tables only

● Import blank cells over existing data

○ Ignore blank cells

2. Select the type of delimited file that you are importing. (If the file is not tab delimited or comma delimited, then you must specify the delimiter that the file uses.)

3. Specify the values for the following:
   - Number of Unique Identifiers in the Import File that match columns in the spreadsheet—Enter the number of columns in the text file that you are importing that match to the number of columns in the spreadsheet. No data in the matched columns is overwritten. Only data from the matched point forward is overwritten. For example, if your spreadsheet and import text file have three columns each, and you indicate “1” for the number of matched columns, then when the data is imported into the spreadsheet, the data in Column 1 of the spreadsheet is not overwritten; however, the data in Columns 2 and 3 of the spreadsheet is overwritten by the data in Columns 2 and 3 of the import file.

⚠ *The correct value for the number of matched columns is critical to ensuring the integrity of the data in the spreadsheet*

   - Data options:
     - Import into tables only—Select this option *only* if you are importing data into table cells in the spreadsheet.
     - Import blank cells over existing data—Allows data in the spreadsheet to be replaced by blank cells.
     - Ignore blank cells—If the import file contains blank cells, do *not* replace the data in the spreadsheet with blank cells.
4. Click Import.

   The Open File dialog box opens.
5. In the Open File dialog box, browse to select and select the file that you are importing, and then click Open.

   A message opens indicating the Import operation was successful.
6. Click OK.

   The message closes. You return to the spreadsheet tab. The imported information is displayed in the spreadsheet.

Exporting Spreadsheet Data

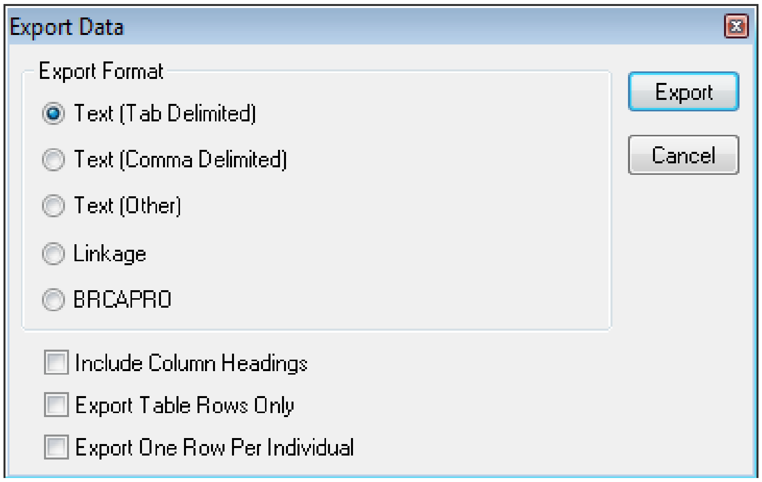
Just as you can import data into a spreadsheet from a text file, you can export data from a spreadsheet to a text file. The file can be a comma delimited file, a tab delimited file, or you can specify another delimiter type. You can export any user-created field as well as system fields.

To export spreadsheet data

1. On the spreadsheet toolbar, click the Export button Export.

   The Export Data dialog box opens.

Figure 4-19: Export Data dialog box



Export Data

Export Format

● Text (Tab Delimited)
○ Text (Comma Delimited)
○ Text (Other)
○ Linkage
○ BRCAPRO

☐ Include Column Headings
☐ Export Table Rows Only
☐ Export One Row Per Individual

2. Select the Export format.
   - If the file is not tab delimited or comma delimited, then you must specify the delimiter that the file uses.
   - If you select Linkage, then the data is exported to a pedigree file format (.PED). In addition to the exported data, the first five columns of file also contains the following pedigree relationship fields in the order indicated—UPN, Father ID, Mother ID, and Gender. You must also specify the way in which the individuals in the pedigree are to be identified. The default value is the UPN (Unique Person Number) for each person in the pedigree, but you can select a different value.
   - If you select BRCAPRO, then the data is exported in a format that can be used in the BRCA Risk Analysis application.

3. Select the data that is to be exported.
    - Export Table Rows Only—If you are exporting table data, and want to export only the table rows that contain data (and not the blank row that indicates a table), then select this option.
    - Export One Row per Individual—If you are exporting table data, and want to maintain a single row per individual (or sample), then select this option.
4. Click Export.

    The Save As dialog box opens. The Save as Type field is automatically populated with the file type of text (.txt) and you cannot change this value.
5. Browse to the location in which the exported file is to be saved, and then in the File name field, enter a name for the file.
6. Click Save.

    A message opens indicating the Export operation was successful.
7. Click OK.

    The message closes. You return to the spreadsheet tab.

Saving and Loading a Spreadsheet Format

After you have generated a spreadsheet with a specific format, you can save the format. You can then retrieve this saved format and load it into another spreadsheet *of the same type.*

The following procedure details the saving and loading of a spreadsheet format that returns the data for all individuals, pedigrees, samples, or markers in a Progeny database. To save and load a spreadsheet format that returns only a specific subset of data, see "Running Spreadsheet Queries" on page 122.

To save a spreadsheet format

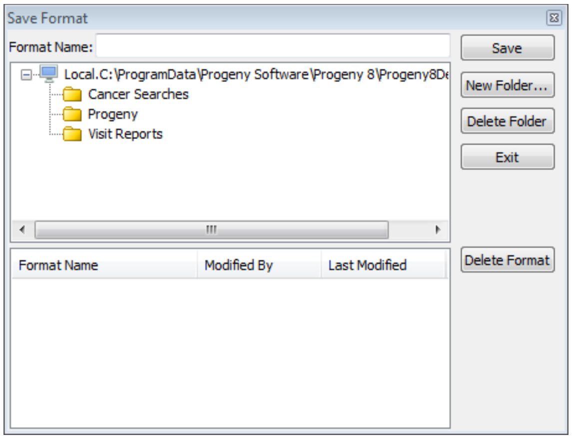
When you save a spreadsheet format, it saves not only the order of the spreadsheet columns, but also, the width of the columns.

1. Format and generate the spreadsheet as needed. See "Generating a Spreadsheet" on page 106.

2. On the spreadsheet toolbar, click the Save Format button .

   The Save Format dialog box opens. It provides three default folders (Cancer Searches, Progeny, and Visit Reports) in which to save the spreadsheet format. (These folders are located in the database that you are currently logged in to and you cannot change this location.)

Figure 4-20: Save Format dialog box



3. Enter a name for the spreadsheet format, and then do one of the following:
   - Select one of the three default folders.
   - Click New Folder, and on the Format Folder dialog box that opens, do the following:
     - Enter the name of the new folder in which to save to format.
     - Select the location for the new folder. The folder can be stored at the root level (the same level as the default folders), or it can be a sub-folder of one of the default folders, or of another folder.
     - Click Save.
4. Click Save on the Save Format dialog box.

   You can now load this saved spreadsheet format and generate a spreadsheet with this format. See "To load a spreadsheet format" below.

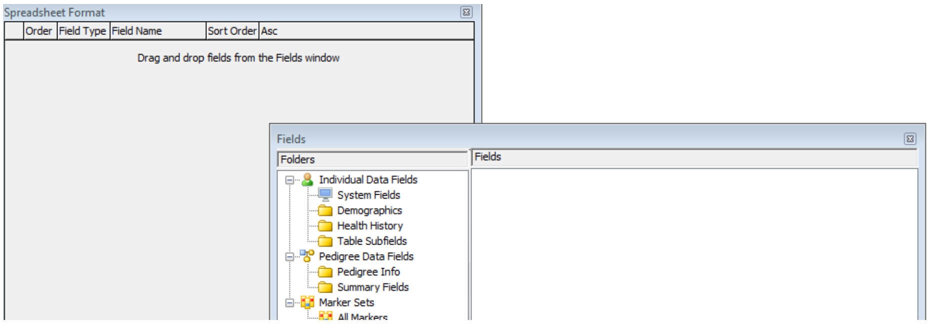
To load a spreadsheet format

You can a retrieve a saved spreadsheet format and load it into another spreadsheet *of the same type.*

1. On the Progeny main window navigation bar, open the window for the item for which you are generating the spreadsheet. For example, if you are generating an Individuals spreadsheet, click the Individuals button to open the Individuals window, and then on the Individuals window, click the Individual Spreadsheet button Indiv SS .

   The Fields dialog box opens on top of a blank Spreadsheet Format window.

Figure 4-21: Fields dialog box and Spreadsheet Format window

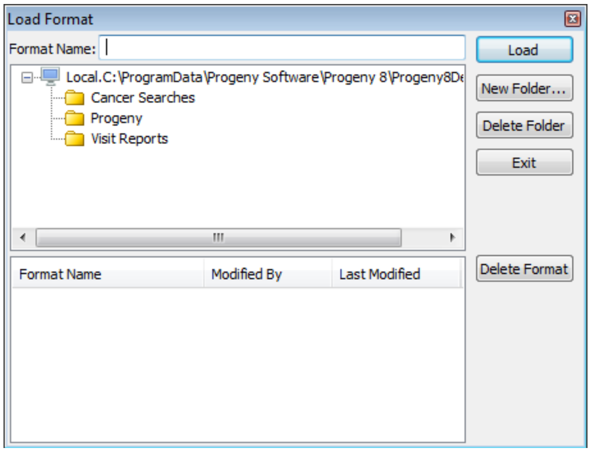


Drag and drop fields from the Fields window

2. On the spreadsheet toolbar, click the Load Format button Load Fmt.

   The Load Format dialog box opens.

Figure 4-22: Load Format dialog box



3. Open the folder that contains the spreadsheet format that you are loading, select the format, and then click Load.

   The Load Format dialog box closes. The Spreadsheet Format window is refreshed with the information for the loaded spreadsheet format.

4. Click the Run button Run to generate the spreadsheet according to the loaded format.

Running Spreadsheet Queries

You can query the Progeny database to retrieve a specific subset of data. You can run a query one time from within a given spreadsheet, or if you need to run the query frequently, you can save the query as part of the spreadsheet format, and then run the query on as-needed basis. When you set up the spreadsheet for the query, the spreadsheet does *not* have to contain the fields against which the query was run. For example, you could set up a query for all female individuals under the age of 50 that have been diagnosed with bilateral breast cancer and the spreadsheet is to display the demographic information for the individuals who meet the query criteria. You would set up the spreadsheet with the following fields—First Name, Last Name, Age at Diagnosis, Current Age, and so on, but you would not need to include the Gender field and the BRCA Diagnosis1 field as these fields would display the same value (Female or BL BR, respectively) for all the individuals who are retrieved by the query.

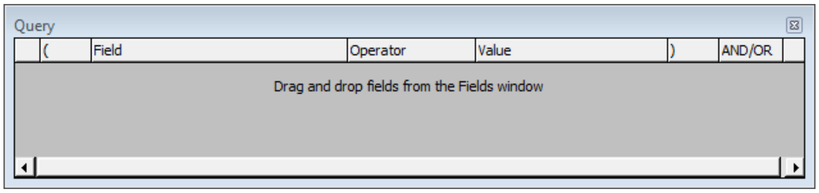
To run a spreadsheet query

1. Create the spreadsheet with the needed fields. (See "Generating a Spreadsheet" on page 106.)

2. On the spreadsheet toolbar, click the Query button .

   The Query dialog box opens.

Figure 4-23: Query dialog box

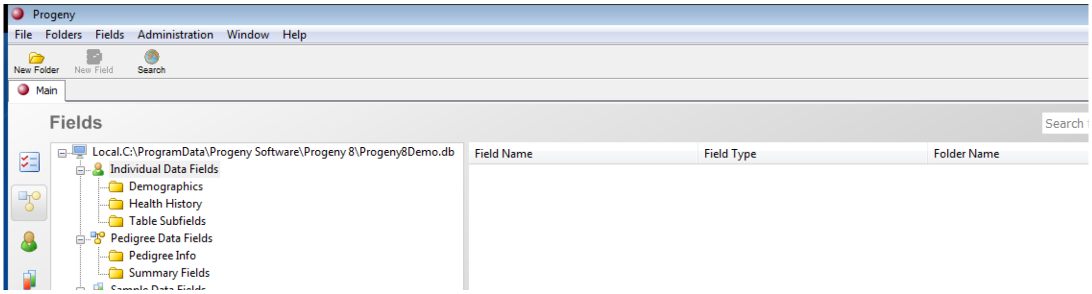


Drag and drop fields from the Fields window

3. On the spreadsheet toolbar, click the Fields button .

   The Fields window opens.

Figure 4-24: Fields window



4. For each field that is to be queried, drag the field from the Fields window to the Field field in the Query dialog box, and then complete the query (Operator, Value, and so on) for the field.

To remove a field from a query, right-click on the query row and click Delete Row.

See “Database Query Format” on page 173 for detailed information about formatting a database query.

5. Click the Run button Run to run the query.

   The results of the query are displayed onscreen in the spreadsheet. If needed, you can now save this query as part of the spreadsheet format and run the query when needed. See “To save a query as part of a spreadsheet format.”

To save a query as part of a spreadsheet format

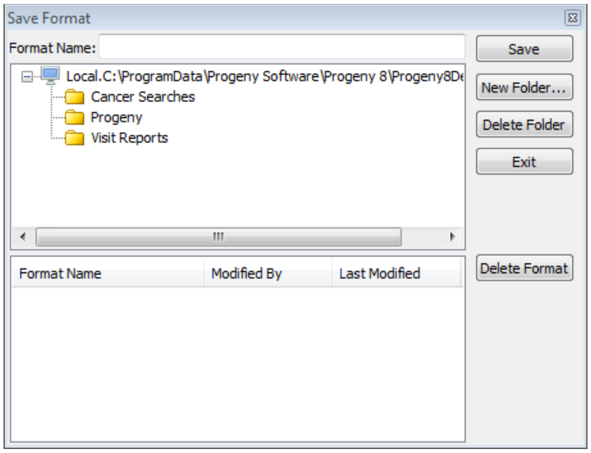
If you have a spreadsheet query that you need to frequently run, you do not need to generate the query “from scratch” every time. Instead, you can save the query as a part of a spreadsheet format and then load the format to run the query.

1. Run the initial query from within the spreadsheet. See “To run a spreadsheet query” on page 122.

2. On the spreadsheet toolbar, click the Save Format button Save Fmt.

   The Save Format dialog box opens. It provides three default folders (Cancer Searches, Progeny, and Visit Reports) in which to save the spreadsheet format. (These folders are located in the database that you are currently logged in to and you cannot change this location.)

Figure 4-25: Save Format dialog box



3. Enter a name for the spreadsheet format, and then do one of the following:
    - Select one of the three default folders.
    - Click New Folder, and on the Format Folder dialog box that opens, do the following:
        - Enter the name of the new folder in which to save to format.
        - Select the location for the new folder. The folder can be stored at the root level (the same level as the default folders), or it can be a sub-folder of one of the default folders, or of another folder.
        - Click Save.
4. Click Save on the Save Format dialog box.

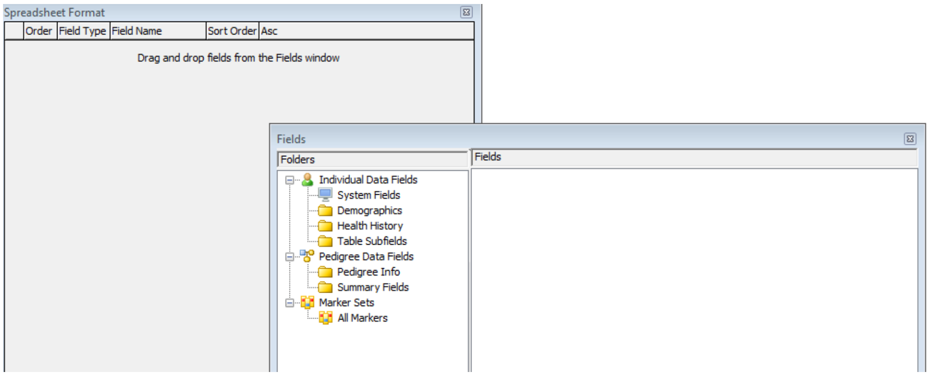
    You can now load this saved spreadsheet format and run the associated query at any time. You can run the query within the spreadsheet (see "To run a saved query within a spreadsheet" below or you can run it from the Progeny main window. (See"Main Window Queries" on page 180.)

To run a saved query within a spreadsheet

1. Open the appropriate window for the spreadsheet. For example, if you are running a query that was saved for an individual spreadsheet, open the Individuals window.
2. On the window toolbar, click the Spreadsheet button. For example, if you have opened the Individuals window, then click the Individual Spreadsheet button Indiv SS.

    The Fields dialog box opens on top of a blank Spreadsheet Format window.

Figure 4-26: Fields dialog box and Spreadsheet Format window

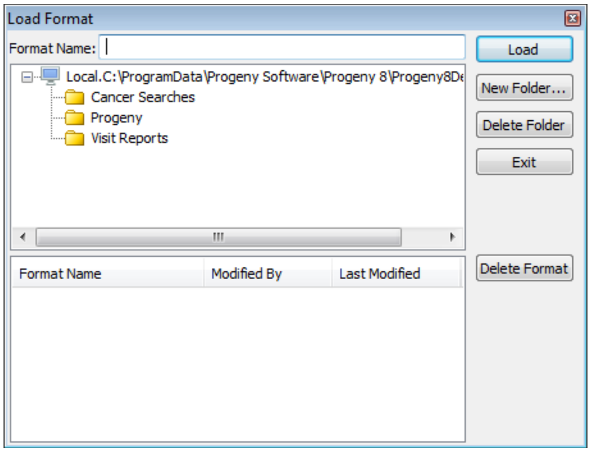


Drag and drop fields from the Fields window

3. On the spreadsheet toolbar, click the Load Format button Load Fmt.

   The Load Format dialog box opens.

Figure 4-27: Load Format dialog box



4. Open the folder that contains the spreadsheet format that you are loading, select the format, and then click Load.

   The Load Format dialog box closes. The Spreadsheet Format window is refreshed with the information for the loaded query format.

5. Click the Run button Run to run the loaded query.

   The results of the query are displayed onscreen in the spreadsheet.

Sorting and Filtering Spreadsheet Data

Sorting determines the order of the data that is displayed in a spreadsheet. For example, do you want to display your data based on a birth date that is sorted in reverse chronological order? You can sort the data in a spreadsheet at any time—immediately after you create a spreadsheet, or after you query the spreadsheet data to retrieve a subset of the data. Different sorting options are available for the different types of data columns (text, date, and numeric). After you select a sorting option, the spreadsheet display is dynamically updated.

You can also filter spreadsheet data. Filters retrieve a specific subset of the spreadsheet data based on specific constraints (or *filters*) that you set. For example, you might want to filter spreadsheet data to show only those individuals that were born in the 1970s. You can set multiple filters for a spreadsheet. Multiple filters are *mutually inclusive*. Only those individuals, pedigrees, samples, or markers that meet *all* the filtering criteria are displayed in the spreadsheet. As with sorting, you can filter the data in a spreadsheet at any time—immediately after you create a spreadsheet, or after you query the spreadsheet data to retrieve an initial subset of the data.

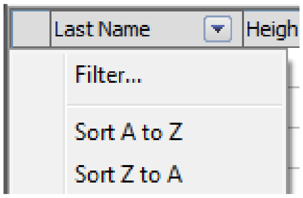
Although sorting and filtering spreadsheet data are two completely separate actions, you can combine them as needed to produce a customized dataset that best fits your business needs. For example, you can sort spreadsheet data based reverse chronological birth dates, and you can then filter the sorted data to show only those individuals that were born in the 1970s.

To sort spreadsheet data

1. Click in the column header for any text, date, or numeric data column.

   A menu opens with a Filter option and sorting options that are specific for the column type.

Figure 4-28: Example of options for a text column



2. Select a sorting option for the column.

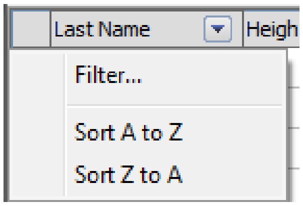
Column	Sorting Options and Description
Text	• Sort A to Z—Sort the data in the column alphabetical order (from A to Z). • Sort Z to A—Sort the data in the column in reverse alphabetical order (from Z to A).
Date	• Sort Oldest to Newest—Sort the data in the column in chronological order. • Sort Newest to Oldest—Sort the data in the column in reverse chronological order.
Numeric	• Sort Smallest to Largest—Sort the data in the column in numerical order. • Sort Largest to Smallest—Sort the data in the column in reverse numerical order.

To filter spreadsheet data

1. Click in the column header for any text, date, or numeric data column.

   A list opens with a Filter option and sorting options that are specific for the column type.

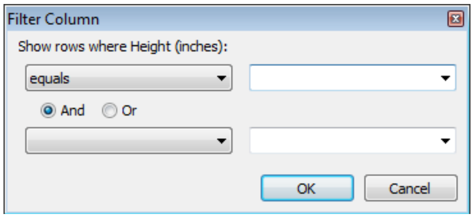
Figure 4-29: Example of options for a text column



2. Select Filter.

   The Filter column dialog box opens.

Figure 4-30: Filter Column dialog box

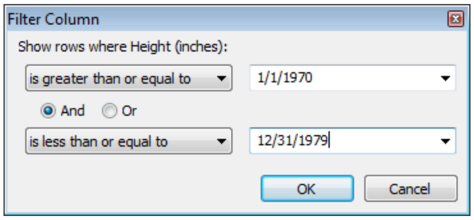


Show rows where Height (inches):
equals
● And ○ Or

3. Set the filter for the column.

   For example, Figure 4-31 shows how to filter spreadsheet data to show only those individuals who were born in the 1970s.

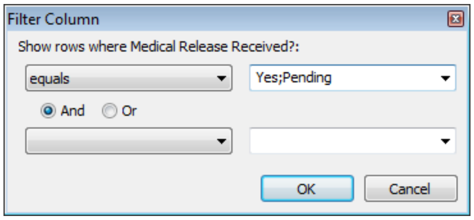
Figure 4-31: Filtering for DOB in the 1970s



Show rows where Height (inches):
is greater than or equal to 1/1/1970
● And ○ Or
is less than or equal to 12/31/1979

In another example, Figure 4-32shows how to filter spreadsheet data based on multiple filter values. The values are separated by a semi-colon (;) which acts an OR operator for the filter. (The filter shown here would filter the spreadsheet data based on medical release forms that have been received (Yes) *or* are Pending.)

Figure 4-32: Filtering for release forms with one of two statuses



Show rows where Medical Release Received?:
equals Yes;Pending
● And ○ Or

4. Click OK.

   The spreadsheet display is updated based on the filters that you have set. Any column for which you have set a filter is marked with a Filter icon .

5. Optionally, at any time, clear a filter by right-clicking on the column header for the filtered column, and on the context menu that opens, clicking Clear Filter.

   The spreadsheet display is dynamically updated to include all of the data in the column.

Printing Spreadsheet Data

After you generate a spreadsheet, you can print the spreadsheet. You can print all the pages in a multipage spreadsheet, or you can print selected pages.

To print a spreadsheet

1. On the spreadsheet toolbar, click the Print button Print .

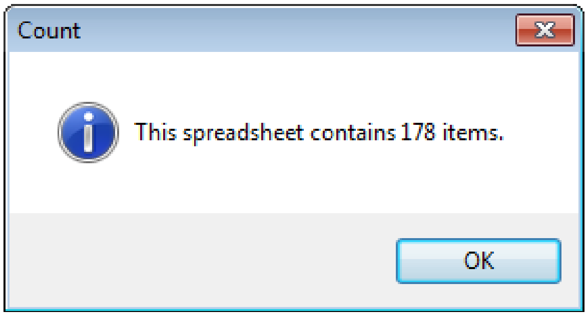
   The Print dialog box opens.

2. On the Print dialog box, select the needed printing options, and then click Print.

Counting Spreadsheet Data

After you generate a spreadsheet, you can click the Count button Count on the spreadsheet toolbar to count the number of individuals, pedigrees, samples, or markers (that is, the number of rows) in the spreadsheet. A Count dialog box opens, indicating the number of items (rows) that the spreadsheet contains.

Figure 4-33: Count dialog box



This spreadsheet contains 178 items.

Chapter 5

Database Security

Database security is the system, processes, and procedures that protect a database from unintended activity be it intentional or unintentional. This chapter details the procedures for setting the appropriate security standards for a Progeny database and its components.

This chapter covers the following topics:

- "Working with Users and Classes" on page 133.
- "Setting Database Field Security" on page 140.
- "Setting Database Folder Security" on page 143.
- "Setting Database Security" on page 145.
- "Viewing Active Connections" on page 147.

With the exception of changing a user password, all functions that are detailed in this chapter are available only to the Progeny administrator. A user can change his/her own password.

Working with Users and Classes

A single user, the Progeny administrator user, is supplied with Progeny. The username for the administrator user is *progeny*, and the *default* administrator password is also *progeny*. Only the progeny user has access to the Administration menu and its options for creating, modifying, and deleting other Progeny users and passwords. As the Progeny administrator, after you add a user, you must set the *security levels* for the user. The security levels for a user determine the application functions that are available to the user. As the Progeny administrator, you can also add user classes. A *user class* groups users based on the access that the users are to have to database fields and folders. All users who you add to the same class have the same level of access to the same database fields and/or folders. As the Progeny administrator, you can also delete users, delete user classes, change the administrator password, and change the passwords for your users.

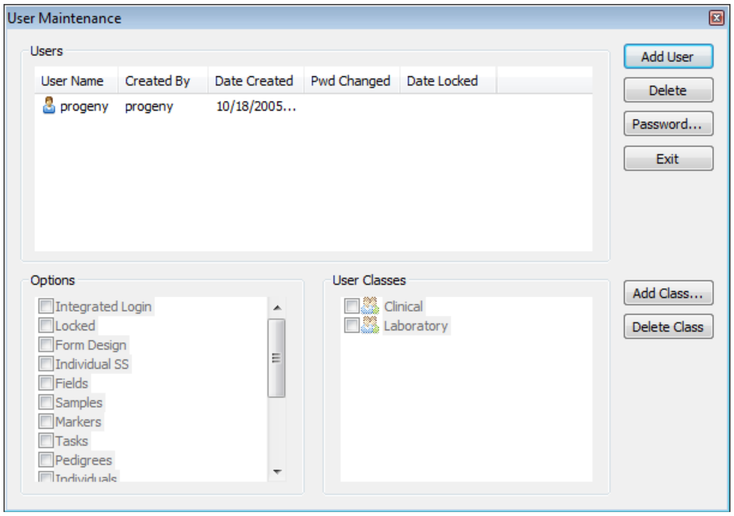
Users can also change their own passwords. See "To change your own password as a user" on page 139.

To add users

1. On the main menu, click Administration > User Maintenance.

   The User Maintenance window opens.

Figure 5-1: User Maintenance window



User Name	Created By	Date Created	Pwd Changed	Date Locked
progeny	progeny	10/18/2005...		

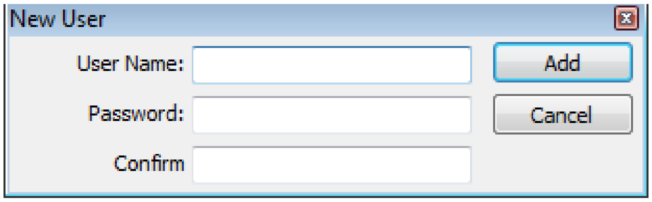
☐ Integrated Login
☐ Locked
☐ Form Design
☐ Individual SS
☐ Fields
☐ Samples
☐ Markers
☐ Tasks
☐ Pedigrees
☐ Individuals

☐ Clinical
☐ Laboratory

2. Click Add User.

   The New User dialog box opens.

Figure 5-2: New User dialog box



3. Enter the user name and password for the user account.

   The user name and password must adhere to the following rules:

   - The user name cannot include any spaces.
   - The first character cannot be a number. Instead, it must be an alphabetic character or one of the following special characters: an underscore (_), an at sign (@), a number sign (#), or a dollar sign ($).
   - The user name can only contain alphabetic characters, numbers, and one or more of the following special characters: an underscore (_), an at sign (@), a number sign (#), or a dollar sign ($).
   - The user name cannot contain a reserved word for an SQL database. See the following: http://www.ianywhere.com/developer/product_manuals/sqlanywhere/0902/en/html/dbrfen9/00000010.htm

   The password is case-sensitive and it must adhere not only to the same rules as the user name, but also, these two rules:

   - The password must be a minimum of six characters and contain at least one number.
   - The password cannot contain the user name.

4. In the Confirm field, enter the password again exactly as you entered it in the Password field.

5. Click Add.

   The Add New User dialog box closes. The new user account is displayed in the Users pane of the User Maintenance window. You can now set security levels for the user account. See “To set the security levels for a user account” on page 135.

To set the security levels for a user account

1. If you have not already done so, on the main menu, click Administration > User Maintenance to open the User Maintenance window.
2. In the Users pane, select the user account for which you are setting the security levels.

   The security levels are enabled in the Options pane.
3. Set the security levels as needed for the user account.

Option	Description
Standard Login	The user must connect to the Progeny database with the user name and password for their Progeny user account.
Integrated Login	Allows the user to connect to the Progeny database without providing an additional user ID or password. Instead, the user authentication is done by the Windows operating system.
LDAP Login	The user’s login must be authenticated to an LDAP directory server.
Locked	Locks the user out of the Progeny database after three unsuccessful attempts to log in.
Form Design	Allow the user to create, edit and add data to datasheets.
Individual SS	Allows the user to create an individual spreadsheet.
Fields	Allows the user access to the Fields window.
Samples	Allows the user access to the Samples window.
Markers	Allows the user access to the Markers window.
Tasks	Allows the user access to the Tasks window.
Pedigrees	Allows the user access to the Pedigrees window.
Individuals	Allows the user access to the Individuals window.
Inventory	Allows the user access to the Inventory window.
Workflows	Allows the user access to the Workflows window.
Containers	Allows the user access to the Containers window.
Genotypes	Allows the user access to the Genotypes window.
Analysis	Allows the user access to the Analysis window.
Orders	Allows the user access to the Orders window.

To delete a user

You can delete a user only if the user is not currently logged in to the Progeny database.

1. On the main menu, click Administration > User Maintenance

   The User Maintenance window opens.

2. In the Users pane, select the user that is being deleted.

3. Click Delete.

   A message opens asking you if you are sure that you want to delete the selected user.

4. Click Yes.

   A message opens indicating that the user was successfully deleted.

5. Click OK to close the message and return to the User Maintenance window.

To add a user class

A *user class* groups users based on the access that the users are to have to database folders and fields. All users who are in the same class have the same level of access to the same database folders and/or fields. By default, when you add a new user class, the Progeny administrator is automatically added to the class.

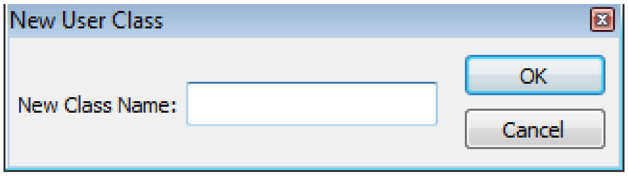
1. On the main menu, click Administration > User Maintenance.

   The User Maintenance window opens.

2. Click Add Class.

   The New User Class dialog box opens.

Figure 5-3: New User Class dialog box



3. Enter the name for the new user class, and then click OK.

   A message opens indicating that the user class was added successfully.

4. Click OK to close the message and return to the User Maintenance window.

   You can now add users to the class. See “To add users to a user class” on page 137.

To add users to a user class

By default, as the Progeny administrator, when you add a new user class, you are automatically added to the class. Only non-administrator users must be explicitly added to a user class.

1. If you have not already done so, on the main menu, click Administration > User Maintenance to open the User Maintenance window.
2. In the Users pane, select the user that you are adding to a class.
3. In the User Classes pane, select the checkbox next to the class or classes to which you are adding the user.
4. Click Exit to close the User Maintenance window.

   The changes are saved when the window closes. All users who are in the same class have the same level of access to the same database fields and/fields. See "Setting Database Field Security" on page 140 and "Setting Database Folder Security" on page 143.

To delete a user class

When you delete a class, you delete only the class and not any users who have been assigned to the class; however, all the users who are assigned to the class lose any database folder and field security privileges that you have set for the class.

1. On the main menu, click Administration > User Maintenance

   The User Maintenance window opens.
2. In the Users pane, select any user *other than* the Progeny administrator.
3. In the User Classes pane, select class that you are deleting. (Do not select the checkbox next to the class.) CTRL-click to select multiple classes.
4. Click Delete.

   A message opens asking you if you are sure that you want to delete the selected class.
5. Click Yes.

   A message opens indicating that the class was successfully deleted.
6. Click OK to close the message and return to the User Maintenance window.

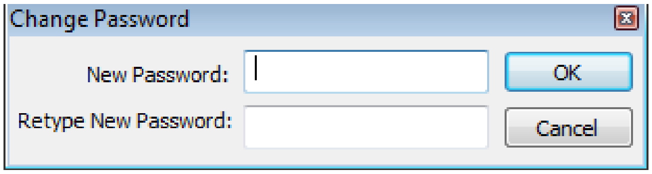
To change the administrator password

As the Progeny administrator, your default password is *progeny*. You can change this password, however, if you do change your password, you must record it in a secure location. The password is encrypted and if you lose it or do not remember it, Progeny cannot recover it for you.

1. On the main menu, click Administration > Change Password.

   The Change Password dialog box opens.

Figure 5-4: Change Password dialog box



2. Enter the new administrator password.

   The new password must adhere to the rules that apply to any user password. See [Password Rules](#).

3. In the Retype New Password field, enter the password again exactly as you entered it in the New Password field.

4. Click OK.

   The Change Password dialog box closes. You remain logged in to the current Progeny session with your old password. The next time that you log in to Progeny, you must log in using your new password.

To change a user password as the Progeny administrator

To change the number of days after which all user passwords (other than the administrator password) expire, see "Setting Database Security" on page 145.

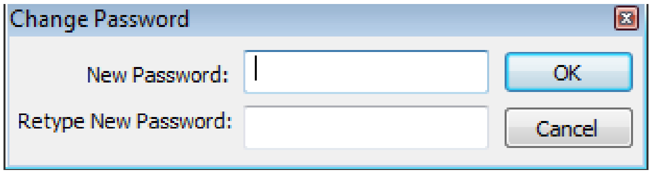
1. On the main menu, click Administration > User Maintenance.

   The User Maintenance window opens.

2. Select the user for whom you are changing the password.

   The Change Password dialog box opens.

Figure 5-5: Change Password dialog box



3. Enter the new user password.

   The new password must adhere to the rules that apply to any user password. See Password Rules.

4. In the Retype New Password field, enter the password again exactly as you entered it in the New Password field.

5. Click OK.

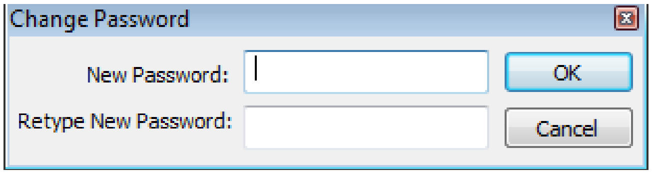
   The Change Password dialog box closes. The user remains logged in to the current Progeny session with their old password. The next time that they log in to Progeny, they must log in using their new password.

To change your own password as a user

1. On the main menu, click Administration > Change Password.

   The Change Password dialog box opens.

Figure 5-6: Change Password dialog box



2. Enter your new user password.

   The new password must adhere to the rules that apply to any user password. See Password Rules.

3. In the Retype New Password field, enter the password again exactly as you entered it in the New Password field.

4. Click OK.

   The Change Password dialog box closes. You remain logged in to the current Progeny session with your old password. The next time that you log in to Progeny, you must log in using your new password.

Setting Database Field Security

When you are adding a new database field, then you have the option of setting security for the field. Security determines the type of access (Read, Write or both) that a specific class of user has for the field. The default security settings for any database field are set to Read and Write for All Users. As the Progeny administrator, if you have yet to add any other user classes, then only two default user classes—Clinical and Laboratory—are displayed for a field; otherwise, all the user classes that you have added are displayed. You can add more classes of users if needed.

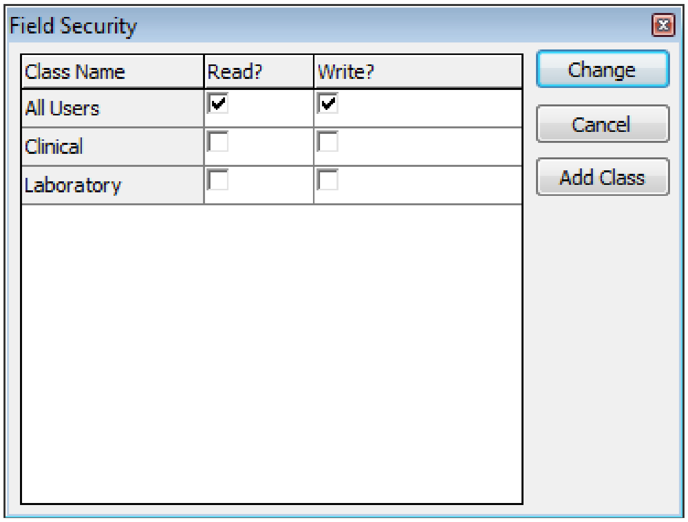
When you create database fields, you typically set the security for the fields on a field by field basis; however, if you want to apply the same security settings for every single field that is contained in the same database folder in a single step, then you can apply the settings at the folder level. See "Setting Database Folder Security" on page 143.

To set database field security

1. If the field is already open in the Add New Field dialog box, go to Step 5; otherwise, go to Step 2.
2. On the navigation bar, click the Fields button to open the Fields window.
3. In the left pane of the Fields window, open the folder that contains the field for which you are setting the security, and then in the right pane of the window, right-click on the field, and on the context menu that opens, click Field Security Level.

   The Field Security dialog box opens.
4. Go to Step 6.

Figure 5-7: Field Security dialog box

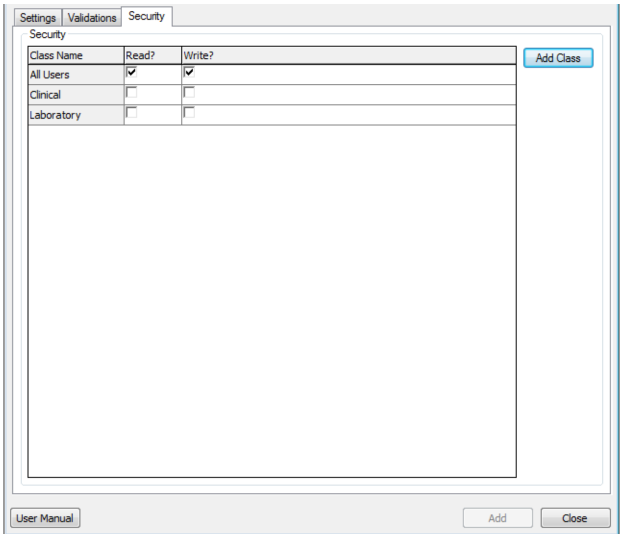


Class Name	Read?	Write?
All Users	☑	☑
Clinical	☐	☐
Laboratory	☐	☐

Chapter 5
Database Security

5. Open the Security tab on the Add Data Field dialog box

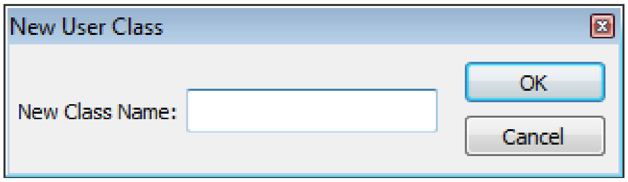
Figure 5-8: Add Data Field dialog box, Security tab



Class Name	Read?	Write?
All Users	☑	☑
Clinical	☐	☐
Laboratory	☐	☐

6. Do one or more of the following:
   - Modify the security for All Users or for the different classes of users.
   - Click Add Class to open the New User Class dialog box to create a new user class, and then set the security for the class.

Figure 5-9: New User Class dialog box



7. Continue to any other necessary tasks for the field, or click Add to add the field the database.

Setting Database Folder Security

When you create database fields, you typically set the security for the fields on a field by field basis; however, if you want to apply the same security settings for every single field that is contained in the same database folder in a single step, then you can set the security at the folder level. The default security settings for any database folder are set to Read Folder and Add/Delete/Modify Fields for All Users. As the Progeny administrator, if you have yet to add any other user classes, then only two default user classes—Clinical and Laboratory—are displayed for a folder; otherwise, all the user classes that you have added are displayed. You can add more classes of users if needed.

To set database folder security

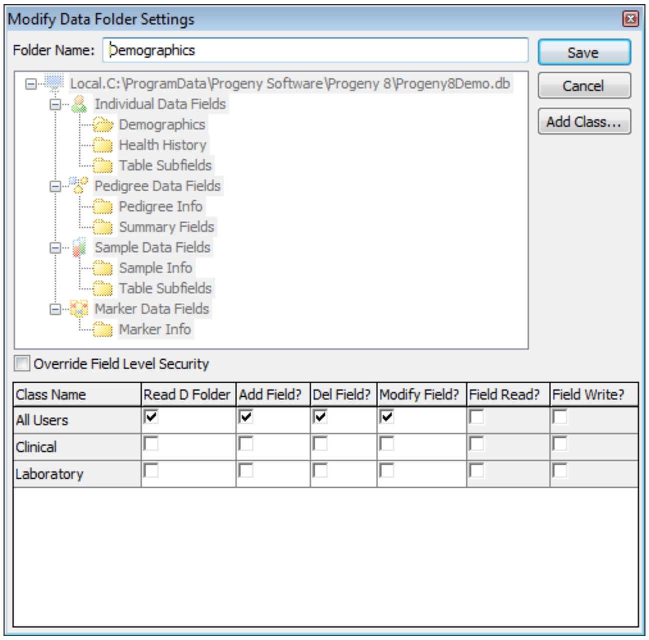
1. On the navigation bar, click the Fields button to open the Fields window.

2. On the Fields window toolbar, right-click on the folder for which you are setting the security, and on the context menu that opens, click Edit Folder Security.

   The Modify Data Folder Settings dialog box opens. The name of the selected database folder is displayed in the Folder Name field.

Although the dialog box is titled "Modify Data Folder Settings," the selected folder is actually a database folder.

Figure 5-10: Modify Data Folder Settings dialog box



Folder Name: Demographics

☐ Override Field Level Security

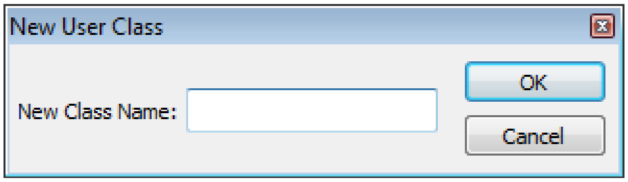
Class Name	Read D Folder	Add Field?	Del Field?	Modify Field?	Field Read?	Field Write?
All Users	☑	☑	☑	☑	☐	☐
Clinical	☐	☐	☐	☐	☐	☐
Laboratory	☐	☐	☐	☐	☐	☐

3. Do one or more of the following:
   - Modify the security settings for All Users or for the different classes of users.
     - Read D Folder?—Open and view the contents of the database folder.
     - Add Field?—Add database fields to the folder.
     - Del Field?—Delete database fields from the folder.
     - Modify Field?—Modify database fields in the folder.

   To maintain database integrity, you typically do not allow all users the ability to add, delete, and modify fields in a database folder. Instead, only the administrator user has full access to all database folders.

   - Click Add Class to open the New User Class dialog box to create a new user class, and then set the folder security for the new class.

   Figure 5-11: New User Class dialog box

   - If you have assigned field-level security to one more fields in the folder, and you want to override the security settings for these fields based on the security settings at the folder level, click Override Field Level Security, and then set the appropriate field-level security for the different classes of users.
     - Field Read?—View the data in the field.
     - Field Write?—Write data to the field.
4. Click Save.

   A message opens indicating the settings for the folder were successfully changed.
5. Click OK to close the message and return to the Fields window.

Setting Database Security

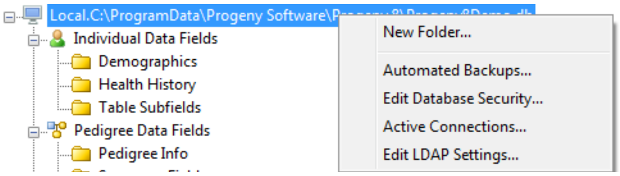
In addition to setting security at the database field level and the database folder level, you can set security at the database level. When you set security at the database level, you can do one or more of the following:

- Set the number of days after which an inactive user is locked out of the database.
- Set the number of days after which a user's password expires.
- Set the security level for adding, deleting, or modifying database folders for a class of users.
- Set the security level for adding, deleting, or modifying *data folders* for a class of users, which are the folders that house the data for individuals, pedigrees, samples, and containers.

To set database security

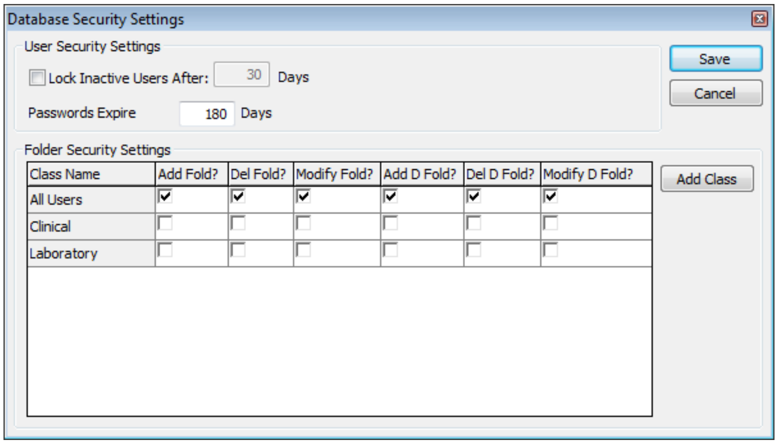
1. Log in to the database for which you are setting the security.
2. On any open window, right-click on the database path, and on the context menu that opens, click Edit Database Security.

Figure 5-12: Database context menu



The Edit Database Security Settings dialog box opens.

Figure 5-13: Edit Database Security Settings dialog box



User Security Settings

☐ Lock Inactive Users After: 30 Days

Passwords Expire 180 Days

Folder Security Settings

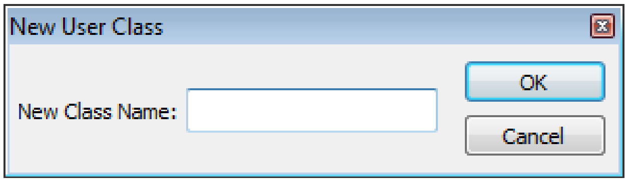
Class Name	Add Fold?	Del Fold?	Modify Fold?	Add D Fold?	Del D Fold?	Modify D Fold?
All Users	☑	☑	☑	☑	☑	☑
Clinical	☐	☐	☐	☐	☐	☐
Laboratory	☐	☐	☐	☐	☐	☐

3. Set the database security as needed.
   - User Security Settings
     - Lock Inactive Users After [ ] Days—Lock out users from the database who have not logged in to the database in the indicated number of days.
     - Passwords Expire After [ ] Days—The number of days after which all passwords for all users (other than the administrator user) expire. If a user attempts to log in to the database with an expired password, they are prompted to change their password "on the fly" so that they can continue logging in. The password must meet all the requirements for a user password. See Password Rules.
   - Folder Security Settings—Do one or more of the following:
     - Modify the security settings for All Users or for the different classes of users.
       - Add Fold?—Add a data folder to the database.
       - Del Fold?—Delete a data folder from the database.
       - Mod Fold?—Modify a data folder in the database.
       - Add D Fold?—Add a database folder to the database.
       - Del D Fold?—Delete a database folder from the database.
       - Modify D Fold?—Modify a database folder in the database.

To maintain database integrity, you typically do not allow all users the ability to add, delete, and modify fields in a database folder.

   - Click Add Class to open the New User Class dialog box to create a new user class, and then set the folder security for the new class.

Figure 5-14: New User Class dialog box



4. Click Save.

   A message opens indicating the settings for the database were successfully changed.

5. Click OK to close the message and return to the application.

Viewing Active Connections

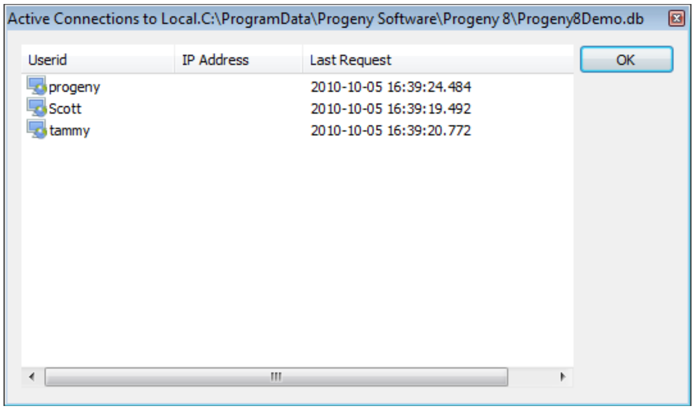
As the Progeny administrator, you can view all active connections to any Progeny database. You typically view active connections for security purposes, for example, to ensure that the database is not being improperly accessed by users. If you determine that a user who is accessing the database should not be, you can edit the database security settings to immediately lock the user out of the database.

To view active connections

1. Log in to the database for which you are viewing the connections.
2. On the main menu, click Administration > Active Connections.

   The Active Connections window opens. This window lists all active connections by user name and IP address. It also lists a date and timestamp of the last login request for the user.

Figure 5-15: Active Connections window



Active Connections to Local.C:\ProgramData\Progeny Software\Progeny 8\Progeny8Demo.db

Userid	IP Address	Last Request
progeny		2010-10-05 16:39:24.484
Scott		2010-10-05 16:39:19.492
tammy		2010-10-05 16:39:20.772

3. Optionally, if you determine that a user who is accessing the database should not be, you can edit the database security settings to immediately lock the user out of the database. See “To set the security levels for a user account” on page 135.

Chapter 6
Database Reporting

Progeny contains a general reporting function to assist you in monitoring and maintaining your database records. You can generate reports for all individuals, pedigrees, markers, and samples in a Progeny database. The reporting function also contains a Query option which you can use to define custom criteria for searching for a specific subset of data in a Progeny database.

This chapter covers the following topics:

- "Generating a Report" on page 151.
- "Saving and Loading Report Formats" on page 155.

Generating a Report

Progeny contains a general reporting function to assist you in monitoring and maintaining your database records. You can generate reports for individuals, pedigrees, samples, and markers.

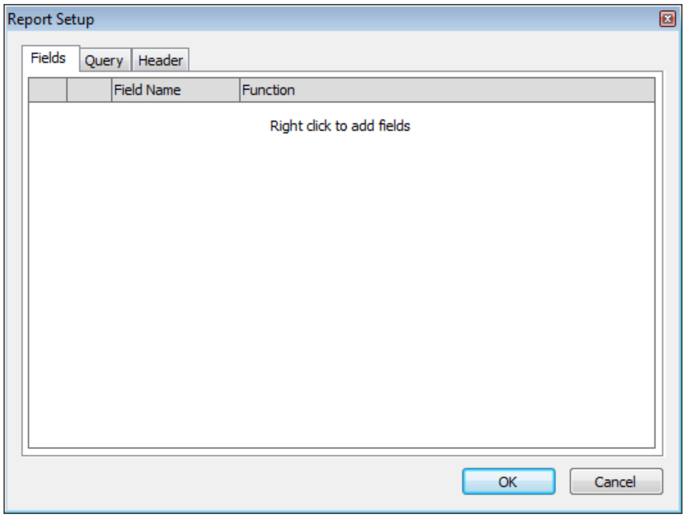
The following procedure details the generation of a Sample report, but, by analogy, you can apply this procedure to generate reports for individuals, pedigrees, and markers.

To generate a report

1. On the Progeny main window navigation bar, click the Samples button to open the Individuals window.
2. On the window toolbar, click the Reporting button .

   The Report Setup dialog box opens. The Fields tab is the active tab.

Figure 6-1: Report Setup dialog box

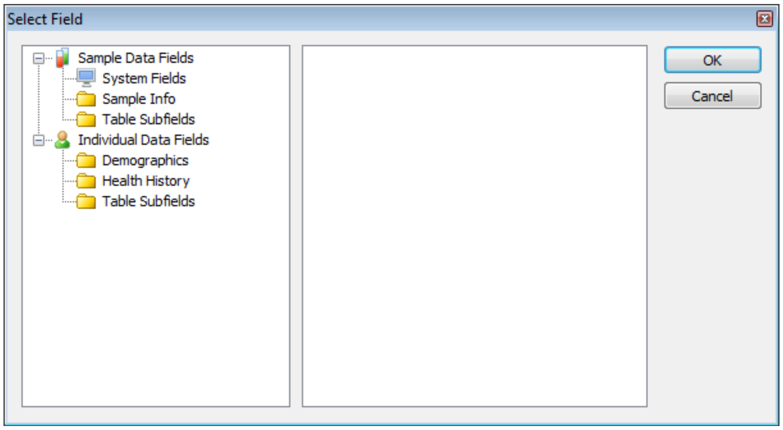


Right click to add fields

3. Right-click on the Report Setup dialog box, and on the context menu that opens, click Add Field.

   The Select Field dialog box opens.

Figure 6-2: Select Field dialog box



4. Select a field from the Select Field dialog box and then click OK.

   The Select Field dialog box closes and the field is displayed on the Fields Tab of the Report Setup dialog box.

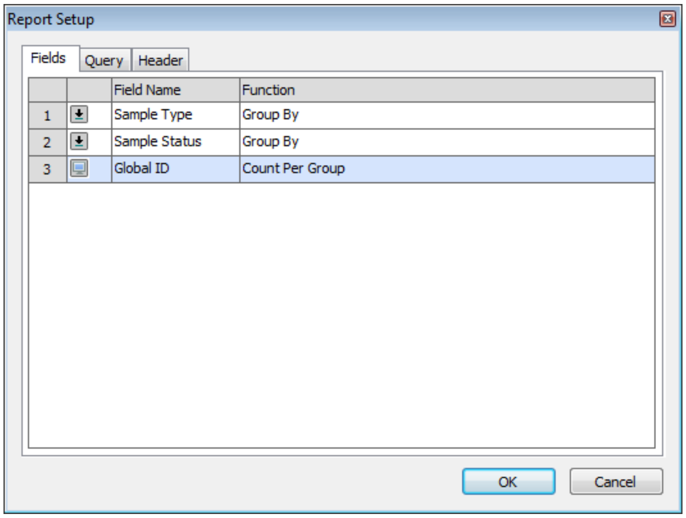
5. Repeat Step 3 and Step 4 for each field that is to be displayed in the report.

⚠ *The order in which you add the fields to the Report Setup dialog box is the order in which they appear (from left to right) as columns in the report. To delete a field from the report, or to change a field section, right-click on the appropriate field, and on the context menu that opens, click Delete Field or Change Field, respectively.*

6. For each report field, select a function.

   The default value is Grouped By. The report output is grouped according to the functions that you select from top to bottom. For example, in Figure 6-3 on page 153, the report is first grouped by Sample Type, and then within each sample type, the report is grouped by Sample Status. If your database contains five sample types and six sample statuses, then your report could contain up to a maximum of 30 rows. If you select one of the Per Group functions (Count Per Group, Max Per Group, or Min Per Group), then for optimum results, this function should be the last function that is selected, and you must select a system field that is relevant for the item that you are counting. (Again, see Figure 6-3 on page 153.) For example, if you are counting samples, then you could select the Barcode system field to count the total number of samples in the database or you could select Global ID to count all the samples in the database that are linked to an individual.

Figure 6-3: Example of a report setup



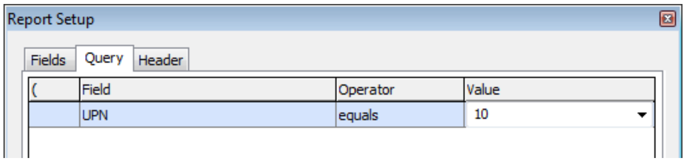
		Field Name	Function
1		Sample Type	Group By
2		Sample Status	Group By
3		Global ID	Count Per Group

7. Optionally, do one or both of the following, or click OK to on the Report Setup dialog box to generate the report.

    - Open the Query tab and define a query to further filter the report results.

      For example, to filter the report described in Figure 6-3 above by samples that are linked to a specific individual, you would set up the query as shown in Figure 6-4 below.

Figure 6-4: Report Setup, example query



(	Field	Operator	Value
	UPN	equals	10

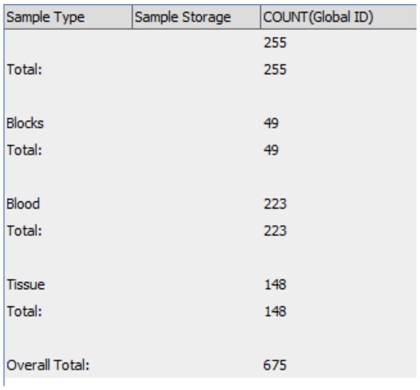
See “Database Query Format” on page 173 for detailed information about formatting a database query.

    - Open the Header tab, and enter a header that is displayed at the top of every page in the report.

8. Click OK.

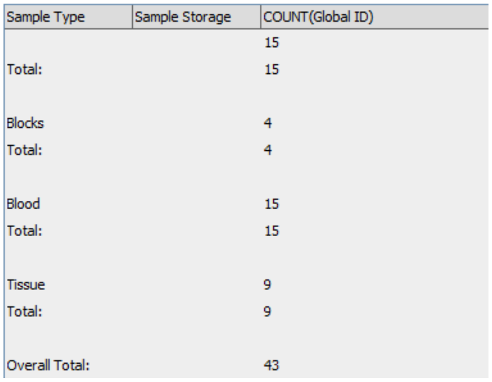
   The Report Setup dialog box closes and the report is generated and displayed onscreen. Figure 6-5 on page 154 shows the Sample report that is generated without the query (675 total samples in the database are linked to an individual). Figure 6-6 on page 154 shows the Sample report that is generated with the query (Of these 675 samples, 43 are linked to the individual whose UPN = 10).

Figure 6-5: Sample report, no query



Sample Type	Sample Storage	COUNT(Global ID)
		255
Total:		255
Blocks		49
Total:		49
Blood		223
Total:		223
Tissue		148
Total:		148
Overall Total:		675

Figure 6-6: Sample report, with query



Sample Type	Sample Storage	COUNT(Global ID)
		15
Total:		15
Blocks		4
Total:		4
Blood		15
Total:		15
Tissue		9
Total:		9
Overall Total:		43

9. Optionally, after you generate a report, you can do one or more of the following:

   - Click the Setup button Setup to open the Report Setup dialog box, modify the report settings, and generate the report again.
   - Click the Print button Print to print the report.
   - Click the Export button Export to export the report. See “Exporting Spreadsheet Data” on page 117.
   - Save the report format for loading and running on as-needed basis. See “Saving and Loading Report Formats” on page 155.

Saving and Loading Report Formats

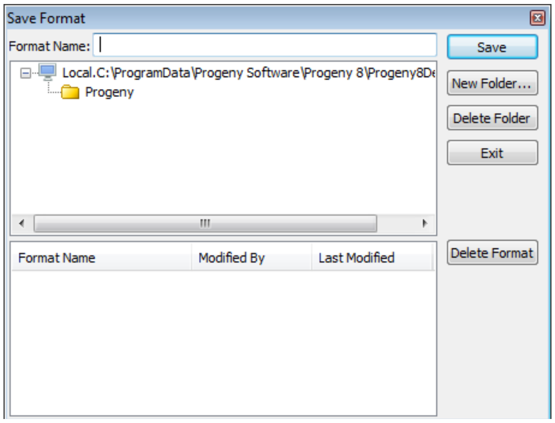
After you have created a report with a specific format, you can save the format. You can then load this saved format and use it to generate another report *of the same type*.

To save a report format

1. Format and generate the report as needed. See "Generating a Report" on page 151.
2. On the report toolbar, click the Save Format button Save Fmt.

   The Save Format dialog box opens. It provides a default folder named Progeny in which to save the report format. (This folder is located in the database that you are currently logged in to and you cannot change this location.)

Figure 6-7: Save Format dialog box



3. Enter a name for the report format, and then do one of the following:
   - Select the Progeny folder.
   - Click New Folder, and on the Format Folder dialog box that opens, do the following:
     - Enter the name of the new folder in which to save to format.
     - Select the location for the new folder. The folder can be stored at the root level (the same level as the Progeny folder), or it can be a sub-folder of the Progeny folder, or of another folder.
     - Click Save.
4. Click Save on the Save Format dialog box.

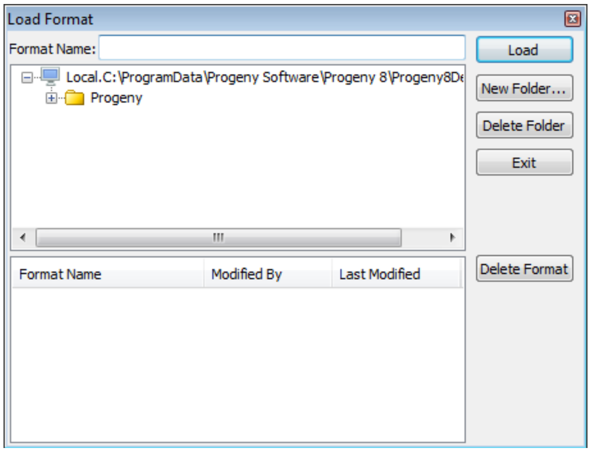
To load a report format

You can a retrieve a saved report format and use it to generate a report *of the same type.*

1. On the Progeny main window navigation bar, open the window for the item for which you are generating the report. For example, if you are generating an Individuals report, click the Samples button to open the Samples window.
2. On the window toolbar, click the Reporting button Reporting .
3. On the window toolbar, click the Load Format button Load Fmt .

   The Load Format dialog box opens.

Figure 6-8: Load Format dialog box



4. Open the folder that contains the report format that you are loading, select the format, and then click Load.

   The Report Setup dialog box opens. The dialog box displays the information for the loaded format (selected fields, functions, and so on).
5. Click OK on the Report Setup dialog box.

   The report is generated and displayed onscreen according to the loaded format.

Chapter 7
Database Organization

Progeny provides two functions—Tasks and Smart Lists—to assist you in managing a Progeny database and organizing the data for easy review and retrieval.

This chapter covers the following topics:

- "Using the Tasks Feature" on page 159.
- "Creating Smart Lists" on page 165.

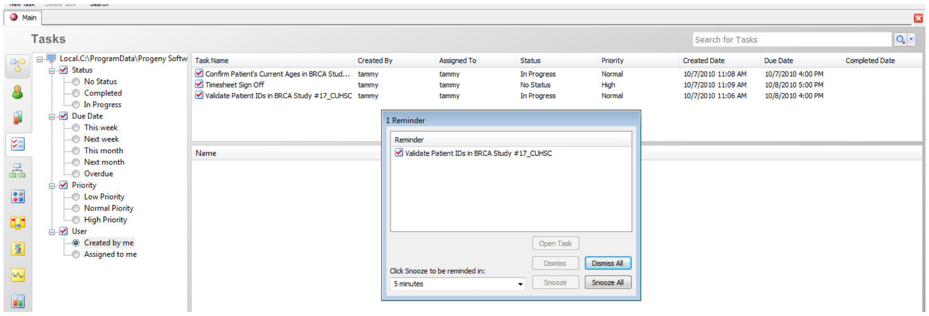
Using the Tasks Feature

The Tasks feature centralizes the database tasks that have been created by you or assigned to you in a single location. After you log into Progeny, if any tasks that are assigned to you have been flagged with a reminder that has a due date less than or equal to the current day's date, then a Reminders dialog box opens in the Tasks main window. The dialog box lists the tasks by name. You can create tasks in the Tasks window and assign the task to yourself or to another user, and you can also edit and delete these tasks. If a task has not been created with a reminder, or if the current date is too soon for a reminder and therefore, the task is not displayed in the Reminders dialog box, you can search for the task in the Tasks window.

To work with tasks in the Reminders dialog box

After you log into Progeny, if any tasks that are assigned to you have been flagged with a reminder that has a due date less than or equal to the current day's date, then a Reminders dialog box opens in the Tasks main window. The dialog box lists the tasks by name.

Figure 7-1: Tasks window with Reminders dialog box



Task Name	Created By	Assigned To	Status	Priority	Created Date	Due Date	Completed Date
☑ Confirm Patient's Current Ages in BRCA Stud...	tammy	tammy	In Progress	Normal	10/7/2010 11:08 AM	10/7/2010 4:00 PM	
☑ Timesheet Sign Off	tammy	tammy	No Status	High	10/7/2010 11:09 AM	10/8/2010 5:00 PM	
☑ Validate Patient IDs in BRCA Study #17_CUHSC	tammy	tammy	In Progress	Normal	10/7/2010 11:06 AM	10/8/2010 4:00 PM	

1 Reminder

Reminder
☑ Validate Patient IDs in BRCA Study #17_CUHSC

Click Snooze to be reminded in: 5 minutes

- To view a task in the Reminders dialog box, select the task and then click Open Task.
- To dismiss a task from the Reminders dialog box (regardless of its status), select the task and click Dismiss. To dismiss all tasks from the Reminders dialog box, click Dismiss All.

When you dismiss a task from the Reminders dialog box, the task is not deleted. A dismissed task can still be returned in a task search. If you dismiss all tasks, the Reminders dialog box closes.

- To change the default task reminder Snooze time from 5 minutes to another time for a single task, select the task, select a different time on the Snooze time dropdown list, and then click Snooze.
- To change the default task reminder Snooze time from 5 minutes to another time for all tasks, select a different time on the Snooze time dropdown list, and then click Snooze All.

If you snooze all reminders, the Reminders dialog box closes.

To create a database task

You can create a database task from the Tasks window, or you can manually associate an item (individual, sample, or pedigree) with a task. If you create a task from the Tasks window, then you must associate an automatic query with the task. When the user selects the task in the Tasks window, the associated query is automatically generated and the results of the query are displayed in the lower right pane of the Tasks window.

Make sure that you are logged in to the Progeny database for which you want to create the task.

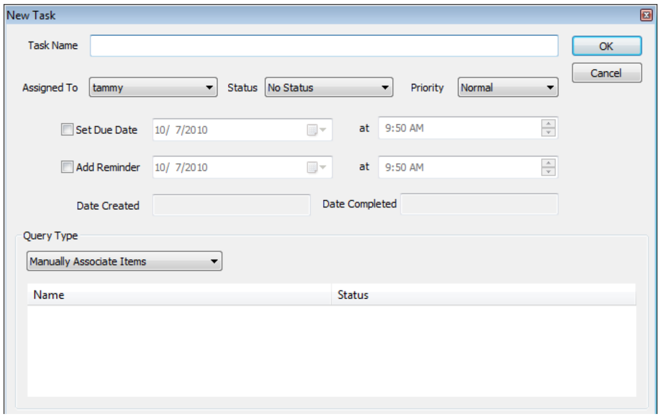
To create a task from the Task window

1. On the Progeny main window, click the Tasks button ☑ to open the Tasks window.

2. On the Tasks window toolbar, click the New Task button ☑ New Task.

   The New Task dialog box opens.

Figure 7-2: New Task dialog box



New Task

Task Name

Assigned To: tammy

Status: No Status

Priority: Normal

☐ Set Due Date 10/ 7/2010 at 9:50 AM

☐ Add Reminder 10/ 7/2010 at 9:50 AM

Date Created

Date Completed

Query Type: Manually Associate Items

3. Enter the identifying information for the task.

Field	Description
Task Name	A descriptive or identifying name for the task.
Assigned To	Dropdown list of all the users for the Progenydatabase.
Status	Dropdown list. Available values are No Status, In Progress, Completed.
Priority	Dropdown list. Available values are Normal, Low, and High.
Set Due Date Add Reminder	Default values are the current day’s date and current time. To modify these values, select the appropriate checkbox to enable the Date and Time fields. **Note:** If you do not set a reminder for a task, then to view the task, you or the user to whom you assigned the task must search for the Task in the Tasks window.

4. To associate an automatic query with the task, select the Query Type (Pedigree Query, Individual Query, or Sample Query), right-click in the Query pane to select the query fields, and then format the query (operator, value, and so on) as needed.

See "Database Query Format" on page 173 for detailed information about formatting a database query.

5. Click OK.

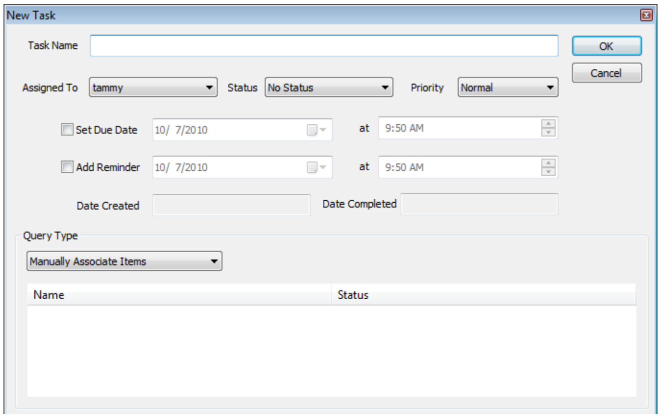
   The Add New Task dialog box closes. The newly created task is displayed in the upper right pane of the Tasks window.

To manually associate an item with a task

1. Right-click on the item (individual, pedigree, or sample) that you are associating with a task, and on the context menu that opens, click New Task.

   The New Task dialog box opens.

Figure 7-3: New Task dialog box



New Task

Task Name

Assigned To: tammy
Status: No Status
Priority: Normal

☐ Set Due Date 10/ 7/2010 at 9:50 AM

☐ Add Reminder 10/ 7/2010 at 9:50 AM

Date Created

Date Completed

Query Type: Manually Associate Items

Name	Status

2. Enter the information for the task.

Field	Description
Task Name	A descriptive or identifying name for the task.
Assigned To	Dropdown list of all the users for the Progenydatabase.
Status	Dropdown list. Available values are No Status, In Progress, Completed.
Priority	Dropdown list. Available values are Normal, Low, and High.
Set Due Date Add Reminder	Default values are the current day's date and current time. To modify these values, select the appropriate checkbox to enable the Date and Time fields. **Note:** If you do not set a reminder for a task, then to view the task, you or the user to whom you assigned the task must search for the Task in the Tasks window.

3. Click OK.

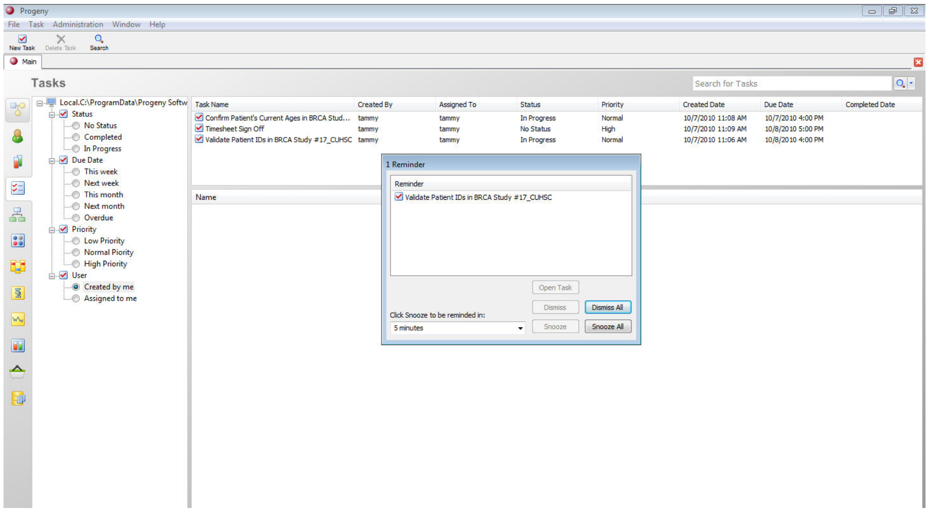
   The Add New Task dialog box closes. The newly created task is displayed in the upper right pane of the Tasks window.

To edit a task

1. Log in to the Progeny database in for which you are editing the tasks.

   If any tasks that are assigned to you have been flagged with a reminder that has a due date less than or equal to the current day's date, then a Reminder dialog box opens in the Tasks main window. The dialog box lists the tasks by name.

Figure 7-4: Tasks window with Reminder dialog box



Task Name	Created By	Assigned To	Status	Priority	Created Date	Due Date	Completed Date
☑ Confirm Patient's Current Ages in BRCA Stud...	tammy	tammy	In Progress	Normal	10/7/2010 11:08 AM	10/7/2010 4:00 PM	
☑ Timesheet Sign Off	tammy	tammy	No Status	High	10/7/2010 11:09 AM	10/8/2010 5:00 PM	
☑ Validate Patient IDs in BRCA Study #17_CUHSC	tammy	tammy	In Progress	Normal	10/7/2010 11:06 AM	10/8/2010 4:00 PM	

Reminder
☑ Validate Patient IDs in BRCA Study #17_CUHSC

Click Snooze to be reminded in: 5 minutes

2. Do one or more of the following:

   - If the task that you are editing is displayed in the Reminders dialog box, select the task, and then click Open Task. The Tasks opens in the Edit Task dialog box. Edit the task as needed.

   - If the task that you are editing is not displayed in the Reminders dialog box, then do one of the following:

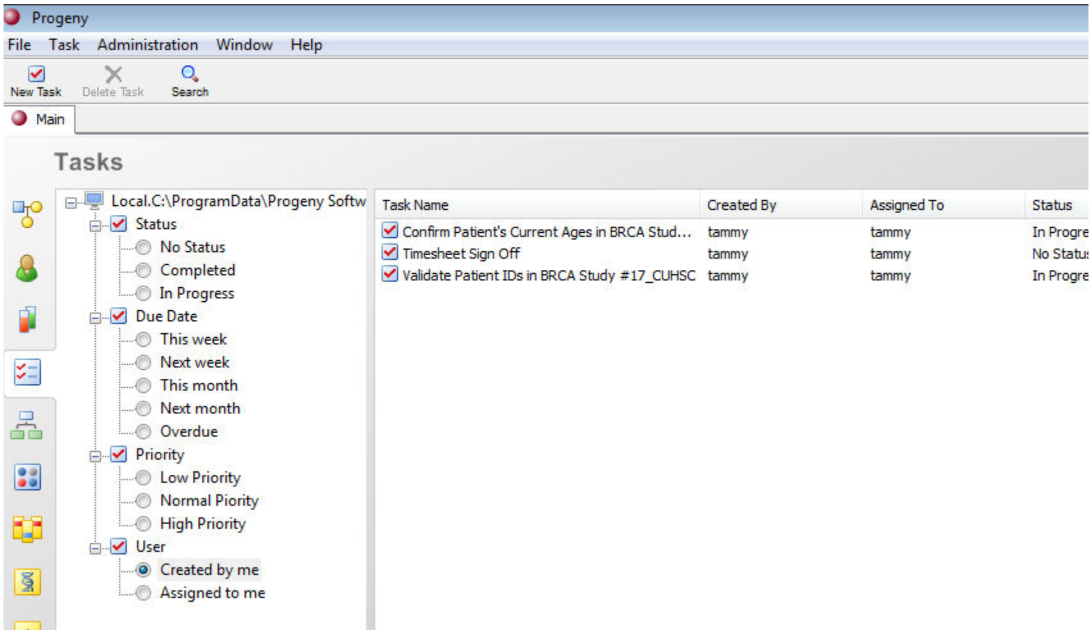
     - Carry out a contextual search for the task. See "Contextual Search" on page 179.

     - Select the appropriate option in the left pane of the Tasks window to search by Status, Due Date, Priority, *or* User.

The search options in the left pane are mutually exclusive. You cannot, for example, search for all tasks that you created that have a high priority. If you search for all tasks that you created, then all tasks that you created are returned regardless of their priority.

The tasks the meet the search criteria are displayed in the upper right pane of the Tasks window. See Figure 7-5 on page 163.

Figure 7-5: Tasks search results in Tasks window

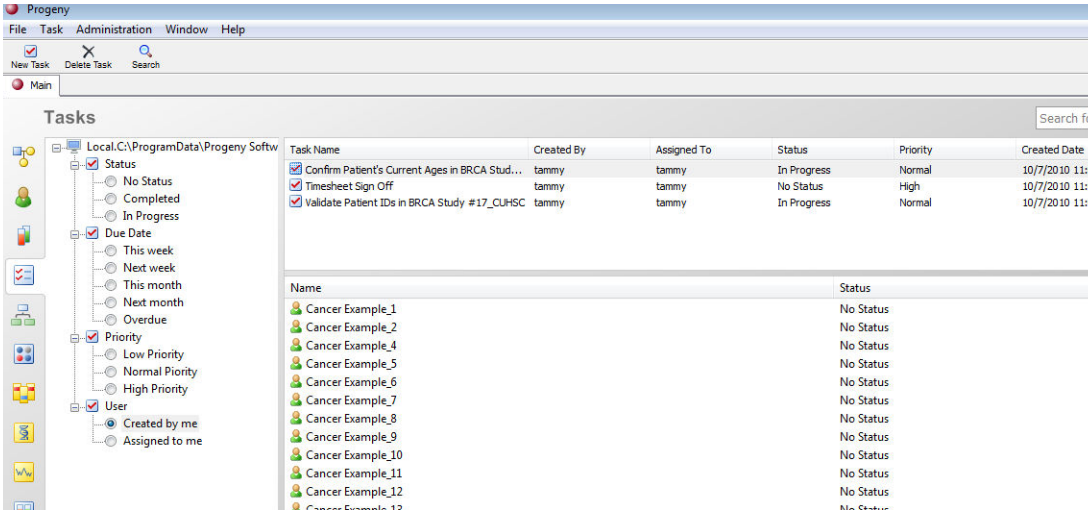


Task Name	Created By	Assigned To	Status
☑ Confirm Patient's Current Ages in BRCA Stud...	tammy	tammy	In Progre
☑ Timesheet Sign Off	tammy	tammy	No Statu
☑ Validate Patient IDs in BRCA Study #17_CUHSC	tammy	tammy	In Progre

3. Double-click on the task in the Tasks window to open the Tasks in the Edit Tasks window and edit the task as needed.

If an automatic query is associated with the selected task, then the results of the query are displayed in the lower pane of the Tasks window. See Figure 7-6 below.

Figure 7-6: Query results for an automatic query associated with a task



Task Name	Created By	Assigned To	Status	Priority	Created Date
☑ Confirm Patient's Current Ages in BRCA Stud...	tammy	tammy	In Progress	Normal	10/7/2010 11:
☑ Timesheet Sign Off	tammy	tammy	No Status	High	10/7/2010 11:
☑ Validate Patient IDs in BRCA Study #17_CUHSC	tammy	tammy	In Progress	Normal	10/7/2010 11:

Name	Status
Cancer Example_1	No Status
Cancer Example_2	No Status
Cancer Example_4	No Status
Cancer Example_5	No Status
Cancer Example_6	No Status
Cancer Example_7	No Status
Cancer Example_8	No Status
Cancer Example_9	No Status
Cancer Example_10	No Status
Cancer Example_11	No Status
Cancer Example_12	No Status

To delete a task

1. Log in to the Progeny database in for which you are deleting the tasks.
2. Optionally, if applicable, to close the Reminders dialog box, Snooze All tasks or Dismiss All Tasks.

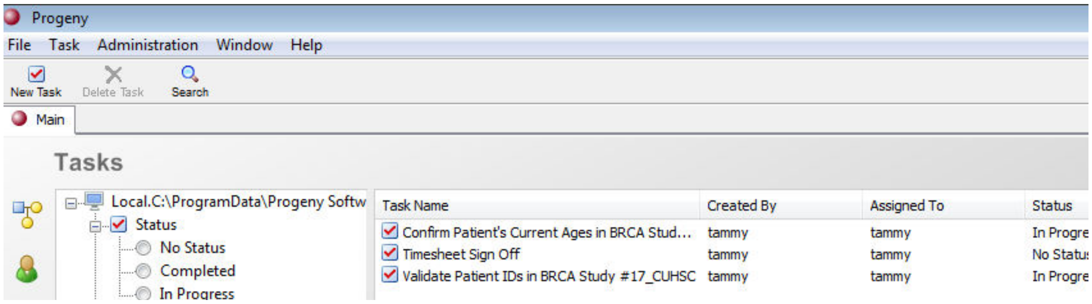
It is recommended to Snooze All Tasks to close the dialog box as Dismissing All Tasks will permanently remove the tasks from the Reminders list.

3. Do one of the following:
   - Carry out a contextual search for the task. See "Contextual Search" on page 179.
   - Select the appropriate option in the left pane of the Tasks window to search by Status, Due Date, Priority, *or* User.

The search options in the left pane are mutually exclusive. You cannot, for example, search for all tasks that you created that have a high priority. If you search for all tasks that you created, then all tasks that you created are returned regardless of their priority.

The tasks the meet the search criteria are displayed in the upper right pane of the Tasks window.

Figure 7-7: Tasks search results in Tasks window



Local.C:\ProgramData\Progeny Softw
- ☑ Status
  - ○ No Status
  - ○ Completed
  - ○ In Progress

Task Name	Created By	Assigned To	Status
☑ Confirm Patient's Current Ages in BRCA Stud...	tammy	tammy	In Progre
☑ Timesheet Sign Off	tammy	tammy	No Statu
☑ Validate Patient IDs in BRCA Study #17_CUHSC	tammy	tammy	In Progre

4. Select the task or tasks that are being deleted, (CTRL-click to select multiple tasks), and then on the Tasks window toolbar, click the Delete Task button.

   A message opens asking you if you are sure that you want to delete the selected tasks.

5. Click Yes.

   The message closes. The selected tasks are deleted.

To search for a task

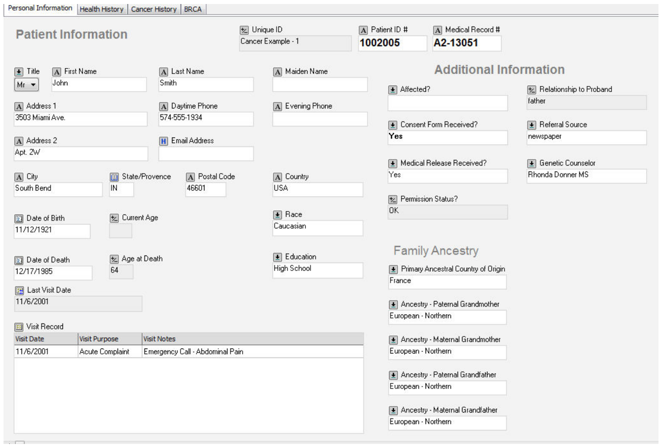
You have two options for searching for a task from the Tasks window:

- You can carry out a contextual search for the task. See "Contextual Search" on page 179.
- You can click the Search icon Search on the Tasks window toolbar to carry out a global search. See "Database Global Search" on page 178.

Creating Smart Lists

When you collect data for an individual, pedigree, marker, and so on, you typically have multiple fields in which to enter the data. For example, if you are collecting data for an individual, the fields in which you must enter data can include First Name, Last Name, Maiden Name, Address 1, Address 2, Address 3, City, State, Zip, Race, DOB, Current Age, Height, Weight, and so on. When you are trying to quickly locate a specific individual, pedigree, or so on in a data folder, it is simply not feasible to display all the fields. Instead, you can customize the fields that are displayed in a *smart list*. A smart list displays only selected fields from all the available data fields and system fields for individuals, pedigrees, samples, markers, and inventories. Smart lists are displayed in the right panes of the Progeny main window. Multiple smarts lists are available for individuals, pedigrees, samples, and inventories. Only a single smart list is available for markers. (See "Smart List types" on page 166.) A smart list can be saved on per user basis so that each user can have his/her own preferred view, or the Progeny administrator can set a single default view for all users. After you or the Progeny Administrator creates smart lists for individuals, pedigrees, and so on, you can carry out a *contextual search*. A contextual search searches only the data that is displayed in the columns in a smart list, which provides a convenient method for quickly retrieving needed data. (See "Contextual Search" on page 179.)

Figure 7-8: Individual Smart List example



Patient Information

Unique ID: Cancer Example - 1
Patient ID #: 1002005
Medical Record #: A2-13051
Title: Mr
First Name: John
Last Name: Smith
Maiden Name:
Address 1: 3503 Miami Ave.
Daytime Phone: 574-555-1934
Evening Phone:
Address 2: Apt. 2W
Email Address:
City: South Bend
State/Provence: IN
Postal Code: 46601
Country: USA
Date of Birth: 11/12/1921
Current Age:
Race: Caucasian
Date of Death: 12/17/1985
Age at Death: 64
Education: High School
Last Visit Date: 11/6/2001

Visit Record

Visit Date	Visit Purpose	Visit Notes
11/6/2001	Acute Complaint	Emergency Call - Abdominal Pain

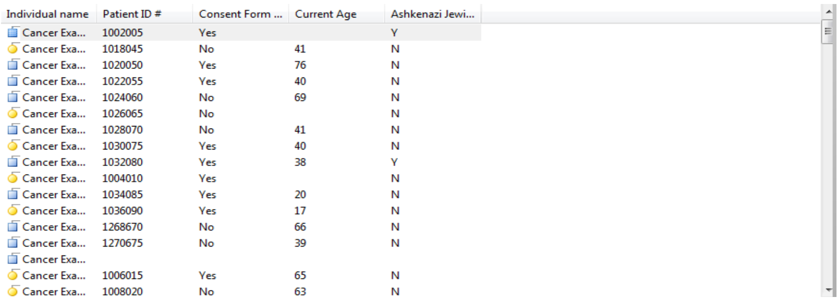
Additional Information

Affected?:
Relationship to Proband: father
Consent Form Received?: Yes
Referral Source: newspaper
Medical Release Received?: Yes
Genetic Counselor: Rhonda Donner MS
Permission Status?: OK

Family Ancestry

Primary Ancestral Country of Origin: France
Ancestry - Paternal Grandmother: European - Northern
Ancestry - Maternal Grandmother: European - Northern
Ancestry - Paternal Grandfather: European - Northern
Ancestry - Maternal Grandfather: European - Northern

Multiple data fields on multiple tabs for collecting individual data.



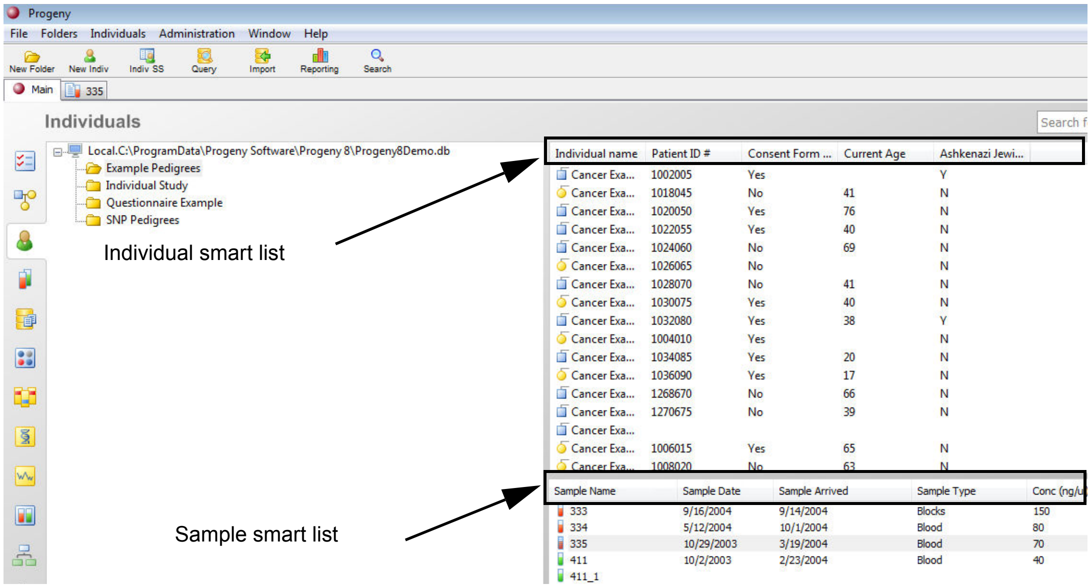
Individual name	Patient ID #	Consent Form ...	Current Age	Ashkenazi Jewi...
Cancer Exa...	1002005	Yes		Y
Cancer Exa...	1018045	No	41	N
Cancer Exa...	1020050	Yes	76	N
Cancer Exa...	1022055	Yes	40	N
Cancer Exa...	1024060	No	69	N
Cancer Exa...	1026065	No		N
Cancer Exa...	1028070	No	41	N
Cancer Exa...	1030075	Yes	40	N
Cancer Exa...	1032080	Yes	38	Y
Cancer Exa...	1004010	Yes		N
Cancer Exa...	1034085	Yes	20	N
Cancer Exa...	1036090	Yes	17	N
Cancer Exa...	1268670	No	66	N
Cancer Exa...	1270675	No	39	N
Cancer Exa...				
Cancer Exa...	1006015	Yes	65	N
Cancer Exa...	1008020	No	63	N

Only a select number of these data fields are displayed in the smart list for individuals.

Smart List types

Multiple smarts lists are available for individuals, pedigrees, samples, and inventories. Only a single smart list is available for markers.

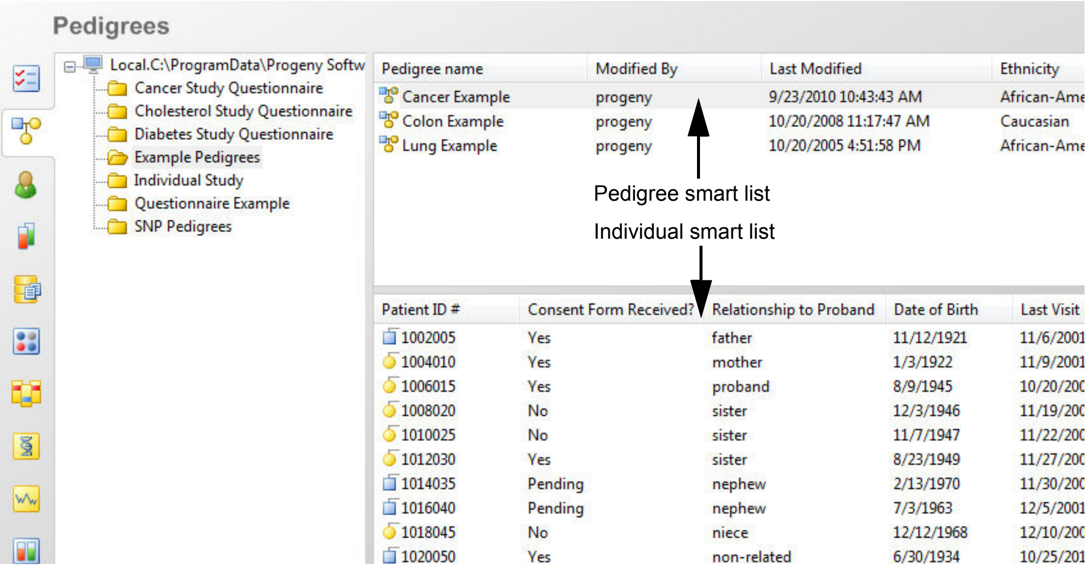
Figure 7-9: Individual smart lists



Individual name	Patient ID #	Consent Form ...	Current Age	Ashkenazi Jewi...
Cancer Exa...	1002005	Yes		Y
Cancer Exa...	1018045	No	41	N
Cancer Exa...	1020050	Yes	76	N
Cancer Exa...	1022055	Yes	40	N
Cancer Exa...	1024060	No	69	N
Cancer Exa...	1026065	No		N
Cancer Exa...	1028070	No	41	N
Cancer Exa...	1030075	Yes	40	N
Cancer Exa...	1032080	Yes	38	Y
Cancer Exa...	1004010	Yes		N
Cancer Exa...	1034085	Yes	20	N
Cancer Exa...	1036090	Yes	17	N
Cancer Exa...	1268670	No	66	N
Cancer Exa...	1270675	No	39	N
Cancer Exa...				
Cancer Exa...	1006015	Yes	65	N
Cancer Exa...	1008020	No	63	N

Sample Name	Sample Date	Sample Arrived	Sample Type	Conc (ng/u
333	9/16/2004	9/14/2004	Blocks	150
334	5/12/2004	10/1/2004	Blood	80
335	10/29/2003	3/19/2004	Blood	70
411	10/2/2003	2/23/2004	Blood	40
411_1				

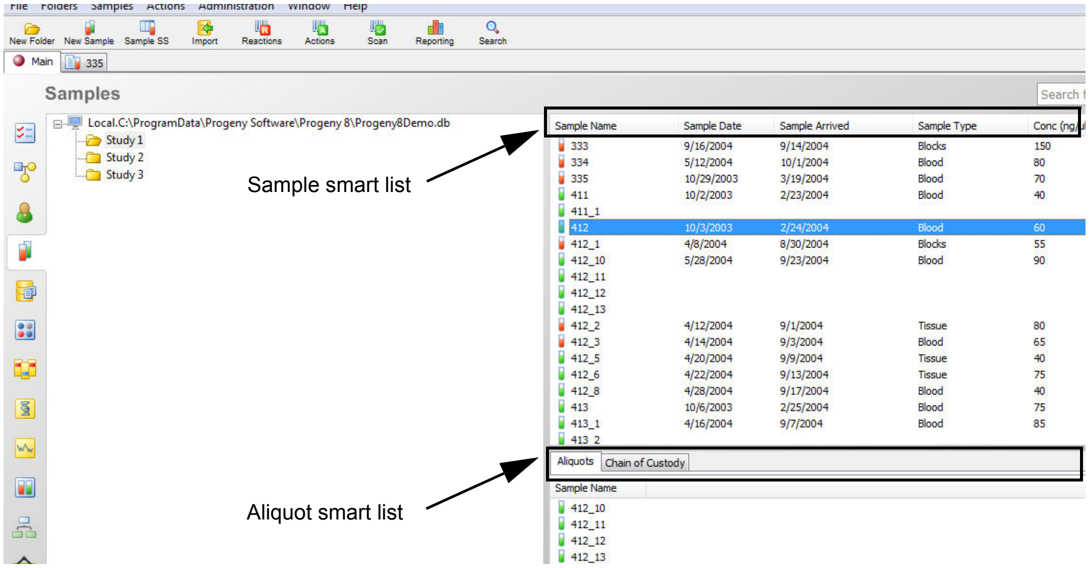
Figure 7-10: Pedigree smart lists



Pedigree name	Modified By	Last Modified	Ethnicity
Cancer Example	progeny	9/23/2010 10:43:43 AM	African-Ame
Colon Example	progeny	10/20/2008 11:17:47 AM	Caucasian
Lung Example	progeny	10/20/2005 4:51:58 PM	African-Ame

Patient ID #	Consent Form Received?	Relationship to Proband	Date of Birth	Last Visit
1002005	Yes	father	11/12/1921	11/6/2001
1004010	Yes	mother	1/3/1922	11/9/2001
1006015	Yes	proband	8/9/1945	10/20/200
1008020	No	sister	12/3/1946	11/19/200
1010025	No	sister	11/7/1947	11/22/200
1012030	Yes	sister	8/23/1949	11/27/200
1014035	Pending	nephew	2/13/1970	11/30/200
1016040	Pending	nephew	7/3/1963	12/5/2001
1018045	No	niece	12/12/1968	12/10/200
1020050	Yes	non-related	6/30/1934	10/25/201

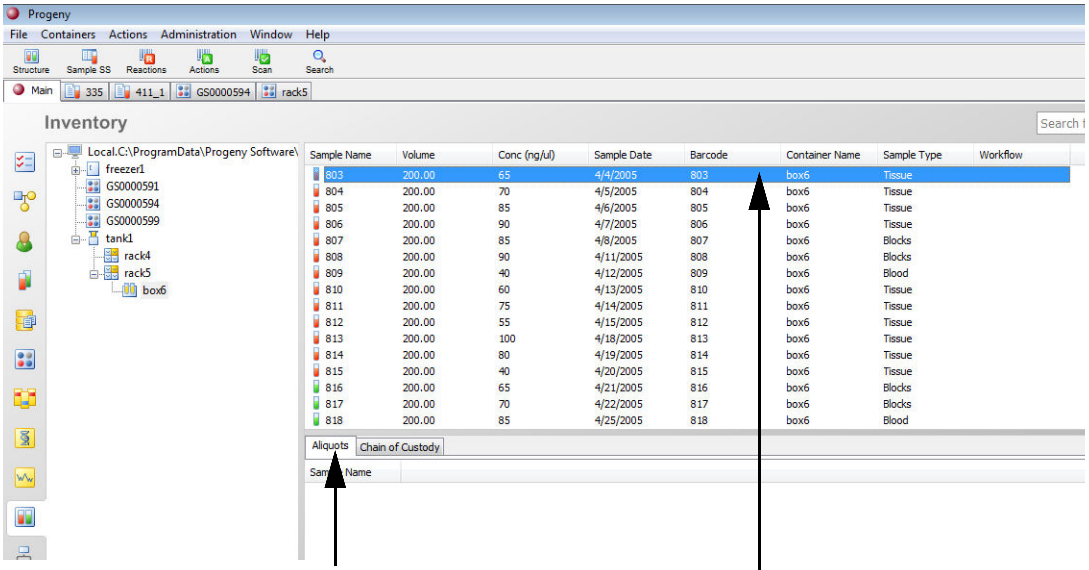
Figure 7-11: Sample smart lists



Sample Name	Sample Date	Sample Arrived	Sample Type	Conc (ng/ul
333	9/16/2004	9/14/2004	Blocks	150
334	5/12/2004	10/1/2004	Blood	80
335	10/29/2003	3/19/2004	Blood	70
411	10/2/2003	2/23/2004	Blood	40
411_1				
412	10/3/2003	2/24/2004	Blood	60
412_1	4/8/2004	8/30/2004	Blocks	55
412_10	5/28/2004	9/23/2004	Blood	90
412_11				
412_12				
412_13				
412_2	4/12/2004	9/1/2004	Tissue	80
412_3	4/14/2004	9/3/2004	Blood	65
412_5	4/20/2004	9/9/2004	Tissue	40
412_6	4/22/2004	9/13/2004	Tissue	75
412_8	4/28/2004	9/17/2004	Blood	40
413	10/6/2003	2/25/2004	Blood	75
413_1	4/16/2004	9/7/2004	Blood	85
413_2				

Sample Name
412_10
412_11
412_12
412_13

Figure 7-12: Inventory smart lists



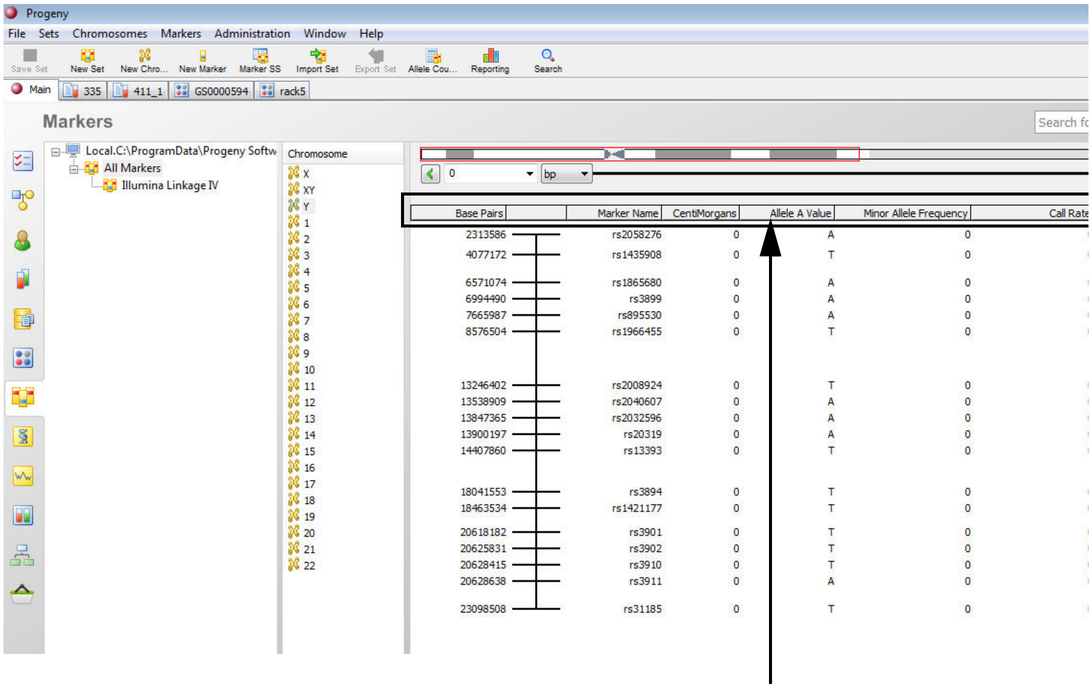
Sample Name	Volume	Conc (ng/ul)	Sample Date	Barcode	Container Name	Sample Type	Workflow
803	200.00	65	4/4/2005	803	box6	Tissue	
804	200.00	70	4/5/2005	804	box6	Tissue	
805	200.00	85	4/6/2005	805	box6	Tissue	
806	200.00	90	4/7/2005	806	box6	Tissue	
807	200.00	85	4/8/2005	807	box6	Blocks	
808	200.00	90	4/11/2005	808	box6	Blocks	
809	200.00	40	4/12/2005	809	box6	Blood	
810	200.00	60	4/13/2005	810	box6	Tissue	
811	200.00	75	4/14/2005	811	box6	Tissue	
812	200.00	55	4/15/2005	812	box6	Tissue	
813	200.00	100	4/18/2005	813	box6	Tissue	
814	200.00	80	4/19/2005	814	box6	Tissue	
815	200.00	40	4/20/2005	815	box6	Tissue	
816	200.00	65	4/21/2005	816	box6	Blocks	
817	200.00	70	4/22/2005	817	box6	Blocks	
818	200.00	85	4/25/2005	818	box6	Blood	

Sample Name

Aliquot smart list

Inventory smart list

Figure 7-13: Markers smart list



Base Pairs	Marker Name	CentiMorgans	Allele A Value	Minor Allele Frequency	Call Rate
2313586	rs2058276	0	A	0	
4077172	rs1435908	0	T	0	
6571074	rs1865680	0	A	0	
6994490	rs3899	0	A	0	
7665987	rs895530	0	A	0	
8576504	rs1966455	0	T	0	
13246402	rs2008924	0	T	0	
13538909	rs2040607	0	A	0	
13847365	rs2032596	0	A	0	
13900197	rs20319	0	A	0	
14407860	rs13393	0	T	0	
18041553	rs3894	0	T	0	
18463534	rs1421177	0	T	0	
20618182	rs3901	0	T	0	
20625831	rs3902	0	T	0	
20628415	rs3910	0	T	0	
20628638	rs3911	0	A	0	
23098508	rs31185	0	T	0	

Markers smart list. Base Pairs, Marker Names, and CentiMorgans are not optional columns. They are always displayed in the Markers smart list. All other columns are optional.

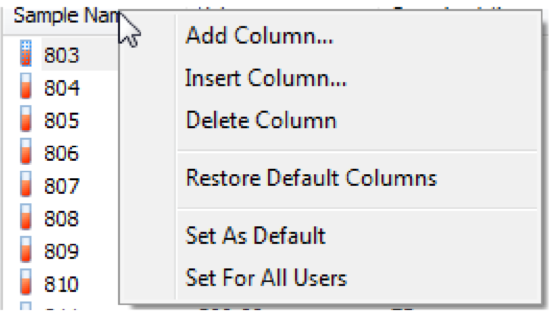
To create a smart list

The following procedure details the creation of an individual smart list, but, by analogy, you can apply this procedure to create smart lists for pedigrees, samples, inventories, and markers.

1. Click the Individuals button to open the Individuals window.
2. Right-click in any of the column headers for a smart list.

   The smart list context menu opens.

Figure 7-14: Smart List context menu



3. Select the appropriate option on the context menu.

Option	Description
Add Column	Add a new column at the end of the smart list.
Insert Column	Add a new column to the to the immediate left of the selected column.
Delete Column	Delete the selected column from the smart list.
Restore Default Columns	Return the smart list to its default view. This view can be the default installation view or it can be a default view that the Progeny administrator has set for all users.
Set as Default	Available only for the Progeny administrator. Sets the current view as the default view for the smart list.
Set for All Users	Available only for the Progeny administrator. Sets the current view as the default view for the smart list for all progeny users.

Remember, after you or the Progeny Administrator creates smart lists for individuals, pedigrees, and so on, you can carry out a contextual search. A contextual search searches only the data that is displayed in the columns in a smart list, which provides a convenient method for quickly retrieving needed data. See "Contextual Search" on page 179.

Chapter 8
Database Queries and Searches

Both queries and searches are an inquiry into the database and both are used to extract data from the database in a readable format according to a user's request. Queries and searches differ primarily in the operators that are used in the request and the allowed format of the request.

This chapter covers the following topics:

Database Query Format

A *database query* is an inquiry into the database that is used to extract data from the database in a readable format according to a user's request. A query can be carried out for a single field in the database, or it can be carried out for multiple fields. For either type of query, after you have selected the fields for the query, you must:

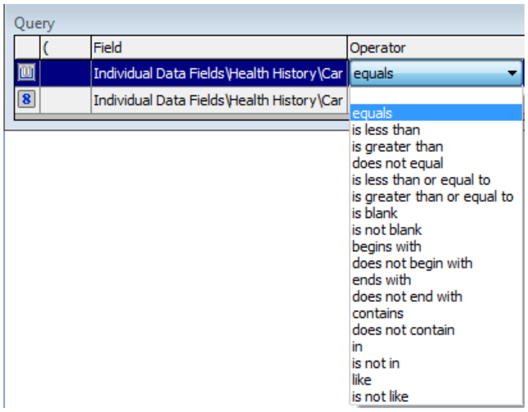
- Specify the operators for the query.
- Specify the values for the query. Depending on the fields that you selected for the query, you must either manually enter a value, or select a value from a table or dropdown list.

In addition, if you are carrying out a multiple fields query, you must specify the Boolean operators (AND/OR) for the query. Optionally, you can also use brackets to apply an order of operations to the query, which determines the queries that must be carried out first in a series of queries.

Query operators

When you are setting up a database query, you must select from a list of operators for the query.

Figure 8-1: List of available operators for a query



Operator	Description
equals	Search for an exact match. For example, if the query field for individuals is the Weight field, and you specify the search criteria as Weight = 175, then only those individuals whose weight is exactly 175 are returned in the search.
is less than	Search for an item that is less than the specified value. For example, if the query field for individuals is the Weight field, and you specify Weight < 175, then only those individuals whose weight is 174 or less are returned in the search.
is greater than	Search for an item that is greater than the specified value. For example, if the query field for individuals is the Weight field, and you specify Weight > 175, then only those individuals whose weight is 176 or greater are returned in the search.

Operator	Description
does not equal	Search for an item that is meets any criteria *other* than what you specify. For example, if the query field for individuals is the Weight field, and you specify Weight ≠ 175, then only those individuals whose weight does not equal 175 (i.e., individuals with weight = 174 or less, or individuals whose weight = 176 or greater) are returned in the search.
is less than or equal to	Search for an item that is less than than the specified value or is an exact match for the specified value. For example, if the query field for individuals is the Weight field, and you specify Weight ≤ 175, then those individuals whose weight is exactly 175 or less are returned in the search.
is greater than or equal to	Search for an item that is greater than than the specified value or is an exact match for the specified value. For example, if the query field for individuals is the Weight field, and you specify Weight ≥ 175, then those individuals whose weight is exactly 175 or greater are returned in the search.
is blank	Search for an item where the specified field contains absolutely no data. For example, if the query field for individuals is the Weight field, and you specify Weight is blank, only those individuals for whom data has *not* been entered into the Weight field are returned in the search. **Note:** A zero (0) is an actual data value.This means that if a zero (0) has been entered into the Weight field for an individual, then the individual is *not* returned in the search.
is not blank	Search for an item where the specified field contains any valid data. For example, if the query field for individuals is the Weight field, and you specify Weight is not blank, all individuals for whom data has been entered into the Weight field are returned in the search. **Note:** A zero (0) is an actual data value.This means that if a zero (0) has been entered into the Weight field for an individual, then the individual *is* returned in the search.
begins with	Search for an item where the specified field contains data that *begins* with the search criteria. For example, if the query field for individuals is the Weight field, and you specify Weight begins with 17, then only those individuals for whom the weight begins with a 17 (17 or 170-179) are returned in the search.
does not begin with	Search for an item where the specified field contains data that *does not begin* with the search criteria. For example, if the query field for individuals is the Weight field, and you specify Weight does not begin with 17, then only those individuals for whom the weight does not begin with a 17 (0-169, 180 -1699, and so on) are returned in the search.
ends with	Search for an item where the specified field contains data that *ends* with the search criteria. For example, if the query field for individuals is the Weight field, and you specify Weight ends with 75, then only those individuals for whom the weight ends with a 75 (75, 175, 275, and so on) are returned in the search.

Operator	Description
does not end with	Search for an item where the specified field contains data that *does not end* with the search criteria. For example, if the query field for individuals is the Weight field, and you specify Weight does not end with 75, then only those individuals for whom the weight does *not* end with a 75 (0-74, 76-174, 176-274, and so on) are returned in the search.
contains	Search for an item where the specified field contains any instance of the search criteria. For example, if the query field for individuals is the Weight field, and you specify Weight contains 75, then all individuals who have a weight in which 75 appears anywhere (75, 175, 275, and so on) are returned in the search.
does not contain	Search for an item where the specified field does *not* contain any instance of the search criteria. For example, if the query field for individuals is the Weight field, and you specify Weight does not contain 75, then all individuals who have a weight in which 75 does not appear (0-74, 76-174, 176-274, and so on) are returned in the search.
in	Allows for comma separated values to be entered into a field so that multiple items can be searched and returned in the search results. For example, if the query field for individuals is the Weight field, and you specify Weight in 75, 80, 85, 90, then all individuals whose weight is exactly 75, 80, 85, or 90 are returned in the search. **Note:** You can copy and paste a list of values from .csv file into a query of this type.
is not in	Allows for comma separated values to be entered into a field so that multiple items can be searched and excluded from the search results. For example, if the query field for individuals is the Weight field, and you specify Weight is not in 75, 80, 85, 90, then all individuals whose weight is *not* exactly 75, 80, 85, or 90 are returned in the search. **Note:** You can copy and paste a list of values from .csv file into a query of this type.
like	A pattern matching search based on the keyword “like.” An underscore (_) is used to match exactly one character, and the percent sign (%) is used to indicate any number of characters. For example, if the query field for individuals is the Weight field, then to search for all individuals whose weight is like 75, select “like” as the operator and enter %75 in the Value field. The % indicates that any number of characters can come before 75, for example, 75, 175, 275, and so on. **Note:** You can use the % anywhere in the search criteria, for example, 75% or 7%5.

Operator	Description
is not like	A pattern matching search based on the keyword “like.” An underscore (_) is used to match exactly one character, and the percent sign (%) is used to indicate any number of characters. For example, if the query field for individuals is the Weight field, then to search for all individuals whose weight is *not* like 75, select “is not like” as the operator and enter %75 in the Value field. The % indicates that any number of characters can come before 75, for example, 0 -74, 176 - 184, 186 - 274, and so on. **Note:** You can use the % anywhere in the search criteria, for example, 75% or 7%5.

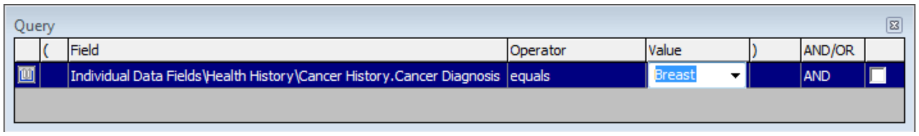
AND/OR operators

You use the Boolean operators AND and OR to narrow or widen your search respectively.

- A search with the Boolean operator AND returns only those items that use *both* the search terms you specify, as in this example: BREAST AND FEMALE.
- A search with the Boolean operator OR returns those items that use *either* search term that you specify, as in this example: BREAST OR FEMALE.

When you set up a single field query, then by default, the AND/OR operator is set to AND, which is ignored by the application. For example, Figure 8-2 shows the query for all individuals with a cancer diagnosis equal to Breast.

Figure 8-2: Singe field query

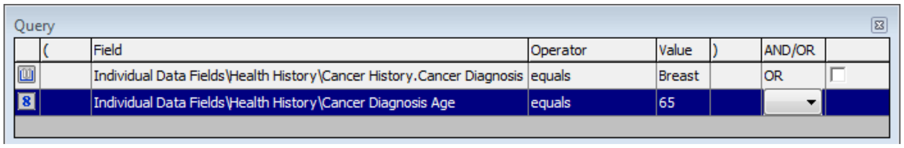


Query

	(	Field	Operator	Value	)	AND/OR	
		Individual Data Fields\Health History\Cancer History.Cancer Diagnosis	equals	Breast		AND	☐

When you set up a multiple fields query, then you must specify the correct operator for the desired query results. For example, Figure 8-3 shows the query for all individuals who have a cancer diagnosis equal to Breast *or* who were diagnosed with any type of cancer at the age of 65.

Figure 8-3: Multi-field query with OR operator

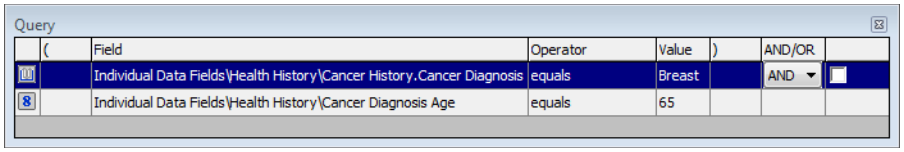


Query

	(	Field	Operator	Value	)	AND/OR	
		Individual Data Fields\Health History\Cancer History.Cancer Diagnosis	equals	Breast		OR	☐
8		Individual Data Fields\Health History\Cancer Diagnosis Age	equals	65			

Figure 8-4 shows the query for all individuals who have a cancer diagnosis equal to Breast *and* who were diagnosed with this type of cancer at the age of 65.

Figure 8-4: Multi-field query with AND operator



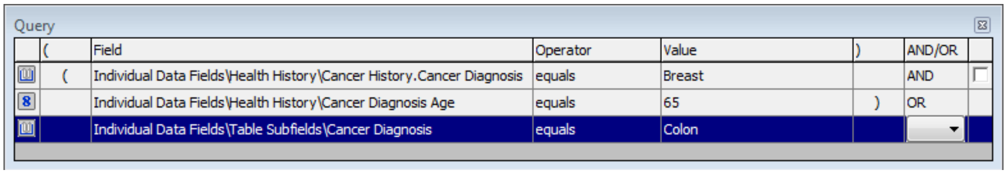
Query

	(	Field	Operator	Value	)	AND/OR	
		Individual Data Fields\Health History\Cancer History.Cancer Diagnosis	equals	Breast		AND	☐
		Individual Data Fields\Health History\Cancer Diagnosis Age	equals	65			

Order of operations for a query

When you carry out a multiple fields query, you can use parentheses to define the order of operations for a query. The order of operations determines the queries that must be carried out first in a series of queries. For example, Figure 8-5 shows a query that first sorts individuals who were diagnosed with breast cancer at the age of 65. The query then sorts individuals who were diagnosed with colon cancer. Because this query uses the OR operator, the query returns individuals who meet *either* query criteria.

Figure 8-5: Order of operations for multi-field query, OR operator

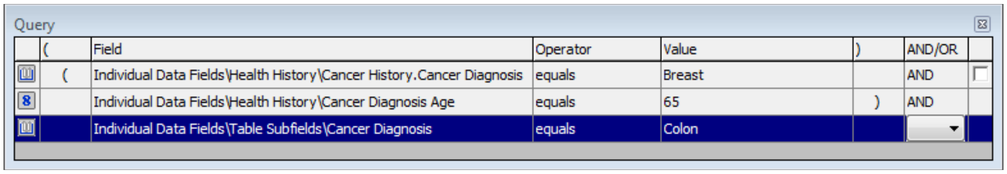


Query

	(	Field	Operator	Value	)	AND/OR	
	(	Individual Data Fields\Health History\Cancer History.Cancer Diagnosis	equals	Breast		AND	☐
		Individual Data Fields\Health History\Cancer Diagnosis Age	equals	65	)	OR	
		Individual Data Fields\Table Subfields\Cancer Diagnosis	equals	Colon			

Figure 8-6 shows a query that first sorts individuals who were diagnosed with breast cancer at the age of 65. The query then sorts individuals who were diagnosed with colon cancer. Because this query uses the AND operator, the query returns only those individuals who meet *both* query criteria.

Figure 8-6: Order of operations for multi-field query, AND operator



Query

	(	Field	Operator	Value	)	AND/OR	
	(	Individual Data Fields\Health History\Cancer History.Cancer Diagnosis	equals	Breast		AND	☐
		Individual Data Fields\Health History\Cancer Diagnosis Age	equals	65	)	AND	
		Individual Data Fields\Table Subfields\Cancer Diagnosis	equals	Colon			

Database Global Search

When you carry out a *database global search*, the entire database is searched for every occurrence of a sequence of characters, or *search string*. You search is limited to the exact order of the characters in the string and you can use the asterisk (*) as a wildcard to extend the search. For example, if you searching for individuals with some form of Bob in either their First Name or Last Name:

- If you enter Bob as the search string, then only those database items that contain the exact value of "Bob" in at least one of the data fields are returned by the search for example, the individual Bob Smith.
- If you enter Bob* as the search string, then the database items that contain the value "Bob" followed by any other characters in at least one of the data fields are returned by the search, for example, the individual Bobbi Smith or the individual James Bobby.
- If you enter *Bob as the search string, then the database items that contain the value "Bob" preceded by any other characters in at least one of the data fields are returned by the search, for example, the individual Jim-Bob Walton.

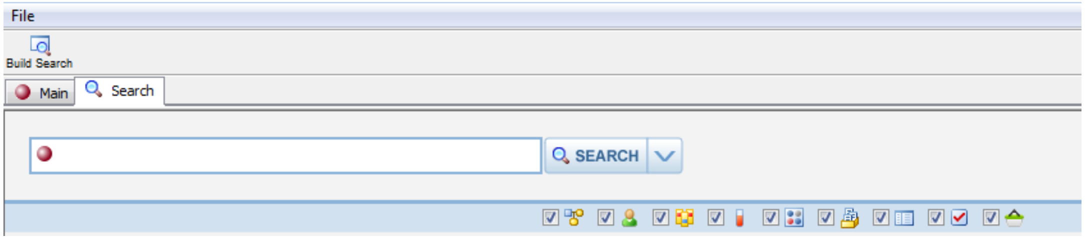
All items that are returned by the search are returned in a hyperlink format, which you can click to go to the referenced item.

To carry out a database global search

1. On the Progeny main window toolbar, click the Search icon Search.

   A blank Search tab opens. By default, all database items for which you can search (from left to right, the icons are for pedigrees, individuals, markers, samples, containers, fields, spreadsheets, tasks, and orders) are selected.

Figure 8-7: Search tab with default search options



2. Optionally, clear the selections for the database items for which you do *not* want to search.
3. In the Search field, enter the search string. Use asterisks as needed to extend the search.
4. Click Search.

   All database items that meet the search criteria are returned by the search. The items are returned in a hyperlink format, which you can click to go to the referenced item.

Contextual Search

When you carry out a *contextual search,* only the data that is displayed in the columns in a smart list is searched. You search is limited to the exact order of the characters in the string and you can use the asterisk (*) as a wildcard to extend the search. For example, when searching an individual smart list where First Name is one of the columns that is displayed:

- If you enter Bob as the search string, then only those individuals that contain the exact value of “Bob” in the First Name field are returned by the search (for example, the individual Bob Smith).
- If you enter Bob* as the search string, then those individuals that contain the value “Bob” followed by any other characters in the First Name field returned by the search, (for example, the individual Bobbi Smith).
- If you enter *Bob as the search string, then those individuals that contain the value “Bob” preceded by any other characters in the First Name field are returned by the search, (for example, the individual Jim-Bob Walton).

A contextual search does not distinguish between identical values in different columns. For example, if an individual smart list also displays the Last Name Column, and you enter Bob* as the search string, then not only is the individual Bobbi Smith returned, but also, the individual James Bobby, where Bobby is contained in the Last Name field. A contextual search is available on every window (Individuals, Pedigrees, Samples, Fields, Containers, and so on) that is opened from the navigation bar on the Progeny main window.

Figure 8-8: Example of an Individuals contextual search field

The application “remembers” the last search string entered for a contextual search. To view and/or select this string, click the dropdown arrow next to the Search icon.

Figure 8-9: Selecting last contextual search string


23

23

To carry out a contextual search

1. In the appropriate contextual search field, do one of the following:
    - Enter new search criteria, or select the dropdown arrow next to the Search icon to select the last search string entered.
    - Click on the dropdown arrow next to the Search icon and select the last search string.
2. Click the Search icon 🔍 Search.

   The smart list is updated with only those items that meet the search criteria.

Main Window Queries

The Main Window Query function allows you to retrieve all queries that were saved as part of a spreadsheet format, run these queries, and display the query results according to the selected query type.

- Spreadsheet—The results of the query are displayed in a spreadsheet format.
- Pedigree—A list of pedigrees that meet the query criteria are displayed. You can double-click a pedigree to open it.
- Individual Datasheet—A list of individual datasheets for all individuals who meet the query criteria is displayed. You can double-click an individual datasheet to open it.

To carry out a Main Window query

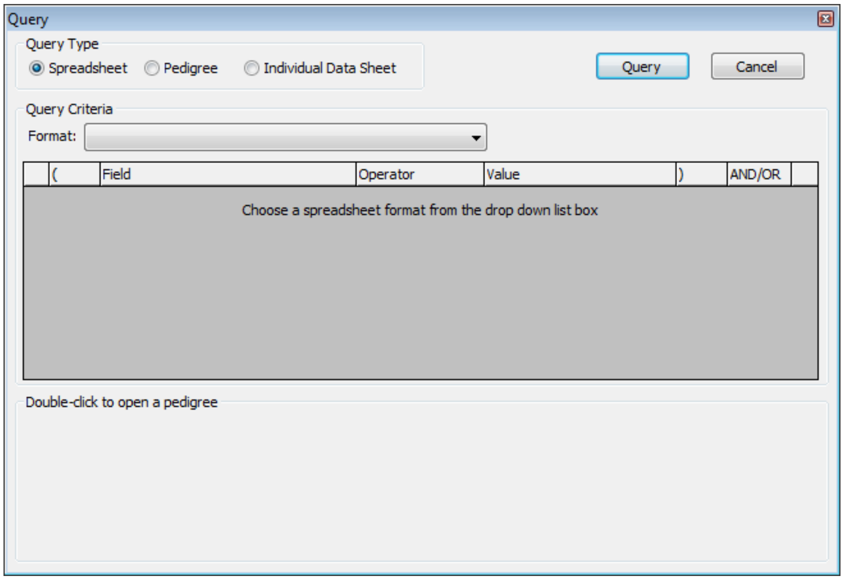
1. On the Progeny main window navigation bar, click the Individuals button or the Pedigrees button .

   The Individuals window or Pedigrees window opens, respectively.

2. On the window toolbar, click the Query button .

   The Query window opens.

Figure 8-10: Query window



Choose a spreadsheet format from the drop down list box

3. Select the query type.

4. On the Query Criteria dropdown list, select the query that is to be run.

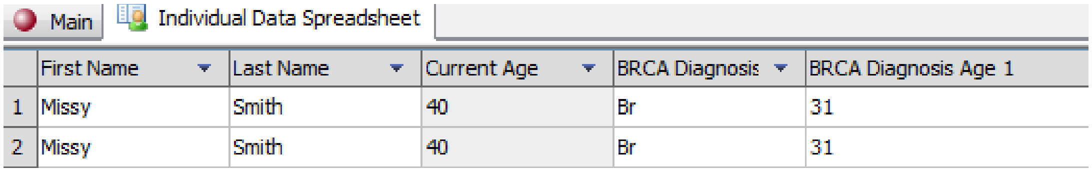
   The Query window is updated with the query criteria (Field, Operator, and so on).

5. Click Query.

   The query is run and the results are according to the selected query type.

   - Spreadsheet—The results of the query are displayed in a spreadsheet format.

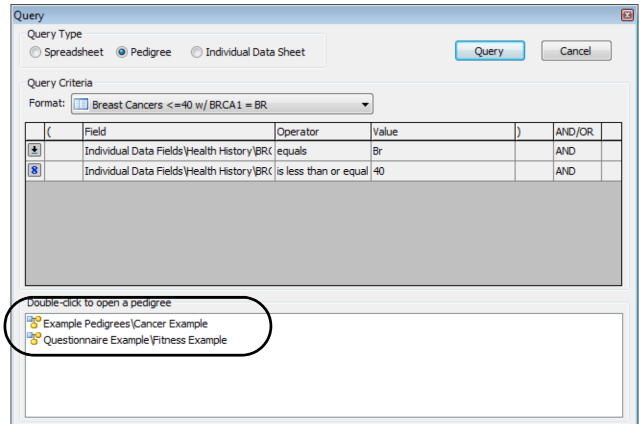
Figure 8-11: Main window query, Spreadsheet query type



	First Name	Last Name	Current Age	BRCA Diagnosis	BRCA Diagnosis Age 1
1	Missy	Smith	40	Br	31
2	Missy	Smith	40	Br	31

- Pedigree—A list of pedigrees that meet the query criteria are displayed in the bottom pane of the Query window. You can double-click a pedigree to open it.

Figure 8-12: Main window query, Pedigree query type



○ Spreadsheet ● Pedigree ○ Individual Data Sheet

Format: Breast Cancers <=40 w/ BRCA1 = BR

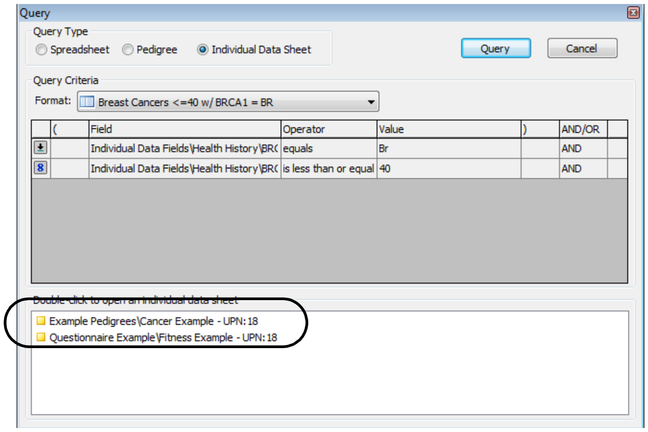
	(	Field	Operator	Value	)	AND/OR
		Individual Data Fields\Health History\BR(	equals	Br		AND
		Individual Data Fields\Health History\BR(	is less than or equal	40		AND

Double-click to open a pedigree

Example Pedigrees\Cancer Example
Questionnaire Example\Fitness Example

- Individual Datasheet—A list of individual datasheets for each individual that meets the query criteria is displayed in the bottom pane of the Query window. You can double-click an individual datasheet to open it.

Figure 8-13: Main window query, Individual Datasheet query type



○ Spreadsheet ○ Pedigree ● Individual Data Sheet

Format: Breast Cancers <=40 w/ BRCA1 = BR

	(	Field	Operator	Value	)	AND/OR
		Individual Data Fields\Health History\BR(	equals	Br		AND
		Individual Data Fields\Health History\BR(	is less than or equal	40		AND

Double-click to open an individual data sheet

Example Pedigrees\Cancer Example - UPN: 18
Questionnaire Example\Fitness Example - UPN: 18

Chapter 9
Database Auditing

Database auditing involves observing a database so that you can be aware of the actions of the database users. Database auditing is often for security purposes, for example, to ensure that information is not accessed by those without the permission to access it, or that only acceptable and allowed changes were made to the data. You use the auditing feature in Progeny to track changes that were made to data in a Progeny database. You can turn the auditing feature on for specific pedigree data fields, individual data fields, and sample fields. After the audit feature is turned on, any changes that are made to the data in these fields for a pedigree, individual, or sample is tracked in the Audit report. The Audit report displays item type, the item name, the old field value, the new field value, the user name for the user who changed the value and a transaction date and time stamp.

This chapter covers the following topics:

- "Activating the Auditing Feature" on page 185.
- "Generating an Audit Report" on page 187.

All functions that are detailed in this chapter are available only to the Progeny administrator.

Activating the Auditing Feature

You use the auditing feature in Progeny to track changes that were made to data in a Progeny database. Activating the audit feature is a two step process. You first must set the audit status for specific data fields. You can set the audit status for pedigree data fields, individual data fields, and sample fields. After you set the audit status for the data fields, you must turn on the auditing feature for the pedigrees, individuals, or samples that use these fields.

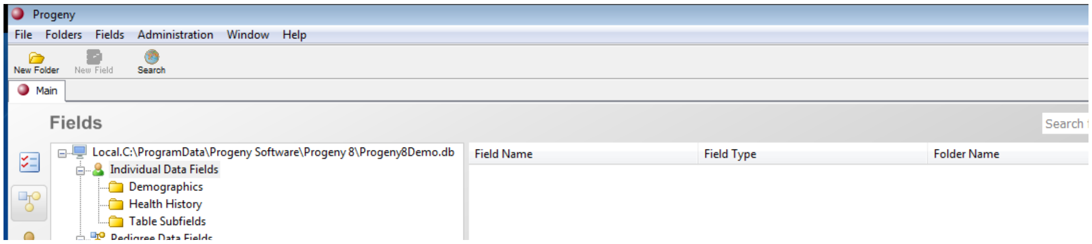
This section details the activation of the auditing feature for samples, but by analogy, you can use this procedure to activate the auditing feature for individuals and pedigrees.

To set the audit status for data fields

1. On the Progeny main window navigation bar, click the Fields button .

   The Fields window opens.

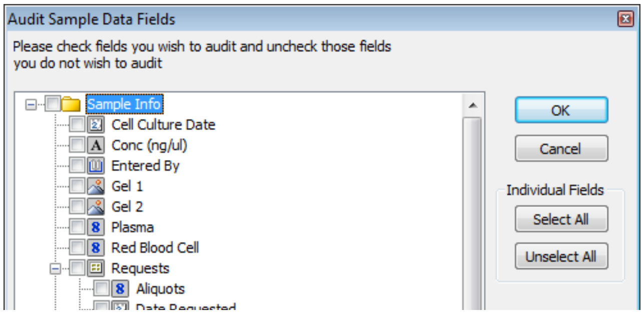
Figure 9-1: Fields window



2. In the left pane of the window, open the individual database folder that contains the fields for which you are setting the audit status.
3. In the right pane of the Fields window, select the field or fields (CTRL-click so select multiple fields) for which you are setting the audit status.
4. Right-click on the selected fields, and on the context menu that opens, click Update Audit Status.

   The Audit Data Fields dialog box opens.

Figure 9-2: Audit Data Fields dialog box



Please check fields you wish to audit and uncheck those fields you do not wish to audit

5. Select the checkbox next to each field that is to be audited. Conversely, clear the checkbox next to each field that is not to be audited.

To select all fields for auditing in a single step, click Select All. Conversely, to remove all fields from auditing, click Unselect All.

6. Click OK.

   A message opens indicating the number of fields that were updated successfully.

7. Click OK to close both the message and the Audit Data Fields dialog box and return to the Fields window.
8. Continue to "To turn on auditing for an individual, pedigree, or sample" below.

To turn on auditing for an individual, pedigree, or sample

1. On the Progeny main window navigation bar, click the Samples button to open the Samples window.
2. In the left pane of the window, open the data folder that contains the samples that are to be audited.
3. In the right pane of the folder, select the sample or samples (CTRL-click to select multiple samples) that are to be audited.
4. Right-click on the selected samples, and on the context menu that opens, click Audit Status, and then click On.

   A message opens indicating that the audit status was successfully changed.

5. Click OK to close the message and return to the Samples window.

   Any changes made to the selected data fields for the selected samples are recorded in the Audit report. See "Generating an Audit Report" on page 187.

Generating an Audit Report

After the auditing feature is turned on, any changes that are made to the data in selected fields for a pedigree, individual, or sample are tracked in the Audit report. The Audit report displays the following data in a spreadsheet format—the item type, the item name, the old field value, the new field value, the user name for the user who changed the value and a transaction date and time stamp.

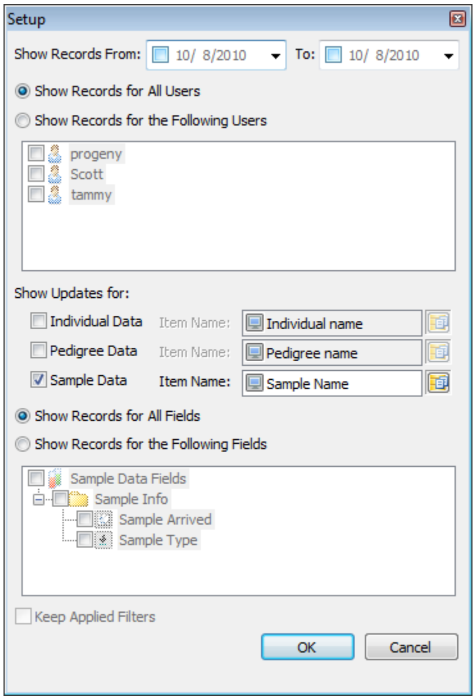
To access the Audit table

The following procedure details how to access the Audit table for samples, but by analogy, you can apply this procedure to individuals and pedigrees.

1. On the Progeny main window navigation bar, click the Samples button to open on the Samples window.
2. On the main menu, click Administration > Field Audit Report.

   The Audit Setup dialog box opens.

Figure 9-3: Audit Setup dialog box



Setup

Show Records From: 10/ 8/2010 To: 10/ 8/2010

● Show Records for All Users

○ Show Records for the Following Users

☐ progeny
☐ Scott
☐ tammy

Show Updates for:

☐ Individual Data Item Name: Individual name
☐ Pedigree Data Item Name: Pedigree name
☑ Sample Data Item Name: Sample Name

● Show Records for All Fields

○ Show Records for the Following Fields

- ☐ Sample Data Fields
  - ☐ Sample Info
    - ☐ Sample Arrived
    - ☐ Sample Type

☐ Keep Applied Filters

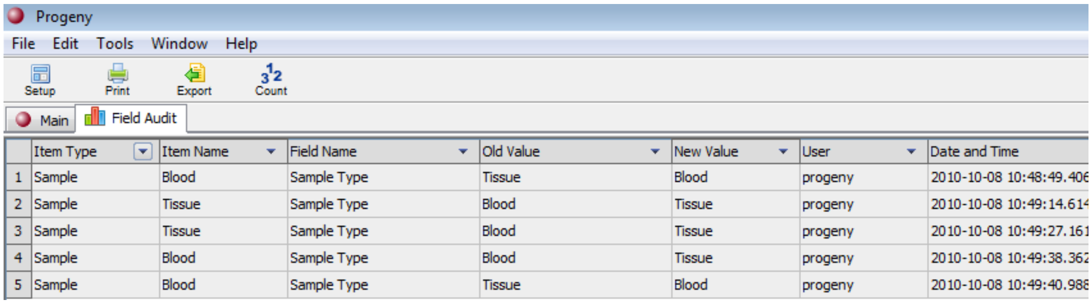
3. Specify the information for the audit.

Option	Description
Date	The ending date can be the same as the beginning date, or you can specify a date range.
• Show Records for All Users • Show Records for the Following Users	If you select Show Records for the Following Users, you can select more than one user.
Show Updates for:	By default, the data type that is selected is based on the window from which you opened the Audit Setup dialog box. For example, if you opened the dialog box from the Samples window, then Sample Data is selected. Indicate how you want to identify/refer to the item for which you are generating the Audit report. This information is displayed in the Item Name column (second column) of the Audit report. • Individual Data - Individual Name (The default value, which is the recommended value). • Pedigree Data—Pedigree Name (The default value, which is the recommend value). • Sample Data—Sample Name or Barcode Number.
• Show Records for All Fields • Show Records for the Following Fields	The fields that are available are based on the selected data type. • Select this option to display all fields for which auditing is turned on in the Audit report. • Select this option, and then select the specific fields for which auditing is turned that are to be displayed in the Audit report.
Keep Applied Filters	Enabled only after you generate the initial report. After you generate the initial report, select Keep Applied Filters, filter one or more columns of data, and then click Run again to generate the report with the applied filters. **Note:** Make sure to clear this option if you do not want to generate the report with the applied filters.

4. Click OK.

The Audit table is generated in a spreadsheet format.

Figure 9-4: Sample Audit table



	Item Type	Item Name	Field Name	Old Value	New Value	User	Date and Time
1	Sample	Blood	Sample Type	Tissue	Blood	progeny	2010-10-08 10:48:49.406
2	Sample	Tissue	Sample Type	Blood	Tissue	progeny	2010-10-08 10:49:14.614
3	Sample	Tissue	Sample Type	Blood	Tissue	progeny	2010-10-08 10:49:27.161
4	Sample	Blood	Sample Type	Blood	Tissue	progeny	2010-10-08 10:49:38.362
5	Sample	Blood	Sample Type	Tissue	Blood	progeny	2010-10-08 10:49:40.988

5. Optionally, after you generate an audit report, you can do one or more of the following:
    - Sort and/or filter the audit data. See “Sorting and Filtering Spreadsheet Data” on page 126.
    - Click the Setup button Setup to open the Audit setup dialog box, modify the report settings, and generate the report again.
    - Click the Print button Print to print the Audit report.
    - Click the Export button Export to export the Audit report. See “Exporting Spreadsheet Data” on page 117.
    - Click the Count button Count to count the number of individuals, pedigrees, or samples (that is, the number of rows) in the spreadsheet. See “Counting Spreadsheet Data” on page 130.

Chapter 10
Database Backup

When you back up a Progeny database, you are essentially making a copy of the database that you can use to restore the original after a data loss or corruption event. It is important to understand that backing up is a process. As long as new data is being created and changes are being made, backups will need to be updated regularly. Progeny provides an Automated Backup function for scheduling automatic backups of a Progeny database on a regular basis. This function allows for the backing up of a database even while the application is running.

This chapter covers the following topics:

- "Scheduling an Automated Database Backup" on page 193.

The Automated Backup function is available only to the Progeny administrator.

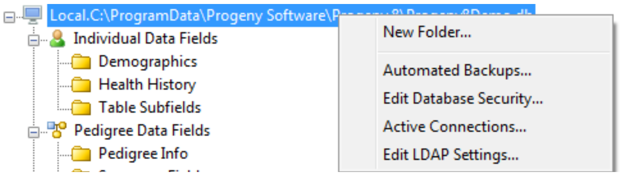
Scheduling an Automated Database Backup

You use the Automated Backup function to schedule the automatic backup of a Progeny database on a regular basis. When you are scheduling a backup, you must specify the name of the backup, the directory folder for the backup, and the backup frequency. When you are specifying the backup frequency, you can schedule the frequency to run on specific days, or to run during a specific timeframe. Also, because you must specify a directory folder for a backup, this means that a new backup to the folder always overwrites an existing backup in the folder, so good practice dictates that you archive your backups on a regular basis.

To schedule an automated database backup

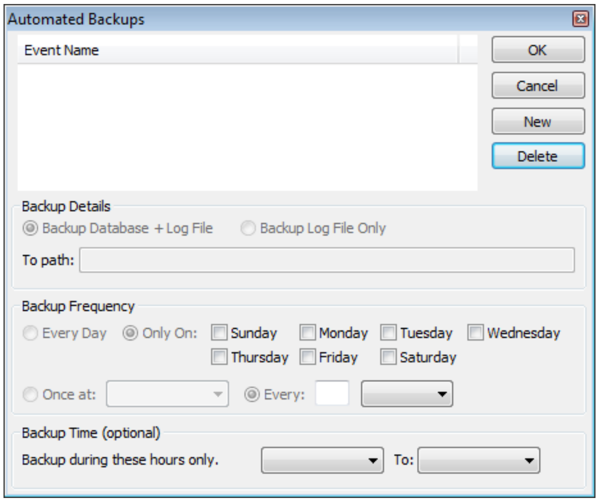
1. Log in to the database for which you are scheduling the backup.
2. On any open window, right-click on the database path, and on the context menu that opens, click Automated Backups.

Figure 10-1: Database context menu



The Automated Backups dialog box opens.

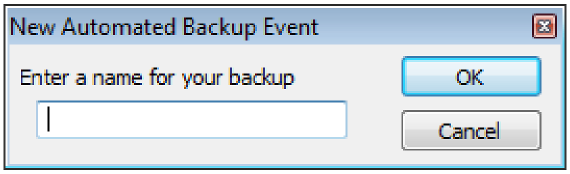
Figure 10-2: Automated Backups dialog box



3. Click New.

   The New Automated Backup Event dialog box opens.

Figure 10-3: New Automated Backup Event dialog box



4. Enter a name for the backup, and then click OK.

   The dialog box closes, and you return to the Automated Backups dialog box. The Backup Details and Backup Frequency Options are enabled.

5. Under Backup Details, do the following:

   - Select one of the following: Back up Database + Log File or Backup Log File Only.

The log file is a transactional log file. You can select this option only if you are certain that log file copy will be kept pristine and in a secure location. Also note that although you can rebuild a database from a transactional log file, the older the file, the more out of date your database will be after rebuilding it, so if you elect to save only the log file, it should not be a one time option.

   - Enter the full directory path, including the folder name, for the backup location.

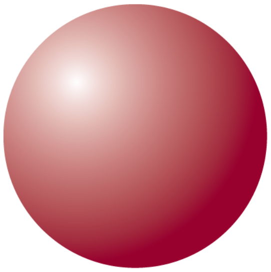
If you are backing up a Progeny database that resides locally, then ideally, this path should be to a network drive, but it can be a directory on your hard drive. If you are backing up a Progeny database that resides on a server, then the backup folder must be mapped to the location on the server where the database resides.

6. Under Backup Frequency, do one of the following:

   - To schedule the frequency based on specific days, select Every Day or Only On (make sure to select a day if you select Only On), and then select a time for Once at.
   - To schedule the frequency based on specific time intervals, select Every, and then enter a specific time interval (hours or minutes), for example, every 1 hour. Optionally, under Backup Time, set the specific timeframe during which these interval backups can run, for example, every 1 hour between 10:00 pm to midnight.

7. Click OK.

Section 2



Progeny Clinical

Section Contents

Chapter 1

Progeny Clinical Terms and Conventions

Progeny Clinical is pedigree and clinical data management software that is ideal for family-based studies. The application provides the ability to draw and manage pedigrees and associated data and the ability to manage and track individuals and their associated data, whether the individual is a member of a pedigree or is a singlet (not a member of a pedigree). Progeny Clinical uses conventions in both its terminology and its output to ensure consistency and accuracy when you are manipulating and analyzing clinical data.

This chapter covers the following topics:

- “Progeny Clinical Terms and Conventions” on page 199.

Progeny Clinical Terms and Conventions

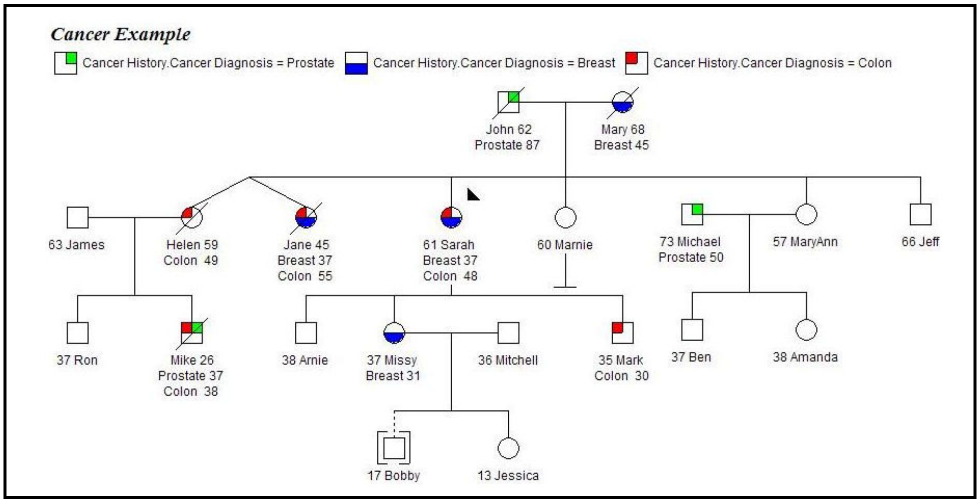
Progeny Clinical provides the ability to draw and manage pedigrees and associated data and the ability to manage and track individuals and their associated data. Progeny Clinical uses conventions in both its terminology and its output to ensure consistency and accuracy when you are manipulating and analyzing clinical data.

- Individual—An *individual* is a single, distinct entity for which data is collected according to an approved protocol. The data can be obtained in a variety of methods, including, but not limited to physically manipulating the individual, taking samples from the individual, interviewing the individual, and so on. An individual can be a *singlet*, which means that the individual is *not* a member of a pedigree, or the individual can be a member of a pedigree. A square icon indicates a male individual, a circle icon indicates a female individual, and a diamond icon indicates an individual of unknown/undetermined gender. Variations of these icons differentiate between singlets and individuals who are a member of a pedigree.

Figure 1-1: Individual icons

- Pedigree—A *pedigree*, also known as a *genogram*, is a diagram that depicts individuals who are related by blood or another factor. Different icons represent different types of individuals. For example, a square icon indicates a male individual, a circle icon indicates a female individual, and a diamond icon indicates an individual of unknown/undetermined gender. Symbols are applied to icons to graphically represent data about the individual, such as individuals with a cancer diagnosis that equals Breast. A legend identifies each symbol. The lines connecting individuals identify the relationship between two individuals, such as marital status. The *icon subtext*, which is the text that is displayed above or below an individual icon on a pedigree, is specific for the individual. The following icon indicates a pedigree: .

Figure 1-2: Example of a Cancer History pedigree



- Sample—A *sample* is a part that is representative of a whole or a set of elements that is drawn from and analyzed to estimate the characteristics of a population. A sample can be an unassociated sample, or it can be associated with an individual. The following icon indicates a sample: 🧪.

Chapter 2
Managing Data Folders

Data folders are the folders that house the data for individuals, pedigrees, samples, and containers. One of the key features of Progeny Clinical is the use of template data folders to organize individuals, pedigrees, and samples. When you create a new individual or pedigree, you must set specific options for the individual or pedigree—the datasheet layout, the pedigree datasheet layout, the icon subtext, and so on, and you must assign the individual or a pedigree to a data folder. Similarly, when you create a new sample, you must specify the sample datasheet layout. If the data folder is a template data folder, then these options are set at the folder level. Every new individual, pedigree, or sample that you assign to the data folder is assigned with exactly the same template folder options, which prevents you from having to assign the options each time that you create an individual, pedigree, or sample. Because the first step in creating a new individual, pedigree, or sample is the selection of its data folder, the creation and management of data folders must be discussed even before the creation of a new individual, pedigree, or sample.

This chapter covers the following topics:

- "Adding Individual and Pedigree Data Folders" on page 203.
- "Adding Sample Data Folders" on page 206.
- "Copying Template Options Between Data Folders or Items" on page 208.
- "Modifying and Deleting Data Folders" on page 217.

Adding Individual and Pedigree Data Folders

When you add a new individual or pedigree data folder, you have the option of adding the folder as a *template* folder or as a non-template folder. A *template* data folder replicates the same properties (the datasheet format, the pedigree datasheet format, the icon subtext, and so on) for all the individuals or pedigrees that are contained in the data folder. Every new individual or pedigree that you add to the data folder is added with exactly the same template folder options, which prevents you from having to assign the options each time that you create an individual or pedigree. If you add a *non-template* data folder, which is a folder without a single template option selected, then you must assign these options each and every time that you add an individual or pedigree to the data folder.

When you add a new individual data folder, an identically named pedigree data folder with the same template options is added. Likewise, when you add a new pedigree data folder, an identically named individual data folder with the same template options is added. This action allows you to include singlets with individuals who are members of a pedigree in the same folder and it also allows you to view and work with individuals who are members of a pedigree separately from the pedigree. In addition, individual data folders and pedigree data folders are linked. Any changes that you make to the options for a data folder on the Individuals window are also made to the same folder on the Pedigrees window and vise-versa.

Progeny Software highly recommends that you create template folders whenever possible; however, in the rare event that you want to use the Copy feature to carry out "one-off" copies of individuals, pedigrees, or samples in a data folder, you can create a non-template folder. See "Copying Template Options Between Data Folders or Items" on page 208.

To add an individual or pedigree data folder

The following procedure details the creation of an individual folder however, by analogy, you can follow this procedure to create a pedigree folder.

1. On the Progeny main window navigation bar, click the Individuals button to open the Individuals window.
2. Select the location for the new folder.

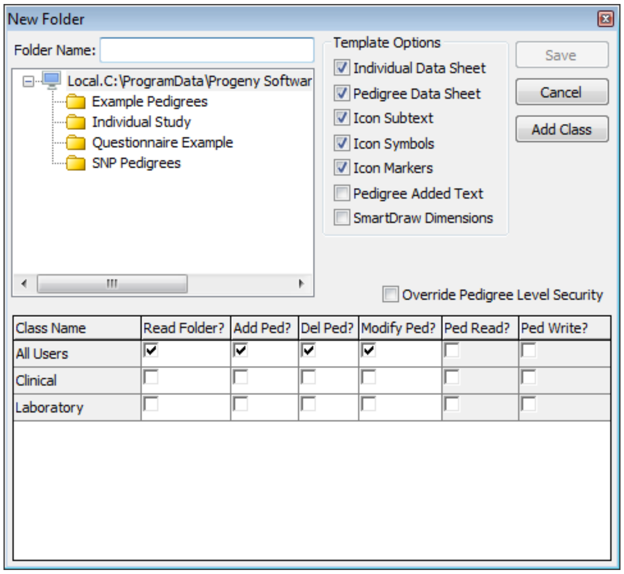
   The folder can be stored at the root level (which is the database that you are currently logged in to), or it can be a sub-folder of another folder.

If needed, you can simply drag a folder to move it to a different location.

3. On the Individuals window toolbar, click the New Folder button New Folder.

   The New Folder dialog box opens. The dialog box contains a list of options that you can set for a template folder. In addition, if you are the Progeny administrator, the dialog box contains options for setting folder security.

Figure 2-1: New Folder dialog box



Folder Name:

Template Options
☑ Individual Data Sheet
☑ Pedigree Data Sheet
☑ Icon Subtext
☑ Icon Symbols
☑ Icon Markers
☐ Pedigree Added Text
☐ SmartDraw Dimensions

☐ Override Pedigree Level Security

Class Name	Read Folder?	Add Ped?	Del Ped?	Modify Ped?	Ped Read?	Ped Write?
All Users	☑	☑	☑	☑	☐	☐
Clinical	☐	☐	☐	☐	☐	☐
Laboratory	☐	☐	☐	☐	☐	☐

4. In the Folder Name field, enter a name for the new data folder.

5. Do one of the following:

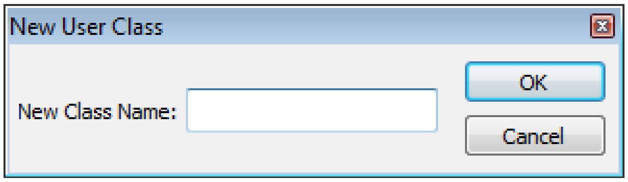
   - If you are creating a non-template folder, then clear all the template options on the New Folder dialog box.
   - If you are creating a template folder, then specify the pertinent template options for the data folder.

Option	Description
Individual datasheet	Selected by default. The same individual datasheet format is used for entering and storing individual data for the individuals who are in the folder.
Pedigree datasheet	Selected by default. The same pedigree datasheet format is used for entering and storing pedigree data for the pedigrees that are in the folder.
Icon Subtext	Selected by default. The same *icon subtext*, which is the text that is displayed above or below an icon on a pedigree, is displayed for every icon on all pedigrees that are in the folder. See “Configuring Pedigree Icons” on page 277.
Icon Symbols	Selected by default. The same *icon symbols*, which are symbols that graphically represent data about on an individual on a pedigree, are used for all pedigrees in the folder. See “Configuring Pedigree Icons” on page 277.

Option	Description
Icon Markers	Selected by default. The same *icon markers*, which are the color codes that are used to identify genotypes (marker values) in pedigrees, are used for all pedigrees in the folder. See "Configuring Pedigree Icons" on page 277.. **Note:** This feature is a Progeny Lab feature and requires the Marker module to be used in Progeny Clinical.
Pedigree Added Text	The same text (header, footer, and/or date) is displayed on the pedigrees that are in the folder. See "Pedigree Properties" on page 271.
SmartDraw Dimensions	All the pedigrees that are in the folder use the same drawing dimensions such as spacing, icon size, and so on. See "Pedigree Properties" on page 271.

6. If you are the Progeny administrator, then do one or more of the following to set the security for the data folder; otherwise, continue to Step 7.
   - Modify the security settings for All Users or for the different classes of users.
     - Read Folder?—Open and view the contents of the data folder.
     - Add Ped?—Add pedigrees to the data folder.
     - Del Ped?—Delete pedigrees from the data folder.
     - Modify Ped?—Modify pedigrees in the data folder.
   - Click Add Class to open the New User Class dialog box to create a new user class, and then set the folder security for the new class.

Figure 2-2: New User Class dialog box



   - If you have assigned security to one more pedigrees in the folder, and you want to override the security settings for these pedigrees based on the security settings at the folder level, click Override Pedigree Level Security, and then set the appropriate pedigree level security for the different classes of users.
     - Ped Read?—View the data in the pedigree.
     - Ped Write?—Write data to the pedigree.
7. Click Save.

   A message opens indicating the settings for the folder were successfully changed.
8. Click OK to close the message and return to the Individuals window.

Adding Sample Data Folders

When you add a new sample data folder, you have the option of making the folder a template folder. If you make the folder a template folder, then all samples that are added to the folder use the same sample datasheet for entering and storing data. If you do not make the folder a template folder, then each time you add a sample to the folder, you must create a new datasheet for the sample.

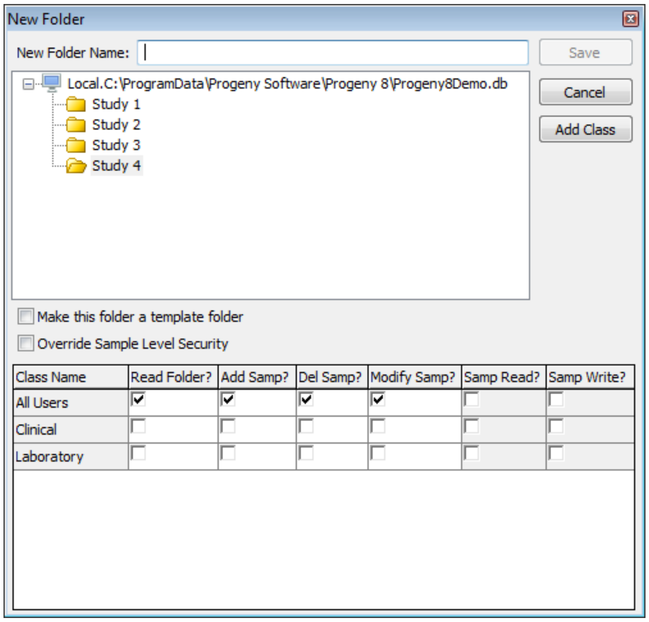
To add a sample data folder

1. On the Progeny main window navigation bar, click the Samples button to open the Samples window.

2. On the Samples window toolbar, click the New Folder button.

   The New Folder dialog box opens. The dialog box contains an option for making a sample folder a template folder. In addition, if you are the Progeny administrator, the dialog box contains options for setting folder security.

Figure 2-3: New Folder dialog box



New Folder

New Folder Name:

Local.C:\ProgramData\Progeny Software\Progeny 8\Progeny8Demo.db
- Study 1
- Study 2
- Study 3
- Study 4

☐ Make this folder a template folder

☐ Override Sample Level Security

Class Name	Read Folder?	Add Samp?	Del Samp?	Modify Samp?	Samp Read?	Samp Write?
All Users	☑	☑	☑	☑	☐	☐
Clinical	☐	☐	☐	☐	☐	☐
Laboratory	☐	☐	☐	☐	☐	☐

3. In the New Folder Name field, enter a name for the new data folder.

4. Optionally, to make this folder a template folder, select Make this folder a template folder.

If you make the folder a template folder, then all samples that are added to the folder use the same sample datasheet for entering and storing data; otherwise, each time you add a sample to the folder, you must create a new datasheet for the sample.

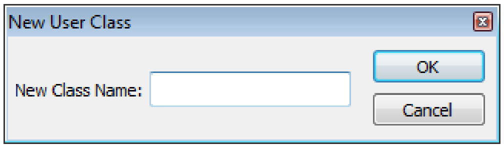
5. Select the location for the new folder.

   The folder can be stored at the root level (which is the database that you are currently logged in to), or it can be a sub-folder of another folder.

If needed, you can simply drag a folder to move it to a different location.

6. If you are the Progeny administrator, then do one or more of the following to set the security for the data folder; otherwise, continue to Step 7.
   - Modify the security settings for All Users or for the different classes of users.
     - Read Folder?—Open and view the contents of the data folder.
     - Add Samp?—Add samples to the data folder.
     - Del Samp?—Delete samples from the data folder.
     - Modify Samp?—Modify samples in the data folder.
   - Click Add Class to open the New User Class dialog box to create a new user class, and then set the folder security for the new class.

Figure 2-4: New User Class dialog box



   - If you have assigned security to one more samples in the folder, and you want to override the security settings for these samples based on the security settings at the folder level, click Override Sample Level Security, and then set the appropriate sample level security for the different classes of users.
     - Samp Read?—View the sample data.
     - Ped Write?—Write data to the sample.
7. Click Save.

   A message opens indicating the settings for the folder were successfully changed.
8. Click OK to close the message and return to the Samples window.

Copying Template Options Between Data Folders or Items

You typically use the Copy feature to apply the same template options to all items (individuals, pedigrees, or samples) that are in the same data folder. The *source* item is the item (individual, pedigree, or sample) *from* which you are copying the template options. The *destination folder* is the data folder *to* which you copying the template options. The destination folder must contain at least one item (individual, pedigree, or sample) and at least one template option must be selected for the folder for the template options to be copied.

Although less common, you can also use the Copy feature to copy template options to a single individual, pedigree, or sample that is in a non-template data folder without affecting the options that are set for the other items in the folder. If you use the Copy feature to copy template options to a single individual, pedigree, or sample that is in a template data folder, then the template options are applied to all items in the folder.

To copy template options to an individual or pedigree data folder

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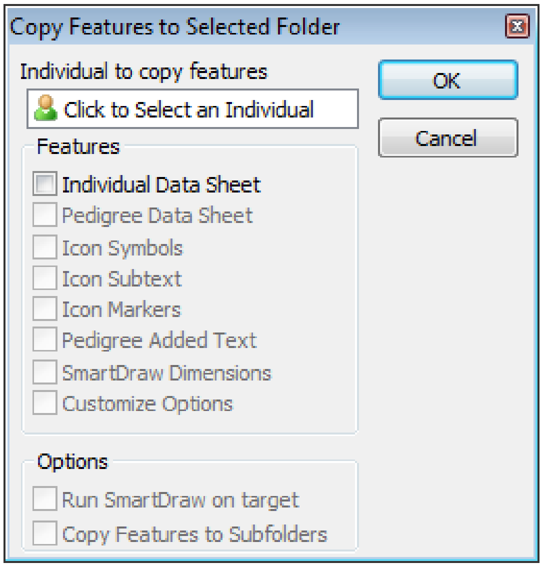
The following procedure details how to copy template options to an individual data folder, but by analogy, you can follow this procedure to copy template options to pedigree data folder.

1. On the Progeny main window navigation bar, click the Individuals button to open the Individuals window.
2. Right-click on the destination folder (which is the individual data folder *to* which you are copying the template options), and on the context menu that opens, click Copy Features to Folder.

Remember, the destination folder must contain at least one item (individual or pedigree) for the template options to be copied.

The Copy Features to Selected folder dialog box opens. See Figure 2-5 on page 209.

Figure 2-5: Copy Features to Selected Folder dialog box



Copy Features to Selected Folder

Individual to copy features

Click to Select an Individual

Features

☐ Individual Data Sheet
☐ Pedigree Data Sheet
☐ Icon Symbols
☐ Icon Subtext
☐ Icon Markers
☐ Pedigree Added Text
☐ SmartDraw Dimensions
☐ Customize Options

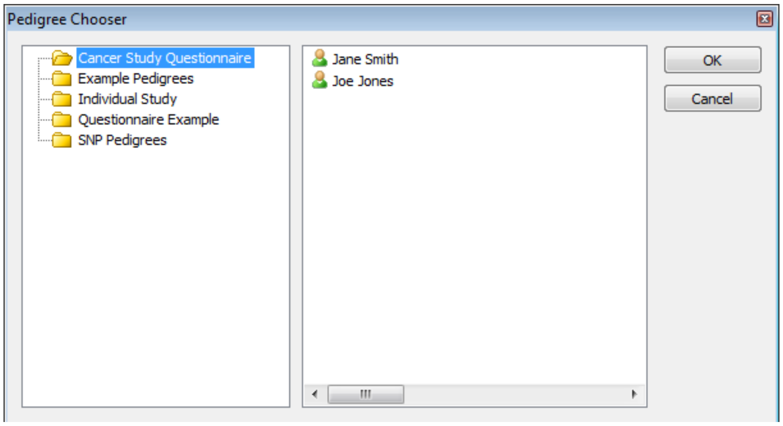
Options

☐ Run SmartDraw on target
☐ Copy Features to Subfolders

3. Click in the field labeled “Click to Select an Individual.”

   The Pedigree Chooser dialog box opens.

Figure 2-6: Pedigree Chooser



Pedigree Chooser

- Cancer Study Questionnaire
- Example Pedigrees
- Individual Study
- Questionnaire Example
- SNP Pedigrees

- Jane Smith
- Joe Jones

4. In the Pedigree Chooser dialog box, select the source individual from whom you are copying the template folder options, and then click OK.

   The Pedigree Chooser dialog box closes. You return to the Copy Features to Selected folder dialog box.

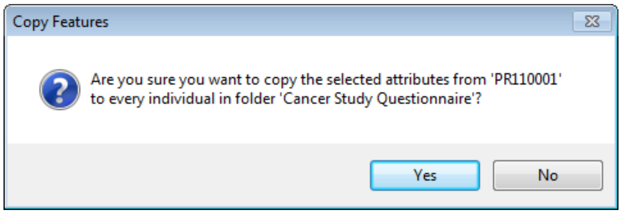
5. Select the source template options that are to be copied.

Option	Description
Features	
Individual datasheet	Available for both individual data folders and pedigree data folders. The same individual datasheet format is used for entering and storing individual data for the individuals who are in the folder.
Pedigree datasheet	Available only for pedigree data folders. The same pedigree datasheet format is used for entering and storing pedigree data for the pedigrees that are in the folder.
Icon Subtext	Available only for pedigree data folders. The same *icon subtext*, which is the text that is displayed above or below an icon on a pedigree, is displayed for every icon on all pedigrees that are in the folder. See "Configuring Pedigree Icons" on page 277.
Icon Symbols	Available only for pedigree data folders. The same *icon symbols,* which are symbols that graphically represent data about on an individual on a pedigree, are used for all pedigrees in the folder. See "Configuring Pedigree Icons" on page 277.
Icon Markers	Available only for pedigree data folders. The same i*con markers*, which are the color codes that are used to identify the genotypes (marker values) in pedigrees, are used for all pedigrees in the folder. See "Configuring Pedigree Icons" on page 277. **Note:** This feature is a Progeny Lab feature and requires the Marker module to be used in Progeny Clinical.
Pedigree Added Text	Available only for pedigree data folders. The same text (header, footer, and/or date) is displayed on the pedigrees that are in the folder. See "Pedigree Properties" on page 271.
SmartDraw Dimensions	Available only for pedigree data folders. All the pedigrees that are in the folder use the same drawing dimensions such as spacing, icon size, and so on. See "Pedigree Properties" on page 271.
Customize Options	Available only for pedigree data folders. All the pedigrees that are in the folder use the same additional custom drawing options that are defined in the Properties dialog box for the pedigree, which includes such things as Show Grid, Snap to Grid, Pedigree Scale Size, and so on. See "Pedigree Properties" on page 271.
Options	
Run SmartDraw on target	Available only for pedigree data folders. Select this option to run SmartDraw on all the pedigrees in the selected destination folder.
Copy Features to SubFolders	Available for both individual and pedigree data folders. Select this option to copy the selected template options not only to the selected destination folder, but also, to all its subfolders.

6. Click OK.

   A Copy Features message opens, asking you if you are sure that you want to copy the selected attributes from the individual that you selected in Step 4 to every individual in the destination folder that you selected in Step 2.

Figure 2-7: Copy Features message



Copy Features

Are you sure you want to copy the selected attributes from 'PR110001' to every individual in folder 'Cancer Study Questionnaire'?

7. Click Yes.

   A Copy Progress dialog box opens, indicating the status of the copy progress.

8. After the copy process is completed, click Close in the Copy Progress dialog box.

   The Copy Progress and Copy Features to Selected folder dialog boxes close. You return to the Individuals window. The selected template options are copied at the data folder level. All individuals that you add to the folder will now use the same datasheet format.

To copy a sample datasheet format to a sample folder

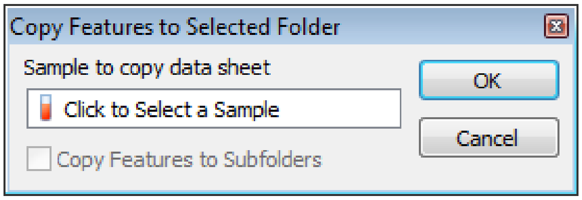
1. On the Progeny main window navigation bar, click the Samples button to open the Samples window.

2. Right-click on the destination folder (which is the sample data folder *to* which you are copying the datasheet format), and on the context menu that opens, click Copy Features to Folder.

Remember, the destination folder must contain at least one sample for the datasheet format to be copied.

The Copy Features to Selected Folder dialog box opens.

Figure 2-8: Copy Features to Samples dialog box



Copy Features to Selected Folder

Sample to copy data sheet

Click to Select a Sample

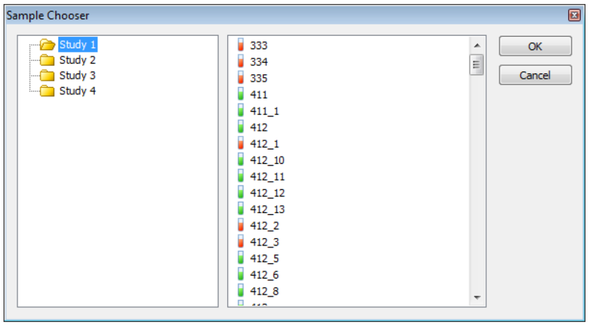
☐ Copy Features to Subfolders

3. Optionally, to copy the sample datasheet format not only to the selected folder, but also, to all of its subfolders, select Copy Features to Subfolders.

4. Click in the field labeled “Click to Select a Sample.”

   The Sample Chooser dialog box opens. This dialog box lists all the available sample data folders and the samples in them.

Figure 2-9: Sample Chooser dialog box



5. In the Sample Chooser dialog box, select the source sample from which you are copying the sample datasheet format, and then click OK.

   The Sample Chooser dialog box closes. The name of the sample that you selected is displayed in the Copy Features to Selected Folders dialog box.

6. Click OK in the Copy Features to Selected Samples dialog box.

   A message opens asking you if you are sure that you want to copy the datasheet format from the sample that you selected in Step 5 to the folder that you selected in Step 2.

7. Click Yes.

   The message closes. The sample datasheet format is copied at the sample folder level. All samples that you add to the folder will now use the same datasheet format.

To copy template options to individuals or pedigrees

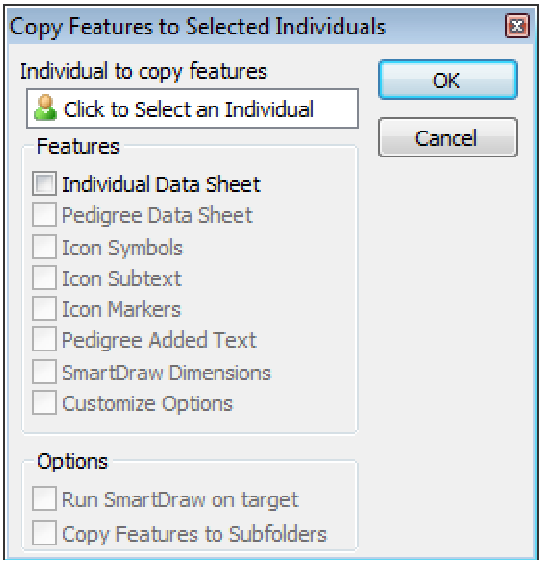
The following procedure describes how to copy template features to a single individual that is in a non-template folder, but by analogy, you can follow this procedure to copy template features to a single pedigree that is in a non-template folder.

1. On the Progeny main window navigation bar, click the Individuals button to open the Individuals window.

2. Do one of the following:
   - If you are copying template options to a single destination individual, (which is the individual *to* which you are copying the template options), then right-click on the individual and on the context menu that opens, click Copy Features to Individual(s).
   - If you are copying template options to multiple destination individuals, CTRL-click to select these multiple individuals, and then right-click and on the context menu that opens, click Copy Features to Individual(s).

   The Copy Features to Selected Individual(s) dialog box opens.

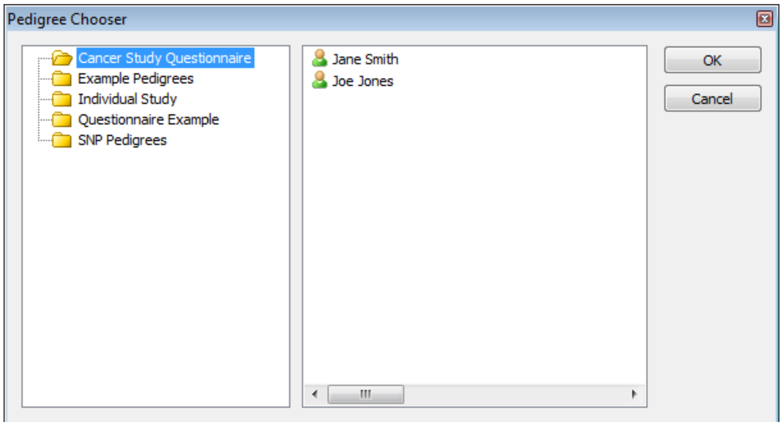
Figure 2-10: Copy Features to Selected Individuals dialog box



3. Click in the field labeled “Click to Select an Individual.”

   The Pedigree Chooser dialog box opens.

Figure 2-11: Pedigree Chooser



4. In the Pedigree Chooser dialog box, select the source individual from whom you are copying the template folder options, and then click OK.

   The Pedigree Chooser dialog box closes. You return to the Copy Features to Selected folder dialog box.

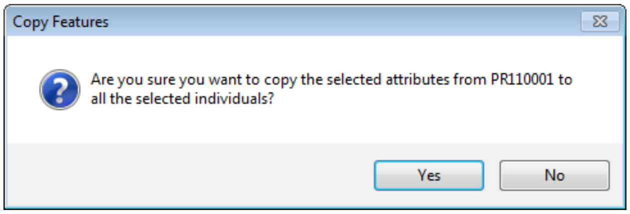
5. Select the source template options that are to be copied.

Option	Description
Features	
Individual datasheet	Available for both individual data folders and pedigree data folders. The same individual datasheet format is used for entering and storing individual data for the individuals who are in the folder.
Pedigree datasheet	Available only for pedigree data folders. The same pedigree datasheet format is used for entering and storing pedigree data for the pedigrees that are in the folder.
Icon Subtext	Available only for pedigree data folders. The same *icon subtext*, which is the text that is displayed above or below an icon on a pedigree, is displayed for every icon on all pedigrees that are in the folder. See "Configuring Pedigree Icons" on page 277.
Icon Symbols	Available only for pedigree data folders. The same *icon symbols,* which are symbols that graphically represent data about on an individual on a pedigree, are used for all pedigrees in the folder. See "Configuring Pedigree Icons" on page 277.
Icon Markers	Available only for pedigree data folders. The same *icon markers*, which are the color codes that are used to identify the genotypes (marker values) in pedigrees, are used for all pedigrees in the folder. See "Configuring Pedigree Icons" on page 277. **Note:** This feature is a Progeny Lab feature and requires the Marker module to be used in Progeny Clinical.
Pedigree Added Text	Available only for pedigree data folders. The same text (header, footer, and/or date) is displayed on the pedigrees that are in the folder. See "Pedigree Properties" on page 271.
SmartDraw Dimensions	Available only for pedigree data folders. All the pedigrees that are in the folder use the same drawing dimensions such as spacing, icon size, and so on. See "Pedigree Properties" on page 271.
Customize Options	Available only for pedigree data folders. All the pedigrees that are in the folder use the same additional custom drawing options that are defined in the Properties dialog box for the pedigree, which includes such things as Show Grid, Snap to Grid, Pedigree Scale Size, and so on. See "Pedigree Properties" on page 271.
Options	
Run SmartDraw on target	Available only for pedigree data folders. Select this option to run SmartDraw on all the pedigrees in the selected destination folder.
Copy Features to SubFolders	N/A.

6. Click OK.

   A Copy Features message opens, asking you if you are sure that you want to copy the selected attributes from the individual that you selected in Step 4 to all the individuals that you selected in Step 2.

Figure 2-12: Copy Features message



Are you sure you want to copy the selected attributes from PR110001 to all the selected individuals?

7. Click Yes.

   A Copy Progress dialog box opens, indicating the status of the copy progress.

8. After the copy process is completed, click Close in the Copy Progress dialog box.

   The Copy Progress and Copy Features to Selected folder dialog boxes close. You return to the Individuals window. The selected template options are copied at the individual level.

To copy a sample datasheet format to samples

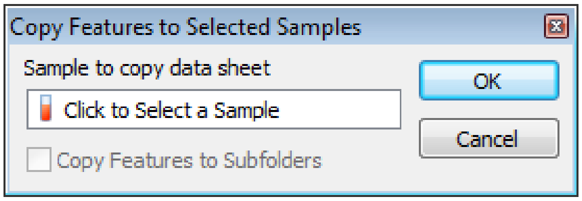
1. On the Progeny main window navigation bar, click the Samples button to open the Samples window.

2. Do one of the following:

   - If you are copying a datasheet format to a single destination sample, (which is the sample *to* which you are copying the format), then right-click on the sample and on the context menu that opens, click Copy Features to Sample(s).
   - If you are copying a datasheet format to multiple destination samples, CTRL-click to select these multiple samples, and then right-click and on the context menu that opens, click Copy Features to Sample(s).

   The Copy Features to Selected Samples dialog box opens.

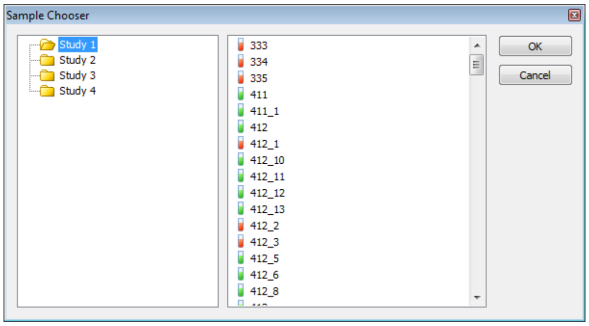
Figure 2-13: Copy Features to Selected Samples dialog box



3. Click in the field labeled “Click to Select a Sample.”

   The Sample Chooser dialog box opens. This dialog box lists all the available sample data folders and the samples in them.

Figure 2-14: Sample Chooser dialog box



4. In the Sample Chooser dialog box, select the source sample *from* which you are copying the sample datasheet format, and then click OK.

   The Sample Chooser dialog box closes. The name of the sample that you selected is displayed in the Copy Features to Samples dialog box.

5. Click OK in the Copy Features to Selected Samples dialog box.

   A message opens asking you if you are sure that you want to copy the datasheet format from the sample that you selected in Step 4 to the samples that you selected in Step 2.

6. Click Yes.

   The message closes. The sample datasheet format is copied at the sample level.

Modifying and Deleting Data Folders

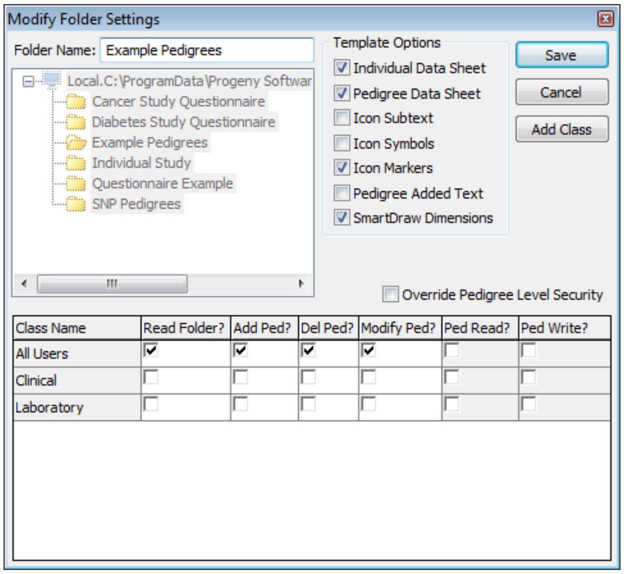
If you are the Progeny administrator, or if your administrator has set certain security levels for your user account, after you set the template options for a data folder, you can always modify the options. Likewise, after you create a non-template folder, you can always modify the folder and set template options for the folder. If you modify the template options for a data folder, then the modified options are applied only to new items (individuals, pedigrees, or samples) that you add to the folder. The modified options do not override the current template options for any existing items in the folder. In addition, if you are the Progeny administrator, you can modify the security levels for a data folder and you can delete a data folder. If you are not the Progeny administrator, then the security levels that your administrator has set for user account determine whether you can delete a data folder.

To modify a data folder

1. Right-click on the data folder that you are modifying, and on the context menu that opens, click Edit Folder.

   The Modify Folder Settings dialog box opens.

Figure 2-15: Modify Folder Settings dialog box for an individual or a pedigree



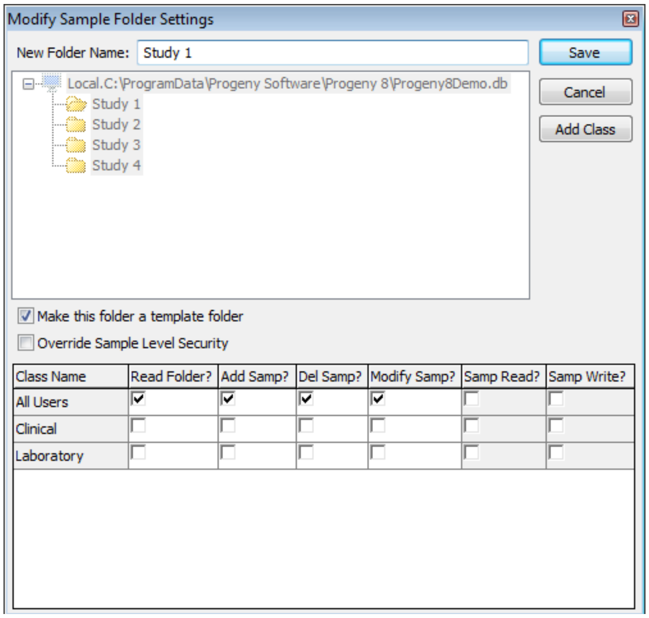
Folder Name: Example Pedigrees

Template Options
☑ Individual Data Sheet
☑ Pedigree Data Sheet
☐ Icon Subtext
☐ Icon Symbols
☑ Icon Markers
☐ Pedigree Added Text
☑ SmartDraw Dimensions

☐ Override Pedigree Level Security

Class Name	Read Folder?	Add Ped?	Del Ped?	Modify Ped?	Ped Read?	Ped Write?
All Users	☑	☑	☑	☑	☐	☐
Clinical	☐	☐	☐	☐	☐	☐
Laboratory	☐	☐	☐	☐	☐	☐

Figure 2-16: Modify Sample Folder Settings dialog box



New Folder Name: Study 1

☑ Make this folder a template folder

☐ Override Sample Level Security

Class Name	Read Folder?	Add Samp?	Del Samp?	Modify Samp?	Samp Read?	Samp Write?
All Users	☑	☑	☑	☑	☐	☐
Clinical	☐	☐	☐	☐	☐	☐
Laboratory	☐	☐	☐	☐	☐	☐

2. Modify the template options for the folder as needed.
3. Do one of the following:
    - If you are the Progeny administrator, then optionally, modify the security for the data folder as needed, and then click Save.
    - If you are not the Progeny administrator, then click Save.

    A message opens indicating the settings for the folder were successfully changed.
4. Click OK to close the message and return to the item (Individuals, Pedigrees, or Samples) window.

To delete a data folder

When you delete a data folder, all the data that is in the folder (individuals, pedigrees, or samples) is deleted as well as any subfolders and all the data that is in the subfolders.

1. Right-click on the data folder that you are deleting, and on the context menu that opens, click Delete Folder.

   A Confirm Delete Folder message opens that asks you to confirm the deletion of the data folder, its data, and any subfolders and all the data in the subfolders.

2. Click OK to confirm the deletion.

   The message closes and you return to the item (Individuals, Pedigrees, or Samples) window.

Chapter 3
Managing Individuals

An *individual* is a single, distinct entity for which data is collected according to an approved protocol. Managing individuals in Progeny Clinical consists of creating new individuals, creating individual shortcuts, creating datasheets for individuals, modifying an individual, creating individual shortcuts, copying, moving, and deleting individuals, moving individuals to a pedigree, and importing individual data.

This chapter covers the following topics:

- "Adding a New Individual" on page 223.
- "Creating a New Individual Datasheet" on page 225.
- "Modifying an Individual" on page 227.
- "Creating Individual Shortcuts" on page 229.
- "Copying and Moving Individuals" on page 231.
- "Deleting an Individual" on page 233.
- "Moving an Individual to a Pedigree" on page 234.

For detailed information about importing individual data, see Chapter B, "Importing Clinical Data," on page 559.

Adding a New Individual

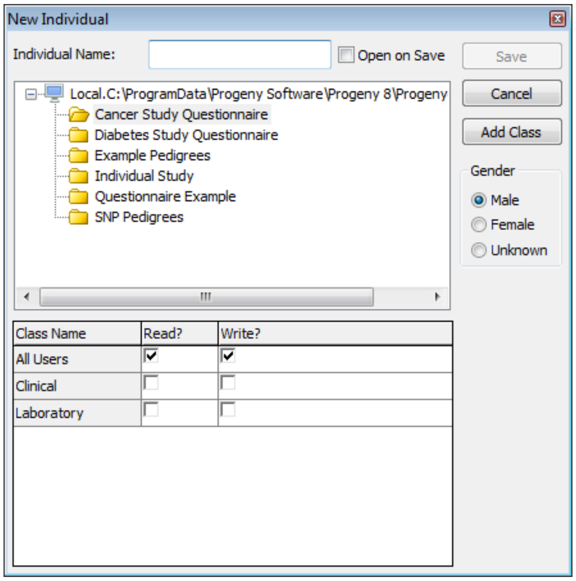
When you first add an individual, the individual is not contained in a pedigree. An individual who is not contained in a pedigree is referred to as a singlet. After you create a singlet, you can move the single to an existing pedigree or to a new pedigree.

To add a new individual

1. On the Progeny main window navigation bar, click the Individuals button to open the Individuals window.
2. On the Individuals window, click the New Individual button New Indiv.

   The New Individual dialog box opens.

Figure 3-1: New Individual dialog box



Individual Name: ☐ Open on Save

Local.C:\ProgramData\Progeny Software\Progeny 8\Progeny
- Cancer Study Questionnaire
- Diabetes Study Questionnaire
- Example Pedigrees
- Individual Study
- Questionnaire Example
- SNP Pedigrees

Gender
● Male
○ Female
○ Unknown

Class Name	Read?	Write?
All Users	☑	☑
Clinical	☐	☐
Laboratory	☐	☐

3. Enter the name for the new individual.
4. Select the data folder to which the individual is being added.
5. Select the gender for the individual.

The Individual Name field and Gender field are system fields. See "Individual System Fields" on page 553.

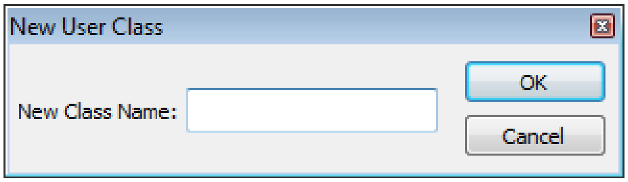
6. Optionally, select Open on Save.

   If the Individual Datasheet template option has been selected for the folder to which you assigned the individual and a datasheet has been created for the folder, after you save the new individual, the formatted datasheet opens in Data Entry mode and you can immediately begin entering data for the individual. If no datasheet has been created for the folder, then a blank datasheet opens in Data Entry mode. You can click Form Design mode and design the datasheet format for the folder before you add any more individuals to the folder. See "Creating a New Individual Datasheet" on page 225.

7. If you are the Progeny administrator, then do one or more of the following to set the security for the individual; otherwise, continue to Step 8.

   - Modify the security settings for All Users or for the different classes of users.
     - Read?—View the data (name and data in the individual datasheet) for the individual.
     - Write?—Write data (change the name and enter data to an individual datasheet) to the individual.
   - Click Add Class to open the New User Class dialog box to create a new user class, and then set the individual security for the new class.

Figure 3-2: New User Class dialog box



8. Click Save.

   A message opens indicating the settings for the individual were successfully changed.

9. Click OK to close the message and return to the Individuals window.

Creating a New Individual Datasheet

You use an individual datasheet to enter and store data for an individual in a Progeny database. All the individuals who are assigned to an individual data folder can use the same datasheet format, or each individual in the folder can use a unique datasheet format. You can create and format an individual datasheet at the time that you add an individual to a data folder, or at a later date.

To create an individual datasheet

1. Create an individual data folder.

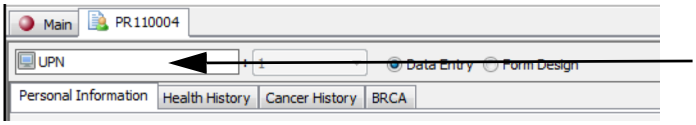
   If all the individuals who are assigned to the folder are to use the same individual datasheet format, make sure to select the Individual Datasheet template option; otherwise, clear it. See "Adding Individual and Pedigree Data Folders" on page 203.

2. Create a new individual (see "Adding a New Individual" on page 223) and add the individual to the data folder. When you are creating the individual, do one of the following:

   - To have a blank datasheet open immediately after you save the individual, select Open on Save. You can click Form Design on this blank datasheet and format the datasheet as needed. If the Individual Datasheet template option has been selected for the data folder, then all the individuals that you subsequently add to the folder will use the same datasheet format for entering and storing data; otherwise, you must format a datasheet for each individual that you add to the folder.
   - To add all individuals to the folder before you create and format the datasheet, do not select Open on Save for any individual whom you add to the folder. After you have added all of the needed individuals to the folder, you can simply double-click on any individual in the folder to open a blank datasheet and format the datasheet as needed. If the Individual Datasheet template option has been selected for the data folder, then all individuals who are currently added to the folder or that you subsequently add to the folder will use this same datasheet format for entering and storing data; otherwise, you must format a datasheet for each individual in the folder.

   See "Creating and Formatting Datasheets" on page 86 for detailed information about creating and formatting an individual datasheet.

When you are entering data into an individual datasheet, by default, the UPN for the individual is displayed above the datasheet. To make it easier for you to identify an individual when you are entering data for the individual, you can display a different field above the datasheet, for example, the Patient ID. To change the field, in Form Design mode, click the Fields button to open the Select Field dialog box, and drag the new field onto the UPN field in the upper left corner of the individual datasheet. The new field and its data are displayed instead of the UPN number.



Change the UPN field to a different field when entering data into an individual datasheet.

Modifying an Individual

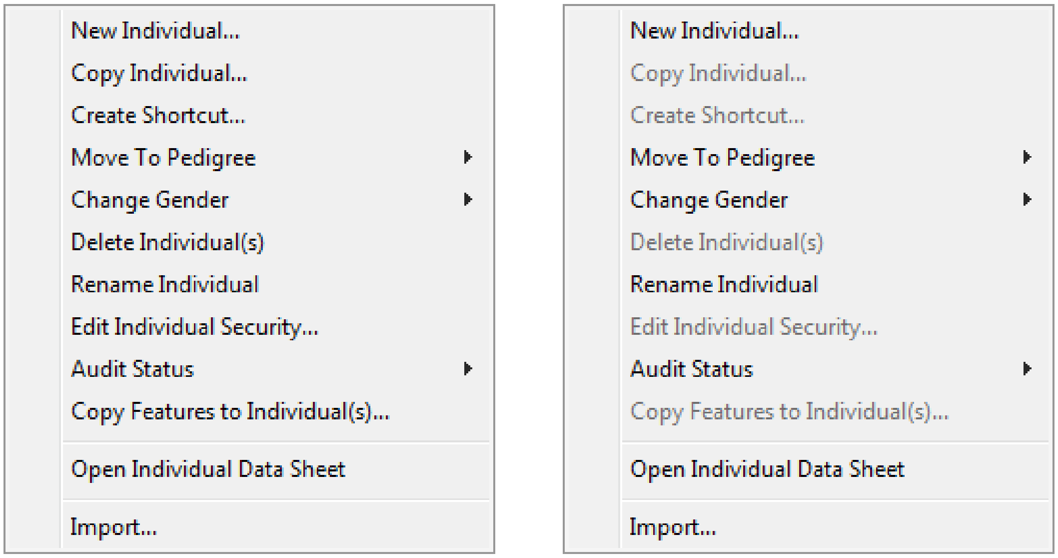
After an individual is created, you can modify the gender for the individual. If you are the Progeny administrator, or your administrator has set Write access for the individual for your user account, you can rename the individual. As the Progeny administrator, you can also modify the security levels for the individual.

To modify an individual

1. On the Progeny main window navigation bar, click the Individuals button to open the Individuals window.
2. Open the data folder that contains the individual that is being modified.
3. Select the individual that is being modified, and on the main menu, click Individuals, and then click the appropriate option.

   The options that are available from the Individuals menu depends on whether the individual is a single or a member of a pedigree.

Figure 3-3: Individuals menu for a singlet and a member of a pedigree



Individuals menu for a singlet.

Individuals menu for a member.

Option	Description
Change Gender	Available only for a singlet. Options are Male, Female, and Unknown. **Note:** You can change the gender of an individual that is included in a pedigree only from the pedigree drawing window. See "Working with Individuals in a Pedigree" on page 296.
Rename Individual	Automatically selects the individual name for modification.

Option	Description

Edit Individual Security	Available only for a singlet. Opens the Individual Security dialog box in which you can do one or both of the following:
	• Modify the security settings for All Users or for the different classes of users.
	  • Read?—View the data (name and data in the individual datasheet) for the individual.
	  • Write?—Write data (change the name and enter data to an individual datasheet) to the individual.
	• Click Add Class to open the New User Class dialog box to create a new user class, and then set the individual security for the new class.

Creating Individual Shortcuts

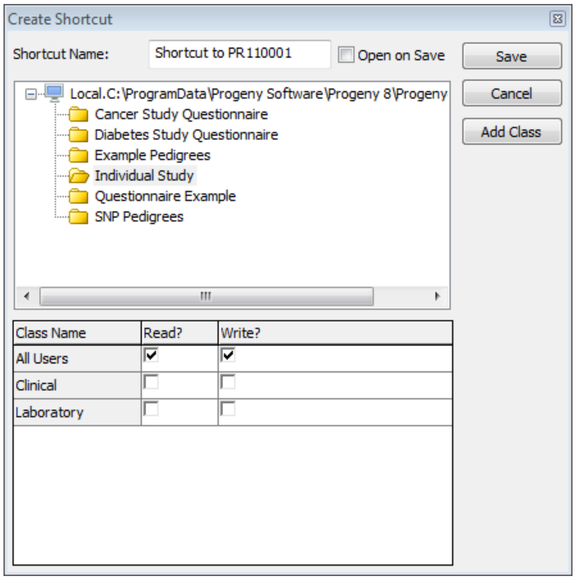
An *individual shortcut* is a link to that points to an individual in a Progeny database. You create an individual shortcut so that you can add an individual to multiple folders without having to copy or duplicate the individual. Although a shortcut points to the same original individual, each shortcut inherits the template options of the folder in which it is contained. For example, you might place an individual shortcut in an individual data folder named Colon Cancer, which has been assigned an individual datasheet that has been specifically designed for entering data that is related to colon cancer. You can also place this same individual shortcut in an individual data folder named Breast Cancer, which has been assigned an individual datasheet that has been specifically designed for entering data related that is related to breast cancer. You can create an individual shortcut only for a singlet.

To create an individual shortcut

1. On the Progeny main window navigation bar, click the Individuals button to open the Individuals window.
2. Open the data folder that contains the individual for which you are creating the shortcut.
3. Select the individual for which you are creating the shortcut, and on the main menu, click Individuals > Create Shortcut.

   The Create Shortcut dialog box opens. The Shortcut Name field is automatically populated with a default value, but you can change this value.

Figure 3-4: Create Shortcut dialog box



Create Shortcut

Shortcut Name: Shortcut to PR110001 ☐ Open on Save

Class Name	Read?	Write?
All Users	☑	☑
Clinical	☐	☐
Laboratory	☐	☐

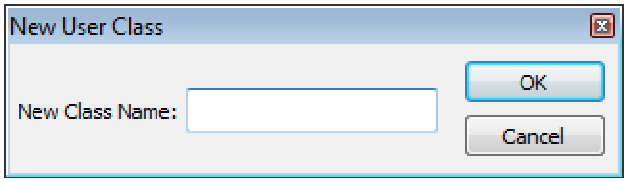
4. Select the folder in which to save the shortcut.

5. Optionally, do one or both of the following:
   - Change the shortcut name.
   - Select Open on Save.

     If the Individual Datasheet template option has been selected for the folder to which you assigned the shortcut and a datasheet has been created for the folder, after you save the shortcut, the formatted datasheet opens in Data Entry mode and you can immediately begin entering data for the individual. If no datasheet has been created for the shortcut, then a blank datasheet opens in Data Entry mode. You can click Form Design mode and design the datasheet format for the folder before you add any more shortcuts to the folder. See "Creating a New Individual Datasheet" on page 225.

6. If you are the Progeny administrator, then do one or more of the following to set the security for the individual; otherwise, continue to Step 7.
   - Modify the security settings for All Users or for the different classes of users.
     - Read?—View the data (name and data in the individual datasheet) for the individual.
     - Write?—Write data (change the name and enter data to an individual datasheet) to the individual.
   - Click Add Class to open the New User Class dialog box to create a new user class, and then set the individual security for the new class.

Figure 3-5: New User Class dialog box



7. Click Save.

   A message opens indicating the settings for the individual were successfully changed.

8. Click OK to close the message and return to the Individuals window.

Copying and Moving Individuals

You can copy an individual between data folders, and you can move an individual between data folders. For any of these actions, the following are important points to note:

- Copying an individual leaves the original individual in its original data folder while putting a copy (or duplicate) of the individual in the new destination folder. Any edits that you make to the copied individual are *not* reflected in the original individual.
- Moving an individual removes the individual from its original data folder and places the individual in a new destination folder. A copy of the original individual is not made.

To copy or move an individual

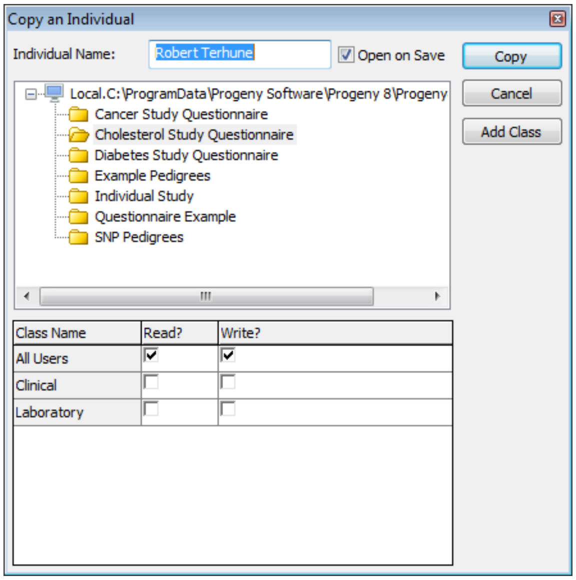
1. On the Progeny main window navigation bar, click the Individuals button 👤 to open the Individuals window.
2. Open the data folder that contains the individual that you are copying or moving, and then continue to one of the following:
    - "To copy an individual between data folders" below.
    - "To move an individual between data folders" on page 232.

To copy an individual between data folders

1. On the main menu, click Individuals > Copy Individual.

   The Copy an Individual dialog box opens.

Figure 3-6: Copy an Individual



Copy an Individual

Individual Name: Robert Terhune

☑ Open on Save

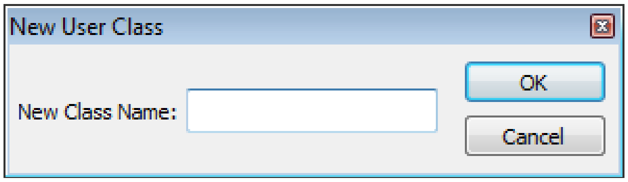
Local.C:\ProgramData\Progeny Software\Progeny 8\Progeny
- Cancer Study Questionnaire
- Cholesterol Study Questionnaire
- Diabetes Study Questionnaire
- Example Pedigrees
- Individual Study
- Questionnaire Example
- SNP Pedigrees

Class Name	Read?	Write?
All Users	☑	☑
Clinical	☐	☐
Laboratory	☐	☐

2. Select the data folder to which the individual is being copied.

3. Optionally, before you copy the individual to a data folder, clear or select the Open on Save option.
4. Optionally, if you are the Progeny administrator, then do one or more of the following to modify the security for the individual; otherwise, continue to Step 5.
   - Modify the security settings for All Users or for the different classes of users.
     - Read?—View the data (name and data in the individual datasheet) for the individual.
     - Write?—Write data (change the name and enter data to an individual datasheet) to the individual.
   - Click Add Class to open the New User Class dialog box to create a new user class, and then set the individual security for the new class.

Figure 3-7: New User Class dialog box



5. Click Copy.

   A message opens indicating that the individual was successfully copied.
6. Click OK to close the message and return to the Individuals window.

To move an individual between data folders

Simply drag the selected individual to the appropriate data folder.

Deleting an Individual

Deleting an individual is a permanent event. After you delete an individual, you cannot recover it from the database. You can delete only singlets from the Individuals window. You must delete individuals who are members of a pedigree from the Pedigree Drawing window. (See "To delete an individual from a pedigree" on page 298.)

To delete an individual

1. On the Progeny main window navigation bar, click the Individuals button to open the Individuals window.
2. Open the data folder that contains the individual that is being deleted.
3. Select the individual that is being deleted (CTRL-click to select multiple individuals), and on the main menu, click Individuals > Delete Individual(s).

   A message opens asking you if you are sure that you want to delete the selected individuals.
4. Click Yes.

   The message closes and the selected individuals are deleted. You return to the Individuals window.

Moving an Individual to a Pedigree

You can move a singlet (an individual who is not contained in a pedigree) to a pedigree at any time. After you move an individual to a pedigree, the icon for the individual is updated to reflect the fact that the individual is now in a pedigree. You can move an individual to an existing pedigree, or you can create a new pedigree at the time that you are moving the individual, and then move the individual to this new pedigree. When you move an individual to a pedigree, the name that you assigned to the individual is retained for the individual in the pedigree. Also, if the individuals are moved to a pedigrees folder for which the Individual Datasheet template option has been selected, then all the individuals in the folder use the same individual datasheet format, which is extremely useful if you want to manually draw a pedigree for these individuals. (See “Manually Drawing a Pedigree” on page 288.)

Figure 3-8: Individual icons

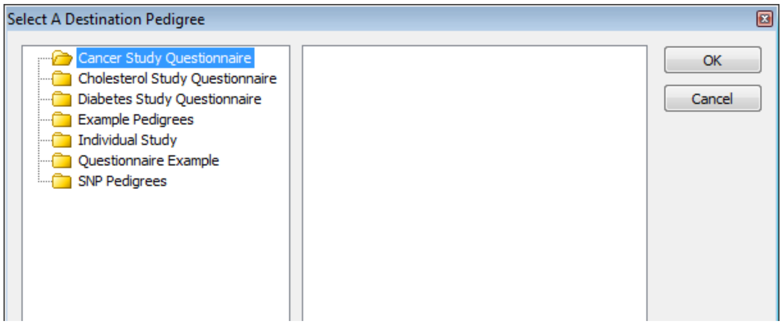
After you move an individual to a pedigree, some options on the Individuals menu are no longer available for the individual such as copying the individual to a data folder, creating a shortcut for the individual, and so on, so make sure that you have carried out all the needed actions for the individual before moving it.

To move an individual to an existing pedigree

1. On the Progeny main window navigation bar, click the Individuals button to open the Individuals window.
2. Open the data folder that contains the individual that you are moving to an existing pedigree.
3. Select the individual that is being moved, and on the main menu, click Individuals > Move to Pedigree > Existing Pedigree.

   The Select a Destination Pedigree dialog box opens.

Figure 3-9: Select a Destination Pedigree dialog box



4. Select the pedigree to which the individual is being moved, and then click OK.

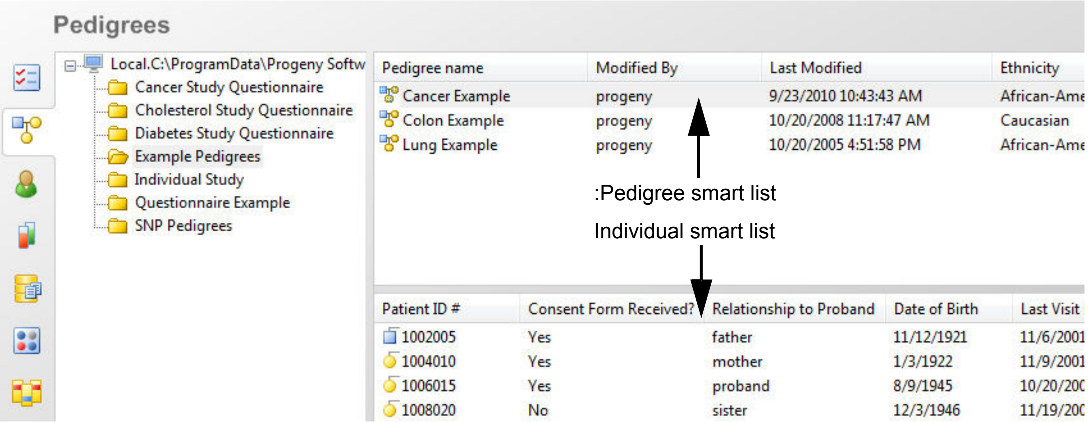
   The Select a Destination Pedigree dialog box closes. You return to the Individuals window. The singlet is removed from the individual data folder.

5. Optionally, to view the individual, open the Pedigrees window and in the correct pedigree data folder, select the pedigree to which you moved the individual.

   The individual is displayed in the Individuals smart list on the Pedigrees window.

After you add an individual to the pedigree, the icon for the individual is displayed in the upper left corner of the pedigree. You can drag the individual to is correct location in the pedigree, and manually add the relationships for the individual. See “Manually Drawing a Pedigree” on page 288.

Figure 3-10: Pedigree smart lists



Pedigree name	Modified By	Last Modified	Ethnicity
Cancer Example	progeny	9/23/2010 10:43:43 AM	African-Ame
Colon Example	progeny	10/20/2008 11:17:47 AM	Caucasian
Lung Example	progeny	10/20/2005 4:51:58 PM	African-Ame

:Pedigree smart list

Individual smart list

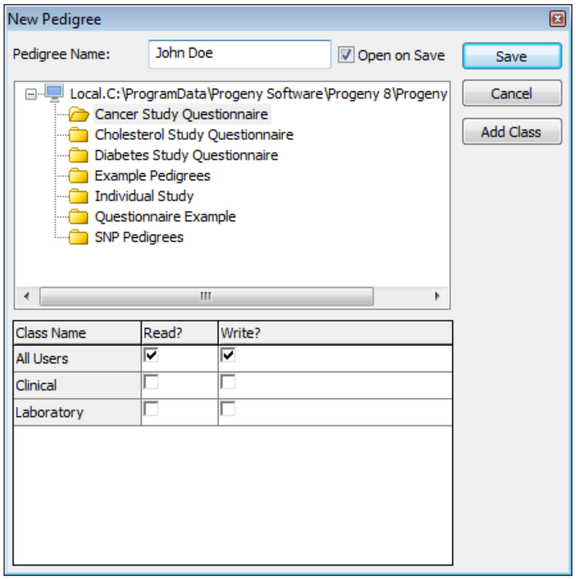
Patient ID #	Consent Form Received?	Relationship to Proband	Date of Birth	Last Visit
1002005	Yes	father	11/12/1921	11/6/2001
1004010	Yes	mother	1/3/1922	11/9/2001
1006015	Yes	proband	8/9/1945	10/20/200
1008020	No	sister	12/3/1946	11/19/200

To move an individual to a new pedigree

1. On the Progeny main window navigation bar, click the Individuals button to open the Individuals window.
2. Open the data folder that contains the individual that you are moving to a new pedigree.
3. Select the individual that is being moved, and on the main menu, click Individuals > Move to Pedigree > New Pedigree.

   The New Pedigree dialog box opens.

Figure 3-11: New Pedigree dialog box



Pedigree Name: John Doe

☑ Open on Save

- Local.C:\ProgramData\Progeny Software\Progeny 8\Progeny
  - Cancer Study Questionnaire
  - Cholesterol Study Questionnaire
  - Diabetes Study Questionnaire
  - Example Pedigrees
  - Individual Study
  - Questionnaire Example
  - SNP Pedigrees

Class Name	Read?	Write?
All Users	☑	☑
Clinical	☐	☐
Laboratory	☐	☐

4. Create the new pedigree. See
5. Click Save.

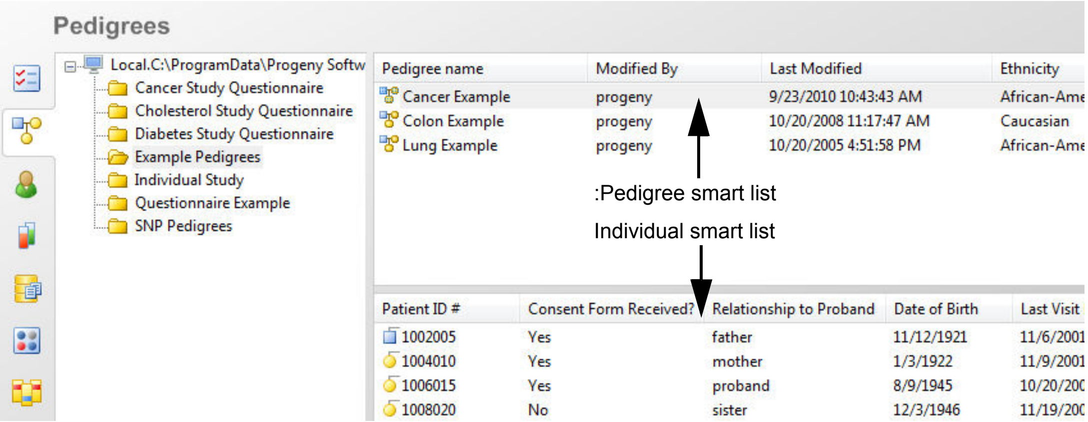
   A message opens indicating that the new pedigree was successfully added.
6. Click OK.

   The message closes. You return to the Individuals window. The singlet is removed from the individual data folder.
7. Optionally, to view the individual, open the Pedigrees window and in the correct pedigree data folder, select the pedigree to which you moved the individual.

   The individual is displayed in the Individuals smart list on the Pedigrees window.

Because this individual is the first individual that has been added to the pedigree, the individual is automatically designated as the proband. You can always change this designation at a later time.

Figure 3-12: Pedigree smart lists



- Local.C:\ProgramData\Progeny Softw
  - Cancer Study Questionnaire
  - Cholesterol Study Questionnaire
  - Diabetes Study Questionnaire
  - Example Pedigrees
  - Individual Study
  - Questionnaire Example
  - SNP Pedigrees

Pedigree name	Modified By	Last Modified	Ethnicity
Cancer Example	progeny	9/23/2010 10:43:43 AM	African-Ame
Colon Example	progeny	10/20/2008 11:17:47 AM	Caucasian
Lung Example	progeny	10/20/2005 4:51:58 PM	African-Ame

Patient ID #	Consent Form Received?	Relationship to Proband	Date of Birth	Last Visit
1002005	Yes	father	11/12/1921	11/6/2001
1004010	Yes	mother	1/3/1922	11/9/2001
1006015	Yes	proband	8/9/1945	10/20/200
1008020	No	sister	12/3/1946	11/19/200

After you add an individual to the pedigree, the icon for the individual is displayed in the upper left corner of the pedigree. You can drag the individual to is correct location in the pedigree, and manually add the relationships for the individual. See "Manually Drawing a Pedigree" on page 288.

Chapter 4
Managing Pedigrees

A *pedigree*, also known as a genogram, is a diagram that depicts individuals who are related by blood or another factor. Managing pedigrees in Progeny Clinical consists of creating new pedigrees, creating pedigrees shortcuts, creating datasheets for pedigrees, modifying an pedigree, creating pedigrees shortcuts, copying, moving, and deleting pedigrees, merging pedigrees, generating sub-pedigrees, printing pedigrees, and importing pedigree data.

This chapter covers the following topics:

For detailed information about importing pedigree data, see Chapter B, "Importing Clinical Data," on page 559.

Adding a New Pedigree

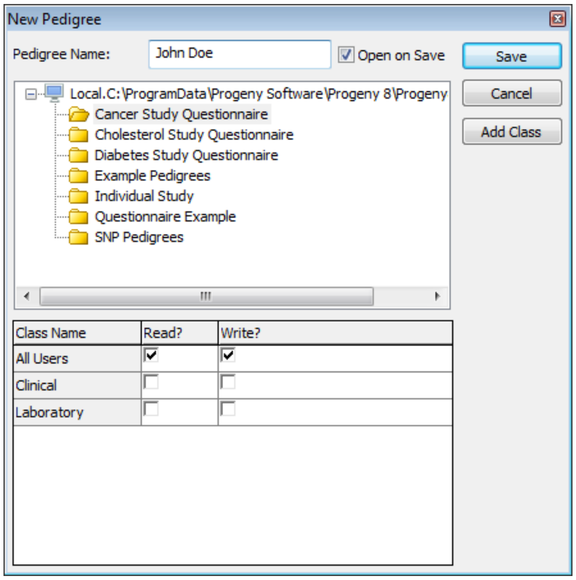
When you add a new pedigree, you are essentially adding a blank canvas, or Pedigree Drawing window, for drawing the pedigree. Adding a new pedigree consists of naming the pedigree and selecting the data folder in which to save the pedigrees.

To add a new pedigree

1. On the Progeny main window navigation bar, click the Pedigrees button to open the Pedigrees window.
2. On the Pedigrees window, click the New Pedigree button New Ped .

   The New Pedigree dialog box opens.

Figure 4-1: New Pedigree dialog box



Pedigree Name: John Doe ☑ Open on Save

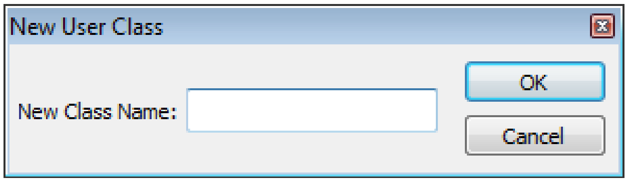
Class Name	Read?	Write?
All Users	☑	☑
Clinical	☐	☐
Laboratory	☐	☐

3. Enter the name for the new pedigree.
4. Select the data folder to which the pedigree is being added.
5. Optionally, click Open on Save.

   If you select this option, then after you save the pedigree, a blank pedigree canvas opens in the Pedigree Drawing window. See Chapter 5, “Drawing and Customizing Pedigrees,” on page 267.

6. If you are the Progeny administrator, then do one or more of the following to set the security for the pedigree; otherwise, continue to Step 7.
   - Modify the security settings for All Users or for the different classes of users.
     - Read?—View the data (name, data in the pedigree datasheet, the pedigree drawing) for the pedigree.
     - Write?—Write data (change the name, enter data in the a pedigree datasheet, draw the pedigree) to the pedigree.
   - Click Add Class to open the New User Class dialog box to create a new user class, and then set the pedigree security for the new class.

Figure 4-2: New User Class dialog box



7. Click Save.

   A message opens indicating the settings for the pedigree were successfully changed.
8. Click OK to close the message and return to the Pedigrees window.

Formatting a Pedigree Datasheet

You use a pedigree datasheet to enter and store data for a pedigree in a Progeny database. When you create a new pedigree, a pedigree datasheet is automatically created for the pedigree. All the pedigrees that are assigned to a pedigree data folder can use the same datasheet format, or each pedigree in the folder can use a unique datasheet format. You can format a pedigree datasheet at the time that you add a pedigree to a data folder, or at a later date.

To format a pedigree datasheet

1. Create a pedigree data folder.

   If all the pedigrees that are assigned to the folder are to use the same pedigree datasheet format, make sure to select the Pedigree Datasheet template option; otherwise, clear it. See “Adding Individual and Pedigree Data Folders” on page 203.

2. Create a new pedigree and add the pedigree to the data folder and then do one of the following:

   - To have a blank datasheet open immediately after you save the pedigree, right-click on the pedigree, and on the context menu that opens, click Open Pedigree Datasheet. You can click Form Design on this blank datasheet and format the datasheet as needed. If the Pedigree Datasheet template option has been selected for the data folder, then all the pedigrees that you subsequently add to the folder will use the same datasheet format for entering and storing data; otherwise, you must format a datasheet for each pedigree that you add to the folder.

   - Add all the needed pedigrees to the pedigree data folder. After you have added all of the needed pedigrees to the folder, right-click on any pedigree in the folder and on the context menu that opens, click Open Pedigree Datasheet. If the Pedigree Datasheet template option has been selected for the data folder, then all pedigrees that are currently added to the folder or that you subsequently add to the folder will use this same datasheet format for entering and storing data; otherwise, you must format a datasheet for each pedigree in the folder.

   See “Creating and Formatting Datasheets” on page 86 for detailed information about creating and formatting a pedigree datasheet.

Modifying a Pedigree

If you are the Progeny administrator, or your administrator has set Write access for the pedigree for your user account, you can rename the pedigree. As the Progeny administrator, you can also modify the security levels for the pedigree.

To modify a pedigree

1. On the Progeny main window navigation bar, click the Pedigrees button to open the Pedigrees window.
2. Open the data folder that contains the pedigree that is being modified.
3. Select the pedigree that is being modified, and on the main menu, click Pedigrees, and then click the appropriate option.

Option	Description
Rename pedigree	Automatically selects the pedigree name for modification.

Edit Pedigree Security	Opens the Pedigree Security dialog box in which you can do one or both of the following:
	• Modify the security settings for All Users or for the different classes of users.
	  • Read?—View the data (name and data in the pedigree datasheet) for the pedigree.
	  • Write?—Write data (change the name and enter data to an pedigree datasheet) to the pedigree.
	• Click Add Class to open the New User Class dialog box to create a new user class, and then set the pedigree security for the new class.

Creating Pedigree Shortcuts

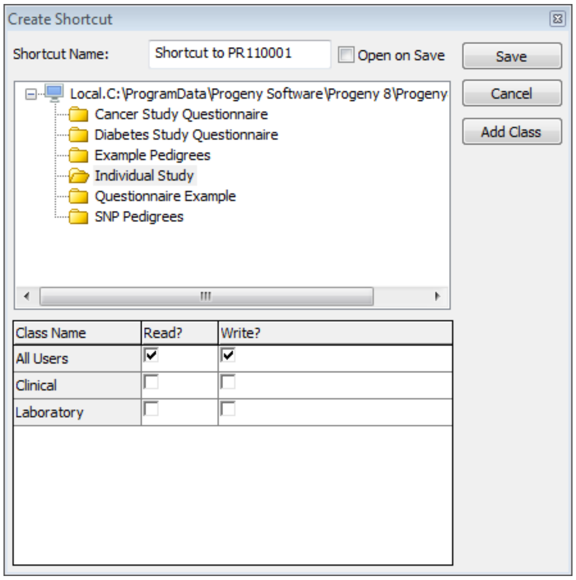
A *pedigree shortcut* is a link to that points to a pedigree in a Progeny database. You create a pedigree shortcut so that you can add a pedigree to multiple folders without having to copy or duplicate the pedigree. Although a shortcut points to the same original pedigree, each shortcut inherits the template options of the folder in which it is contained. For example, you might place a pedigree shortcut in a pedigree data folder named Diabetes Pedigrees, which has been assigned a pedigree datasheet that has been specifically designed for entering data that is related to the diabetic individuals who are contained in the pedigree. You can also place this same pedigree shortcut in a pedigree data folder named High Blood Pressure Pedigrees, which has been assigned a pedigree datasheet that has been specifically designed for entering data related that is related to the hypertensive individuals who are contained in the pedigree.

To create a pedigree shortcut

1. On the Progeny main window navigation bar, click the Pedigrees button to open the Pedigrees window.
2. Open the data folder that contains the pedigree for which you are creating the shortcut.
3. Select the pedigree for which you are creating the shortcut, and on the main menu, click Pedigrees > Create Shortcut.

   The Create Shortcut dialog box opens. The Shortcut Name field is automatically populated with a default value, but you can change this value.

Figure 4-3: Create Shortcut dialog box



Shortcut Name: Shortcut to PR110001 ☐ Open on Save

Local.C:\ProgramData\Progeny Software\Progeny 8\Progeny
- Cancer Study Questionnaire
- Diabetes Study Questionnaire
- Example Pedigrees
- Individual Study
- Questionnaire Example
- SNP Pedigrees

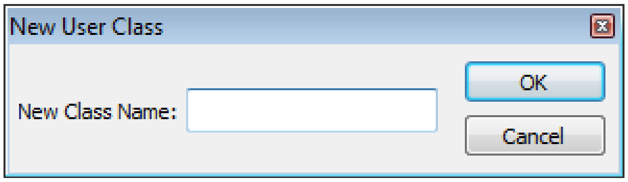
Class Name	Read?	Write?
All Users	☑	☑
Clinical	☐	☐
Laboratory	☐	☐

4. Select the folder in which to save the shortcut.

5. Optionally, do one or both of the following:
    - Change the shortcut name.
    - Select Open on Save.

      If you select this option, then after you save the pedigree shortcut, the pedigree opens in the Pedigree Drawing window. See Chapter 5, “Drawing and Customizing Pedigrees,” on page 267.
6. If you are the Progeny administrator, then do one or more of the following to set the security for the pedigree; otherwise, continue to Step 7.
    - Modify the security settings for All Users or for the different classes of users.
        - Read?—View the data (name, data in the pedigree datasheet, the pedigree drawing) for the pedigree.
        - Write?—Write data (change the name, enter data in the a pedigree datasheet, draw the pedigree) to the pedigree.
    - Click Add Class to open the New User Class dialog box to create a new user class, and then set the pedigree security for the new class.

Figure 4-4: New User Class dialog box



7. Click Save.

   A message opens indicating the settings for the pedigree were successfully changed.
8. Click OK to close the message and return to the Pedigrees window.

Copying and Moving Pedigrees between Data Folders

You can copy a pedigree between data folders, and you can move a pedigree between data folders. For any of these actions, the following are important points to note:

- Copying a pedigree leaves the original pedigree in its original data folder while putting a copy (or duplicate) of the pedigree in the new destination folder. Any edits that you make to the copied pedigree are *not* reflected in the original pedigree.
- Moving a pedigree removes the pedigree from its original data folder and places the pedigree in a new destination folder. A copy of the original pedigree is not made.

To copy or move a pedigree between data folders

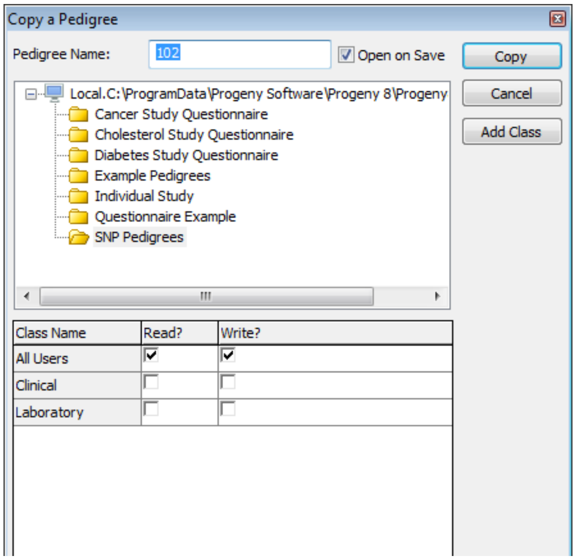
1. On the Progeny main window navigation bar, click the Pedigrees button to open the Pedigrees window.
2. Open the data folder that contains the pedigree that you are copying or moving, and then continue to one of the following:
    - "To copy a pedigree between data folders" below.
    - "To move a pedigree between data folders" on page 248.

To copy a pedigree between data folders

1. On the main menu, click Pedigrees > Copy a Pedigree.

   The Copy a Pedigree dialog box opens.

Figure 4-5: Copy a Pedigree dialog box



Pedigree Name: 102

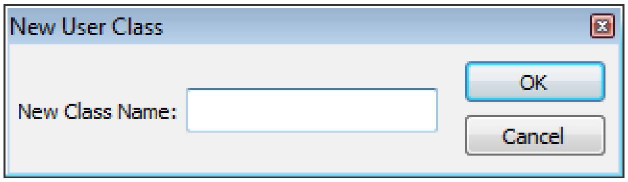
☑ Open on Save

Local.C:\ProgramData\Progeny Software\Progeny 8\Progeny
- Cancer Study Questionnaire
- Cholesterol Study Questionnaire
- Diabetes Study Questionnaire
- Example Pedigrees
- Individual Study
- Questionnaire Example
- SNP Pedigrees

Class Name	Read?	Write?
All Users	☑	☑
Clinical	☐	☐
Laboratory	☐	☐

2. Select the data folder to which the pedigree is being copied.
3. Optionally, before you copy the pedigree to a data folder, clear or select the Open on Save option.
4. Optionally, if you are the Progeny administrator, then do one or more of the following to modify the security for the pedigree; otherwise, continue to Step 5.
    - Modify the security settings for All Users or for the different classes of users.
        - Read?—View the data (name, data in the pedigree datasheet, the pedigree drawing) for the pedigree.
        - Write?—Write data (change the name, enter data in the a pedigree datasheet, draw the pedigree) to the pedigree.
    - Click Add Class to open the New User Class dialog box to create a new user class, and then set the pedigree security for the new class.

Figure 4-6: New User Class dialog box



5. Click Copy.

   A message opens indicating that the pedigree was successfully copied.
6. Click OK to close the message and return to the Individuals window.

To move a pedigree between data folders

Simply drag the selected pedigree to the appropriate data folder.

Copying a Pedigree between Databases as a Text File

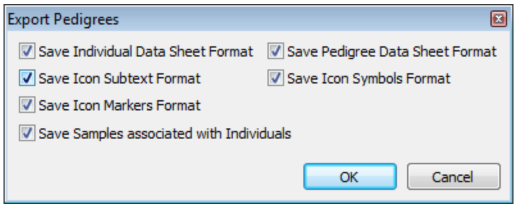
When you copy a pedigree between databases as a text file, you can copy pedigree data, individual data, sample data, and markers.

To copy a pedigree between databases as a text file

1. Launch Progeny and log into the database from which you are coping the pedigrees.
2. On the Progeny main window navigation bar, click the Pedigrees button to open the Pedigrees window.
3. Open the data folder that contains the pedigree that you are copying.
4. Select the pedigree that you are copying, (CTRL-click to select multiple pedigrees) and on the main menu, click Pedigrees > Save Selected Pedigrees as Txt.

   The Export Pedigrees dialog box opens. This dialog box lists all the options that can be exported with the pedigrees. By default, all options are selected.

Figure 4-7: Export Pedigrees dialog box

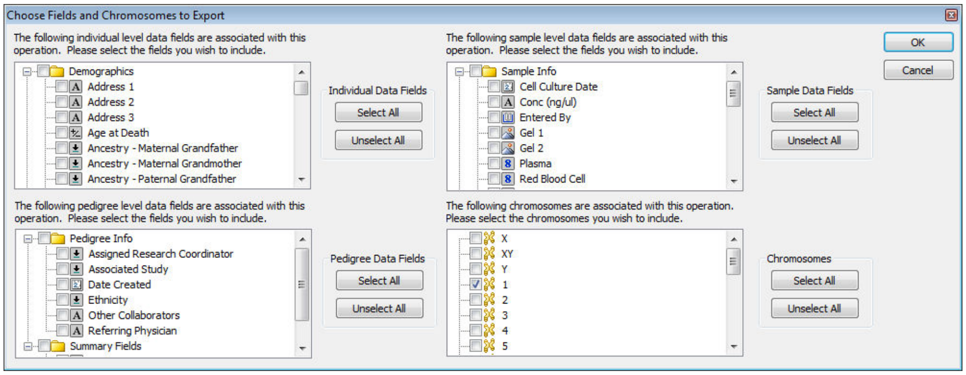


☑ Save Individual Data Sheet Format
☑ Save Pedigree Data Sheet Format
☑ Save Icon Subtext Format
☑ Save Icon Symbols Format
☑ Save Icon Markers Format
☑ Save Samples associated with Individuals

5. Optionally, clear any options that are not be exported with the pedigrees, and then click OK.

   The Export Pedigrees dialog box closes and the Choose Fields and Chromosome to Export dialog box opens.

Figure 4-8: Choose Fields and Chromosome to Export dialog box



The following individual level data fields are associated with this operation. Please select the fields you wish to include.

- ☐ Demographics
  - ☐ Address 1
  - ☐ Address 2
  - ☐ Address 3
  - ☐ Age at Death
  - ☐ Ancestry - Maternal Grandfather
  - ☐ Ancestry - Maternal Grandmother
  - ☐ Ancestry - Paternal Grandfather

The following pedigree level data fields are associated with this operation. Please select the fields you wish to include.

- ☐ Pedigree Info
  - ☐ Assigned Research Coordinator
  - ☐ Associated Study
  - ☐ Date Created
  - ☐ Ethnicity
  - ☐ Other Collaborators
  - ☐ Referring Physician
- ☐ Summary Fields

The following sample level data fields are associated with this operation. Please select the fields you wish to include.

- ☐ Sample Info
  - ☐ Cell Culture Date
  - ☐ Conc (ng/ul)
  - ☐ Entered By
  - ☐ Gel 1
  - ☐ Gel 2
  - ☐ Plasma
  - ☐ Red Blood Cell

The following chromosomes are associated with this operation. Please select the chromosomes you wish to include.

- ☐ X
- ☐ XY
- ☐ Y
- ☑ 1
- ☐ 2
- ☐ 3
- ☐ 4
- ☐ 5

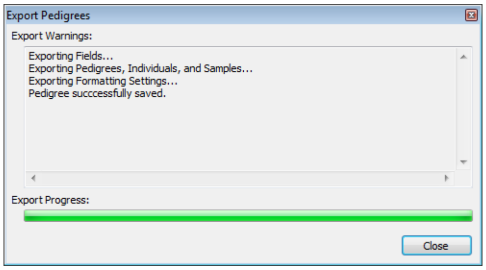
6. Select the data fields and chromosomes that are to be exported with the pedigrees, and then click OK.

   The Open dialog box opens.

7. Enter a name for the exported pedigrees file (the file type is set to .txt and you cannot change this), select a location in which to save the file, and then click Open.

   An Export Pedigrees dialog box opens, indicating the status of the export.

Figure 4-9: Export Pedigrees dialog box



```
Exporting Fields...
Exporting Pedigrees, Individuals, and Samples...
Exporting Formatting Settings...
Pedigree succcessfully saved.
```

8. When the export is complete, click Close.

9. On the Progeny main menu, click File > Exit to log out of the database from which you are copying the pedigrees, and then continue to "To load a pedigree text file" below.

To load a pedigree text file

1. Launch Progeny and log into the database *to* which you are copying the pedigrees.

2. On the Progeny main window navigation bar, click the Pedigrees button to open the Pedigrees window.

3. Select the data folder into which you are copying the pedigree.

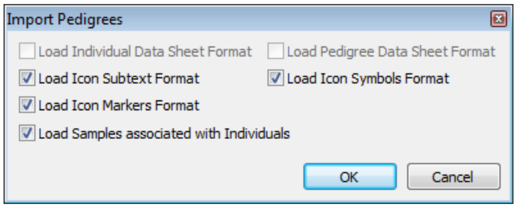
4. On the main menu, click Pedigrees > Load Pedigree(s) from Txt.

   The Open dialog box opens.

5. Locate the pedigree .txt file that you are loading, and then click Open.

   The Import Pedigrees dialog box opens. This dialog box lists all the options that were imported with the selected pedigree.

Figure 4-10: Import Pedigrees dialog box

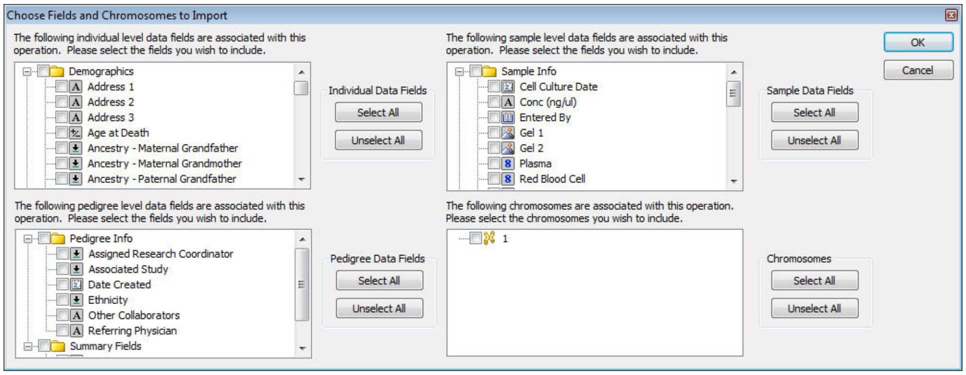


☐ Load Individual Data Sheet Format ☐ Load Pedigree Data Sheet Format
☑ Load Icon Subtext Format ☑ Load Icon Symbols Format
☑ Load Icon Markers Format
☑ Load Samples associated with Individuals

6. You can leave the options as-is, or clear the options that are not to be imported with the pedigree.
7. Click OK.

   The Choose Fields and Chromosome to Import dialog box opens. This dialog box lists all the data fields and chromosomes that are associated with the imported pedigree.

Figure 4-11: Choose Fields and Chromosomes to Import dialog box



The following individual level data fields are associated with this operation. Please select the fields you wish to include.

The following sample level data fields are associated with this operation. Please select the fields you wish to include.

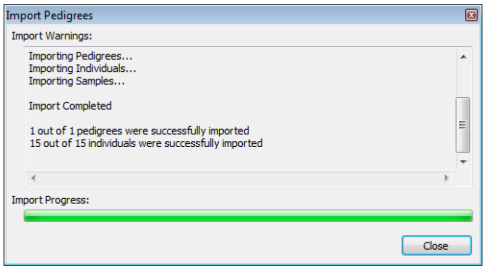
The following pedigree level data fields are associated with this operation. Please select the fields you wish to include.

The following chromosomes are associated with this operation. Please select the chromosomes you wish to include.

8. Select the data fields and chromosomes that are to be imported with the pedigree, and then click OK.

   The Import Pedigrees dialog box opens, indicating the status of the import.

Figure 4-12: Import Pedigrees dialog box



```
Importing Pedigrees...
Importing Individuals...
Importing Samples...

Import Completed

1 out of 1 pedigrees were successfully imported
15 out of 15 individuals were successfully imported
```

9. When the import is complete, click Close.
   - Individuals in the pedigree are imported into the a folder that is named identically to the folder into which you imported the pedigrees. (Remember, when you create a new individual data folder, an identically named pedigree data folder with the same template options is created. Likewise, when you create a new pedigree data folder, an identically named individual data folder with the same template options is created.)
   - Samples are imported into a folder that is named Imported Samples.
   - The folder structure for the imported database fields is recreated in the database into which you are importing the pedigrees, and the database fields are imported into the appropriate folders.

Copying a Pedigree between Databases as an XML File

When you copy a pedigree between databases as an .xml file, you can copy pedigree data, individual data, and markers. You *cannot* copy sample data. Also, to be able to select the data fields and markers that are to be copied (versus having all data fields and markers copied by default), you must use the Save as XML and Load From XML options that are available on the context menu for an open pedigree, and not the options that are available from the main menu.

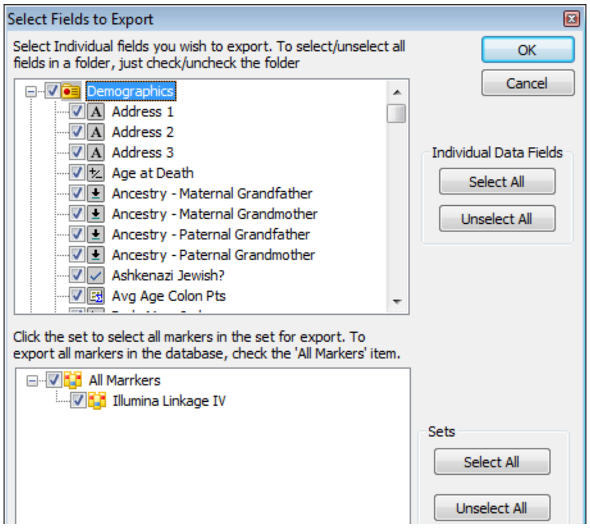
To copy a pedigree between databases as an XML file

1. Launch Progeny and log into the database *from* which you are coping the pedigree.
2. On the Progeny main window navigation bar, click the Pedigrees button to open the Pedigrees window.
3. Select the data folder that contains the pedigree that you are copying.
4. Open the pedigree that you are saving as an .xml file, right-click in the Pedigree Drawing window, and on the context menu that opens, click Save As XML.

   The Save As dialog box opens.
5. Enter a name for the exported pedigrees file (the file type is set to .xml and you cannot change this), select a location in which to save the file, and then click Save.

   The Select Fields to Export dialog box opens. This dialog box lists all the pedigree data fields, individual data fields, and markers that are available for exporting for the pedigree. By default, all data fields and markers are selected for exporting.

Figure 4-13: Select Fields to Export dialog box



Select Fields to Export

Select Individual fields you wish to export. To select/unselect all fields in a folder, just check/uncheck the folder

- ☑ Demographics
  - ☑ Address 1
  - ☑ Address 2
  - ☑ Address 3
  - ☑ Age at Death
  - ☑ Ancestry - Maternal Grandfather
  - ☑ Ancestry - Maternal Grandmother
  - ☑ Ancestry - Paternal Grandfather
  - ☑ Ancestry - Paternal Grandmother
  - ☑ Ashkenazi Jewish?
  - ☑ Avg Age Colon Pts

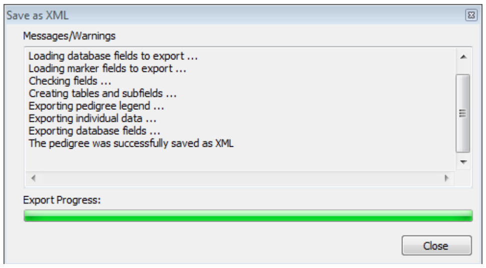
Click the set to select all markers in the set for export. To export all markers in the database, check the 'All Markers' item.

- ☑ All Marrkers
  - ☑ Illumina Linkage IV

6. Optionally, clear the selections for the data fields and/or markers that are *not* to be exported, and then click OK.

   The Save as XML dialog box opens, indicating the status of the export.

Figure 4-14: Save ax XML dialog box



Loading database fields to export ...
Loading marker fields to export ...
Checking fields ...
Creating tables and subfields ...
Exporting pedigree legend ...
Exporting individual data ...
Exporting database fields ...
The pedigree was successfully saved as XML

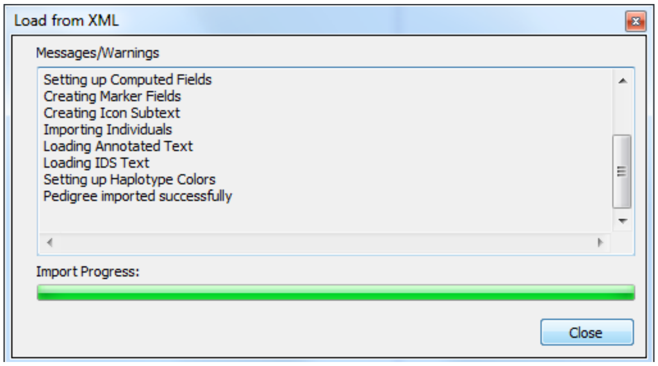
7. When the export is complete, click Close.
8. On the Progeny main menu, click File > Exit to log out of the database from which you are copying the pedigrees, and then continue to "To load a pedigree XML file" on page 253.

To load a pedigree XML file

1. Launch Progeny and log into the database *to* which you are copying the pedigrees.
2. On the Progeny main window navigation bar, click the Pedigrees button to open the Pedigrees window.
3. Select the data folder into which you are copying the pedigree.
4. Create a new pedigree in this data folder. (Make sure that Open on Save is selected so that a blank Pedigree Drawing window opens after you save the pedigree.)
5. Right-click on the blank Pedigree Drawing window, and on the context menu that opens, click Import XML Files.

   A Load from XML dialog box opens that indicates the progress of importing the pedigree XML file.

Figure 4-15:



Setting up Computed Fields
Creating Marker Fields
Creating Icon Subtext
Importing Individuals
Loading Annotated Text
Loading IDS Text
Setting up Haplotype Colors
Pedigree imported successfully

6. After the XML file is imported, click Close.

   The Load from XML dialog box closes. The pedigree, along with all the data that was imported with the pedigree, is displayed onscreen.

Importing FAM Files

You can import multiple Cyrillic pedigrees (FAM files) into a Progeny database.

To import FAM files

1. Launch Progeny and log into the database *into* which you are coping the pedigree.
2. On the Progeny main window navigation bar, click the Pedigrees button to open the Pedigrees window.
3. Select the data folder into which you are copying the pedigrees.
4. On the main menu, click Pedigrees > Import FAM Files.

   The Browse for Folder dialog box opens.
5. Browse to the location that contains the FAM files, and then click OK.

   A Progeny Import Module dialog box opens, indicating the status of the import.
6. When the import is complete, click Close.

Exporting to BRCA

You can export database fields in a pedigree in a format that can be used in the BRCA Risk Analysis application.

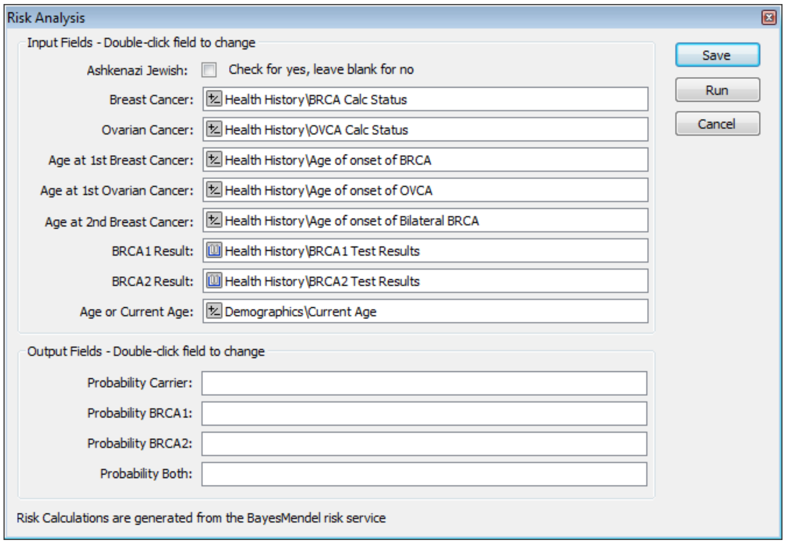
You must have internet access as the BRCA Risk Analysis software is located on a web server that Progeny automatically accesses.

To export to BRCA

1. On the Progeny main window navigation bar, click the Pedigrees button to open the Pedigrees window.
2. Select the data folder that contains the pedigree from which you are exporting the database fields.
3. Open the pedigree that contains the fields that you are exporting, right-click in the Pedigree Drawing window, and on the context menu that opens, click Risk Analysis > BRCA.

   The Risk Analysis dialog box opens.

Figure 4-16: Risk Analysis dialog box



Input Fields - Double-click field to change

Ashkenazi Jewish: ☐ Check for yes, leave blank for no
Breast Cancer: Health History\BRCA Calc Status
Ovarian Cancer: Health History\OVCA Calc Status
Age at 1st Breast Cancer: Health History\Age of onset of BRCA
Age at 1st Ovarian Cancer: Health History\Age of onset of OVCA
Age at 2nd Breast Cancer: Health History\Age of onset of Bilateral BRCA
BRCA1 Result: Health History\BRCA1 Test Results
BRCA2 Result: Health History\BRCA2 Test Results
Age or Current Age: Demographics\Current Age

Output Fields - Double-click field to change

Probability Carrier:
Probability BRCA1:
Probability BRCA2:
Probability Both:

Risk Calculations are generated from the BayesMendel risk service

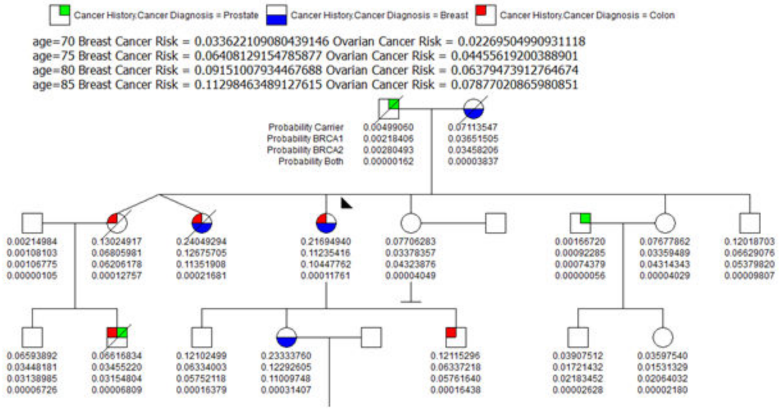
4. Locate all of the fields within the database that BRCA Risk Analysis program requires.

Progeny ships these files in the Health History folder within the Progeny Demo.db database; however, you can identify your own fields as long as the values are consistent with what BRCA expects. Figure 4-16 above illustrates what the BRCA Risk Analysis setup looks like if you used the fields that are shipped in the demo database.

5. Click Save, and then click Run.

   Progeny accesses the web server on which the BRCA Risk Analysis software is loaded. The results of the analysis are returned—percentage risks for carrier, BRCA1, BRCA2, and both BRCA1 and BRCA2—are displayed for each individual on the pedigree. The lifetime risks for breast and ovarian cancer for the proband are also displayed.

Figure 4-17: BRCA Risk Analysis results displayed on a pedigree



```
age=70 Breast Cancer Risk = 0.033622109080439146 Ovarian Cancer Risk = 0.02269504990931118
age=75 Breast Cancer Risk = 0.06408129154785877 Ovarian Cancer Risk = 0.04455619200388901
age=80 Breast Cancer Risk = 0.09151007934467688 Ovarian Cancer Risk = 0.06379473912764674
age=85 Breast Cancer Risk = 0.11298463489127615 Ovarian Cancer Risk = 0.07877020865980851
```

Copying and Pasting Pedigrees into Third Party Applications

You can copy and paste a pedigree into the third party applications Microsoft Word or Microsoft Powerpoint, and you can copy and paste a pedigree into another pedigree in Progeny. When you are copying and pasting a pedigree into a third party application, note the following:

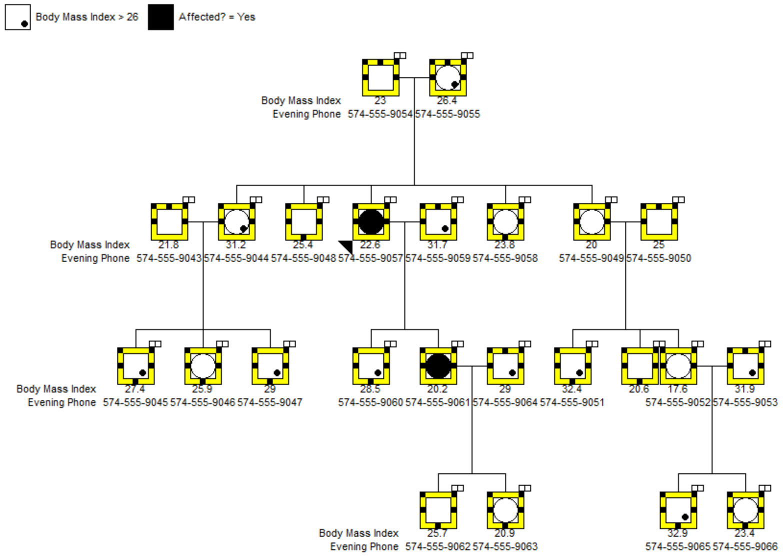
- Ideally you should not modify the pedigree after you have pasted it. This means that you should have the pedigree formatted and drawn to the appropriate specifications before you copy it.
- Any icon subtext or haplotypes that are displayed on the pedigree are also copied; however, any static text that is displayed on the pedigree is not copied. If needed, you can copy this text separately.
- If you absolutely must edit the pedigree after you paste it, then you must right-click on the pedigree, and on the context menu that opens, click Edit > Picture.

To copy and paste a pedigree into a third party application

1. Open the pedigree that is being copied, right-click anywhere in the Pedigree Drawing window, and on the context menu that opens, click Edit > Select All.

   Every individual icons in the pedigree become a double yellow square with handles on it, indicating that is has been selected.

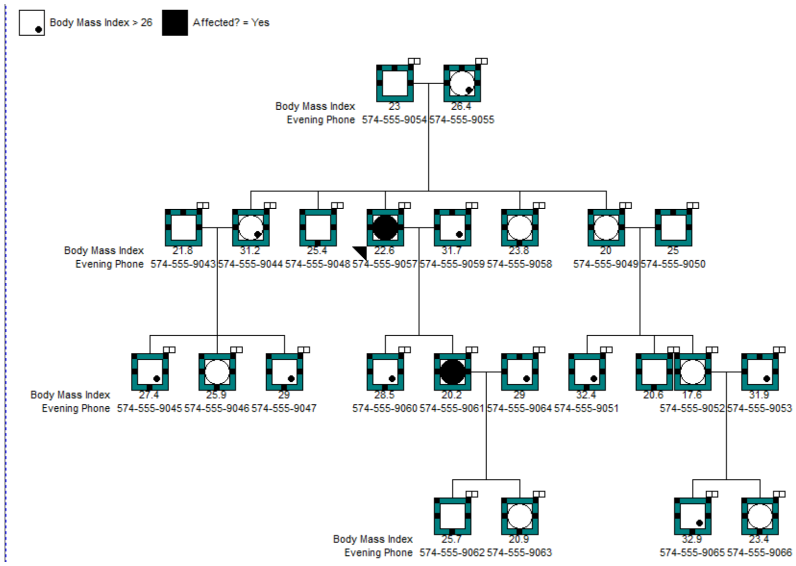
Figure 4-18: Pedigree with all icons selected



2. Do one of the following:
   - On the main menu, click Edit > Copy.
   - Use the standard keyboard copy command of CTRL + C.
   - Right-click anywhere in the Pedigree Drawing window, and on the context menu that opens, click Copy.

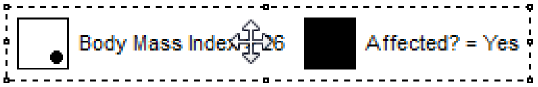
   Every individual icons in the pedigree become a double green square with handles on it, indicating that is has been selected for copying.

Figure 4-19: Pedigree with all icons selected for copying



3. Open a blank Word document or PowerPoint slide, and use standard menu or keyboard commands to paste the pedigree.
4. After pasting the pedigree:
   - To edit the pedigree, right-click on the pedigree, and on the context menu that opens, click Edit > Picture.
   - To copy the static text to the pedigree:
     - Click on the static text in the pedigree to select it. (The static text is displayed in a text box with handles and the cursor changes to a set of double-headed arrows.)

Figure 4-20: Selected static text on a pedigree



     - Right-click on the selected text and select Copy or use the standard keyboard copy command of CTRL + C to copy the selected text, and then use standard menu or keyboard commands to paste the text into the pedigree.

Merging Pedigrees

If you have two pedigrees that are in the same database and all the individuals in both pedigrees are from the same family, you can merge the pedigrees. When you merge pedigrees, all the data that is associated with each individual in the pedigree remains intact.

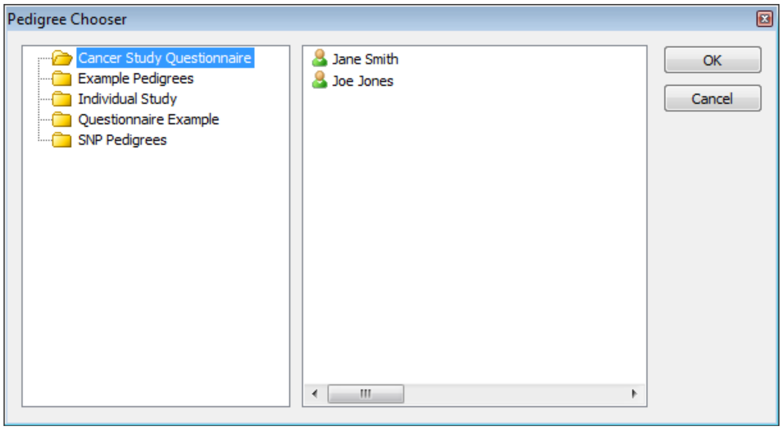
You can merge only original pedigrees. You cannot merge copies of original pedigrees.

To merge pedigrees

1. On the Progeny main window navigation bar, click the Pedigrees button to open the Pedigrees window.
2. Open the data folder that contains the pedigree that is being merged into another pedigree.
3. Select the pedigree that is being merged into another pedigree, and on the main menu, click Pedigrees > Merge Pedigree into Existing Pedigree.

   The Pedigree Chooser dialog box opens.

Figure 4-21: Pedigree Chooser dialog box



4. Select the pedigree *into* which you are merging another pedigree, and then click OK.

   A message opens indicating that the pedigrees were successfully merged.

5. Click OK to close the message and return to the Pedigrees window.

   The entry for the pedigree that was merged is no longer displayed in the window. Only the entry for the pedigree into which the merge occurred is displayed. For example, if you merged a pedigree named Patient 102 into a pedigree named Patient 110, then the entry for Patient 102 is no longer displayed in the Pedigrees window. Only the entry for Patient 110 is displayed.

Deleting a Pedigree

Deleting a pedigree is a permanent event. After you delete a pedigree, you cannot recover it from the database.

To delete a pedigree

1. On the Progeny main window navigation bar, click the Pedigrees button to open the Pedigrees window.
2. Open the data folder that contains the pedigree that is being deleted.
3. Select the pedigree that is being deleted (CTRL-click to select multiple pedigrees), and on the main menu, click Pedigrees > Delete Pedigree(s).

   A message opens asking you if you are sure that you want to delete the selected pedigrees.
4. Click Yes.

   The message closes and the selected pedigrees are deleted. You return to the Pedigrees window.

Generating a Spreadsheet for the Individuals in a Pedigree

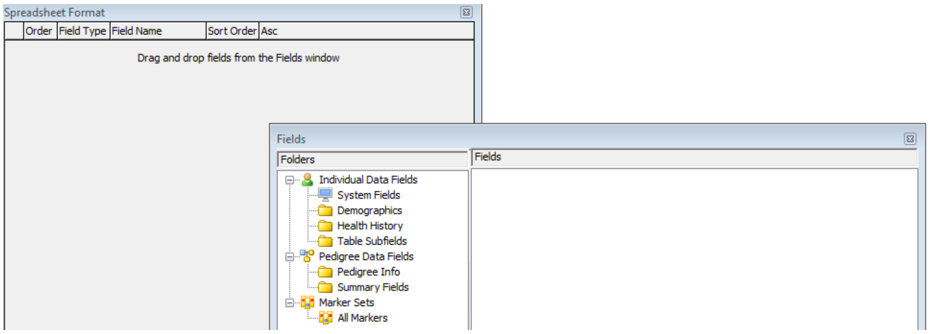
The generation of a spreadsheet for all individuals in a Progeny database has already been discussed in Chapter 4, “Spreadsheet Basics,” on page 103. You can also generate a spreadsheet of that consists solely of the individuals in a selected pedigree.

To generate a spreadsheet for the individuals in a pedigree

1. Open the appropriate pedigree in the Pedigree Drawing window.
2. On the window’s toolbar, click the Spreadsheet button Spreadsheet.

   The Fields dialog box opens on top of the Spreadsheet Format window.

Figure 4-22: Fields dialog box and Spreadsheet Format window



Drag and drop fields from the Fields window

3. Drag the fields (including any system fields) that are to be displayed in the spreadsheet from the Fields dialog box onto the Spreadsheet Format window.
4. Click the Run button Run to generate the spreadsheet.

All the rules and caveats for entering data into a spreadsheet, loading and saving formats, running queries, and so on still apply to a spreadsheet that was just generated just for individuals in a selected pedigree. See Chapter 4, “Spreadsheet Basics,” on page 103.

5. Click the Save button Save to save the spreadsheet.

Creating a Sub-Pedigree

A *sub-pedigree* is simply a subset of individuals from an existing pedigree. The data that is associated with each individual in a sub-pedigree is the actual data for the individual. To view the pedigree with selected members hidden, you would simply create a sub-pedigree and save it for later retrieval. For instance, you might want to save a subset of a pedigree in which only the first degree relatives of the proband are displayed. You simply create a subset of the pedigree where these are the only individuals shown on the pedigree. Some important points to note about a sub-pedigree are the following:

- There are no limits as to the number of sub-pedigrees that you can create for a given pedigree.
- You can add individuals to a pedigree only from within the pedigree, and not from within any sub-pedigrees.
- Any changes that you make to the structure or data in the pedigree are reflected in the associated sub-pedigrees as well. For instance, if you delete the proband from the pedigree, the proband is also deleted from any associated sub-pedigrees.
- Any changes that you make to the *structure* of a sub-pedigree are *not* reflected in the pedigree. For instance, if you delete the proband from a sub-pedigree, the proband is *not* deleted in the pedigree.
- Any changes that you make to the *data* for an individual in a sub-pedigree *are* reflected in the pedigree. (Remember, the data that is associated with each individual in a sub-pedigree is the actual data for the individual.)
- You can open the individual datasheet for an individual in a sub-pedigree exactly the same way that you open it for an individual in a pedigree. Simply right-click on the individual, and on the context menu that opens, click Open Individual Datasheet.
- You can generate a spreadsheet for all the individuals who are in a sub-pedigree in exactly the same way you generate a spreadsheet for all the individuals in a pedigrees. Open the sub-pedigree, and on the Pedigree Drawing window toolbar, click the click the Spreadsheet button. (See "To generate a spreadsheet for the individuals in a pedigree" on page 262.)

To create a sub-pedigree

The following procedure details the creation of a sub-pedigree for all 1st degree relatives of a proband in a pedigree; however, by analogy, you can follow this procedure to create any sub-pedigree as needed.

1. Open the pedigree for which you are creating a sub-pedigree in the Pedigree Drawing window.

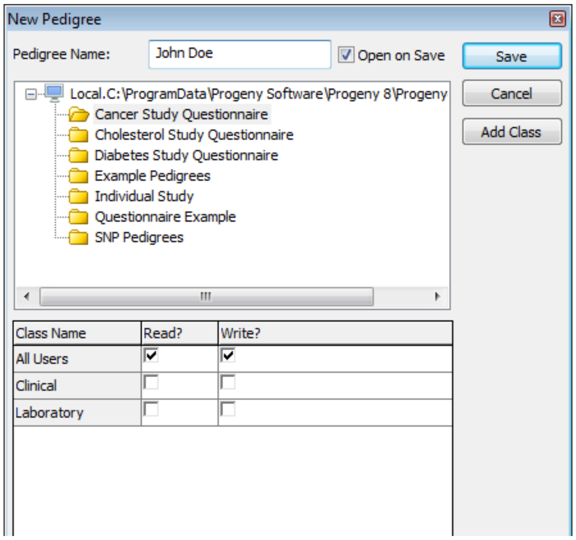
2. Right-click on the proband, and on the context menu that opens, click Select > 1st Degree.

   All individuals who are first degree relatives to the proband are selected in the pedigree.

3. On the Pedigree Drawing window toolbar, click the New Sub-Pedigree button .

   The New Pedigree dialog box opens.

Figure 4-23: New Pedigree dialog box



Pedigree Name: John Doe

☑ Open on Save

- Local.C:\ProgramData\Progeny Software\Progeny 8\Progeny
  - Cancer Study Questionnaire
  - Cholesterol Study Questionnaire
  - Diabetes Study Questionnaire
  - Example Pedigrees
  - Individual Study
  - Questionnaire Example
  - SNP Pedigrees

Class Name	Read?	Write?
All Users	☑	☑
Clinical	☐	☐
Laboratory	☐	☐

4. Enter the name for the new sub-pedigree.

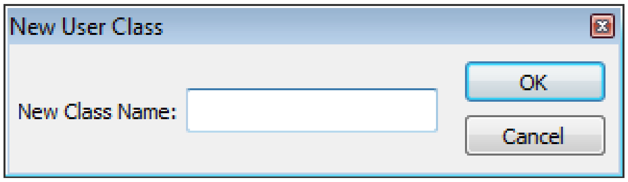
5. Select the data folder to which the sub-pedigree is being added.

6. Optionally, click Open on Save.

   If you select this option, then after you save the pedigree, the sub-pedigree opens in the Pedigree Drawing window. See Chapter 5, “Drawing and Customizing Pedigrees,” on page 267.

7. If you are the Progeny administrator, then do one or more of the following to set the security for the sub-pedigree; otherwise, continue to Step 8.
   - Modify the security settings for All Users or for the different classes of users.
     - Read?—View the data (name, data in the pedigree datasheet, the pedigree drawing) for the pedigree.
     - Write?—Write data (change the name, enter data in the a pedigree datasheet, draw the pedigree) to the pedigree.
   - Click Add Class to open the New User Class dialog box to create a new user class, and then set the pedigree security for the new class.

Figure 4-24: New User Class dialog box



8. Click Save.

   A message opens indicating the settings for the pedigree were successfully changed.
9. Click OK to close the message and open the sub-pedigree in the Pedigrees Drawing window.

Printing a Pedigree

You can print a pedigree that is displayed in the Pedigree Drawing window.

To print a pedigree

1. Open that pedigree that is to be printed in the Pedigree Drawing window.
2. Optionally, set one or more of the following options:
   - To see where the edge of each pedigree page is, make sure that Show Page Breaks is selected on the Progeny tab of the Properties dialog box. (See “Properties dialog box, Progeny tab” on page 271.) If this option is selected, then blue lines are displayed at the exact point at which the page stops printing and moves to the next page (Print Preview). Page numbers are displayed in the bottom right corner of each page in the order of how the pages print.
   - Landscape is the default mode for printing. To change this, on the main menu, click File > Printer Setup, and on the Print Setup dialog box, select Portrait.
   - To automatically scale the pedigree to print on a single page, right-click on the opened pedigree, and on the context menu that opens, click Fit to Page. To return the pedigree to is original scale, enter the appropriate value for he Pedigree Scale option on the Pedigree tab of the Properties dialog box. See “Properties dialog box, Pedigree tab” on page 272.
3. On the pedigree toolbar, click the Print button Print .

   The Print dialog box opens.
4. On the Print dialog box, select the needed printing options, and then click Print.

   The pedigree is printed exactly as it is displayed onscreen, including the header, the footer, and the legends.

Chapter 5

Drawing and Customizing Pedigrees

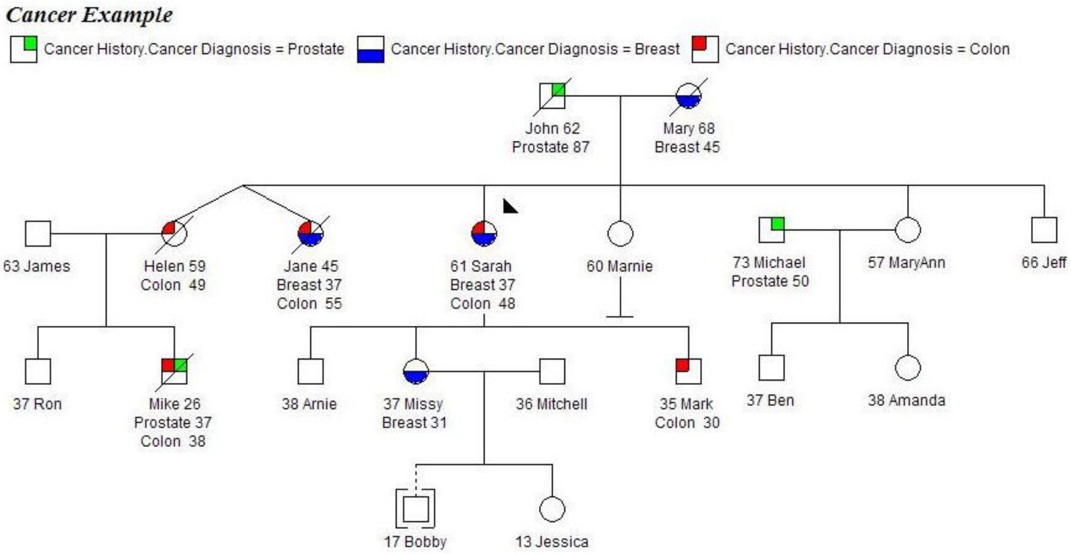
A *pedigree*, also known as a *genogram*, is a diagram that depicts individuals who are related by blood or another factor. When you create a new pedigree, you are essentially creating a blank canvas for drawing the pedigree. (This blank canvas is referred to as the Pedigree Drawing window.) Drawing of a pedigree consists of identify the icons that are to be used in the pedigree, including their subtext and symbols, adding individuals to the pedigree, deleting individuals from a pedigree, adding and modifying relationships among individuals in the pedigree, and so on.

This chapter covers the following topics:

Overview of a Pedigree

A *pedigree*, also known as a genogram, is a diagram that depicts individuals who are related by blood or another factor. Different icons represent different types of individuals. For example, a square icon indicates a male individual, a circle icon indicates a female individual, and a diamond icon indicates an individual of unknown/undetermined gender. Symbols are applied to icons to graphically represent data about the individual, such as individuals with a cancer diagnosis that equals Breast. A legend identifies each symbol. The lines connecting individuals identify the relationship between two individuals, such as marital status. The icon subtext, which is the text that is displayed above or below an individual icon on a pedigree, is specific for the individual. Figure 5-1 below shows a pedigree that details the cancer history for the members of a family.

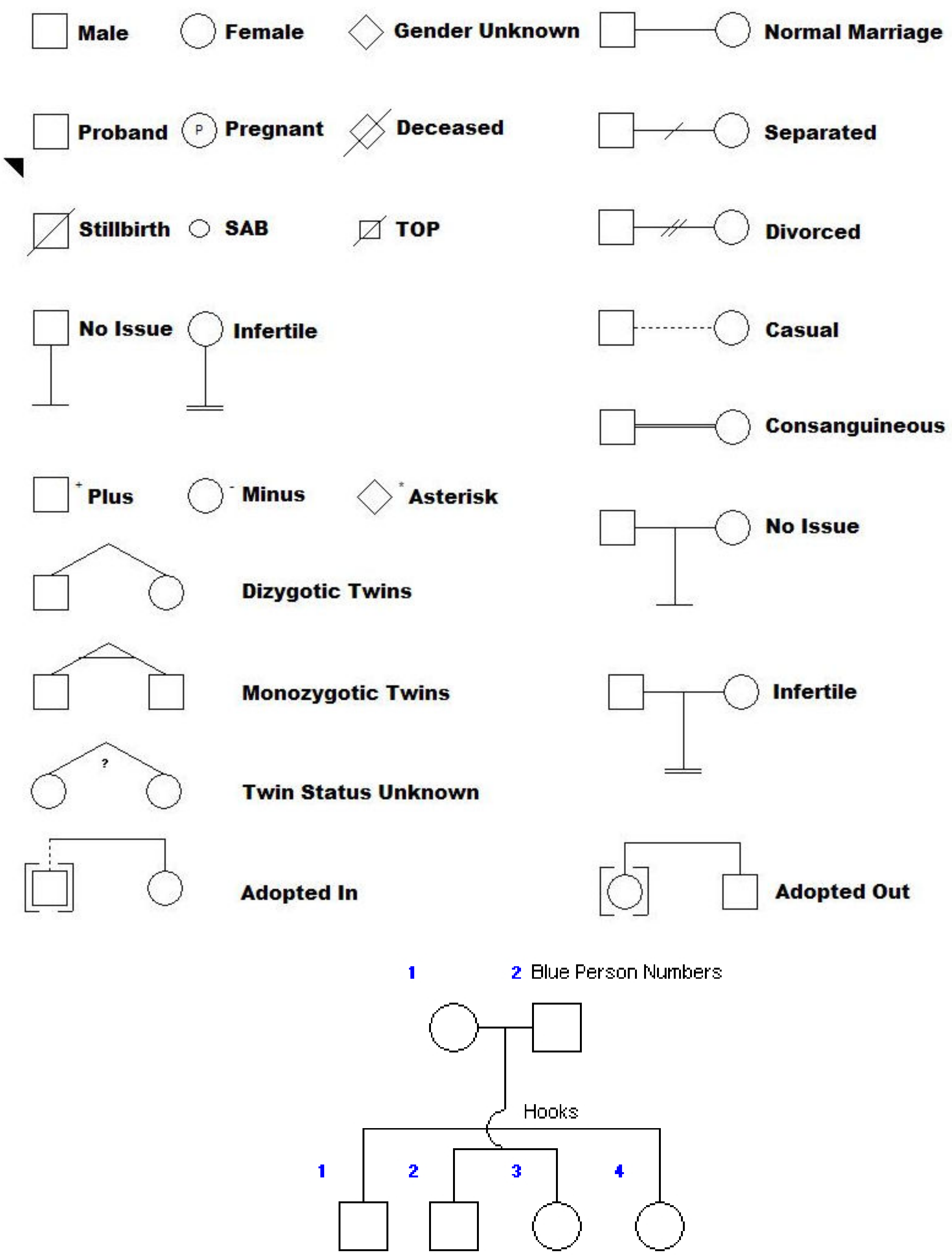
Figure 5-1: Example of a pedigree



Overview of Pedigree Icons

Although there are no definitive standards when drawing pedigrees, there are published guidelines for the human genetics market. Progeny uses pedigree icons based on the guidelines published in the *American Journal of Human Genetics (1995)* Bennet, et al.

Figure 5-2: Icons used in pedigrees drawn in Progeny



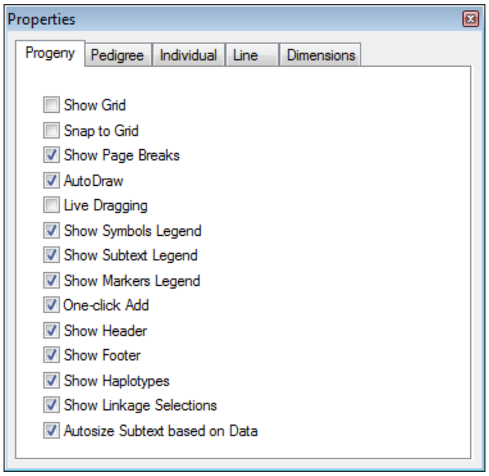
Pedigree Properties

The Properties dialog box displays all the options that you can set for controlling the drawing and displaying of a pedigree. Although some of these options might not make sense right now, it is important for you to be aware of them so that when they are referenced later in this chapter, you are able to correctly modify and apply the properties when you are drawing pedigrees. You open the Properties dialog box by clicking on the Properties button on the toolbar for any open pedigree.

The dialog box has five tabs—Progeny, Pedigree, Individual, Line, and Dimensions. By default, the Progeny tab is the active tab when the dialog box first opens.

Properties dialog box, Progeny tab

Figure 5-3: Properties dialog box, Progeny tab



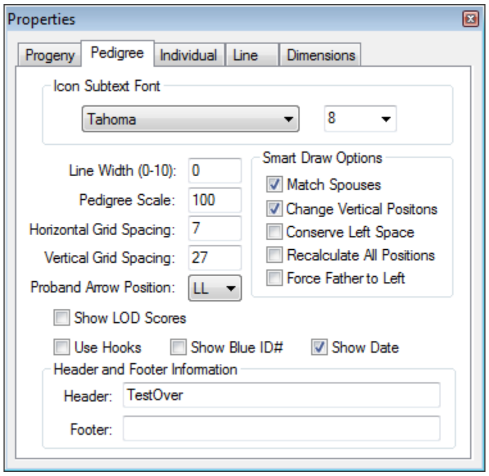
☐ Show Grid
☐ Snap to Grid
☑ Show Page Breaks
☑ AutoDraw
☐ Live Dragging
☑ Show Symbols Legend
☑ Show Subtext Legend
☑ Show Markers Legend
☑ One-click Add
☑ Show Header
☑ Show Footer
☑ Show Haplotypes
☑ Show Linkage Selections
☑ Autosize Subtext based on Data

Option	Description
Show Grid	Displays a grid on the pedigree canvas.
Snap to Grid	When moving an icon in the pedigree, aligns (or “snaps”) the icon to the nearest intersection of lines in the grid, even if the grid is not visible.
Show Page Breaks	Displays the edges of the print pages in Print Preview mode.
AutoDraw	Automatically runs SmartDraw every time you add an individual to a pedigree. You can then define your SmartDraw options. See “Smart Draw Options” in “Properties dialog box, Pedigree tab” on page 272.
Live Dragging	Relationship lines move with the icon when you reposition the icon.
Show Symbols Legend	Displays the legend for the symbols that are used in the pedigree.
Show Subtext Legend	Displays the legend for the icon subtext (database fields) that are displayed in the pedigree.
One-click Add	Selected by default. Allows you to click on specific handles on an individual icon to automatically add a relationship to the individual. (You do not have to manually add relationships from the palette or drag lines between icons to create relationships).

Option	Description
Show Header Show Footer	Displays a header or footer on each page of the pedigree. **Note:** You set the text for the header and footer on the Pedigree tab.
Show Haplotypes	Display a colored-coded legend for markers that are displayed on a pedigree.
Show Linkage Selections	Displays sample status (Sample/Plate/Gentoyped) on the pedigree and indicates whether individual has been “Included in Analysis.”

Properties dialog box, Pedigree tab

Figure 5-4: Properties dialog box, Pedigree tab



Icon Subtext Font: Tahoma, 8

Line Width (0-10): 0

Pedigree Scale: 100

Horizontal Grid Spacing: 7

Vertical Grid Spacing: 27

Proband Arrow Position: LL

Smart Draw Options
☑ Match Spouses
☑ Change Vertical Positons
☐ Conserve Left Space
☐ Recalculate All Positions
☐ Force Father to Left

☐ Show LOD Scores

☐ Use Hooks ☐ Show Blue ID# ☑ Show Date

Header and Footer Information
Header: TestOver
Footer:

Option	Description
Icon Subtext Font	The font type and font size used for the icon subtext.
LIne Width	The width of the relationship lines used in the pedigree. Increasing the value increases the line width.
Pedigree Scale	Size of the pedigree, from 0 to 800%.
Grid Spacing Horizontal Grid Spacing Vertical	If Show Grid is selected on the Progeny tab, then change these values to adjust the spacing between the grid lines.
Proband Arrow Position	Change the position of the solid black arrowhead that identifies the proband on a pedigree. Values are UL (for upper left), UR (for upper right), LL (for lower left), and LR (for lower right).

Option	Description
Smart Draw Options	• Match Spouses—Keep spouses next to each other at all times on the pedigree. • Change Vertical Positons—Maintain vertical positions of individuals at all times on the pedigree. • Converse Left Space—Aligns the pedigree to the left edge of the page. • Recalculate All Positions—As you add an individual to a pedigree, the redrawing of the entire pedigree is recalculated as a whole. • Force Father to the Left—Forces each spouse combination to keep the Father on the right and the Mother on the left.
Show LOD Scores	Displays a table with LOD scores for the markers that are listed for each individual.
Use Hooks	Distinguishes between lines that cross over one another. **Note:** See "Overview of Pedigree Icons" on page 270 for a graphical depiction of hooks.
Show Blue ID #	Display a blue number next to an icon in a pedigree to indicate the ordering of individuals from left to right in a generation. **Note:** See "Overview of Pedigree Icons" on page 270 for a graphical depiction of blue numbers. You can change the position of blue numbers on the Dimensions tab.
Show Date	Display the current day's date in the upper left hand corner of the pedigree.
Header and Footer Information	Optional text-entry fields for header and footer information. **Note:** You set the display options for the header and footer on the Progeny tab.

Properties dialog box, Individual tab

You use the options on the Individual tab to change the properties of an individual icon. Select the icon the pedigree for which you are changing the properties (the selected icon becomes a double yellow square with handles on it), and then open the Individual tab on the Properties dialog box, and change the values for any and all options as needed.

Figure 5-5: Selected icon and relationship attachment points

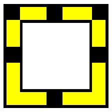
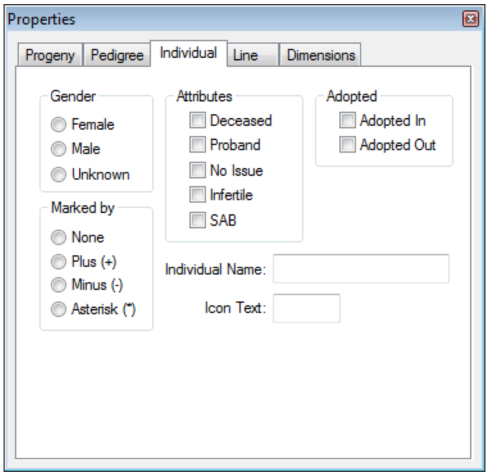


Figure 5-6: Properties dialog box, Individual tab



Option	Description
Gender	Change the gender of the selected individual.
Attributes	Select the attributes for the selected individual.
Adopted	Indicate the adoption status for the selected individual.
Marked By	Place the indicated symbol next to the selected individual.
Individual Name	Every individual in Progeny is assigned an individual name (a system field). When you are drawing a pedigree in Progeny the software automatically assigns an individual name to an individual. The default format for the Individual Name is: pedigree name _UPN. If needed, you can edit this default name here.
Icon Text	Enter in text that is to be displayed *inside* the individual icon. The text can be any number of alphanumeric characters or special characters.

Properties dialog box, Line tab

You use the options on the Line tab to change the properties of a relationship line. Select the line on the pedigree for which you are changing the properties, (a black dot is displayed at each end of a selected line), then open the Line tab on the Properties dialog box, and change the values for any and all options as needed.

Figure 5-7: Example of a selected line in a pedigree

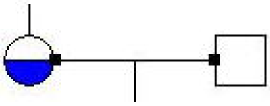
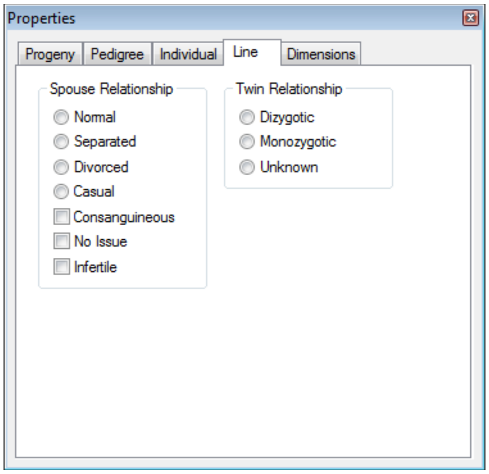


Figure 5-8: Properties dialog box, Line tab

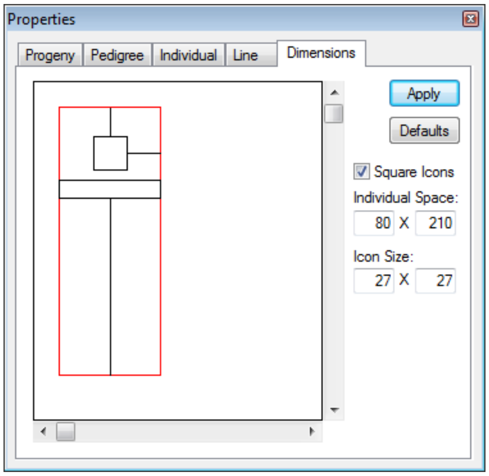


Option	Description
Spouse Relation	Applicable only for a selected spouse relationship line. The displayed line indicates the relationship between the spouses.
Twin Relationship	Applicable only for a selected twin relationship line. The displayed line indicates the relationship between the twins.

Properties dialog box, Dimensions tab

You use the options on the Dimensions tab to change the dimensions (Individual Space or Icon Size) of a pedigree.

Figure 5-9: Properties dialog box, Dimensions tab



☑ Square Icons

Individual Space: 80 X 210

Icon Size: 27 X 27

Option	Description
Individual Space	The space between individual icons in a pedigree.

<table>
<tr><th>Option</th><th>Description</th></tr>
<tr><td>Icon Size</td><td>The size of the icons that represent individuals in a pedigree.
Note: If Square Icons is selected, then the Icon Size is identical in both height and width.</td></tr>
<tr><td colspan="2">**Note:** You can also manually adjust the individual space and icon size. To move any object on the pedigree, simply click and hold your left mouse button on the object, drag the object to its new position, and then release the button. To change the size of an object, place the cursor on the edges of the object until the cursor changes to a double-headed arrow, and then drag the edge as needed to increase or decrease the size of the object.</td></tr>
</table>

Configuring Pedigree Icons

Configuring the icons that are used in a pedigree consists at a minimum of the following:

- Configuring the *icon subtext*, which is the text that is displayed above or below every icon on a pedigree.
- Configuring the *icon symbols*, which are symbols that graphically represent data about an individual on a pedigree.

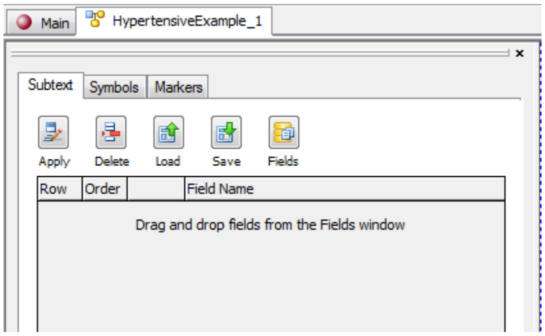
Also, if your implementation of Progeny Clinical contains the Marker module, you can also configure the subtext for marker icons, which are the color codes that are used to identify genotypes (marker values) in pedigrees.

To configure the icons for a pedigree

1. On the Progeny main window navigation bar, click the Pedigrees button to open the Pedigrees window.
2. Open the data folder that contains the pedigree for which you are configuring the icons.
3. Double-click on the pedigree name to open the Pedigree Drawing window, and on the window's main menu, click View > Icons.

   The Icon window opens in the left pane of the Pedigree Drawing window. The window has at least two tabs—Subtext and Symbols. (By default, the Subtext tab is the active tab.) In addition, if your implementation of Progeny Clinical contains the Marker module, then the window has a third tab—Markers.

Figure 5-10: Icon window, Subtext tab



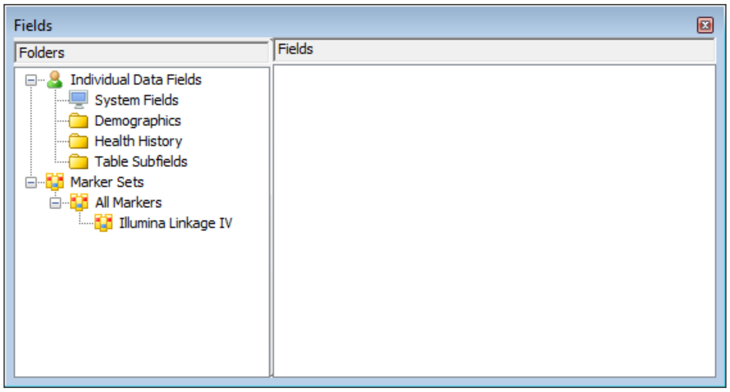
Drag and drop fields from the Fields window

4. Continue to one of the following:
   - "To configure the icon subtext for a pedigree" on page 278.
   - "To configure the icon symbols for a pedigree" on page 280.
   - "To configure icon markers for a pedigree" on page 283.

To configure the icon subtext for a pedigree

1. Click the Fields button to open the Fields dialog box.

Figure 5-11: Fields dialog box



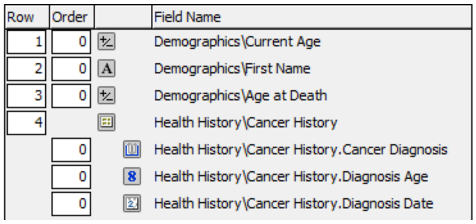
2. Drag each field that is to be displayed in the icon subtext from the Fields dialog box to the blank Subtext tab. When you are dragging the fields, note the following:

   - The order in which you drag the fields is the order from top to bottom in which the fields are displayed under an icon. (The Row Number for the field.)
   - You can change the row number for a field to change its display order. To display field above an icon, enter a negative row number, for example, -1.
   - The Order Number for a field indicates the order in which the fields that are contained in the same row are displayed. To change the order of fields within the same row, change the Order Number for the fields.
   - You can display table fields in icon subtext. When you drag a table field from the Field dialog box to the Subtext tab, all the table subfields are included under the table name. To include a table subfield in the icon subtext, enter a number in the blank field next to the table field. The number indicates the order in which the table subfields are displayed (from to top to bottom) in the icon subtext. If you drag a lookup table to the Subtext tab, then only the lookup table field is displayed on the tab. The lookup table subfields are not displayed.
   - If the data for a given subtext field is longer than nine characters, you must adjust the dimensions for the pedigree so that the entire icon subtext can be displayed. See "Properties dialog box, Dimensions tab" on page 275.
   - If you add a field in error, or decide that you want to delete a field, select the field, and then click the Delete button .

3. After you have ordered the icon subtext, click the Apply button Apply .

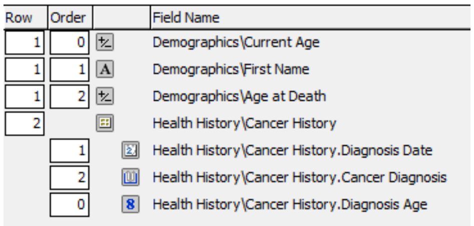
   Figure 5-12 below shows the ordering of the fields for icon subtext, and the resulting subtext.

Figure 5-12: Example of recording fields for icon subtext on a pedigree



Row	Order	Field Name
1	0	Demographics\Current Age
2	0	Demographics\First Name
3	0	Demographics\Age at Death
4		Health History\Cancer History
	0	Health History\Cancer History.Cancer Diagnosis
	0	Health History\Cancer History.Diagnosis Age
	0	Health History\Cancer History.Diagnosis Date

The order of the subtext fields after the initial selection.



Row	Order	Field Name
1	0	Demographics\Current Age
1	1	Demographics\First Name
1	2	Demographics\Age at Death
2		Health History\Cancer History
	1	Health History\Cancer History.Diagnosis Date
	2	Health History\Cancer History.Cancer Diagnosis
	0	Health History\Cancer History.Diagnosis Age

The reordering of the subtext fields and the subtext that results.

4. Do one of the following:

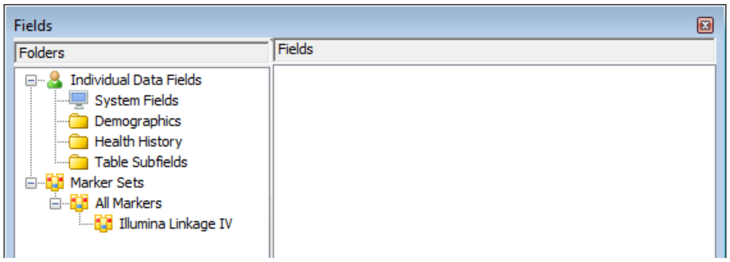
   - Click the Save button Save on the Pedigree Drawing window toolbar to save the icon subtext for the pedigree. You can always return to the pedigree and continue configuring the icons as needed.
   - Continue configuring the icons for the pedigree.

After you configure and save the icon subtext for a pedigree, you can the subtext as a format, and then load the format for other pedigrees. See "Saving and Loading Icon Formats" on page 285.

To configure the icon symbols for a pedigree

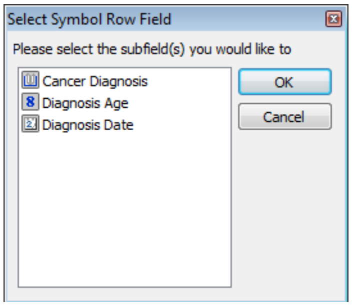
1. Open the Symbols tab.
2. Click the Fields button Fields to open the Fields dialog box.

Figure 5-13: Fields dialog box



3. Drag each field that is to be represented by a symbol from the Fields dialog box to the blank Symbols tab. When you are dragging the fields, note the following:
   - You can graphically represent the value for any database field, including system fields, and you can graphically represent ranges such as individuals with a current age > 50.
   - The order in which you drag the fields is the order from top to bottom in which the symbols are applied to the icon.
   - If you select a table field, then the Select Symbol Row Field dialog box opens. This dialog box lists all the table subfields. You must select the table subfields that are to be used as symbol rows. If you select a lookup table field, then only the lookup field is added to the Symbols tab. The lookup table subfields are not.

Figure 5-14: Select Symbol Row Field dialog box



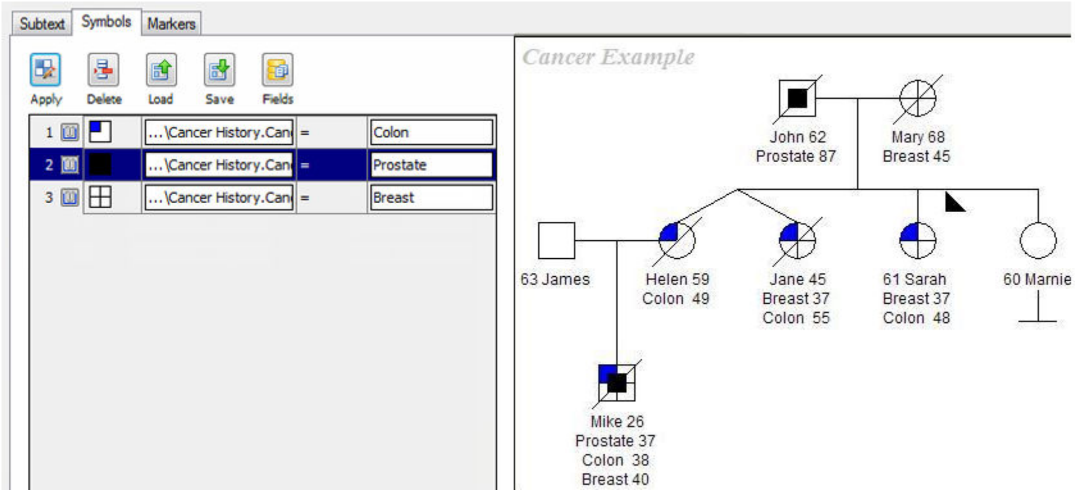
Please select the subfield(s) you would like to

   - You can drag the same field multiple times if the field multiple symbols are to be used for the field. For example, if you are creating a pedigree that shows the cancer history for a family, you could drag the Cancer Diagnosis field multiple times to apply the symbols for Cancer Diagnosis = Colon, Cancer Diagnosis = Prostate, and Cancer Diagnosis = Breast.

4. After you have selected all the fields to which symbols are to be applied, do the following for each field:
    - Click in the blank field next to the symbol field to open a dropdown list from which you can select the symbol for the field.

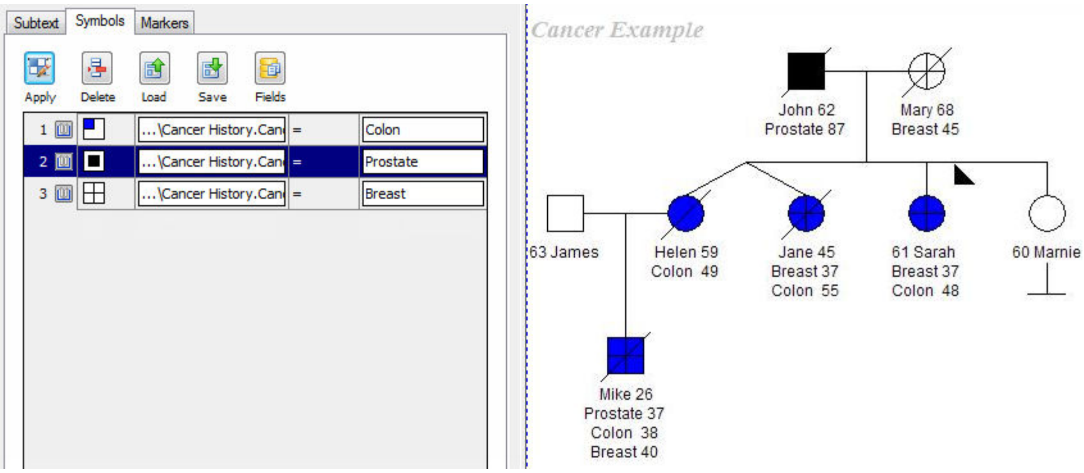
Because the order in which you drag the fields is the order from top to bottom in which the symbols are applied to the icon. make sure that you select symbols that do not overlay each other. See

Figure 5-15: Example of overlaying symbols



1	◰	...\Cancer History.Can	=	Colon
2	■	...\Cancer History.Can	=	Prostate
3	⊞	...\Cancer History.Can	=	Breast

Based on the order in which the symbols shown above are applied, then all three symbols would be visible when applied to the same icon (such as the case for the icon for the individual named Mike shown in the pedigree above).



1	◰	...\Cancer History.Can	=	Colon
2	▣	...\Cancer History.Can	=	Prostate
3	⊞	...\Cancer History.Can	=	Breast

Based on the order in which the symbols shown above are applied, if you selected the values shown above for symbol 1 and symbol 2, then if all three symbols were to be applied to an icon, symbol 1 would overlay symbol 2 and not be visible (such as the case for the icon for the individual named Mike shown in the pedigree above).

- Click in the blank field to the immediate right of the symbol field to open a dropdown list from which you can select an operator for the field. (See “Query operators” on page 173 for a detailed explanation of the operators.)
- Click in the blank field to the immediate right of the operator field and to select or enter a value for the dropdown list.
- If you add a field in error, or decide that you want to delete a field, select the field, and then click the Delete button Delete .

5. After you have selected all the necessary icon symbols, click the Apply button Apply .

6. Do one of the following:

   - Click the Save button Save on the Pedigree Drawing window toolbar to save the icon symbols for the pedigree. You can always return to the pedigree and continue configuring the icons as needed.
   - Continue configuring the icons for the pedigree.

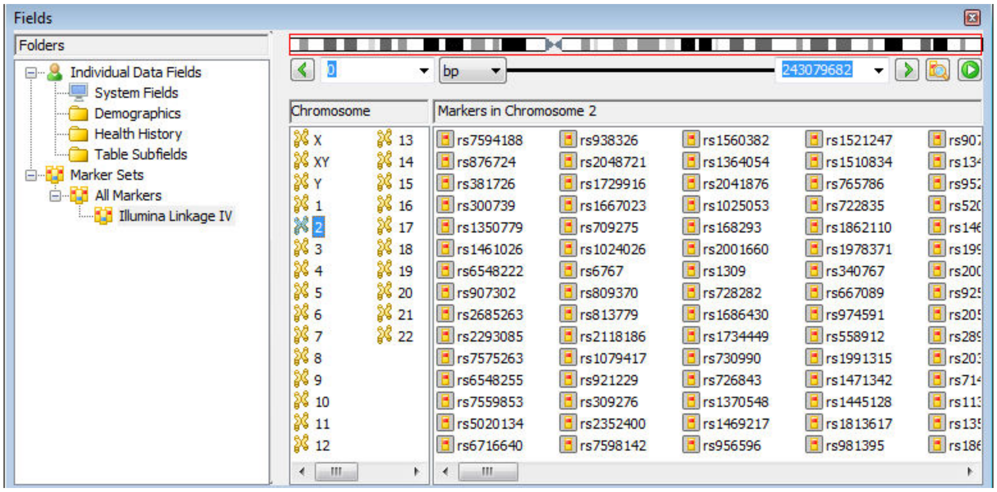
After you configure and save the icon subtext for a pedigree, you can the subtext as a format, and then load the format for other pedigrees. See “Saving and Loading Icon Formats” on page 285.

To configure icon markers for a pedigree

1. Open the Markers tab.
2. Click the Fields button Fields to open the Fields dialog box.

   The left pane of the dialog box lists available marker sets in the Progeny database. Select All Markers to open the list of available sets, and then select one of the sets to view the information for the markers contained in that set. The middle pane is the Chromosome List pane, which lists the chromosomes on which you can view or add markers. Select a chromosome to display an image of the chromosome above the top of the right pane. A list of the markers and SNPs that are found in the selected chromosome is displayed below the image in the right pane.

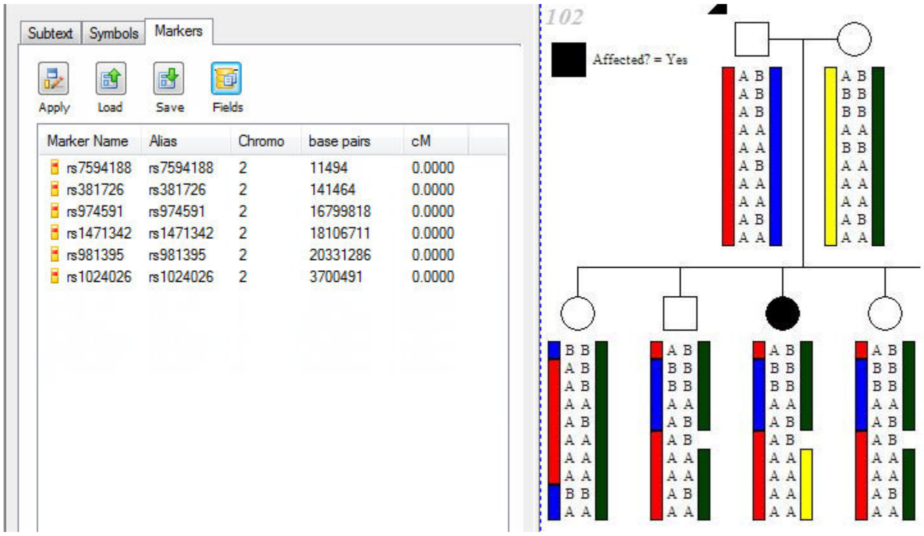
Figure 5-16: Fields dialog box for icon markers



3. Drag each marker that is to be displayed on the pedigree from the Fields dialog box to the blank Marker tab. As you select the markers that are to be displayed on the pedigree, note the following:
   - Make sure to drag the markers in order of *ascending* bps. The order in which you drag the markers is the order in which they are displayed under each icon in the pedigree
   - If you add a marker in error, or you decide you want to delete a specific marker, or all markers, then right-click on the *marker name* on the Markers tab, and on the context menu that opens, click Remove selected marker. To remove all markers in a single, right-click anywhere on the Markers tab, and on the context menu that opens, click Remove all markers.

   See Figure 5-17 on page 284 for an example of a pedigree that shows marker information.

Figure 5-17: Example of a pedigree showing icon markers



Marker Name	Alias	Chromo	base pairs	cM
rs7594188	rs7594188	2	11494	0.0000
rs381726	rs381726	2	141464	0.0000
rs974591	rs974591	2	16799818	0.0000
rs1471342	rs1471342	2	18106711	0.0000
rs981395	rs981395	2	20331286	0.0000
rs1024026	rs1024026	2	3700491	0.0000

4. After you have selected all the necessary icon symbols, click the Apply button Apply.

5. Do one of the following:

    - Click the Save button Save on the Pedigree Drawing window toolbar to save the icon symbols for the pedigree. You can always return to the pedigree and continue configuring the icons as needed.
    - Continue configuring the icons for the pedigree.

After you configure and save the icon subtext for a pedigree, you can the subtext as a format, and then load the format for other pedigrees. See "Saving and Loading Icon Formats" on page 285.

Saving and Loading Icon Formats

After you have configured the necessary icons (subtext, symbols, and markers) for a pedigree, you can save each configuration as an icon format. You can then load this format and apply it when needed to other pedigrees.

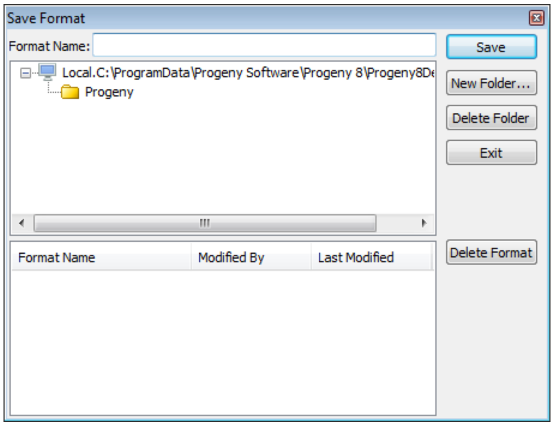
To save an icon format

The following procedure details how to save an icon subtext format, but by analogy, you can follow this procedure to save an icon symbol format and an icon marker format.

1. After you have configured the necessary icon subtext format, click the Save button .

   The Save Format dialog box opens. It provides a single default folders, Progeny, in which to save the icon format. (This folder is located in the database that you are currently logged in to and you cannot change this location.)

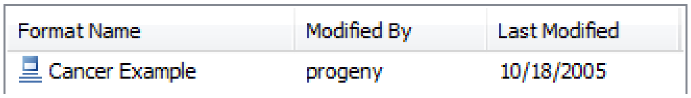
Figure 5-18: Save Format dialog box



2. Enter a name for the icon format, and then do one of the following:
   - Select the default folder.
   - Click New Folder, and on the Format Folder dialog box that opens, do the following:
     - Enter the name of the new folder in which to save to format.
     - Select the location for the new folder. The folder can be stored at the root level (the same level as the default folders), or it can be a sub-folder of another folder.
     - Click Save.

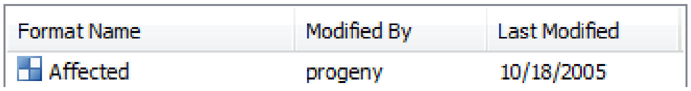
Ideally, you should save the different icon formats in different folders; however, if you save them in the save folder, then different icons are used to indicate the different formats. See Figure 5-19 on page 286.

Figure 5-19: Saved icon formats



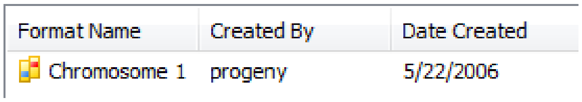
Format Name	Modified By	Last Modified
Cancer Example	progeny	10/18/2005

Saved icon subtext format.



Format Name	Modified By	Last Modified
Affected	progeny	10/18/2005

Saved icon subtext format.



Format Name	Created By	Date Created
Chromosome 1	progeny	5/22/2006

Saved icon marker format.

3. Click Save on the Save Format dialog box.

   You can now load this saved icon format and use it when drawing another pedigree. See "To load an icon format" below.

To load an icon format

You can load multiple saved formats (subtext, symbols, and markers) for a pedigree. The formats that are available for loading are specific for each tab. For example, if you are loading a subtext format, then the Subtext tab must be open. When you click the Load button on this tab, then the Load Format dialog box shows only the icon subtext formats that are available for loading. If you are loading different icon formats, then you must repeat Step 4 through Step 6 of the following procedure for each format that you are loading.

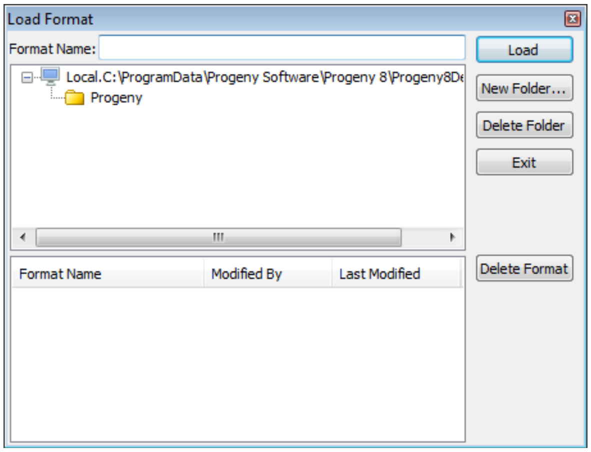
1. On the Progeny main window navigation bar, click the Pedigrees button to open the Pedigrees window.
2. Open the data folder that contains the pedigree for which you are loading the format(s).
3. Double-click on the pedigree name to the pedigree in the Pedigree Drawing window, and on the window's main menu, click View > Icons.

   The Icon window opens in the left pane of the Pedigree Drawing window.
4. Open the tab for which you are loading the format. For example, if you are loading a subtext format, then open the Subtext tab.

5. Click the Load button Load .

   The Load Format dialog box opens.

Figure 5-20: Load Format dialog box



6. Open the folder that contains the icon format that you are loading, select the format, and then click Load.

   The Load Format dialog box closes. The opened tab is refreshed with the information for the loaded icon format.

Manually Drawing a Pedigree

To manually draw a pedigree, you must manually add each individual that is to be contained in the pedigree, and you must manually add all the necessary relationships for each individual. Four ways of manually drawing a pedigree are available to you in Progeny. Although these methods are presented here as separate and distinct methods, you can actually combine various aspects from each of them and develop an approach that best suits your working needs. These methods are the following:

- Use the palette to add individuals to the pedigree and assign relationships between individuals. See “To manually draw a pedigree using the palette” on page 289.
- Use the palette to add individuals to the pedigree and then use the One-click Add function to assign relationships between individuals. See “To manually draw a pedigree using the One-click Add option” on page 291.
- Use the palette to add individuals to the pedigree and then use the Add Relation option on the pedigree context menu to assign relationships between individuals. See “To manually drawing a pedigree using the palette and Add Relation context menu option” on page 293.
- Create individuals in an individuals folder for which the Individual Datasheet template option has been selected, and then move these individuals from the individuals folder to a new or existing pedigree. See “To manually draw a pedigree after adding and moving individuals to a pedigree” on page 294.

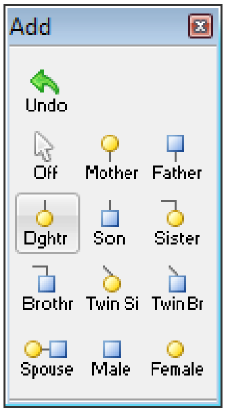
To manually draw a pedigree using the palette

Before you can use the palette to add relationships for an individual in pedigree, you must first add the individual as either a male or female. You can then add relationships (a Mother, a Father, a Son, and so on) for the individual.

1. On the Pedigree Drawing window toolbar, click the Palette button Palette.

   The Palette dialog box opens.

Figure 5-21: Palette dialog box



2. Click the Male or Female icon in the Palette dialog box and then click in the Pedigree Drawing window to add the selected individual as an unattached male or female to the pedigree.

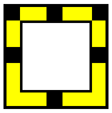
   Each time that you click in the Pedigree Drawing window, the icon is added to the pedigree until you click Off. For example, to add four unattached males to a pedigree, click the Male icon in the palette, click on the pedigree four times, and then click Off. After you have added an unattached individual to a pedigree, you can add the relationships for the individual.

To remove an icon from the pedigree, click Undo on the palette. This action removes the icons in the same order in which they were added- that is, the first icon that you added to the pedigree is the first icon that is deleted from the pedigree.

3. Click on the individual icon to which you are adding the relationships.

   The icon to which you are adding the relationships becomes a double yellow square with handles on it.

Figure 5-22: Selected icon and relationship attachment points



4. Click on the appropriate relationship icon on the palette, and then click on the selected individual icon. For example, to add a father relationship to an individual icon, click the Father icon on the palette, and then click on the selected individual icon. Repeat this step until you have added all the necessary relationships to an individual icon. When adding relationships to an individual icon, note the following:
    - Make sure to click Off on the Palette between selections of relationships.
    - If you add a relationship in error, or want to delete a relationship, click on the relationship line, (a black dot appears at each end of a selected line) and then click the [Delete] key on your keyboard.
    - To distinguish monozygotic and dizygotic twin relationships, or to change the properties of any other line (for example, to show a divorced relationship between spouses), see "Properties dialog box, Line tab" on page 274.
5. Optionally, do one or more of the following:
    - To add static text to the pedigree (free-standing text that is not tied to any icon on a pedigree), click the Add Text button Add Text to open a blank text box for entering the static text.

To resize the text box, drag the top, side, or corner handles. To move the text box to its needed location on the pedigree, click and hold your mouse pointer on the center of the text box and drag the text box to the correct location on the datasheet.

- If you have icons configured for the pedigree, and you want to display this information for the individuals on the pedigree, double-click on each individual icon to open the datasheet for the individual and enter the data for the individual.

6. When you are done adding individuals and their relationships to the pedigree, click the Save button Save .

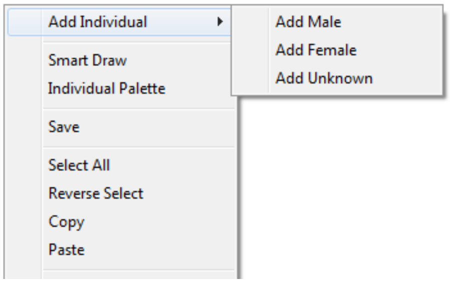
To manually draw a pedigree using the One-click Add option

The One-click Add function must be selected on the Properties dialog box. See "Properties dialog box, Progeny tab" on page 271.

1. Do one of the following:

    - Add all necessary individual icons to the pedigree using the palette. (See Step 1 and Step 2 of "To manually draw a pedigree using the palette" on page 289.)
    - Right-click anywhere in the blank Pedigree Drawing window, and on the context menu that opens, click Add Individual, and then click Add Male, Add Female, or Add Unknown as needed. Repeat this step until you have added all the necessary individual icons to the pedigree.

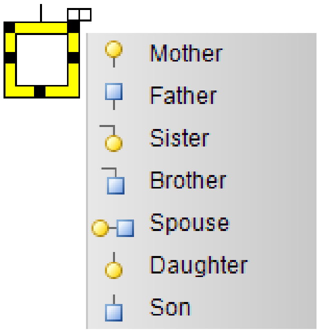
Figure 5-23:



2. Click on an icon to which you want to add relationships.

    The icon becomes a double yellow square and a list of relationships that you can add to the icon opens.

Figure 5-24: Selected icon with list of relationships



3. Select *each* relationship that is to be added to the icon. For example, to add a sister to the icon, click Sister on the list. To add a brother to the icon, click Brother on the list.

    The list of relationships open until you click on any blank white space in the Pedigree drawing window.

4. Repeat Step 2 and Step 3 until you have added all the necessary relationships for all individuals in the pedigree.

> *To distinguish monozygotic and dizygotic twin relationships, or to change the properties of any other line (for example, to show a divorced relationship between spouses), see "Properties dialog box, Line tab" on page 274.*

5. Optionally, do one or more of the following:
    - To add static text to the pedigree (free-standing text that is not tied to any icon on a pedigree), click the Add Text button Add Text to open a blank text box for entering the static text.

> *To resize the text box, drag the top, side, or corner handles. To move the text box to its needed location on the pedigree, click and hold your mouse pointer on the center of the text box and drag the text box to the correct location on the datasheet.*

    - If you have icons configured for the pedigree, and you want to display this information for the individuals on the pedigree, double-click on each individual icon to open the datasheet for the individual and enter the data for the individual.

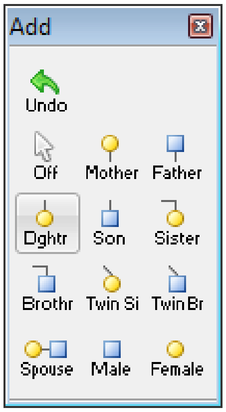
6. When you are done adding individuals and their relationships to the pedigree, click the Save button Save .

To manually drawing a pedigree using the palette and Add Relation context menu option

1. On the Pedigree Drawing window toolbar, click the Palette button Palette.

   The Palette dialog box opens.

Figure 5-25: Palette dialog box



2. Click the Male or Female icon in the Palette dialog box and then click in the Pedigree Drawing window to add the selected individual as an unattached male or female to the pedigree.

   Each time that you click in the Pedigree Drawing window, the icon is added to the pedigree until you click Off. For example, to add four unattached males to a pedigree, click the Male icon in the palette, click on the pedigree four times, and then click Off. After you have added an unattached individual to a pedigree, you can add the relationships for the individual.

To remove an icon from the pedigree, click Undo on the palette. This action removes the icons in the same order in which they were added- that is, the first icon that you added to the pedigree is the first icon that is deleted from the pedigree.

3. Right-click on an individual icon, and on the context menu that opens, click Add Relation, and then select the appropriate relation (Mother, Father, Sister, and so on) from the context menu.

4. Optionally, do one or more of the following:
    - To add static text to the pedigree (free-standing text that is not tied to any icon on a pedigree), click the Add Text button Add Text to open a blank text box for entering the static text.

To resize the text box, drag the top, side, or corner handles. To move the text box to its needed location on the pedigree, click and hold your mouse pointer on the center of the text box and drag the text box to the correct location on the datasheet.

- To distinguish monozygotic and dizygotic twin relationships, or to change the properties of any other line (for example, to show a divorced relationship between spouses), see "Properties dialog box, Line tab" on page 274.
- If you have icons configured for the pedigree, and you want to display this information for the individuals on the pedigree, double-click on each individual icon to open the datasheet for the individual and enter the data for the individual.

5. When you are done adding individuals and their relationships to the pedigree, click the Save button Save .

To manually draw a pedigree after adding and moving individuals to a pedigree

After you move individuals to a pedigree (see "Moving an Individual to a Pedigree" on page 234), all the icons for all the individuals are clustered in the upper left hand corner of the pedigree.

1. To move each icon, click and hold the left mouse button on the icon, and then drag the icon to its new location in the pedigree.
2. Use any of the available methods for manually drawing a pedigree. See
    - "To manually draw a pedigree using the palette" on page 289.
    - "To manually draw a pedigree using the One-click Add option" on page 291.
    - "To manually drawing a pedigree using the palette and Add Relation context menu option" on page 293.

3. Optionally, do one or more of the following:
    - To add static text to the pedigree (free-standing text that is not tied to any icon on a pedigree), click the Add Text button Add Text to open a blank text box for entering the static text.

To resize the text box, drag the top, side, or corner handles. To move the text box to its needed location on the pedigree, click and hold your mouse pointer on the center of the text box and drag the text box to the correct location on the datasheet.

    - If you have icons configured for the pedigree, and you want to display this information for the individuals on the pedigree, double-click on each individual icon to open the datasheet for the individual and enter the data for the individual.
4. When you are done adding individuals and their relationships to the pedigree, click the Save button Save .

Working with Individuals in a Pedigree

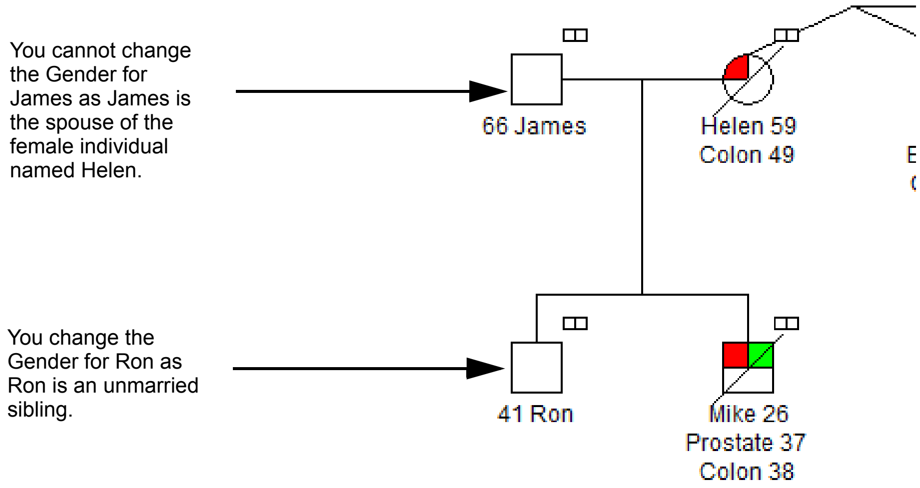
For any individual in a pedigree, you can do one or more of the following:

- Change the gender and/or vital status (Alive or Deceased). See "To change the gender and/or vital status of an individual in a pedigree" below.
- Move an individual or groups of individuals to another location in the pedigree. See "To move an individual in a pedigree" on page 297.
- Delete an individual from a pedigree. See "To delete an individual from a pedigree" on page 298.
- Select an individual based on its relationship. See "To select individuals in a pedigree based on relationships" on page 298.
- Correct any Mendelian errors for individuals for which haplotypes are displayed. See "To correct Mendelian errors for individuals in a pedigree" on page 300.
- View all the samples that are associated with an individual in a pedigree. See "To view all the samples associated with an individual in a pedigree" on page 301.

To change the gender and/or vital status of an individual in a pedigree

You can change the gender of an individual in a pedigree only if the individual is not in a *prohibitive relationship*. For example, if an individual female in a pedigree has a spouse relationship, you cannot change the individual from female to male.

Figure 5-26: Changing the gender of an individual in a pedigree



You cannot change the Gender for James as James is the spouse of the female individual named Helen.

You change the Gender for Ron as Ron is an unmarried sibling.

To change the gender and/or vital status of an individual in the pedigree, right-click on the individual, and on the context menu that opens, select Change Gender or Change Vital Status as appropriate. The icon for the individual is updated accordingly.

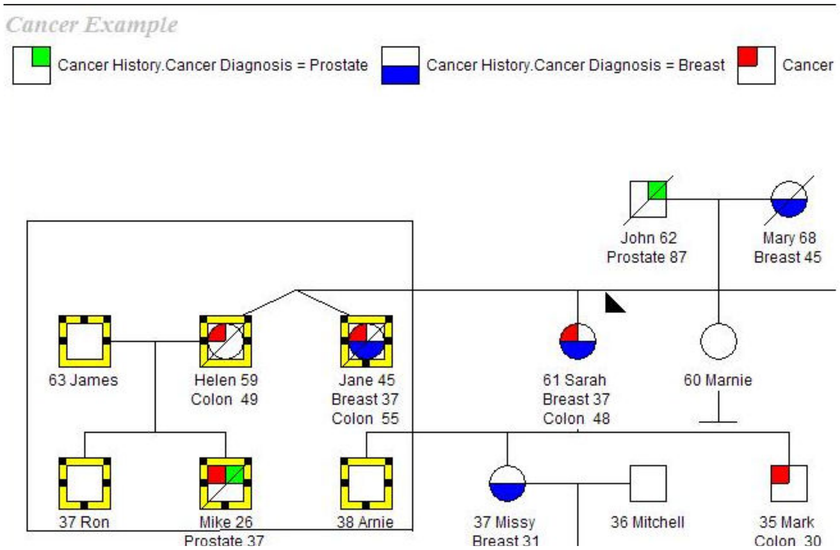
To move an individual in a pedigree

To move a single individual, simply drag the individual to its new location in the pedigree. To move a group of individuals, to the following:

1. Press and hold the left mouse button, and then drag the cursor around the group of individuals that are being moved.

   A box is drawn around the selected individuals.

Figure 5-27: Selecting multiple individuals to move in a pedigree



2. Click on one selected individual in the group, and then drag the entire group to its new location in the pedigree.

When you are moving individuals in the pedigree, if you reach the edge of the Pedigree Drawing window, the window automatically scrolls, allowing you to move across the entire pedigree without having to drop the individual.

3. After you have moved the needed individuals to their new locations, click the Save button Save .

To delete an individual from a pedigree

You can delete one or more individuals from a pedigree or you can delete individuals not only from the pedigree, but also, from the database.

1. Select the individual that is to be deleted from the pedigree. (CTRL-click to select multiple individuals).
2. Do one of the following:
    - Press the [Delete] key on your keyboard.
    - Right-click on any of the selected individuals, and on the context menu that opens, click Remove Individual From Pedigree or Delete Individual(s) from Database, as appropriate.
3. After you have deleted the needed individuals from the pedigree, click the Save button Save .

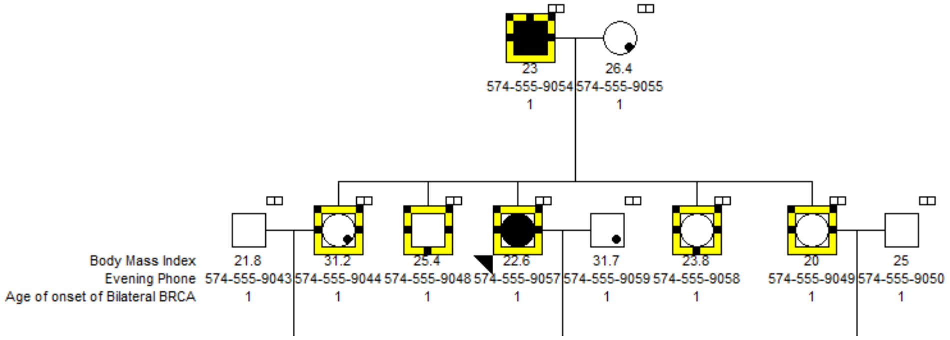
To select individuals in a pedigree based on relationships

You can select individuals in a pedigree based on their relationships such as first degree relationships, spouses, and so on. You can also select individuals in a pedigree based on relationships that they do not have, for example, all individuals who are not first degree relatives for an individual. This is known as a *reverse selection*.

To select an individual based on a relationship

Right-click on the individual in the pedigree, and on the context menu that opens, click Select, and then select the appropriate relationship. All the individuals that meet the relationship criteria are selected in the pedigree.

Figure 5-28: Selecting based on relationship - all first degree relatives shown for a selected individual

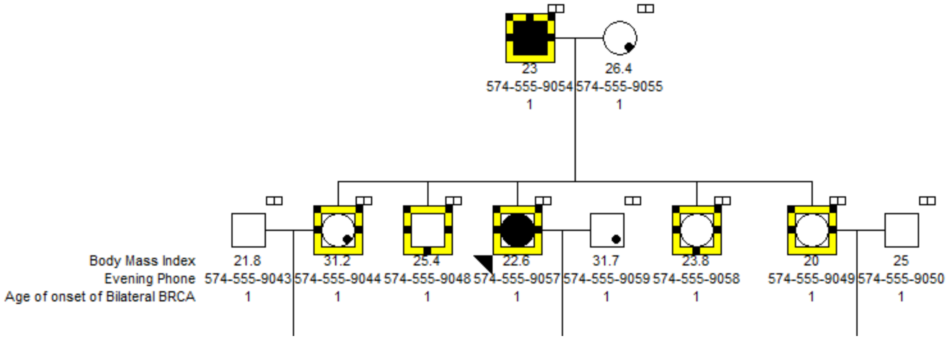


To selected an individual based on a reverse relationship

1. Right-click on the individual in the pedigree, and on the context menu that opens, click Select, and then select the appropriate relationship, for example First Degree.

   All the individuals that meet the relationship criteria are selected in the pedigree.

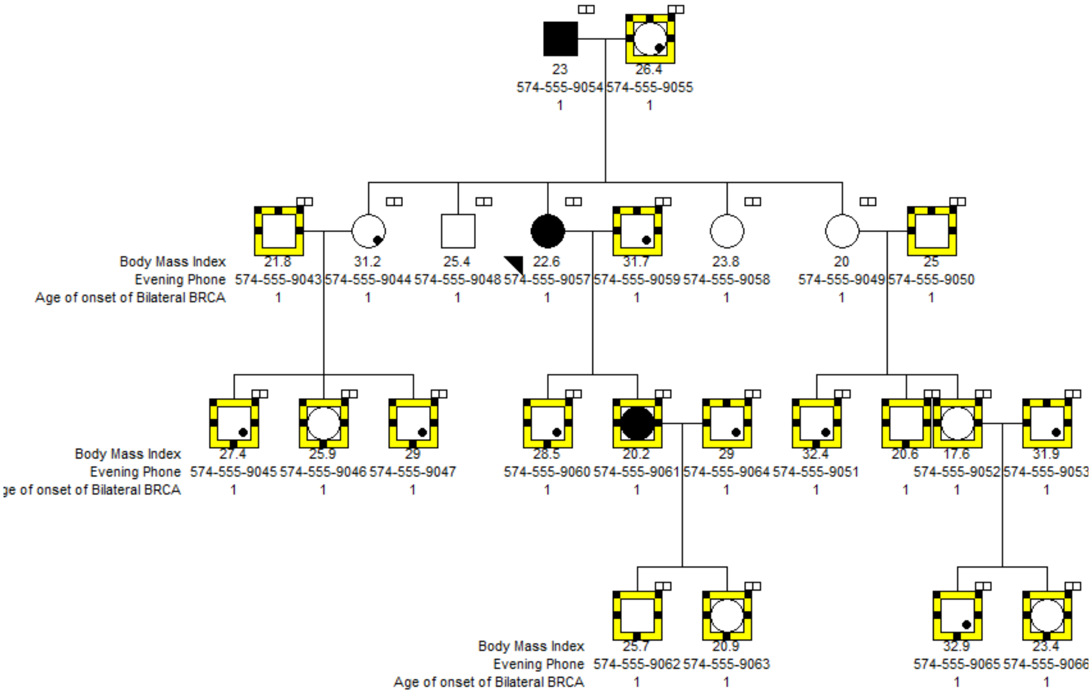
Figure 5-29: Selecting individuals based on relationship - all first degree relatives shown for a selected individual



2. With these individuals still selected in the pedigree, right-click on the pedigree, and on the context menu that opens, click Reverse Select.

   All the individuals that do no meet the relationship criteria are now selected in the pedigree.

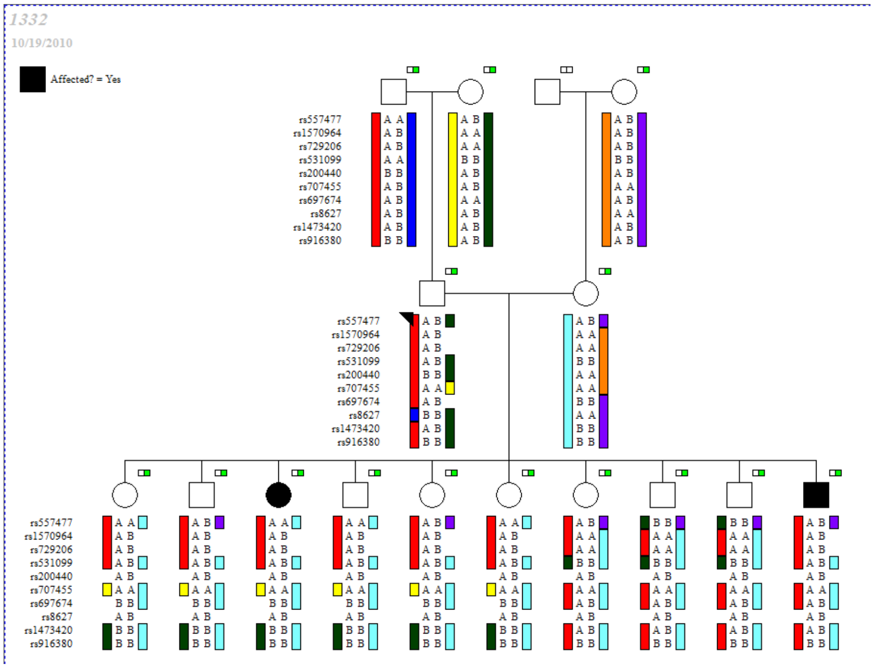
Figure 5-30: Selecting individuals based on a reverse relationship - all non-first degree relatives are shown for the selected individual



To correct Mendelian errors for individuals in a pedigree

1. Open the pedigree for which you are correcting the Mendelian errors.

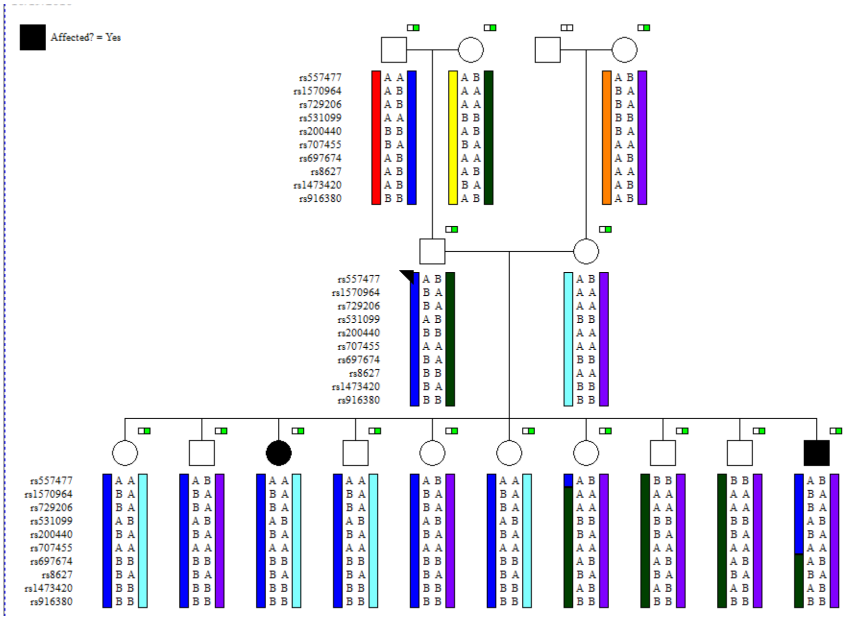
Figure 5-31: Pedigree showing Mendelian errors in individuals' haplotypes



2. Click the Haplotype button Haplotype on the Pedigree Drawing window toolbar.

   The Mendelian errors are corrected for all pertinent individuals in the pedigree.

Figure 5-32: Pedigree with Mendelian errors corrected

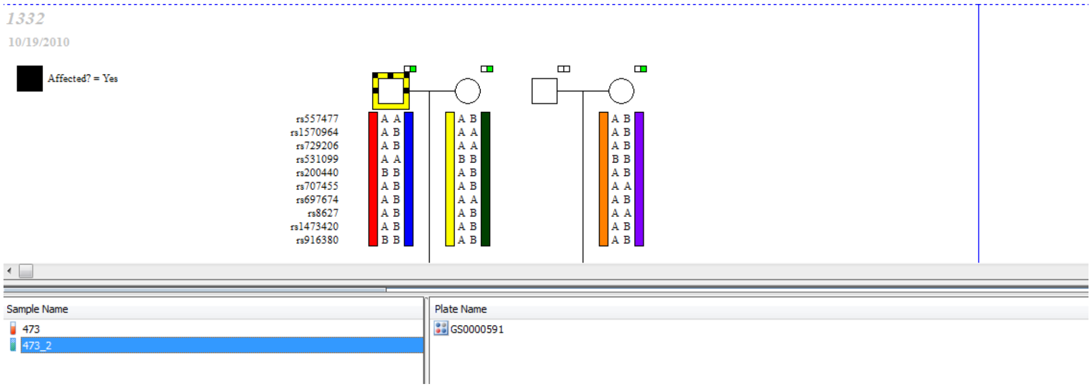


To view all the samples associated with an individual in a pedigree

1. Select the individual for whom you are viewing the samples.
2. Click the Samples button on the Pedigree Drawing window toolbar.

   A Samples Pane and Containers pane opens below the pedigree. The Samples pane lists all the samples that are associated with the selected individual. To view information about a sample, select the sample in the Samples pane.

Figure 5-33: Viewing samples associated with an individual in a pedigree



rs557477	A A	A B	A B
rs1570964	A B	A A	A B
rs729206	A B	A A	A B
rs531099	A A	B B	B B
rs200440	B B	A B	A B
rs707455	A B	A B	A A
rs697674	A B	A A	A B
rs8627	A B	A B	A A
rs1473420	A B	A B	A B
rs916380	B B	A B	A B

Sample Name	Plate Name
473	GS0000591
473_2	

3. To close the Samples and Containers panes, click the Samples button again.

Adding an Individual Shadow to a Pedigree

The *individual shadow* is a feature that indicates a complex marital relationship that otherwise would be shown as a single line that crossed the entire pedigree. For instance, you can add a shadow to display an individual in a second generation who is married to an individual in the first generation. An individual who is a shadow in pedigree is denoted with a thin, dark gray rectangle above its icon. A gray UPN number is displayed to the bottom right of the icon of the shadowed individual, indicating the UPN of the original individual on the pedigree.

Figure 5-34: Example of a individual shadow

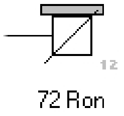
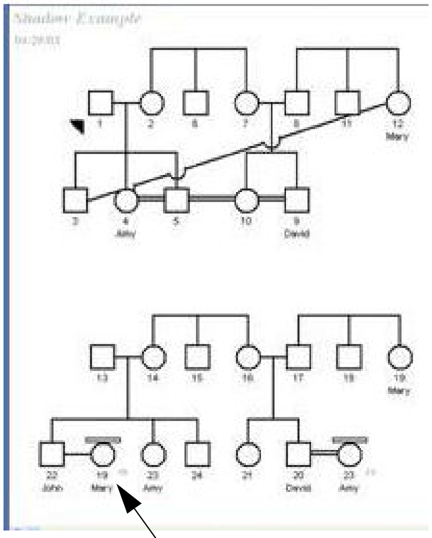


Figure 5-35: Example of a shadow in a pedigree



In the pedigree shown on top, Mary, a first generation individual is married to John, a second generation individual. The spouse line crossed the entire pedigree, from the upper right corner to the lower left corner, but even with hooks to show criss-crossing lines, the relationship is hard to discern.

In the pedigree shown on bottom, Mary, a first generation individual who is married to John, a second generation individual, is shown as a shadow next to John.

Shadow of Mary next to John.

The individual shadow icon is actually the same icon as the original individual. As a result, if you double-click on the icon to access the individual datasheet, the individual datasheet of the original individual on the pedigree is opened. To locate the original individual on the pedigree, right-click on the shadow icon and then click Jump (shadow) to select the icon for the original individual on the pedigree.

The One-click Add option cannot be selected for a pedigree in which you are creating a shadow individual. To turn off the One-click Add option, open the Progeny tab on the Properties dialog box, and clear the option. See "Properties dialog box, Progeny tab" on page 271.

To add an individual shadow to a pedigree

1. On the pedigree, select one of the spouse icons, press and hold the [CTRL] key, and from either of the spouse handles on the selected icon, drag a line to the other spouse icon.
2. Release the [CTRL] key only *after* the a set of crosshairs is displayed in the center of the spouse icon *to* which you are dragging the line.

   The shadow of the spouse icon is displayed next to the icon *from* which you dragged the line. For example, if you drag a line from the spouse John to the spouse Mary, then a shadow of Mary is displayed next to John.

Creating a Pedigree Thumbnail

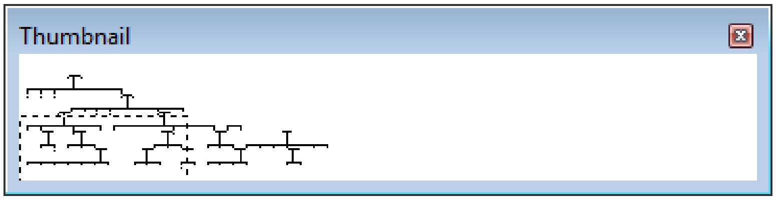
You use the Show Thumbnails option to create a *pedigree thumbnail*, which is a specific area of a pedigree in which to work without having to scroll up or down or left or right.

To create a pedigree thumbnail

1. On the Pedigree tab of the Properties dialog box, set the needed working scale for the pedigree. For example, set the scale to 200%. See "Properties dialog box, Pedigree tab" on page 272.
2. Right-click anywhere on a *blank* section of the pedigree, and on the context menu that opens, click Show Thumbnail.

   The entire pedigree is displayed in the Thumbnail window.

Figure 5-36: Thumbnail window showing a pedigree



3. In the Thumbnail window, click on the area of the pedigree in which you want to work.

   The pedigree is scaled in the Pedigree Drawing window to show only those individuals in the selected area. The Thumbnail window remains open.
4. Repeat Step 3 as many times as needed to complete your work on the pedigree.
5. After you have completed the necessary work on the pedigree, close the Thumbnail window, and then if needed, on the Pedigree tab of the Properties dialog box, reset the pedigree scale to its original value.

Chapter 6
Managing Samples

A *sample* is a part that is representative of a whole or a set of elements that is drawn from and analyzed to estimate the characteristics of a population. A sample can be an unassociated sample, or it can be associated with an individual. Managing samples in Progeny Clinical consists of creating new samples, creating sample datasheets, modifying samples, deleting samples, and importing sample data.

This chapter covers the following topics:

- "Manually Adding a New Sample" on page 307.
- "Creating a New Sample Datasheet" on page 311.
- "Modifying a Sample" on page 312.
- "Deleting a Sample" on page 313.

For detailed information about importing sample data, see Appendix B, "Importing Clinical Data," on page 559.

Manually Adding a New Sample

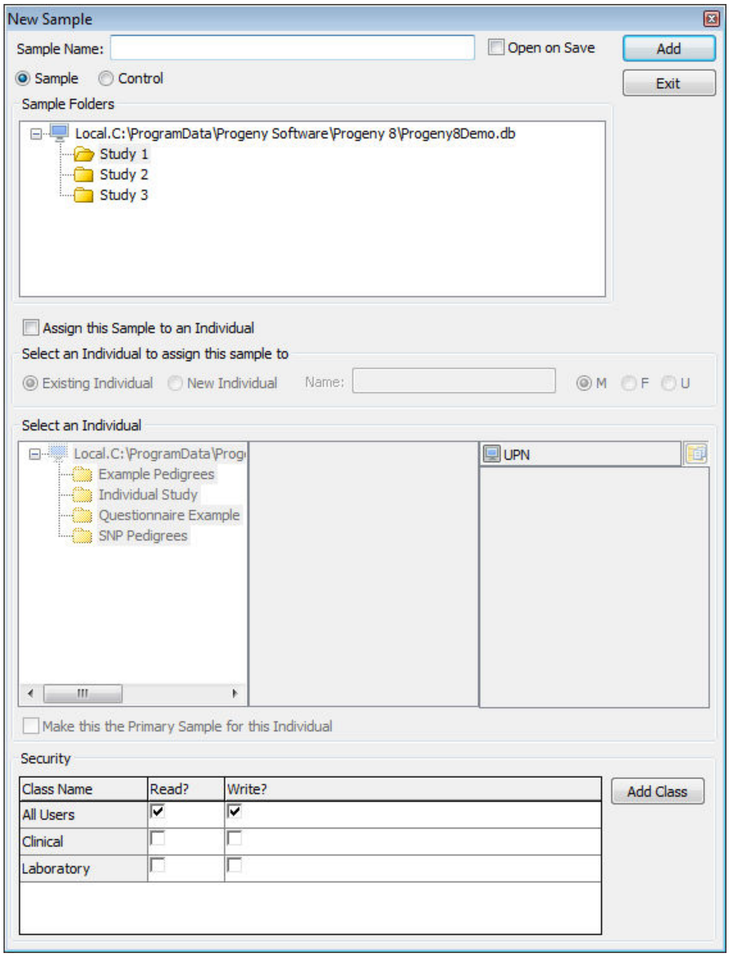
When you add a new sample to a Progeny database, you can add the sample as an unassociated sample, or you can associate the sample with an individual. You can add the sample as a “true” sample, or you can add the sample as a control.

To add a new sample

1. On the Progeny main window navigation bar, click the Samples button to open the Samples window.
2. On the Samples window, click the New Samples button.

   The New Sample dialog box opens.

Figure 6-1: New Sample dialog box



New Sample

Sample Name:

☐ Open on Save

● Sample ○ Control

Sample Folders

Local.C:\ProgramData\Progeny Software\Progeny 8\Progeny8Demo.db
  - Study 1
  - Study 2
  - Study 3

☐ Assign this Sample to an Individual

Select an Individual to assign this sample to

● Existing Individual ○ New Individual Name: ● M ○ F ○ U

Select an Individual

Local.C:\ProgramData\Prog
  - Example Pedigrees
  - Individual Study
  - Questionnaire Example
  - SNP Pedigrees

UPN

☐ Make this the Primary Sample for this Individual

Security

Class Name	Read?	Write?
All Users	☑	☑
Clinical	☐	☐
Laboratory	☐	☐

3. Enter the name for the new sample.

4. Select Sample.
5. Select the data folder to which the sample is being added.
6. Optionally, Select Open on Save.

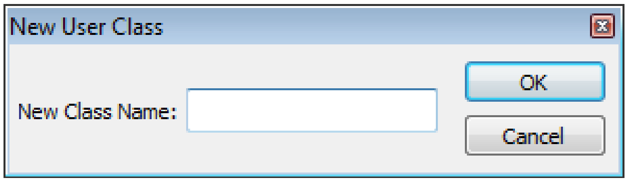
   If you select this option, then after you save the sample, the sample datasheet opens for the sample.

7. Optionally, assign the sample to an individual.
   - If you select Existing Individual, then you must select the individual from the available individuals in the database. The individual can be contained in an individual data folder or in a pedigree. If you select a pedigree, then after you select the pedigree, you must select the appropriate individual from the pedigree. In either case, the UPN is the default value for identifying the individual, but you can click the Fields button to open the Select Fields dialog box, and select another value for identifying the individual.
   - If you select New Individual, then you must enter a name for the individual, indicate the gender, and select a data folder to which to add the individual.
8. Optionally, if you assigned the sample to an individual, indicate if this sample is to be the primary sample for the individual.

If a sample is marked as the primary sample for an individual, then this is the sample that is exported when selecting an individual for a custom genotype export. See "Creating and Running a Custom Genotype Export" on page 439.

9. If you are the Progeny administrator, then do one or more of the following to set the security for the individual; otherwise, continue to Step 10.
   - Modify the security settings for All Users or for the different classes of users.
     - Read?—View the data (name and data in the sample datasheet) for the sample.
     - Write?—Write data (change the name and enter data to an sample datasheet) to the sample.
   - Click Add Class to open the New User Class dialog box to create a new user class, and then set the individual security for the new class.

Figure 6-2: New User Class dialog box



10. Click Save.

    A message opens indicating the settings for the sample were successfully changed.

11. Click OK to close the message and return to the Samples window.

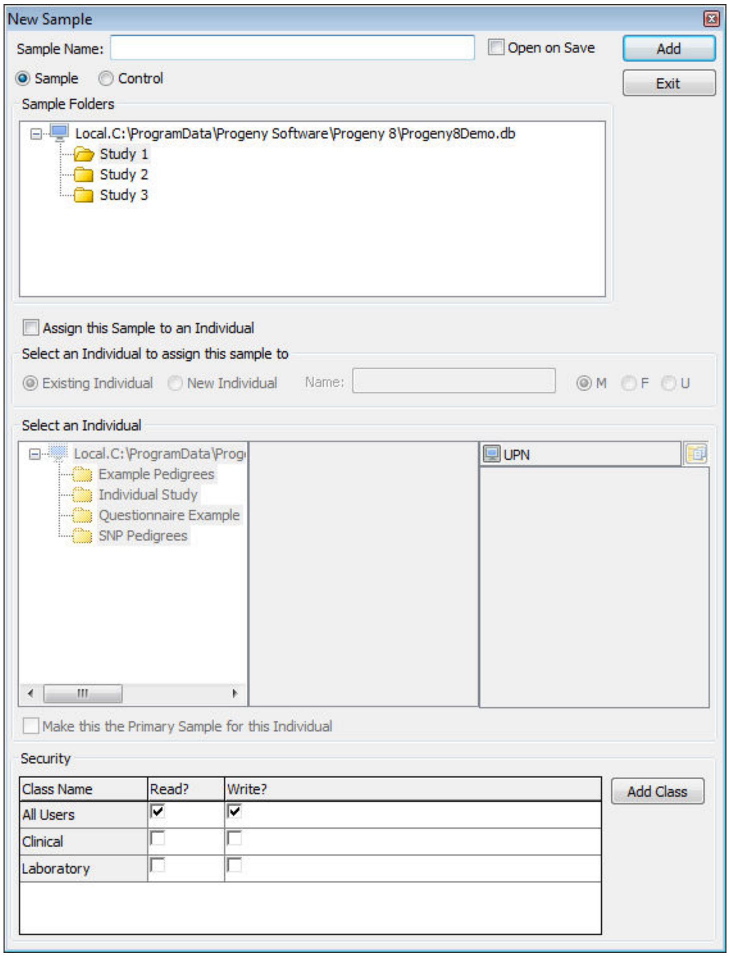
To add a new control

1. On the Progeny main window navigation bar, click the Samples button to open the Samples window.

2. On the Samples window, click the New Samples button New Sample.

   The New Sample dialog box opens.

Figure 6-3: New Sample dialog box



Class Name	Read?	Write?
All Users	☑	☑
Clinical	☐	☐
Laboratory	☐	☐

3. Enter the name for the new sample.

4. Select Control.

5. Select the data folder to which the sample is being added.

6. Optionally, Select Open on Save.

   If you select this option, then after you save the control, the sample datasheet opens for the control.

7. Click Save.

   A message opens indicating the settings for the sample were successfully changed.

8. Click OK to close the message and return to the Samples window.

Creating a New Sample Datasheet

You use a sample datasheet to enter and store data for a sample in a Progeny database. All the samples that are assigned to a sample data folder can use the same datasheet format, or each sample in the folder can use a unique datasheet format. You can create and format a sample datasheet at the time that you add a sample to a data folder, or at a later date.

To create a sample datasheet

1. Create a sample data folder.

   If all the samples that are assigned to the folder are to use the same sample datasheet format, make sure to select the Make this folder a template folder option; otherwise, clear it. See "Adding Sample Data Folders" on page 206.

2. Create a new sample and add the sample to the data folder. When you are creating the sample, do one of the following:

   - To have a blank datasheet open immediately after you save the sample, select Open on Save. You can click Form Design on this blank datasheet and format the datasheet as needed. If the Make this folder a template folder option has been selected for the data folder, then all the samples that you subsequently add to the folder will use the same datasheet format for entering and storing data; otherwise, you must format a datasheet for each sample that you add to the folder.
   - To add all samples to the folder before you create and format the datasheet, do not select Open on Save for any sample that you add to the folder. After you have added all of the needed samples to the folder, double-click on any sample in the folder to open a blank datasheet and format the datasheet as needed. If the Make this folder a template folder option has been selected for the data folder, then all samples that are currently added to the folder or that you subsequently add to the folder will use this same datasheet format for entering and storing data; otherwise, you must format a datasheet for each sample in the folder.

   See "Creating and Formatting Datasheets" on page 86 for detailed information about creating and formatting a sample datasheet.

Modifying a Sample

If you are the Progeny administrator, or your administrator has set Write access for the sample for your user account, you can rename a sample and modify the sample (such as assigning a sample to an individual.) As the Progeny administrator, you can also modify the security levels for the sample.

To modify a sample

1. On the Progeny main window navigation bar, click the Samples button to open the Samples window.
2. Open the data folder that contains the sample that is being modified.
3. Select the sample that is being modified, and on the main menu, click Samples, and then click the appropriate option.

Option	Description
Rename sample	Automatically selects the sample name for modification.
Edit Sample	Opens the Edit Sample dialog box in which you can edit the information for the sample (such as assigning the sample to an individual).
Edit Sample Security	Opens the Sample Security dialog box in which you can do one or both of the following: • Modify the security settings for All Users or for the different classes of users. • Read?—View the data (name and data in the pedigree datasheet) for the pedigree. • Write?—Write data (change the name and enter data to an pedigree datasheet) to the pedigree. • Click Add Class to open the New User Class dialog box to create a new user class, and then set the pedigree security for the new class.

4. Click Copy.

   A message opens indicating that the sample was successfully copied.

5. Click OK to close the message and return to the Samples window.

Deleting a Sample

Deleting a sample is a permanent event. After you delete a sample, you cannot recover it from the database.

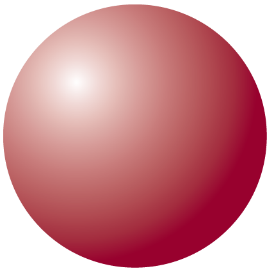
To delete a sample

1. On the Progeny main window navigation bar, click the Samples button to open the Samples window.
2. Open the data folder that contains the sample that is being deleted.
3. Select the sample that is being deleted (CTRL-click to select multiple samples), and on the main menu, click Samples > Delete Sample(s).

   A message opens asking you if you are sure that you want to delete the selected samples.
4. Click Yes.

   The message closes and the selected samples are deleted. You return to the Samples window.

Section 3



Progeny Lab

Section Contents

Chapter 1

Conventions and Samples Management in Progeny Lab

Progeny Lab is software that is designed for the management of whole genome association, targeted genotyping, and linkage studies. Progeny Lab is *always* sold with Progeny Clinical. As a result, Progeny Lab uses the same terms and conventions as Progeny Clinical. Also, many of the functions that are available in Progeny Lab, such as creating sample data folders, creating samples, importing samples, and so on, have already been detailed in the Progeny Clinical section in this manual, and therefore, do not need to be repeated in detail here. Instead, a summary list of these functions is provided in this chapter, and a link to a detailed discussion about each function is provided.

This chapter covers the following topics:

- "Conventions and Sample Management in Progeny Lab" on page 319.

Chapter 1
Conventions and Samples Management in Progeny Lab

Conventions and Sample Management in Progeny Lab

Progeny Lab is software that is designed for the management of whole genome association, targeted genotyping and linkage studies. Progeny Lab is *always* sold with Progeny Clinical. As a result, Progeny Lab uses the same terms and conventions as Progeny Clinical. Also, many of the functions that are available in Progeny Lab, such as creating sample data folders, creating samples, importing samples, and so on, have already been detailed in the Progeny Clinical section in this manual, and therefore, do not need to be repeated in detail here. Instead, a summary list of these functions is provided in this chapter, and a link to a detailed discussion about each function is provided.

- Terms and Conventions—Progeny Lab uses conventions in both its terminology and its output to ensure consistency and accuracy when you are manipulating and analyzing genetic data. The terms that are used in Progeny Lab are identical to those used in Progeny Clinical. See "Progeny Clinical Terms and Conventions" on page 197.
- Sample Management—Like Progeny Clinical, sample management in Progeny Lab consists of adding, modifying, and deleting sample folders, adding, modifying, and deleting samples, copying sample features, creating sample datasheets, and importing sample data. See the following for detailed information in the Progeny Clinical section about each of these sample management functions:
  - Adding, modifying and deleting sample folders (including copying samples features)—Chapter 2, "Managing Data Folders," on page 201.
  - Adding, modifying, and deleting samples (including creating a new sample datasheet)—Chapter 6, "Managing Samples," on page 305.
  - Importing sample data—Appendix B, "Importing Clinical Data," on page 559.

Chapter 1
Conventions and Samples Management in Progeny Lab

Chapter 2

Managing Markers

Progeny Lab provides functionality for adding markers from an entire genome-wide set (Affymetrix 10K, 100K or 500K, ABI 10cM, SNPlex or TaqMan, Illumina Custom, Golden Gate, 300K, 550K, or 650K, Sequenom, or any other user customized sets), from specific whole chromosomes, or from markers from a specific genomic region. Managing marker sets in Progeny Lab consists of importing marker sets, creating new marker sets, creating marker set formats,

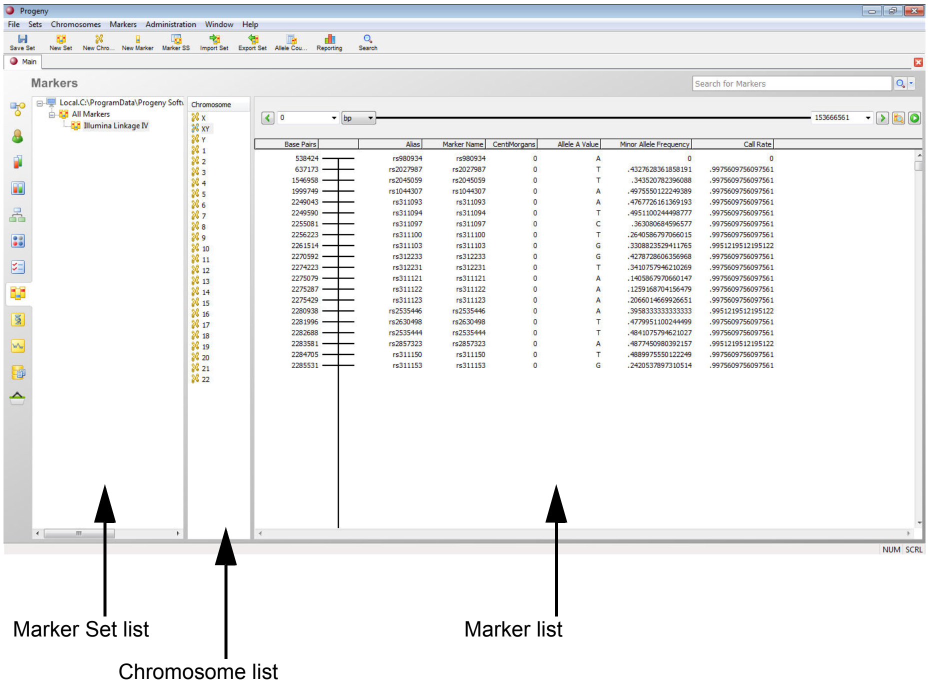
This chapter covers the following topics:

Markers Window

Progeny Lab provides functionality for adding markers from an entire genome-wide set (Affymetrix 10K, 100K or 500K, ABI 10cM, SNPlex or TaqMan, Illumina Custom, Golden Gate, 300K, 550K, or 650K, Sequenom, or any other user customized sets), from specific whole chromosomes, or from markers from a specific genomic region. The Markers window, which displays the information for a loaded marker set, is slightly different in its layout than for the Individuals, Pedigrees, or Samples window.

- The left pane displays the Market Set list, which is a list of marker sets that are available in a Progeny database. Select All Markers to view all available marker sets. Select one of the marker sets to view information only for the markers in the selected set.
- The middle pane displays the Chromosome list, which is a list of the chromosomes in the marker set. Select a chromosome in the list to view an image of the chromosome above the right pane.
- The right pane displays the Markers list, which is a list of markers and SNPs for a selected chromosome. From this pane, you can view or update the marker name, the marker alias, and the marker distance information.

Figure 2-1: Markers window



Base Pairs	Alias	Marker Name	CentiMorgans	Allele A Value	Minor Allele Frequency	Call Rate
538424	rs980934	rs980934	0	A	0	0
637173	rs2027987	rs2027987	0	T	.4327628361858191	.9975609756097561
1546958	rs2045059	rs2045059	0	T	.343520782396088	.9975609756097561
1999749	rs1044307	rs1044307	0	A	.4975550122249389	.9975609756097561
2249043	rs311093	rs311093	0	A	.4767726161369193	.9975609756097561
2249590	rs311094	rs311094	0	T	.4951100244498777	.9975609756097561
2255081	rs311097	rs311097	0	C	.363080684596577	.9975609756097561
2256223	rs311100	rs311100	0	T	.2640586797066015	.9975609756097561
2261514	rs311103	rs311103	0	G	.3308823529411765	.9951219512195122
2270592	rs312233	rs312233	0	G	.4278728606356968	.9975609756097561
2274223	rs312231	rs312231	0	T	.3410757946210269	.9975609756097561
2275079	rs311121	rs311121	0	A	.1405867970660147	.9975609756097561
2275287	rs311122	rs311122	0	A	.1259168704156479	.9975609756097561
2275429	rs311123	rs311123	0	A	.2066014669926651	.9975609756097561
2280938	rs2535446	rs2535446	0	A	.3958333333333333	.9951219512195122
2281996	rs2630498	rs2630498	0	T	.4779951100244499	.9975609756097561
2282688	rs2535444	rs2535444	0	T	.4841075794621027	.9975609756097561
2283581	rs2857323	rs2857323	0	A	.4877450980392157	.9951219512195122
2284705	rs311150	rs311150	0	T	.4889975550122249	.9975609756097561
2285531	rs311153	rs311153	0	G	.2420537897310514	.9975609756097561

Importing Marker Sets

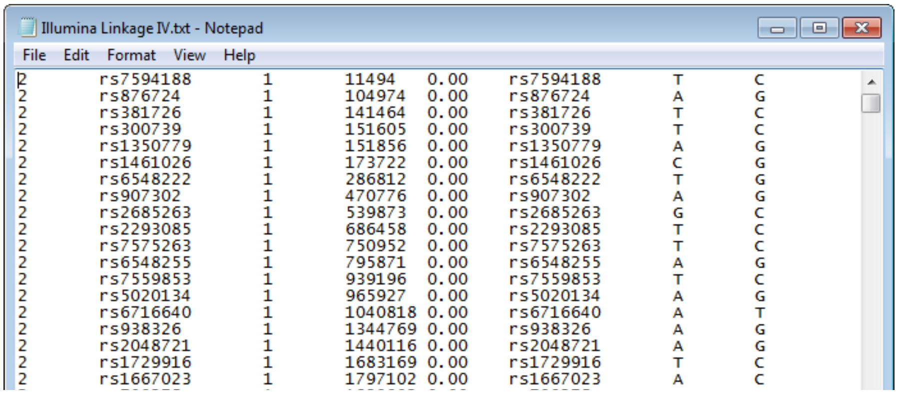
You use the Import Marker Set function to import complete marker sets into a Progeny database. You can import marker set information to update existing an existing marker set and you can import marker set information to create an entirely new marker set. For a *standard* import, the import file must be one of three allowed file types—a Standard (Progeny) format, an Illumina OP A Manifest, or an Affymetrix NetAffix Annotation File. (See "To import a standard marker set" on page 325.) If the import file is not one of these three allowed file types, then the file must be in a custom format and you must carry out a *custom* import. (See "To import a custom marker set" on page 326.)

Standard Progeny format

A Standard (Progeny) format must be a text file with a specific structure. Columns 1 through 4 are required. Columns 5 through 8 are optional. Each optional column must be located in its allocated column order. To use columns 7 and 8, you must have values in columns 5 and 6.

Column	Description
1	Chromosome – Chromosome on which the microsatellite or SNP is located.
2	Marker Name – Unique alphanumeric name or ID of the microsatellite or SNP.
3	Type – 0 to signify a microsatellite, 1 to signify a SNP
4	Base Pairs – Total number base pairs from the beginning of chromosome at which the marker is located.
5	cM – centiMorgan distance from the beginning of chromosome.
6	Alias Name – Alternative display name that is associated with the marker or SNP. For example, Affymetrix genotype calls uses the Affymetrix SNP ID instead of the rs number. If an alias name is not imported, the marker name is displayed in the marker map.
7	Allele A Value – Expected SNP value (ACGT).
8	Allele B Value – Stores expected ACG or T value. Available only for SNPs.

Figure 2-2: Example of a Standard (Progeny) import file

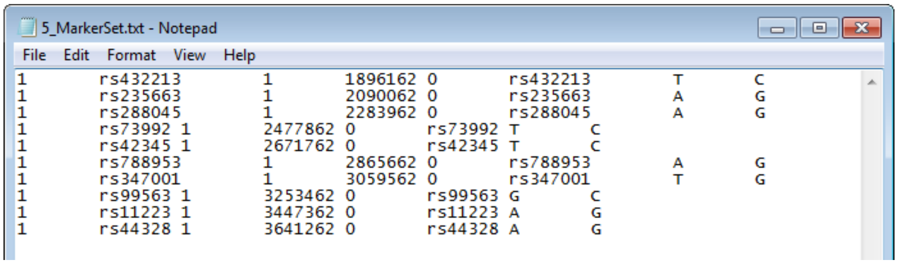


```
2        rs7594188      1       11494   0.00    rs7594188       T       C
2        rs876724       1       104974  0.00    rs876724        A       G
2        rs381726       1       141464  0.00    rs381726        T       C
2        rs300739       1       151605  0.00    rs300739        T       C
2        rs1350779      1       151856  0.00    rs1350779       A       G
2        rs1461026      1       173722  0.00    rs1461026       C       G
2        rs6548222      1       286812  0.00    rs6548222       T       G
2        rs907302       1       470776  0.00    rs907302        A       G
2        rs2685263      1       539873  0.00    rs2685263       G       C
2        rs2293085      1       686458  0.00    rs2293085       T       C
2        rs7575263      1       750952  0.00    rs7575263       T       C
2        rs6548255      1       795871  0.00    rs6548255       A       G
2        rs7559853      1       939196  0.00    rs7559853       T       C
2        rs5020134      1       965927  0.00    rs5020134       A       G
2        rs6716640      1       1040818 0.00    rs6716640       A       T
2        rs938326       1       1344769 0.00    rs938326        A       G
2        rs2048721      1       1440116 0.00    rs2048721       A       G
2        rs1729916      1       1683169 0.00    rs1729916       T       C
2        rs1667023      1       1797102 0.00    rs1667023       A       C
```

Custom import file format

In a custom import, you must identify the columns that contain the data that is to be imported into a Progeny database. The file can contain fields that currently exist in Progeny database as well as fields that do not currently exist in the Progeny database. At a minimum, the file must contain the Marker Name, the Chromo Name and the bp fields. Also, because all the marker sets that are defined in a custom file can be SNPs, microsatellites, or a mixture of both, then the file must also contain a column for designating the marker type (0 indicates a microsatellite, and 1 indicates an SNP).

Figure 2-3: Example of a custom import file



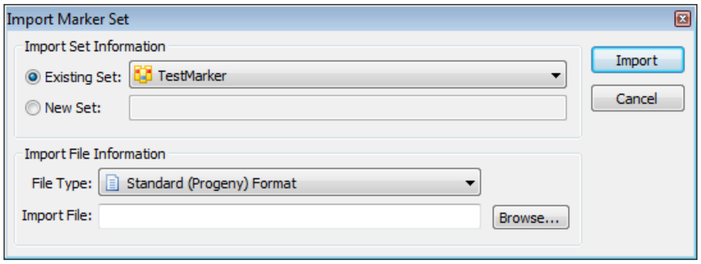
```
1       rs432213        1       1896162 0       rs432213        T       C
1       rs235663        1       2090062 0       rs235663        A       G
1       rs288045        1       2283962 0       rs288045        A       G
1       rs73992 1       2477862 0       rs73992 T       C
1       rs42345 1       2671762 0       rs42345 T       C
1       rs788953        1       2865662 0       rs788953        A       G
1       rs347001        1       3059562 0       rs347001        T       G
1       rs99563 1       3253462 0       rs99563 G       C
1       rs11223 1       3447362 0       rs11223 A       G
1       rs44328 1       3641262 0       rs44328 A       G
```

To import a standard marker set

1. On the Markers window toolbar, click the Import button Import.

   The Import Marker Set dialog box opens.

Figure 2-4: Import Marker Set dialog box



● Existing Set: TestMarker

○ New Set:

File Type: Standard (Progeny) Format

Import File:

2. If you are importing import marker set information to update existing an existing marker set, then select Existing Set; otherwise, select New Set, and then enter a name for the new marker set.
3. Select one of the following three file types—Standard (Progeny) format, Illumina OPA Manifest, or Affymetrix NetAffix Annotation File.
4. Click Browse to browse to and select the marker set import file.
5. Click Import.

   An Import Markers dialog box opens, indicating the progress of the import. When the import process is complete, a Market Set complete message opens, indicating the total number of marker sets that were successfully imported.

6. Click OK to close the message and return to the Markers window.

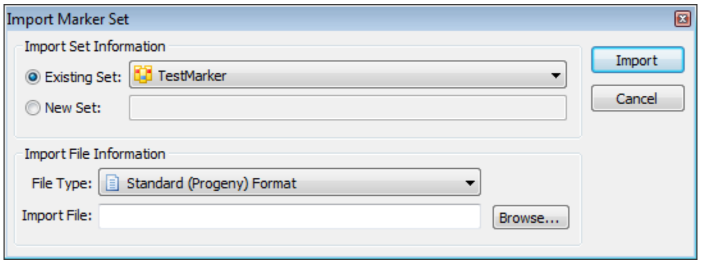
   The imported marker set is selected in the Markers window, and the information for the imported marker set is displayed in the window.

To import a custom marker set

1. On the Markers window toolbar, click the Import button .

   The Import Marker Set dialog box opens.

Figure 2-5: Import Marker Set dialog box



Import Marker Set

Import Set Information

● Existing Set: TestMarker

○ New Set:

Import File Information

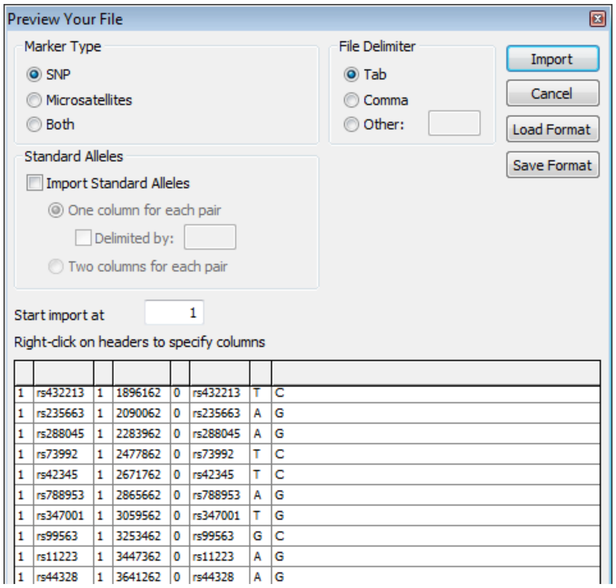
File Type: Standard (Progeny) Format

Import File:

2. If you are importing import marker set information to update existing an existing marker set, then select Existing Set; otherwise, select New Set, and then enter a name for the new marker set.
3. Select Custom Format for the file type.
4. Click Browse to browse to and select the marker set import file, and then click Import.

   An Import dialog box opens. The imported file is displayed in the Import Preview pane (bottom pane) of the dialog box.

Figure 2-6: Import dialog box



Preview Your File

Marker Type

● SNP

○ Microsatellites

○ Both

File Delimiter

● Tab

○ Comma

○ Other:

Standard Alleles

☐ Import Standard Alleles

● One column for each pair

☐ Delimited by:

○ Two columns for each pair

Start import at 1

Right-click on headers to specify columns

1	rs432213	1	1896162	0	rs432213	T	C
1	rs235663	1	2090062	0	rs235663	A	G
1	rs288045	1	2283962	0	rs288045	A	G
1	rs73992	1	2477862	0	rs73992	T	C
1	rs42345	1	2671762	0	rs42345	T	C
1	rs788953	1	2865662	0	rs788953	A	G
1	rs347001	1	3059562	0	rs347001	T	G
1	rs99563	1	3253462	0	rs99563	G	C
1	rs11223	1	3447362	0	rs11223	A	G
1	rs44328	1	3641262	0	rs44328	A	G

5. Select the delimiter that is used for the data in the import file. If you select Other, you must specify the character that is used for the delimiter.

6. Select the marker type that is contained in the import file. If you select SNP *and* your import file contains data for standard alleles, go to Step 7; otherwise, go to Step 8.

7. Select Import Standard Alleles, and then indicate how the data is represented.

    - One column for each pair - The standard alleles are contained within a single column. You must mark Allele AB in the Preview pane.
    - Two columns for each pair - The standard alleles are in separate columns. You must mark Allele A and Allele B in the Preview pane.

8. Specify starting row for the import.

9. In the Import Preview pane (the bottom pane of the Import dialog box), for each field that *exists* in the Progeny database, right-click in the column header and manually assign the appropriate heading. When you are finished assigning column headers to the existing fields, if your file contains only fields that are found in the Progeny database, then go to Step 11; otherwise, go to Step 10.

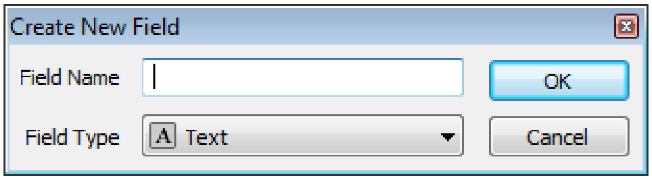
At a minimum, the file must contain the Marker Name, the Chromo Name, and the bp. If the file contains mixture of SNPs and microsatellites, then the file must also contain a column for designating the marker type (0 indicates a microsatellite, and 1 indicates an SNP).

10. For each field that is not contained in the Progeny database, right-click in the field, and then do one of the following:

    - To have the data imported into a new database field, select Create New Field.

      The Add a new Field dialog box opens. Enter a name for the new field in this dialog box, and optionally, select a different field type. The field will be created and the data for the individual will be imported into this field during the import process.

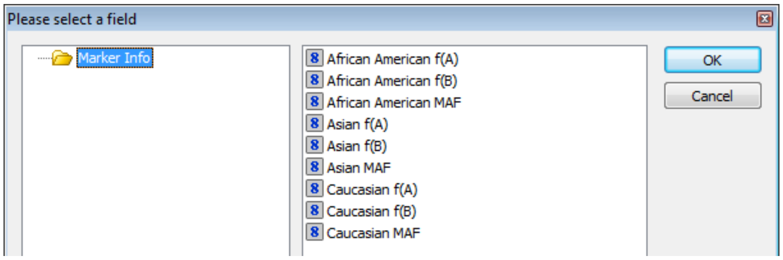
Figure 2-7: Add a New Field dialog box



- To have the data imported into an existing database, field, select Choose Existing Field.

  The Select Field dialog box opens, from which you can select an existing marker database field into which to import the data.

Figure 2-8: Select Field dialog box



Optionally, after you label a column, you can do one or both of the following:

- *To remove a column from the import, right-click on the column, and on the context menu that opens, select Ignore This Column.*
- *To update a column a column after it has been labeled, right-click on the column, and on the context menu that opens, select a different column label.*

11. Click Import.

    A Progeny Import Module dialog box opens, indicating the status of the import.

12. When the import is complete, click Close.

Saving and Loading an Import Format

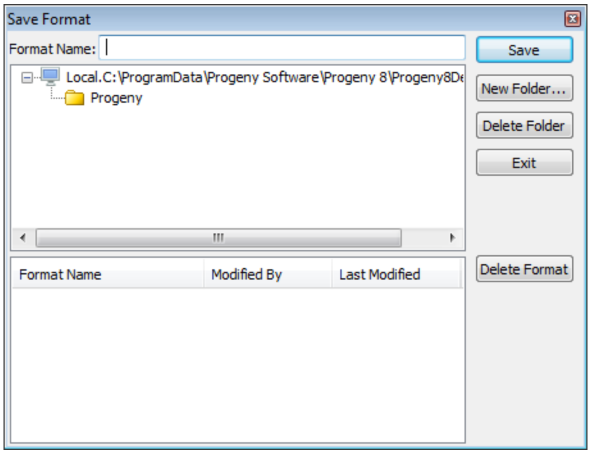
After you have set up an import format for a custom marker set, you can save the format. You can then load this saved format and run it on as-needed basis.

To save an import format

1. Set up the import format for the custom marker set, but do not click Import. See “To import a custom marker set” on page 326.
2. Click Save Format on the Import dialog box.

   The Save Format dialog box opens. It provides a default folder named Progeny in which to save the import format. (This folder is located in the database that you are currently logged in to and you cannot change this location.)

Figure 2-9: Save Format dialog box



3. Enter a name for the import format, and then do one of the following:
   - Select the Progeny folder.
   - Click New Folder, and on the Format Folder dialog box that opens, do the following:
     - Enter the name of the new folder in which to save to format.
     - Select the location for the new folder. The folder can be stored at the root level (the same level as the Progeny folder), or it can be a sub-folder of the Progeny folder, or of another folder.
     - Click Save.
4. Click Save on the Save Format dialog box.

   You can then load this saved format and run it on as-needed basis. See “To load an import format” on page 330.

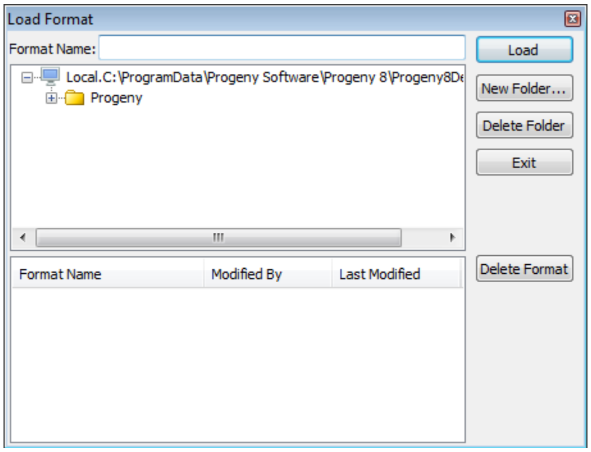
To load an import format

You can a retrieve a saved import format for a custom marker set and load it to import a data file with the appropriate type of data.

1. Open the Import dialog box. (See Step 1 through Step 4 of "To import a custom marker set" on page 326.)
2. On the Import dialog box, click the Load Format button Load Fmt.

   The Load Format dialog box opens.

Figure 2-10: Load Format dialog box



3. Open the folder that contains the import format that you are loading, select the format, and then click Load.

   The Import dialog box is refreshed with the loaded format. You can now browse to and select the import file, and then click Import to import the data according to the selected format.

Manually Adding New Markers

You can add custom markers from “scratch” in Progeny Lab by manually entering the information for the markers. The markers can be microsatellites or SNPs. You can add the new markers to an existing chromosome in an existing marker set, or you can add a new market set and/or new chromosome for the new markers as needed. You can add a new marker set and/or a new chromosome before you add the new markers, or you can add them at the time that you are adding the new markers.

To create a custom marker set by importing a file, see “To import a custom marker set” on page 326.

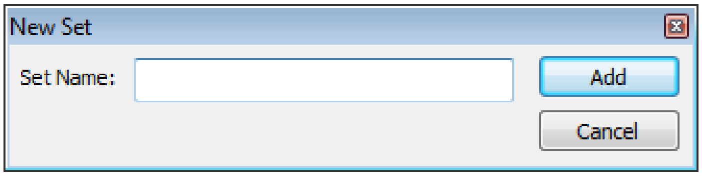
To add a new marker set

When you add a new marker set, you are essentially creating a placeholder for adding markers. All new marker sets are added at the root level (All Markers) for marker sets.

1. On the Markers window toolbar, make sure that All Markers is selected in the Marker Set pane.
2. Click the New Set button .

   The New Set dialog box opens.

Figure 2-11: New Set dialog box



3. Enter a name for the new marker set, and then click Add.

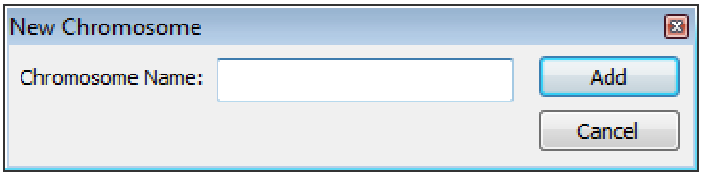
   The New Set dialog box closes. The new marker set is displayed in the Marker List in the Markers window.

To add a new chromosome

1. On the Markers window toolbar, click the New Chromosome button New Chro.. .

   The New Chromosome dialog box opens.

Figure 2-12: New Chromosome dialog box



2. Enter a name for the new chromosome, and then click Add.

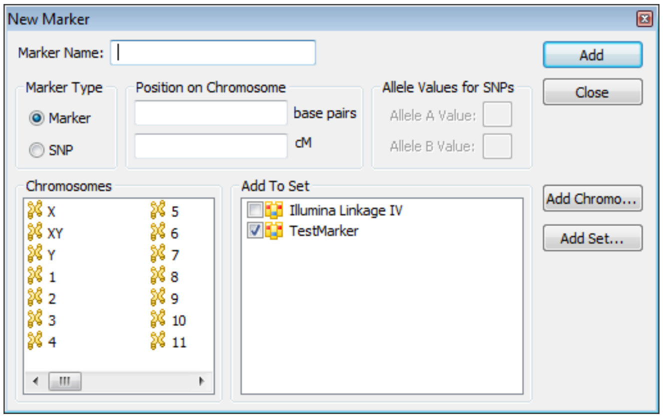
   The New Chromosome dialog box closes. The new chromosome is displayed in the Chromosome List in the Markers window.

To manually add new markers

1. On the Markers window toolbar, click the New Marker button New Marker .

   The New Marker dialog box opens.

Figure 2-13: New Marker dialog box



2. Enter the name for the new marker.
3. Select the appropriate marker type—Marker (microsatellite) or SNP.
4. Enter the position for the marker in base pairs for a microsatellite or cM for an SNP.
5. If the marker is an SNP, then enter the allele values for Allele A and Allele B. (Allowed values are A, C, G, or T).

6. Select the chromosome on which the marker is located.

If the chromosome does not exist, then click Add Chromo to open the New Chromosome dialog box and add a new chromosome.

7. Do one of the following:

    - To add the marker at the All Markers level, do not select any marker sets in the Add to Set pane.
    - To ad the marker to a specific marker sets, select these marker sets in the Add to Set pane.

If the marker set does not exist, then click Add Set to open the New Set dialog box, and add a new marker set.

8. Click Add.

    The Add a New Marker dialog box closes. The new marker is added to the marker list on the selected chromosome.

Modifying Marker Information

You can modify the following information for a marker in a marker set:

- The base pair size
- The marker name (Available only at the All Markers level)
- The marker alias (Applicable only for custom or imported markers.)
- The cM distance

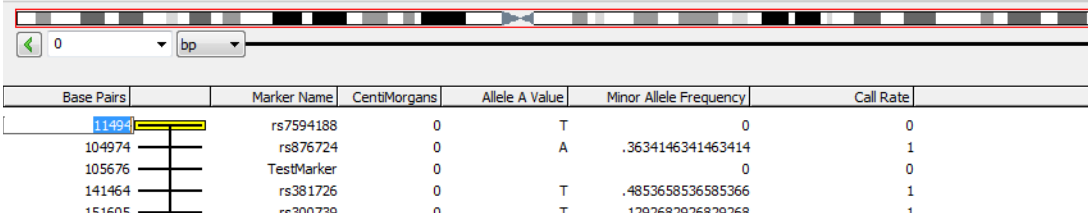
To modify marker information

1. Locate the marker for which you are modifying the information in the Markers window.

If you are modifying the marker name, then you must locate the marker at the All Markers level. You can modify the marker alias only for custom or imported markers.

2. Click *once* on the information that you modifying to select it, and then modify the information as needed.

Figure 2-14: Example of a marker bps selected for modifying



Base Pairs		Marker Name	CentiMorgans	Allele A Value	Minor Allele Frequency	Call Rate
11494		rs7594188	0	T	0	0
104974		rs876724	0	A	.3634146341463414	1
105676		TestMarker	0		0	0
141464		rs381726	0	T	.4853658536585366	1

Deleting Markers

You can delete a marker from a marker set, or you can delete a marker from a Progeny database.When you delete a marker from a set, the marker is not deleted from the database. The marker is still listed at the All Markers level, and can be added back to the set, or to another set. To delete a marker from the database, you must delete the marker at the all Markers level.

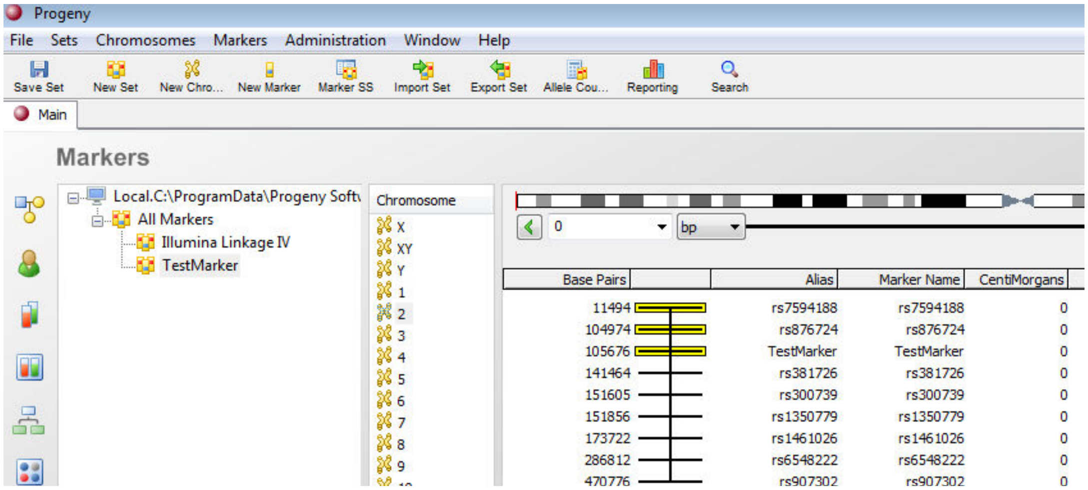
To delete a marker from a set

1. Locate the markers that you are deleting in the Markers window.

⚠ *The markers must be in a marker set, and not at the All Markers level.*

2. Select the marker that is to be deleted (CTRL-click to select multiple markers), and then do one of the following:
    - Press the [Delete] key on your keyboard.
    - Right-click on any of the selected markers, and on the context menu that opens, click Remove Selected Marker(s) from the Set.

Figure 2-15: Example of a markers selected for deletion from a set



Base Pairs		Alias	Marker Name	CentiMorgans
11494		rs7594188	rs7594188	0
104974		rs876724	rs876724	0
105676		TestMarker	TestMarker	0
141464		rs381726	rs381726	0
151605		rs300739	rs300739	0
151856		rs1350779	rs1350779	0
173722		rs1461026	rs1461026	0
286812		rs6548222	rs6548222	0
470776		rs907302	rs907302	0

3. A message opens asking you if you are sure that you want to delete the selected markers.
4. Click Yes.

   The message closes and the markers are deleted.

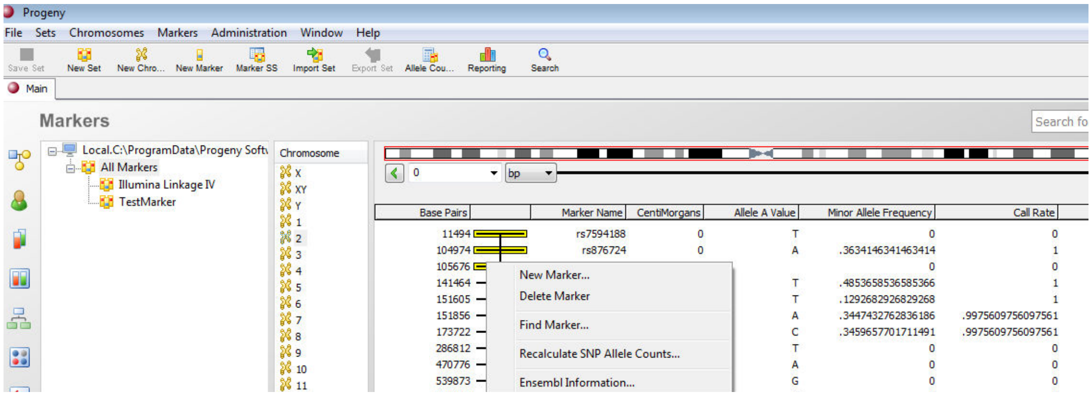
To delete a marker from the database

1. Make sure that you are logged in to the dabase from which you are deleting the marker.
2. Locate the marker that you are deleting in the Markers window.

⚠ *The markers must be at the All Markers level.*

3. Select the marker that is to be deleted (CTRL-click to select multiple markers), and then do one of the following:
   - Press the [Delete] key on your keyboard.
   - Right-click on any of the selected markers, and on the context menu that opens, click Delete Marker.

Figure 2-16: Example of a markers selected for deletion from a the database



Base Pairs	Marker Name	CentiMorgans	Allele A Value	Minor Allele Frequency	Call Rate
11494	rs7594188	0	T	0	0
104974	rs876724	0	A	.3634146341463414	1
105676				0	0
141464			T	.4853658536585366	1
151605			T	.1292682926829268	1
151856			A	.3447432762836186	.9975609756097561
173722			C	.3459657701711491	.9975609756097561
286812			T	0	0
470776			A	0	0
539873			G	0	0

4. A message opens asking you if you are sure that you want to delete the selected markers.
5. Click Yes.

   The message closes and the markers are deleted.

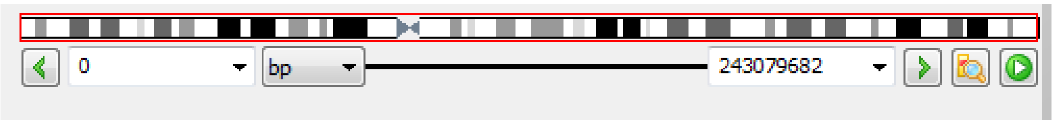
Searching for a Marker

Two methods are available to you for searching for a specific marker in a Progeny database—the Marker filter and the Find Marker function.

To search using the Marker filter

The Marker filter is located in the right pane of the Markers window above the Markers list. A figure of a chromosome is displayed above the filter. When the Markers window first opens, the entire chromosome is surrounded by a red location rectangle. The bp range for all the markers in the All Markers list is displayed.

Figure 2-17: Marker filter



Do one of the following:

- On the dropdown list, select the option by which to search (bp, cM, name, or alias information), enter the search criteria, and then click the Run button to search for the markers that meet the criteria.
- Carry out a contextual search for the marker or markers. See "Contextual Search" on page 179.

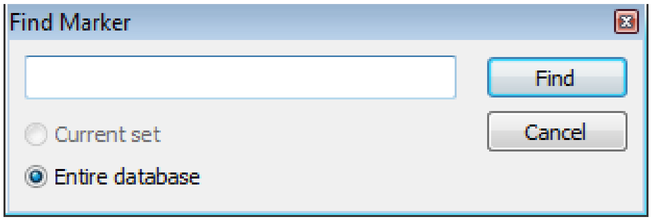
The markers that meet the search criteria are displayed in the Markers list, and the location rectangle is moved to the appropriate area on the chromosome. If you entered a distance as a search criteria (either bp or CM), then you can click the Jump buttons at either end of the filter to continue searching based on the distance criteria. For example, if your search filter is set from 1000000 bp to 2000000 bp, then click the Jump Forward button to change the filter to 200000 through 3000000 bp and update the Markers list accordingly.

To search using the Find Marker function

1. Click the Find Marker button below the chromosome image.

   The Find Marker dialog box opens.

Figure 2-18: Find Marker dialog box



○ Current set

● Entire database

2. Enter the name or alias of the marker for which you are searching.

You must enter the marker name or alias exactly as it is stored in the database, but the search is not case-sensitive. For example, RS238976 and rs238976 return exactly the same marker.

3. Select Current Set or Entire database.

Any marker set can be selected if you select Entire database. If you select Current Set, make sure that the set that you want to search is indeed the selected set in the Markers window.

4. Click Find.

   If the marker is found, Progeny switches the view to the corresponding set and chromosome and highlights the marker.

Exporting Marker Sets

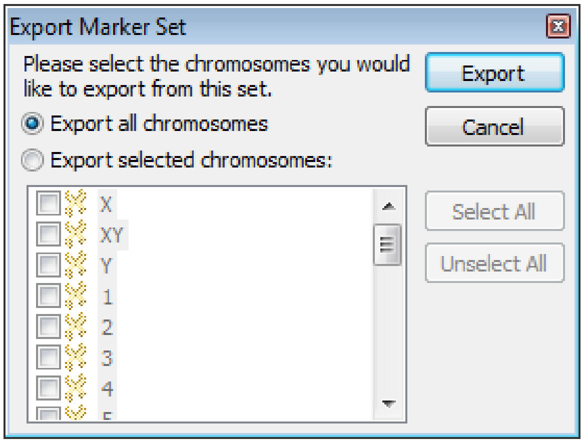
You can export marker sets for chromosomes including positioning information. You can export marker sets for all chromosomes, or for only selected chromosomes. A Marker Set export file is formatted according to the Standard (Progeny) file format.

To export marker sets

1. On the Markers window, select the marker set for which you are carrying out the export.
2. On the Markers window toolbar, click the Export Set button Export Set .

   The Export Marker Set dialog box opens.

Figure 2-19: Export Marker Set dialog box



Export Marker Set

Please select the chromosomes you would like to export from this set.

● Export all chromosomes

○ Export selected chromosomes:

3. Select Export all chromosomes, or select Export selected chromosomes, and then select the chromosomes for which the marker sets are to be exported.
4. Click Export.

   The Save As dialog box opens. The Save as Type field is automatically populated with the file type of text (.txt) and you cannot change this value.
5. Browse to the location in which the exported file is to be saved, and then in the File name field, enter a name for the file.
6. Click Save.

   A message opens indicating the Export operation was successful.
7. Click OK to close the message and return to the Markers window.

Recalculating Allele Counts for a Marker Set

You use the Allele Counts function to update the counts of AA, AB, BB, and NoCall counts for each SNP, which, in turn, allows for the calculation of the Hardy Weinberg p-value, the minor allele frequency, the degree of heterozygosity, and call rates. You might also want to recalculate allele counts if you have manually updated genotypes.

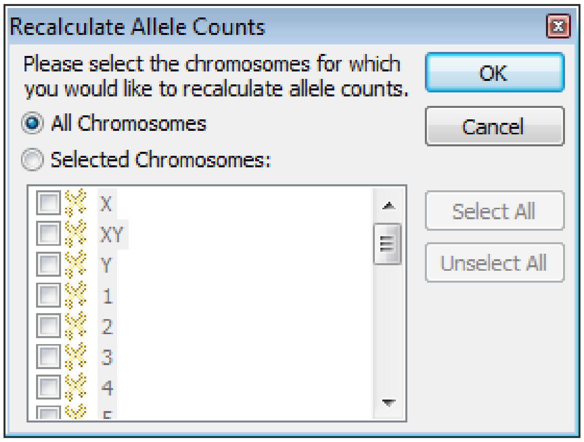
To recalculate allele counts for a marker set

1. On the Markers window, select the marker set for which you are recalculating the allele count.

2. On the Markers window toolbar, click the Export Set button Allele Cou... .

   The Recalculate Allele Counts dialog box opens.

Figure 2-20: Recalculate Allele Counts dialog box



Recalculate Allele Counts

Please select the chromosomes for which you would like to recalculate allele counts.

● All Chromosomes

○ Selected Chromosomes:

☐ X
☐ XY
☐ Y
☐ 1
☐ 2
☐ 3
☐ 4

3. Select All chromosomes, or select Selected chromosomes, and then select the chromosomes for which the allele counts are to be recalculated.

4. Click OK.

   A Recalculate Allele Counts dialog box opens, indicating the progress of recalculating the allele counts.

5. When the recalculation is complete, click Close to close the dialog box and return to the Markers window.

Formatting a Marker Datasheet

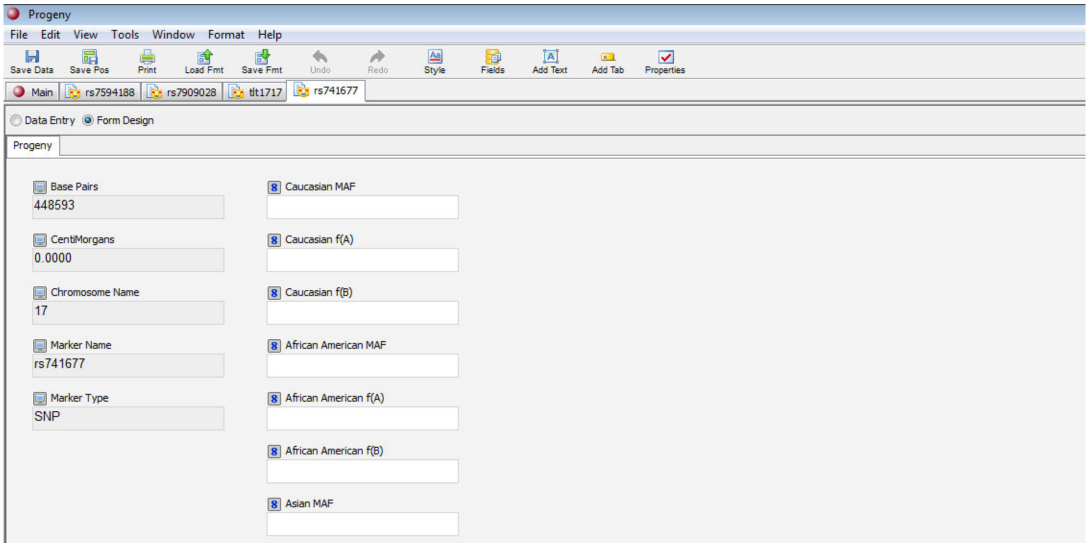
You use a marker datasheet to enter and store data for a marker in a Progeny database. When you create a new marker, a marker datasheet is automatically created for the marker. All marker datasheets are created with the same five system fields and the same nine Marker Info fields. You can add more system fields and Marker Info fields to a marker datasheet. All markers that are in the same set use the same datasheet format.

To format a marker datasheet

1. On the Markers window, select the marker set for which you are formatting the datasheet.
2. Double-click one of the markers in the marker set.

   The marker datasheet opens.

Figure 2-21: Marker datasheet



○ Data Entry ● Form Design

Base Pairs: 448593
CentiMorgans: 0.0000
Chromosome Name: 17
Marker Name: rs741677
Marker Type: SNP

3. If needed, you can add more fields to the datasheet. See Chapter 3, “Datasheet Basics,” on page 83.

Chapter 3
Managing Genotypes

Progeny Lab provides functionality for importing genotypes directly from supported file formats such as Illumina, Affymetrix, ABI, Sequenom, as well as other formats. You can also manually enter genotypes.

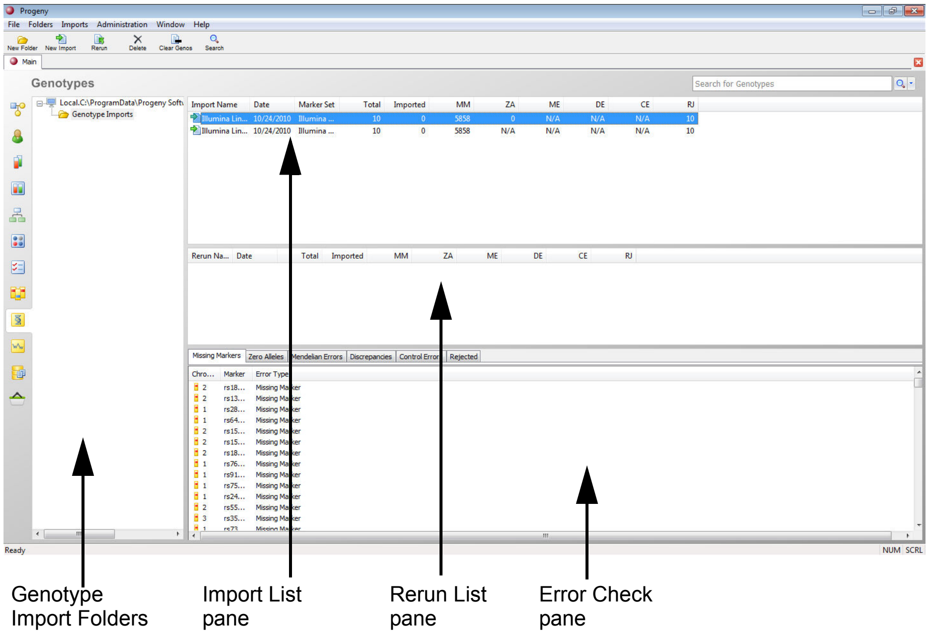
This chapter covers the following topics:

The Genotypes Window

The Genotypes window, which displays the information for imported genotypes is slightly different in its layout than for the Individuals, Pedigrees, or Samples window.

- The left pane displays the genotype import folders, which are the folders that hold all of the genotypes that have been imported into a Progeny database.
- The upper right pane displays the Genotype Import list, which is a list of all the imports that are contained ina specific genotype import folder. The pane displays the following information (from left to right) for an import—the import name, the import date, the name of the marker set used for comparison and error checking the import, the total number of markers in the set, the total number of markers imported, the total number of missing markers (MM) in the import, the total number of zero alleles (ZA) in the import, the total number of Mendelian errors (ME) in the import, the total number of discrepancies in the import, the total number of control errors (CE) in the import, and the total number of data lines rejected from the import.
- The middle right pane displays the Rerun Import list, which is a list of all the imports that were rerun for an original import. The pane displays the same information for a rerun as the top pane displays for an original import.
- The bottom right pane, or Error Check pane, displays expanded information for each error check that was carried out for an original import or a rerun. To view the results of a specific type of error check for an import or rerun, select the import or rerun in the appropriate pane of the Genotypes window, and then open the needed tab in the Error Check pane. (By default, the Missing Markers tab is the active tab for the pane when the Genotypes window first opens.)

Figure 3-1: Genotypes window



Import Name	Date	Marker Set	Total	Imported	MM	ZA	ME	DE	CE	RJ
Illumina Lin...	10/24/2010	Illumina ...	10	0	5858	0	N/A	N/A	N/A	10
Illumina Lin...	10/24/2010	Illumina ...	10	0	5858	N/A	N/A	N/A	N/A	10

Chro...	Marker	Error Type
2	rs18...	Missing Marker
2	rs13...	Missing Marker
1	rs28...	Missing Marker
1	rs64...	Missing Marker
2	rs15...	Missing Marker
2	rs15...	Missing Marker
2	rs18...	Missing Marker
1	rs76...	Missing Marker
1	rs91...	Missing Marker
1	rs75...	Missing Marker
1	rs24...	Missing Marker
2	rs55...	Missing Marker
3	rs35...	Missing Marker

Importing Genotypes

Progeny Lab provides functionality for importing genotype files in one of three ways:

- Using a Standard Import format.
- Using one of the following third party formats—Illumina, ABI, or Affymetrix.
- Using a Custom Import format.

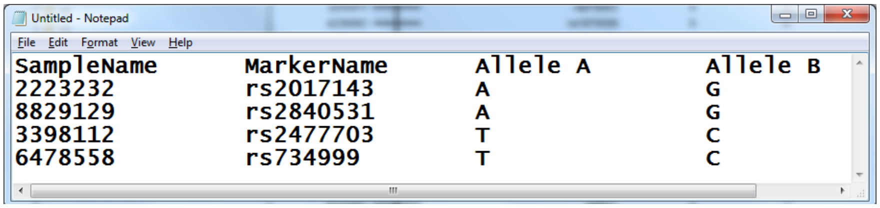
The Custom Import Format is the preferred option because you can specify the exact layout of the file you are importing, which includes designating the data that is contained in each column of the file to ensure compatibility.

Standard Import format

A Standard Import format must be a tab-delimited text file with a specific structure.

Column	Description
1	The sample name. All alphanumeric characters are allowed, and there is no limit on the number of characters.
2	The marker name. All alphanumeric characters are allowed, and there is no limit on the number of characters.
3	The value for allele 1. **Note:** For microsatellites, there are no restrictions on the data that can be displayed in this column. For SNPs, the value can be either an A or a B, or it can be an A, C, G, or T.
4	The value for allele 2. **Note:** For microsatellites, there are no restrictions on the data that can be displayed in this column. For SNPs, the value can be either an A or a B, or it can be an A, C, G, or T.

Figure 3-2: Example of a Standard import file



```
SampleName      MarkerName      Allele A        Allele B
2223232         rs2017143       A               G
8829129         rs2840531       A               G
3398112         rs2477703       T               C
6478558         rs734999        T               C
```

Illumina Final Report Format

The Illumina Final Report Format is an output format that is generated by the Illumina platform. Because of the number of iterations that can cause compatibility issues with the Progeny application, Progeny strongly recommends that you use the Custom Import Format instead. By using the Custom Import Format, you can specify the file layout and import the data as indicated in the file.

ABI

The ABI format is an output format that is generated by the Applied Biosystems by Life Technologies platform. Because of the number of iterations that can cause compatibility issues with the Progeny application, Progeny strongly recommends that you use the Custom Import Format instead. By using the Custom Import Format, you can specify the file layout and import the data as indicated in the file.

Affymetrix files

The Affymetrix CHP file, the Affymetrix GDAS Text Output Format , and the Affymetrix GTYPE Text Output Format are output formats that are generated by the Affymetrix platform.

- Each Affymetrix CHP file contains a single sample. The Affymetrix file name is either the exact name of the sample name or it can also contain an underscore with additional text, such as 223339_axt3343. If the file contains an underscore with additional text, Progeny ignores this additional text during the import. For instance, 223339_axt3343 is imported as 223339.
- Because of the number of iterations that can cause compatibility issues with the Progeny application, Progeny strongly recommends that you use the Custom Import Format in lieu of either the Affymetrix GDAS Text Output Format or the Affymetrix GTYPE Text Output Format. By using the Custom Import Format, you can specify the file layout and import the data as indicated in the file.

Custom import file format

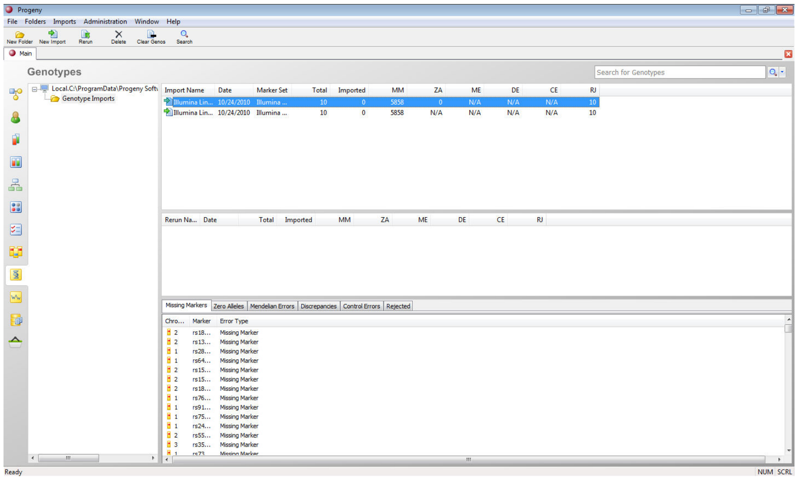
A custom genotype file can have one of three formats:

- One row per call—Calls in row, with the following columns: Unique ID, Marker Name, Allele 1, and Allele 2.
- One row per sample—Samples in rows with markers in columns
- One row per marker—Markers in rows with samples in columns

To import genotypes

1. On the navigation bar, click the Genotypes button to open the Genotypes window.

Figure 3-3:   Genotypes window



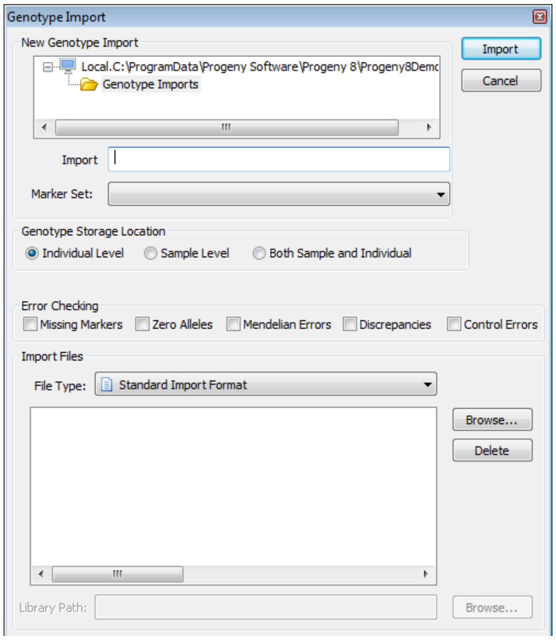
2. Select the folder in which to store the imported genotypes.

You can add a new folder if needed. See “Adding, Editing and Deleting Database Folders” on page 81.

3. On the Genotypes window toolbar, click the New Import button New Import .

   The Genotype Import dialog box opens.

Figure 3-4:   Genotype Import dialog box



Genotype Storage Location: ● Individual Level ○ Sample Level ○ Both Sample and Individual

Error Checking: ☐ Missing Markers ☐ Zero Alleles ☐ Mendelian Errors ☐ Discrepancies ☐ Control Errors

File Type: Standard Import Format

4. Define the import.
    - In the top pane of the dialog box, select the folder in which to import the genotype data.
    - In the Import field, enter a name for the genotype import.
    - On the Marker Set dropdown list, select the marker set against which the genotype data is to be verified.

      Progeny verifies the imported genotype data by matching the markers that are contained in the import against the markers that are listed in the selected marker set. All error checking that is carried out on the import is based on this selected marker set. For example, markers that are defined in the marker set, but are not found in the import file, are flagged as missing markers.

This step assumes that you have previously created the needed marker set for comparison. If you need to create or edit a marker set, see "Managing Markers" on page 321.

- Indicate the level at which the genotype information is to be stored—with the individual only, with the sample only, or at both the individual and sample level.

If you select at both the individual and sample level, you are duplicating the genotype data in the database. As a result, the preferred option is at the sample level only.

- Select the type of error checking that is to be carried out—Missing Markers, Zero Alleles, Mendelian Errors, Discrepancies, and/or Control Errors.

For a complete explanation of each type of error checking method, see "Importing Genotypes" on page 346.

5. Continue to one of the following:
    - "To complete a standard import" on page 349.
    - "To complete a custom import" on page 350.

To complete a standard import

1. Select one of the following standard import formats—Standard Import Format, Illumina Final Report Format, Affymetrix CHP File, Affymetrix GDAS Text Output Format, or Affymetrix GTYPE Text Output Format.

If you are using an Affymetrix Library, then you must also specify the path for the library, In the Library path field, click Browse to open the Browse for Folder dialog box and browse to and select the folder for the library.

2. Click Browse to browse to and select the genotype import files.

3. Click Import.

   A dialog box opens, indicating the progress of the import. When the process is complete, a message opens indicating that the import was successfully completed.

4. Click OK to close the message and the dialog box.

   You return to the Genotypes window. The import is listed in the top pane of the Genotypes window.

5. To view the results of a specific type of error check for the import, select the import in the top pane of the Genotypes window, and then open the appropriate tab in the Error Check (bottom) pane.

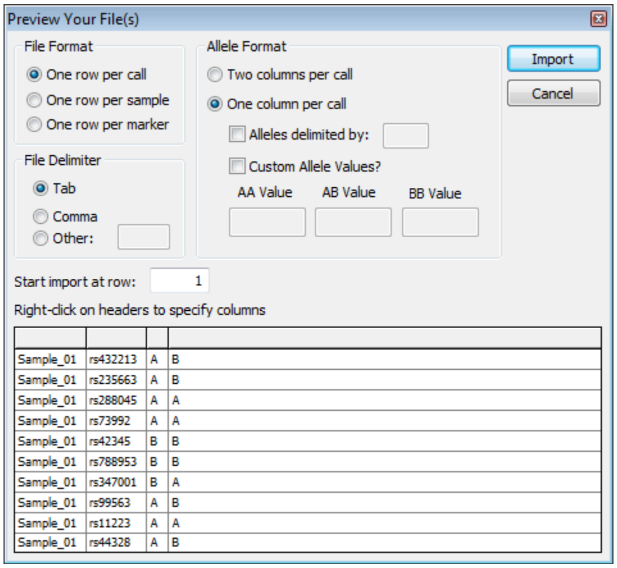
To complete a custom import

1. Select Custom Format for the file type.

2. Click Browse to browse to and select the genotypes import file.

   An Import dialog box opens. The imported file is displayed in the Import Preview pane (bottom pane) of the dialog box.

Figure 3-5: Import dialog box



File Format
● One row per call
○ One row per sample
○ One row per marker

File Delimiter
● Tab
○ Comma
○ Other:

Allele Format
○ Two columns per call
● One column per call
☐ Alleles delimited by:
☐ Custom Allele Values?
AA Value
AB Value
BB Value

Start import at row: 1

Right-click on headers to specify columns

Sample_01	rs432213	A	B
Sample_01	rs235663	A	B
Sample_01	rs288045	A	A
Sample_01	rs73992	A	A
Sample_01	rs42345	B	B
Sample_01	rs788953	B	B
Sample_01	rs347001	B	A
Sample_01	rs99563	A	B
Sample_01	rs11223	A	A
Sample_01	rs44328	A	B

3. Indicate the format of your custom file.

4. Select the delimiter that is used for the data in the import file. If you select Other, you must specify the character that is used for the delimiter.

5. Indicate the format for the allele calls in the file.

   - Two columns per call—Each allele call is in a separate column. Continue to Step 7.
   - One column per call—Both allele calls are in the same column. Continue to Step 6.

6. Optionally, do one or both of the following:
    - Select Alleles delimited by, and then specify the delimiter.
    - Select Custom Allele Values, and then enter the appropriate allele values.
7. Specify the starting row for the import.
8. In the Import Preview pane (the bottom pane of the Import dialog box), for each field, right-click in the column header and manually assign the appropriate heading.
    - One row per call requires a Sample Name column and a Marker Name column. If Two columns per call is selected, you must indicate the Allele A and Allele B columns. If One Column per call is selected, you must indicate the Allele AB column.
    - One row per sample requires a Sample Name column. If two columns per call is selected, you must indicate the Allele A and Allele B columns. If One Column per call is selected, you must indicate the Allele AB column.
    - One row per marker requires a Marker Name. If two columns per call is selected, you must indicate the Allele A and Allele B columns. If One Column per call is selected, you must indicate the Allele AB column.
9. Click Import.

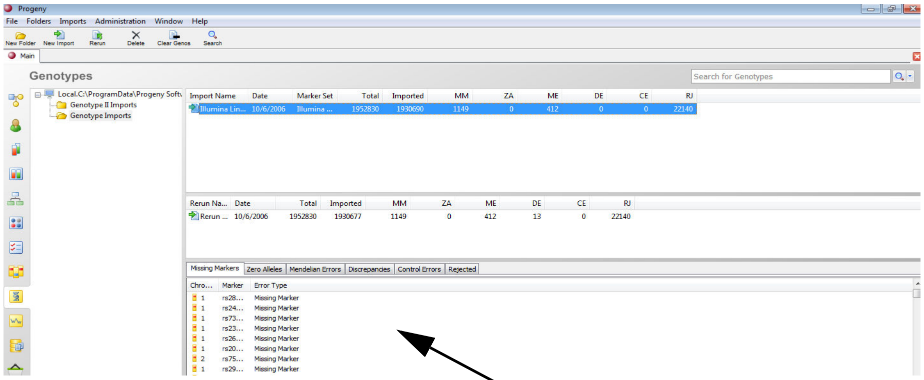
    A dialog box opens, indicating the progress of the import. When the process is complete, a message opens indicating that the import was successfully completed.
10. Click OK to close the message and the dialog box.

    You return to the Genotypes window. The import is listed in the top pane of the Genotypes window.
11. To view the results of a specific type of error check for the import, select the import in the top pane of the Genotypes window, and then open the appropriate tab in the Error Check (bottom) pane.

Error Checks for Genotype Imports

Progeny Lab provides functionality for importing genotypes directly from supported file formats such as Illumina, Affymetrix, ABI, Sequenom, as well as other formats. When you import genotypes, an option is available for carrying out specific error checks—Missing Markers, Zero Alleles, Mendelian errors, Discrepancies, Control Errors, and Rejected—on the data. Error Check results are displayed in the bottom pane of the Genotypes window. To view the results of a specific type of error check for an import, select the import in the top pane of the Genotypes window, and then open the appropriate tab in the Error Check (bottom) pane. (By default, the Missing Markers tab is the active tab for the pane.)

Figure 3-6: Selected genotype import and error checking results displayed in bottom pane



Import Name	Date	Marker Set	Total	Imported	MM	ZA	ME	DE	CE	RJ
Illumina Lin...	10/6/2006	Illumina ...	1952830	1930690	1149	0	412	0	0	22140

Rerun Na...	Date	Total	Imported	MM	ZA	ME	DE	CE	RJ
Rerun ...	10/6/2006	1952830	1930677	1149	0	412	13	0	22140

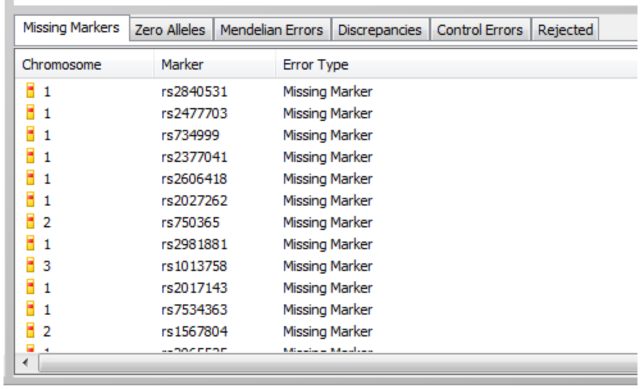
Chro...	Marker	Error Type
1	rs28...	Missing Marker
1	rs24...	Missing Marker
1	rs73...	Missing Marker
1	rs23...	Missing Marker
1	rs26...	Missing Marker
1	rs20...	Missing Marker
2	rs75...	Missing Marker
1	rs29...	Missing Marker

Error Check pane

Missing Markers tab

When you import genotypes, you must select a marker set to compare the import file against. In a Missing Markers error check, Progeny compares the markers that are contained in the import file against the markers that are listed in the selected marker set. All error checking that is carried out on the import is based on this selected marker set. For example, markers that are defined in the marker set, but are not found in the import file, are flagged as missing markers.

Figure 3-7: Missing Markers tab

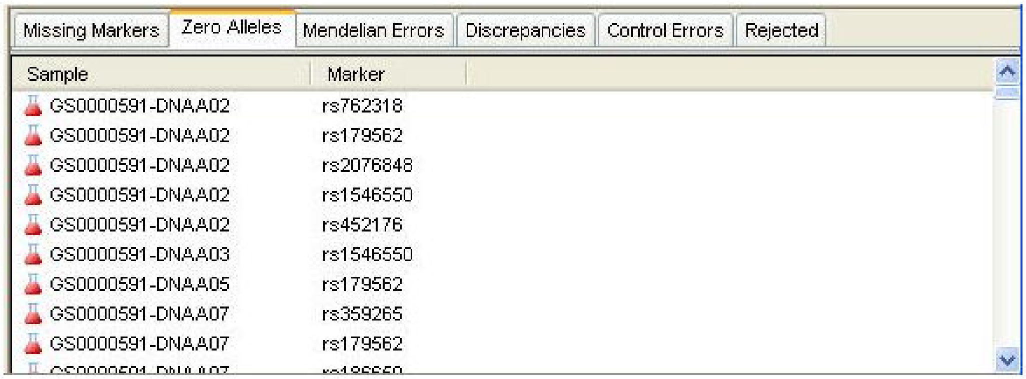


Chromosome	Marker	Error Type
1	rs2840531	Missing Marker
1	rs2477703	Missing Marker
1	rs734999	Missing Marker
1	rs2377041	Missing Marker
1	rs2606418	Missing Marker
1	rs2027262	Missing Marker
2	rs750365	Missing Marker
1	rs2981881	Missing Marker
3	rs1013758	Missing Marker
1	rs2017143	Missing Marker
1	rs7534363	Missing Marker
2	rs1567804	Missing Marker

Zero Alleles tab

In a Zero Alleles error check, Progeny checks each sample for all markers and identifies any markers that contain *zero alleles,* which occurs when the value for a microsatellite cannot be determined. As a result, a zero (0) is displayed for the marker value. The Zero Alleles tab displays the sample name and the corresponding marker that contains a zero allele.

Figure 3-8: Zero Alleles tab

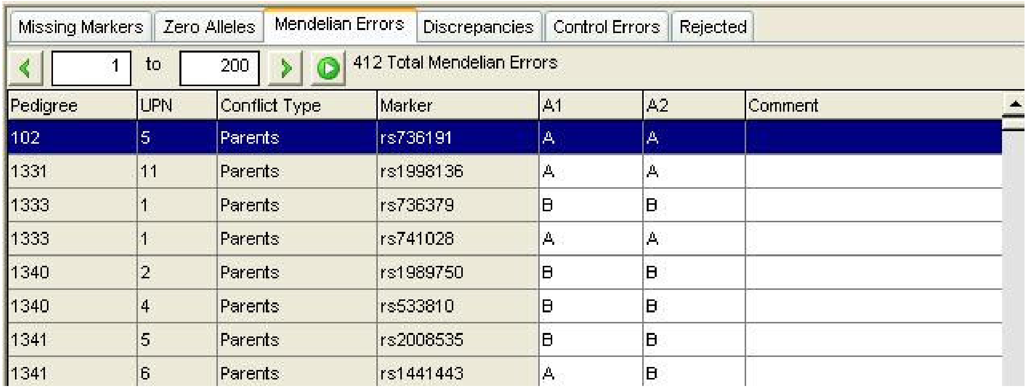


Sample	Marker
GS0000591-DNAA02	rs762318
GS0000591-DNAA02	rs179562
GS0000591-DNAA02	rs2076848
GS0000591-DNAA02	rs1546550
GS0000591-DNAA02	rs452176
GS0000591-DNAA03	rs1546550
GS0000591-DNAA05	rs179562
GS0000591-DNAA07	rs359265
GS0000591-DNAA07	rs179562

Mendelian Errors tab

In a Mendelian Errors check, Progeny compares the data for each allele against the relationship structure of the pedigree and verifies the compatibility. Any discrepancies are identified as Mendelian errors, and are displayed on the Mendelian Errors tab.

Figure 3-9: Mendelian Errors tab



412 Total Mendelian Errors

Pedigree	UPN	Conflict Type	Marker	A1	A2	Comment
102	5	Parents	rs736191	A	A	
1331	11	Parents	rs1998136	A	A	
1333	1	Parents	rs736379	B	B	
1333	1	Parents	rs741028	A	A	
1340	2	Parents	rs1989750	B	B	
1340	4	Parents	rs533810	B	B	
1341	5	Parents	rs2008535	B	B	
1341	6	Parents	rs1441443	A	B	

The first four columns in this tab (Pedigree, UPN, Conflict Type, and Marker) are system-generated fields and therefore, are not editable. The final three columns (A1, A2, and Comment) are editable fields. You can change the value of either Allele 1 or Allele 2 to resolve any conflicts as well as enter comments in the Comment field for record keeping purposes. You can edit a Mendelian error directly on the Mendelian Errors tab, or you can edit the Mendelian error directly in the pedigree.

To edit a Mendelian error on the Mendelian errors tab

1. Select the error that you are correcting on the Mendelian errors tab.
2. Edit the value as needed, and then right-click on the edited value, and on the context menu that opens, click Save Changes.
3. Repeat Step 1 and Step 2 to correct all the Mendelian errors.
4. Select a row for which you corrected the Mendelian error (CTRL-click to select multiple rows), right-click on any of the selected row, and then on the context menu that opens, click Rerun Mendelian Checks on All Selected Rows.

   The Mendelian checks are rerun for all the rows to ensure that the error was properly corrected.

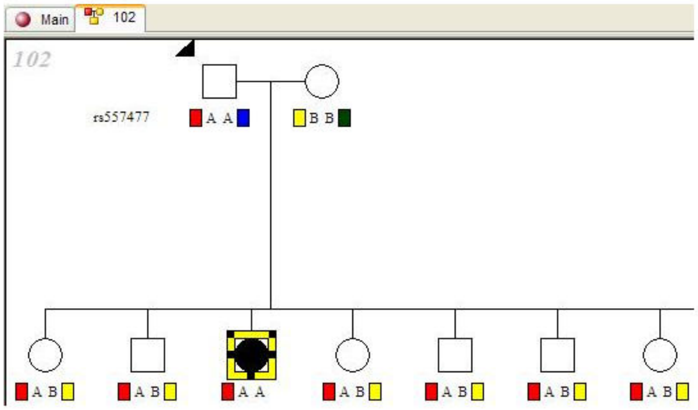
   A message opens, indicating that the Mendelian error rerun was successfully completed. It also indicates the number of errors that were corrected, and that the corrected rows have been disabled.
5. Click OK to close the message to return to the Mendelian Errors tab.
6. Optionally, to delete a disabled row, select the row (CTRL-click to select multiple rows), right-click on any selected row, and on the context menu that opens, click Delete All Selected Rows.

To edit a Mendelian error in the pedigree

1. On the Mendelian Errors tab, right-click on the error that you are editing, and on the context menu that opens, click Open Error to Pedigree.

   The pedigree that contains the individual with the Mendelian error opens. The specific marker is loaded in the pedigree, and the allele information is displayed as a haplotype for the affected individual.

Figure 3-10: Opened pedigree with Mendelian error



2. To edit the value, click on the allele value and enter the correct value.

3. Close the pedigree, making sure to answer the prompt about saving the changes.

   After you correct the error in the pedigree, you return to the Mendelian Errors tab. The row that contained the error is disabled.

4. Right-click on any corrected error row, and on the context menu that opens, click Rerun Mendelian Checks on All Selected Rows.

   The Mendelian checks are rerun for all the row to ensure that the error was properly corrected.

   A message opens, indicating that the Mendelian error rerun was successfully completed. It also indicates the number of errors that were corrected, and that the corrected rows have been disabled.

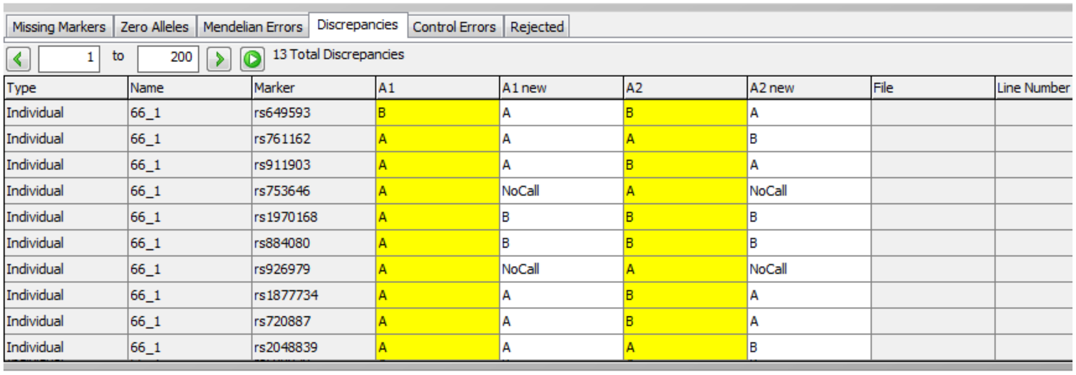
5. Click OK to close the message to return to the Mendelian Errors tab.

6. Optionally, to delete a disabled row, select the row (CTRL-click to select multiple rows), right-click on any selected row, and on the context menu that opens, click Delete All Selected Rows.

Discrepancies tab

The Discrepancies tab lists any discrepancies that were found between an original genotype import and a rerun of the import. The first three fields on the tab (Pedigree, UPN, and Marker) are system fields, and are not editable. The next four fields display the original value for allele 1 (A1), the new value for A1, the original value for allele 2 (A2), and the new value for A2, respectively. When the tab first opens, the original values for A1 and A2 (highlighted in yellow on the tab) are the values that are stored in the database. You can resolve these discrepancies from the Discrepancies tab, or you can resolve these discrepancies from the pedigree. You can also export the information that is displayed on the Discrepancies tab to a text file.

Figure 3-11: Discrepancies tab



13 Total Discrepancies

Type	Name	Marker	A1	A1 new	A2	A2 new	File	Line Number
Individual	66_1	rs649593	B	A	B	A		
Individual	66_1	rs761162	A	A	A	B		
Individual	66_1	rs911903	A	A	B	A		
Individual	66_1	rs753646	A	NoCall	A	NoCall		
Individual	66_1	rs1970168	A	B	B	B		
Individual	66_1	rs884080	A	B	B	B		
Individual	66_1	rs926979	A	NoCall	A	NoCall		
Individual	66_1	rs1877734	A	A	B	A		
Individual	66_1	rs720887	A	A	B	A		
Individual	66_1	rs2048839	A	A	A	B		

To change the view on the tab, enter new values for the beginning and ending discrepancy range, and then click the Run button ▶*. You can click the Jump buttons at either end of the filter to update the display according to the range that you specified. For example, if your search filter is set from 1 to 200 to show the first 200 discrepancies, then click the Jump Forward button* › *to change the range to 200 to 400 and update the display accordingly.*

To resolve discrepancies from the Discrepancies tab

1. To resolve the discrepancy for an allele, click on the new value for the allele.

   The new value for the allele is now highlighted in yellow, indicating this is the value that is to be stored for the allele in the database, and the original value now has no background color (white), indicating that the original value is to be rejected.

2. After you have you have determined which values to store in the database and which values to reject for both A1 and A2 for each marker, select a row (CTRL-click to select multiple rows), and then right-click on any selected row, and on the context menu that opens, click Resolve Selected Discrepancies.

   The selected discrepancies are removed from the Discrepancies tab and the changes that you made are saved in the Progeny database. The selections that you made are used when data is exported for analysis.

To resolve discrepancies from the pedigree

1. Right-click on the discrepancy on the Discrepancies tab, and on the context menu that opens, click Open Pedigree to Error.

   The pedigree is displayed onscreen.

2. Make the changes directly in the displayed pedigree.
3. Close the pedigree to return to the Discrepancies tab.
4. Select the changed value in either the A1 New or A2 New column.

   The new value for the allele is now highlighted in yellow, indicating this is the value that is to be stored for the allele in the database, and the original value now has no background color (white), indicating that the original value is to be rejected.

5. After you have you have determined which values to store in the database and which values to reject for both A1 and A2 for each marker, select a row (CTRL-click to select multiple rows), and then right-click on any selected row, and on the context menu that opens, click Resolve Selected Discrepancies.

   The selected discrepancies are removed from the Discrepancies tab and the changes that you made are saved in the Progeny database. The selections that you made are used when data is exported for analysis.

To export discrepancies to a text file

1. Right-click on any row on the Discrepancies tab, and on the context menu that opens, click Export to File.
2. Specify the name and location for the export file.

   The exported file contains all the discrepancies, including the original call and the change that was committed to the database.

Control Errors tab

The Control Errors Tab lists any controls where the expected value for A1 and A2 is different that what was returned in the genotype file that was imported. The expected calls are listed in the columns A1 Control and A2 Control. The returned incorrect calls are listed in A1 and A2 columns. To export the control errors to a text file, right-click anywhere on the tab, and on the context menu that opens, click Export to File. After a control is identified as an error, all the data for the marker in the genotype import will be rejected. The resulting rejected markers are listed on the Rejected tab with the reason “Entire Marker invalid due to control error.”

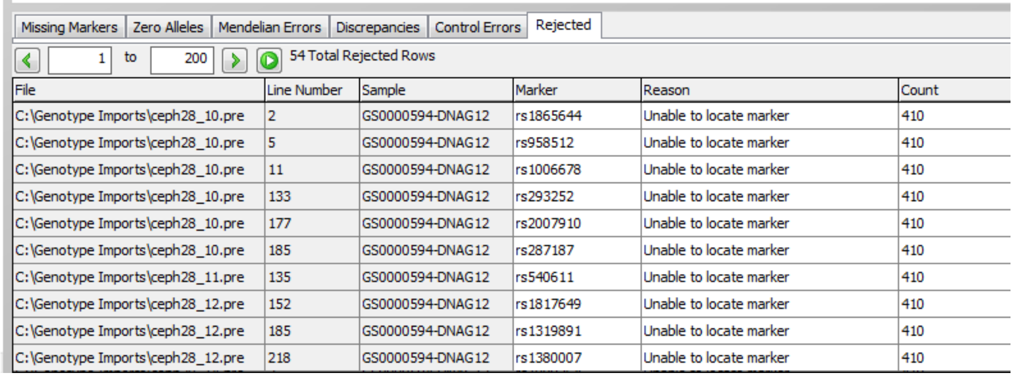
Rejected tab

The Rejected tab lists all the data in the genotype import file that was rejected for one of the following reasons:

- There is no match in the database with a sample name that appears in the genotype import. The sample name must exist in the database to store the genotype information.
- There is no match in the database with a marker that appears in the genotype import. The marker must exist in the database to store the genotype information.
- If duplicate markers and samples are contained in the genotype import, and the values for both are zero, the second marker/sample entry is rejected.
- If the expected Allele A value or Allele B value is not stored for a given SNP or marker in the Markers module, then the SNP or marker is rejected.
- If a field cannot be updated during the import process (for example, another user is updating a Sample Name field during your import process), then the data that references the field is rejected.
- If any database error occurs during the import process, then the field that failed to record data is listed on the Rejected tab along with the value that could not be recorded.

None of the fields on this tab is editable. The first three columns (File, Line, Sample) list the file that contained the rejected data, the line number where the error check occurred in the file, and the sample that contained the error, respectively. The remaining three columns (Marker, Reason, Count) list the marker that contains the error, the reason for the rejection, and the count for multiple error rows, respectively.

Figure 3-12: Rejected tab



File	Line Number	Sample	Marker	Reason	Count
C:\Genotype Imports\ceph28_10.pre	2	GS0000594-DNAG12	rs1865644	Unable to locate marker	410
C:\Genotype Imports\ceph28_10.pre	5	GS0000594-DNAG12	rs958512	Unable to locate marker	410
C:\Genotype Imports\ceph28_10.pre	11	GS0000594-DNAG12	rs1006678	Unable to locate marker	410
C:\Genotype Imports\ceph28_10.pre	133	GS0000594-DNAG12	rs293252	Unable to locate marker	410
C:\Genotype Imports\ceph28_10.pre	177	GS0000594-DNAG12	rs2007910	Unable to locate marker	410
C:\Genotype Imports\ceph28_10.pre	185	GS0000594-DNAG12	rs287187	Unable to locate marker	410
C:\Genotype Imports\ceph28_11.pre	135	GS0000594-DNAG12	rs540611	Unable to locate marker	410
C:\Genotype Imports\ceph28_12.pre	152	GS0000594-DNAG12	rs1817649	Unable to locate marker	410
C:\Genotype Imports\ceph28_12.pre	185	GS0000594-DNAG12	rs1319891	Unable to locate marker	410
C:\Genotype Imports\ceph28_12.pre	218	GS0000594-DNAG12	rs1380007	Unable to locate marker	410

To change the view on the tab, enter new values for the beginning and ending rejected range, and then click the Run button ▶*. You can click the Jump buttons at either end of the filter to continue searching based on the range that you specified. For example, if your search filter is set from 1 to 200 to show the first 200 rejected samples, then click the Jump Forward button* › *to change the range to 200 to 400 and update the display accordingly.*

Rerunning a Genotypes Import

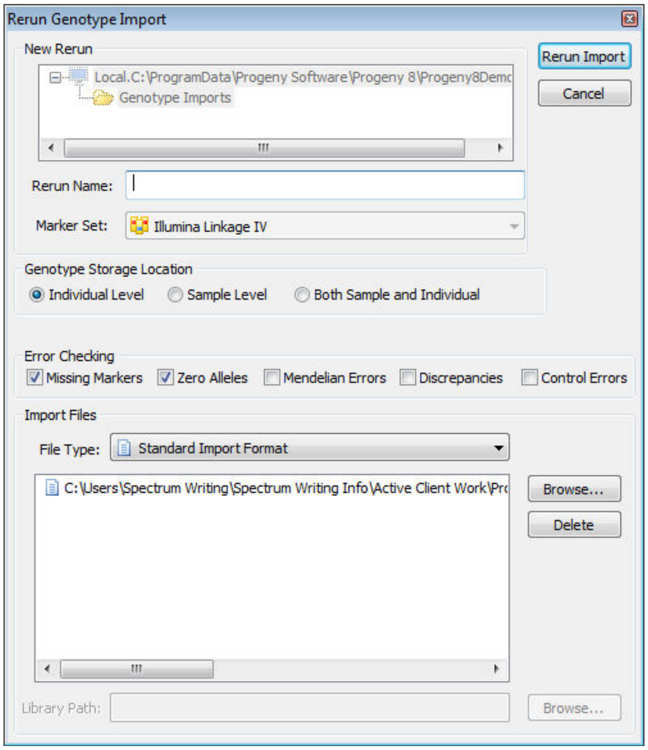
After you run an original genotypes import, and then make all the needed corrections to the import, you can run the import again.

To rerun a genotypes import

1. On the Genotypes window, in the Import List pane, select the original import that is to be rerun, and then on the window toolbar, click the Rerun button Rerun.

   The Rerun Genotype Import dialog box opens.

Figure 3-13: Rerun Genotype Import dialog box



Rerun Genotype Import

New Rerun

Local.C:\ProgramData\Progeny Software\Progeny 8\Progeny8Dem
Genotype Imports

Rerun Name:

Marker Set: Illumina Linkage IV

Genotype Storage Location

● Individual Level ○ Sample Level ○ Both Sample and Individual

Error Checking

☑ Missing Markers ☑ Zero Alleles ☐ Mendelian Errors ☐ Discrepancies ☐ Control Errors

Import Files

File Type: Standard Import Format

C:\Users\Spectrum Writing\Spectrum Writing Info\Active Client Work\Pr

Library Path:

When this dialog box opens:

- The marker set that was used for the original import is automatically selected for the rerun, and you cannot change this value.
- The Error Checking options that were selected for the original import are also automatically selected, however, you can change these selections.
- The file type that was used for the original import is automatically selected for the rerun, however, you can change this selection.

If you are using an Affymetrix Library, then you must also specify the path for the library, In the Library path field, click Browse to open the Browse for Folder dialog box and browse to and select the folder for the library.

- The files that were used for the original import are displayed in the lower pane of the dialog box. You can change this list of files, if needed, including deleting files, and selecting new files.

2. After you have made all the necessary modifications for the rerun, click Rerun Import.

   A dialog box opens, indicating the progress of the import. When the process is complete, a message opens indicating that the import was successfully completed.

3. Click OK to close the message and the dialog box.

   You return to the Genotypes window. The import is listed in the middle pane of the Genotypes window. Any discrepancies between the original import and the rerun are listed on the Discrepancies tab.

Manually Entering Genotype Data

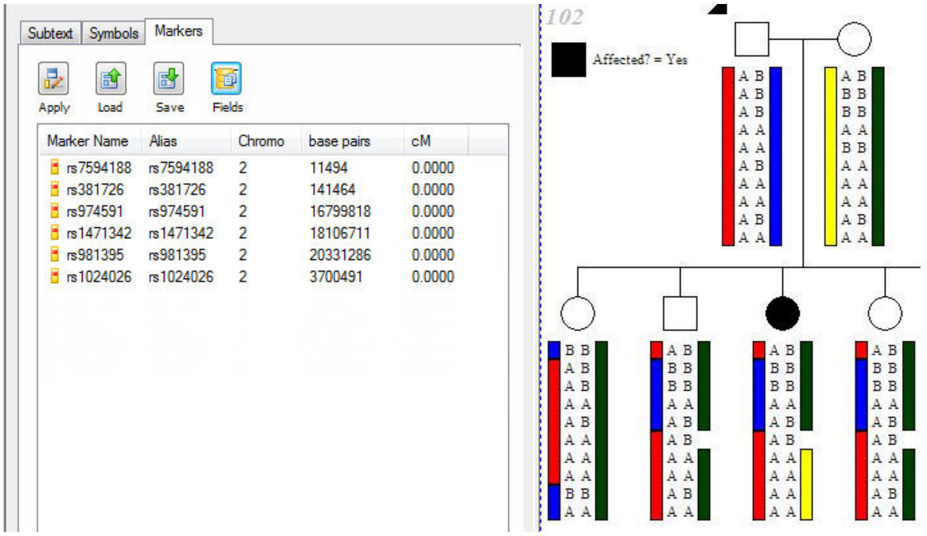
Instead of importing genotype data into a Progeny database, you can manually enter data.

If you manually enter genotype data, no error checking of the data is automatically carried out of the data.

Four options are available for manually entering genotype data:

- You can enter genotype data using icon markers on a pedigree. See "To configure icon markers for a pedigree" on page 283.

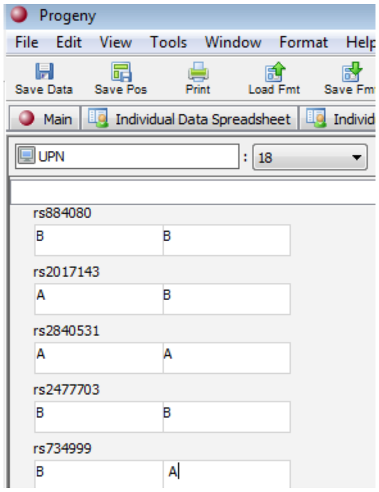
Figure 3-14: Example of a pedigree showing icon markers



Marker Name	Alias	Chromo	base pairs	cM
rs7594188	rs7594188	2	11494	0.0000
rs381726	rs381726	2	141464	0.0000
rs974591	rs974591	2	16799818	0.0000
rs1471342	rs1471342	2	18106711	0.0000
rs981395	rs981395	2	20331286	0.0000
rs1024026	rs1024026	2	3700491	0.0000

- You can enter genotype data into the marker fields on a datasheet for an individual. See "Creating and Formatting Datasheets" on page 86.

Figure 3-15: Marker data in an individual datasheet



UPN : 18

rs884080
B B

rs2017143
A B

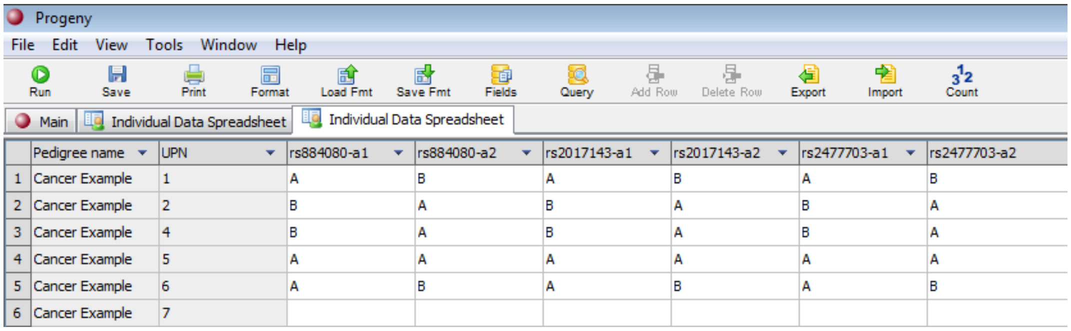
rs2840531
A A

rs2477703
B B

rs734999
B A

- You can enter genotype data directly into the marker fields in an spreadsheet for an individual. For example, select the pedigree on the Pedigrees window, and then on the window toolbar, click the Individual Spreadsheet button. Select the system fields of Pedigree Name and UPN and the appropriate marker fields, and then run the spreadsheet. The marker field is automatically split into two fields representing the paternal allele in a1 and the maternal allele in a2. See “Generating a Spreadsheet” on page 106.

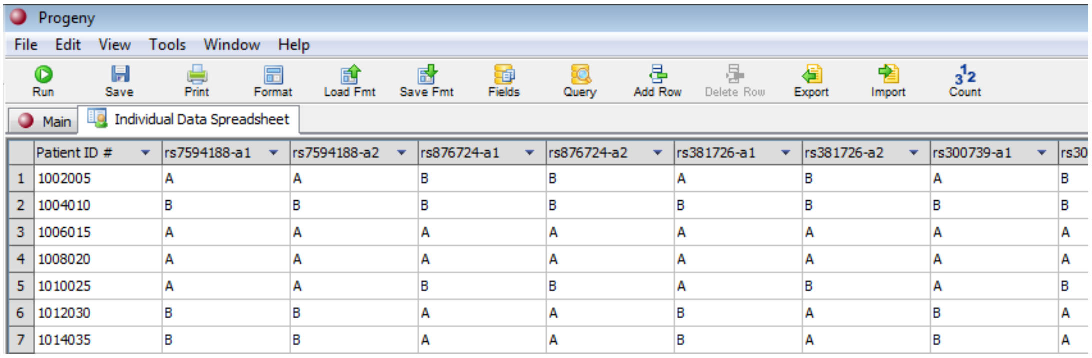
Figure 3-16: Entering genotype data into an individual spreadsheet



	Pedigree name	UPN	rs884080-a1	rs884080-a2	rs2017143-a1	rs2017143-a2	rs2477703-a1	rs2477703-a2
1	Cancer Example	1	A	B	A	B	A	B
2	Cancer Example	2	B	A	B	A	B	A
3	Cancer Example	4	B	A	B	A	B	A
4	Cancer Example	5	A	A	A	A	A	A
5	Cancer Example	6	A	B	A	B	A	B
6	Cancer Example	7						

- You can import data from a text file into the marker fields in a spreadsheet for an individual. For example, select a field that matches the individuals in the spreadsheet to the individuals in the text file such as Patient ID #, and the appropriate marker fields, and then run the spreadsheet. The marker field is automatically split into two fields representing the paternal allele in a1 and the maternal allele in a2. After running the spreadsheet, import the marker data. See “To import data into a spreadsheet” on page 115.

Figure 3-17: Importing genotype data into an individual spreadsheet



	Patient ID #	rs7594188-a1	rs7594188-a2	rs876724-a1	rs876724-a2	rs381726-a1	rs381726-a2	rs300739-a1	rs30
1	1002005	A	A	B	B	A	B	A	B
2	1004010	B	B	B	B	B	B	B	B
3	1006015	A	A	A	A	A	A	A	A
4	1008020	A	A	A	A	A	A	A	A
5	1010025	A	A	B	B	A	B	A	B
6	1012030	B	B	A	A	B	A	B	A
7	1014035	B	B	A	A	B	A	B	A

Clearing Genotype Data

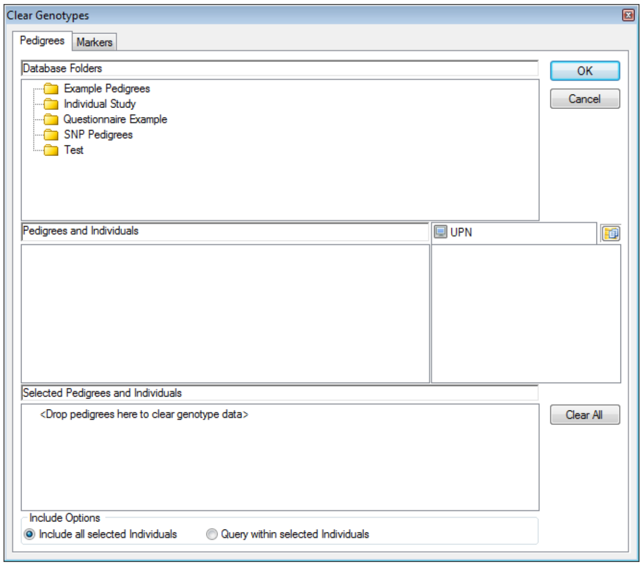
You use the Clear Genotypes function to clear genotype data from selected individuals in selected pedigrees.

To clear genotype data

1. On the Genotypes window toolbar, click the Clear Genotypes button Clear Genos.

   The Clear Genotype dialog box opens. By default, the Pedigrees tab is the active tab.

Figure 3-18: Clear Genotypes dialog box, Pedigrees tab



● Include all selected Individuals ○ Query within selected Individuals

2. In the Database Folders (top) pane of the dialog box, select the folder that contains the pedigrees for which the genotype data is to be cleared.
3. In the Pedigrees and Individuals (left middle) pane of the dialog, select the pedigree (CTRL-click to select multiple pedigrees) for which the genotype data is to be cleared.

   The individuals that are contained in a selected pedigree are displayed in the right middle pane of the dialog box. By default, the UPN is the identifier used for the individuals.

Optionally, you can click the Fields button next to the Individuals list to open the Select Field dialog box and select a different identifier, such as the Global ID, for individuals in a pedigree.

4. Drag the selected pedigrees to the Selected Pedigrees and Individuals (bottom) pane of the dialog box.

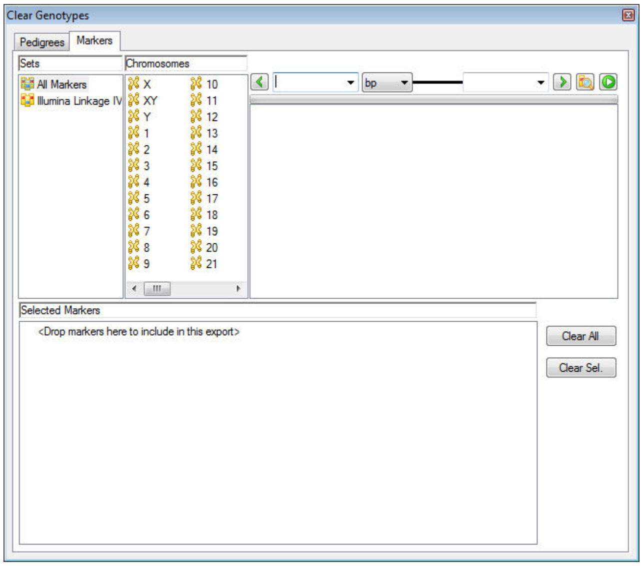
5. Do one of the following:
   - To delete the genotype data for all individuals in all selected pedigrees, select Include all selected individuals.
   - To delete the genotype data only for those individuals who meet selected criteria, select Query within selected individuals, and then click the Query button to open the Query dialog box and define a new query, or load a saved query format.

For detailed information about defining a query, see Chapter 8, "Database Queries and Searches," on page 171.

6. Open the Markers tab, and then do one of the following:
   - To clear an entire marker set, drag the marker set from the Sets (top right) pane of the dialog box to the Selected Markers (bottom) pane.
   - To clear the all the markers for a specific chromosome, drag the chromosome from the Chromosomes (top middle) pane of the dialog box to the Selected Markers (bottom) pane.
   - To clear only specific markers, select the marker (CTRL-click to select multiple markers) from the top right pane to the Selected Markers (bottom) pane.

To search for a specific marker or markers, you can use the marker search functions. See "Searching for a Marker" on page 337.

Figure 3-19: Clear Genotypes dialog box, Markers tab



7. Open the Pedigrees tab, and then click OK on the tab.

   A message opens, asking you if you are sure that you want to clear the genotype data.

8. Click Yes to close the message.

   A dialog box opens, indicating the status of clearing the genotype data.

9. When the status is complete, click Close to close the dialog box and return to the Genotypes window.

Chapter 4
Linkage Exports

Progeny Lab provides all the functionality needed for managing genetic linkage studies, including managing linkage exports. Managing linkage formats consists of creating and running linkage exports, saving linkage export formats for running on an as-needed basis, rerunning linkage exports, importing LOD scores, and deleting linkage exports.

This chapter covers the following topics:

- "Creating and Running a Linkage Export" on page 369.
- "Saving and Loading a Linkage Export Format" on page 377.
- "Viewing and Rerunning a Linkage Export" on page 379.
- "Importing LOD Scores" on page 381.
- "Displaying LOD Scores on a Pedigree" on page 382.
- "Deleting a Linkage Export" on page 383.

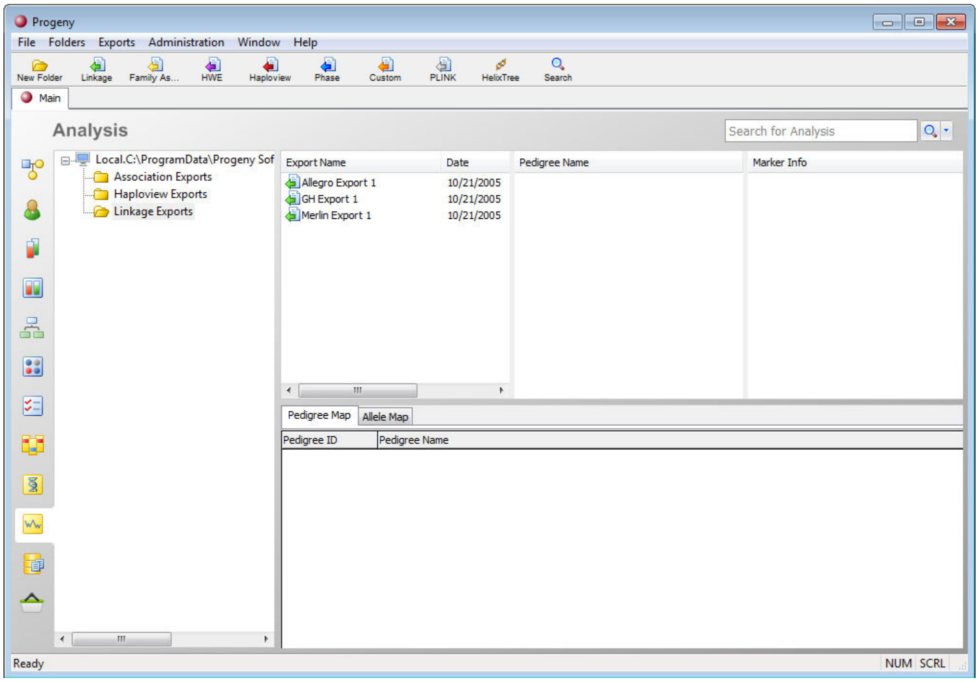
Creating and Running a Linkage Export

You can export MLINK, Genehunter, MEGA2, Allegro, and Merlin linkage formats in Progeny Lab. You must first create the linkage export, and then you can run the linkage export.

To create a linkage export

1. On the main window navigation bar, click the Analysis button to open the Analysis window.

Figure 4-1: Analysis window



Local.C:\ProgramData\Progeny Sof
- Association Exports
- Haploview Exports
- Linkage Exports

Export Name	Date	Pedigree Name	Marker Info
Allegro Export 1	10/21/2005		
GH Export 1	10/21/2005		
Merlin Export 1	10/21/2005		

Pedigree ID	Pedigree Name

2. On the Analysis window, select the folder in which to the linkage export is to be saved.

You can add a new folder if needed. Click the New Folder button on the window toolbar to open the New Folder dialog box, in which you can enter a name for a new Analysis folder and select its location (at the root level or as a sub-folder of another folder.)

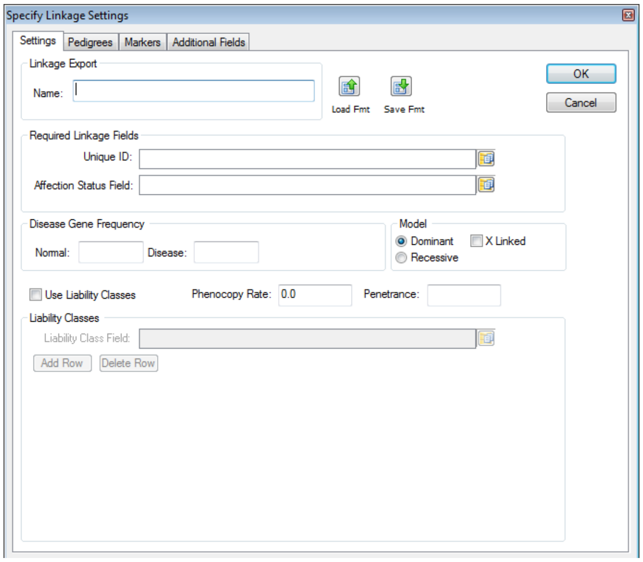
3. On the window toolbar, click the Linkage button .

   The Specify Linkage Settings dialog box opens. By default, the Settings tab is the active tab.

4. Specify the necessary linkage settings on all four tabs of the dialog box. See:
    - "Specify Linkage Settings dialog box, Settings tab" on page 370.
    - "Specify Linkage Settings dialog box, Pedigrees tab" on page 371.
    - "Specify Linkage Settings dialog box, Markers tab" on page 373.
    - "Specify Linkage Settings dialog box, Additional Fields tab" on page 375.
5. After you specify the necessary linkage settings on all four tabs, return to the Settings tab, and then click OK on the tab.
6. Continue to "To run a linkage export" on page 375.

Specify Linkage Settings dialog box, Settings tab

Figure 4-2: Specify Linkage Settings dialog box, Settings tab



● Dominant ☐ X Linked
○ Recessive

☐ Use Liability Classes

Phenocopy Rate: 0.0

Penetrance:

1. Enter the settings for the linkage export.

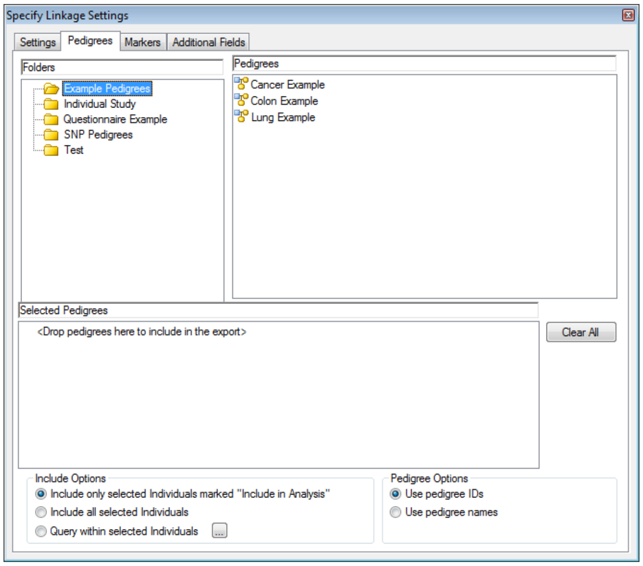
Option	Description
Linkage Export	
Linkage Export Name	Name or description of the linkage export.
Required Linkage Fields	
Unique ID	Click the Fields button to the right of the Unique ID field to open the Select Field dialog box and select the field that represents the unique ID for each individual that is to be included in the linkage export.
Affection Status Field	Click the Fields button to the right of the Affection Status Field to open the Select Field dialog box and select the field that represents the affected status for each individual that is to be included in the linkage export.

Option	Description
Disease Gene Frequency	
Normal Disease	Enter the appropriate values for Normal and Disease gene frequency. **Note:** The gene frequencies, when totaled, must equal 1.0.
Model	
• Dominant • Recessive	Select one value.
X Linked	Select if relevant.
Use Liability Classes	Select if applicable, and then click the Fields button to the right of the Liability Class Field to open the Select Field dialog box and select the field that holds the liability class values. A table opens in the Liability Classes (bottom) pane of the dialog box for identifying the values for the liability classes. To add a row to the table, click Add Row. **Note:** For X-Linked models, specify three female values and two male values; otherwise, specify three values and leave the remaining blank.
Phenocopy Rate Penetrance	Available only if Use Liability Classes is *not* selected.

2. Continue specifying any other linkage export settings as needed; otherwise, return to the Settings tab, click OK, and then continue to "To run a linkage export" on page 375.

Specify Linkage Settings dialog box, Pedigrees tab

Figure 4-3: Specify Linkage Settings dialog box, Pedigrees tab



● Include only selected Individuals marked "Include in Analysis"
○ Include all selected Individuals
○ Query within selected Individuals

● Use pedigree IDs
○ Use pedigree names

1. In the Folders (top left) pane of the dialog box, select the folder that contains the pedigrees for which the linkage export is being created.

2. In the Pedigrees (top right) pane of the dialog, select the pedigree (CTRL-click to select multiple pedigrees) for which the linkage export is being created.

3. Drag the selected pedigrees to the Selected Pedigrees (bottom) pane of the dialog box.
4. Select one of the following:
   - To include only those individuals in a pedigree who have been specifically marked for inclusion in an analysis, select Include only selected individuals marked “Include in Analysis.” (See “To select individuals in a pedigree for inclusion in an analysis” below.)
   - To include all individuals in all the selected pedigrees are included in the linkage export, select Include all selected individuals.
   - To include only those individuals in the export linkage who meet specific criteria, select Query within selected individuals, and then click the Query button to open the Query dialog box and define a new query, or load a saved query format.

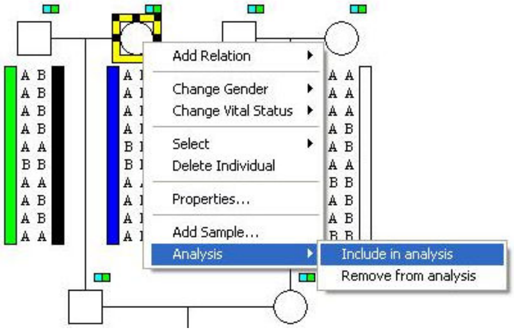
For detailed information about defining a query, see Chapter 8, “Database Queries and Searches,” on page 171.

5. Select one of the following:
   - Use Pedigree IDs—Converts a text-based pedigree name into a numerical ID.
   - Use pedigree names—Use pedigree names as-is.
6. Continue specifying any other linkage export settings as needed; otherwise, return to the Settings tab, click OK, and then continue to “To run a linkage export” on page 375.

To select individuals in a pedigree for inclusion in an analysis

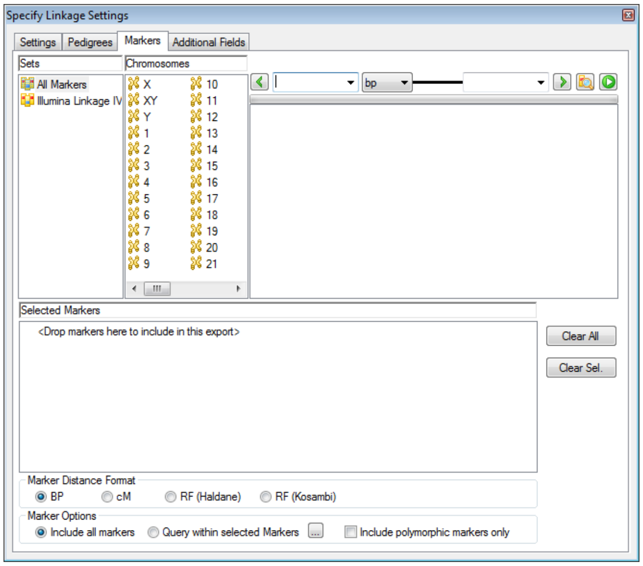
If you select the option Include only selected individuals marked “Include in Analysis,” then you must open each affected pedigree, and manually select the appropriate individuals. You can select a single individual, or CTRL-click to select multiple individuals, and then right-click on any selected individual, and on the context menu that opens, click Include in analysis.

Figure 4-4: Selecting individuals for analysis



Specify Linkage Settings dialog box, Markers tab

Figure 4-5: Specify Linkage Settings dialog box, Markers tab



Marker Distance Format
● BP ○ cM ○ RF (Haldane) ○ RF (Kosambi)

Marker Options
● Include all markers ○ Query within selected Markers ☐ Include polymorphic markers only

1. Do one of the following:
   - To include an entire marker set in the analysis, drag the marker set from the Sets (top right) pane of the dialog box to the Selected Markers (bottom) pane.
   - To include all the markers for a specific chromosome in the analysis, drag the chromosome from the Chromosomes (top middle) pane of the dialog box to the Selected Markers (bottom) pane.
   - To include only specific markers in the analysis, select the marker (CTRL-click to select multiple markers) from the top right pane to the Selected Markers (bottom) pane.

To search for a specific marker or markers, you can use the marker search functions. See "Searching for a Marker" on page 337.

2. Specify the intermarker distance format that is to be exported.
   - BP or cM exports the exact distance between the markers in base pairs or centiMorgans, respectively.
   - RF (Haldane) and RF (Kosambi) exports the distance between the markers based on the Haldane recombination factor or the Kosambi recombination factor, respectively.

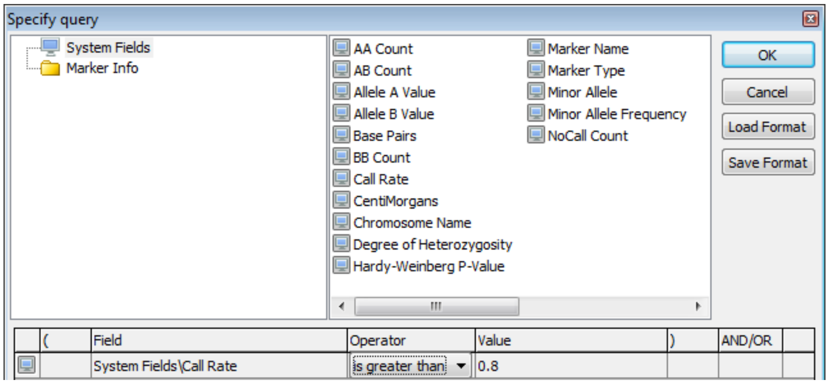
3. Select one of the following:

   - To include all of the markers in the Selected Markers pane in the linkage export, select Include all markers.
   - To include only those markers in the Selected Markers pane in the linkage export that meet specific criteria, select Query within selected markers, and then click the Query button to open the Query dialog box and define a new query, or load a saved query format.

For detailed information about defining a query, see Chapter 8, “Database Queries and Searches,” on page 171.

If you specify a query, then you can carry out additional marker filtering, and filter the selected SNPs by Hardy Weinberg p-value, Minor Allele Frequency, Degree of Heterozygosity, and/or Call Rates. For example, to include only those SNPs that have a call rate higher than 80%, you would select the Call Rate system field and enter > 0.8 as the operator and value. You can use this additional filtering criteria only if there is allele count data stored on a per SNP basis.

Figure 4-6: Additional marker filtering

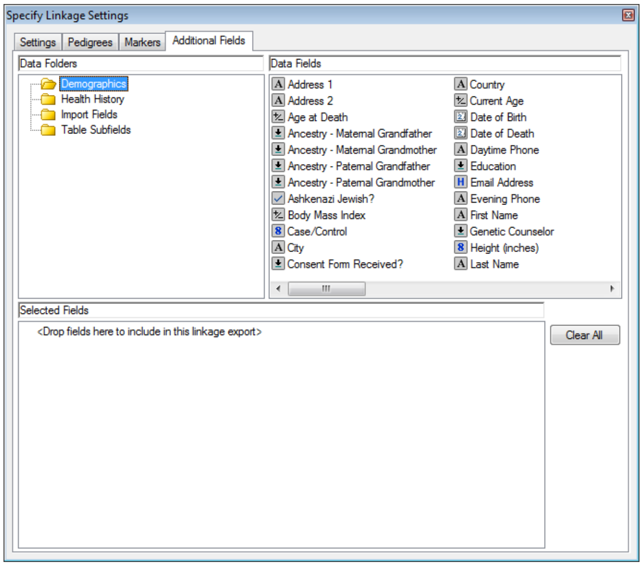


(	Field	Operator	Value	)	AND/OR
	System Fields\Call Rate	is greater than	0.8		

4. Optionally, select Include polymorphic markers only to further filter the selected markers and export only those markers that have at least one heterozygous genotype.
5. Continue specifying any other linkage export settings as needed; otherwise, return to the Settings tab, click OK, and then continue to “To run a linkage export” on page 375.

Specify Linkage Settings dialog box, Additional Fields tab

Figure 4-7: Specify Linkage Settings dialog box, Additional Fields tab

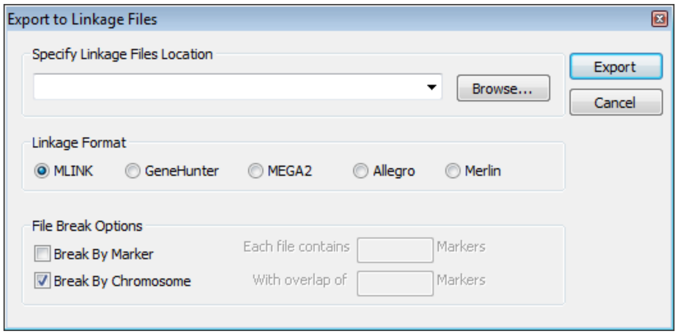


1. Specify additional individual level database fields that are to be included in the linkage export.
2. Continue specifying any other linkage export settings as needed; otherwise, return to the Settings tab, click OK, and then continue to "To run a linkage export" below.

To run a linkage export

After you specify the necessary linkage settings on all four tabs, you must return to the Settings tab, and then click OK on the tab. The Export to Linkage Files dialog box opens.

Figure 4-8: Export to Linkage Files dialog box



1. Click Browse to open the Browse for Folder dialog box, and browse to and select the folder in which the linkage export files are be stored.

If you have previously run linkage exports, then any previously selected locations are available in a dropdown list in the Browse field. You can always select a value from this list.

2. Select the appropriate linkage format.
3. Select one or both file break options.
    - Break by Marker—Indicate how many markers are to be contained in each linkage file. If you select this option, you must also indicate the number of overlapping markers in each file.
    - Break by Chromosome—Creates a new file for each chromosome that is exported.
4. Click Export.

    A dialog box opens, indicating the status of the linkage export.
5. When the export is complete, click Close to close the dialog box and return to the Analysis window.
6. Load the files that were created by the linkage export into your analysis software to produce LOD files that you can import into Progeny. See “Importing LOD Scores” on page 381.

Saving and Loading a Linkage Export Format

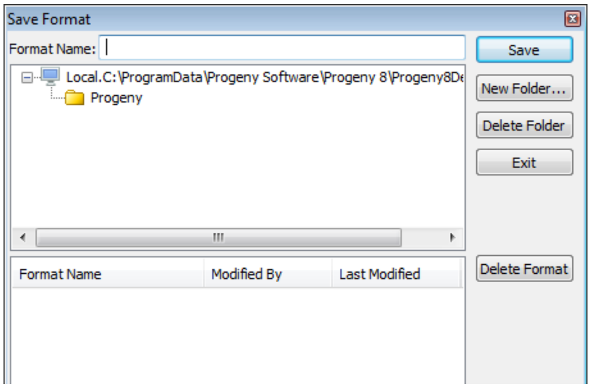
After you have set up an linkage export format, you can save the format. You can then load this saved format and run it on as-needed basis.

To save a linkage export format

1. Set up the linkage export format but do *not* run the format See “Creating and Running a Linkage Export” on page 369.
2. Click the Save Format button Save Fmt on the Specify Linkage Settings dialog box.

   The Save Format dialog box opens. It provides a default folder named Progeny in which to save the export format. (This folder is located in the database that you are currently logged in to and you cannot change this location.)

Figure 4-9: Save Format dialog box



3. Enter a name for the linkage export format, and then do one of the following:
   - Select the Progeny folder.
   - Click New Folder, and on the Format Folder dialog box that opens, do the following:
     - Enter the name of the new folder in which to save to format.
     - Select the location for the new folder. The folder can be stored at the root level (the same level as the Progeny folder), or it can be a sub-folder of the Progeny folder, or of another folder.
     - Click Save.
4. Click Save on the Save Format dialog box.

   You can then load this saved format and run it on as-needed basis. See “To load a linkage export format” on page 378.

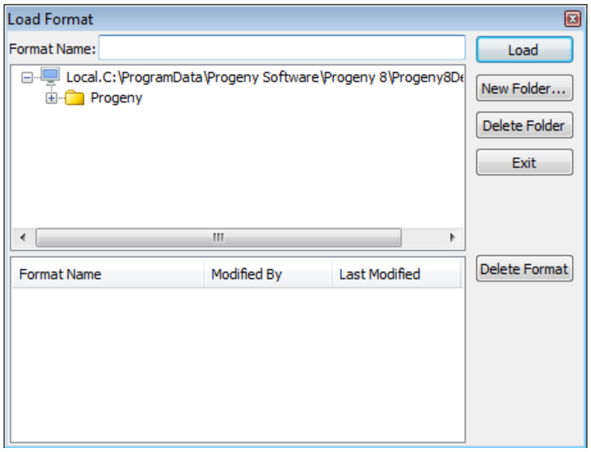
To load a linkage export format

You can a retrieve a saved linkage export format and run it on as-is needed based.

1. Open the Specify Linkage Settings dialog box. (See Step 1 through Step 3 of “To create a linkage export” on page 369.)
2. On the dialog box, click the Load Format button Load Fmt .

   The Load Format dialog box opens.

Figure 4-10: Load Format dialog box



3. Open the folder that contains the linkage export format that you are loading, select the format, and then click Load.

   The Specify Linkage Export Settings dialog box is refreshed with the loaded format. You can modify the format as needed (for example, modify the information on the Pedigrees tab), and export the linkage format.

Viewing and Rerunning a Linkage Export

You can view information about any linkage exports that were previously run on the Analysis window, and you can rerun any linkage export as necessary.

To view and rerun a linkage export

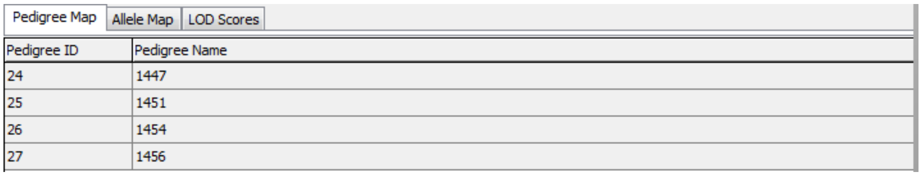
1. On the Analysis window, select the linkage export that you want to view.

   Three tabs open in the bottom pane of the window—Pedigree Map, Allele Map, and LOD Scores. By default, the Pedigree Map tab is the active tab.

2. Open and view the information on each tab as necessary.

   - The Pedigree Map tab displays the mapping of the original pedigree name to the pedigree ID generated for the export file. These values are not editable; however, you can sort this information by clicking the heading for either the Pedigree ID or the Pedigree Name.

Figure 4-11: Pedigree Map tab



Pedigree ID	Pedigree Name
24	1447
25	1451
26	1454
27	1456

   - The Allele Map tab displays the mapping of the original calls for each marker to the allele number generated for the export file. These values are not editable; however, you can sort the data by clicking the heading for either the Maker, Allele, or Call.

Figure 4-12: Allele Map tab

Marker	Allele	Call
rs10098	1	A
rs10098	2	B
rs1012959	1	A
rs1012959	2	B
rs1014803	1	A
rs1014803	2	B

You can also right-click on either of these tabs and open a context menu with options for copying the information on the tab, exporting the information on the tab to a text file, or printing the information on the tab.

   - The LOD Scores tab is initially blank. You must import the LOD scores for the linkage export. See “Importing LOD Scores” on page 381.

3. Optionally, to rerun the linkage export, right-click on the selected export, and on the context menu that opens, click Open Export.

   The Specify Linkage Settings dialog box opens. You can now modify any of the needed settings and click OK on the Settings tab to rerun the export. See "Creating and Running a Linkage Export" on page 369.

Importing LOD Scores

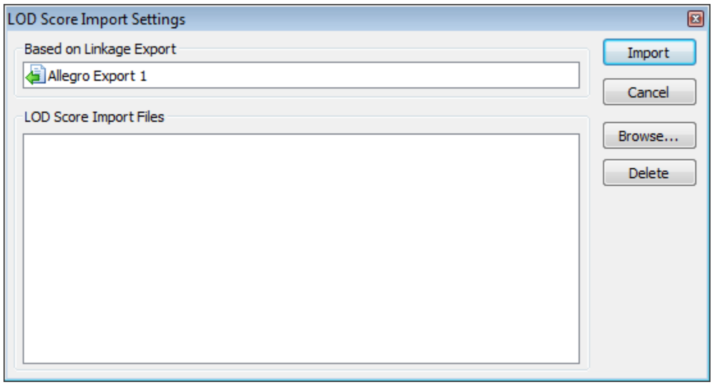
After you run a linkage export, the LOD Scores tab is initially blank for a selected export. You must import the LOD scores for the linkage export to populate the tab.

To import LOD scores

1. On the Analysis window, right-click on the linkage export for which you are importing the LOD scores, and on the context menu that opens, click Import LOD scores.

   The LOD Score Import Settings dialog box opens.

Figure 4-13: LOD Score Import Settings dialog box



Based on Linkage Export: Allegro Export 1

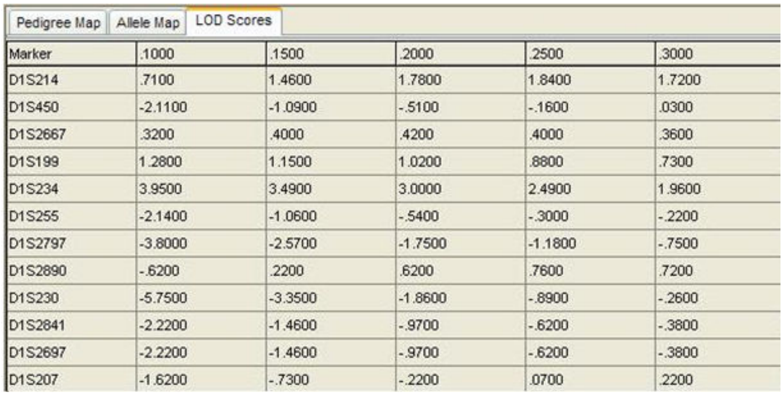
2. Click Browse to open the Open dialog box and browse to and select the LOD Score text files for the linkage export.

Remember, you loaded the files that were created by the linkage export into your analysis software to produce these LOD files.

3. Click Import.

   The LOD scores for each marker are displayed on the LOD Scores tab on the Analysis window for the selected linkage export.

Figure 4-14: LOD Scores tab



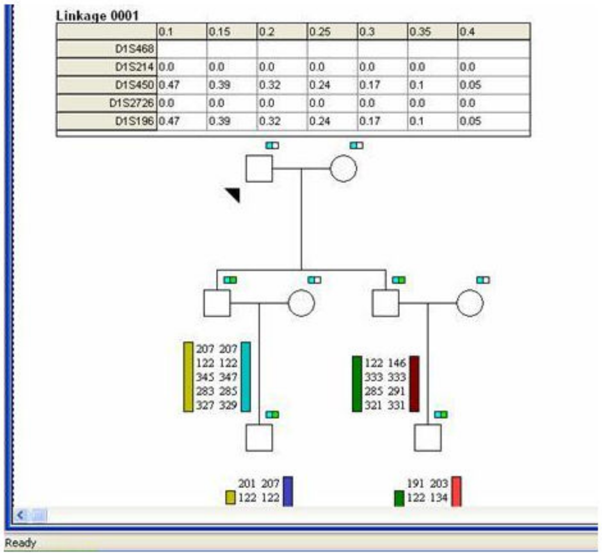
Marker	.1000	.1500	.2000	.2500	.3000
D1S214	.7100	1.4600	1.7800	1.8400	1.7200
D1S450	-2.1100	-1.0900	-.5100	-.1600	.0300
D1S2667	.3200	.4000	.4200	.4000	.3600
D1S199	1.2800	1.1500	1.0200	.8800	.7300
D1S234	3.9500	3.4900	3.0000	2.4900	1.9600
D1S255	-2.1400	-1.0600	-.5400	-.3000	-.2200
D1S2797	-3.8000	-2.5700	-1.7500	-1.1800	-.7500
D1S2890	-.6200	.2200	.6200	.7600	.7200
D1S230	-5.7500	-3.3500	-1.8600	-.8900	-.2600
D1S2841	-2.2200	-1.4600	-.9700	-.6200	-.3800
D1S2697	-2.2200	-1.4600	-.9700	-.6200	-.3800
D1S207	-1.6200	-.7300	-.2200	.0700	.2200

Displaying LOD Scores on a Pedigree

In addition to displaying LOD scores on the LOD Scores tab on the Analysis window, you can display LOD scores on a pedigree. To display the LOD scores on a pedigree, note the following:

- You must load the files that were created by the linkage export into your analysis software to produce the needed LOD files, and then you must import these LOD files into Progeny. See “Importing LOD Scores” on page 381.
- When you are drawing the pedigree, you must select the markers that you are to be displayed on the pedigree. See “To configure icon markers for a pedigree” on page 283.
- Show LOD Scores must be selected on the Pedigree tab of the Properties dialog box. See “Pedigree Properties” on page 271.

Figure 4-15: Displaying LOD scores on a pedigree



Linkage 0001

	0.1	0.15	0.2	0.25	0.3	0.35	0.4
D1S468							
D1S214	0.0	0.0	0.0	0.0	0.0	0.0	0.0
D1S450	0.47	0.39	0.32	0.24	0.17	0.1	0.05
D1S2726	0.0	0.0	0.0	0.0	0.0	0.0	0.0
D1S196	0.47	0.39	0.32	0.24	0.17	0.1	0.05

Deleting a Linkage Export

You can delete a linkage export by doing one of the following:

- Right-clicking on the linkage export in the Analysis window, and on the context menu that opens, clicking Delete Export.
- Selecting the linkage export in the Analysis window, and then clicking the [Delete] key on your keyboard.

Chapter 5
Family Based Associations

Progeny Lab provides all the functionality needed for managing genetic linkage studies, including managing family-based associations. Managing family-based associations consists of creating and running family-based association exports, saving family-based association export formats for running on an as-needed basis, and deleting family-based association exports.

This chapter covers the following topics:

Chapter 5
Family Based Associations

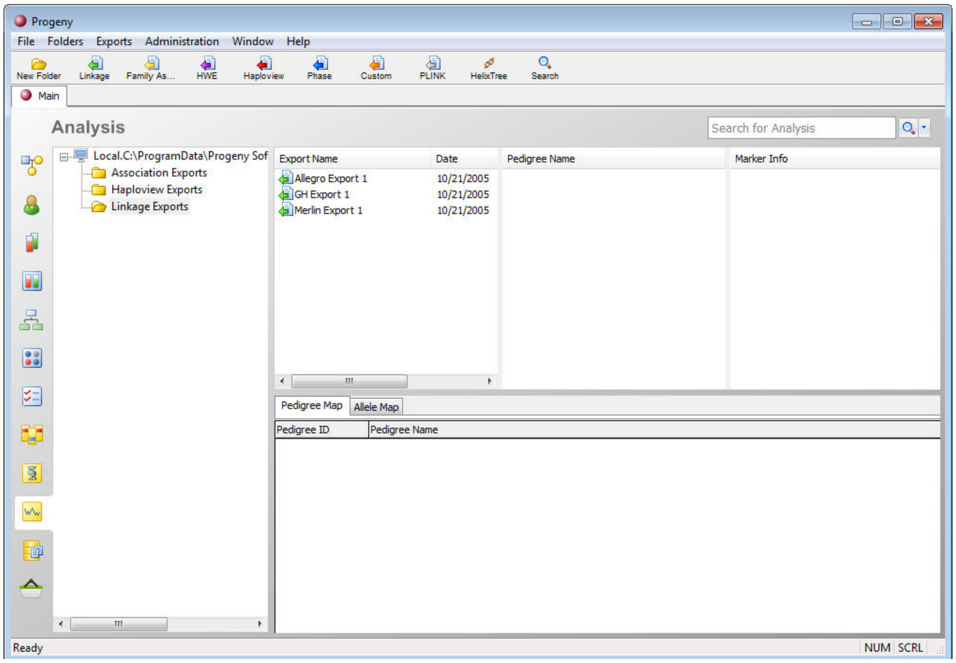
Creating and Running a Family-Based Association Export

You can export FBAT and QTDT association formats in.Progeny Lab. You must first create the association export, and then you can run the association export.

To create a family-based association export

1. On the main window navigation bar, click the Analysis button to open the Analysis window.

Figure 5-1: Analysis window



Export Name	Date	Pedigree Name	Marker Info
Allegro Export 1	10/21/2005		
GH Export 1	10/21/2005		
Merlin Export 1	10/21/2005		

2. On the Analysis window, select the folder in which to the association export is to be saved.

You can add a new folder if needed. Click the New Folder button on the window toolbar to open the New Folder dialog box, in which you can enter a name for a new Analysis folder and select its location (at the root level or as a sub-folder of another folder.)

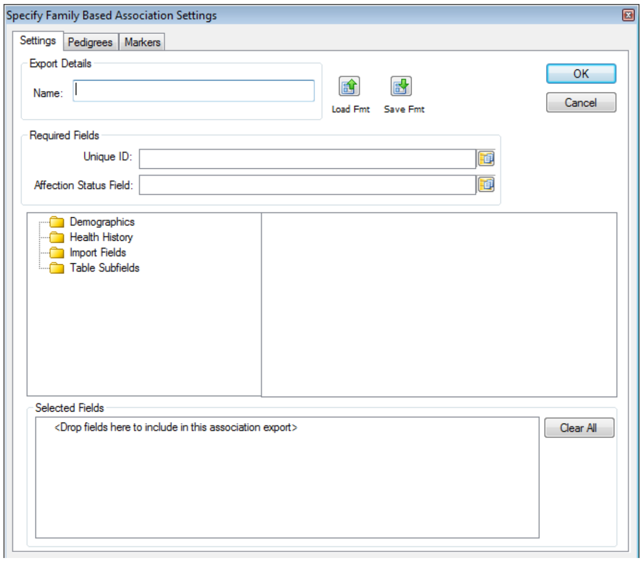
3. On the window toolbar, click the Family Association button Family As... .

The Specify Family Based Association Settings dialog box opens. By default, the Settings tab is the active tab.

4. Specify the necessary association settings on all three tabs of the dialog box. See:
   - "Specify Family Based Association Settings dialog box, Settings tab" on page 388.
   - "Specify Family Based Association Settings dialog box, Pedigrees tab" on page 389.
   - "Specify Family Based Association Settings dialog box, Markers tab" on page 391.
5. After you specify the necessary association settings on all three tabs, return to the Settings tab, and then click OK on the tab.
6. Continue to "To run a family-based association export" on page 392.

Specify Family Based Association Settings dialog box, Settings tab

Figure 5-2: Specify Family Based Association Settings dialog box, Settings tab



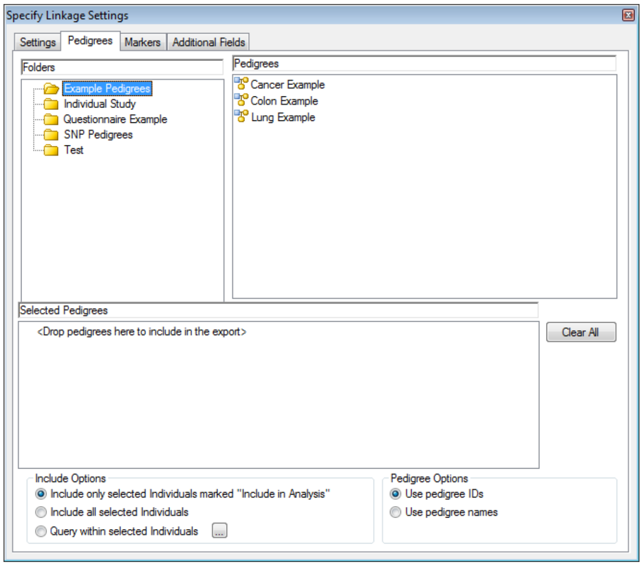
1. Specify the name for the association export and the required fields for the export.

Option	Description
Export Details	
Name	Name or description of the association export.
Required Fields	
Unique ID	Click the Fields button to the right of the Unique ID field to open the Select Field dialog box and select the field that represents the unique ID for each individual that is to be included in the association export.
Affection Status Field	Click the Fields button to the right of the Affection Status Field to open the Select Field dialog box and select the field that represents the affected status for each individual that is to be included in the association export.

2. Select the fields that are to be included in the association export by doing the following:
    - In the Folders (middle left) pane of the dialog box, select the folder that contains the individual data fields that are to be included in the association export.
    - In the Fields pane (middle right) pane of the dialog, select the fields (CTRL-click to select multiple fields) that are to be included in the association export.
    - Drag the selected fields to the Selected fields (bottom) pane of the dialog box.
3. Continue specifying any other family-based export settings as needed; otherwise, return to the Settings tab, click OK, and then continue to "To run a family-based association export" on page 392.

Specify Family Based Association Settings dialog box, Pedigrees tab

Figure 5-3: Specify Family Based Association Settings dialog box, Pedigrees tab



Include Options
● Include only selected Individuals marked "Include in Analysis"
○ Include all selected Individuals
○ Query within selected Individuals

Pedigree Options
● Use pedigree IDs
○ Use pedigree names

1. In the Folders (top left) pane of the dialog box, select the folder that contains the pedigrees for which the linkage export is being created.
2. In the Pedigrees (top right) pane of the dialog, select the pedigree (CTRL-click to select multiple pedigrees) for which the linkage export is being created.
3. Drag the selected pedigrees to the Selected Pedigrees (bottom) pane of the dialog box.

4. Select one of the following:
   - To include only those individuals in a pedigree who have been specifically marked for inclusion in an analysis, select Include only selected individuals marked "Include in Analysis." (See "To select individuals in a pedigree for inclusion in an analysis" on page 390.)
   - To include all individuals in all the selected pedigrees are included in the linkage export, select Include all selected individuals.
   - To include only those individuals in the export linkage who meet specific criteria, select Query within selected individuals, and then click the Query button to open the Query dialog box and define a new query, or load a saved query format.

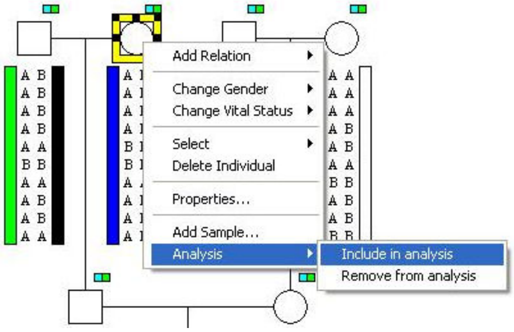
For detailed information about defining a query, see Chapter 8, "Database Queries and Searches," on page 171.

5. Select one of the following:
   - Use Pedigree IDs—Converts a text-based pedigree name into a numerical ID.
   - Use pedigree names—Use pedigree names as-is.
6. Continue specifying any other family-based export settings as needed; otherwise, return to the Settings tab, click OK, and then continue to "To run a family-based association export" on page 392.

To select individuals in a pedigree for inclusion in an analysis

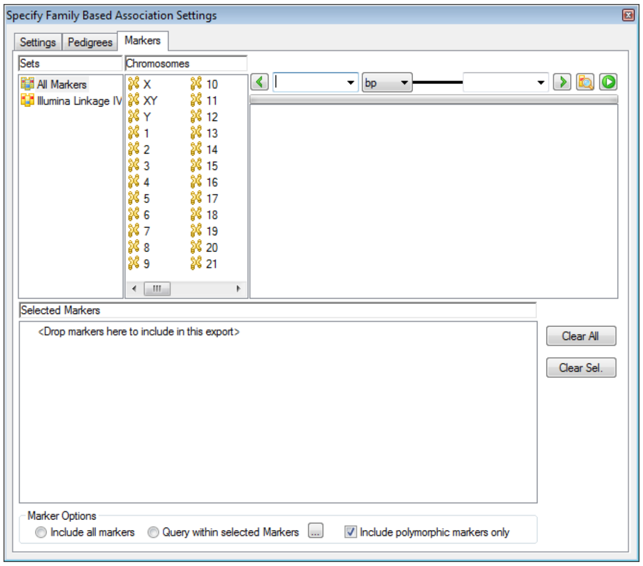
If you select the option Include only selected individuals marked "Include in Analysis," then you must open each affected pedigree, and manually select the appropriate individuals. You can select a single individual, or CTRL-click to select multiple individuals, and then right-click on any selected individual, and on the context menu that opens, click Include in analysis.

Figure 5-4: Selecting individuals for analysis



Specify Family Based Association Settings dialog box, Markers tab

Figure 5-5: Specify Family Based Association Settings dialog box, Markers tab



1. Do one of the following:
   - To include an entire marker set in the analysis, drag the marker set from the Sets (top right) pane of the dialog box to the Selected Markers (bottom) pane.
   - To include all the markers for a specific chromosome in the analysis, drag the chromosome from the Chromosomes (top middle) pane of the dialog box to the Selected Markers (bottom) pane.
   - To include only specific markers in the analysis, select the marker (CTRL-click to select multiple markers) from the top right pane to the Selected Markers (bottom) pane.

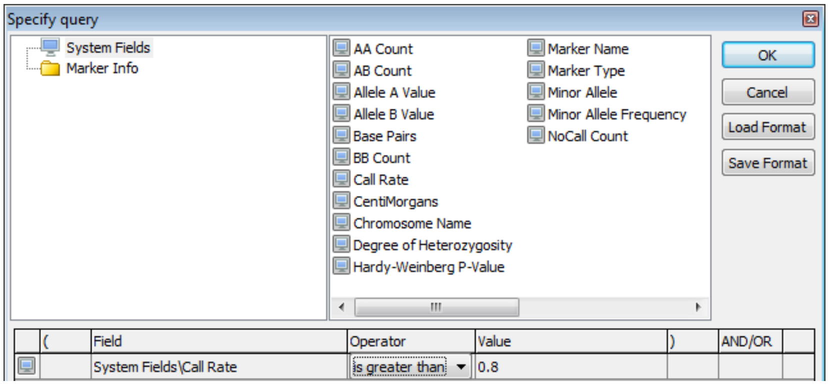
To search for a specific marker or markers, you can use the marker search functions. See "Searching for a Marker" on page 337.

2. Select one of the following:
   - To include all of the markers in the Selected Markers pane in the linkage export, select Include all markers.
   - To include only those markers in the Selected Markers pane in the linkage export that meet specific criteria, select Query within selected markers, and then click the Query button to open the Query dialog box and define a new query, or load a saved query format.

For detailed information about defining a query, see Chapter 8, "Database Queries and Searches," on page 171.

If you specify a query, then you can carry out additional marker filtering, and filter the selected SNPs by Hardy Weinberg p-value, Minor Allele Frequency, Degree of Heterozygosity, and/or Call Rates. For example, to include only those SNPs that have a call rate higher than 80%, you would select the Call Rate system field and enter > 0.8 as the operator and value. You can use this additional filtering criteria only if there is allele count data stored on a per SNP basis.

Figure 5-6: Additional marker filtering



(	Field	Operator	Value	)	AND/OR
	System Fields\Call Rate	is greater than	0.8		

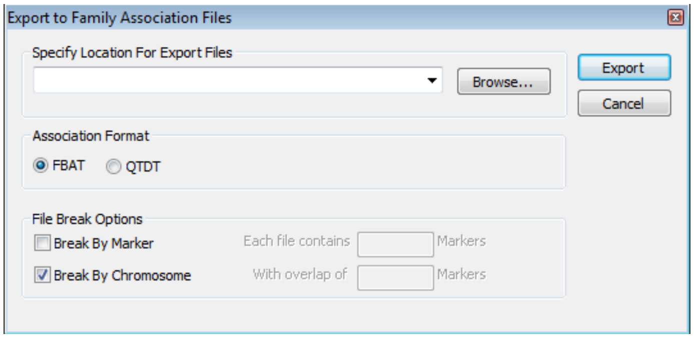
3. Optionally, select Include polymorphic markers only to further filter the selected markers and export only those markers that have at least one heterozygous genotype.

4. Continue specifying any other family-based export settings as needed; otherwise, return to the Settings tab, click OK, and then continue to "To run a family-based association export" below.

To run a family-based association export

After you specify the necessary export settings on all three tabs, you must return to the Settings tab, and then click OK on the tab. The Export to Family Association Files dialog box opens.

Figure 5-7: Export to Family Association Files dialog box



● FBAT ○ QTDT

☐ Break By Marker

☑ Break By Chromosome

1. Click Browse to open the Browse for Folder dialog box, and browse to and select the folder in which the association export files are to be stored.

If you have previously run association exports, then any previously selected locations are available in a dropdown list in the Browse field. You can always select a value from this list.

2. Select the appropriate association format.
3. Select one or both file break options.
    - Break by Marker—Indicate how many markers are to be contained in each linkage file. If you select this option, you must also indicate the number of overlapping markers in each file.
    - Break by Chromosome—Creates a new file for each chromosome that is exported.
4. Click Export.

    A dialog box opens, indicating the status of the association export.
5. When the export is complete, click Close to close the dialog box and return to the Analysis window.

Saving and Loading a Family Based Association Export Format

After you have set up a family-based association export format, you can save the format. You can then load this saved format and run it on as-needed basis.

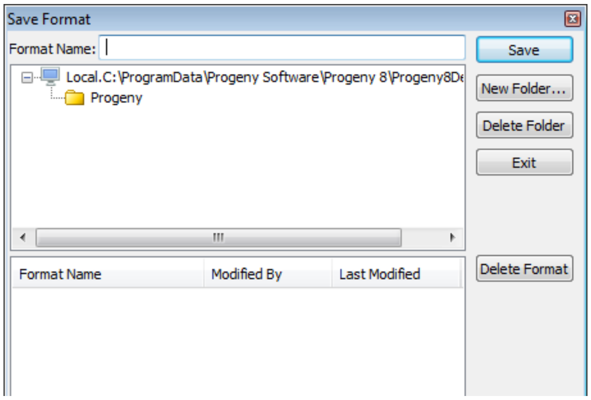
To save a family-based association export format

1. Set up the family-based association export format but do *not* run the format See “Creating and Running a Family-Based Association Export” on page 387.

2. Click the Save Format button Save Fmt on the Specify Family Based Association Settings dialog box.

   The Save Format dialog box opens. It provides a default folder named Progeny in which to save the export format. (This folder is located in the database that you are currently logged in to and you cannot change this location.)

Figure 5-8: Save Format dialog box



3. Enter a name for the association export format, and then do one of the following:
   - Select the Progeny folder.
   - Click New Folder, and on the Format Folder dialog box that opens, do the following:
     - Enter the name of the new folder in which to save to format.
     - Select the location for the new folder. The folder can be stored at the root level (the same level as the Progeny folder), or it can be a sub-folder of the Progeny folder, or of another folder.
     - Click Save.

4. Click Save on the Save Format dialog box.

   You can then load this saved format and run it on as-needed basis. See “To load a family-based association export format” on page 395.

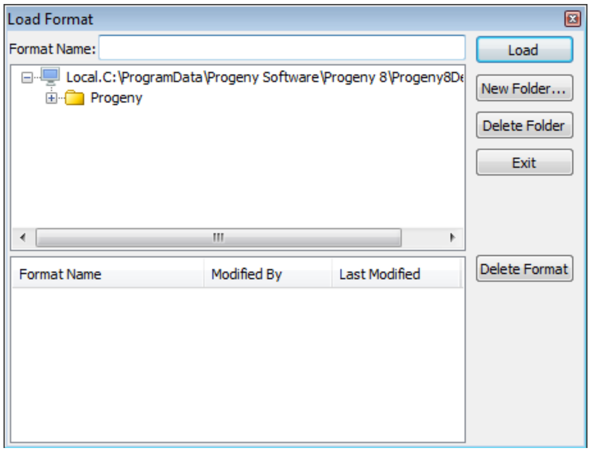
To load a family-based association export format

You can a retrieve a saved family-based association export format and run it on as-is needed based.

1. Open the Specify Family Based Association Settings dialog box. (See Step 1 through Step 3 of "To create a family-based association export" on page 387.)
2. On the dialog box, click the Load Format button Load Fmt .

   The Load Format dialog box opens.

Figure 5-9: Load Format dialog box



3. Open the folder that contains the association export format that you are loading, select the format, and then click Load.

   The Specify Family Based Association Export Settings dialog box is refreshed with the loaded format. You can modify the format as needed (for example, modify the information on the Pedigrees tab), and export the association format.

Viewing and Rerunning a Family-Based Association Export

You can view information about any family-based association exports that were previously run on the Analysis window, and you can rerun any association export as necessary.

To view and rerun a family-based association export

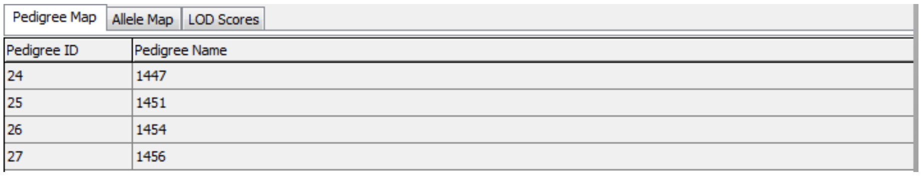
1. On the Analysis window, select the association export that you want to view.

   Two tabs open in the bottom pane of the window—Pedigree Map and Allele Map. By default, the Pedigree Map tab is the active tab.

2. Open and view the information on each tab as necessary.

   - The Pedigree Map tab displays the mapping of the original pedigree name to the pedigree ID generated for the export file. These values are not editable; however, you can sort this information by clicking the heading for either the Pedigree ID or the Pedigree Name.

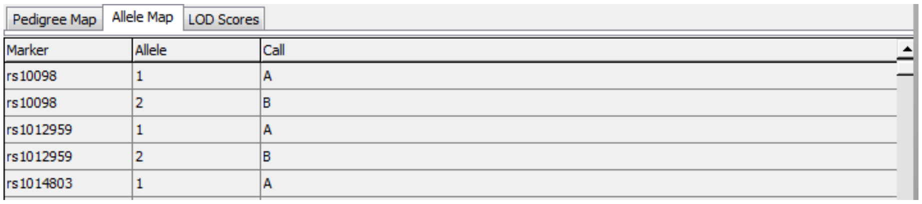
Figure 5-10: Pedigree Map tab



Pedigree ID	Pedigree Name
24	1447
25	1451
26	1454
27	1456

   - The Allele Map tab displays the mapping of the original calls for each marker to the allele number generated for the export file. These values are not editable; however, you can sort the data by clicking the heading for either the Maker, Allele, or Call.

Figure 5-11: Allele Map tab



Marker	Allele	Call
rs10098	1	A
rs10098	2	B
rs1012959	1	A
rs1012959	2	B
rs1014803	1	A

You can also right-click on either of these tabs and open a context menu with options for copying the information on the tab, exporting the information on the tab to a text file, or printing the information on the tab.

3. Optionally, to rerun the association export, right-click on the selected export, and on the context menu that opens, click Open Export.

   The Specify Family Based Association Settings dialog box opens. You can now modify any of the needed settings and click OK on the Settings tab to rerun the export. See "Creating and Running a Family-Based Association Export" on page 387.

Deleting a Family-Based Association Export

You can delete a family-based association export by doing one of the following:

- Right-clicking on the association export in the Analysis window, and on the context menu that opens, clicking Delete Export.
- Selecting the association export in the Analysis window, and then clicking the [Delete] key on your keyboard.

Chapter 6
Hardy Weinberg Test

Progeny Lab provides all the functionality needed for creating Hardy Weinberg tests and working with the results.

This chapter covers the following topics:

Chapter 6
Hardy Weinberg Test

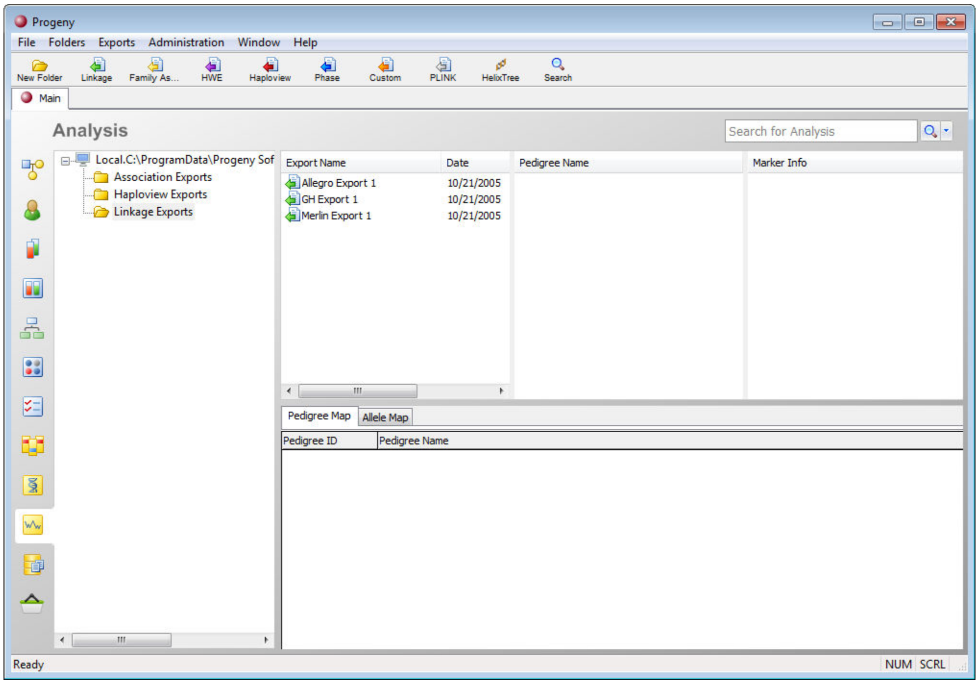
Creating and Running a Hardy Weinberg Export

Progeny Lab provides all the functionality needed for creating a Hardy Weinberg export and working with the results. You must first create the export, and then you can run the export.

To create a Hardy Weinberg export

1. On the main window navigation bar, click the Analysis button to open the Analysis window.

Figure 6-1: Analysis window



Export Name	Date	Pedigree Name	Marker Info
Allegro Export 1	10/21/2005		
GH Export 1	10/21/2005		
Merlin Export 1	10/21/2005		

2. On the Analysis window, select the folder in which to the association export is to be saved.

You can add a new folder if needed. Click the New Folder button on the window toolbar to open the New Folder dialog box, in which you can enter a name for a new Analysis folder and select its location (at the root level or as a sub-folder of another folder.)

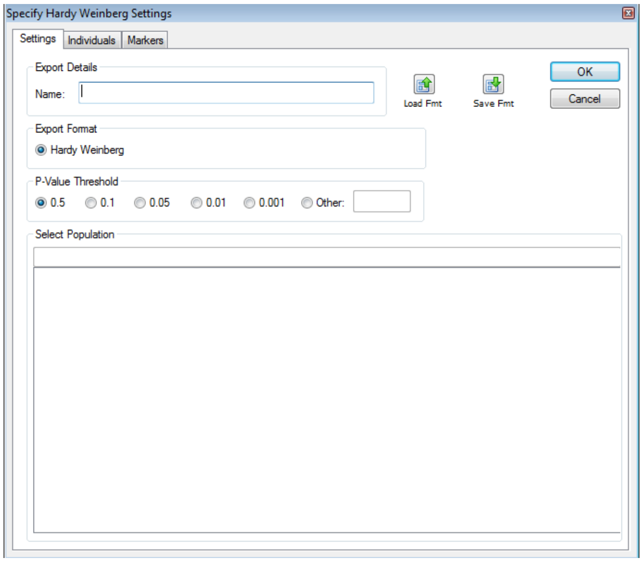
3. On the window toolbar, click the Hardy Weinberg button HWE.

   The Specify Hardy Weinberg Settings dialog box opens. By default, the Settings tab is the active tab.

4. Specify the necessary association settings on all three tabs of the dialog box. See:
   - "Specify Hardy Weinberg Settings dialog box, Settings tab" on page 402.
   - "Specify Hardy Weinberg Settings dialog box, Individuals tab" on page 403.
   - "Specify Hardy Weinberg Settings dialog box, Markers tab" on page 404.
5. After you specify the necessary settings on all three tabs, return to the Settings tab, and then click OK on the tab.
6. Continue to "To run a Hardy Weinberg export."

Specify Hardy Weinberg Settings dialog box, Settings tab

Figure 6-2: Specify Hardy Weinberg Settings dialog box, Settings tab



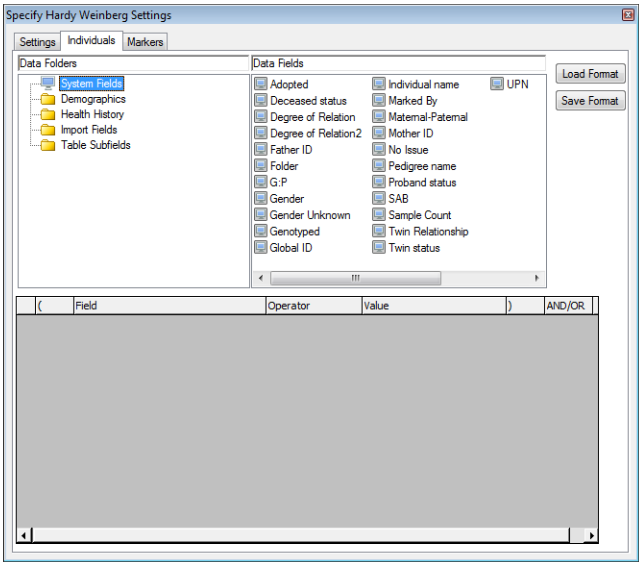
Export Format: ● Hardy Weinberg

P-Value Threshold: ● 0.5 ○ 0.1 ○ 0.05 ○ 0.01 ○ 0.001 ○ Other:

1. Specify the name for the Hardy Weinberg export.
2. Select from one of the preset values for the p-value threshold, or click Other, and then enter the p-value threshold.
3. Continue specifying any other Hardy Weinberg export settings as needed; otherwise, return to the Settings tab, click OK, and then continue to "To run a Hardy Weinberg export" on page 405.

Specify Hardy Weinberg Settings dialog box, Individuals tab

Figure 6-3: Specify Hardy Weinberg Settings dialog box, Individuals tab



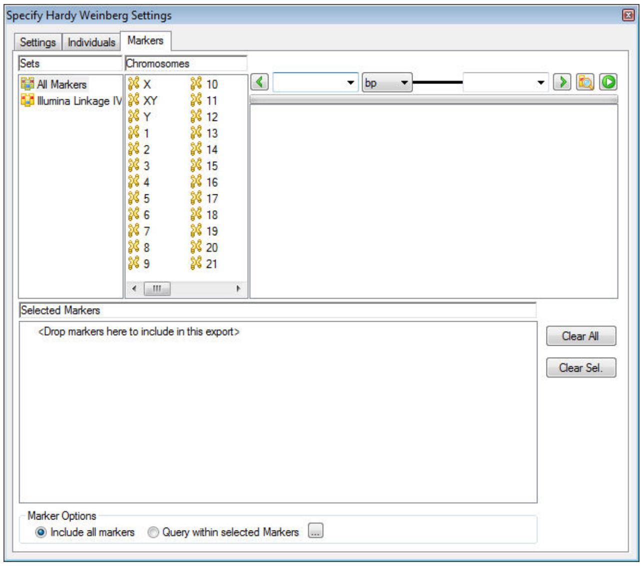
1. Define a query to select those individuals that are to be included in your Hardy Weinberg test.

For detailed information about defining a query, see Chapter 8, "Database Queries and Searches," on page 171.

2. Continue specifying any other Hardy Weinberg export settings as needed; otherwise, return to the Settings tab, click OK, and then continue to "To run a Hardy Weinberg export" on page 405.

Specify Hardy Weinberg Settings dialog box, Markers tab

Figure 6-4: Specify Hardy Weinberg Settings dialog box, Markers tab



1. Do one of the following:
   - To include an entire marker set in the analysis, drag the marker set from the Sets (top right) pane of the dialog box to the Selected Markers (bottom) pane.
   - To include all the markers for a specific chromosome in the analysis, drag the chromosome from the Chromosomes (top middle) pane of the dialog box to the Selected Markers (bottom) pane.
   - To include only specific markers in the analysis, select the marker (CTRL-click to select multiple markers) from the top right pane to the Selected Markers (bottom) pane.

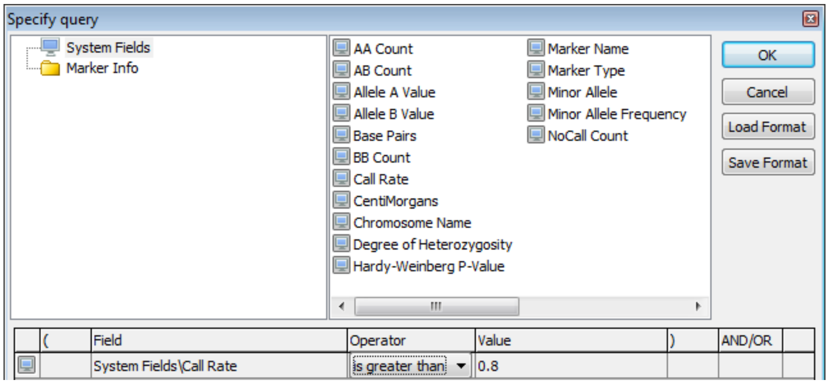
To search for a specific marker or markers, you can use the marker search functions. See "Searching for a Marker" on page 337.

2. Select one of the following:
   - To include all of the markers in the Selected Markers pane in the linkage export, select Include all markers.
   - To include only those markers in the Selected Markers pane in the linkage export that meet specific criteria, select Query within selected markers, and then click the Query button to open the Query dialog box and define a new query, or load a saved query format.

For detailed information about defining a query, see Chapter 8, "Database Queries and Searches," on page 171.

If you specify a query, then you can carry out additional marker filtering, and filter the selected SNPs by Minor Allele Frequency, Degree of Heterozygosity, and/or Call Rates. For example, to include only those SNPs that have a call rate higher than 80%, you would select the Call Rate system field and enter > 0.8 as the operator and value. You can use this additional filtering criteria only if there is allele count data stored on a per SNP basis.

Figure 6-5: Additional marker filtering



(	Field	Operator	Value	)	AND/OR
	System Fields\Call Rate	is greater than	0.8		

3. Continue specifying any other Hardy Weinberg export settings as needed; otherwise, return to the Settings tab, click OK, and then continue to "To run a Hardy Weinberg export" below.

To run a Hardy Weinberg export

1. After you specify the necessary export settings on all three tabs, you must return to the Settings tab, and then click OK on the tab.

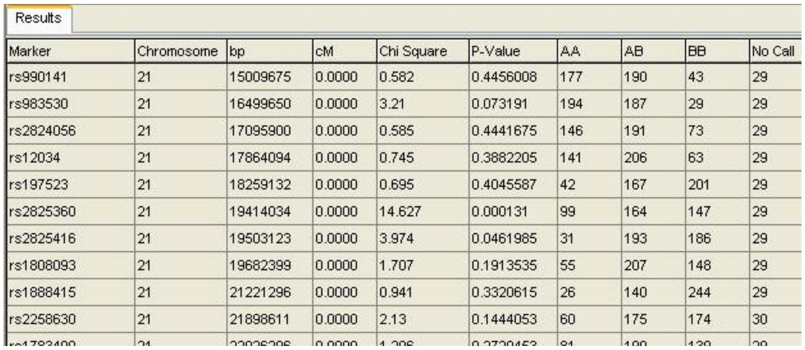
   A Export Status dialog box opens, indicating the progress of the export.

2. After the export is completed, click Close to close the Export Status dialog box and return to the Analysis window.

   The resulting are displayed on the Results tab in the bottom pane of the Analysis window.

Remember, the results might not contain all the markers that you selected. If you specified a lower p-value threshold, then the higher p-value results are not included.

Figure 6-6: Results tab



Marker	Chromosome	bp	cM	Chi Square	P-Value	AA	AB	BB	No Call
rs990141	21	15009675	0.0000	0.582	0.4456008	177	190	43	29
rs983530	21	16499650	0.0000	3.21	0.073191	194	187	29	29
rs2824056	21	17095900	0.0000	0.585	0.4441675	146	191	73	29
rs12034	21	17864094	0.0000	0.745	0.3882205	141	206	63	29
rs197523	21	18259132	0.0000	0.695	0.4045587	42	167	201	29
rs2825360	21	19414034	0.0000	14.627	0.000131	99	164	147	29
rs2825416	21	19503123	0.0000	3.974	0.0461985	31	193	186	29
rs1808093	21	19682399	0.0000	1.707	0.1913535	55	207	148	29
rs1888415	21	21221296	0.0000	0.941	0.3320615	26	140	244	29
rs2258630	21	21898611	0.0000	2.13	0.1444053	60	175	174	30

Column	Description
Marker	The name of the marker.
Chromosome	The name of the chromosome.
bp	The base pair information for the chromosome.
cM	The cM information for the marker.
Chi Square	The calculated Chi Square value for the marker.
P-Value	The corresponding p-value for the marker.
AA	The number of AA calls in the Hardy Weinberg test.
AB	The number of AB calls in the Hardy Weinberg test.
BB	The number of BB calls in the Hardy Weinberg test.
No Calls	The number of No Calls in the Hardy Weinberg test.

Saving and Loading a Hardy Weinberg Export Format

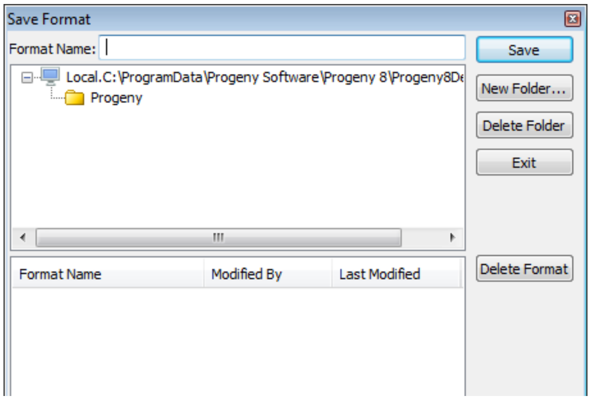
After you have set up a Hardy Weinberg export format, you can save the format. You can then load this saved format and run it on as-needed basis.

To save a Hardy Weinberg export format

1. Set up the Hardy Weinberg export format but do *not* run the format See “Creating and Running a Hardy Weinberg Export” on page 401.
2. Click the Save Format button Save Fmt on the Specify Hardy Weinberg Settings dialog box.

   The Save Format dialog box opens. It provides a default folder named Progeny in which to save the export format. (This folder is located in the database that you are currently logged in to and you cannot change this location.)

Figure 6-7: Save Format dialog box



3. Enter a name for the Hardy Weinberg export format, and then do one of the following:
   - Select the Progeny folder.
   - Click New Folder, and on the Format Folder dialog box that opens, do the following:
     - Enter the name of the new folder in which to save to format.
     - Select the location for the new folder. The folder can be stored at the root level (the same level as the Progeny folder), or it can be a sub-folder of the Progeny folder, or of another folder.
     - Click Save.
4. Click Save on the Save Format dialog box.

   You can then load this saved format and run it on as-needed basis. See “To load a Hardy Weinberg export format” on page 408.

To load a Hardy Weinberg export format

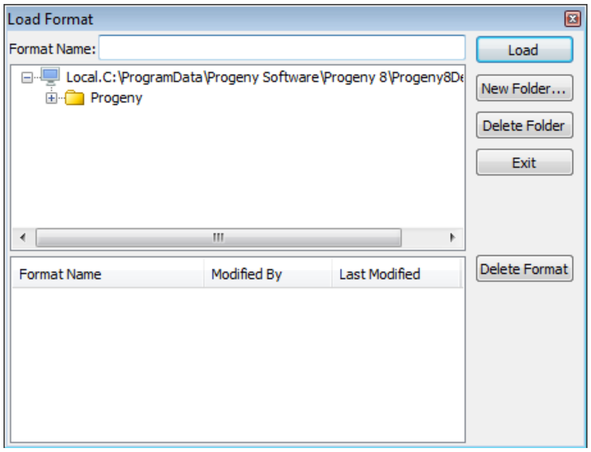
You can a retrieve a saved Hardy Weinberg export format and run it on as-is needed based.

1. Open the Specify Hardy Weinberg Settings dialog box. (See Step 1 through Step 3 of “Creating and Running a Hardy Weinberg Export” on page 401.)

2. On the dialog box, click the Load Format button Load Fmt .

   The Load Format dialog box opens.

Figure 6-8: Load Format dialog box



3. Open the folder that contains the Hardy Weinberg export format that you are loading, select the format, and then click Load.

   The Specify Hardy Weinberg Settings dialog box is refreshed with the loaded format. You can modify the format as needed (for example, modify the information on the Markers tab), and export the format. See “Creating and Running a Hardy Weinberg Export” on page 401.

Viewing and Rerunning a Hardy Weinberg Export

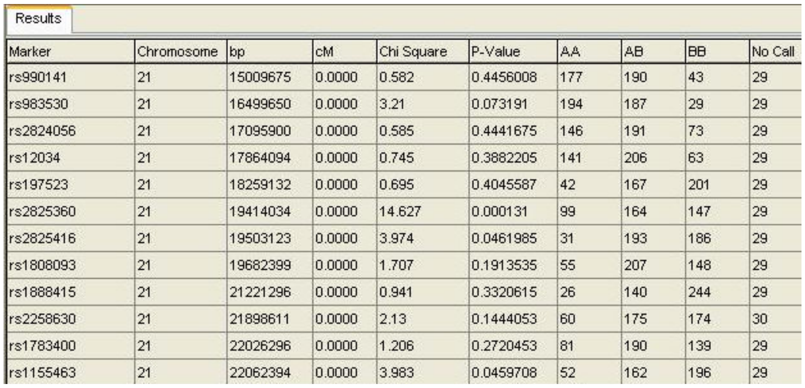
You can view information about any Hardy Weinberg exports that were previously run on the Analysis window, and you can rerun any Hardy Weinberg export as necessary.

To view and rerun a Hardy Weinberg export

1. On the Analysis window, select the Hardy Weinberg export that you want to view.

   A single tab—the Results tab—opens in the bottom pane of the window.

Figure 6-9: Results tab



Marker	Chromosome	bp	cM	Chi Square	P-Value	AA	AB	BB	No Call
rs990141	21	15009675	0.0000	0.582	0.4456008	177	190	43	29
rs983530	21	16499650	0.0000	3.21	0.073191	194	187	29	29
rs2824056	21	17095900	0.0000	0.585	0.4441675	146	191	73	29
rs12034	21	17864094	0.0000	0.745	0.3882205	141	206	63	29
rs197523	21	18259132	0.0000	0.695	0.4045587	42	167	201	29
rs2825360	21	19414034	0.0000	14.627	0.000131	99	164	147	29
rs2825416	21	19503123	0.0000	3.974	0.0461985	31	193	186	29
rs1808093	21	19682399	0.0000	1.707	0.1913535	55	207	148	29
rs1888415	21	21221296	0.0000	0.941	0.3320615	26	140	244	29
rs2258630	21	21898611	0.0000	2.13	0.1444053	60	175	174	30
rs1783400	21	22026296	0.0000	1.206	0.2720453	81	190	139	29
rs1155463	21	22062394	0.0000	3.983	0.0459708	52	162	196	29

You can also right-click on the tab and open a context menu with options for copying the information on the tab, exporting the information on the tab to a text file, or printing the information on the tab.

2. Optionally, to rerun the Hardy Weinberg export, right-click on the selected export, and on the context menu that opens, click Open Export.

   The Specify Hardy Weinberg Settings dialog box opens. You can now modify any of the needed settings and click OK on the Settings tab to rerun the export. See "Creating and Running a Hardy Weinberg Export" on page 401.

Deleting a Hardy Weinberg Export

You can delete a Hardy Weinberg export by doing one of the following:

- Right-clicking on the export in the Analysis window, and on the context menu that opens, clicking Delete Export.
- Selecting the export in the Analysis window, and then clicking the [Delete] key on your keyboard.

Chapter 7
Haploview Exports

Progeny Lab provides all the functionality needed for creating haploview exports and working with the results.

This chapter covers the following topics:

- "Creating and Running a Haploview Export" on page 413.
- "Saving and Loading a Haploview Export Format" on page 420.
- "Viewing and Rerunning a Haploview Export" on page 422.
- "Deleting a Haploview Export" on page 423.

To create and run haploview exports, Haploview must be installed locally.

Creating and Running a Haploview Export

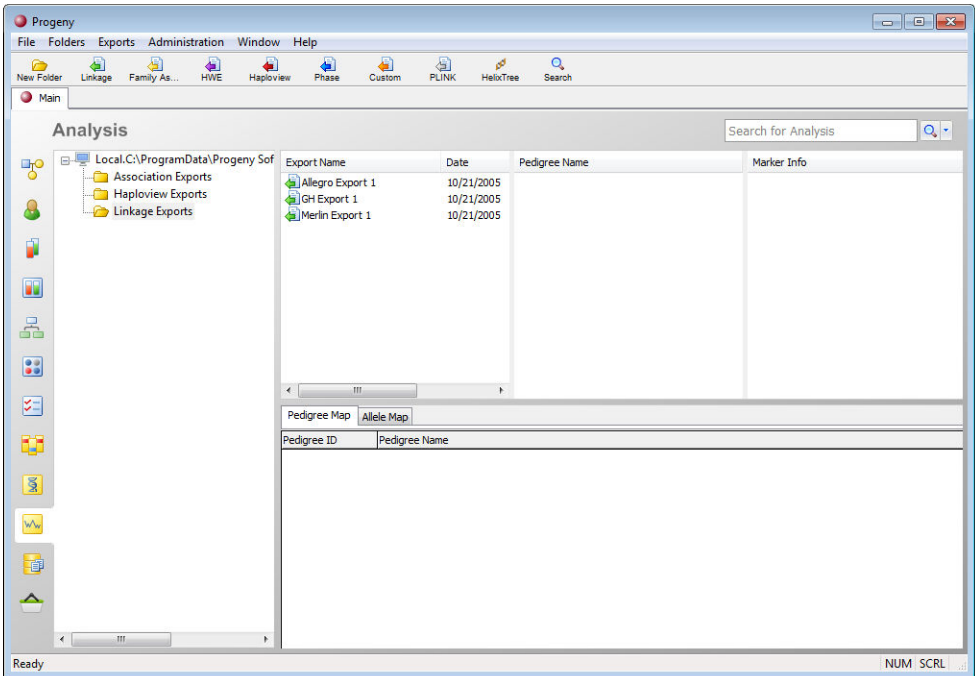
Progeny Lab provides all the functionality needed for creating haploview exports and working with the results. You must first create the export, and then you can run the export.

To create and run Haploview exports, Haploview must be installed locally.

To create a Haploview export

1. On the main window navigation bar, click the Analysis button to open the Analysis window.

Figure 7-1: Analysis window



Export Name	Date	Pedigree Name	Marker Info
Allegro Export 1	10/21/2005		
GH Export 1	10/21/2005		
Merlin Export 1	10/21/2005		

2. On the Analysis window, select the folder in which to the haploview export is to be saved.

You can add a new folder if needed. Click the New Folder button on the window toolbar to open the New Folder dialog box, in which you can enter a name for a new Analysis folder and select its location (at the root level or as a sub-folder of another folder.)

3. On the window toolbar, click the Haploview button Haploview.

   The Specify Haploview Export Settings dialog box opens. By default, the Settings tab is the active tab.

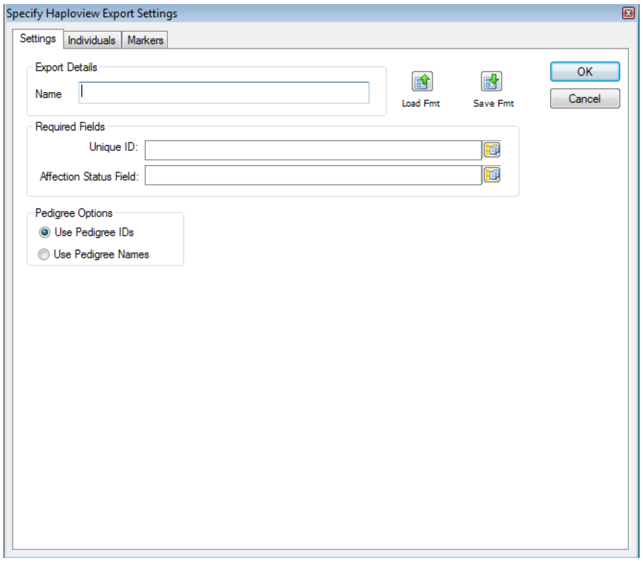
4. Specify the necessary association settings on all three tabs of the dialog box. See:
   - "Specify Haploview Export Settings dialog box, Settings tab" on page 414.
   - "Specify Haploview Export Settings dialog box, Individuals tab" on page 415.
   - "Specify Haploview Export Settings dialog box, Markers tab" on page 416.

5. After you specify the necessary export settings on all three tabs, return to the Settings tab, and then click OK on the tab.

6. Continue to "To run a Haploview export."

Specify Haploview Export Settings dialog box, Settings tab

Figure 7-2: Specify Haploview Export Settings dialog box, Settings tab



1. Specify the settings for the Haploview export.

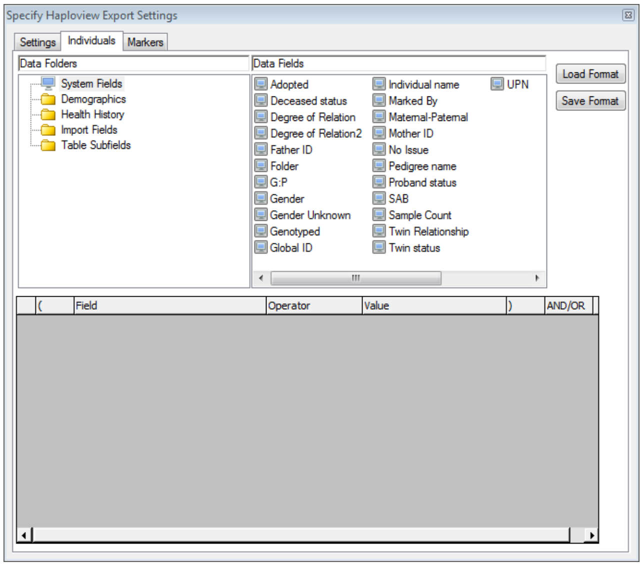
Option	Description
Export Details	
Name	Name or description of the haploview export.
Required Fields	
Unique ID	Click the Fields button to the right of the Unique ID field to open the Select Field dialog box and select the field that represents the unique ID for each individual that is to be included in the haploview export.

Option	Description
Affection Status Field	Click the Fields button to the right of the Affection Status Field to open the Select Field dialog box and select the field that represents the affected status for each individual that is to be included in the haploview export.
Pedigree Options	
Use Pedigree IDs	Converts a text-based pedigree name into a numerical ID.
Use pedigree names	Use pedigree names as-is.

2. Continue specifying any other Haploview export settings as needed; otherwise, return to the Settings tab, click OK, and then continue to "To run a Haploview export" on page 418.

Specify Haploview Export Settings dialog box, Individuals tab

Figure 7-3: Specify Haploview Export Settings dialog box, Individuals tab



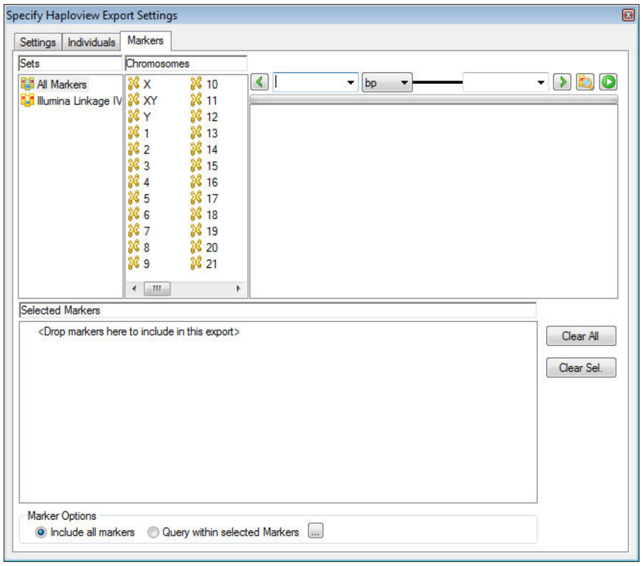
1. Define a query to select those individuals that are to be included in your haploview export.

For detailed information about defining a query, see Chapter 8, "Database Queries and Searches," on page 171.

2. Continue specifying any other Haploview export settings as needed; otherwise, return to the Settings tab, click OK, and then continue to "To run a Haploview export" on page 418.

Specify Haploview Export Settings dialog box, Markers tab

Figure 7-4: Specify Haploview Export Settings dialog box, Markers tab



1. Do one of the following:
   - To include an entire marker set in the analysis, drag the marker set from the Sets (top right) pane of the dialog box to the Selected Markers (bottom) pane.
   - To include all the markers for a specific chromosome in the analysis, drag the chromosome from the Chromosomes (top middle) pane of the dialog box to the Selected Markers (bottom) pane.
   - To include only specific markers in the analysis, select the marker (CTRL-click to select multiple markers) from the top right pane to the Selected Markers (bottom) pane.

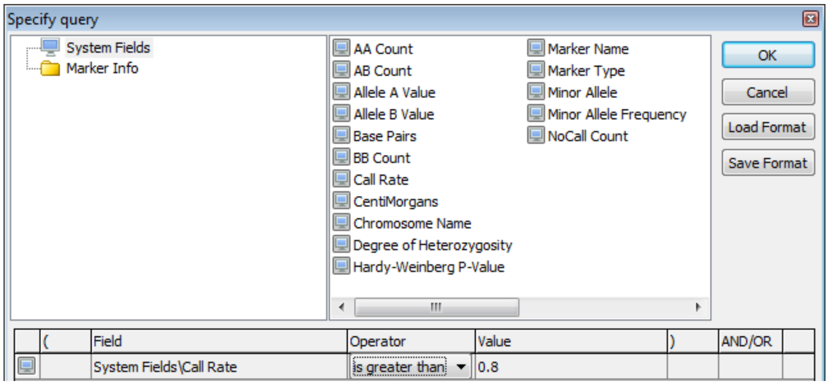
To search for a specific marker or markers, you can use the marker search functions. See "Searching for a Marker" on page 337.

2. Select one of the following:
   - To include all of the markers in the Selected Markers pane in the linkage export, select Include all markers.
   - To include only those markers in the Selected Markers pane in the linkage export that meet specific criteria, select Query within selected markers, and then click the Query button to open the Query dialog box and define a new query, or load a saved query format.

For detailed information about defining a query, see Chapter 8, "Database Queries and Searches," on page 171.

If you specify a query, then you can carry out additional marker filtering, and filter the selected SNPs by Hardy Weinberg p-value, Minor Allele Frequency, Degree of Heterozygosity, and/or Call Rates. For example, to include only those SNPs that have a call rate higher than 80%, you would select the Call Rate system field and enter > 0.8 as the operator and value. You can use this additional filtering criteria only if there is allele count data stored on a per SNP basis.

Figure 7-5: Additional marker filtering



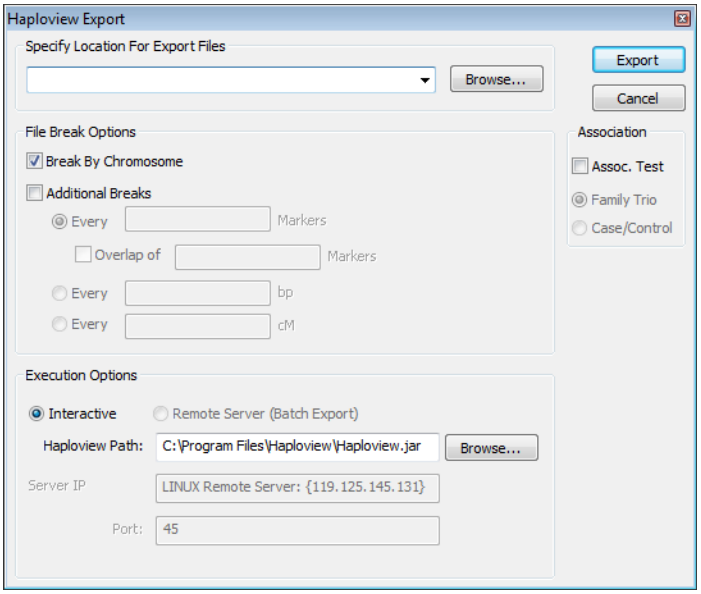
(	Field	Operator	Value	)	AND/OR
	System Fields\Call Rate	is greater than	0.8		

3. Continue specifying any other Haploview export settings as needed; otherwise, return to the Settings tab, click OK, and then continue to "To run a Haploview export" on page 418.

To run a Haploview export

After you specify the necessary export settings on all three tabs, you must return to the Settings tab, and then click OK on the tab. The Haploview Export dialog box opens.

Figure 7-6: Haploview Export dialog box



Haploview Export

Specify Location For Export Files

Browse...

Export

Cancel

File Break Options

☑ Break By Chromosome

☐ Additional Breaks

● Every Markers

☐ Overlap of Markers

○ Every bp

○ Every cM

Association

☐ Assoc. Test

● Family Trio

○ Case/Control

Execution Options

● Interactive ○ Remote Server (Batch Export)

Haploview Path: C:\Program Files\Haploview\Haploview.jar Browse...

Server IP LINUX Remote Server: {119.125.145.131}

Port: 45

1. Click Browse to open the Browse for Folder dialog box, and browse to and select the folder in which the haploview export files are to be stored.

If you have previously run haploview exports, then any previously selected locations are available in a dropdown list in the Browse field. You can always select a value from this list.

2. Optionally to select an association format, select Association Test, and then select Family Trios or Case/Controls.

3. Select one or both file break options.
   - Break by Chromosome—Creates a new file for each chromosome that is exported.
   - Additional Breaks
     - Every [ ] Markers—Indicates how many markers are to be contained in each export file. If you select this option, you must also indicate the number of overlapping markers in each file.
     - Every [ ] bp—Indicates how many base pairs are to be included in each file.
     - Every [ ] cM—Indicates how many centiMorgans are to be included in each file.

The break options can overlap. For example, select to Break by Chromosome and then by every 1000000 bp within the chromosome.

4. Only the Interactive execution is currently available. The default path to the Haploview executable is displayed in the Haploview Path field. You can leave this location as-is, or you can click Browse to open the Open the dialog box and browse to and select a different location for the executable.
5. Click Export.

   An Export to Haploview dialog box opens, indicating the status of the haploview export.
6. When the export is complete, click Close to close the dialog box and return to the Analysis window.

   After Haploview has completed the necessary calculations, a Haploview window opens showing the result of the calculations.

Saving and Loading a Haploview Export Format

After you have set up a Haploview export format, you can save the format. You can then load this saved format and run it on as-needed basis.

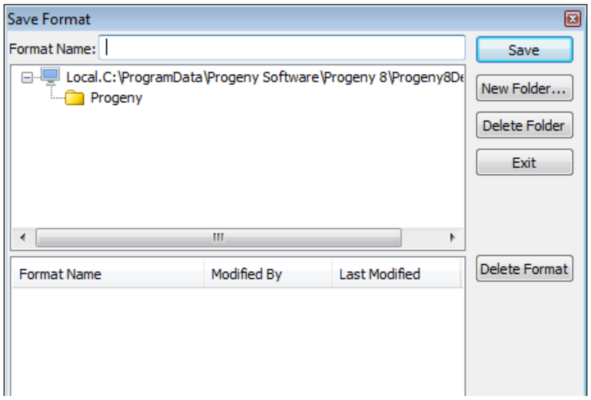
To save a Haploview export format

1. Set up the haploview export format but do *not* run the format See “Creating and Running a Haploview Export” on page 413.

2. Click the Save Format button Save Fmt on the Specify Haploview Export Settings dialog box.

   The Save Format dialog box opens. It provides a default folder named Progeny in which to save the export format. (This folder is located in the database that you are currently logged in to and you cannot change this location.)

Figure 7-7: Save Format dialog box



3. Enter a name for the Haploview export format, and then do one of the following:
   - Select the Progeny folder.
   - Click New Folder, and on the Format Folder dialog box that opens, do the following:
     - Enter the name of the new folder in which to save to format.
     - Select the location for the new folder. The folder can be stored at the root level (the same level as the Progeny folder), or it can be a sub-folder of the Progeny folder, or of another folder.
     - Click Save.

4. Click Save on the Save Format dialog box.

   You can then load this saved format and run it on as-needed basis. See “To load a Haploview export format” on page 421.

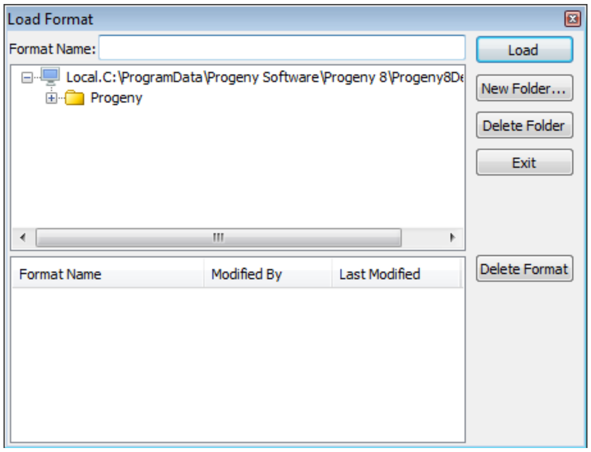
To load a Haploview export format

You can a retrieve a saved Haploview export format and run it on as-is needed based.

1. Open the Specify Haploview Export Settings dialog box. (See Step 1 through Step 3 of "To create a Haploview export" on page 413.)
2. On the dialog box, click the Load Format button Load Fmt .

   The Load Format dialog box opens.

Figure 7-8: Load Format dialog box



3. Open the folder that contains the Haploview export format that you are loading, select the format, and then click Load.

   The Specify Haploview Export Settings dialog box is refreshed with the loaded format. You can modify the format as needed (for example, modify the information on the Markers tab), and export the format. See "Creating and Running a Haploview Export" on page 413.

Viewing and Rerunning a Haploview Export

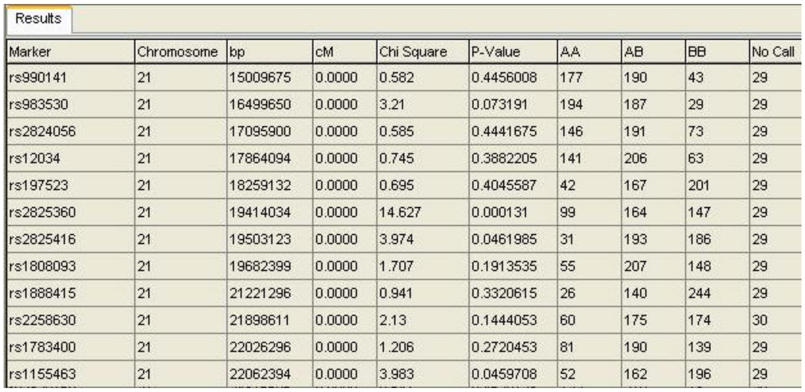
You can view information about any haploview exports that were previously run on the Analysis window, and you can rerun any haploview export as necessary.

To view and rerun a haploview export

1. On the Analysis window, select the haploview export that you want to view.

   A single tab—the Results tab—opens in the bottom pane of the window.

Figure 7-9: Results tab



Marker	Chromosome	bp	cM	Chi Square	P-Value	AA	AB	BB	No Call
rs990141	21	15009675	0.0000	0.582	0.4456008	177	190	43	29
rs983530	21	16499650	0.0000	3.21	0.073191	194	187	29	29
rs2824056	21	17095900	0.0000	0.585	0.4441675	146	191	73	29
rs12034	21	17864094	0.0000	0.745	0.3882205	141	206	63	29
rs197523	21	18259132	0.0000	0.695	0.4045587	42	167	201	29
rs2825360	21	19414034	0.0000	14.627	0.000131	99	164	147	29
rs2825416	21	19503123	0.0000	3.974	0.0461985	31	193	186	29
rs1808093	21	19682399	0.0000	1.707	0.1913535	55	207	148	29
rs1888415	21	21221296	0.0000	0.941	0.3320615	26	140	244	29
rs2258630	21	21898611	0.0000	2.13	0.1444053	60	175	174	30
rs1783400	21	22026296	0.0000	1.206	0.2720453	81	190	139	29
rs1155463	21	22062394	0.0000	3.983	0.0459708	52	162	196	29

You can also right-click on the tab and open a context menu with options for copying the information on the tab, exporting the information on the tab to a text file, or printing the information on the tab.

2. Optionally, to rerun the haploview export, right-click on the selected export, and on the context menu that opens, click Open Export.

   The Specify Haploview Export Settings dialog box opens. You can now modify any of the needed settings and click OK on the Settings tab to rerun the export. See “Creating and Running a Haploview Export” on page 413.

Deleting a Haploview Export

You can delete a Haploview export by doing one of the following:

- Right-clicking on the export in the Analysis window, and on the context menu that opens, clicking Delete Export.
- Selecting the export in the Analysis window, and then clicking the [Delete] key on your keyboard.

Chapter 8
Phase Exports

Progeny Lab provides all the functionality needed for creating phase exports and working with the results.

This chapter covers the following topics:

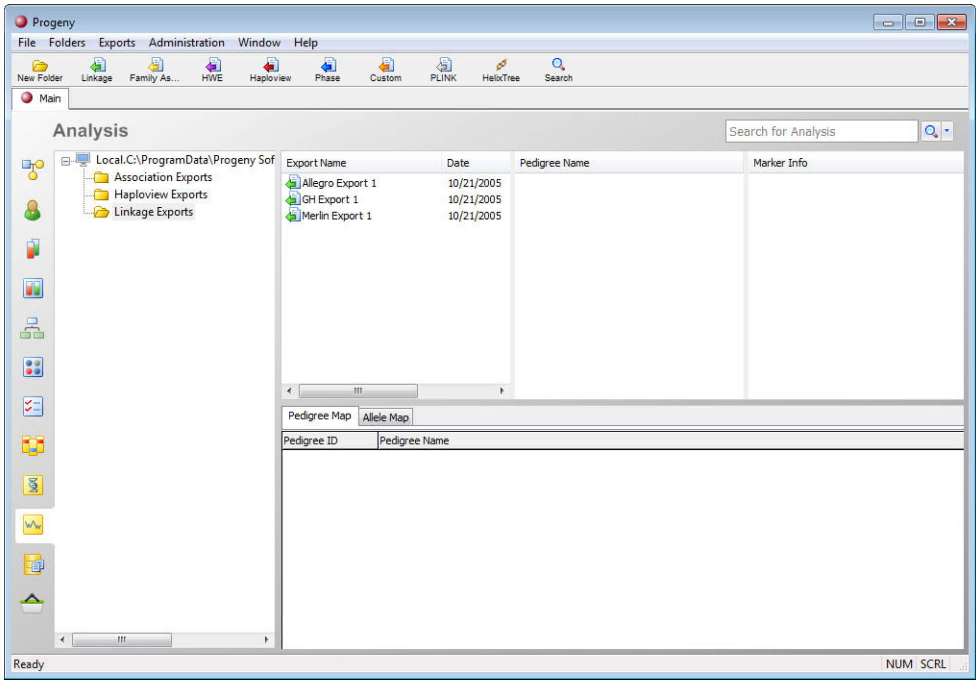
Creating and Running a Phase Export

Progeny Lab provides all the functionality needed for creating phase exports and working with the results. You must first create the phase export, and then you can run the export.

To create a phase export

1. On the main window navigation bar, click the Analysis button to open the Analysis window.

Figure 8-1: Analysis window



Export Name	Date	Pedigree Name	Marker Info
Allegro Export 1	10/21/2005		
GH Export 1	10/21/2005		
Merlin Export 1	10/21/2005		

2. On the Analysis window, select the folder in which to the phase export is to be saved.

> *You can add a new folder if needed. Click the New Folder button on the window toolbar to open the New Folder dialog box, in which you can enter a name for a new Analysis folder and select its location (at the root level or as a sub-folder of another folder.)*

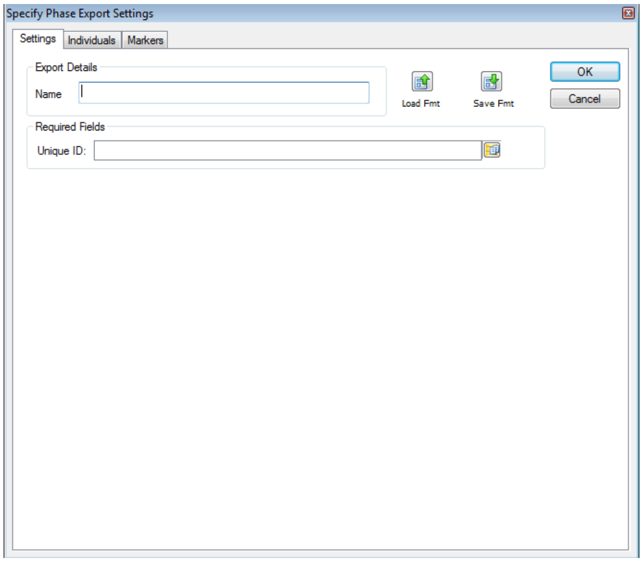
3. On the window toolbar, click the Phase button Phase .

   The Specify Phase Export Settings dialog box opens. By default, the Settings tab is the active tab.

4. Specify the necessary export settings on all three tabs of the dialog box. See:
    - "Specify Phase Export Settings dialog box, Settings tab" on page 428.
    - "Specify Phase Export Settings dialog box, Individuals tab" on page 429.
    - "Specify Phase Export Settings dialog box, Markers tab" on page 430.
5. After you specify the necessary export settings on all three tabs, return to the Settings tab, and then click OK on the tab.
6. Continue to "To run a phase export."

Specify Phase Export Settings dialog box, Settings tab

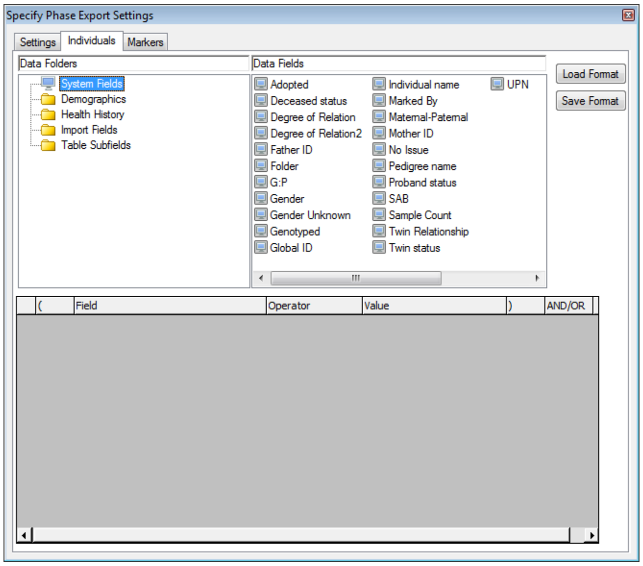
Figure 8-2: Specify Phase Export Settings dialog box, Settings tab



1. Specify the name for the phase export,
2. Click the Fields button to the right of the Unique ID field to open the Select Field dialog box and select the field that represents the unique ID for each individual that is to be included in the phase export.
3. Continue specifying any other phase export settings as needed; otherwise, return to the Settings tab, click OK, and then continue to "To run a phase export" on page 431.

Specify Phase Export Settings dialog box, Individuals tab

Figure 8-3: Specify Phase Export Settings dialog box, Individuals tab



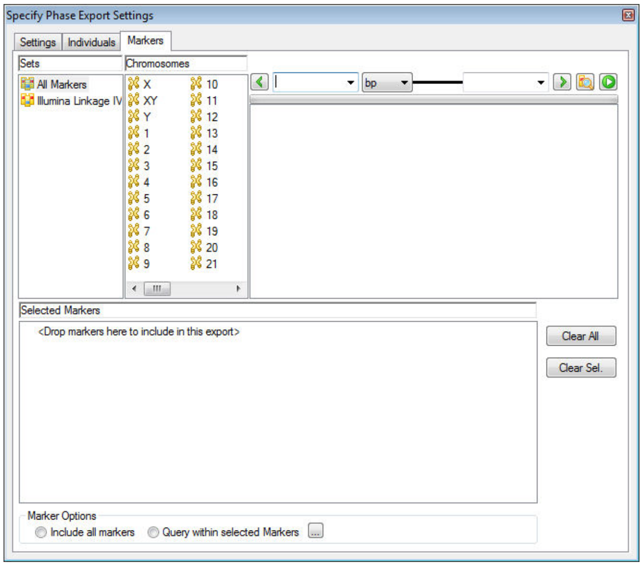
1. Define a query to select those individuals that are to be included in your phase export.

For detailed information about defining a query, see Chapter 8, "Database Queries and Searches," on page 171.

2. Continue specifying any other phase export settings as needed; otherwise, return to the Settings tab, click OK, and then continue to "To run a phase export" on page 431.

Specify Phase Export Settings dialog box, Markers tab

Figure 8-4: Specify Phase Export Settings dialog box, Markers tab



1. Do one of the following:
   - To include an entire marker set in the analysis, drag the marker set from the Sets (top right) pane of the dialog box to the Selected Markers (bottom) pane.
   - To include all the markers for a specific chromosome in the analysis, drag the chromosome from the Chromosomes (top middle) pane of the dialog box to the Selected Markers (bottom) pane.
   - To include only specific markers in the analysis, select the marker (CTRL-click to select multiple markers) from the top right pane to the Selected Markers (bottom) pane.

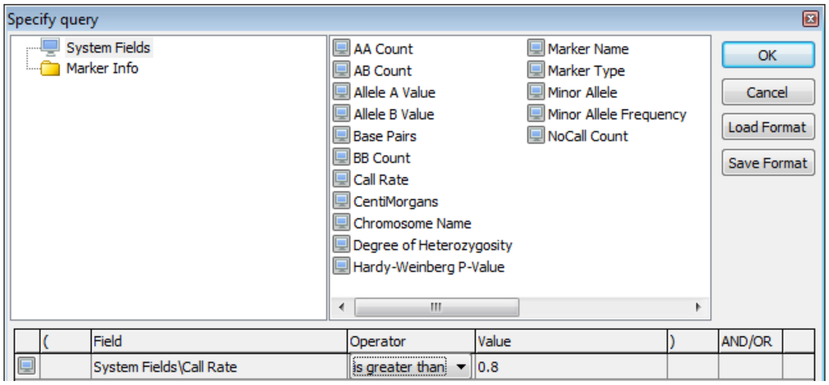
To search for a specific marker or markers, you can use the marker search functions. See "Searching for a Marker" on page 337.

2. Select one of the following:
   - To include all of the markers in the Selected Markers pane in the linkage export, select Include all markers.
   - To include only those markers in the Selected Markers pane in the linkage export that meet specific criteria, select Query within selected markers, and then click the Query button to open the Query dialog box and define a new query, or load a saved query format.

For detailed information about defining a query, see Chapter 8, "Database Queries and Searches," on page 171.

If you specify a query, then you can carry out additional marker filtering, and filter the selected SNPs by Hardy Weinberg p-value, Minor Allele Frequency, Degree of Heterozygosity, and/or Call Rates. For example, to include only those SNPs that have a call rate higher than 80%, you would select the Call Rate system field and enter > 0.8 as the operator and value. You can use this additional filtering criteria only if there is allele count data stored on a per SNP basis.

Figure 8-5: Additional marker filtering



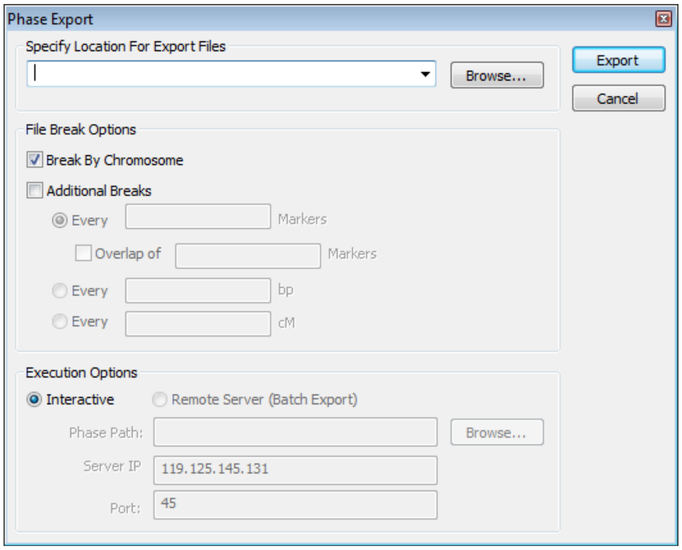
(	Field	Operator	Value	)	AND/OR
	System Fields\Call Rate	is greater than	0.8		

3. Continue specifying any other phase export settings as needed; otherwise, return to the Settings tab, click OK, and then continue to“To run a phase export” below.

To run a phase export

After you specify the necessary export settings on all three tabs, you must return to the Settings tab, and then click OK on the tab. The Phase Export dialog box opens.

Figure 8-6: Phase Export dialog box



☑ Break By Chromosome

☐ Additional Breaks

● Interactive

Server IP 119.125.145.131

Port: 45

1. Click Browse to open the Browse for Folder dialog box, and browse to and select the folder in which the phase export is to be stored.

If you have previously run phase exports, then any previously selected locations are available in a dropdown list in the Browse field. You can always select a value from this list.

2. Select one or both file break options.
   - Break by Chromosome—Creates a new file for each chromosome that is exported.
   - Additional Breaks
     - Every [ ] Markers—Indicates how many markers are to be contained in each export file. If you select this option, you must also indicate the number of overlapping markers in each file.
     - Every [ ] bp—Indicates how many base pairs are to be included in each file.
     - Every [ ] cM—Indicates how many centiMorgans are to be included in each file.

The break options can overlap. For example, select to Break by Chromosome and then by every 1000000 bp within the chromosome.

Execution options are currently not applicable.

3. Click Export.

   An Export to Phase dialog box opens, indicating the status of the phase export. When the export is complete, click Close to close the dialog box and return to the Analysis window.

Saving and Loading a Phase Export Format

After you have set up a phase export format, you can save the format. You can then load this saved format and run it on as-needed basis.

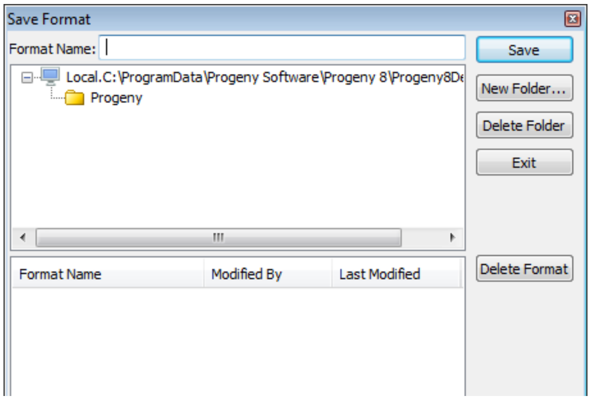
To save a phase export format

1. Set up the phase export format but do *not* run the format See “Creating and Running a Phase Export” on page 427.

2. Click the Save Format button Save Fmt on the Specify Phase Export Settings dialog box.

   The Save Format dialog box opens. It provides a default folder named Progeny in which to save the export format. (This folder is located in the database that you are currently logged in to and you cannot change this location.)

Figure 8-7: Save Format dialog box



3. Enter a name for the phase export format, and then do one of the following:
   - Select the Progeny folder.
   - Click New Folder, and on the Format Folder dialog box that opens, do the following:
     - Enter the name of the new folder in which to save to format.
     - Select the location for the new folder. The folder can be stored at the root level (the same level as the Progeny folder), or it can be a sub-folder of the Progeny folder, or of another folder.
     - Click Save.
4. Click Save on the Save Format dialog box.

   You can then load this saved format and run it on as-needed basis. See “To load a phase export format” on page 434.

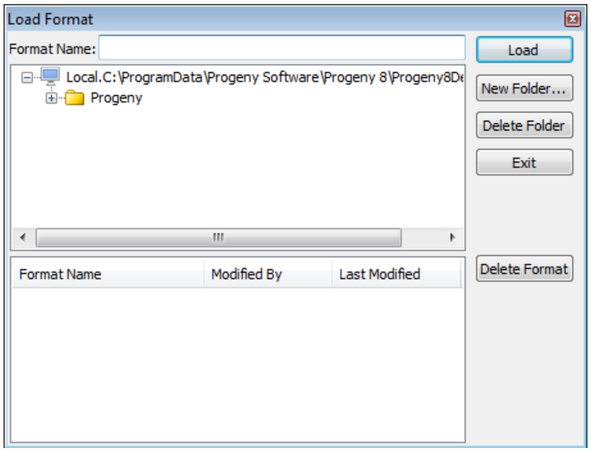
To load a phase export format

You can a retrieve a saved phase export format and run it on as-is needed based.

1. Open the Specify Phase Export Settings dialog box. (See Step 1 through Step 3 of “To create a phase export” on page 427.)
2. On the dialog box, click the Load Format button Load Fmt .

   The Load Format dialog box opens.

Figure 8-8: Load Format dialog box



3. Open the folder that contains the phase export format that you are loading, select the format, and then click Load.

   The Specify Phase Export Settings dialog box is refreshed with the loaded format. You can modify the format as needed (for example, modify the information on the Markers tab), and export the format. See “Creating and Running a Phase Export” on page 427.

Viewing and Rerunning a Phase Export

You can view information about any phase exports that were previously run on the Analysis window, and you can rerun any phase export as necessary.

To view and rerun a phase export

1. On the Analysis window, select the phase export that you want to view.

   A single tab—the Results tab—opens in the bottom pane of the window.

You can also right-click on the tab and open a context menu with options for copying the information on the tab, exporting the information on the tab to a text file, or printing the information on the tab.

2. Optionally, to rerun the phase export, right-click on the selected export, and on the context menu that opens, click Open Export.

   The Specify Phase Export Settings dialog box opens. You can now modify any of the needed settings and click OK on the Settings tab to rerun the export. See "Creating and Running a Phase Export" on page 427.

Deleting a Phase Export

You can delete a phase export by doing one of the following:

- Right-clicking on the export in the Analysis window, and on the context menu that opens, clicking Delete Export.
- Selecting the export in the Analysis window, and then clicking the [Delete] key on your keyboard.

Chapter 9
Custom Genotype Exports

Progeny Lab provides all the functionality needed for creating custom genotype exports and working with the results.

This chapter covers the following topics:

- "Creating and Running a Custom Genotype Export" on page 439.
- "Saving and Loading a Custom Genotype Export Format" on page 447.
- "Viewing and Rerunning a Custom Genotype Export" on page 449.
- "Deleting a Custom Genotype Export" on page 450.

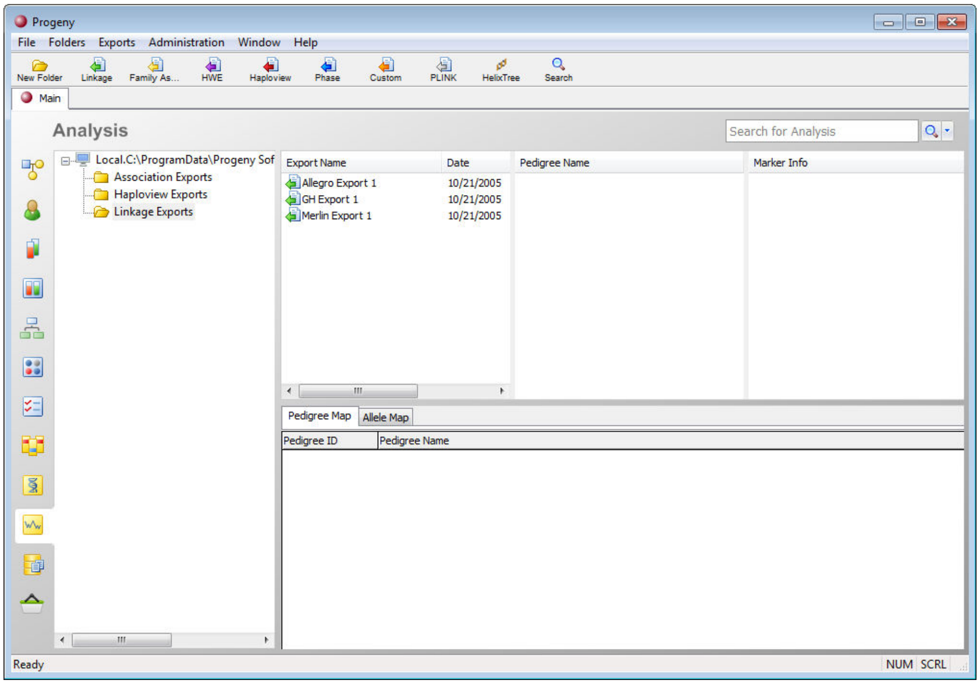
Creating and Running a Custom Genotype Export

Progeny Lab provides all the functionality needed for creating custom genotype exports and working with the results. You must first create the custom export, and then you can run the export.

To create a custom genotype export

1. On the main window navigation bar, click the Analysis button to open the Analysis window.

Figure 9-1: Analysis window



Export Name	Date
Allegro Export 1	10/21/2005
GH Export 1	10/21/2005
Merlin Export 1	10/21/2005

2. On the Analysis window, select the folder in which to the custom export is to be saved.

You can add a new folder if needed. Click the New Folder button on the window toolbar to open the New Folder dialog box, in which you can enter a name for a new Analysis folder and select its location (at the root level or as a sub-folder of another folder.)

3. On the window toolbar, click the Custom button .

   The Specify Custom Export Settings dialog box opens. By default, the Settings tab is the active tab.

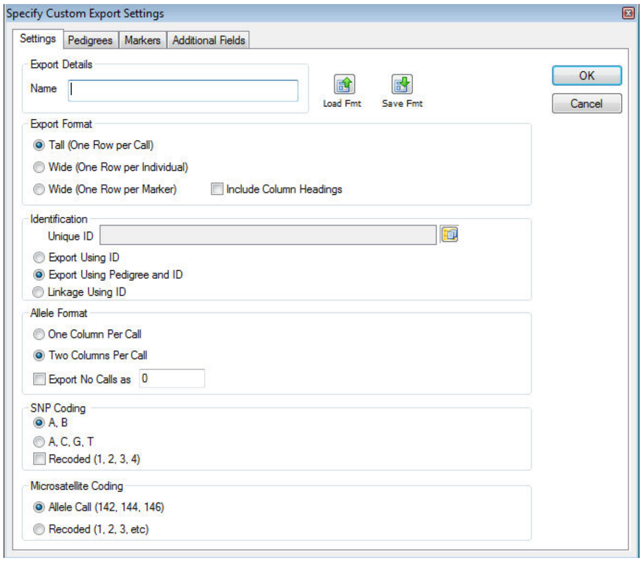
4. Specify the necessary export settings on all four tabs of the dialog box. See:
   - "Specify Custom Export Settings dialog box, Settings tab" on page 440.
   - "Specify Custom Export Settings dialog box, Pedigrees tab" on page 442.
   - "Specify Custom Export Settings dialog box, Markers tab" on page 443.
   - "Specify Custom Export Settings dialog box, Additional Fields tab" on page 445.

5. After you specify the necessary export settings on all four tabs, return to the Settings tab, and then click OK on the tab.

6. Continue to "To run a custom genotype export."

Specify Custom Export Settings dialog box, Settings tab

Figure 9-2: Specify Custom Export Settings dialog box, Settings tab



Export Details
Name

Export Format
● Tall (One Row per Call)
○ Wide (One Row per Individual)
○ Wide (One Row per Marker) ☐ Include Column Headings

Identification
Unique ID
○ Export Using ID
● Export Using Pedigree and ID
○ Linkage Using ID

Allele Format
○ One Column Per Call
● Two Columns Per Call
☐ Export No Calls as 0

SNP Coding
● A, B
○ A, C, G, T
☐ Recoded (1, 2, 3, 4)

Microsatellite Coding
● Allele Call (142, 144, 146)
○ Recoded (1, 2, 3, etc)

1. Specify the settings for the custom export.

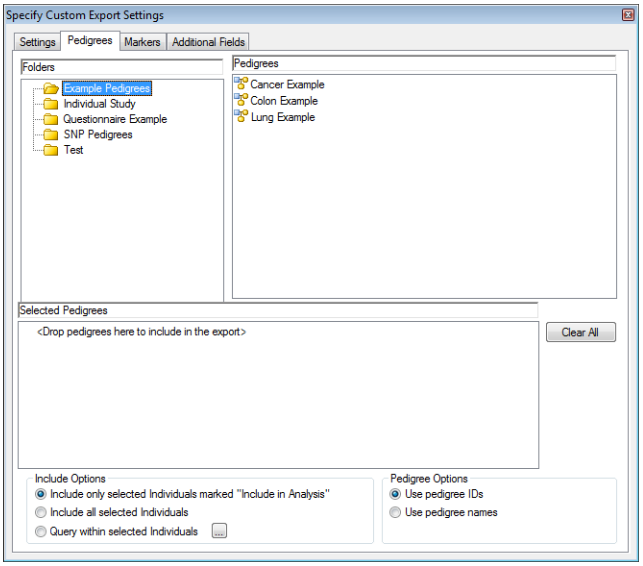
Option	Description
Export Details	
Name	Name or description of the custom export.

Option	Description
Export Format	
• Tall (One Row per Call) • Wide (One Row per Individual) • Wide (One Row per Marker)	• Unique ID, Marker Name, Allele 1, and Allele 2 • Individuals in rows and markers in columns (Two columns per call) • Markers in rows and individuals in columns (Two columns per call)
Affection Status Field	Click the Fields button to the right of the Affection Status Field to open the Select Field dialog box and select the field that represents the affected status for each individual that is to be included in the PLINK export.
Pedigree Options	
Use Pedigree IDs Use pedigree names	Converts a text-based pedigree name into a numerical ID. Use pedigree names as-is.
Identification	
Click the Fields button next to the Unique ID field to open the Select Field dialog box and select the identifier, such as the Global ID, for the individuals being exported, then select one of the identification options.	
• Export Using ID • Export Using Pedigree and UPN • Linkage Using ID	• Use the selected ID to identify the individuals being exported. • Use the pedigree and the selected ID to identify the individuals being exported. • When you select an ID, the same ID field is exported to specify the Mother and Father.
Allele Format	
• One Column Per Call • Two Columns Per Call	• For example, AB is shown in a single column. • For example, A is shown in one column and B is shown in the second column.
Export No Calls as	Optional. The default value is 0, but you can enter another value.
SNP Coding	
• A, B • A, C, G, T	• Show alleles as A or B. • Show alleles as A, C, G, or T. **Note:** If you select A, C, G, or T, you can select Recoded (1, 2, 3, 4) and show the alleles as 1, 2, 3, or 4 instead of A, C, G, or T.
Microsatellite Coding	
• Allele Call • Recoded (1, 2, 3, etc.)	• Use the actual allele call in the export. • Recode the allele call to 1, 2, 3, and so on in the export.

2. Continue specifying any other custom export settings as needed; otherwise, return to the Settings tab, click OK, and then continue to "To run a custom genotype export" on page 446.

Specify Custom Export Settings dialog box, Pedigrees tab

Figure 9-3: Specify Custom Export Settings dialog box, Pedigrees tab



Example Pedigrees
Individual Study
Questionnaire Example
SNP Pedigrees
Test

Cancer Example
Colon Example
Lung Example

<Drop pedigrees here to include in the export>

Include Options
● Include only selected Individuals marked "Include in Analysis"
○ Include all selected Individuals
○ Query within selected Individuals

Pedigree Options
● Use pedigree IDs
○ Use pedigree names

1. In the Folders (top left) pane of the dialog box, select the folder that contains the pedigrees for which the linkage export is being created.
2. In the Pedigrees (top right) pane of the dialog, select the pedigree (CTRL-click to select multiple pedigrees) for which the linkage export is being created.
3. Drag the selected pedigrees to the Selected Pedigrees (bottom) pane of the dialog box.
4. Select one of the following:
    - To include only those individuals in a pedigree who have been specifically marked for inclusion in an analysis, select Include only selected individuals marked “Include in Analysis.” (See “To select individuals in a pedigree for inclusion in an analysis” below.)
    - To include all individuals in all the selected pedigrees are included in the linkage export, select Include all selected individuals.
    - To include only those individuals in the export linkage who meet specific criteria, select Query within selected individuals, and then click the Query button to open the Query dialog box and define a new query, or load a saved query format.

For detailed information about defining a query, see Chapter 8, “Database Queries and Searches,” on page 171.

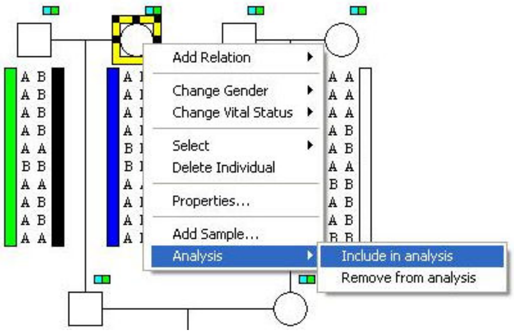
5. Select one of the following:
    - Use Pedigree IDs—Converts a text-based pedigree name into a numerical ID.
    - Use pedigree names—Use pedigree names as-is.

6. Continue specifying any other custom export settings as needed; otherwise, return to the Settings tab, click OK, and then continue to "To run a custom genotype export" on page 446.

To select individuals in a pedigree for inclusion in an analysis

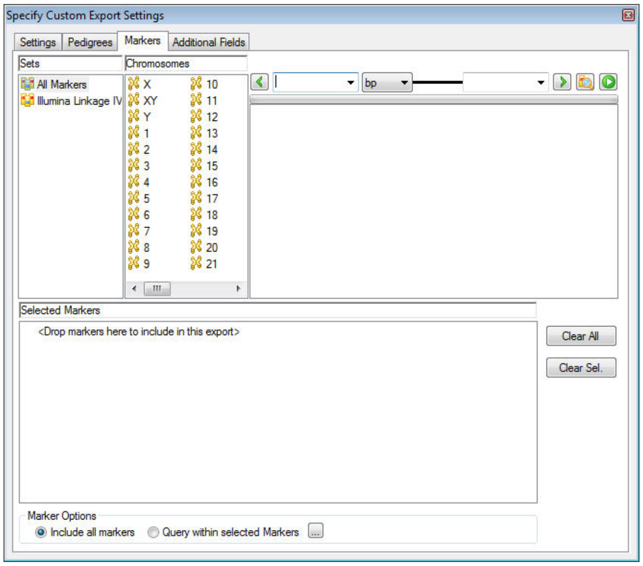
If you select the option Include only selected individuals marked "Include in Analysis," then you must open each affected pedigree, and manually select the appropriate individuals. You can select a single individual, or CTRL-click to select multiple individuals, and then right-click on any selected individual, and on the context menu that opens, click Include in analysis.

Figure 9-4: Selecting individuals for analysis



Specify Custom Export Settings dialog box, Markers tab

Figure 9-5: Specify Custom Export Settings dialog box, Markers tab



Marker Options: ● Include all markers ○ Query within selected Markers

1. Do one of the following:
    - To include an entire marker set in the analysis, drag the marker set from the Sets (top right) pane of the dialog box to the Selected Markers (bottom) pane.
    - To include all the markers for a specific chromosome in the analysis, drag the chromosome from the Chromosomes (top middle) pane of the dialog box to the Selected Markers (bottom) pane.
    - To include only specific markers in the analysis, select the marker (CTRL-click to select multiple markers) from the top right pane to the Selected Markers (bottom) pane.

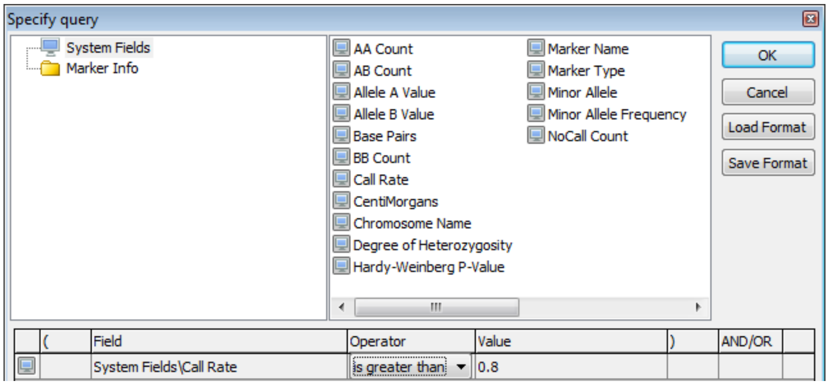
To search for a specific marker or markers, you can use the marker search functions. See "Searching for a Marker" on page 337.

2. Select one of the following:
    - To include all of the markers in the Selected Markers pane in the linkage export, select Include all markers.
    - To include only those markers in the Selected Markers pane in the linkage export that meet specific criteria, select Query within selected markers, and then click the Query button to open the Query dialog box and define a new query, or load a saved query format.

For detailed information about defining a query, see Chapter 8, "Database Queries and Searches," on page 171.

If you specify a query, then you can carry out additional marker filtering, and filter the selected SNPs by Hardy Weinberg p-value, Minor Allele Frequency, Degree of Heterozygosity, and/or Call Rates. For example, to include only those SNPs that have a call rate higher than 80%, you would select the Call Rate system field and enter > 0.8 as the operator and value. You can use this additional filtering criteria only if there is allele count data stored on a per SNP basis.

Figure 9-6: Additional marker filtering

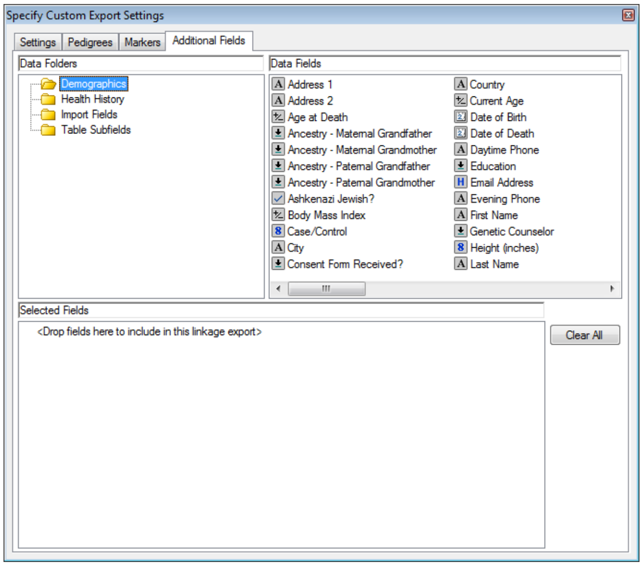


	(	Field	Operator	Value	)	AND/OR
		System Fields\Call Rate	is greater than	0.8		

3. Continue specifying any other custom export settings as needed; otherwise, return to the Settings tab, click OK, and then continue to “To run a custom genotype export” on page 446.

Specify Custom Export Settings dialog box, Additional Fields tab

Figure 9-7: Specify Custom Export Settings dialog box, Additional Fields tab

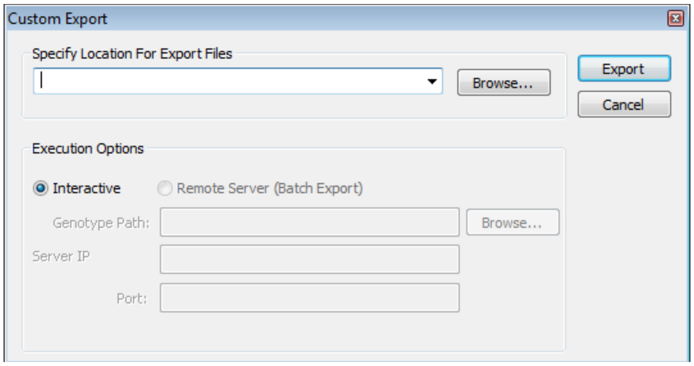


1. Specify additional individual level database fields that are to be included in the custom genotype export.
2. Continue specifying any other custom export settings as needed; otherwise, return to the Settings tab, click OK, and then continue to “To run a custom genotype export” on page 446.

To run a custom genotype export

After you specify the necessary export settings on all fours tabs, you must return to the Settings tab, and then click OK on the tab. The Custom Export dialog box opens.

Figure 9-8: Custom Export dialog box



1. Click Browse to open the Browse for Folder dialog box, and browse to and select the folder in which the custom export files are to be stored.

If you have previously run custom exports, then any previously selected locations are available in a dropdown list in the Browse field. You can always select a value from this list.

Execution options are currently not applicable.

2. Click Export.

   An Custom Export dialog box opens, indicating the status of the custom export.

3. When the export is complete, click Close to close the dialog box and return to the Analysis window.

Saving and Loading a Custom Genotype Export Format

After you have set up a custom genotype export format, you can save the format. You can then load this saved format and run it on as-needed basis.

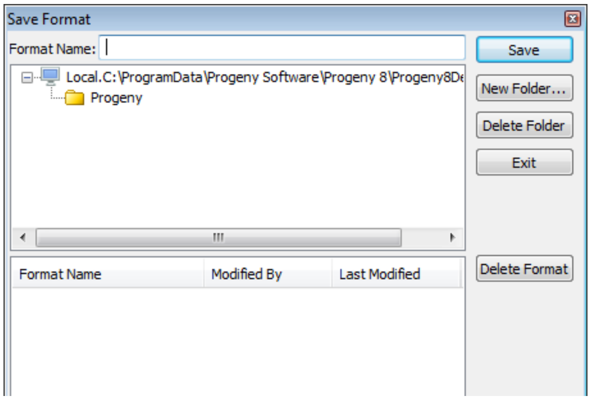
To save a custom genotype export format

1. Set up the custom genotype export format but do *not* run the format See “Creating and Running a Custom Genotype Export” on page 439.

2. Click the Save Format button Save Fmt on the Specify Custom Export Settings dialog box.

   The Save Format dialog box opens. It provides a default folder named Progeny in which to save the export format. (This folder is located in the database that you are currently logged in to and you cannot change this location.)

Figure 9-9: Save Format dialog box



3. Enter a name for the custom export format, and then do one of the following:
   - Select the Progeny folder.
   - Click New Folder, and on the Format Folder dialog box that opens, do the following:
     - Enter the name of the new folder in which to save to format.
     - Select the location for the new folder. The folder can be stored at the root level (the same level as the Progeny folder), or it can be a sub-folder of the Progeny folder, or of another folder.
     - Click Save.
4. Click Save on the Save Format dialog box.

   You can then load this saved format and run it on as-needed basis. See “To load a custom genotype export format” on page 448.

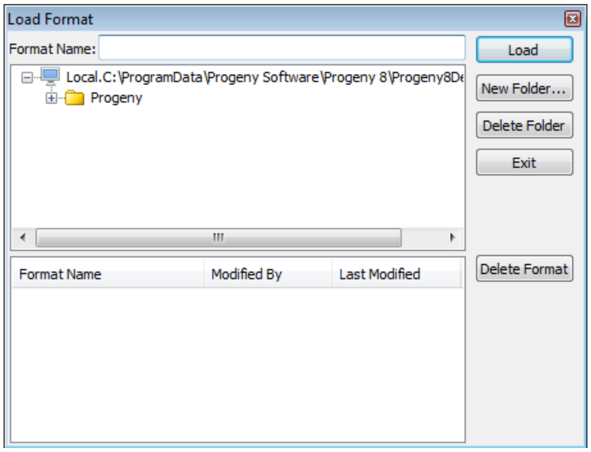
To load a custom genotype export format

You can a retrieve a saved custom genotype export format and run it on as-is needed based.

1. Open the Specify Custom Export Settings dialog box. (See Step 1 through Step 3 of "To create a custom genotype export" on page 439.)
2. On the dialog box, click the Load Format button Load Fmt.

   The Load Format dialog box opens.

Figure 9-10: Load Format dialog box



3. Open the folder that contains the custom export format that you are loading, select the format, and then click Load.

   The Specify Custom Export Settings dialog box is refreshed with the loaded format. You can modify the format as needed (for example, modify the information on the Markers tab), and export the format. See "Creating and Running a Custom Genotype Export" on page 439.

Viewing and Rerunning a Custom Genotype Export

You can view information about any custom genotype exports that were previously run on the Analysis window, and you can rerun any custom genotype exports as necessary.

To view and rerun a custom genotype export

1. On the Analysis window, select the phase export that you want to view.

   A single tab—the Results tab—opens in the bottom pane of the window.

You can also right-click on the tab and open a context menu with options for copying the information on the tab, exporting the information on the tab to a text file, or printing the information on the tab.

2. Optionally, to rerun the custom export, right-click on the selected export, and on the context menu that opens, click Open Export.

   The Specify Custom Export Settings dialog box opens. You can now modify any of the needed settings and click OK on the Settings tab to rerun the export. See "Creating and Running a Custom Genotype Export" on page 439.

Deleting a Custom Genotype Export

You can delete a custom genotype export by doing one of the following:

- Right-clicking on the export in the Analysis window, and on the context menu that opens, clicking Delete Export.
- Selecting the export in the Analysis window, and then clicking the [Delete] key on your keyboard.

Chapter 10
PLINK Exports

Progeny Lab provides all the functionality needed for creating PLINK exports and working with the results.

This chapter covers the following topics:

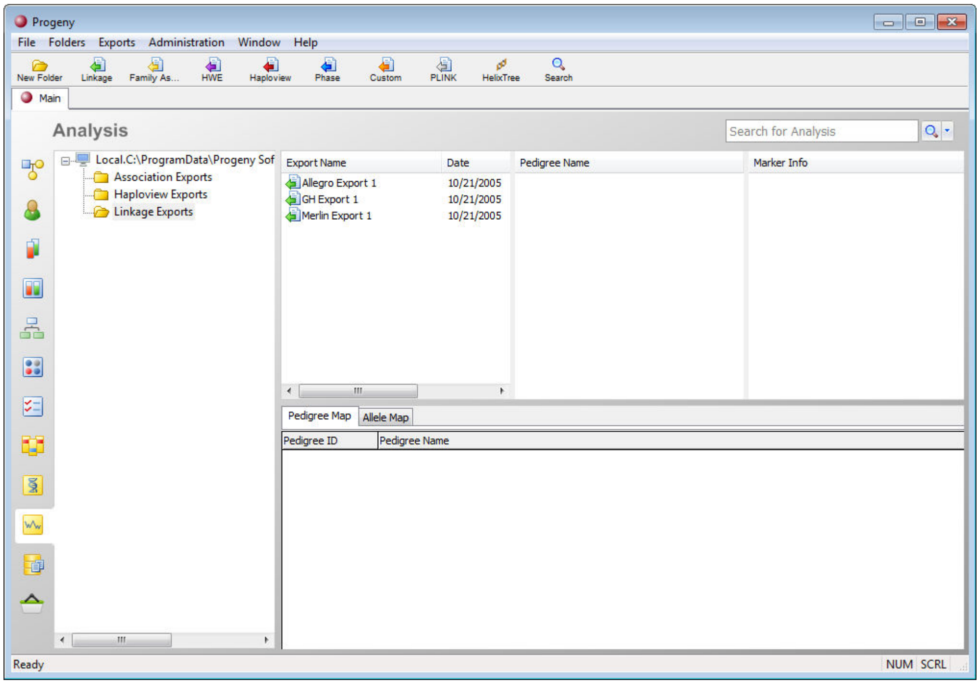
Creating and Running a PLINK Export

Progeny Lab provides all the functionality needed for creating PLINK exports and working with the results. You must first create the export, and then you can run the export.

To create a PLINK export

1. On the main window navigation bar, click the Analysis button to open the Analysis window.

Figure 10-1: Analysis window



Export Name	Date	Pedigree Name	Marker Info
Allegro Export 1	10/21/2005		
GH Export 1	10/21/2005		
Merlin Export 1	10/21/2005		

2. On the Analysis window, select the folder in which to the phase export is to be saved.

You can add a new folder if needed. Click the New Folder button on the window toolbar to open the New Folder dialog box, in which you can enter a name for a new Analysis folder and select its location (at the root level or as a sub-folder of another folder.)

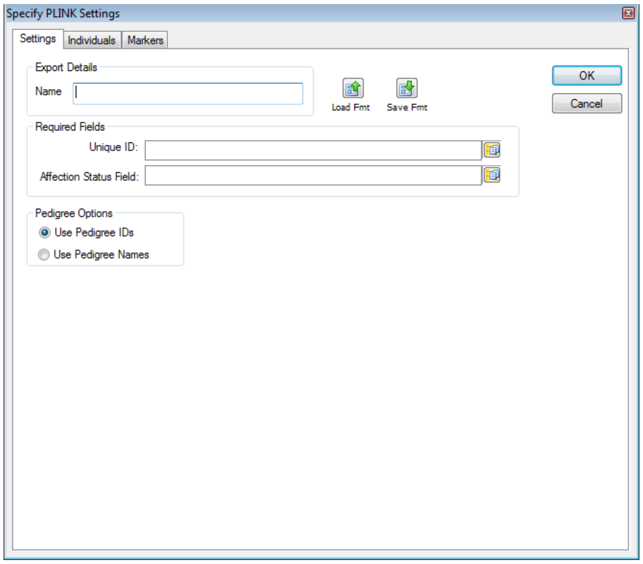
3. On the window toolbar, click the PLINK button .

   The Specify Phase Export Settings dialog box opens. By default, the Settings tab is the active tab.

4. Specify the necessary export settings on all three tabs of the dialog box. See:
   - "Specify PLINK Export Settings dialog box, Settings tab" on page 454.
   - "Specify PLINK Export Settings dialog box, Individuals tab" on page 455.
   - "Specify PLINK Export Settings dialog box, Markers tab" on page 456.
5. After you specify the necessary export settings on all three tabs, return to the Settings tab, and then click OK on the tab.
6. Continue to "To run a PLINK export."

Specify PLINK Export Settings dialog box, Settings tab

Figure 10-2: Specify PLINK Export Settings dialog box, Settings tab



● Use Pedigree IDs
○ Use Pedigree Names

1. Specify the name for the PLINK export, the required fields for the export, and the pedigree options for the export.

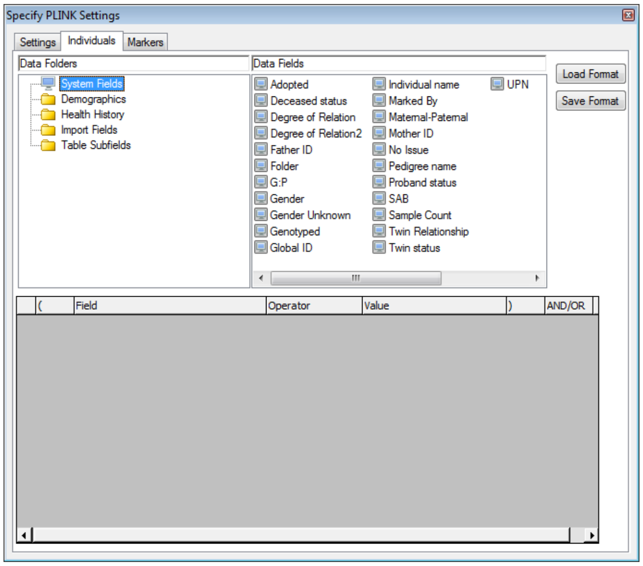
Option	Description
Export Details	
Name	Name or description of the PLINK export.
Required Fields	
Unique ID	Click the Fields button to the right of the Unique ID field to open the Select Field dialog box and select the field that represents the unique ID for each individual that is to be included in the PLINK export.
Affection Status Field	Click the Fields button to the right of the Affection Status Field to open the Select Field dialog box and select the field that represents the affected status for each individual that is to be included in the PLINK export.

Option	Description
Pedigree Options	
Use Pedigree IDs	Converts a text-based pedigree name into a numerical ID.
Use pedigree names	Use pedigree names as-is.

2. Continue specifying any other PLINK export settings as needed; otherwise, return to the Settings tab, click OK, and then continue to "To run a PLINK export" on page 457.

Specify PLINK Export Settings dialog box, Individuals tab

Figure 10-3: Specify Phase Export Settings dialog box, Individuals tab



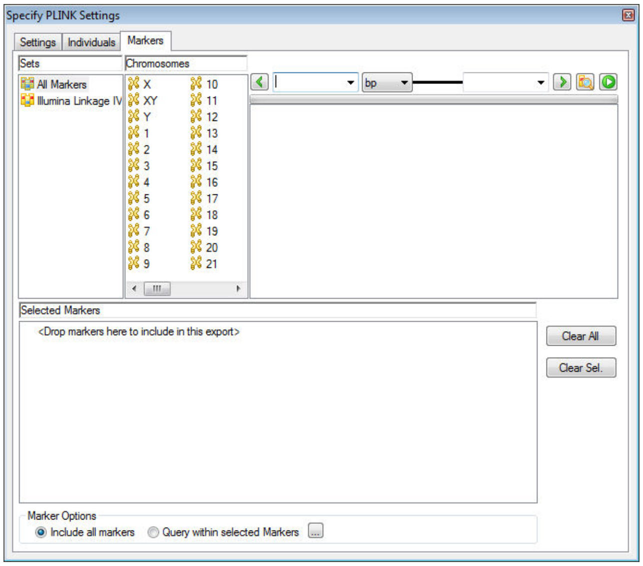
1. Define a query to select those individuals that are to be included in your Phase export.

For detailed information about defining a query, see Chapter 8, "Database Queries and Searches," on page 171.

2. Continue specifying any other PLINK export settings as needed; otherwise, return to the Settings tab, click OK, and then continue to "To run a PLINK export" on page 457.

Specify PLINK Export Settings dialog box, Markers tab

Figure 10-4: Specify PLINK Export Settings dialog box, Markers tab



1. Do one of the following:
   - To include an entire marker set in the analysis, drag the marker set from the Sets (top right) pane of the dialog box to the Selected Markers (bottom) pane.
   - To include all the markers for a specific chromosome in the analysis, drag the chromosome from the Chromosomes (top middle) pane of the dialog box to the Selected Markers (bottom) pane.
   - To include only specific markers in the analysis, select the marker (CTRL-click to select multiple markers) from the top right pane to the Selected Markers (bottom) pane.

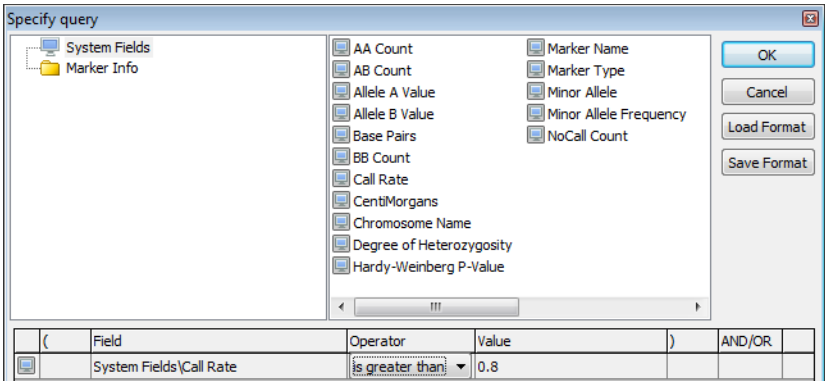
To search for a specific marker or markers, you can use the marker search functions. See "Searching for a Marker" on page 337.

2. Select one of the following:
   - To include all of the markers in the Selected Markers pane in the linkage export, select Include all markers.
   - To include only those markers in the Selected Markers pane in the linkage export that meet specific criteria, select Query within selected markers, and then click the Query button to open the Query dialog box and define a new query, or load a saved query format.

For detailed information about defining a query, see Chapter 8, "Database Queries and Searches," on page 171.

If you specify a query, then you can carry out additional marker filtering, and filter the selected SNPs by Hardy Weinberg p-value, Minor Allele Frequency, Degree of Heterozygosity, and/or Call Rates. For example, to include only those SNPs that have a call rate higher than 80%, you would select the Call Rate system field and enter > 0.8 as the operator and value. You can use this additional filtering criteria only if there is allele count data stored on a per SNP basis.

Figure 10-5: Additional marker filtering



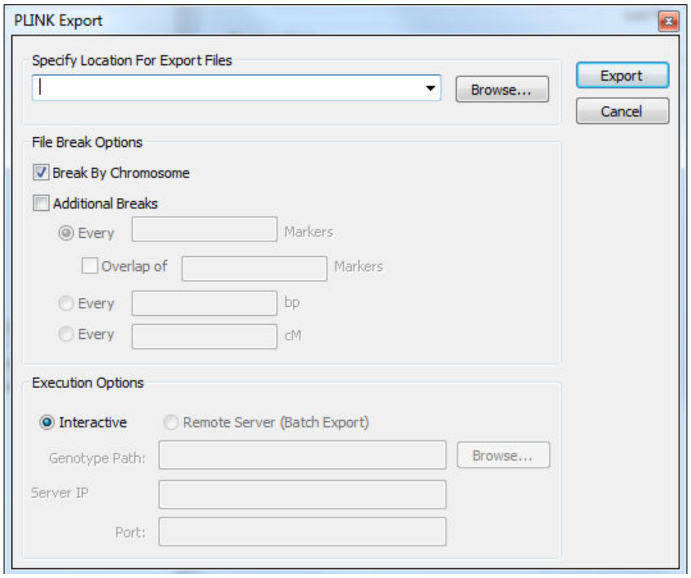
	(	Field	Operator	Value	)	AND/OR
		System Fields\Call Rate	is greater than	0.8		

3. Continue specifying any other PLINK export settings as needed; otherwise, return to the Settings tab, click OK, and then continue to "To run a PLINK export" below.

To run a PLINK export

After you specify the necessary export settings on all three tabs, you must return to the Settings tab, and then click OK on the tab. The PLINK Export dialog box opens.

Figure 10-6: PLINK Export dialog box



☑ Break By Chromosome

● Interactive

1. Click Browse to open the Browse for Folder dialog box, and browse to and select the folder in which the PLINK exports files are to be stored.

If you have previously run PLINK exports, then any previously selected locations are available in a dropdown list in the Browse field. You can always select a value from this list.

2. Select one or both file break options.
   - Break by Chromosome—Creates a new file for each chromosome that is exported.
   - Additional Breaks
     - Every [ ] Markers—Indicates how many markers are to be contained in each export file. If you select this option, you must also indicate the number of overlapping markers in each file.
     - Every [ ] bp—Indicates how many base pairs are to be included in each file.
     - Every [ ] cM—Indicates how many centiMorgans are to be included in each file.

The break options can overlap. For example, select to Break by Chromosome and then by every 1000000 bp within the chromosome.

Execution options are currently not applicable.

3. Click Export.

   An Export to PLINK dialog box opens, indicating the status of the phase export.

4. When the export is complete, click Close to close the dialog box and return to the Analysis window.

Saving and Loading a PLINK Export Format

After you have set up a PLINK export format, you can save the format. You can then load this saved format and run it on as-needed basis.

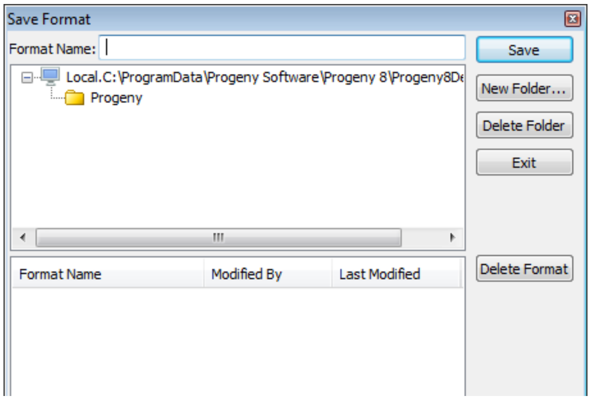
To save a PLINK export format

1. Set up the PLINK export format but do *not* run the format See “Creating and Running a PLINK Export” on page 453.

2. Click the Save Format button Save Fmt on the Specify PLINK Export Settings dialog box.

   The Save Format dialog box opens. It provides a default folder named Progeny in which to save the export format. (This folder is located in the database that you are currently logged in to and you cannot change this location.)

Figure 10-7: Save Format dialog box



3. Enter a name for the PLINK export format, and then do one of the following:
   - Select the Progeny folder.
   - Click New Folder, and on the Format Folder dialog box that opens, do the following:
     - Enter the name of the new folder in which to save to format.
     - Select the location for the new folder. The folder can be stored at the root level (the same level as the Progeny folder), or it can be a sub-folder of the Progeny folder, or of another folder.
     - Click Save.
4. Click Save on the Save Format dialog box.

   You can then load this saved format and run it on as-needed basis. See “To load a PLINK export format” on page 460.

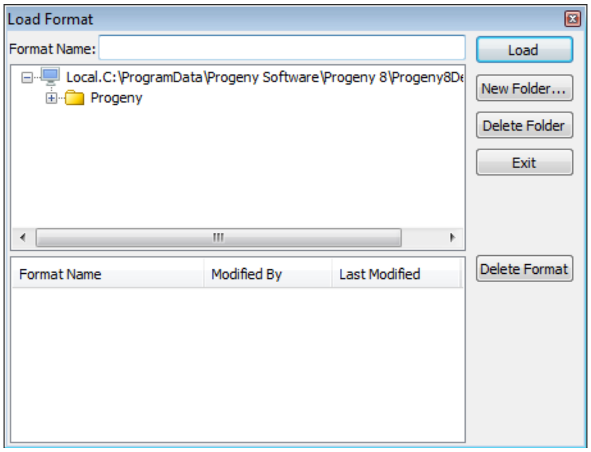
To load a PLINK export format

You can a retrieve a saved PLINK export format and run it on as-is needed based.

1. Open the Specify PLINK Export Settings dialog box. (See Step 1 through Step 3 of "To create a PLINK export" on page 453.)
2. On the dialog box, click the Load Format button Load Fmt.

   The Load Format dialog box opens.

Figure 10-8: Load Format dialog box



Local.C:\ProgramData\Progeny Software\Progeny 8\Progeny8D
Progeny

3. Open the folder that contains the PLINK export format that you are loading, select the format, and then click Load.

   The Specify PLINK Export Settings dialog box is refreshed with the loaded format. You can modify the format as needed (for example, modify the information on the Markers tab), and export the format. See "Creating and Running a PLINK Export" on page 453.

Viewing and Rerunning a PLINK Export

You can view information about any PLINK exports that were previously run on the Analysis window, and you can rerun any PLINK export as necessary.

To view and rerun a PLINK export

1. On the Analysis window, select the PLINK export that you want to view.

   A single tab—the Results tab—opens in the bottom pane of the window.

You can also right-click on the tab and open a context menu with options for copying the information on the tab, exporting the information on the tab to a text file, or printing the information on the tab.

2. Optionally, to rerun the PLINK export, right-click on the selected export, and on the context menu that opens, click Open Export.

   The Specify PLINK Export Settings dialog box opens. You can now modify any of the needed settings and click OK on the Settings tab to rerun the export. See “Creating and Running a PLINK Export” on page 453.

Deleting a PLINK Export

You can delete a PLINK export by doing one of the following:

- Right-clicking on the export in the Analysis window, and on the context menu that opens, clicking Delete Export.
- Selecting the export in the Analysis window, and then clicking the [Delete] key on your keyboard.

Chapter 11

HelixTree Exports

Progeny Lab provides all the functionality needed for creating HelixTree exports and working with the results.

This chapter covers the following topics:

- “Creating and Running a HelixTree Export” on page 465.
- “Saving and Loading a HelixTree Export Format” on page 471.
- “Viewing and Rerunning a HelixTree Export” on page 473.
- “Deleting a HelixTree Export” on page 474.

To create and run HelixTree exports, HelixTree must be installed locally.

Creating and Running a HelixTree Export

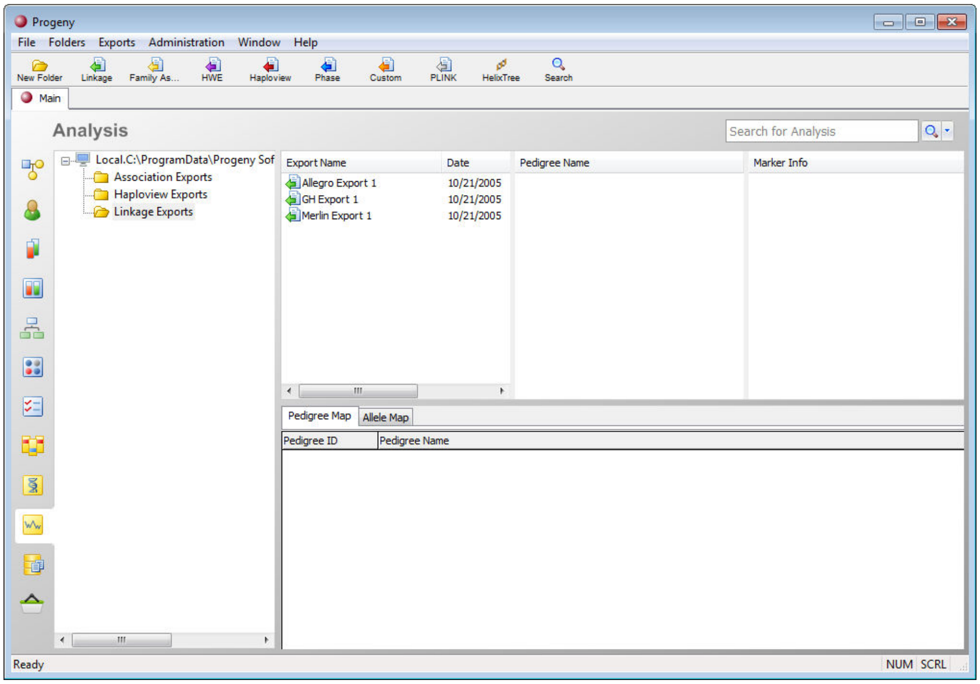
Progeny Lab provides all the functionality needed for creating HelixTree exports and working with the results. You must first create the export, and then you can run the export.

To create and run HelixTree exports, HelixTree must be installed locally.

To create a HelixTree export

1. On the main window navigation bar, click the Analysis button to open the Analysis window.

Figure 11-1: Analysis window



Export Name	Date	Pedigree Name	Marker Info
Allegro Export 1	10/21/2005		
GH Export 1	10/21/2005		
Merlin Export 1	10/21/2005		

2. On the Analysis window, select the folder in which to the phase export is to be saved.

You can add a new folder if needed. Click the New Folder button on the window toolbar to open the New Folder dialog box, in which you can enter a name for a new Analysis folder and select its location (at the root level or as a sub-folder of another folder.)

3. On the window toolbar, click the Phase button HelixTree .

   The Specify HelixTree Settings dialog box opens. By default, the Settings tab is the active tab.

4. Specify the necessary export settings on all three tabs of the dialog box. See:

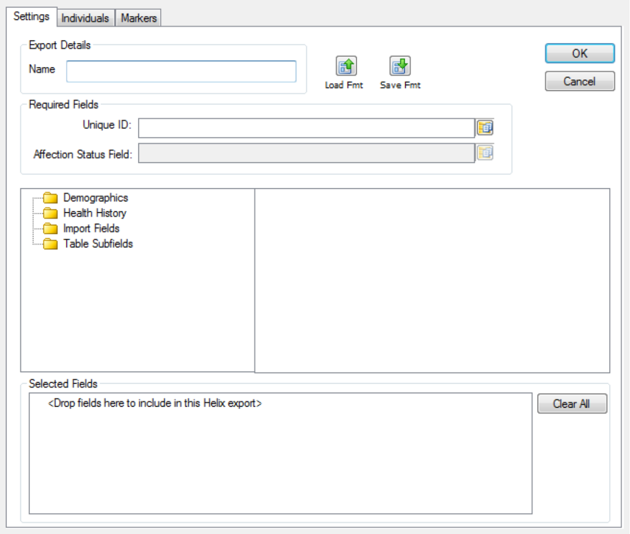
   - "Specify HelixTree Settings dialog box, Settings tab" on page 466.
   - "Specify HelixTree Settings dialog box, Individuals tab" on page 467.
   - "Specify HelixTree Export Settings dialog box, Markers tab" on page 468.

5. After you specify the necessary export settings on all three tabs, return to the Settings tab, and then click OK on the tab.

6. Continue to "To run a HelixTree export."

Specify HelixTree Settings dialog box, Settings tab

Figure 11-2: Specify Phase Export Settings dialog box, Settings tab



1. Specify the name for the export and the required fields for the export.

Option	Description
Export Details	
Name	Name or description of the export.
Required Fields	
Unique ID	Click the Fields button to the right of the Unique ID field to open the Select Field dialog box and select the field that represents the unique ID for each individual that is to be included in the export.

Option	Description
Affection Status Field	Click the Fields button to the right of the Affection Status Field to open the Select Field dialog box and select the field that represents the affected status for each individual that is to be included in the export. **Note:** This is appearing on the dialog box, but is not available.

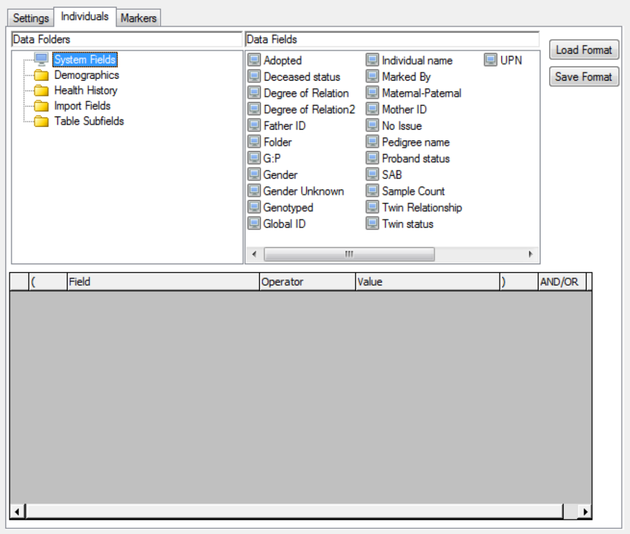
2. Select the fields that are to be included in the export by doing the following:
    - In the Folders (middle left) pane of the dialog box, select the folder that contains the individual data fields that are to be included in the export.
    - In the Fields pane (middle right) pane of the dialog, select the fields (CTRL-click to select multiple fields) that are to be included in the export.
    - Drag the selected fields to the Selected fields (bottom) pane of the dialog box.

At least two fields must be selected to carry out a HelixTree export.

3. Continue specifying any other HelixTree export settings as needed; otherwise, return to the Settings tab, click OK, and then continue to "To run a HelixTree export" on page 469.

Specify HelixTree Settings dialog box, Individuals tab

Figure 11-3: Specify HelixTree Settings dialog box, Individuals tab



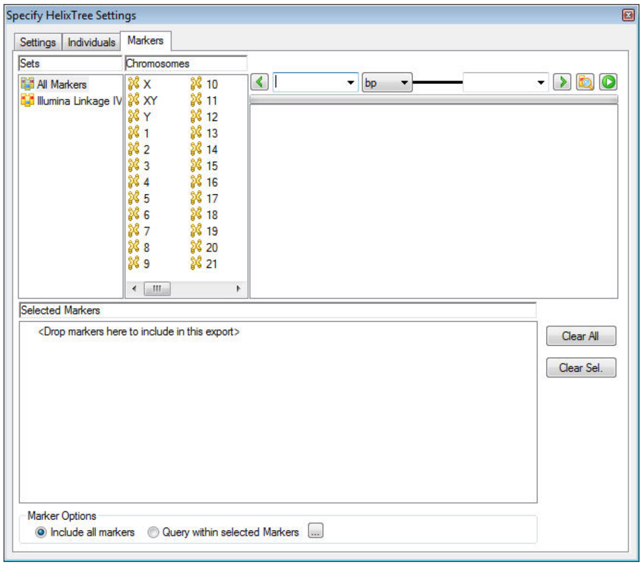
1. Define a query to select those individuals that are to be included in your HelixTree export.

For detailed information about defining a query, see Chapter 8, "Database Queries and Searches," on page 171.

2. Continue specifying any other HelixTree export settings as needed; otherwise, return to the Settings tab, click OK, and then continue to "To run a HelixTree export" on page 469.

Specify HelixTree Export Settings dialog box, Markers tab

Figure 11-4: Specify HelixTree Settings dialog box, Markers tab



● Include all markers ○ Query within selected Markers

1. Do one of the following:
    - To include an entire marker set in the analysis, drag the marker set from the Sets (top right) pane of the dialog box to the Selected Markers (bottom) pane.
    - To include all the markers for a specific chromosome in the analysis, drag the chromosome from the Chromosomes (top middle) pane of the dialog box to the Selected Markers (bottom) pane.
    - To include only specific markers in the analysis, select the marker (CTRL-click to select multiple markers) from the top right pane to the Selected Markers (bottom) pane.

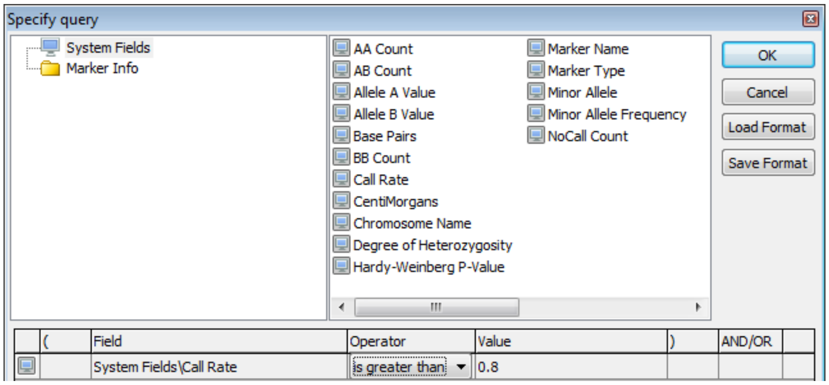
To search for a specific marker or markers, you can use the marker search functions. See "Searching for a Marker" on page 337.

2. Select one of the following:
    - To include all of the markers in the Selected Markers pane in the export, select Include all markers.
    - To include only those markers in the Selected Markers pane in the export that meet specific criteria, select Query within selected markers, and then click the Query button to open the Query dialog box and define a new query, or load a saved query format.

For detailed information about defining a query, see Chapter 8, "Database Queries and Searches," on page 171.

If you specify a query, then you can carry out additional marker filtering, and filter the selected SNPs by Hardy Weinberg p-value, Minor Allele Frequency, Degree of Heterozygosity, and/or Call Rates. For example, to include only those SNPs that have a call rate higher than 80%, you would select the Call Rate system field and enter > 0.8 as the operator and value. You can use this additional filtering criteria only if there is allele count data stored on a per SNP basis.

Figure 11-5: Additional marker filtering



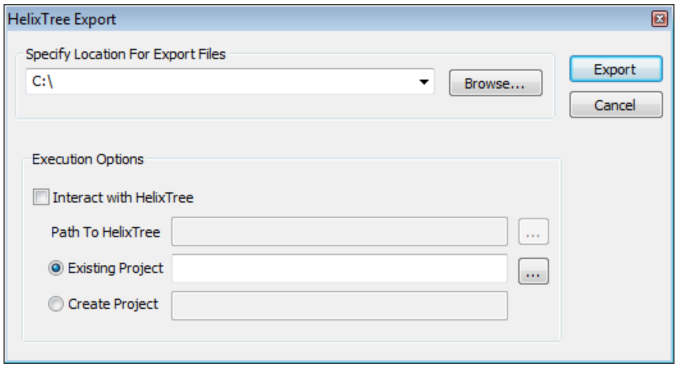
(	Field	Operator	Value	)	AND/OR
	System Fields\Call Rate	is greater than	0.8		

3. Continue specifying any other HelixTree export settings as needed; otherwise, return to the Settings tab, click OK, and then continue to "To run a HelixTree export" below.

To run a HelixTree export

After you specify the necessary export settings on all three tabs, you must return to the Settings tab, and then click OK on the tab. The HelixTree Export dialog box opens.

Figure 11-6: HelixTree Export dialog box



Specify Location For Export Files: C:\

Execution Options

☐ Interact with HelixTree

Path To HelixTree

● Existing Project

○ Create Project

1. Click Browse to open the Browse for Folder dialog box, and browse to and select the folder in which the HelixTree export files are to be stored.

If you have previously run HelixTree exports, then any previously selected locations are available in a dropdown list in the Browse field. You can always select a value from this list.

2. Select the execution options:
    - Interact with HelixTree—Select this option to open HelixTree after the files have been exported.
    - Path to HelixTree—Available only if you select Interact with HelixTree. Click the Browse button to open the Browse for Folder dialog box, and browse to and select the HelixTree executable.
    - Select one of the following:
        - Existing Project—Select this option and then click the Browse button to open the Save As dialog box and select an existing HelixTree projects to which to add these export files.
        - Create Project—Select this option to create a new HelixTree project.
3. Click Export.

    An Export to HelixTree dialog box opens, indicating the status of the export.
4. When the export is complete, click Close to close the dialog box and return to the Analysis window.

Saving and Loading a HelixTree Export Format

After you have set up a HelixTree export format, you can save the format. You can then load this saved format and run it on as-needed basis.

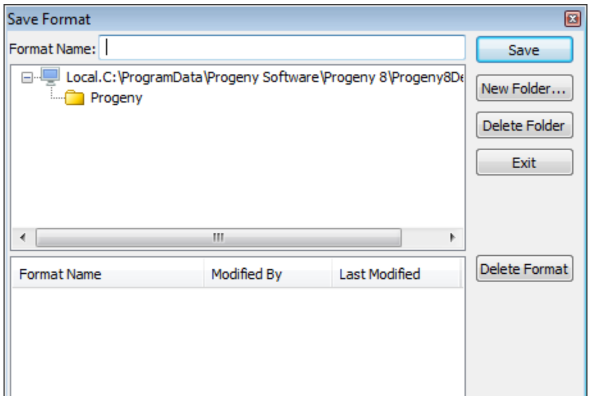
To save a HelixTree export format

1. Set up the HelixTree export format but do *not* run the format See "Creating and Running a HelixTree Export" on page 465.

2. Click the Save Format button Save Fmt on the Specify HelixTree Settings dialog box.

   The Save Format dialog box opens. It provides a default folder named Progeny in which to save the export format. (This folder is located in the database that you are currently logged in to and you cannot change this location.)

Figure 11-7: Save Format dialog box



3. Enter a name for the export format, and then do one of the following:
   - Select the Progeny folder.
   - Click New Folder, and on the Format Folder dialog box that opens, do the following:
     - Enter the name of the new folder in which to save to format.
     - Select the location for the new folder. The folder can be stored at the root level (the same level as the Progeny folder), or it can be a sub-folder of the Progeny folder, or of another folder.
     - Click Save.
4. Click Save on the Save Format dialog box.

   You can then load this saved format and run it on as-needed basis. See "To load a HelixTree export format" on page 472.

To load a HelixTree export format

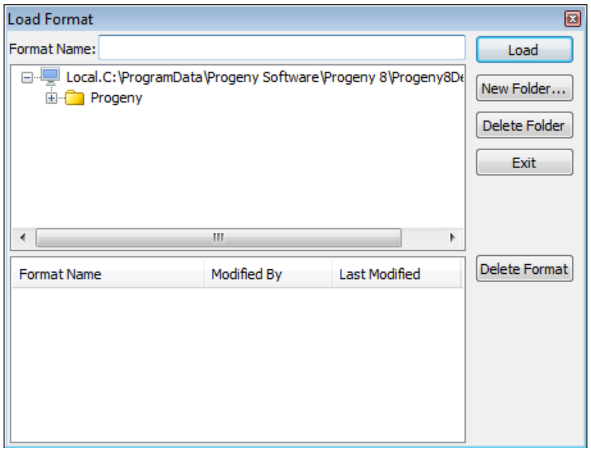
You can a retrieve a saved phase export format and run it on as-is needed based.

1. Open the Specify HelixTree Settings dialog box. (See Step 1 through Step 3 of “To create a HelixTree export” on page 465.)

2. On the dialog box, click the Load Format button Load Fmt.

   The Load Format dialog box opens.

Figure 11-8: Load Format dialog box



3. Open the folder that contains the HelixTree export format that you are loading, select the format, and then click Load.

   The Specify HelixTree Settings dialog box is refreshed with the loaded format. You can modify the format as needed (for example, modify the information on the Markers tab), and export the format. See “Creating and Running a HelixTree Export” on page 465.

Viewing and Rerunning a HelixTree Export

You can view information about any HelixTree exports that were previously run on the Analysis window, and you can rerun any phase export as necessary.

To view and rerun a HelixTree export

1. On the Analysis window, select the HelixTree export that you want to view.

   A single tab—the Results tab—opens in the bottom pane of the window.

You can also right-click on the tab and open a context menu with options for copying the information on the tab, exporting the information on the tab to a text file, or printing the information on the tab.

2. Optionally, to rerun the HelixTree export, right-click on the selected export, and on the context menu that opens, click Open Export.

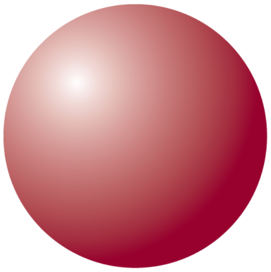
   The Specify HelixTree Settings dialog box opens. You can now modify any of the needed settings (for example, modify information on the Markers tab) and click OK on the Settings tab to rerun the export. See "Creating and Running a HelixTree Export" on page 465.

Deleting a HelixTree Export

You can delete a phase export by doing one of the following:

- Right-clicking on the export in the Analysis window, and on the context menu that opens, clicking Delete Export.
- Selecting the export in the Analysis window, and then clicking the [Delete] key on your keyboard.

Section 4



Progeny LIMS

Section Contents

Chapter 1

Progeny LIMS Terms, Conventions and Components

Progeny LIMS is software that is designed for managing any type of sample and associated data in a fully customizable multi-level inventory system with the freedom to create any laboratory workflow. Progeny LIMS uses conventions in both its terminology and its output to ensure consistency and accuracy when you are manipulating and analyzing sample data.

This chapter covers the following topics:

- "Progeny LIMS Terms and Conventions" on page 479.
- "Progeny LIMS Components" on page 480.

Progeny LIMS Terms and Conventions

Progeny LIMS is software that is designed for managing any type of sample and associated data in a fully customizable multi-level inventory system with the freedom to create any laboratory workflow. Progeny LIMS uses conventions in both its terminology and its output to ensure consistency and accuracy when you are manipulating and analyzing sample data.

- Sample—A *sample* is a part that is representative of a whole or a set of elements that is drawn from and analyzed to estimate the characteristics of a population. A sample can be an unassociated sample, or it can be associated with an individual. The following icon indicates a sample: 🧪.
- Container—A *container* is any receptacle in which a sample is held. A container can be as broad as a freezer and as a granular as a plate, for example, Freezer > Racks > Boxes > Plates. The following icon indicates a container: ▦.

Progeny LIMS Components

To use all of the features that are available to you in Progeny LIMS efficiently and effectively, you must understand the function/purpose of the following four critical components and their relationship with each other.

- Sample database fields—*Sample database fields* are stored at the sample record level. Sample database fields house the data that you enter for a sample in a Progeny database. Sample Name, Sample Type, Sample Status, and so on are examples of sample database fields. It is critical that you have defined all of the necessary sample database fields in a Progeny database *before* you can work with any of the other three LIMS components. See Chapter 2, “Progeny Database Design,” on page 39 in the Progeny Core Database Functionality section.
- Reactions—A *reaction* is a system or user-defined trigger that is used to update sample records. Reactions can carry out a wide range of tasks, including, but not limited to, updating date sample data fields with set values or prompt users for input values, creating new sample and aliquot records, updating container locations, sending print commands to barcode label printers, assigning samples to individuals in the database and moving samples from one workflow to another.See Chapter 3, “Managing Reactions,” on page 497.
- Actions—An *action* is a series of reactions. An action can be carried out on a single sample, a batch of samples, a container of samples, including plates. All of the reactions that are contained in an action must be carried out successfully for the action to be completed. For example, the action Update Sample Information can consist of the following three reactions—Update Sample Concentration, Update Sample Status, and Update Sample Type. To complete the Update Sample action, a user must enter the concentration for the sample (for example, 10 mg/dl), a sample type (for example, Pre-Dosage or Post-Dosage), and a sample status (for example, Thawed or Frozen). See “Managing Actions” on page 505.
- Workflow—A *workflow, (*also referred to as a *sample workflow)* is a collection of actions that have been arranged into a step-by-step procedure. A workflow is made up of multiple stages, with each stage associated with exactly one action. After a sample is placed into a workflow, the movement of the sample from one stage to the next can be tracked and recorded until the sample is ultimately exhausted and removed from the workflow. See Chapter 6, “Managing Workflows,” on page 535.

Chapter 2
Managing Containers

A *container* is any receptacle in which a sample is held. A container can be as broad as a freezer and as a granular as a plate, for example, Freezer > Racks > Boxes > Plates. Managing containers consists of adding new containers, modifying and deleting containers, updating sample positions in containers, and importing and exporting container information.

This chapter covers the following topics:

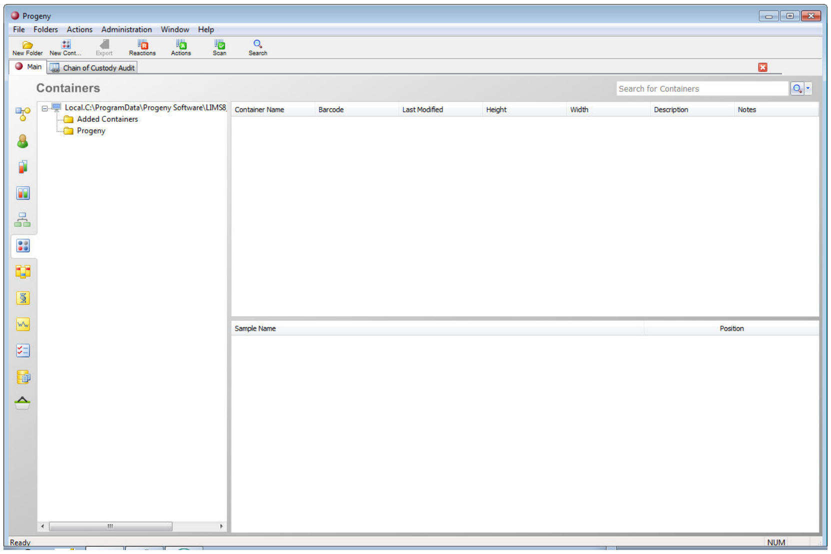
Adding a New Container

A *container* is any receptacle in which a sample is held. A container can be as broad as a freezer and as a granular as a plate, for example, Freezer > Racks > Boxes > Plates. You can add the following containers in Progeny—freezer, shelf, box, refrigerator, rack, or plate. Adding a new container consists of naming the container, and suppling a barcode and the dimensions for the container. In addition, if you are the Progeny administrator, you can set the security for the container. You can add a container as a standalone container, or you can add a container as a child container. For example, you can create a rack, and then from within the rack (the parent container), you can add a box or a plate (the child container).

To add a new container as a standalone container

1. On the Progeny main window navigation bar, click the Containers button to open the Containers window.

Figure 2-1: Containers window



2. Select the folder to which the new container is being added.

You can add a new folder if needed. Click the New Folder button on the window toolbar to open the New Folder dialog box, in which you can enter a name for a new Container folder and select its location (at the root level or as a sub-folder of another folder.)

3. On the window toolbar, click the New Container button to open a dropdown list of the containers that you can add, and then select the container that you are adding.

   The New <Container> dialog box opens.

4. Enter the information for the new container.

The following dialog box is that for a New Plate; however, for any new container, the New Container dialog box contains the same two tabs—a Settings tab for entering the container name, the container barcode, the container dimensions, and an optional description and/or notes about the container, and a Security tab for setting security for the container.

Figure 2-2: *New Plate dialog box*

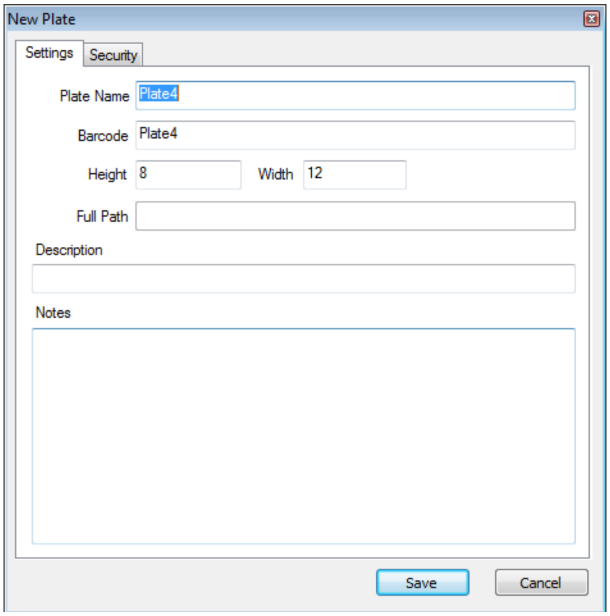
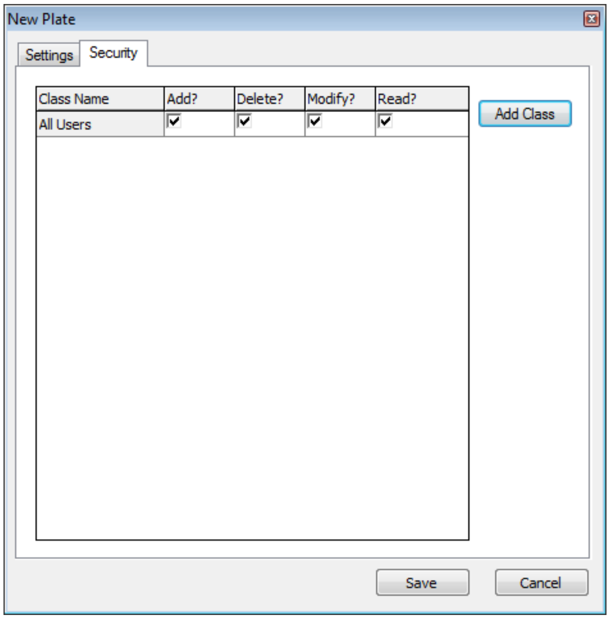


Plate Name: Plate4
Barcode: Plate4
Height: 8
Width: 12
Full Path:

Option	Description
Container Name	The default name is ContainerTypeNumber, where ContainerType is Plate, Shelf, and so on, and Number is auto-incremented. For example, the first time that you add a new plate, the Plate Name is set to Plate1. If you use the default name for your containers, then the second time you add a plate, the default name is Plate2, and so on. You can modify the name to accommodate your own naming schemes.
Barcode	The default barcode is the default Container Name. You can use this value, or you can modify it as needed.
Height Width	The dimensions for the container. Standard dimensions are used for the default values, but you can modify them as needed.
Full Path	The full path to the container location for a shelf, box, rack or plate. For example, for a plate, the path could be -80Freezer\80_shelf\Rack1. **Note:** If you add a shelf, box, rack, or plate as a child container, you do not have to enter this value manually, Instead, this field is automatically populated with the correct path and you cannot change this value. See "To add a child container" on page 486.
Description Notes	Optional fields

5. Open the Security tab, and set the security for the container.

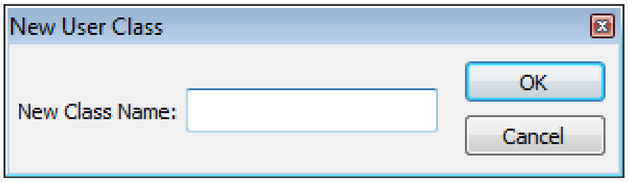
Figure 2-3: New Container dialog box, Security tab



Class Name	Add?	Delete?	Modify?	Read?
All Users	☑	☑	☑	☑

6. Do one or more of the following:
   - Modify the security for All Users.
   - Click Add Class to open the New User Class dialog box to create a new user class, and then set the security for the class.

Figure 2-4: New User Class dialog box



7. Click Save.

   The New Container dialog box closes. The new container is added to the Progeny database.

To add a child container

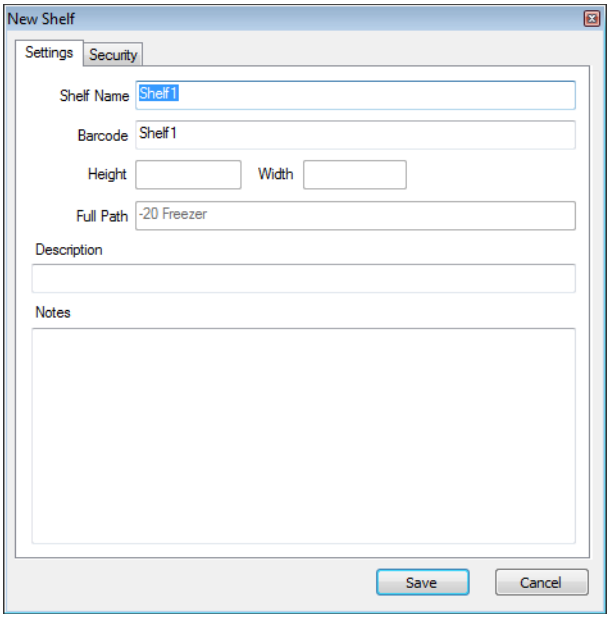
When you add a child container, the full path to the container is automatically populated, which provides an error free way of locating containers. You can add the following child containers:

- You can add a shelf to a freezer or refrigerator.
- You can add a box or a rack to a shelf.
- You can add a box or a plate to a rack.

1. Add the parent container. For example, if you want to add a shelf to a freezer, add the freezer. See "To add a new container as a standalone container" on page 483.
2. Right-click on the parent container in the Containers window, and on the context menu that opens, select the child container that you are adding. For example, if you are adding a shelf to a freezer, then right-click on the freezer, and then click Add Shelf.

   The New Container dialog box opens. The Full Path field is automatically populated for the child container and you cannot edit this value.

Figure 2-5: New Container dialog box when adding a child container



New Shelf

Shelf Name: Shelf1
Barcode: Shelf1
Height:
Width:
Full Path: -20 Freezer
Description:
Notes:

3. Enter the information for the child container as you would for any other container, and then click Save.

Modifying and Deleting a Container

Any user can modify any of the non-security settings for a container. If you are the Progeny administrator, you can also modify the security settings. You can delete a container only if the container does not have any samples in it. If the container has samples, then you must first remove the samples from the container.

To modify a container

1. On the Progeny main window navigation bar, click the Containers button to open the Containers window.
2. Open the data folder that contains the container that you are modifying.
3. Right-click on the container that you are modifying, and on the context menu that opens, click Edit.

   The Edit Container dialog box opens.
4. Edit the information for the container as needed, and then click Save.

Option	Description
Container Name	The default name is ContainerTypeNumber, where ContainerType is Plate, Shelf, and so on, and Number is auto-incremented. For example, the first time that you add a new plate, the Plate Name is set to Plate1. If you use the default name for your containers, then the second time you add a plate, the default name is Plate2, and so on. You can modify the name to accommodate your own naming schemes.
Barcode	The default barcode is the default Container Name. You can use this value, or you can modify it as needed.
Height Width	The dimensions for the container. Standard dimensions are used for the default values, but you can modify them as needed.
Full Path	The full path to the container location for a shelf, box, rack or plate. For example, for a plate, the path could be -80Freezer\80_shelf\Rack1. **Note:** If this container has been added as a child container, for example, the container is a rack that was added as a child container to a shelf, then this field is not editable.
Description Notes	Optional fields.

To delete a container

1. On the Progeny main window navigation bar, click the Containers button to open the Containers window.
2. Open the data folder that contains the container that you are deleting.
3. Right-click on the container that you are modifying, and on the context menu that opens, click Delete.

The Delete option is available only if there are no samples in the container. To delete a container with samples, you must first remove the samples from the container by running an action that contains the system reaction "Remove from Container." This reaction removes all samples from the container without deleting the sample records from the database. See Chapter 5, "Carrying out Actions on a Sample in the Scan Window," on page 528.

Manually Updating Sample Well Positions in a Plate or a Box

After you have added a plate or box, you can manually update the positions of the samples in the plate or box. You can manually update the well positions by dragging samples to their correct positions, or you can simply enter the appropriate sample number for a well position.

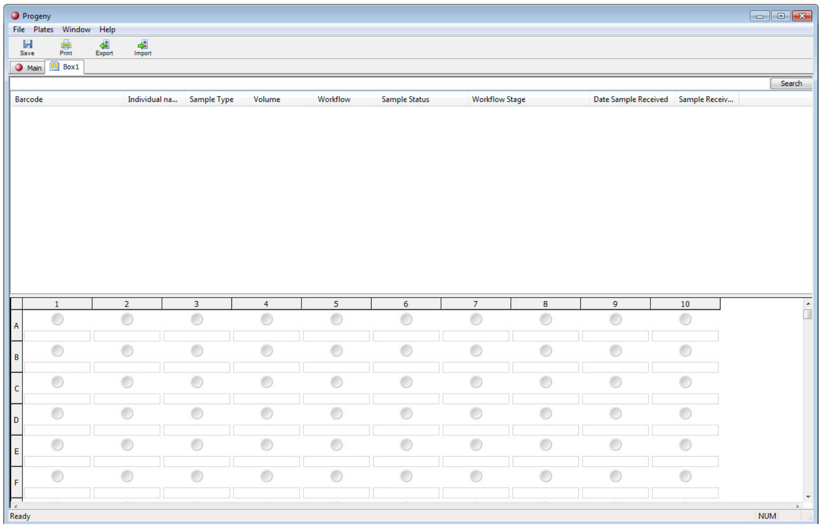
You can also use actions to automatically update sample positions in a container or remove a sample from a container. See Chapter 4, "Managing Actions," on page 505.

To drag samples to their well positions in a plate or a box

1. On the Progeny main window navigation bar, click the Containers button to open the Containers window.
2. Open the data folder that contains the container for which you are modifying the well positions.
3. Double-click on the container for which you are modifying the well positions.

   The Container Viewer opens. A search field is displayed at the top of the viewer.

Figure 2-6: Container Viewer

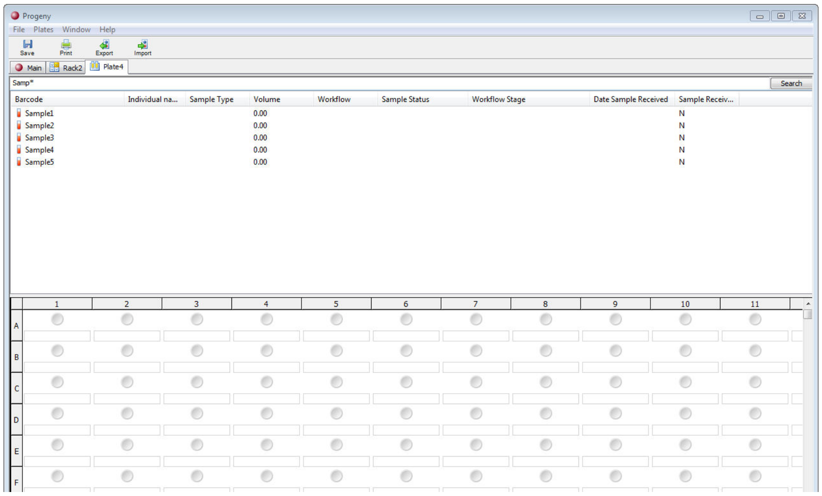


4. In the Search field, enter the criteria to search for the appropriate samples, and then click Search.

   The samples that meet the search criteria are displayed in the upper pane of the Container Viewer.

You search is limited to the exact order of the characters in the string and you can use the asterisk (*) as a wildcard to extend the search. For example, Blood will return Blood1, Blood2, Blood_1, Blood_2, and so on.*

Figure 2-7: Container Viewer with samples retrieved by a search



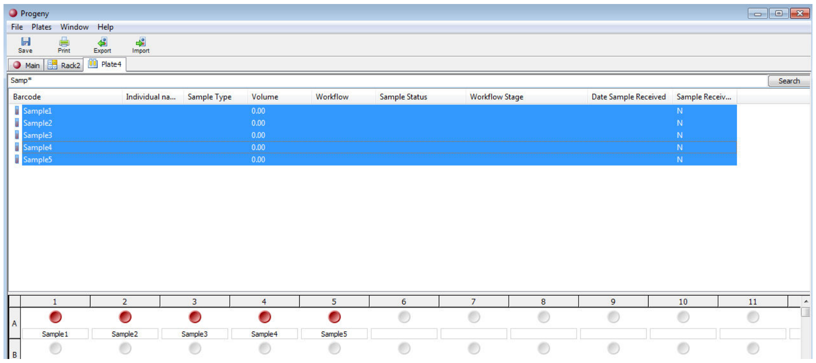
Samp*

Barcode	Individual na...	Sample Type	Volume	Workflow	Sample Status	Workflow Stage	Date Sample Received	Sample Receiv...
Sample1			0.00					N
Sample2			0.00					N
Sample3			0.00					N
Sample4			0.00					N
Sample5			0.00					N

5. Select a sample (CTRL-click to select multiple samples), and then drag the selected samples to the appropriate position on the plate or box.

   If you are dragging multiple samples, then the first selected sample is placed in the well to which the samples were dragged. The remaining samples are placed from left to right in the remaining available wells in the row, and then if applicable, moving down one row at a time, from left to right in the rows below.

Figure 2-8: Samples positioned in plate or box

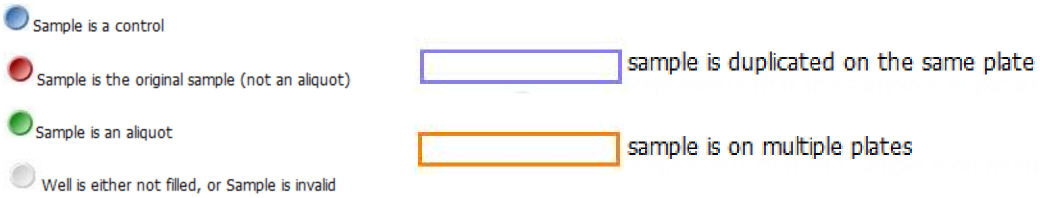


Samp*

Barcode	Individual na...	Sample Type	Volume	Workflow	Sample Status	Workflow Stage	Date Sample Received	Sample Receiv...
Sample1			0.00					N
Sample2			0.00					N
Sample3			0.00					N
Sample4			0.00					N
Sample5			0.00					N

The well colors indicate the type of sample that is placed in a well and the colors around the Sample Name field indicate whether a sample is duplicated on the sample plate or box or in multiple plates or boxes.

Figure 2-9: Color coding for samples in wells

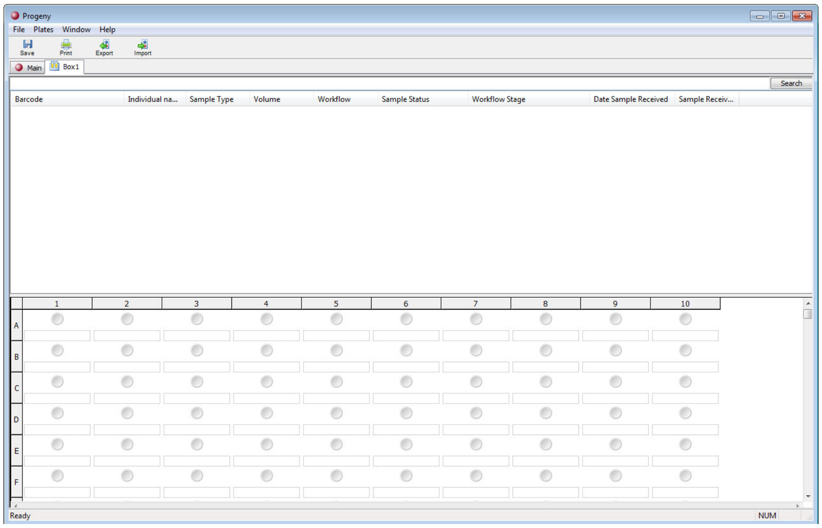


To manually enter positions for a sample in a plate or a box

1. On the Progeny main window navigation bar, click the Containers button to open the Containers window.
2. Open the data folder that contains the container for which you are modifying the well positions.
3. Double-click on the container for which you are modifying the well positions.

   The Container Viewer opens.

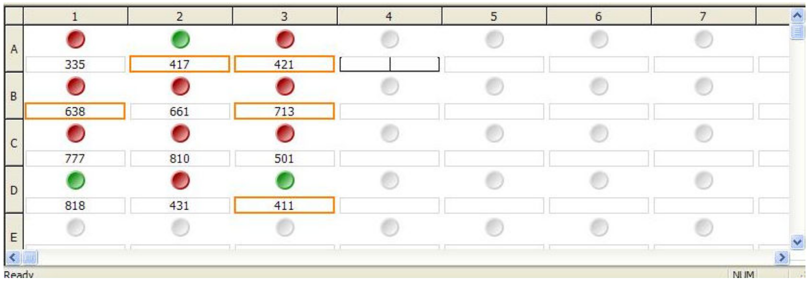
Figure 2-10: Container Viewer



4. Select the text field below a well position, and then enter the sample number for the position.

   If the sample has not yet been added to the Progeny database, then the well color does not change.

Figure 2-11: Manually entering samples in wells



	1	2	3	4	5	6	7
A	335	417	421				
B	638	661	713				
C	777	810	501				
D	818	431	411				
E							

Exporting Container Information

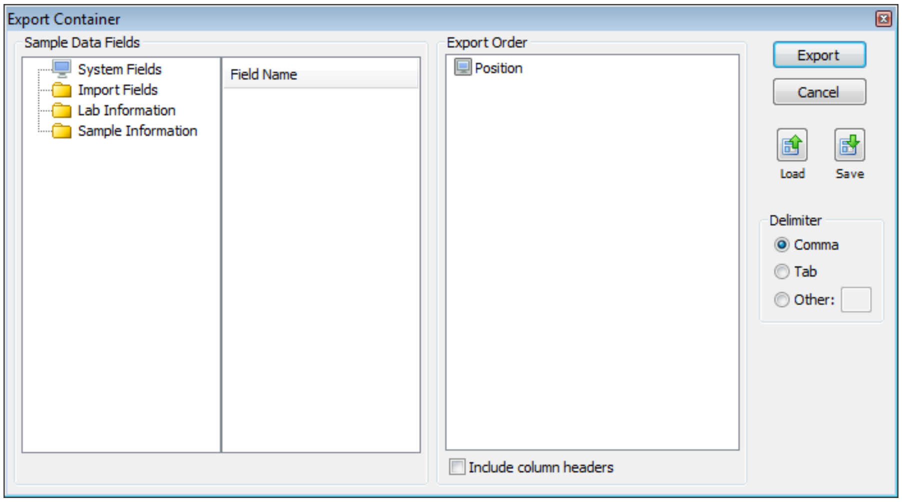
You can export container information to a text file.

To export container information

1. On the Progeny main window navigation bar, click the Containers button to open the Containers window.
2. Open the data folder that contains the container for which you are exporting the information.
3. Select the container for which you are exporting the information, and on the Container window toolbar, click the Export button Export.

   The Export Containers dialog box opens.

Figure 2-12: Export Containers dialog box



4. In the Sample Data Fields (left) pane of the dialog box, open the data folder that contains the fields that you are exporting.

   The fields are displayed in the Field Name (middle) pane dialog box.
5. Drag the fields that are being exported to the Export Order (right) pane of the dialog box.

The order in which you drag the fields is the order in which the fields are exported in the text file. You can drag the fields in the Export Order pane to reorder them. To remove a field from the export, right-click on the field and click Remove.

6. Optionally, to include column headings in the export, select Include column headers.

7. Specify the delimiter for the export file.

   If the delimiter is not a tab or a comma, then you must select Other, and then enter the delimiter.

8. Click Export.

   The Save as Type field is automatically populated with the file type of text (.txt) and you cannot change this value.

9. Browse to the location in which the export file is to be saved, and then in the File name field, enter a name for the text file.

10. Click Save.

    A message opens indicating that the export was successful.

11. Click OK to close the message.

    The Export Container dialog box remains open.

Saving and Loading a Container Export File Format

After you have set up a container export format, you can save the format. You can then load this saved format and run it on as-needed basis.

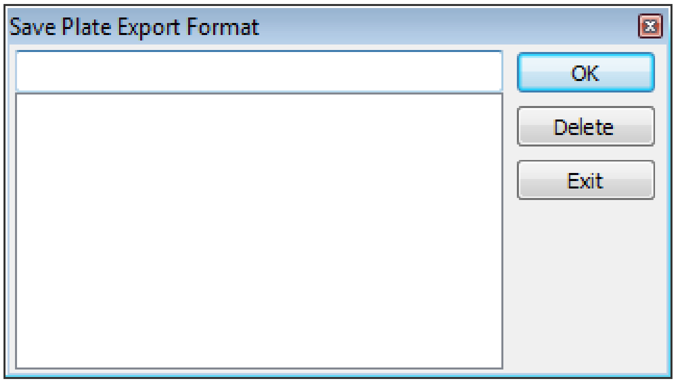
To save a container export format

1. Set up the container export format but do *not* run the format See “Exporting Container Information” on page 493.
2. Click the Save Format button Save Fmt on the Export Container dialog box.

   The Save Plate Export Format dialog box opens.

Although the dialog box is named Save Plate Export Format, you can use this dialog box to save the export format for any container—freezer, shelf, box, and so on.

Figure 2-13: Save Plate Export Format dialog box



3. Enter a name for the container export format.
4. Click Save.

   You can then load this saved format and run it on as-needed basis. See “To load a container export format” on page 496.

To load a container export format

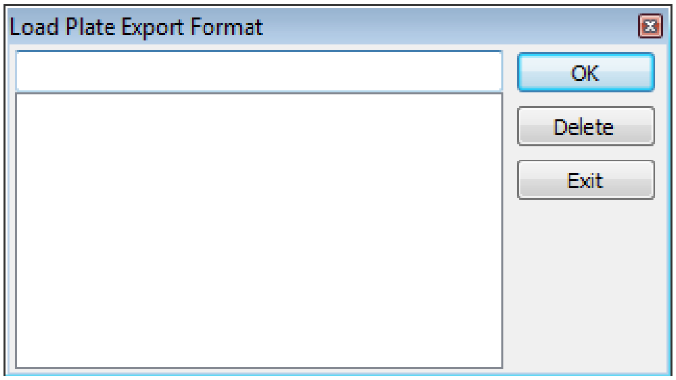
You can a retrieve a saved container export format and run it on as-is needed based.

1. Open the Export Container dialog box.
2. On the dialog box, click the Load Format button Load Fmt .

   The Load Plate Export Format dialog box opens.

Although the dialog box is named Load Plate Export Format, you can use this dialog box to load an export format for any container—freezer, shelf, box, and so on.

Figure 2-14: Load Plate Export Format dialog box



3. Select the container export format that you are loading, and then click Load.

   The Export Container dialog box is refreshed with the loaded format. You can modify the format as needed, and then export the format. See “Exporting Container Information” on page 493.

Chapter 3
Managing Reactions

A *reaction* is a system or user-defined trigger that is used to update sample records. Managing reactions consists of adding, modifying, and deleting reactions.

This chapter covers the following topics:

- "Adding a Reaction" on page 498.
- "Editing a Reaction" on page 502.
- "Deleting a Reaction" on page 504.

Adding a Reaction

A *reaction* is a system or user-defined trigger that is used to update sample records. A reaction always results in the updating or modifying of a single database field. For example, if a reaction is named Update Sample Status, and the reaction type is Update Value for the Sample Status field, then a prompt that could open for the Sample Status field is “Please Enter a Sample Status.” You can add a reaction to a Progeny database from the Inventory window, the Containers window, or the Workflows window.

The following procedure describes how to add a new reaction for changing a field value and for defining sample barcode settings. You can also add reactions for creating and naming new samples and aliquots, but because creating and naming samples and aliquots are part of sample maintenance, these reactions are discussed in Chapter 5, “Managing Samples,” on page 519.

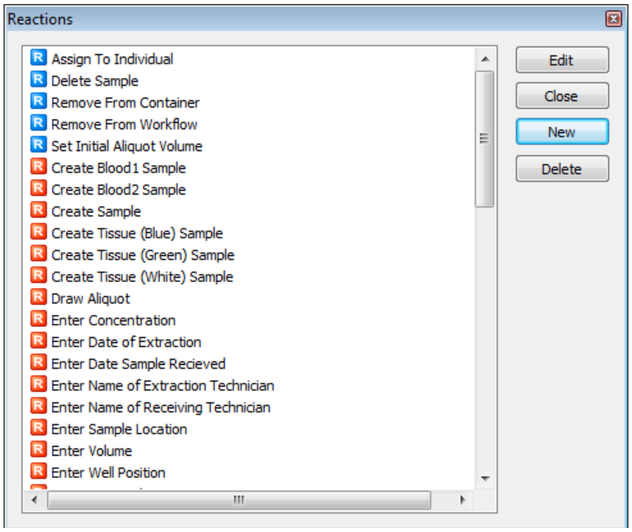
To add a new reaction

1. Open one of the following windows—Inventory, Containers, or Workflows.

2. On the window toolbar, click the Reactions button .

   The Reactions dialog box opens. This dialog box lists all of the reactions that are available in the Progeny database that you are currently logged in to. Reactions that are marked with a blue Reaction icon are system reactions that are always available in every Progeny database and are not editable. Reactions that are marked with a red Reaction icon are user-defined reactions and are editable.

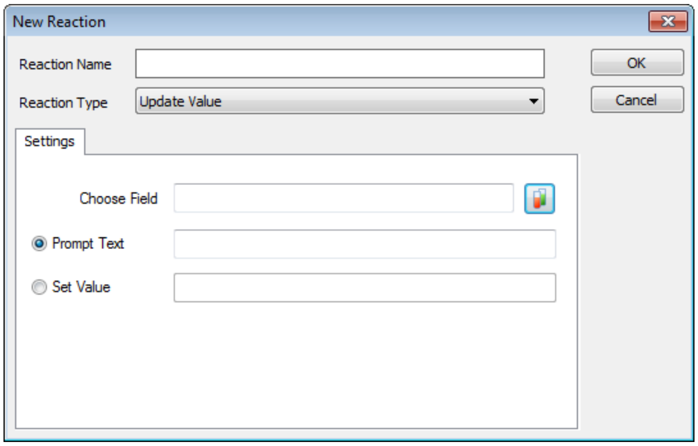
Figure 3-1: Reactions dialog box



3. Click New.

   The New Reaction dialog box opens.

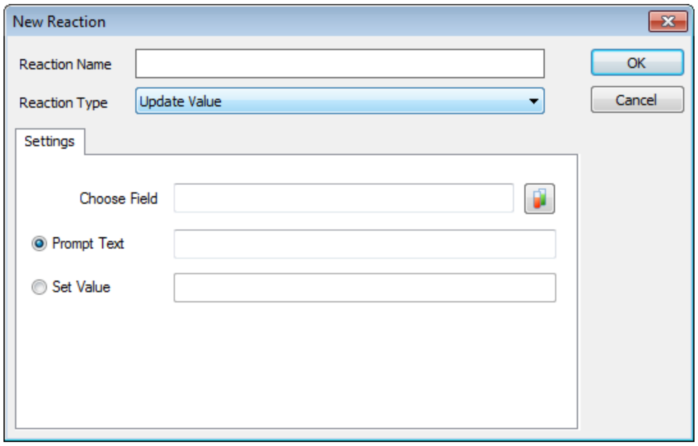
Figure 3-2: New Reaction dialog box



4. Enter the name for the new reaction.
5. Select the reaction type.
   - Update Value—Override the current value in a data field. Go to Step 6.
   - Decrease Value—Subtract an amount from the current value in a data field. Go to Step 6.
   - Increase Value—Add an amount to the current value in a data field. Go to Step 6.
   - Print—Print the barcode label for a sample or send a print command to print a barcode label for a sample or batch of samples. Go to Step 7.
   - Create Sample—See "Adding a Create Sample Reaction" on page 521.
   - Create Aliquot—See "Adding a Create Aliquot Reaction" on page 524.

6. If you selected Update Value, Decrease Value, or Increase Value, then the New Reaction dialog box is refreshed with options for selecting the sample field on which to carry out the action, and whether the reaction is to be a prompt, or an automatic response.

Figure 3-3: New Reaction dialog box, Update Value selected



Reaction Type: Update Value

● Prompt Text

○ Set Value

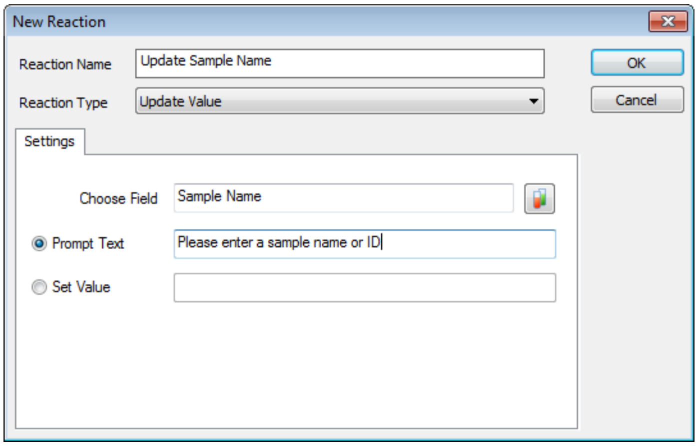
Do the following, and then click OK to add the new reaction.

- Click the Sample button next to the Choose Field field to open the Select Field dialog box and select the field on which the action is to be carried out.
- Select the reaction type—Prompt or Set Value.

A Prompt is typically used for variables, such as "Please enter a Sample ID or Name." A Set Value is typically used for static values that required no manual intervention. Instead of a prompt appearing, the software automatically enters the value in the background, for example, "Mark Sample as Exhausted."

Figure 3-4 below is an example of a reaction in which Update Value was selected for the Reaction Type. In this reaction, the value of the Sample Name field is to be updated, and the prompt that is given for the reaction is "Please Enter Sample Name or ID."

Figure 3-4: Example of an Update Value reaction



Reaction Name: Update Sample Name

Reaction Type: Update Value

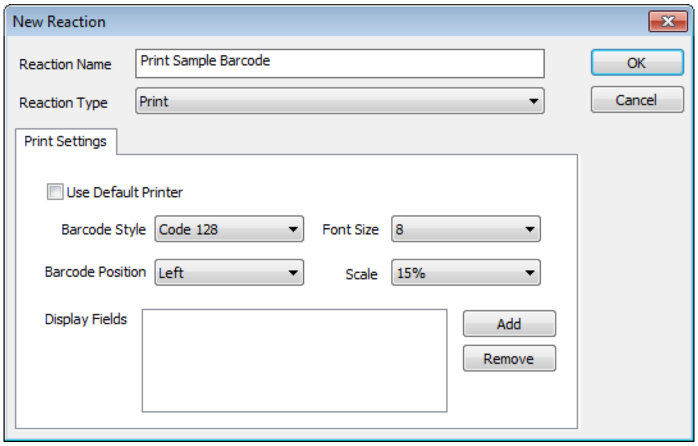
Choose Field: Sample Name

● Prompt Text: Please enter a sample name or ID

○ Set Value

7. If you selected Print, then the New Reaction dialog box is refreshed with an option for printing the barcode from the default printer, as well as options for the barcode style, and the barcode position.

Figure 3-5: New Reaction dialog box, Print selected



Reaction Name: Print Sample Barcode
Reaction Type: Print
☐ Use Default Printer
Barcode Style: Code 128
Font Size: 8
Barcode Position: Left
Scale: 15%
Display Fields

Do the following, and then click OK to add the new reaction.

- Optionally, select Use Default Printer. (If you do not select this option, then every time this reaction is run, a user is prompted to select a printer to use.)
- Select the barcode style. Codes 128, 93, and 39 are standard one dimensional barcoding languages. Data matrix is a two-dimensional barcoding language.
- Select the barcode position (where the barcode is to be printed on the barcode label), font size, scale (the percentage of the barcode label that is to be used for printing the barcode), and display fields (the additional fields that are to be displayed on the barcode).

Editing a Reaction

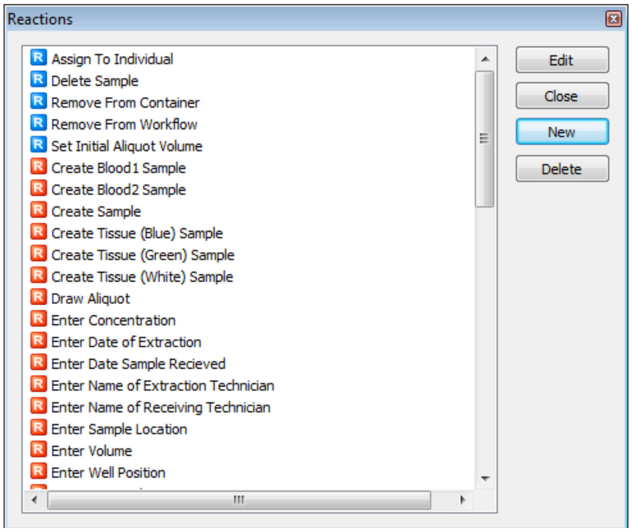
You can edit any user-defined reaction. You cannot edit the system reactions that are defined for every Progeny database.

To edit a reaction

1. Open one of the following windows—Inventory, Containers, or Workflows.
2. On the window toolbar, click the Reactions button .

   The Reactions dialog box opens. This dialog box lists all of the reactions that are available in the Progeny database that you are logged in to. Reactions that are marked with a blue Reaction icon are system reactions that are always available in every Progeny database and are not editable. Reactions that are marked with a red Reaction icon are user-defined reactions and are editable.

Figure 3-6: Reactions dialog box

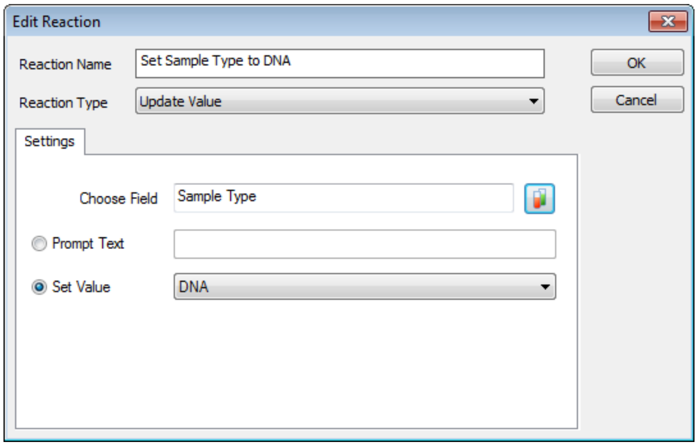


Assign To Individual
Delete Sample
Remove From Container
Remove From Workflow
Set Initial Aliquot Volume
Create Blood1 Sample
Create Blood2 Sample
Create Sample
Create Tissue (Blue) Sample
Create Tissue (Green) Sample
Create Tissue (White) Sample
Draw Aliquot
Enter Concentration
Enter Date of Extraction
Enter Date Sample Recieved
Enter Name of Extraction Technician
Enter Name of Receiving Technician
Enter Sample Location
Enter Volume
Enter Well Position

3. Select the user-defined reaction that you are editing, and then click Edit.

   The Edit Reaction dialog box opens. The dialog box displays the reaction as it is currently defined.

Figure 3-7: Edit Reaction dialog box



Edit Reaction

Reaction Name: Set Sample Type to DNA

Reaction Type: Update Value

Settings

Choose Field: Sample Type

○ Prompt Text

● Set Value: DNA

4. Edit the reaction as needed, and then click OK to save the edited reaction.

Deleting a Reaction

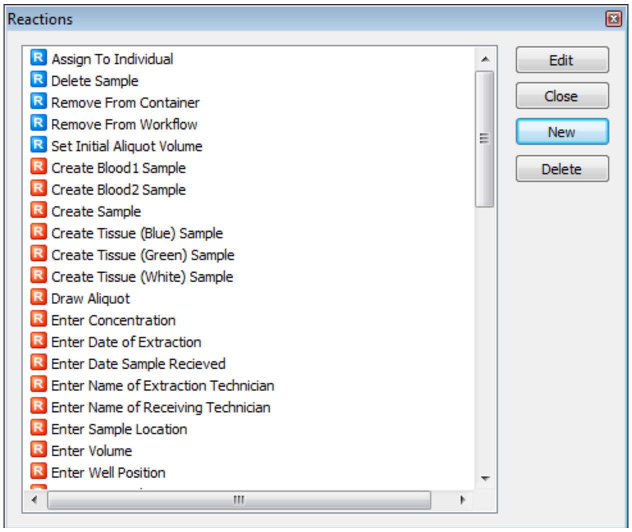
You can delete any user-defined reaction. You cannot delete the system reactions that are defined for every Progeny database.

To delete a reaction

1. Open one of the following windows—Inventory, Containers, or Workflows.
2. On the window toolbar, click the Reactions button Reactions.

   The Reactions dialog box opens. This dialog box lists all of the reactions that are available in the Progeny database that you are logged in to. Reactions that are marked with a blue Reaction icon are system reactions that are always available in every Progeny database and are not editable. Reactions that are marked with a red Reaction icon are user-defined reactions and are editable.

Figure 3-8: Reactions dialog box



- Assign To Individual
- Delete Sample
- Remove From Container
- Remove From Workflow
- Set Initial Aliquot Volume
- Create Blood1 Sample
- Create Blood2 Sample
- Create Sample
- Create Tissue (Blue) Sample
- Create Tissue (Green) Sample
- Create Tissue (White) Sample
- Draw Aliquot
- Enter Concentration
- Enter Date of Extraction
- Enter Date Sample Recieved
- Enter Name of Extraction Technician
- Enter Name of Receiving Technician
- Enter Sample Location
- Enter Volume
- Enter Well Position

3. Select the user-defined reaction that you are deleting (CTRL-click to select multiple reactions), and then click Delete.

   A message opens asking you if you are sure that you want to delete the selected reactions.
4. Click Yes.

   The message closes, and the selected reactions are deleted.

Chapter 4
Managing Actions

An *action* is a series of reactions. An action can be carried out on a single sample, a batch of samples, a container of samples, or a plate. Managing reactions consists of adding, modifying, and deleting actions.

This chapter covers the following topics:

Adding an Action

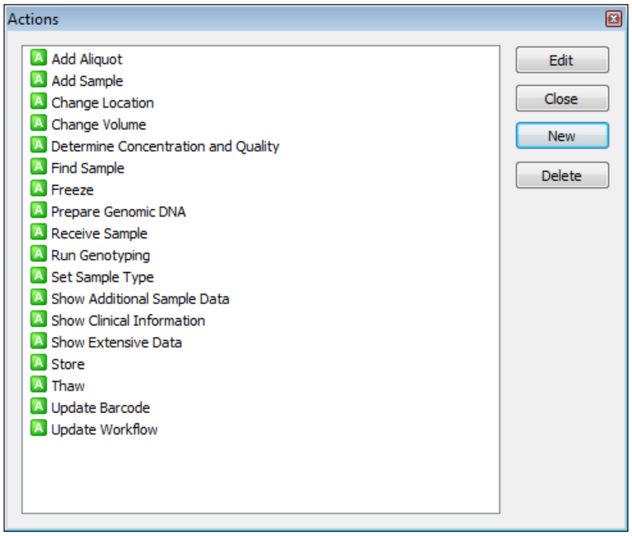
An *action* is a series of reactions. An action can be carried out on a single sample, a batch of samples, a container of samples, or a plate. You can add an action to a Progeny database from the Inventory window, the Containers window, or the Workflows window. When you add an action, you can add it "from scratch," or you can copy an existing action and modify it as necessary to make a new action.

To add a new action

1. Open one of the following windows—Inventory, Containers, or Workflow.
2. On the window toolbar, click the Actions button Actions.

   The Actions dialog box opens. This dialog box lists all of the actions that have been defined for the Progeny database that you are logged in to.

Figure 4-1: Actions dialog box



Actions

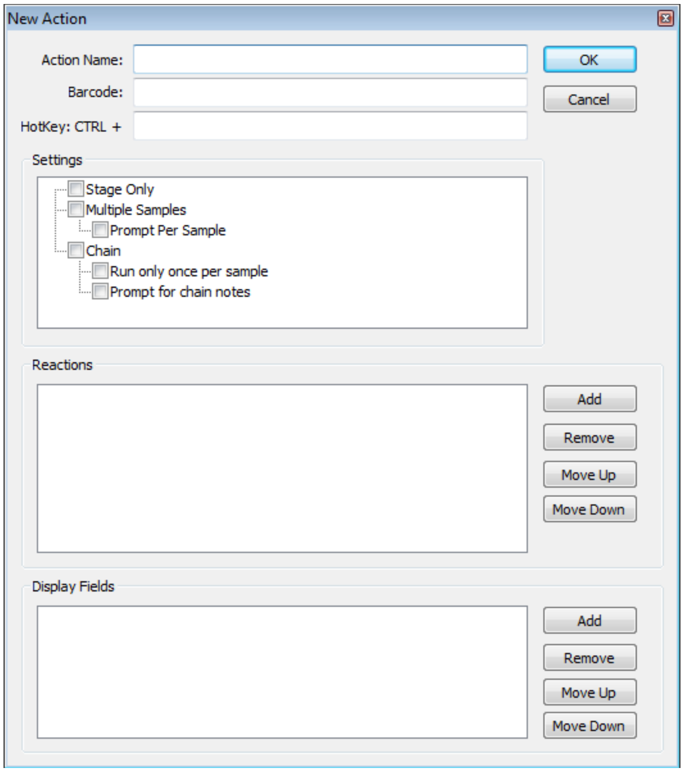
Add Aliquot
Add Sample
Change Location
Change Volume
Determine Concentration and Quality
Find Sample
Freeze
Prepare Genomic DNA
Receive Sample
Run Genotyping
Set Sample Type
Show Additional Sample Data
Show Clinical Information
Show Extensive Data
Store
Thaw
Update Barcode
Update Workflow

The remainder of this procedure describes how to add a new action "from scratch." To add a new action by copying an existing action, select the action that is to be copied, click Copy, and then continue to Step 4.

3. Click New.

   The New Action dialog box opens.

Figure 4-2: New Action dialog box



4. Enter the information for the new action.

Option	Description
Name	The name of the action.
Barcode	The barcode that is associated with the action. When this barcode is scanned into Progeny,or manually entered in the Scan window, the action is initiated. See “Carrying out Actions on a Sample in the Scan Window” on page 528. **Note:** You set the barcoding language, position, scale, and font for action barcodes in the Action Barcode Settings dialog box. See “Specifying Action Barcode Settings” on page 512.
Hotkey: CTRL +	The keystroke combination that initiates a selected action in the Scan window. See “Carrying out Actions on a Sample in the Scan Window” on page 528.
Stage Only	Select this option if the action is to be carried out only from within a workflow (a stage action). **Note:** If the action is carried out outside of a workflow, then it is referred to as an *open action*.
Multiple Samples	Select this option if the action can be carried out on multiple samples at the same time. This is known as batch operation of samples.

Option	Description
Prompt Per Sample	Applicable only for Multiple Samples. A prompt opens for each selected sample when the action is initiated for the sample.
Chain	Select this option to log the action carried out on the sample into the Chain of Custody for the sample. The action is logged with the name of the user who carried out the action on the sample along with a date and timestamp.
Run only once per sample	Applicable only for Chain. Select this option to allow the indicated action to be carried out only once for any given sample if the action has already been logged into the Chain of Custody for the sample.
Prompt for chain notes	Applicable only for Chain. Select this option to allow the user to enter notes/comments about the action that is being logged into the Chain of Custody for the sample.
Prompt for number of samples to create	Displayed only if the first reaction in a series of reactions is of the type Create Sample and the reaction is set to Accept Default as the sample name. Select this option to open a prompt in which a user can specify the number of samples to create.
Prompt for number of aliquots to create	Displayed only if the first reaction in a series of reactions is of the type Create Aliquot and the reaction is set to Accept Default as the aliquot name. Select this option to open a prompt in which a user can specify the number of aliquots to create.

5. In the Reactions pane, click Add to open the Reactions dialog box and select the reactions (CTRL-click to select multiple reactions) that are to be contained in the action.

The order in which you add the reactions to the action is the order in which they are carried out. To change the order, select a reaction, and then click Move Up or Move Down as needed.

6. Optionally, in the Display Fields pane, click Add to open the Select Fields dialog box and select the fields that are to display information when the reaction is carried out.

The fields are for informational purposes only, and are typically used to provide confirming or clarifying information for a reaction. For example, if you are entering the volume for an aliquot, and the aliquot naming scheme does not include the parent name, then you could select the Parent Name field for the reaction to confirm that you are entering the correct information for the correct aliquot.

7. Click OK to close the New Action dialog box and return to the Actions dialog box.

   The the action is added to the Progeny database.

Setting an Action as a Default Action

If needed, you can set an action to be your *default* action. A default action is initiated every time that you open the Scan window (see “Carrying out Actions on a Sample in the Scan Window” on page 528) from the Progeny main window toolbar. A default action is very similar to a hotkey for an action (see Hotkey on page 508); however, you do not have to remember specific keystrokes for carrying out the action.

A default action is set on a per user basis. Every user can set up his/her own default action.

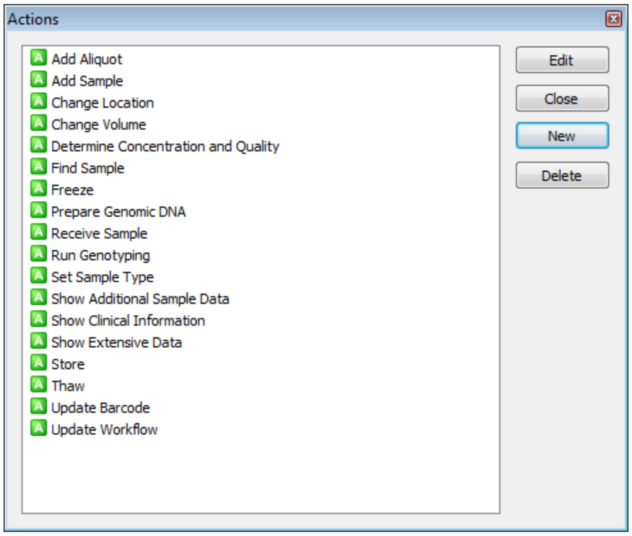
To set an action as a default action

1. Open one of the following windows—Inventory, Containers, or Workflows.

2. On the window toolbar, click the Actions button Actions .

   The Actions dialog box opens. This dialog box lists all of the actions that have been defined for the Progeny database that you are logged in to.

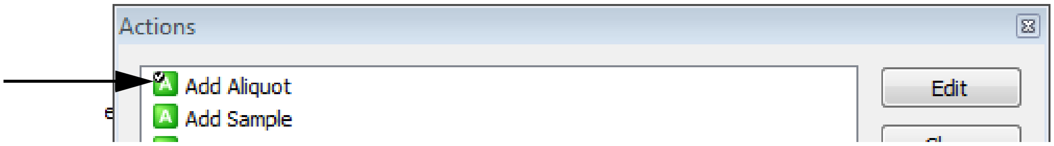
Figure 4-3: Actions dialog box



3. Right-click on the action that is to be your default action, and on the context menu that opens, click Set as Default Action.

   The action is marked with a black check mark in the Actions dialog box.

Figure 4-4: Default action indicated in the Actions dialog box



Conversely, to clear a default action, right-click on the action, and on the context menu that opens, click Remove as Default Action.

Specifying Action Barcode Settings

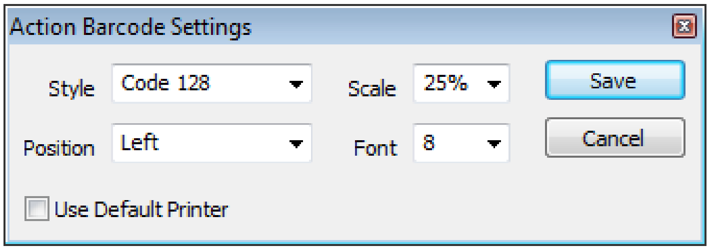
When you create an action, you have the option of specifying a barcode for the action. When you scan this barcode into Progeny, or manually enter the barcode in the Scan window, the action is initiated. (See (see "Carrying out Actions on a Sample in the Scan Window" on page 528.) A very typical use for action barcodes is to create a "cheat sheet," which is essentially a piece of paper that contains labels, with each label having one action barcode printed on it. You can scan the barcodes on these labels to minimize your dependency on manually entering information to carry out a procedure in Progeny LIMS.

To specify action barcode settings

1. Open one of the following windows—Inventory, Containers, or Workflows.
2. On the window main menu, click Actions > Action Barcode Settings.

   The Action Barcode Settings dialog box opens.

Figure 4-5: Action Barcode Settings dialog box



Style: Code 128
Scale: 25%
Position: Left
Font: 8
☐ Use Default Printer

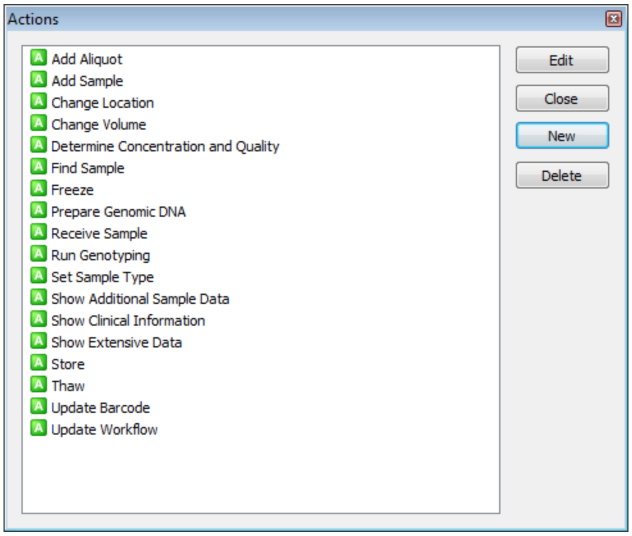
3. Specify the print settings for your action barcodes, and also indicate if are to use your system's default printer to print the barcodes.

The settings that you specify here are global settings and apply to all action barcodes. If you do not select Use Default Printer, then you when you print an action barcode, you are prompted to select a printer.

4. On the window toolbar, click the Actions button Actions .

   The Actions dialog box opens. This dialog box lists all of the actions that have been defined for the Progeny database that you are logged in to.

Figure 4-6: Actions dialog box



5. For each action barcode that is to be printed on a label, right-click on the appropriate action, and then on the context menu that opens, click Print Barcode.

   The barcode is printed according to the settings that you specified in Step 3.

Make sure that you have the appropriate label sheet queued in the printer.

You can now paste all these printed labels on a sheet of paper and in the Scan window use Progeny's barcode scanning function to scan a label to carry out an action. (See "Carrying out Actions on a Sample in the Scan Window" on page 528.) If you have a barcode label printed for every action that you must carry out, then you can carry out an entire procedure in LIMS without ever having to use a mouse and/or a keyboard.

Setting Security for an Action

If you are the Progeny administrator, then you set security for actions.

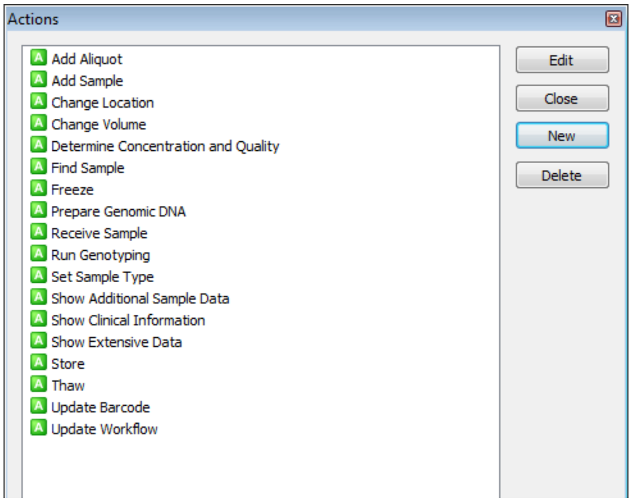
To set security for an action

1. Open one of the following windows—Inventory, Containers, or Workflows.

2. On the window toolbar, click the Actions button .

   The Actions dialog box opens. This dialog box lists all of the actions that have been defined for the Progeny database that you are logged in to.

Figure 4-7: Actions dialog box

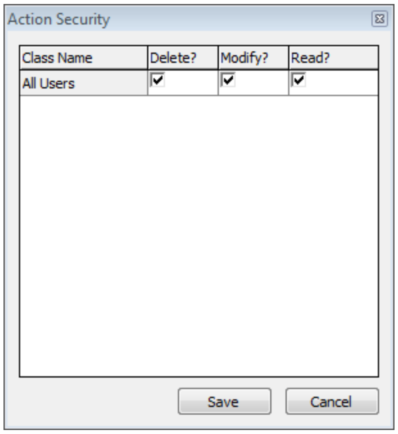


- Add Aliquot
- Add Sample
- Change Location
- Change Volume
- Determine Concentration and Quality
- Find Sample
- Freeze
- Prepare Genomic DNA
- Receive Sample
- Run Genotyping
- Set Sample Type
- Show Additional Sample Data
- Show Clinical Information
- Show Extensive Data
- Store
- Thaw
- Update Barcode
- Update Workflow

3. Right-click on an action, and on the context menu that opens, click Security Settings.

   The Action Security dialog box opens. This dialog box lists all the classes of users that have been defined for the database that you are logged in to.

Figure 4-8: Action Security dialog box



Class Name	Delete?	Modify?	Read?
All Users	☑	☑	☑

4. Modify the security for All Users or for the different classes of users.
   - Delete?—The users can delete the action.
   - Modify?—The users can modify the action.
   - Read?—The users can carry out the action.
5. Click OK.

Editing an Action

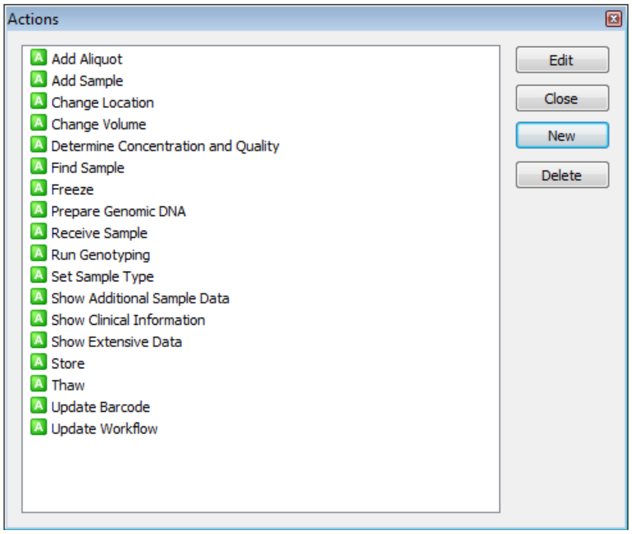
If your administrator has set the correct security, then you can edit an action. As the Progeny administrator, you can always edit any action.

To edit an action

1. Open one of the following windows—Inventory, Containers, or Workflows.
2. On the window toolbar, click the Actions button .

   The Actions dialog box opens. This dialog box lists all of the actions that have been defined for the Progeny database that you are logged in to.

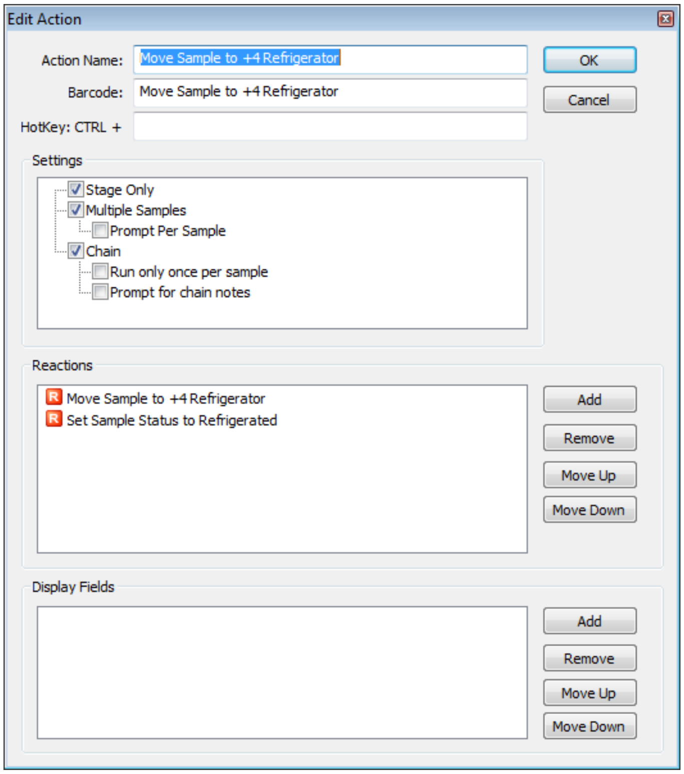
Figure 4-9: Actions dialog box



3. Select the action that you are editing, and then click Edit.

   The Edit Action dialog box opens. The dialog box displays the action as it is currently defined.

Figure 4-10: Edit Reaction dialog box



Action Name: Move Sample to +4 Refrigerator
Barcode: Move Sample to +4 Refrigerator
HotKey: CTRL +

Settings
- ☑ Stage Only
- ☑ Multiple Samples
  - ☐ Prompt Per Sample
- ☑ Chain
  - ☐ Run only once per sample
  - ☐ Prompt for chain notes

Reactions
- Move Sample to +4 Refrigerator
- Set Sample Status to Refrigerated

Display Fields

4. Modify the action as needed, and then click OK to save the modified action.

Deleting an Action

If your administrator has set the correct security, then you can delete an action. As the Progeny administrator, you can always delete any action.

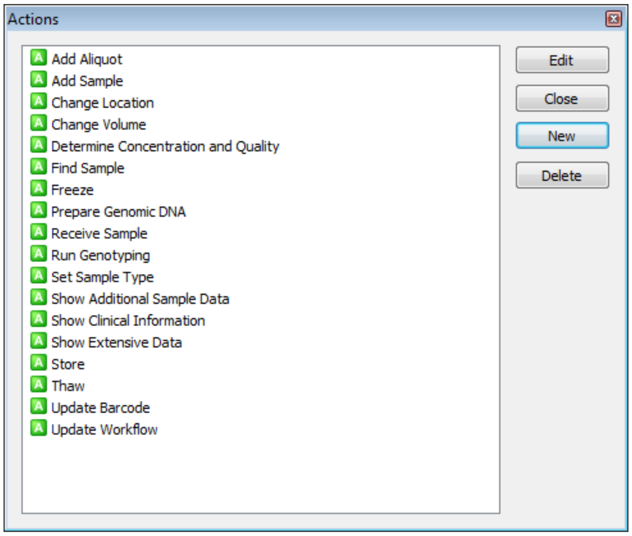
If you delete an action that is part of a workflow, then the action is also deleted from the workflow. You must edit the workflow to accommodate the gap in the workflow. See Chapter 6, "Managing Workflows," on page 535.

To edit an action

1. Open one of the following windows—Inventory, Containers, or Workflows.
2. On the window toolbar, click the Actions button Actions .

   The Actions dialog box opens. This dialog box lists all of the actions that have been defined for the Progeny database that you are logged in to.

Figure 4-11: Actions dialog box



Add Aliquot
Add Sample
Change Location
Change Volume
Determine Concentration and Quality
Find Sample
Freeze
Prepare Genomic DNA
Receive Sample
Run Genotyping
Set Sample Type
Show Additional Sample Data
Show Clinical Information
Show Extensive Data
Store
Thaw
Update Barcode
Update Workflow

3. Select the action that you are deleting (CTRL-click to select multiple actions), and then click Delete.

   A message opens prompting you to delete the selected reactions.
4. Click Yes.

   The message closes. The selected reactions are deleted from the Progeny database.

Chapter 5

Managing Samples

A *sample* is a part that is representative of a whole or a set of elements that is drawn from and analyzed to estimate the characteristics of a population. A sample can be an unassociated sample, or it can be associated with an individual. Managing samples in Progeny LIMS consists of creating new samples, carrying out actions on samples, generating sample reports, assigning samples to workflows and moving a sample through a workflow, modifying samples, deleting samples, importing sample data. In Progeny LIMS, you accomplish all of these tasks through use of actions.

This chapter covers the following topics:

- "Adding a Create Sample Reaction" on page 521.
- "Adding a Create Aliquot Reaction" on page 524.
- "Carrying out Actions on a Sample in the Scan Window" on page 528.
- "Creating a New Sample Datasheet" on page 531.
- "Generating a Chain of Custody Audit Report" on page 532.

For detailed information about importing sample data, see Appendix B, "Importing Clinical Data," on page 559. For detailed information about assigning a sample to a workflow and moving a sample through a workflow, see

Adding a Create Sample Reaction

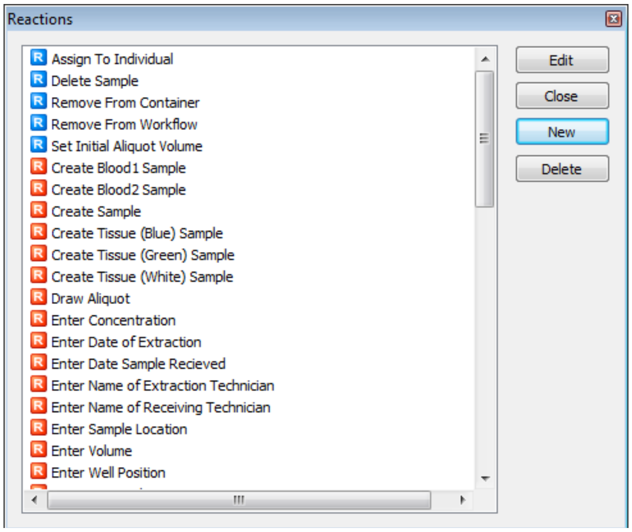
A *reaction* is a system or user-defined trigger that is used to update sample records. A reaction always results in the updating or modifying of a single database field. In Progeny LIMS, you use reactions to create new samples. When you add a reaction for creating new samples, you must also define the naming schema for the samples. You can add a single reaction that simply sequentially numbers all samples as they are added to a Progeny database, or you can add multiple reactions with each reaction creating a different type of sample and each sample type having a unique naming schema. For example, you could add a reaction named Create Blood Samples with a naming schema that results in samples named Blood1, Blood2, Blood3, and so on and you could add a reaction named Create Tissue Samples with a naming schema that results in samples named Tissue1, Tissue2, Tissue3, and so on.

To add a create sample reaction

1. Open one of the following windows—Inventory, Containers, or Workflow.
2. On the window toolbar, click the Reactions button Reactions.

   The Reactions dialog box opens. This dialog box lists all of the reactions that are available in the Progeny database that you are currently logged in to.

Figure 5-1: Reactions dialog box

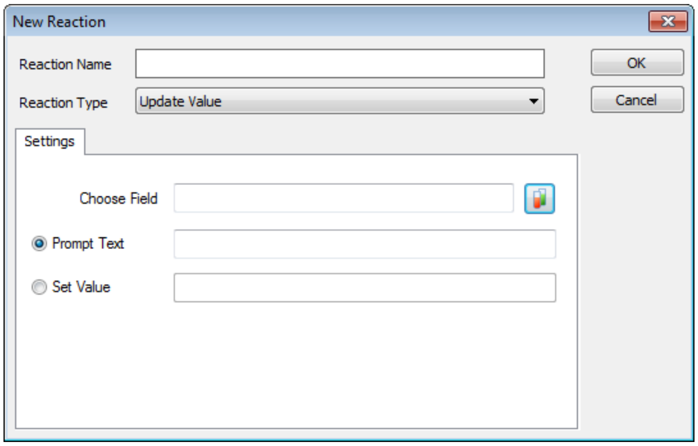


- Assign To Individual
- Delete Sample
- Remove From Container
- Remove From Workflow
- Set Initial Aliquot Volume
- Create Blood1 Sample
- Create Blood2 Sample
- Create Sample
- Create Tissue (Blue) Sample
- Create Tissue (Green) Sample
- Create Tissue (White) Sample
- Draw Aliquot
- Enter Concentration
- Enter Date of Extraction
- Enter Date Sample Recieved
- Enter Name of Extraction Technician
- Enter Name of Receiving Technician
- Enter Sample Location
- Enter Volume
- Enter Well Position

3. Click New.

   The New Reaction dialog box opens.

Figure 5-2: New Reaction dialog box



Reaction Name:

Reaction Type: Update Value

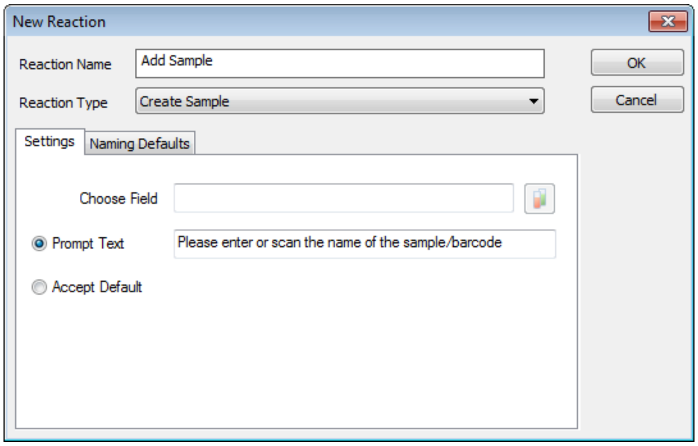
● Prompt Text:

4. In the Reaction Name field, enter an appropriate name such as Add Sample or Create Sample.

5. On the Reaction Type dropdown list, select Create Sample.

   The New Reaction dialog box is refreshed with two tabs—Settings and Naming Defaults. The Settings tab is the active tab.

Figure 5-3: New Reaction dialog box, Settings tab



Reaction Name: Add Sample

Reaction Type: Create Sample

● Prompt Text: Please enter or scan the name of the sample/barcode

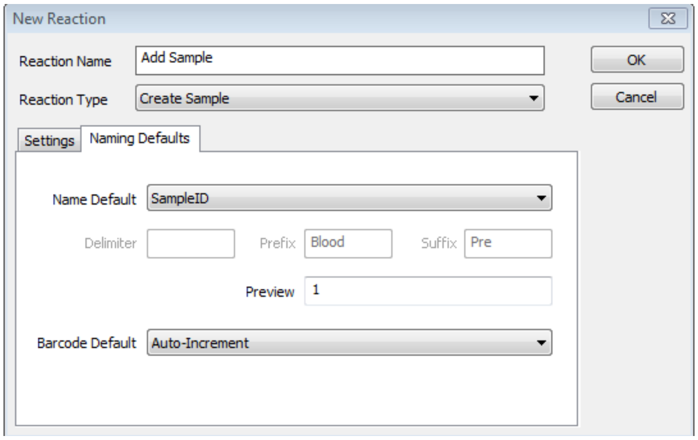
6. Do one of the following:

   - If the sample barcodes were *not* originated in Progeny (that is you are going to scan sample barcodes as the samples are received), then select Prompt Text, and in the Prompt Text field, enter the prompt that is given to a user for adding a new sample.
   - If the sample barcodes originated in Progeny (that is, the sample barcodes are already in the Progeny database), then select Accept Default.

7. Open the Naming Defaults tab, do one of the following to specify the naming scheme for your samples, and then click OK to create the reaction.

   - Leave the Name Default set to SampleID and Barcode Default to Auto-increment to increment every sample that is added to the database. The sample names are simply sequential numbers—1, 2, 3, and so on as shown in the Preview field.

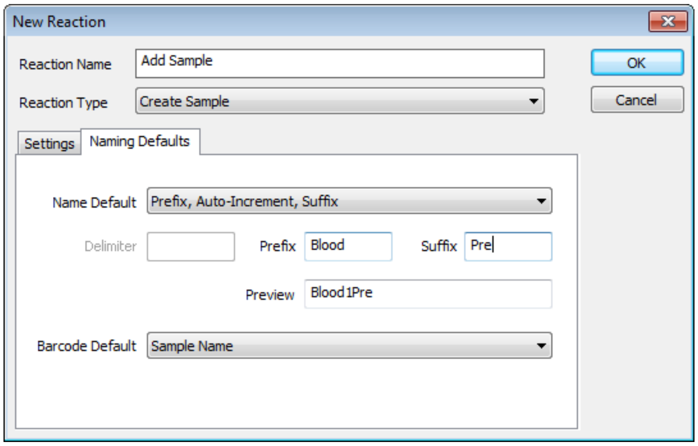
Figure 5-4: New Reaction dialog box, Naming Defaults tab



Reaction Name: Add Sample
Reaction Type: Create Sample
Name Default: SampleID
Delimiter:
Prefix: Blood
Suffix: Pre
Preview: 1
Barcode Default: Auto-Increment

   - Select Prefix, Auto-Increment, Suffix for the Name Default, and select Sample Name for Barcode Default to create a unique barcode naming convention that autoincrements every sample that is added to the database. The sample names are sequentially numbered and are uniquely identified through the use of a prefix and/or suffix, for example, Blood1Pre, Blood2Pre, Blood3Pre, and so on as shown in the Preview field.

Figure 5-5: New Reaction dialog box, Naming Defaults tab



Reaction Name: Add Sample
Reaction Type: Create Sample
Name Default: Prefix, Auto-Increment, Suffix
Delimiter:
Prefix: Blood
Suffix: Pre
Preview: Blood1Pre
Barcode Default: Sample Name

With this approach, you can create multiple reactions with each reaction creating a different type of sample and each sample type having a unique naming schema. For example, you could create a reaction named Create Blood Samples with a naming schema that results in samples named Blood1, Blood2, and so on, and you could create a reaction named Create Tissue Samples with a naming schema that results in samples named Tissue1, Tissue2, and so on.

Adding a Create Aliquot Reaction

A *reaction* is a system or user-defined trigger that is used to update sample records.A reaction always results in the updating or modifying of a single database field. In Progeny LIMS, you use reactions to create new aliquots. When you add a reaction for creating new aliquots, you must also define the naming schema for the aliquots. You can add a single reaction that simply sequentially numbers all aliquots as they are added to a Progeny database, or you can add multiple reactions with each reaction creating a different type of aliquot and each aliquot type having a unique naming schema. For example, you could add a reaction named Create Blood Aliquots with a naming schema that results in samples named Blood1, Blood2, Blood3, and so on and you could add a reaction named Create Serum Aliquots with a naming schema that results in samples named Serum1, Serum2, Serum3, and so on.

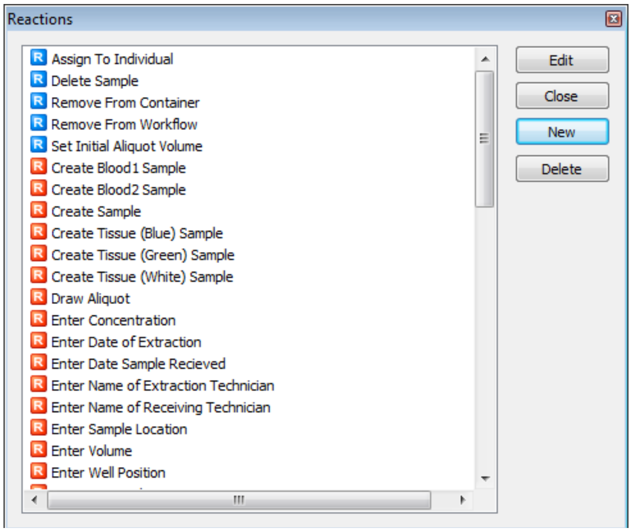
To add a create aliquot reaction

1. Open one of the following windows—Inventory, Containers, or Workflow.

2. On the window toolbar, click the Reactions button Reactions.

   The Reactions dialog box opens. This dialog box lists all of the reactions that are available in the Progeny database that you are currently logged in to.

Figure 5-6: Reactions dialog box



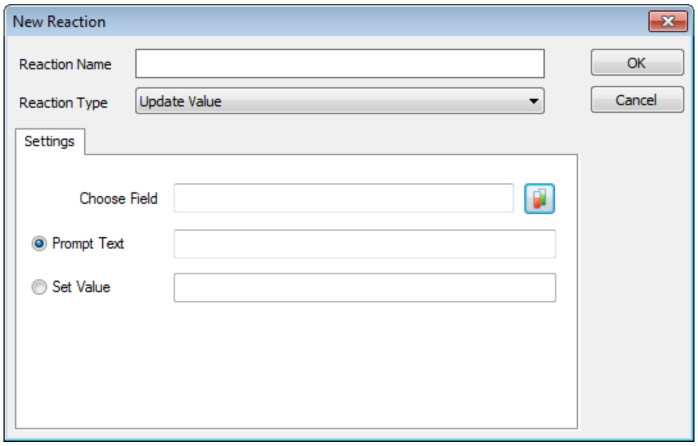
Reactions

- Assign To Individual
- Delete Sample
- Remove From Container
- Remove From Workflow
- Set Initial Aliquot Volume
- Create Blood1 Sample
- Create Blood2 Sample
- Create Sample
- Create Tissue (Blue) Sample
- Create Tissue (Green) Sample
- Create Tissue (White) Sample
- Draw Aliquot
- Enter Concentration
- Enter Date of Extraction
- Enter Date Sample Recieved
- Enter Name of Extraction Technician
- Enter Name of Receiving Technician
- Enter Sample Location
- Enter Volume
- Enter Well Position

3. Click New.

   The New Reaction dialog box opens.

Figure 5-7: New Reaction dialog box



Reaction Name:

Reaction Type: Update Value

● Prompt Text

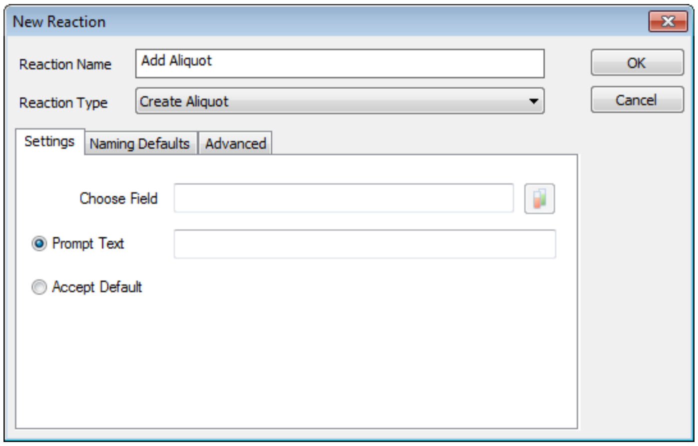
○ Set Value

4. In the Reaction Name field, enter an appropriate name such as Add Aliquot or Create Aliquot.

5. On the Reaction Type dropdown list, select Create Aliquot.

   The New Reaction dialog box is refreshed with three tabs—Settings, Naming Defaults, and Advanced. The Settings tab is the active tab.

Figure 5-8: New Reaction dialog box, Settings tab



Reaction Name: Add Aliquot

Reaction Type: Create Aliquot

● Prompt Text

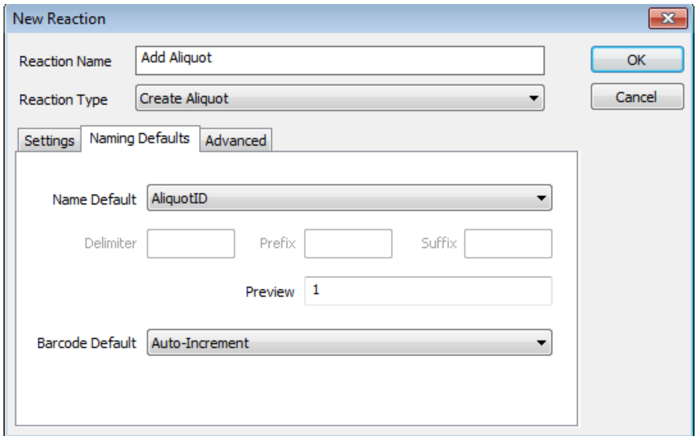
○ Accept Default

6. Do one of the following:

   - If the sample barcodes were *not* originated in Progeny (that is you are going to scan sample barcodes as the samples are received), then select Prompt Text, and in the Prompt Text field, enter the prompt that is given to a user for adding a new sample.
   - If the sample barcodes originated in Progeny (that is, the sample barcodes are already in the Progeny database), then select Accept Default.

7. Open the Naming Defaults tab, and then do one of the following to specify the naming scheme for your samples.
   - Leave the Name Default set to SampleID and Barcode Default to Auto-increment to increment every sample that is added to the database. The sample names are simply sequential numbers—1, 2, 3, and so on as shown in the Preview field.

Figure 5-9: New Reaction dialog box, Naming Defaults tab



New Reaction

Reaction Name: Add Aliquot

Reaction Type: Create Aliquot

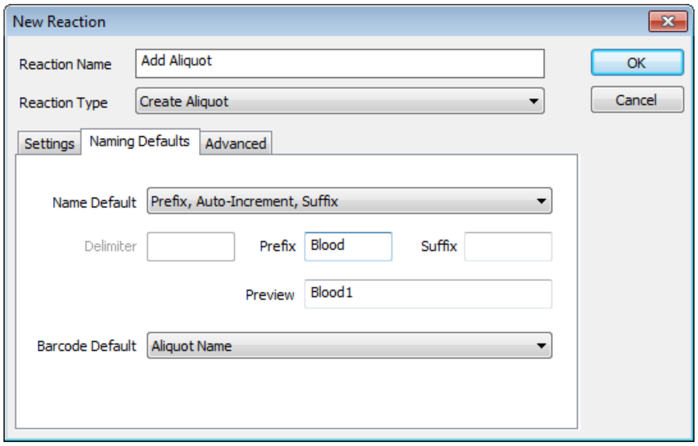
Name Default: AliquotID

Preview: 1

Barcode Default: Auto-Increment

   - Select Prefix, Auto-Increment, Suffix for the Name Default, and select Aliquot Name for Barcode Default to create a unique barcode naming convention that autoincrements every sample that is added to the database. The sample names are sequentially numbered and are uniquely identified through the use of a prefix and/or suffix, for example, Blood1, Blood2, Blood3, and so on as shown in the Preview field.

Figure 5-10: New Reaction dialog box, Naming Defaults tab



New Reaction

Reaction Name: Add Aliquot

Reaction Type: Create Aliquot

Name Default: Prefix, Auto-Increment, Suffix

Prefix: Blood

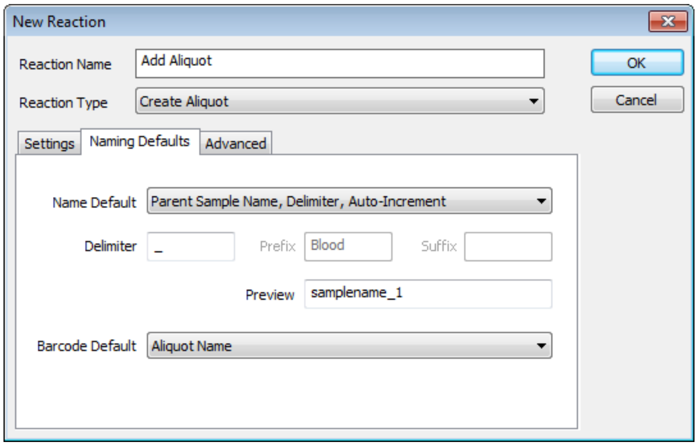
Preview: Blood1

Barcode Default: Aliquot Name

With this approach, you can create multiple reactions with each reaction creating a different type of aliquot and each aliquot type having a unique naming schema. For example, you could create a reaction named Create Blood Aliquots with a naming schema that results in samples named Blood1, Blood2, Blood3, and so on and you could create a reaction named Create Serum Aliquots with a naming schema that results in samples named Serum1, Serum2, Serum3, and so on.

- Select Parent Sample Name, Delimiter, Auto-Increment and select Aliquot Name for Barcode Default to create a unique barcode naming convention that autoincrements every sample that is added to the database. The sample names are sequentially numbered and are uniquely identified through the use of the parent name and a delimiter, for example, SampleParentName_1, SampleParent_2, SampleName_3, and so on as shown in the Preview field.

Figure 5-11: New Reaction dialog box, Naming Defaults tab

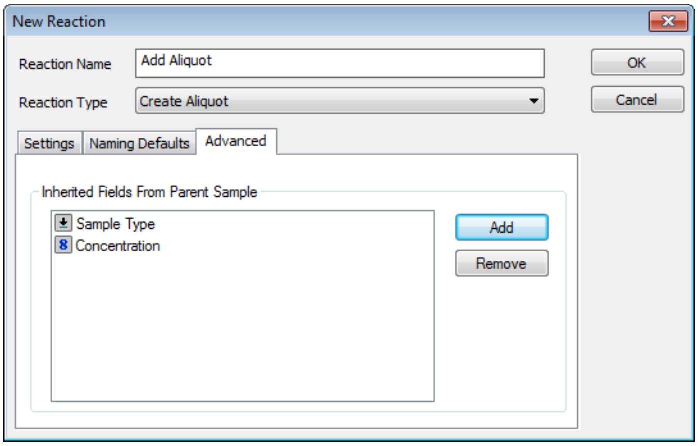


Reaction Name: Add Aliquot
Reaction Type: Create Aliquot
Name Default: Parent Sample Name, Delimiter, Auto-Increment
Delimiter: _
Prefix: Blood
Suffix:
Preview: samplename_1
Barcode Default: Aliquot Name

With this approach, you can create multiple reactions with each reaction creating a different type of aliquot and each aliquot type having a unique naming schema based on the parent sample name.

8. Open the Advanced tab, and then click Add to open the Select Fields dialog box to select the data fields that the aliquot is to inherit from the parent sample.

Figure 5-12: New Reaction dialog box, Advanced tab



Reaction Name: Add Aliquot
Reaction Type: Create Aliquot
Inherited Fields From Parent Sample
Sample Type
Concentration

9. Click OK to add the new reaction.

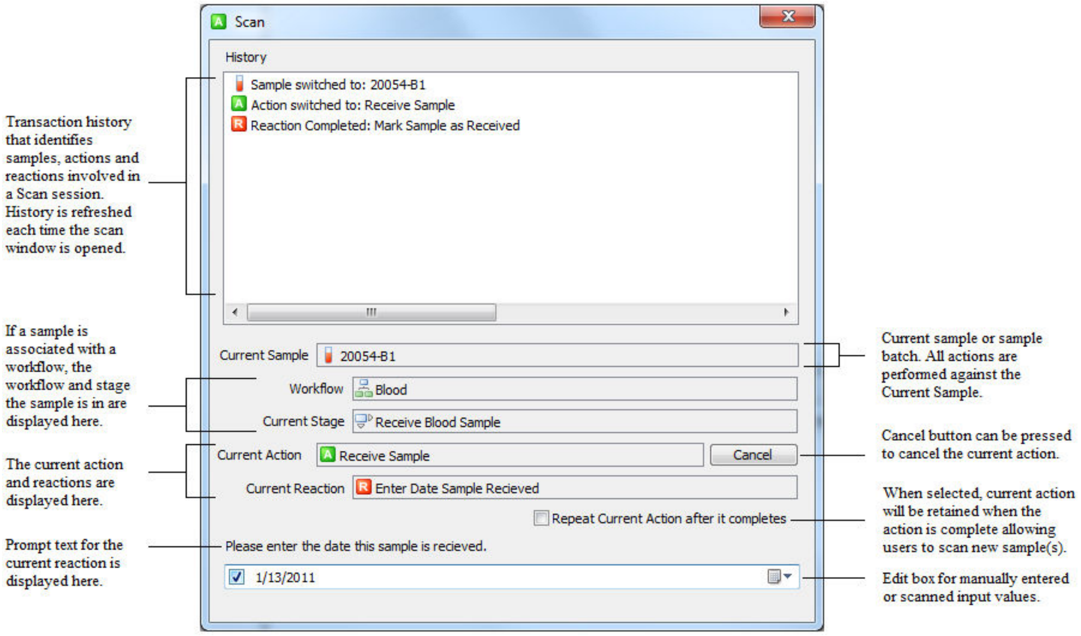
Carrying out Actions on a Sample in the Scan Window

An *action* is a series of reactions. An action can be carried out on a single sample, a batch of samples, or a container of samples, including plates. All of the reactions that are contained in an action must be carried out successfully for the action to be completed. In Progeny LIMS, you carry out actions on a sample, either standalone, or when it is included in workflow stages, in the *Scan window*. You can open the Scan window in one of three ways:

- By clicking the Scan button Scan on the toolbar for the Samples, Inventory, Workflows, or Containers windows.
- By right-clicking on a selected sample, a batch of samples, or a container, including plates, and on the context menu that opens, clicking Actions, and then selecting an action.
- By selecting a sample, a batch of samples, or a container, including plates, and then entering the appropriate Hotkey combination (for example, CTRL + s) for an action.

The Scan window displays critical information about a sample, including its history, the sample or sample batch number, and the current sample action and reaction. The Scan window also contains options for canceling the current action, retaining the current action, and manually entering or scanning action barcodes. After your LIMS implementation is completely operational, you can limit your interaction with Progeny solely to this window.

Figure 5-13: Scan window



Sample switched to: 20054-B1
Action switched to: Receive Sample
Reaction Completed: Mark Sample as Received

Current Sample: 20054-B1
Workflow: Blood
Current Stage: Receive Blood Sample
Current Action: Receive Sample
Current Reaction: Enter Date Sample Recieved

☐ Repeat Current Action after it completes

Please enter the date this sample is recieved.

☑ 1/13/2011

Transaction history that identifies samples, actions and reactions involved in a Scan session. History is refreshed each time the scan window is opened.

If a sample is associated with a workflow, the workflow and stage the sample is in are displayed here.

The current action and reactions are displayed here.

Prompt text for the current reaction is displayed here.

Current sample or sample batch. All actions are performed against the Current Sample.

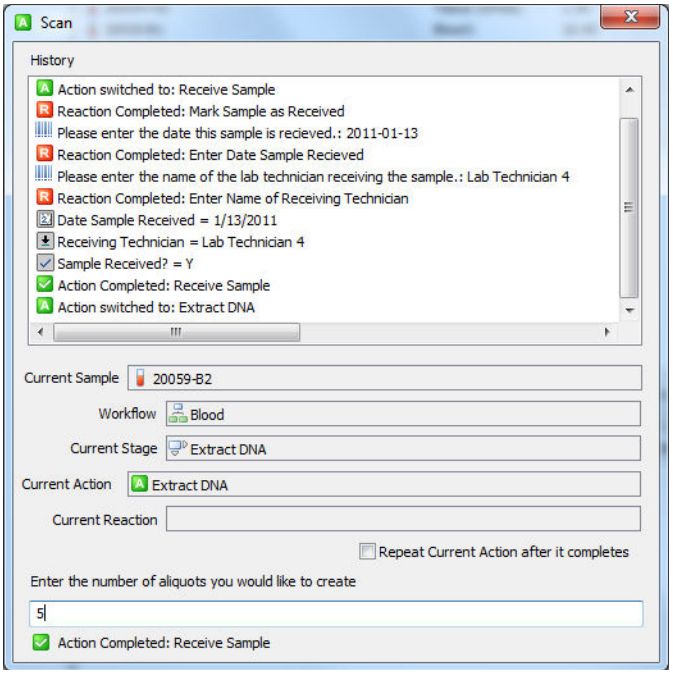
Cancel button can be pressed to cancel the current action.

When selected, current action will be retained when the action is complete allowing users to scan new sample(s).

Edit box for manually entered or scanned input values.

Figure 5-14 and Figure 5-15 below show actions being carried out on a single sample in the Scan window and for a batch of samples in the Scan window. Both windows show the history of an action being carried out from beginning to end. In addition, Figure 5-14 shows that multiple actions can be carried out for samples in a single Scan session. You do not have to open a Scan window for each action that you want to carry out on a sample.

Figure 5-14: Carrying out multiple actions for a single sample in the Scan window



History

Action switched to: Receive Sample
Reaction Completed: Mark Sample as Received
Please enter the date this sample is recieved.: 2011-01-13
Reaction Completed: Enter Date Sample Recieved
Please enter the name of the lab technician receiving the sample.: Lab Technician 4
Reaction Completed: Enter Name of Receiving Technician
Date Sample Received = 1/13/2011
Receiving Technician = Lab Technician 4
Sample Received? = Y
Action Completed: Receive Sample
Action switched to: Extract DNA

Current Sample: 20059-B2
Workflow: Blood
Current Stage: Extract DNA
Current Action: Extract DNA
Current Reaction:

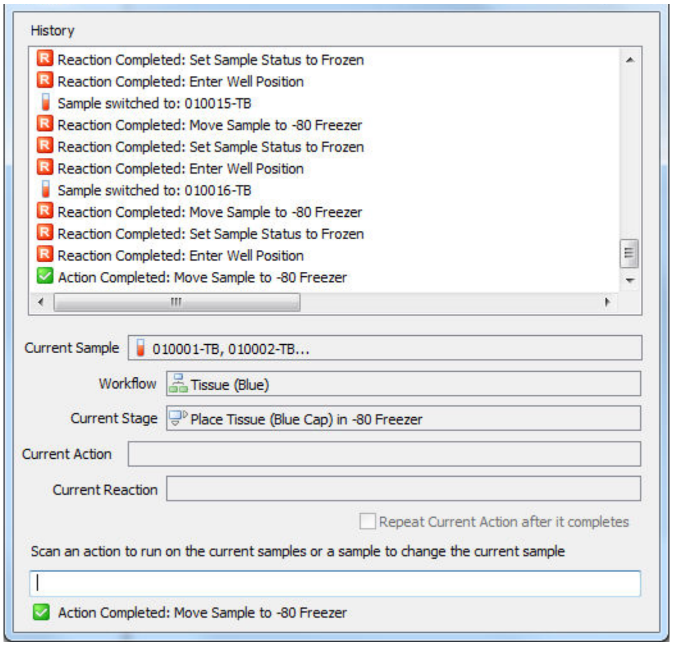
☐ Repeat Current Action after it completes

Enter the number of aliquots you would like to create

5

Action Completed: Receive Sample

Figure 5-15: Carrying out an action for a batch of samples in the Scan window



History

Reaction Completed: Set Sample Status to Frozen
Reaction Completed: Enter Well Position
Sample switched to: 010015-TB
Reaction Completed: Move Sample to -80 Freezer
Reaction Completed: Set Sample Status to Frozen
Reaction Completed: Enter Well Position
Sample switched to: 010016-TB
Reaction Completed: Move Sample to -80 Freezer
Reaction Completed: Set Sample Status to Frozen
Reaction Completed: Enter Well Position
Action Completed: Move Sample to -80 Freezer

Current Sample: 010001-TB, 010002-TB...
Workflow: Tissue (Blue)
Current Stage: Place Tissue (Blue Cap) in -80 Freezer
Current Action:
Current Reaction:

☐ Repeat Current Action after it completes

Scan an action to run on the current samples or a sample to change the current sample

Action Completed: Move Sample to -80 Freezer

For assistance with setting up Scan modes for your samples, contact http://www.progenygenetics.com/support/support_contact.html.

Creating a New Sample Datasheet

You use a sample datasheet to *manually* enter and store data for a sample in a Progeny database. All the samples that are assigned to a sample data folder can use the same datasheet format, or each sample in the folder can use a unique datasheet format. You can create and format a sample datasheet at the time that you add a sample to a data folder, or at a later date.

To create a sample datasheet

1. Create a sample data folder.

   If all the samples that are assigned to the folder are to use the same sample datasheet format, make sure to select the Make this folder a template folder option; otherwise, clear it. See "Adding Sample Data Folders" on page 206.

2. Do one of the following:

   - Create a new sample and add the sample to the data folder. Double-click on the sample in the folder to open a blank datasheet and format the datasheet as needed. If the Make this folder a template folder option has been selected for the data folder, then all the samples that you subsequently add to the folder will use the same datasheet format for entering and storing data; otherwise, you must format a datasheet for each sample that you add to the folder.

   - Add all the needed samples to the data folder. After you have added all of the needed samples to the folder, double-click on any sample in the folder to open a blank datasheet and format the datasheet as needed. If the Make this folder a template folder option has been selected for the data folder, then all samples that are currently added to the folder or that you subsequently add to the folder will use this same datasheet format for entering and storing data; otherwise, you must format a datasheet for each sample in the folder.

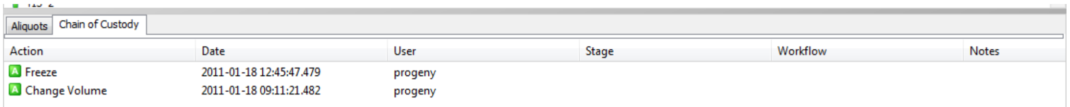
If data has been added to a sample through an action, and the database field that holds this data has been added to the sample datasheet (for example, Sample Type), then when you open the sample datasheet, this field is already populated with the data (for example, Frozen or Thawed).

See "Creating and Formatting Datasheets" on page 86 for detailed information about creating and formatting a sample datasheet.

Generating a Chain of Custody Audit Report

When you are creating an action, you have the option of including the action in the *chain of custody*. The chain of custody is an action audit trail. Any action that has been marked for inclusion in the chain of custody is timestamped with the time that the action was carried out, the name of the user (user name) who carried out the action, the action ID, and if the sample is included in a workflow, the workflow stage ID and the workflow ID. You can generate a chain of custody for every sample in a Progeny database. This information is displayed on the Chain of Custody tab on the Samples window and on the Inventory window.

Figure 5-16: Chain of Custody tab



Action	Date	User	Stage	Workflow	Notes
Freeze	2011-01-18 12:45:47.479	progeny			
Change Volume	2011-01-18 09:11:21.482	progeny			

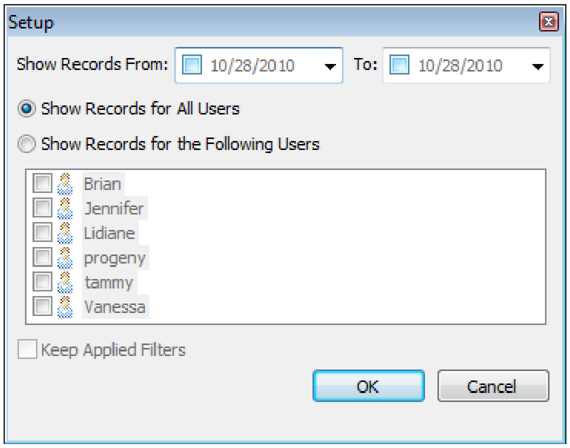
You can generate a Chain of Custody Audit report to filter the Chain of Custody records for every sample in a Progeny database.

To generate a Chain of Custody Audit report

1. Open the Samples or Inventory window, and on the main menu, click Administration > Chain of Custody Audit.

   The Setup dialog box opens.

Figure 5-17: Setup dialog box



Show Records From: ☐ 10/28/2010 To: ☐ 10/28/2010

● Show Records for All Users

○ Show Records for the Following Users

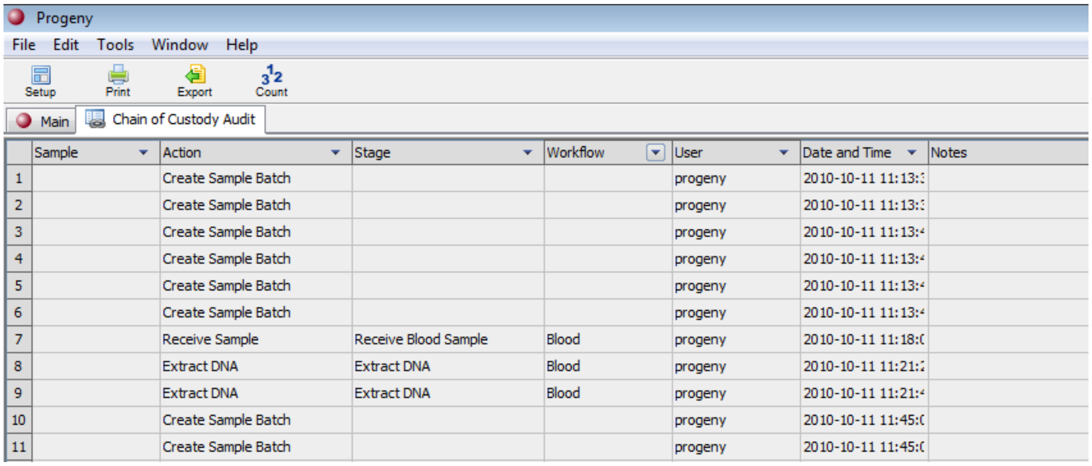
☐ Brian
☐ Jennifer
☐ Lidiane
☐ progeny
☐ tammy
☐ Vanessa

☐ Keep Applied Filters

2. Set the report filtering options:
    - Date—The default value for both the From and To dates is the current day's date. Select a From date and/or a To date. Leave both date fields blank to retrieve all records in the database. Leave date field blank to have the results be open-ended. For example, if you enter a From date and leave the To date empty, all records that were generated between the From date and the current day's date are retrieved.
    - User—The default value is to show the records for all users. You can select Show Records for the following users, and then select the specific users for whom to retrieve the records.
3. Click OK.

    The Chain of Custody Audit report is generated onscreen in a spreadsheet format.

Figure 5-18: Chain of Custody Audit report



	Sample	Action	Stage	Workflow	User	Date and Time	Notes
1		Create Sample Batch			progeny	2010-10-11 11:13:	
2		Create Sample Batch			progeny	2010-10-11 11:13:	
3		Create Sample Batch			progeny	2010-10-11 11:13:	
4		Create Sample Batch			progeny	2010-10-11 11:13:	
5		Create Sample Batch			progeny	2010-10-11 11:13:	
6		Create Sample Batch			progeny	2010-10-11 11:13:	
7		Receive Sample	Receive Blood Sample	Blood	progeny	2010-10-11 11:18:	
8		Extract DNA	Extract DNA	Blood	progeny	2010-10-11 11:21:	
9		Extract DNA	Extract DNA	Blood	progeny	2010-10-11 11:21:	
10		Create Sample Batch			progeny	2010-10-11 11:45:	
11		Create Sample Batch			progeny	2010-10-11 11:45:	

4. Optionally, after you generate an Chain of Custody Audit report, you can do one or more of the following:
    - Sort and/or filter the audit data. See "Sorting and Filtering Spreadsheet Data" on page 126.
    - Click the Setup button Setup to open the Audit setup dialog box, modify the report settings, and generate the report again.
    - Click the Print button Print to print the Audit report.
    - Click the Export button Export to export the Audit report. See "Exporting Spreadsheet Data" on page 117.
    - Click the Count button Count to count the number of individuals, pedigrees, or samples (that is, the number of rows) in the spreadsheet. See "Counting Spreadsheet Data" on page 130.

Chapter 6
Managing Workflows

Workflow—A *workflow*, (also referred to as a *sample workflow*) is a collection of actions that have been arranged into a step-by-step procedure. A workflow is made up of multiple stages, with each stage associated with exactly one action. After a sample is placed into a workflow, the movement of the sample from one stage to the next can be tracked and recorded until the sample is ultimately exhausted and removed from the workflow. Managing a workflow includes creating, modifying, and deleting workflows, assigning a sample to a workflow, and moving a sample through a workflow.

This chapter covers the following topics:

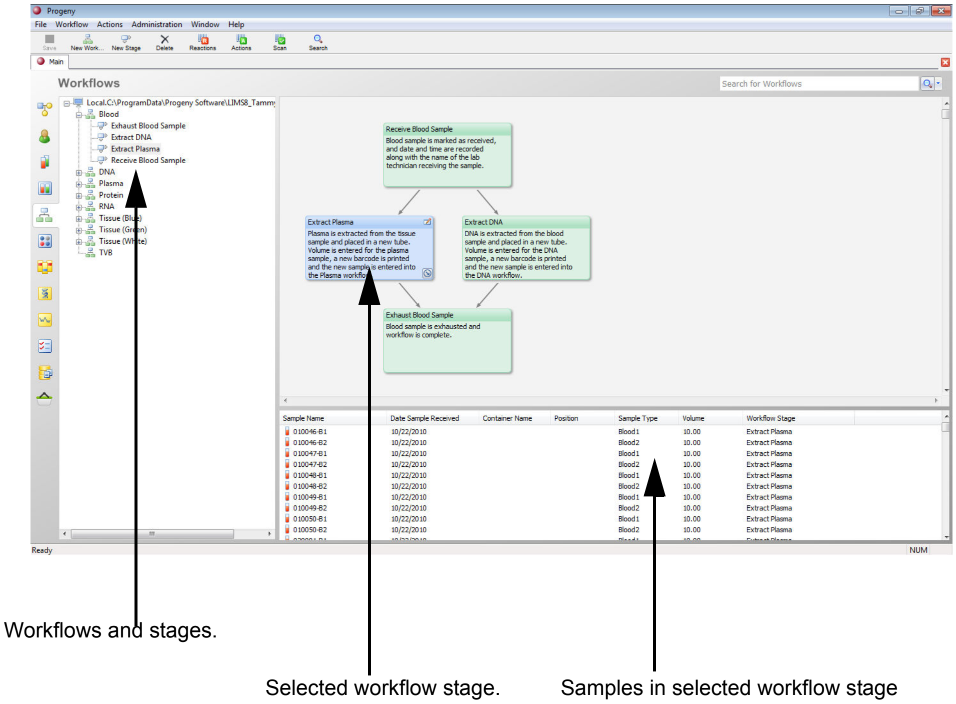
- “Workflows Window” on page 537.
- “Creating a New Workflow” on page 538.
- “Setting Workflow Security” on page 542.
- “Modifying and Deleting a Workflow Stages” on page 544.
- “Deleting a Workflow” on page 545.
- “Assigning a Sample to a Workflow” on page 546.
- “Moving Samples through a Workflow” on page 548.

Workflows Window

The Workflow function in Progeny allows you to create a workflow that outlines the path that a sample must take as it is moved through a laboratory. You have full control to decide the stages the sample must pass through and the action to be carried out on sample at each stage of the workflow. The Workflows window displays information about every workflow that you have created in a Progeny database.

- The left pane in the Workflows window lists all the workflows that are available in a Progeny database. Select a workflow to view all the stages associated with a workflow.
- The top right pane is a graphical representation of a workflow, or a *workflow drawing*, with each stage identified in a green square. By default, the first time that you select a workflow in the left pane, all the samples that are assigned to a workflow are displayed in the bottom right pane of the window. To view only those samples in a specific stage, select the stage. The selected stage is highlighted in blue, and all the samples that are assigned to the stage are displayed in the bottom right pane of the window.

Figure 6-1: Workflows window



Receive Blood Sample
Blood sample is marked as received, and date and time are recorded along with the name of the lab technician receiving the sample.

Extract Plasma
Plasma is extracted from the tissue sample and placed in a new tube. Volume is entered for the plasma sample, a new barcode is printed and the new sample is entered into the Plasma workflow.

Extract DNA
DNA is extracted from the blood sample and placed in a new tube. Volume is entered for the DNA sample, a new barcode is printed and the new sample is entered into the DNA workflow.

Exhaust Blood Sample
Blood sample is exhausted and workflow is complete.

Sample Name	Date Sample Received	Container Name	Position	Sample Type	Volume	Workflow Stage
010046-B1	10/22/2010			Blood1	10.00	Extract Plasma
010046-B2	10/22/2010			Blood2	10.00	Extract Plasma
010047-B1	10/22/2010			Blood1	10.00	Extract Plasma
010047-B2	10/22/2010			Blood2	10.00	Extract Plasma
010048-B1	10/22/2010			Blood1	10.00	Extract Plasma
010048-B2	10/22/2010			Blood2	10.00	Extract Plasma
010049-B1	10/22/2010			Blood1	10.00	Extract Plasma
010049-B2	10/22/2010			Blood2	10.00	Extract Plasma
010050-B1	10/22/2010			Blood1	10.00	Extract Plasma
010050-B2	10/22/2010			Blood2	10.00	Extract Plasma

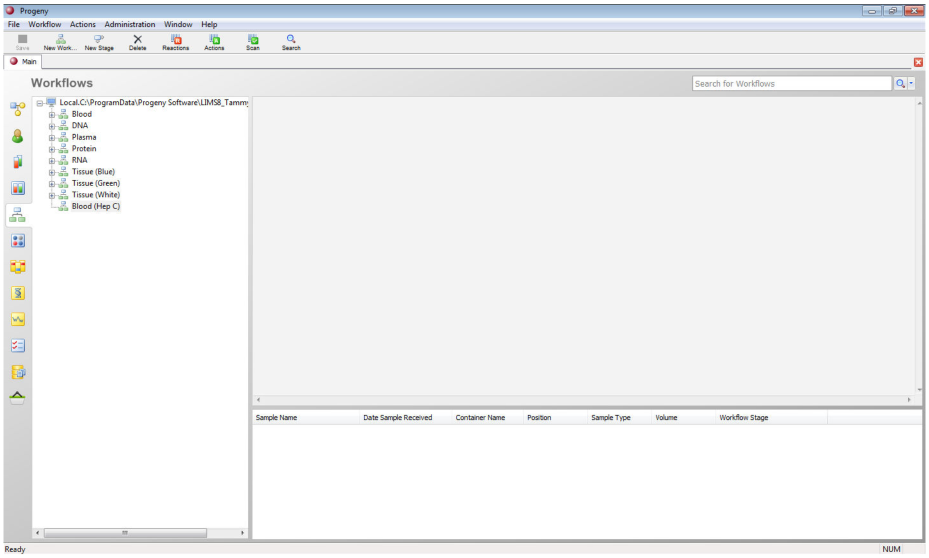
Creating a New Workflow

Creating a new workflow consists of three steps—naming the workflow, adding stages to the workflow, and connecting the workflow stages.

To name a workflow

1. On the Progeny main window navigation bar, click the Workflows button to open the Workflows window.

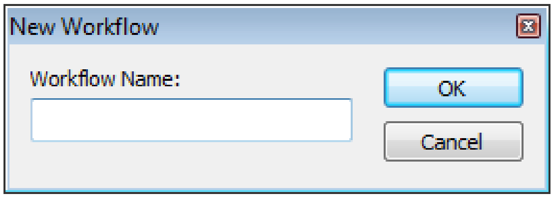
Figure 6-2: Workflows window



2. On the window toolbar, click the New Workflow button New Work...

   The New Workflow dialog box opens.

Figure 6-3: New Workflow dialog box



3. Enter a name for the new workflow, and then click OK.

   The New Workflow dialog box closes. The new workflow is displayed in the right pane of the Workflows window and by default, it is the selected workflow.

4. Continue to "To add stages to a workflow" on page 539.

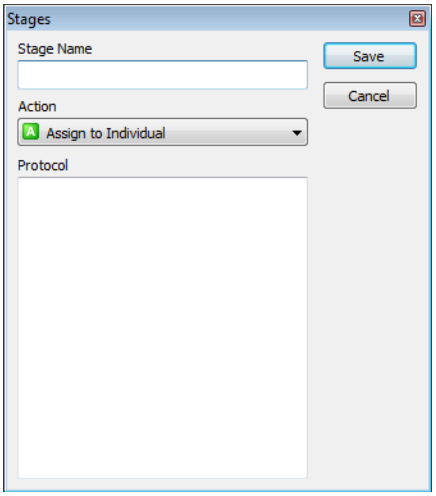
To add stages to a workflow

1. If you have not already done so, open the Workflows window and select the workflow to which you are adding the stages.

2. On the window toolbar, click the New Stage button New Stage .

   The Stages dialog box opens.

Figure 6-4: Stages dialog box



Action

Assign to Individual

3. Enter the name for the stage and on the Action dropdown list, select the action for the stage.

4. Optionally, in the Protocol field, enter a description about the stage.

The stage name and protocol are displayed on the workflow graphic in the right pane of the Workflows window.

5. Click Save.

6. Repeat Step 2 through Step 5 until you have added all the necessary stages for the workflow.

7. Continue to “To connect workflow stages” on page 540.

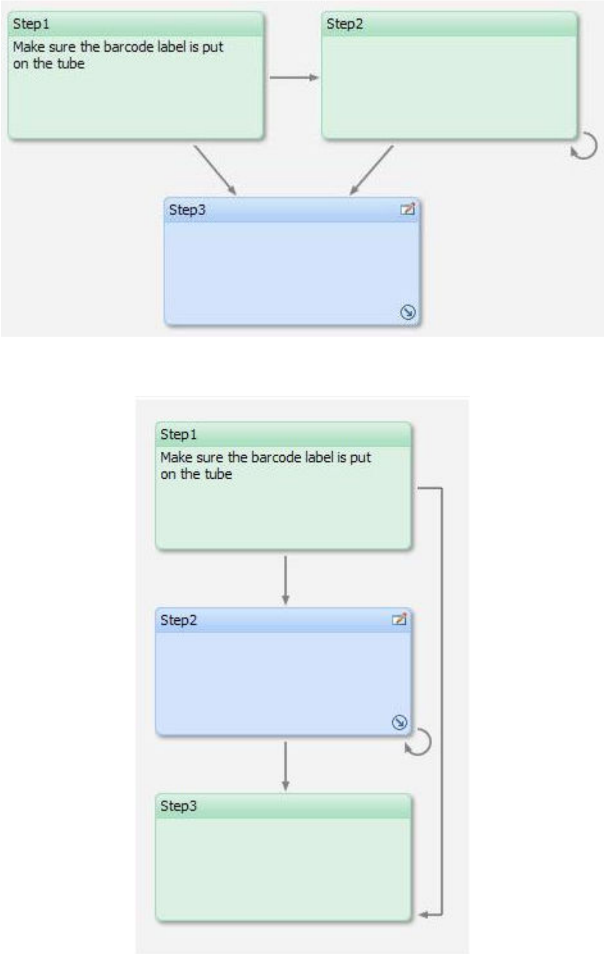
To connect workflow stages

1. If you have not already done so, open the Workflows window and select the workflow for which you are connecting the stages.
2. Connect or disconnect the stages as needed doing one or more of the following:
   - To connect one stage to another stage, click and drag the Arrow icon in the lower right corner.

When you are connecting workflow stages, you can connect them horizontally, vertically, or use a combination of these. Figure 6-5 below illustrates this concept. Both workflows that are shown are identical.

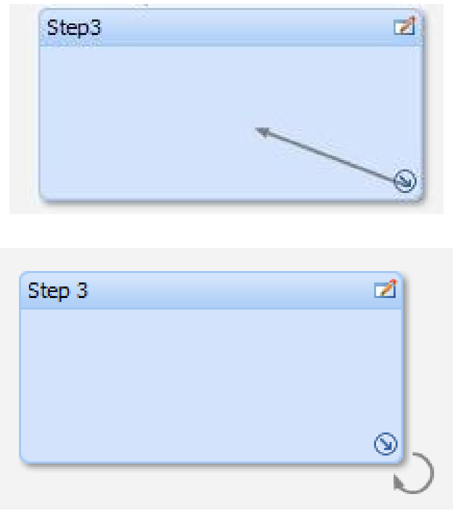
Figure 6-5: Workflow orientation

- Step1 is the only starting point of the workflow. When a sample is assigned to the workflow, Step1 is the first Next Stage.
- Step1 has Next Stages of Step2 or Step3.
- Step2 has Next Stages of Step2 or Step3.
- Step3 is the conclusion of the workflow.



- To indicate that a stage is to be repeated, click and drag the Arrow icon for the stage to the center of the stage graphic. The Arrow icon changes to a Repeat icon.

Figure 6-6: Indicating that the workflow stage is to be repeated



- To disconnect a stage, repeat the action that connected the two stages. For example, if you connected Stage 1 to Stage 2, and decide that you need to disconnect Stage 1 from Stage 2, simply repeat the action for connecting Stage 1 and Stage 2 and the stages are disconnected. To remove the Repeat indication from a stage, simply click and drag the Arrow icon for the stage to the center of the stage graphic icon again.

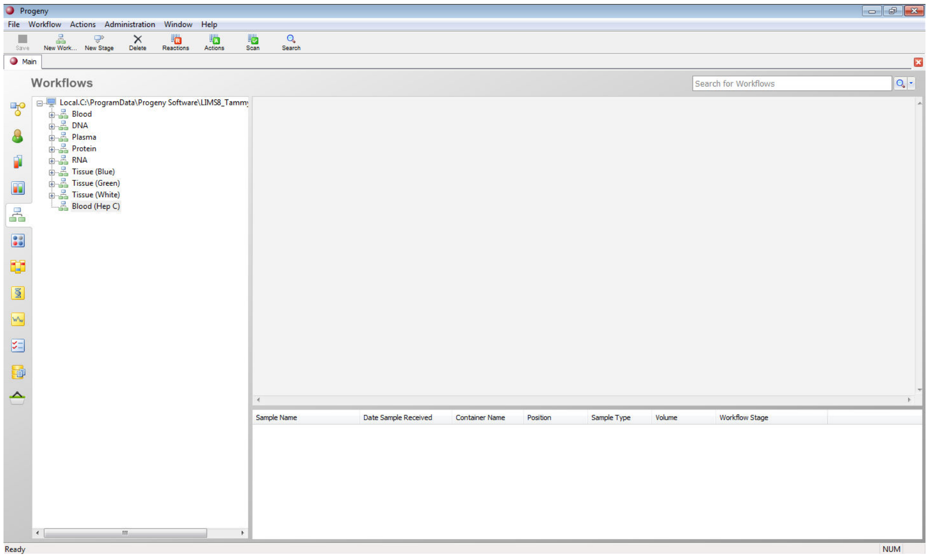
Setting Workflow Security

As the Progeny administrator, you can set the security for a workflow.

To set security for a workflow

1. On the Progeny main window navigation bar, click the Workflows button to open the Workflows window.

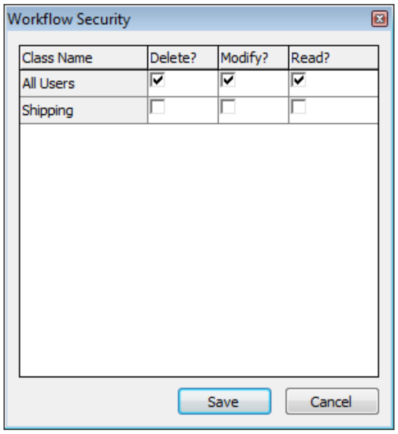
Figure 6-7: Workflows window



2. Right-click on the workflow for which you are setting the security and click Security Settings.

   The Workflow Security dialog box opens. This dialog box lists all the classes of users that have been defined for the database that you are logged in to.

Figure 6-8: Workflow Security dialog box



Class Name	Delete?	Modify?	Read?
All Users	☑	☑	☑
Shipping	☐	☐	☐

3. Modify the security for All Users or for the different classes of users.
   - Delete?—The users can delete the workflow and/or stages n the workflow.
   - Modify?—The users can modify the workflow and/or stages in the workflow.
   - Read?—The users can carry out the workflow.
4. Click OK.

Modifying and Deleting a Workflow Stages

If your administrator has assigned you the correct security, you can modify workflow stages even if samples are currently assigned to the stage. As the Progeny administrator, you can always modify workflow stages even if samples are currently assigned to the stage. If your administrator has assigned you the correct security, you can delete a workflow stages if no samples are assigned to the stage. As the Progeny administrator, you can always delete a workflow stages if no samples are assigned to the stage. If samples are assigned to a stage, you must first move all of the samples that are in the stage onto the next stage.

To modify a workflow stage

1. On the Progeny main window navigation bar, click the Workflows button to open the Workflows window.
2. Select the workflow for which you are modifying the stage.

   The workflow drawing is displayed in the top right pane of the window.
3. Click the Edit button in the upper right hand corner of the stage that you are modifying.

   The Stage dialog box opens.
4. Modify the information as needed for the stage, and then click Save.

To delete a stage

1. On the Progeny main window navigation bar, click the Workflows button to open the Workflows window.
2. Select the workflow for which you are deleting the stage.

   The workflow drawing is displayed in the top right pane of the window.
3. Select the stage that you are deleting either in the workflow drawing, or in the right pane of the Workflows window, and then click the Delete button on the window toolbar.

   A message opens asking you if you are sure that you want to delete the stage.
4. Click Yes.

   The messages closes and the stage is deleted.

Deleting a Workflow

If your administrator has assigned you the correct security, you can delete a workflow only if there are no samples assigned to the workflow, or if no samples are currently being moved through the workflow. As the Progeny administrator, you can always delete a workflow only if there are no samples assigned to the workflow, or if no samples are currently being moved through the workflow. If samples are assigned to the workflow, you must first remove the samples from the workflow, or move the samples through the workflow to complete the workflow.

To delete a workflow

1. On the Progeny main window navigation bar, click the Workflows button to open the Workflows window.
2. Select the workflow that you are deleting.
3. On the window toolbar, click the Delete button .

   A message opens asking you if you are sure that you want to delete the workflow.
4. Click Yes.

   The messages closes and the workflow is deleted.

Assigning a Sample to a Workflow

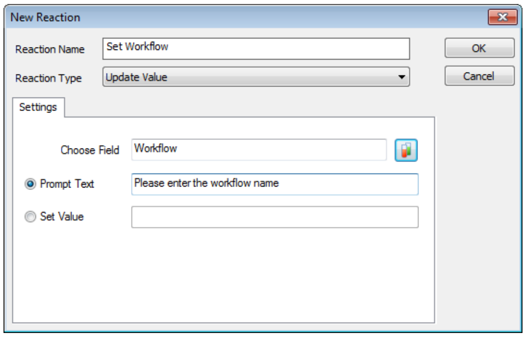
After you have created a workflow, you can assign the needed samples to the workflow. To assign a sample to a workflow you must first create an Update Workflow reaction. After you create this action, you can use it repeatedly to assign any number of samples to any workflow.

To assign a sample to a workflow

1. Add a reaction named Set Workflow. See “Adding a Reaction” on page 498.

Workflow is a system field.

Figure 6-9: Adding the Set Workflow reaction



New Reaction

Reaction Name: Set Workflow

Reaction Type: Update Value

Settings

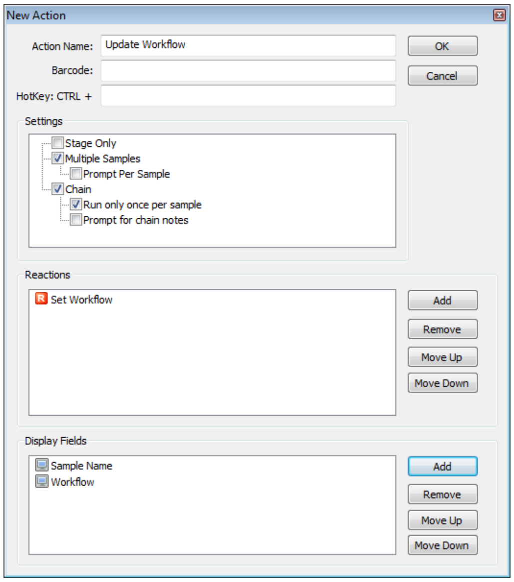
Choose Field: Workflow

● Prompt Text: Please enter the workflow name

○ Set Value:

2. Add an action named Update Workflow that includes the Set Workflow reaction. See “Adding an Action” on page 507.

Figure 6-10: Adding the Update Workflow action



New Action

Action Name: Update Workflow

Barcode:

HotKey: CTRL +

Settings

- ☐ Stage Only
- ☑ Multiple Samples
  - ☐ Prompt Per Sample
- ☑ Chain
  - ☑ Run only once per sample
  - ☐ Prompt for chain notes

Reactions

- Set Workflow

Display Fields

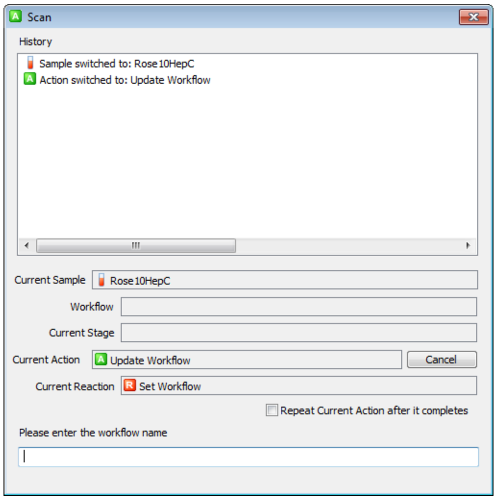
- Sample Name
- Workflow

3. Open the Inventory or Samples window and locate the sample that you are adding to the workflow.

4. Right-click on the sample, and on the context menu that opens, click Actions > Update Workflow.

   The Scan dialog box opens. The cursor is located in the field that prompts you to enter the workflow name.

Figure 6-11: Scan dialog box for adding a sample to a workflow



Sample switched to: Rose10HepC
Action switched to: Update Workflow

Current Sample: Rose10HepC
Workflow:
Current Stage:
Current Action: Update Workflow
Current Reaction: Set Workflow
☐ Repeat Current Action after it completes

5. Enter the name of the workflow, and then press [Enter] on your keyboard.

   The Scan dialog box is refreshed with the message Action Completed: Update Workflow. The sample can now be moved through the stages of the workflow. See "Moving Samples through a Workflow" on page 548.

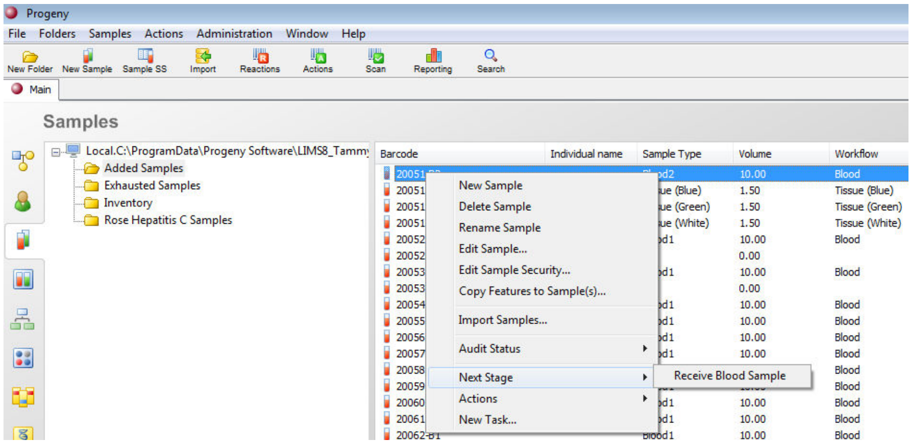
You must enter the name exactly as it is shown on the Workflows window (including capitalization and spacing) or an error message opens indicating that the workflow does not exist.

Moving Samples through a Workflow

Three options are available to you for moving a sample or a batch of samples through a workflow. If actions that are marked with “Chain” are carried out on sample, then the Chain of Custody for the sample is updated as the sample moves through the workflow.

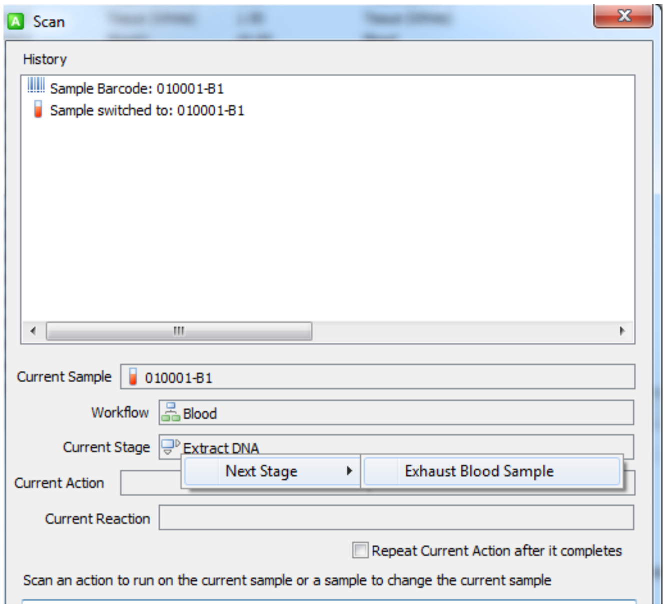
- From *any* window that displays samples (Individuals window, Pedigrees window, Samples window, and so on), right-click on the sample (CTRL-click to select multiple samples), and on the context menu that opens, click Next Stage, and then select the appropriate workflow stage.

Figure 6-12: Moving a sample through a workflow from the Samples window



- Open the Scan window, scan or enter the sample or container barcode, and then, right-click in the Current Stage field, and on the Next Stage dropdown list that opens, select the appropriate stage for the samples.

Figure 6-13: Moving a sample through a workflow from the Scan window



Sample Barcode: 010001-B1
Sample switched to: 010001-B1

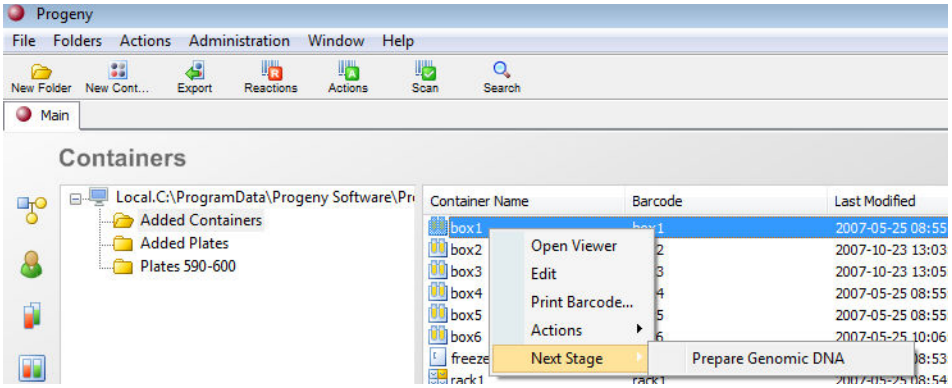
Current Sample: 010001-B1
Workflow: Blood
Current Stage: Extract DNA
Current Action:
Current Reaction:

☐ Repeat Current Action after it completes

Scan an action to run on the current sample or a sample to change the current sample

- On the Containers window, right-click on a container, and on the context menu that opens, click Next Stage, and then select the appropriate workflow stage.

Figure 6-14: Moving a sample batch through a workflow from the Containers window



Any action that is to be carried out on a container must be identified as a batch action.

Appendix A
System Fields

System fields are read-only fields that Progeny automatically stores for a record. Each record type (individual, pedigree, sample, and marker) has its own unique system fields.

This appendix covers the following topics:

- "Individual System Fields" on page 553.
- "Pedigree System Fields" on page 555.
- "Sample System Fields" on page 556.
- "Marker System Fields" on page 558.

Individual System Fields

Field Name	Description	Value Stored
Adopted	Defines an individual as adopted	1=True; 0=False
Deceased Status	Defines an individual as deceased	1=True; 0=False
Degree of Relation[1]	Defines the degree of relation to the proband	0-infinity
Degree of Relation2[2]	Defines the degree of relation to the proband	0-16
Father ID	Defines the UPN for the father of an individual	0-infinity
Folder	Lists the name of a folder that contains the individual	Name of folder
G:P	Generation number:Person number	1:1-infinity
Gender	Defines individual as male or female	M=male; F=Female
Gender Unknown	Defines individual gender as unknown	0=False;1=True
Genotyped	Defines if an individual is gentoyped	0=No;1=Yes
Global ID	Unique number assigned to every individual in a database	1-infinity
Individual Name	Lists the name of the individual	Name of individual
Marked By	Defines individual marked by a sign	0=false, 1=+, 2=-, 3=*
Mother ID	Defines the UPN for the mother of an individual	0-infinity
No Issue	Defines an individual marked by No Issue	0=False;1=True
Pedigree Name	Lists the name of the pedigree that contains the individual	Name of pedigree
Proband Status	Defines an individual as a proband	0=False;1=True
SAB	Defines an individual as still-born	0=False;1=True
Sample Count	Counts the number of samples for an individual	0-infinity
Sample Name	Lists the name of each sample for the individual	Name of sample
Twin Relationship	Lists the type of twin relationship for the individual	Monozygotic, Dizygotic, Unknown
Twin Status	Value for identifying twins	0=Not Twin;1=1st set, 3=2nd set; 5=3rd set, and so on

Field Name	Description	Value Stored
UPN	Lists the unique number of the individual in a pedigree	0-infinity

1. Defines the degree of relation of the specific individual to the proband. For example, a value of 1 is a first degree relative, the value of 2 is a second degree relative, and so on.
2. Defines a more specific relationship to the proband based on the following code system:

Code	Description
1	Proband
2	Brother or Sister
3	Son or Daughter
4	Parent
5	Paternal Grandparent
6	Paternal Aunt or Uncle
7	Maternal Grandparent
8	Maternal Aunt or Uncle
13	Nephew or Niece
14	Husband or Wife
15	Brother or Sister-in-Law
16	Identical Twin of Proband

Pedigree System Fields

Field Name	Description	Value Stored
Audit Status	Indicates whether auditing is turned on for the pedigree	On or Off
Folder	Lists the name of the folder that contains the pedigree	Name of folder
Last Modified	Lists the date when the pedigree was last modified.	Date of last modification
Modified By	Lists the name of the user who last modified the pedigree	Name of user
Pedigree Name	Lists the name of the pedigree	Name of pedigree

Sample System Fields

Field Name	Description	Value Stored
Adopted	Defines an individual as adopted	1=True; 0=False
Deceased Status[1]	Defines an individual as deceased	1=True; 0=False
Degree of Relation	Defines the degree of relation to the proband	0-infinity
Degree of Relation2[2]	Defines the degree of relation to the proband	0-14
Father ID	Defines the UPN for the father of an individual	0-infinity
G:P	Generation number:Person number	1:1-infinity
Gender	Defines individual as male or female	M=male; F=Female
Gender Unknown	Defines individual gender as unknown	0=False;1=True
Global ID	Unique number assigned to every individual in a database	1-infinity
Individual Name	Lists the name of the individual	Name of individual
Marked By	Defines individual marked by a sign	0=false, 1=+, 2=-, 3=*
Mother ID	Defines the UPN for the mother of an individual	0-infinity
No Issue	Defines an individual marked by No Issue	0=False;1=True
Parent Sample Name	Lists the name of the parent sample for an aliquot	Name of parent sample
Pedigree Name	Lists the name of the pedigree that contains the individual	Name of pedigree
Plate Count	Counts the number of wells that contain the sample	0-infinity
Position	Lists the location of the sample within a container	0-infinity
Proband Status	Defines an individual as a proband	0=False;1=True
SAB	Defines an individual as still-born	0=False;1=True
Sample Audit Status	Indicates whether auditing is turned on or off for the sample	On or Off
Sample Folder	Lists the name of the folder that contains the sample	Name of sample folder
Sample Name	Lists the name of the sample	Name of sample

Field Name	Description	Value Stored
Twin Relationship	Lists the type of twin relationship for the individual	Monozygotic, Dizygotic, Unknown
Twin Status	Value for identifying twins	0=Not Twin;1=1st set, 3=2nd set; 5=3rd set, and so on
UPN	Lists the unique number of the individual in a pedigree	0-infinity
Volume	Lists the current sample volume	0-infinity
Workflow	Lists the name of the workflow with which the sample is associated	Name of workflow
Workflow stage	Lists the name of the workflow stage that was last completed for the sample	Name of workflow stage

1. Defines the degree of relation of the specific individual to the proband. For example, a value of 1 is a first degree relative, the value of 2 is a second degree relative, and so on.
2. Defines a more specific relationship to the proband based on the following code system:

Code	Description
1	Proband
2	Brother or Sister
3	Son or Daughter
4	Parent
5	Paternal Grandparent
6	Paternal Aunt or Uncle
7	Maternal Grandparent
8	Maternal Aunt or Uncle
13	Nephew or Niece
14	Husband or Wife
15	Brother or Sister-in-Law
16	Identical Twin of Proband

Marker System Fields

Field Name	Description	Value Stored
Base Pairs	Value entered for base pairs	0-infinity
CentiMorgans	Value entered for CentiMorgans	0-infinity
Chromosome Name	Name of the chromosome where marker is located	0-infinity
Marker Name	List name of the microsatellite or SNP	Name of marker
Marker Type	Defines the type of marker	Marker or SNP
AA Count	Count of AA calls per SNP	0-infinity
AB Count	Count of AB calls per SNP	0-infinity
BB Count	Count of BB calls per SNP	0-infinity
NoCall Count	Count of NoCalls per SNP	0-infinity
Call Rate	Comparison of AA + AB + BB calls versus NoCalls per SN:P	0-infinity
Degree of Heterozygosity	Proportion of heterozygotes per SNP	0-1
Hardy-Weinberg P-Value	P-value results for Hardy-Weinberg tests per SNP	0-1
Minor Allele Frequency	Ratio of the allele that is less common to the total number of alleles (2) per SNP	0-.5
Minor Allele	Stores the minor allele	A or B
Allele A Value	Stores the expected value for Allele A	ACG or T
Allele B Value	Stores the expected value for Allele B	ACG or T

Appendix B

Importing Clinical Data

You use the Import module to import external pedigrees, individuals, and samples that *do not already exist* in a Progeny database. You can also use the Import module to import data that updates individuals and samples that already exist in the database. The data can be contained in any non-complex field (not a computed field, not a summary field, and so on) *other* than a table field. If you import pedigrees that do not already exist in the database, Progeny automatically draws the pedigree and imports all the associated data fields as well.

If you need to import table data for pedigrees, individuals, or samples, you must use the spreadsheet import function. See "To import data into a spreadsheet" on page 115.

This appendix covers the following topics:

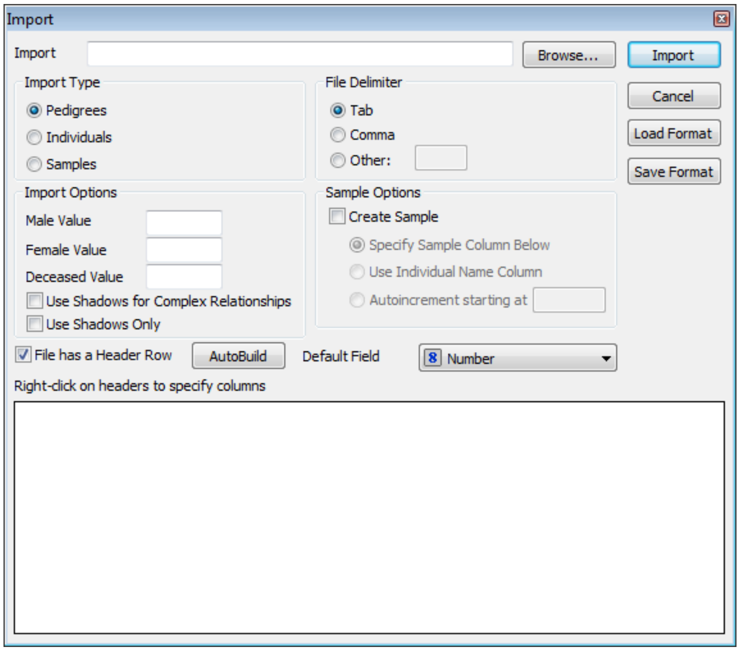
- "Overview of the Import Module" on page 561.
- "Running the Import Module" on page 564.

Overview of the Import Module

You use the Import module to import three types of external data that *do not already exist* in a Progeny database—pedigrees, individuals not contained in pedigrees, and samples. You can also use the Import module to import data that updates individuals and samples that already exist in the database. The data can be contained in any non-complex field (not a computed field, not a summary field, and so on) *other* than a table field. If you import pedigrees that do not already exist in the database, Progeny automatically draws the pedigree and imports all the associated data fields as well. If you import pedigrees and individuals, you are importing *individual level data fields*. If you import samples, you are importing *sample level data fields*.

If you need to import table data for pedigrees, individuals, or samples, you must use the spreadsheet import function. See "To import data into a spreadsheet" on page 115.

Figure B-1: Import module dialog box (for pedigrees)



Import Type: ● Pedigrees ○ Individuals ○ Samples

File Delimiter: ● Tab ○ Comma ○ Other:

Sample Options: ☐ Create Sample

Import Options: ☐ Use Shadows for Complex Relationships ☐ Use Shadows Only

☑ File has a Header Row

Default Field: Number

Right-click on headers to specify columns

All pedigree data and all individual data must be contained in separate text files that have a specific structure. The sample text file can contain be imported as a standalone file, or the sample data can be attached to a pedigree or an individual. Any type of import file can contain fields that exist in the Progeny database as well as fields that do not exist in the Progeny database. If the fields do not exist in the Progeny database, then the fields must be *of the same type*—that is, they must all be text fields, they must all be number fields, and so on. After you import the file, if needed, you can change the field type for these undefined fields. The import options that are available on the Import dialog box depend on whether you are importing pedigree data, individual data, or sample data.

Import file structure for pedigrees

Five columns of the pedigree text file must contain data that defines the pedigree structure—Pedigree Name, Individual Name, Gender, Mother ID, and Father ID. The remaining columns can contain relationship information (spouse, twin status, sibling, and so on) and then individual information (first name, last name, date of birth, and so on).

Pedigree Import Required Columns

- Pedigree Name – Unique alphanumeric ID for the pedigree name.
- Individual Name – Unique alphanumeric ID for the individual name. (Must be unique per pedigree)
- Father ID – Unique alphanumeric ID for the father name.
- Mother ID – Unique alphanumeric ID for the mother name.
- Gender – Distinction between male and female. (If field is blank or uses a value that is or different from the Male/Female values, gender is marked as Unknown.)

Pedigree Import Optional Columns

- Child – Unique alphanumeric ID for the child name.
- Sibling – Unique alphanumeric ID for the sibling name.
- Spouse 1 – Unique alphanumeric ID for the first spouse name.
- Spouse 2 – Unique alphanumeric ID for the second spouse name.
- Twin Status – Number used to identify a set of twins. For instance, the first set of twins within a pedigree would all have the number 1. The second set of twins would have the number 2, and so on.
- Twin Relationship – Twin designation: monozygotic or dizygotic
- Proband Status – If your proband is not the first person listed for each pedigree, designate the correct proband in this column with the value of 1.
- Deceased – Value specified in Import Options on the Import Module dialog box for pedigrees.
- Sample Name - Alphanumeric ID for sample name if “Create Sample/Specify Sample Column Below” is selected in Sample Options on the Import Module dialog box for pedigrees.

Import file structure for individuals

Two columns of an individual text file must contain the individual name (or ID) and gender. The remaining columns can contain any other information for the individual such as first name, last name, date of birth, and so on.

Individual Import Required Columns

- Individual Name - Alphanumeric ID for each individual. (Must be unique per individual.)
- Gender – Distinction between male and female. (If field is blank or uses a value that is or different from the Male/Female values, gender is marked as Unknown)

Individual Import Optional Columns

- Deceased – Value specified in Import Options on the Import Module dialog box for individuals.
- Sample Name - Alphanumeric ID for sample name if "Create Sample/Specify Sample Column Below" is selected in Sample Options on the Import Module dialog box for individuals.

Import file structure for samples

One column of a sample text file must contain the sample name (or ID). The remaining columns can contain other relevant information about the sample such as container name, barcode, and so on.

Sample Import Required Column

- Sample Name - Alphanumeric ID for the sample name. (Must be unique per sample.)

Sample Import Optional Columns

- Container Name - Allows you to place a sample into a container that already exists in the database
- Barcode - Unique label ID assigned to a sample for tracking its location in a container.
- Volume - Numeric value for the quantity of available sample.
- Parent Sample Name - Alphanumeric ID of the original sample from which the aliquot was derived.
- Workflow Name - Allows you to place a sample into a workflow that already exists in the database.
- Position - Exact location within the container.

Running the Import Module

You can run the Import module from the Pedigrees window, the Individuals window, or the Samples window. The type of data that is selected for importing and the folders in which the data is imported all depend on the window from which you opened the Import module.

To run the import module

1. Open the Pedigrees, Individuals, or Samples window and select a folder on the window.
2. Click the Import button Import on the Pedigrees, Individuals, or Samples window toolbar.

   If you clicked the Import button from:

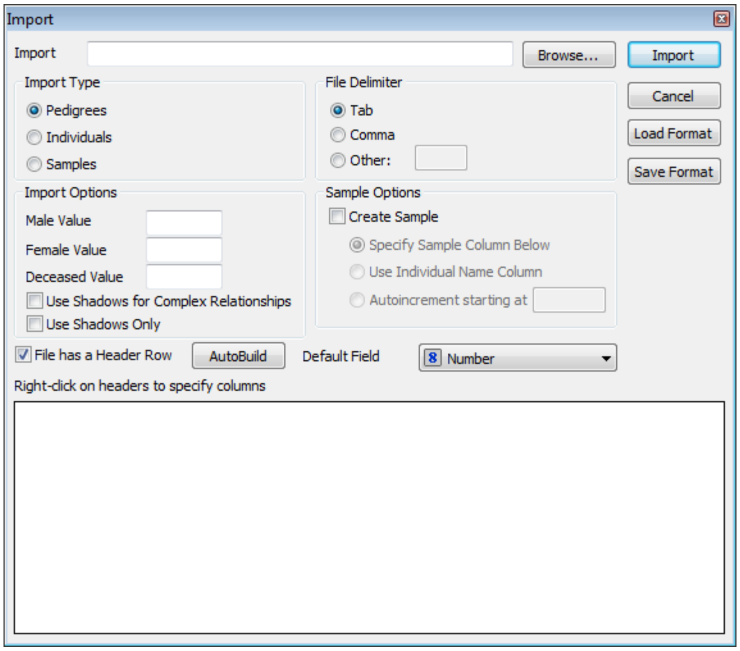
   - the Pedigrees window, then Pedigrees is selected for the Import Type.
   - the Individuals window, then Individual is selected for the Import Type.
   - the Samples window, then Samples is selected as the Import Type.

   You can, however, import any of the three types of data from any access point.

   - If you opened the Import module from the Pedigrees window, then the pedigree data is imported into the pedigree folder that you selected on the Pedigrees window. If you opened the Import module from either the Individuals or Samples window, and selected Pedigrees as the Import Type, then the pedigree data is imported into a new folder, Imported Pedigrees, that is stored at the root level for the Individuals or Samples window.
   - If you opened the Import module from the Individuals window, then the individual data is imported into the individual folder that you selected on the Individuals window. If you opened the Import module from either the Pedigrees or Samples window, and selected Individual as the Import Type, then the individual data is imported into a new folder, Imported Individuals, that is stored at the root level for the Pedigrees or Samples window.
   - If you opened the Import module from the Samples window, then the sample data is imported into the sample folder that you selected on the Samples window. If you opened the Import module from either the Pedigrees or Individuals window, and selected Sample as the Import Type, then the sample data is imported into a new folder, Imported Samples, that is stored at the root level for the Pedigrees or Individuals window.
3. Continue to one of the following:
   - "To import pedigree data" on page 565.
   - "To import individual data" on page 569.
   - "To import sample data" on page 573.

To import pedigree data

Figure B-2: Import module dialog box (for pedigrees)



1. Click Browse to browse to and select the data file that is being imported.

   The imported file is displayed in the Import Preview pane (bottom pane) of the dialog box.

2. Select the delimiter that is used for the data in the import file. If you select Other, you must specify the character that is used for the delimiter.

3. Specify the Import Options for the file:

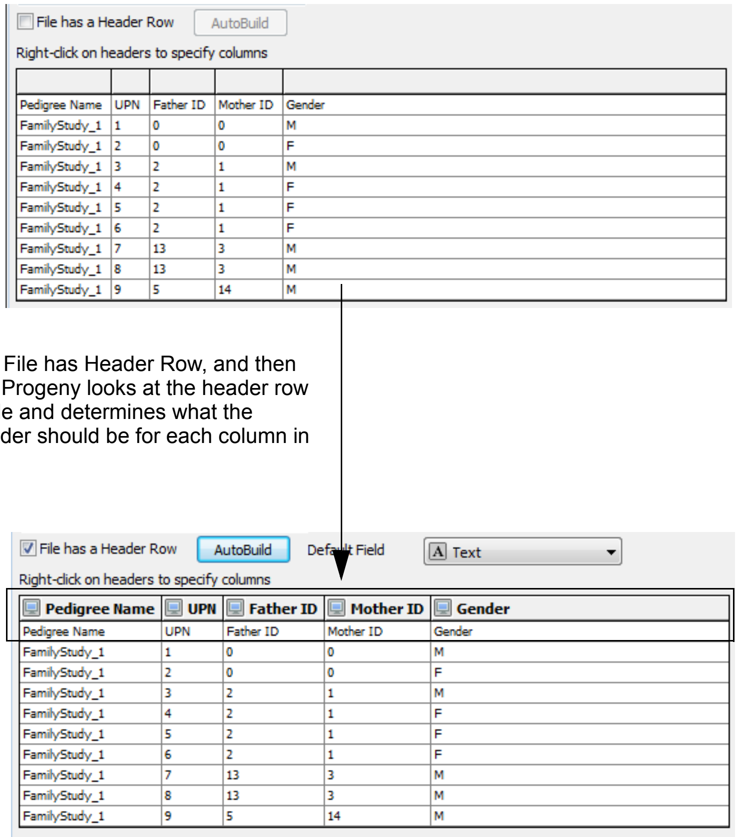
   - Male Value - Specify the value used that is to be used for males in the Gender column in your file (for example, 1, M, Male).
   - Female Value - Specify the value that is to be used for females in the Gender column in your file (for example, 2, F, Female).
   - Deceased Value - Specify the value that is to indicate deceased in the Deceased column in your file (for example, 1, D).
   - Use Shadow for Complex Relationships - Shadow is a feature that allows you to a show a complex marital relationship that otherwise would be shown as a single line that would cross the entire pedigree.
   - Use Shadows Only—Show only shadows on the pedigree. (Used in the event of consanguinity.)

4. If sample data is to be imported with the pedigree data, select Create Sample, and then specify the Sample Options for the file.
    - Specify Sample Column Below - Select this option if you are specifying a column that contains your Sample Name in the import preview.
    - Use Individual Name column - Select this option if the newly created samples will use the name from the Individual Name column that is specified in the import preview.
    - Auto increment starting at - Select this option to create sample for each individual in the pedigree and auto increment the sample number starting at the number specified.
5. In the Import Preview pane (the bottom pane of the Import dialog box), do one of the following:
    - If your import file has a header row, then select File has Header Row, and then click AutoBuild. Also, if your import file contains fields that do not currently exist in the Progeny database, select the field type on the Default Field dropdown list. (The default value is Text.)

      Progeny looks at the header row in your import file and determines what the appropriate header should be for each column in the data file. (See Figure B-3 on page 567.) If your import file contains fields that do *not* exist in the Progeny database, Progeny creates these fields in the Progeny database, assigns the headers that are in the import file as the column headers, and imports the data that is in each column into the newly created field. Continue to Step 7.
    - If your import file does not have a header row, then you must right-click in the header for each column and manually assign the appropriate column heading. (See Figure B-4 on page 567.) If your contains fields that do *not* exist in the Progeny database, then continue to Step 6; otherwise, continue to Step 7.

If you do not agree with an automatic heading that Progeny has assigned to a column, you can also use the manual option to assign a different heading.

Figure B-3: Import file with header row

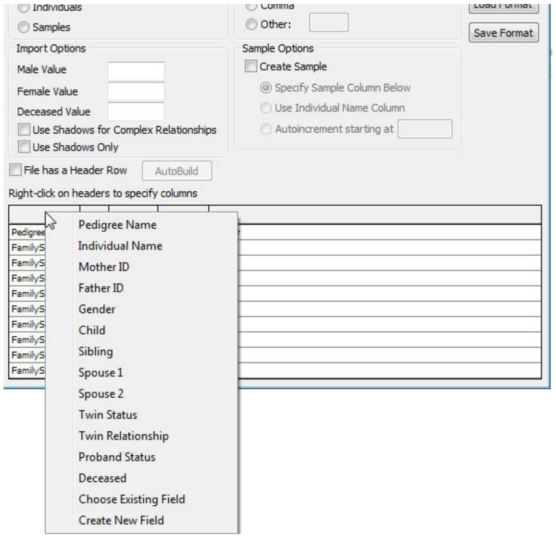


Pedigree Name	UPN	Father ID	Mother ID	Gender
FamilyStudy_1	1	0	0	M
FamilyStudy_1	2	0	0	F
FamilyStudy_1	3	2	1	M
FamilyStudy_1	4	2	1	F
FamilyStudy_1	5	2	1	F
FamilyStudy_1	6	2	1	F
FamilyStudy_1	7	13	3	M
FamilyStudy_1	8	13	3	M
FamilyStudy_1	9	5	14	M

After you select File has Header Row, and then click AutoBuild, Progeny looks at the header row in your import file and determines what the appropriate header should be for each column in the data file.

Pedigree Name	UPN	Father ID	Mother ID	Gender
Pedigree Name	UPN	Father ID	Mother ID	Gender
FamilyStudy_1	1	0	0	M
FamilyStudy_1	2	0	0	F
FamilyStudy_1	3	2	1	M
FamilyStudy_1	4	2	1	F
FamilyStudy_1	5	2	1	F
FamilyStudy_1	6	2	1	F
FamilyStudy_1	7	13	3	M
FamilyStudy_1	8	13	3	M
FamilyStudy_1	9	5	14	M

Figure B-4: Manually assigning a column heading

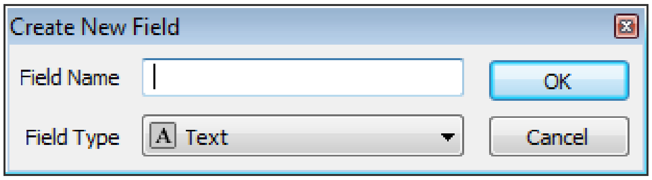


6. For each field that is not contained in the Progeny, right-click in the field, and then do one of the following:

   - To have the data imported into a new database field, select Create New Field.

     The Add a new Field dialog box opens. Enter a name for the new field in this dialog box, and optionally, select a different field type. The field will be created and the data for the individual will be imported into this field during the import process.

Figure B-5: Add a New Field dialog box

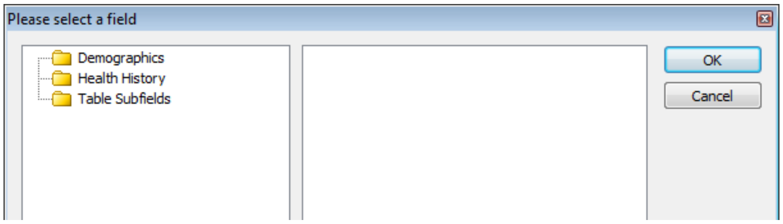


Remember, when you import pedigree data, you are importing individual level data fields. As a result, after the import process is complete, this field can be found in an individual data fields folder named Import Fields on the Fields window.

   - To have the data imported into an existing database, field, select Choose Existing Field.

     The Select Field dialog box opens, from which you can select an existing individual database field into which to import the data.

Figure B-6: Select Field dialog box



Optionally, after you label a column, you can do one or both of the following:

- *To remove a column from the import, right-click on the column, and on the context menu that opens, select Ignore This Column.*
- *To update a column a column after it has been labeled, right-click on the column, and on the context menu that opens, select a different column label.*

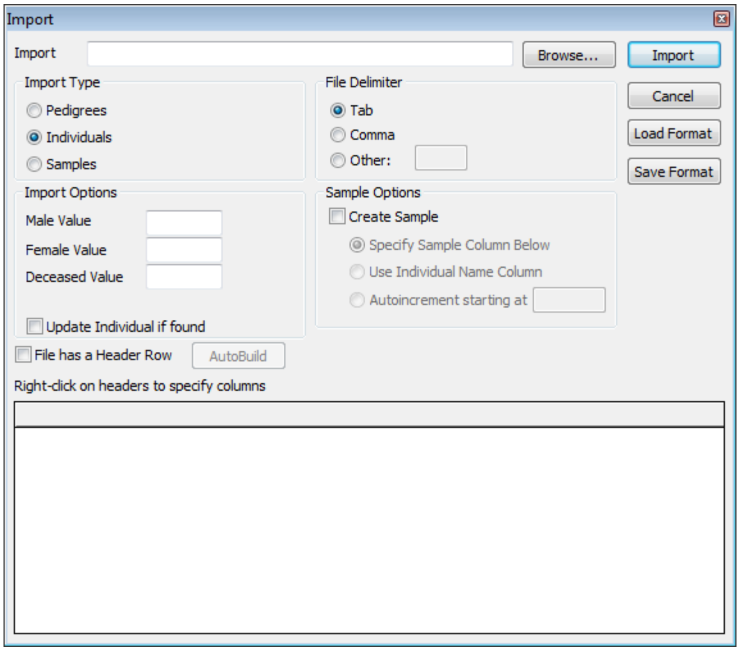
7. Click Import.

   A Progeny Import Module dialog box opens, indicating the status of the import.

8. When the import is complete, click Close.

To import individual data

Figure B-7: Import module dialog box (for individuals)



1. Click Browse to browse to and select the data file that is being imported.

   The imported file is displayed in the Import Preview pane (bottom pane) of the dialog box.

2. Select the delimiter that is used for the data in the import file. If you select Other, you must specify the character that is used for the delimiter.

3. Specify the Import Options for the file:

   - Male Value - Specify the value used that is to be used for males in the Gender column in your file (for example, 1, M, Male).
   - Female Value - Specify the value that is to be used for females in the Gender column in your file (for example, 2, F, Female).
   - Deceased Value - Specify the value that is to indicate deceased in the Deceased column in your file (for example, 1, D).
   - Update Individual if Found—Select this option to update the field values for an individual if the individual is found to already exist in the Progeny database.

4. If sample data is to be imported with the individual data, select Create Sample, and then specify the Sample Options for the file.

    - Specify Sample Column Below - Select this option if you are specifying a column that contains your Sample Name in the import preview.
    - Use Individual Name column - Select this option if the newly created samples will use the name from the Individual Name column that is specified in the import preview.
    - Auto increment starting at - Select this option to create sample for each individual in the pedigree and auto increment the sample number starting at the number specified.

5. In the Import Preview pane (the bottom pane of the Import dialog box), do one of the following:

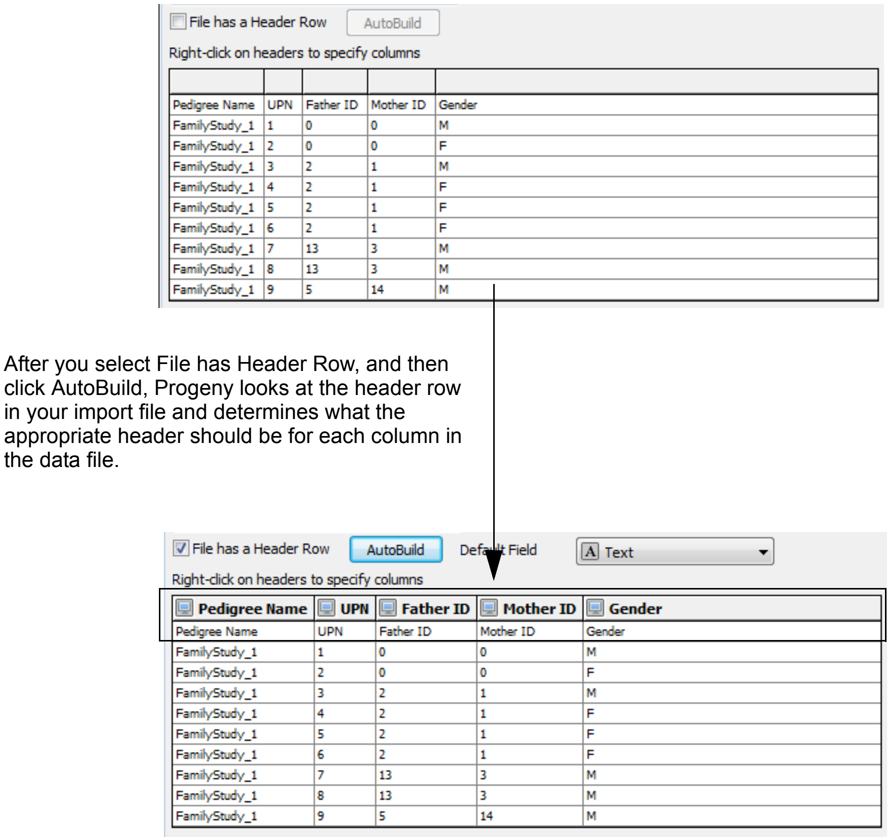
    - If your import file has a header row, then select File has Header Row, and then click AutoBuild. Also, if your import file contains fields that do not currently exist in the Progeny database, select the field type on the Default Field dropdown list. (The default value is Text.)

      Progeny looks at the header row in your import file and determines what the appropriate header should be for each column in the data file. (See Figure B-8 on page 571.) If your import file contains fields that do *not* exist in the Progeny database, Progeny creates these fields in the Progeny database, assigns the headers that are in the import file as the column headers, and imports the data that is in each column into the newly created field. Continue to Step 7.

    - If your import file does not have a header row, then you must right-click in each column header and manually assign the appropriate column heading. (See Figure B-9 on page 571.) If your contains fields that do *not* exist in the Progeny database, then continue to Step 6; otherwise, continue to Step 7.

If you do not agree with the an automatic heading that Progeny has assigned to a column, you can also use the manual option to assign a different heading.

Figure B-8: Import file with header row

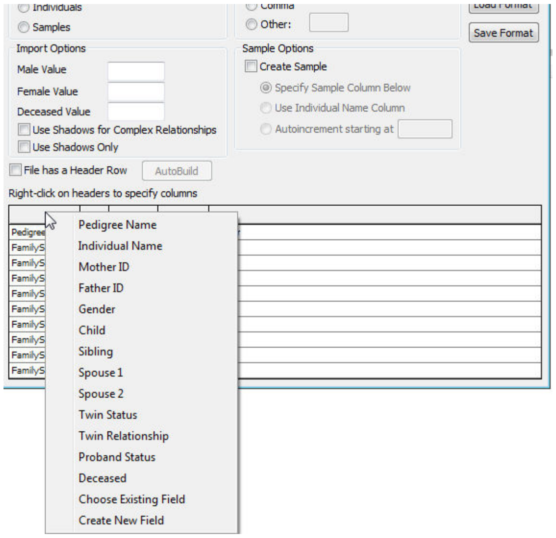


Pedigree Name	UPN	Father ID	Mother ID	Gender
FamilyStudy_1	1	0	0	M
FamilyStudy_1	2	0	0	F
FamilyStudy_1	3	2	1	M
FamilyStudy_1	4	2	1	F
FamilyStudy_1	5	2	1	F
FamilyStudy_1	6	2	1	F
FamilyStudy_1	7	13	3	M
FamilyStudy_1	8	13	3	M
FamilyStudy_1	9	5	14	M

After you select File has Header Row, and then click AutoBuild, Progeny looks at the header row in your import file and determines what the appropriate header should be for each column in the data file.

Pedigree Name	UPN	Father ID	Mother ID	Gender
Pedigree Name	UPN	Father ID	Mother ID	Gender
FamilyStudy_1	1	0	0	M
FamilyStudy_1	2	0	0	F
FamilyStudy_1	3	2	1	M
FamilyStudy_1	4	2	1	F
FamilyStudy_1	5	2	1	F
FamilyStudy_1	6	2	1	F
FamilyStudy_1	7	13	3	M
FamilyStudy_1	8	13	3	M
FamilyStudy_1	9	5	14	M

Figure B-9: Manually assigning a column heading

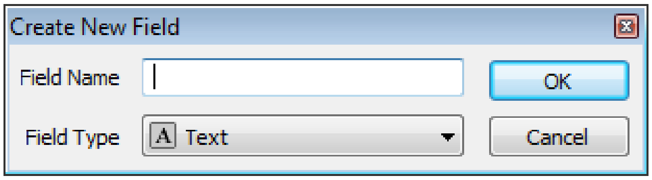


6. For each field that is not contained in the Progeny database, right-click in the field, and then do one of the following:

   - To have the data imported into a new database field, select Create New Field.

     The Add a new Field dialog box opens. Enter a name for the new field in this dialog box, and optionally, select a different field type. The field will be created and the data for the individual will be imported into this field during the import process.

Figure B-10: Add a New Field dialog box

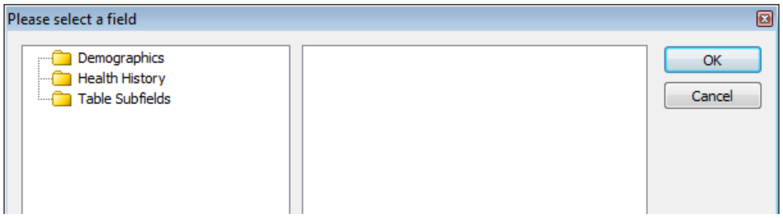


After the import process is complete, this field can be found in an Individual Data Fields folder named Import Fields on the Fields window.

   - To have the data imported into an existing database, field, select Choose Existing Field.

     The Select Field dialog box opens, from which you can select an existing individual database field into which to import the data.

Figure B-11: Select Field dialog box



Optionally, after you label a column, you can do one or both of the following:

- *To remove a column from the import, right-click on the column, and on the context menu that opens, select Ignore This Column.*
- *To update a column a column after it has been labeled, right-click on the column, and on the context menu that opens, select a different column label.*

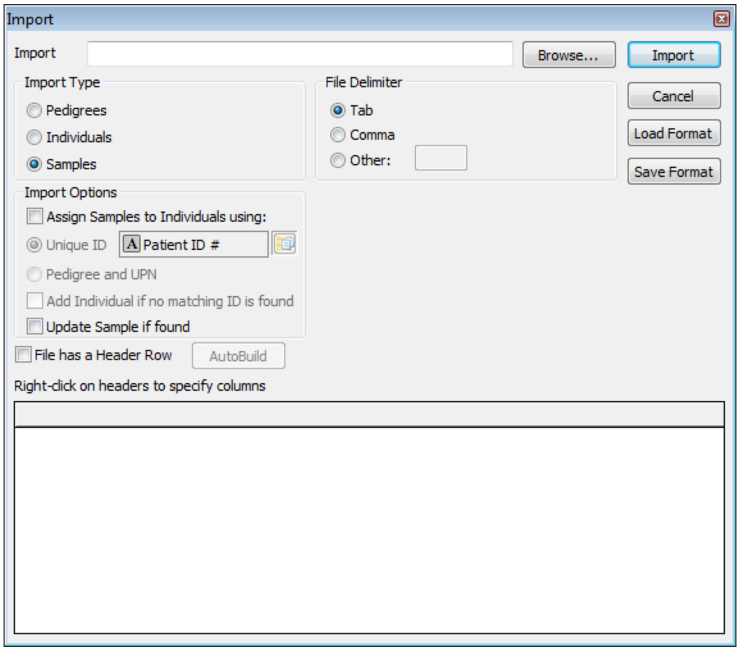
7. Click Import.

   A Progeny Import Module dialog box opens, indicating the status of the import.

8. When the import is complete, click Close.

To import sample data

Figure B-12: Import module dialog box (for samples)



1. Click Browse to browse to and select the data file that is being imported.

   The imported file is displayed in the Import Preview pane (bottom pane) of the dialog box.

2. Select the delimiter that is used for the data in the import file. If you select Other, you must specify the character that is used for the delimiter.

3. Specify the Import Options for the file:

   - Unique ID - Specify the Unique ID field used to connect your new samples with an existing individual in the database.
   - Pedigree and UP - Connect your new samples with a Pedigree and UPN combination that already exists in the database.
   - Add Individual if no matching ID is found - Select this option to add a new individual if one of the previous matching criteria is not met.
   - Update Sample if Found—Select this option to update the field values for a sample if the sample is found to already exist in the Progeny database.

4. In the Import Preview pane (the bottom pane of the Import dialog box), do one of the following:

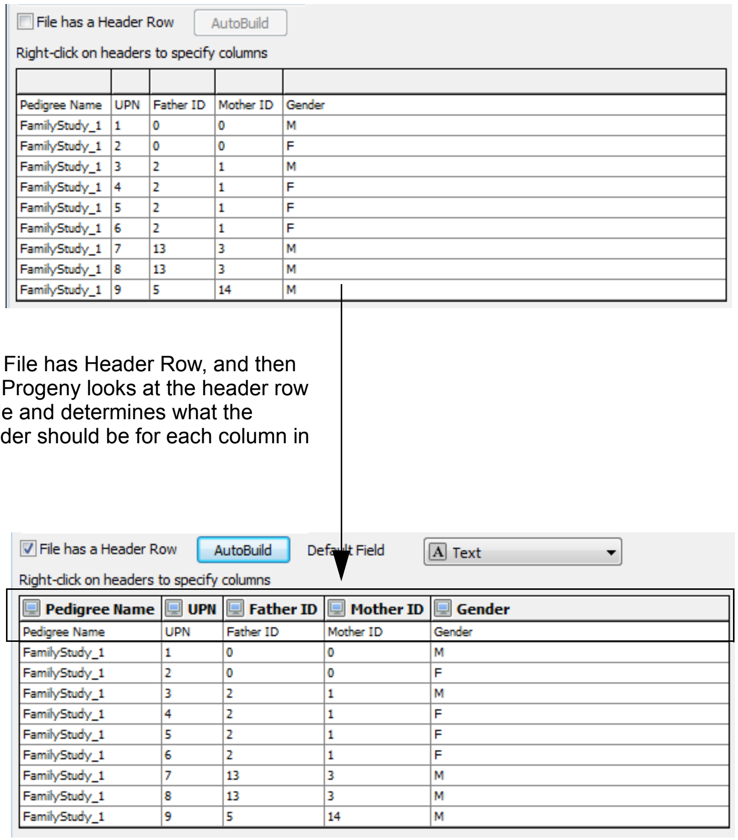
   - If your import file does have a header row, then select File has Header Row, and then click AutoBuild. In addition, if your import file contains fields that do not currently exist in the Progeny database, select the field type on the Default Field dropdown list. (The default value is Text.)

     Progeny looks at the header row in your import file and determines what the appropriate header should be for each column in the data file. (See Figure B-13 below.) Also, if your import file contains fields that do *not* exist in the Progeny database, Progeny creates these fields in the Progeny database, assigns the headers that are in the import file as the column headers, and imports the data that is in each column into the newly created field. Continue to Step 6.

   - If your import file does *not* have a header row, then you must right-click in each column header and manually assign the appropriate column heading. (See Figure B-14 on page 575.) If your contains fields that do *not* exist in the Progeny database, then continue to Step 5; otherwise, continue to Step 6.

If you do not agree with the an automatic heading that Progeny has assigned to a column, you can also use the manual option to assign a different heading.

Figure B-13: Import file with header row



☐ File has a Header Row

Right-click on headers to specify columns

Pedigree Name	UPN	Father ID	Mother ID	Gender
FamilyStudy_1	1	0	0	M
FamilyStudy_1	2	0	0	F
FamilyStudy_1	3	2	1	M
FamilyStudy_1	4	2	1	F
FamilyStudy_1	5	2	1	F
FamilyStudy_1	6	2	1	F
FamilyStudy_1	7	13	3	M
FamilyStudy_1	8	13	3	M
FamilyStudy_1	9	5	14	M

After you select File has Header Row, and then click AutoBuild, Progeny looks at the header row in your import file and determines what the appropriate header should be for each column in the data file.

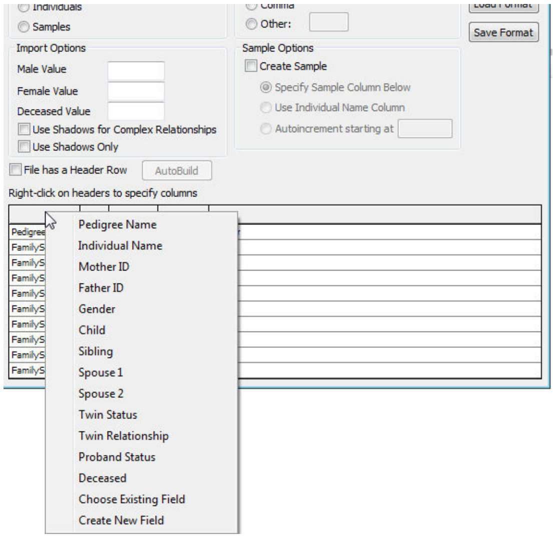
☑ File has a Header Row

Default Field: Text

Right-click on headers to specify columns

Pedigree Name	UPN	Father ID	Mother ID	Gender
Pedigree Name	UPN	Father ID	Mother ID	Gender
FamilyStudy_1	1	0	0	M
FamilyStudy_1	2	0	0	F
FamilyStudy_1	3	2	1	M
FamilyStudy_1	4	2	1	F
FamilyStudy_1	5	2	1	F
FamilyStudy_1	6	2	1	F
FamilyStudy_1	7	13	3	M
FamilyStudy_1	8	13	3	M
FamilyStudy_1	9	5	14	M

Figure B-14: Manually assigning a column heading

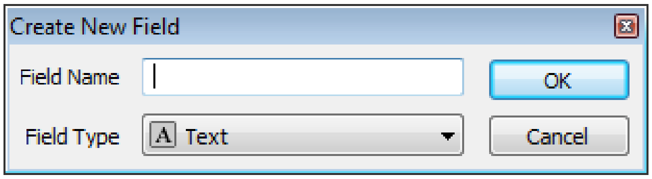


5. For each field that is not contained in the Progeny, right-click in the field, and then do one of the following:

- To have the data imported into a new database field, select Create New Field.

  The Add a new Field dialog box opens. Enter a name for the new field in this dialog box, and optionally, select a different field type. The field will be created and the data for the individual will be imported into this field during the import process.

Figure B-15: Add a New Field dialog box

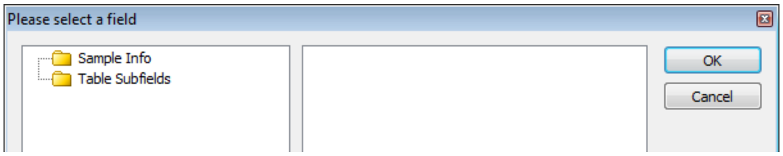


After the import process is complete, this field can be found in a Sample Data Fields folder named Import Fields on the Fields window.

- To have the data imported into an existing database, field, select Choose Existing Field.

  The Select Field dialog box opens, from which you can select an existing individual database field into which to import the data.

Figure B-16: Select Field dialog box



Optionally, after you label a column, you can do one or both of the following:

- *To remove a column from the import, right-click on the column, and on the context menu that opens, select Ignore This Column.*
- *To update a column a column after it has been labeled, right-click on the column, and on the context menu that opens, select a different column label.*

6. Click Import.

   A Progeny Import Module dialog box opens, indicating the status of the import.

7. When the import is complete, click Close.

Saving and Loading an Import Format

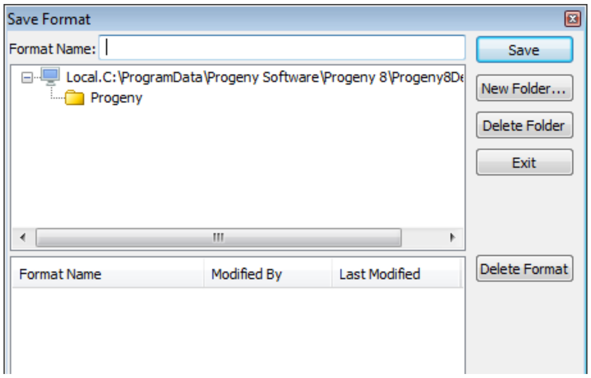
After you have set up an import format for pedigrees, individuals, or samples, you can save the format. You can then load this saved format and run it on as-needed basis.

To save an import format

1. Set up the import format for the pedigrees, individuals, or samples, but do not click Import. See:
    - "To import pedigree data" on page 565.
    - "To import individual data" on page 569.
    - "To import sample data" on page 573.
2. Click Save Format on the Import dialog box.

    The Save Format dialog box opens. It provides a default folder named Progeny in which to save the import format. (This folder is located in the database that you are currently logged in to and you cannot change this location.)

Figure B-17: Save Format dialog box



3. Enter a name for the import format, and then do one of the following:
    - Select the Progeny folder.
    - Click New Folder, and on the Format Folder dialog box that opens, do the following:
        - Enter the name of the new folder in which to save to format.
        - Select the location for the new folder. The folder can be stored at the root level (the same level as the Progeny folder), or it can be a sub-folder of the Progeny folder, or of another folder.
        - Click Save.
4. Click Save on the Save Format dialog box.

    You can then load this saved format and run it on as-needed basis. See "To load an import format" on page 578.

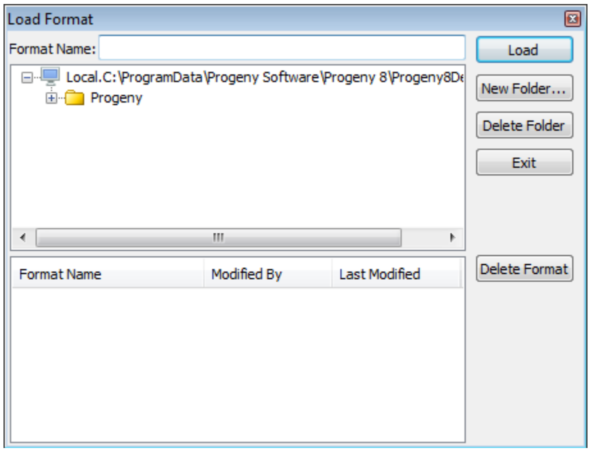
To load an import format

You can a retrieve a saved import format and load it to import a data file with the appropriate type of data. For example, if you retrieve a saved pedigree import, then you must select a text file that contains pedigree data for importing.

1. Open the Import module.
2. On the Import dialog box, click the Load Format button Load Fmt.

   The Load Format dialog box opens.

Figure B-18: Load Format dialog box



3. Open the folder that contains the import format that you are loading, select the format, and then click Load.

   The Import dialog box is refreshed with the loaded format. You can now browse to and select the import file, and then click Import to import the data according to the selected format.

Index