

PMx User Manual

Version 1.0

for PMx v. 1.0.20120115



A Contribution of the IUCN/SSC Conservation Breeding Specialist Group

About this Manual:

This PMx User Manual was developed in concert with the programmers of the PMx software program for intensive population management and with contributions by zoo population management advisors from around the globe. This version (1.0) is written to reflect the options and functionality of PMx version 1.0.20120115. The IUCN/SSC Conservation Breeding Specialist Group will oversee periodic revisions to the user manual as PMx continues to be expanded and updated. This manual is distributed free of charge with the PMx software and is available on the PMx and CBSG websites.

Please send any suggestions, additions or corrections to:

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This manual is currently being translated into Chinese (Mandarin), Japanese and Spanish. Please contact CBSG or the programmers if you are interested in providing translation for other languages for either the PMx software program and/or the user manual.

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SECTION 1: USING PMx

INTRODUCTION TO PMx

Overview and Purpose

PMx provides a suite of tools to support the genetic and demographic management of pedigreed animal populations, through analysis of data typically recorded in a “studbook”. Most such populations will be captive (*ex situ*), but PMx can also be used for managing wild populations for which intensive monitoring allows for at least a partial pedigree to be determined. PMx was designed to guide primarily the management of populations for which there is a desire to maintain the genetic diversity as close as possible to the source population, such as is often the case for conservation breeding programs for wildlife species. However, it can also be useful for management of domesticated livestock, such as rare breeds, or closed populations for which a primary concern is the protection of diversity. PMx provides no guidance on selective breeding for augmenting phenotypic characteristics, and the genetic methods provided in PMx are designed specifically to minimize genetic change due to either selection or drift.

PMx was derived from pedigree analysis programs that assume sexual reproduction with two discrete sexes. Some of its calculations are based on bisexual reproduction, and some of the terminology and data presentation in PMx implies such a breeding system. However, algorithms have been added to PMx that allow comparable calculations to be conducted on species with other breeding systems, such as cloning, hermaphroditic selfing, and haplodiploidy. In addition, PMx provides some methods for estimating genetic parameters when pedigree data are partly missing, when there are multiple possible parents, or when the entities being managed are groups of organisms (rather than diploid individuals) derived from mixing and/or sampling of ancestral groups or individuals. With these new extensions of pedigree analysis methods, PMx may be useful for management of some plant, fungus, or prokaryote populations, although no attempt has been made to facilitate analyses of non-animal populations.

PMx contains sections (modules) for **Demography**, **Genetics**, determining **Goals** for population management, and recording **Recommendations**:

The **Demography** section provides life table projections of population growth (and associated parameters) from observed birth and death rates, the ability to model the effects of changes in rates, tools for exploring the impacts of different management strategies (e.g., harvest or supplementation), and means to determine the numbers of births or deaths needed to achieve demographic goals.

The **Genetics** section provides analysis of the genetic diversity retained over generations, kinships and related metrics (e.g., inbreeding coefficients), measures of genetic value of individuals, tools for selecting individuals for pairing or culling to maximize retention of genetic diversity, and means to examine the genetic effects of partitioning the population into smaller management units.

The **Goals** section integrates demographic and genetic analyses into a modeling tool for determining the combination of demographic values (e.g., population size, growth rate, generation time) and genetic values (e.g., effective population size, starting gene diversity) that will achieve a goal for sustaining a desired level of gene diversity over time.

Finally, a **Recommendations** section provides a means to record and report the breeding and transfer recommendations for each individual.

These sections provide an array of options regarding assumptions to be made about the data, methods of analysis, and output variables to summarize results. These are described in detail in this manual.

This manual does not provide full documentation of the concepts behind the management of pedigreed populations nor of the algorithms employed by PMx. Many of the algorithms may be described briefly in a future appendix, but a complete documentation is impractical. A summary of the methodologies is presented in Ballou *et al.* (2010), and overviews of PMx and genetic methods can be found in three papers currently in press (Ivy and Lacy; Lacy; Lacy *et al.*). Be aware, however, that PMx provides some new approaches and uses new algorithms that are not yet fully documented in any published reference.

History of PMx

PMx was derived from the PM2000 software package (Pollak *et al.* 2000), incorporating all analyses of PM2000 and adding a substantial number of new analyses and options. PMx also incorporates the analyses of MateRx (Ballou *et al.* 2001) and MetaMK (Ballou 1999). PM2000 was itself a combination of the capabilities of the programs GENES (written by Robert Lacy), DEMOG (written by Laurie Bingaman Lackey and Jonathan Ballou), and CAPACITY (written by Jonathan Ballou), as well as adding some new features. Many people, especially including members of the AZA Small Population Management Advisory Group (SPMAG), the EAZA European Population Management Advisory Group (EPMAG), and the IUCN SSC Conservation Breeding Specialist Group (CBSG), were involved in developing the algorithms used in these various programs and provided assistance with software design and testing.

PMx, like its predecessor programs, was designed to work with pedigree data maintained by the SPARKS studbook software that was developed and is distributed by the International Species Information System (ISIS 2011). More so than PM2000, however, PMx is designed also to accept pedigree data from a variety of database programs, as long as the data can be transferred in specified formats. In particular, the developers of PopLink studbook software (Faust *et al.* 2009), as well as Laurie Bingaman Lackey of ISIS, who provides support and ongoing improvements to SPARKS, have worked closely with the developers of PMx to ensure that data can smoothly move to PMx. PMx can also accept data maintained in other studbook database systems, and specifications for PMx input files are provided in *Appendix D*.

New Features: From PM2000 to PMx

PMx includes all of the data analyses available in PM2000 as well as many additional features. The major new options in PMx include:

- Ability to set age class length to intervals other than one year (shorter or longer)
- Stochastic population projections
- Projections for non-reproducing populations
- Projections based on scheduled supplementations and/or removals
- Ability to project availability of individuals for reintroduction over time
- Ability to handle breeding systems other than bi-sexual reproduction (e.g., cloning, selfing)
- Inclusion of probabilities for multiple possible parents
- Ability to assign probability of success to recommended breeding pairs
- Mate Suitability Index matrices (previously available in MateRx)
- Ability to assess genetic impact of transfers between management groups
- Increased ability to incorporate group management strategies
- Increased ability to import data from a variety of datasets

Additional new features will be added over time in subsequent versions.

GETTING STARTED

System Requirements

PMx version 1.0 is written in the C# programming language, developed with Microsoft Visual Studio 2010, for the Microsoft .NET Framework (version 4) running on Windows operating systems. It has been tested on Windows XP and Windows 7, but it is likely that it will work also on older versions of Windows. It can probably be run on Apple Mac OS running Windows emulators, but no versions have been compiled specifically for Mac, Unix, Linux, or other operating systems. PMx can run on 32-bit or 64-bit processors. Users should have the latest service packs for their OS, and must also have installed the Microsoft .NET Framework, version 4. The web installer for the .NET is available at the Microsoft download center (www.microsoft.com/downloads). The memory requirements of PMx depend on the size of the studbook being analyzed. The minimum RAM increases proportional to the square of the population size, and the required RAM can be quite large. A population with 1000 animals selected for analysis (usually, the living animals) will typically require about 10 MB of RAM to hold the calculations; a population of 10,000 will require about 1 GB of available RAM. Moreover, if the population is large (more than about 1000), the program can be very slow and require large graphics memory to hold the extensive tables of data that are available for viewing in PMx. Some of the tables that require the most memory can be optionally disabled in PMx, and the default is that PMx will not display the largest tables (e.g., the kinship matrix) for large studbooks.

Installation

The PMx installation package can be downloaded from: www.vortex9.org/PMx/PMx.html. This installation package should be saved to the local computer, and then run. It is likely that Administrator rights will be required to install PMx, and during installation it may be necessary to authorize the installation program to make changes to the computer. PMx is believed to be free of any malicious code, and we do not collect any information about you or your system during the download, installation, or use of program. *However, we can make no warranty that the copy of PMx you download and install is valid and cannot change your system in unwanted ways. Always protect yourself through the use of anti-virus software.*

PMx can be installed in the default location (usually C:\Program Files\PMx) or in any location on your hard disk. Depending on the version of Windows under which it is installed and the system settings on your computer, it may be beneficial (or even required) to install it in a specific location to which you have installation rights. Also, depending on the security settings on the computer, it may be necessary to run it under Administration rights, or to specify when PMx is opened that the program is authorized to make changes to files and folders. If the program does not run when you try to start it, right-click on the program file and run it as an "Administrator". Short-cuts to PMx should also specify that the program should run in Administrator mode. On some Windows systems, the hassle of needing additional rights to run the program can be avoided by installing the program within folders for user documents, rather than within Program Files; but on other systems programs are required to be placed within Program Files. If you have trouble getting PMx to install and run, try installing it in a different folder. We know of no reason why PMx could not be installed on and run from a server, but such configurations have not been tested and no support can be provided to troubleshoot site-specific installation problems. If you wish to reinstall PMx, you may be required to first uninstall the prior version. If you wish to keep a backup of prior versions, save the installation package files, rather than having multiple versions of PMx installed simultaneously. Uninstalling PMx will not remove any project files that you created.

Creating a New Project

To create a new PMx project, open PMx and click *New Project*. Specify a *Project Name* and *Project Description* to identify the project, and the name of the PMx project file (default name is the project name with the extension *.pmxproj). Type in, or browse using the button, and choose the primary input file, which will differ depending upon the program (and version) that was used to create the export files (see below). Click *Next*. On the following screen, you have the ability to include optional data input files. Click *Create*, and PMx will create your project and open the main PMx window at the **Project Notes** screen. The name of the project will appear in the top window bar. **Note: The PMx window may disappear temporarily while the project is being created; this can take several seconds for large studbooks – please wait for the PMx window to reappear.**

Below is a summary table of those files needed to create a PMx project from various versions of the SPARKS and PopLink database programs – see the detailed instructions on how to create these data exports from each program.

	SPARKS 1.6x	SPARKS 1.5x	PopLink 2.1	PopLink 1.3
Primary Input File	exchange.csv	exchange.dbf	*.ped	*.ped
Demography Input File(s)	(Not needed; included in exchange.csv)	*.prn files	*.prn files (basic) Analytical Survival Statistics Included Individuals Table.csv (advanced)	
Census File	pmxcens.csv	exhcens.txt	Exhcens.txt	Exhcens.txt
UDFs File	(Not needed; included in exchange.csv)		gc_UDF.csv	Not possible

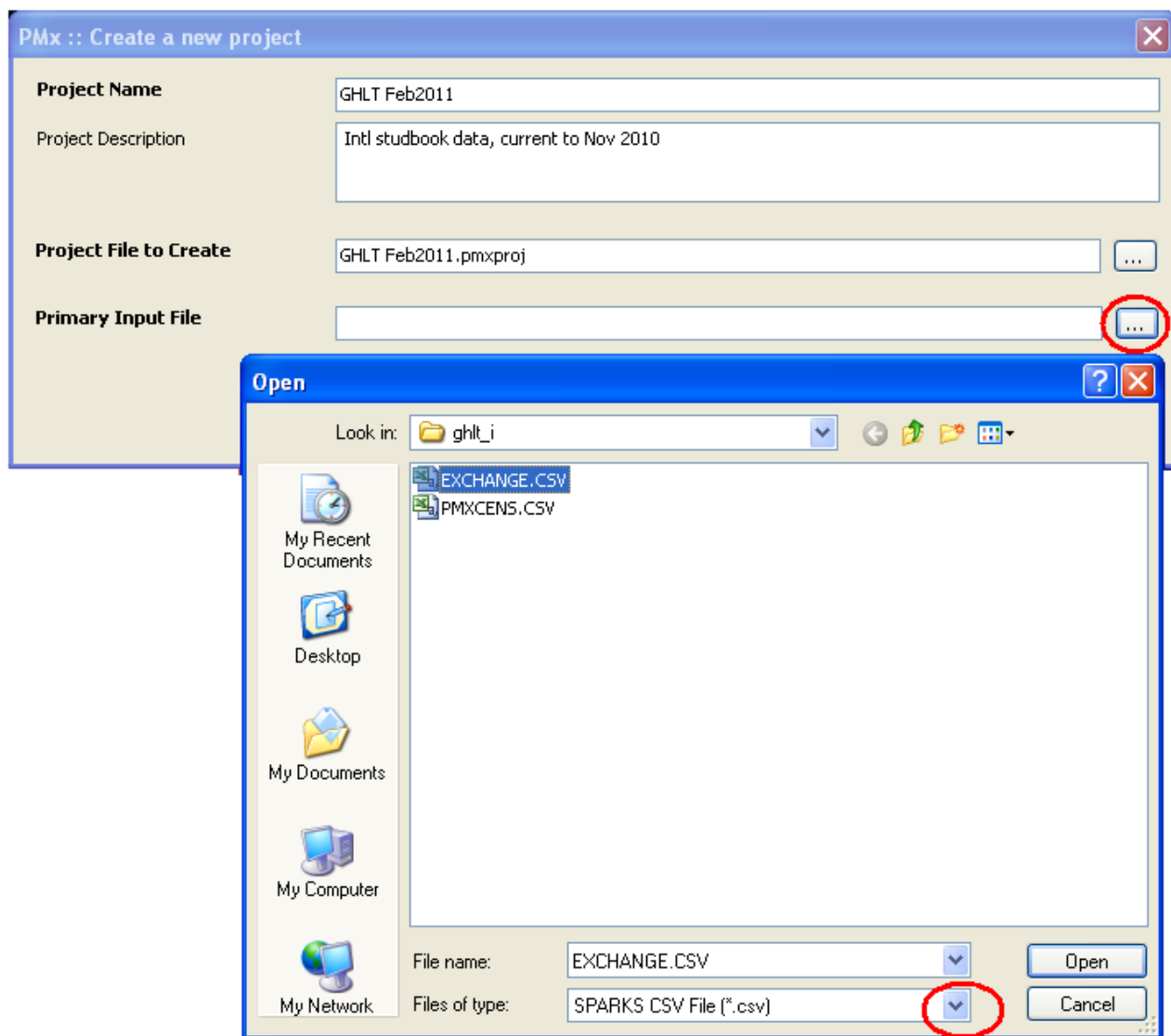
Creating a Project from SPARKS 1.6x

Export from SPARKS:

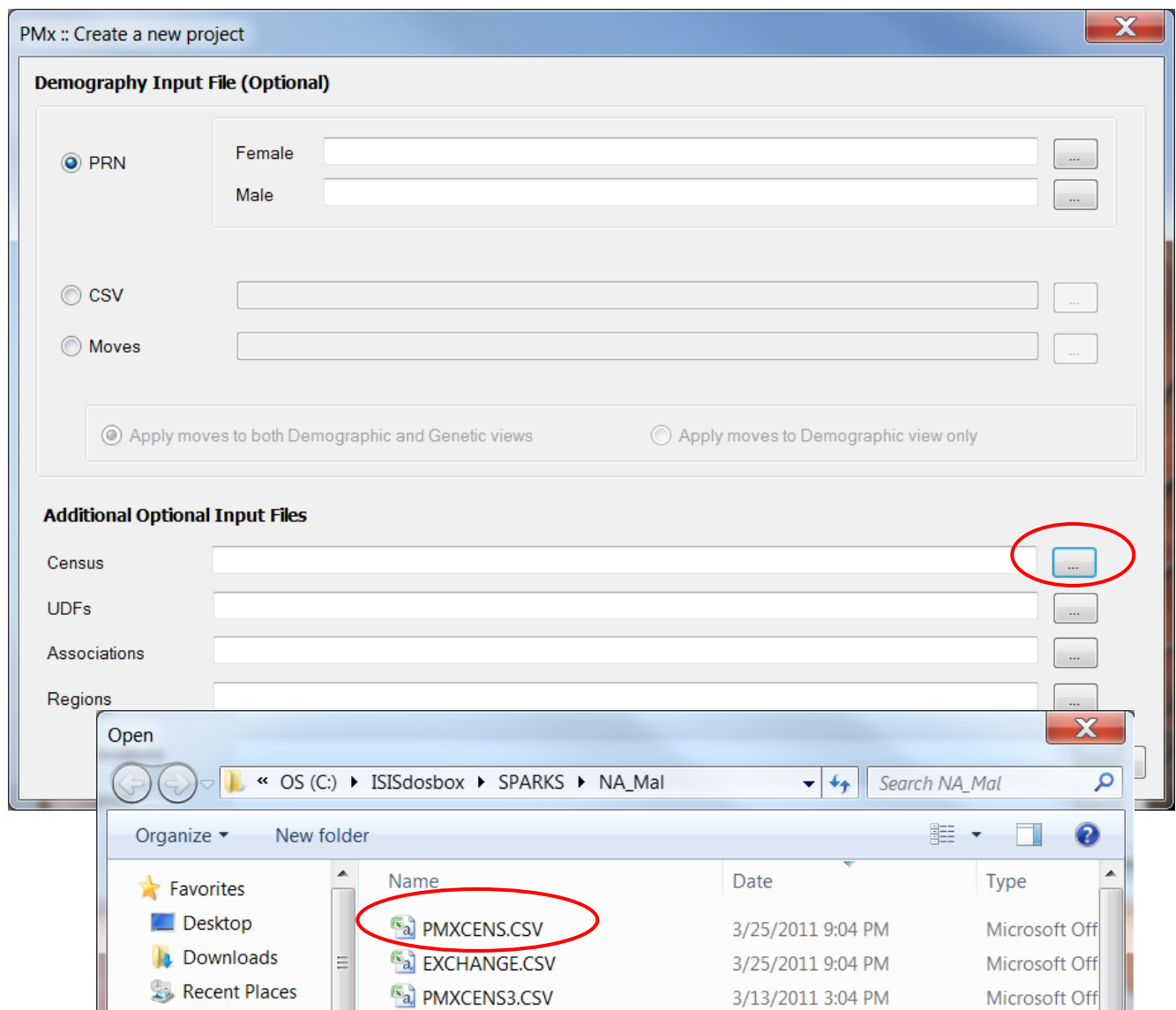
1. From the SPARKS main menu, select *Reports*.
2. Use the *Left* arrow key  to open the *View Criteria* as needed. The *Date Span* for the export will default to 1 Jan 1800 - today's date; otherwise, set a date span sufficient to include sensible demographic data associated with modern management and the lifespan of the species. *Geographic* or *Association* views may be used, as well as *User Defined Fields*. The *ESCAPE* key will return you to the *Reports* menu. *Note that this is quite different than the export to PM2000. The genetic, demographic and census data files are created in a single pass.*
3. From the *Reports* menu, select *Analysis > Export Data To > PMx*. The default name for the genetic/demographic export will be *exchange.csv* (you are given the option to change it). The census export is automatically named *pmxcens.csv*. If there are any available UDFs, you may add them. The export will run, and the resulting files will be saved in the studbook folder.
4. Close SPARKS.

Import into PMx:

1. Open PMx. Pick *New Project* and enter a project name. Including the species name and a date can be helpful as projects accumulate over time.
2. The *Project File to Create* name will automatically update to reflect this project name.
3. Either manually type in the *Primary Input File* information or click on the button at the end of this field and browse to the appropriate SPARKS studbook folder. Change the file type to display .csv files. Choose *exchange.csv*, and click on *Next*.



4. No *Demography Input File* needs to be specified because SPARKS 1.6 places into the *Primary Input File* (*exchange.csv*) the demographic information that is required by PMx. However, additional records of moves of individuals into or out of the population can optionally be specified either as CSV files or as *Moves* files (see *Appendix D* for details on the format of these additional demography files). If additional demographic data are provided in files other than the *Primary Input File*, then these data can be applied only to demographic analyses or can be used also to define which individuals were in or out of the population throughout the Genetic History (see **Genetic Overview** and **Graphs** tabs in *Section 4* of the manual).
5. Under *Additional Optional Input Files*, add the *pmxcens.csv* file (found in the studbook folder) to the *Census*. You may also add any of the *.fed* files (usually found in the SPARKS folder, but possibly in the studbook folder) to *Associations* and/or *.rgn* files to *Regions*.
6. No additional files are needed for UDFs, as they are already included in the SPARKS 1.6 export, although new UDFs that were not in the studbook can be added as an optional UDF (*.udf file).
7. Click on *Create*. Once PMx opens to the opening **Project Notes** screen, select **File > Save Project**.



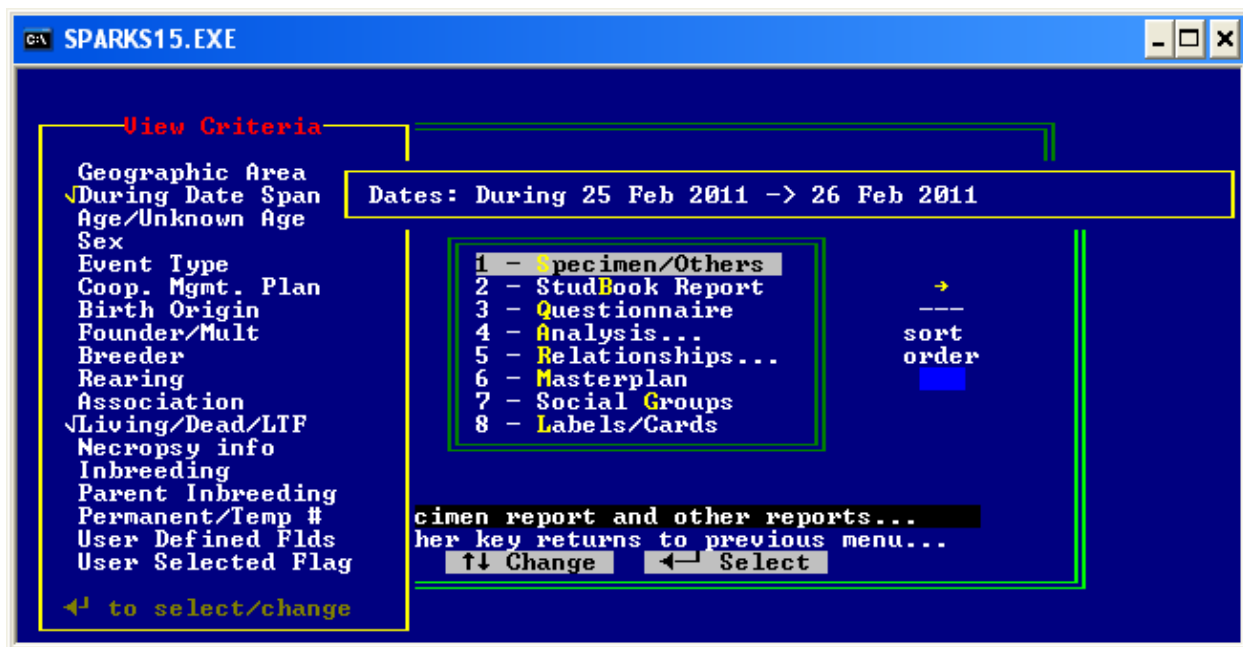
Creating a Project from SPARKS 1.5x

Export from SPARKS:

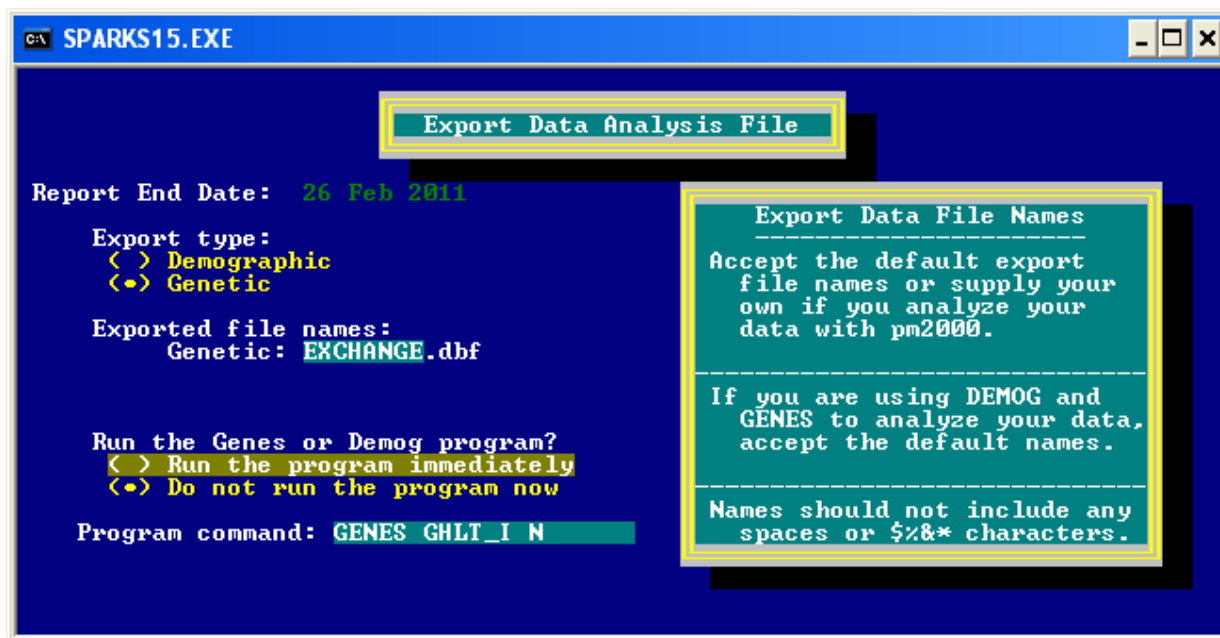
Data are exported in three parts from SPARKS 1.54 or 1.56, similar to how exports are done for PM2000:

Genetic export:

1. From the SPARKS main menu, select *Reports*.
2. Use the *Left* arrow key **←** to open the *View Criteria* as needed. Set the *Date Span* for the export from yesterday's date to today's date, **During** the date span. Also set *Living/Dead/LTF* to *Lived during date span*. *Geographic* or *Association* views may be used, as well as *User Defined Fields*. The *ESCAPE* key will return you to the *Reports* menu.

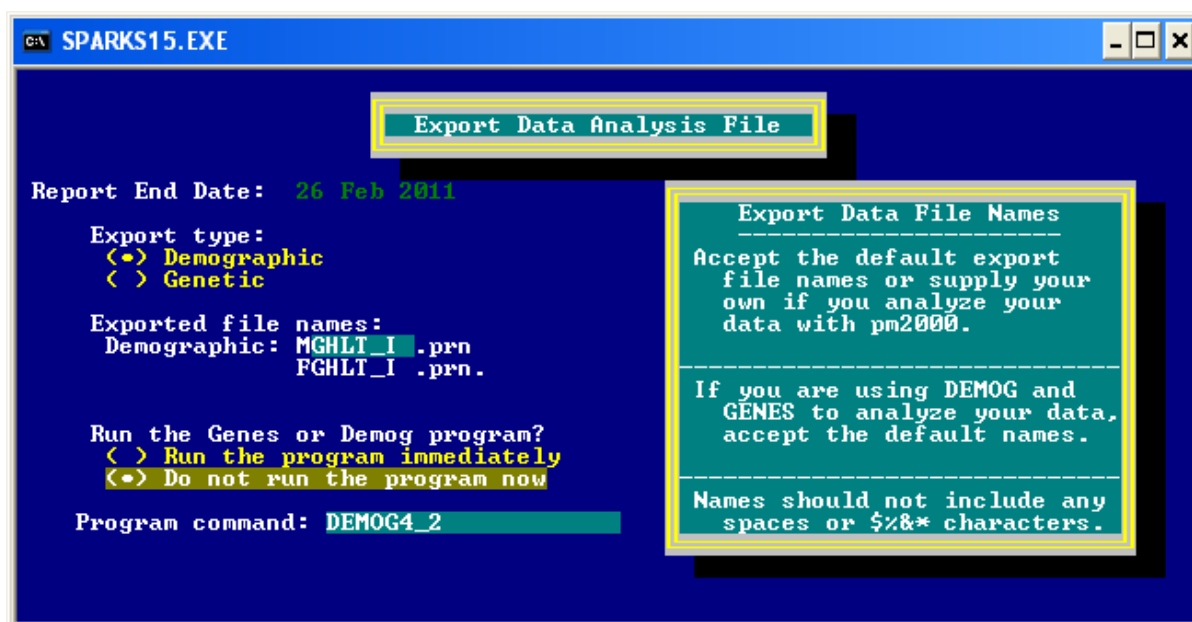


3. From the *Reports* menu, select *Analysis > Export Data*. Use the *Down* arrow key **↓** to move to *Genetic* and then use the *Space* bar on the keyboard to choose *Genetic*. Use the *Down* arrow key to move to the next field. The default name for the export will be EXCHANGE.dbf (you may change this). Select *Do not run the program now*. Use the *Down* arrow key to move through the rest of the screen. [To run Genes or Demog, consult the SPARKS manual.]
4. You will be asked if you wish to include animals released to the wild in the calculations. It would be unusual to answer yes.
5. The export will be created and stored in the studbook folder.
6. Close SPARKS or reset the *View Criteria* for a demographic import (see below).



Demographic export:

1. From the *Reports*, use the *Left* arrow key to open the *View Criteria*.
2. Change the *Date Span* dates to an interval that includes modern management and takes into account the lifespan of the species. Select **During** the date span. *Geographic* or *Association* views may be used, as well as *User Defined Fields*.
3. From the *Reports* menu, select *Analysis > Export Data*.
4. While at the *Demographic* choice, use the *Space* bar on the keyboard to choose *Demographic*. Use the *Down* arrow key to continue down the screen. The default names for the export will be M<studbook name>.prn for males and F<studbook name>.prn for females (these can be changed). Use the *Down* arrow key to move through the rest of the screen.
5. The export will be created and stored in the studbook folder.



Census export:

1. From the *Reports* menu, select *Analysis > Census > Census Report*. Run the report to the screen.
2. Use the *ESCAPE* key to close the report. There is no need to adjust the *View Criteria* for this report. Various reports will be created and stored in the studbook folder.

Import into PMx:

1. Open PMx. Pick *New Project* and enter a project name. Including the species name and a date can be helpful as projects accumulate over time.
2. The *Project File to Create* name will automatically update to reflect this project name.
3. Either manually type in the *Primary Input File* information or click on the button at the end of this field and browse to the appropriate SPARKS studbook folder. Change the file type to display *.dbf* files. Choose *exchange.dbf*, and click on *Next*.

PMx :: Create a new project

Project Name GHLT Intl data pm2000 export files

Project Description Example for using pm2000-style files for import

Project File to Create GHLT Intl data pm2000 export files.pmxproj ...

Primary Input File C:\SparksDW\glt_j\EXCHANGE.DBF ...

Cancel Next >>

4. Add the required *.prn* files for females and males to the project by browsing to the appropriate SPARKS studbook folder. If *Demography Input Files* are not specified, then PMx will not provide any demographic analyses or modeling of goals, because the *Primary Input File* provided by SPARKS 1.5 (*exchange.dbf*) does not contain the necessary data to allow the demographic calculations to be done.
5. As with data import from SPARK 1.6, additional records of moves of individuals into or out of the population can be specified either as *CSV* files or as *Moves* files, and these data can optionally be applied to define also the movements of individuals in and out of the genetically managed population. Any such additional demographic files would need to be created in a program other than SPARKS.
6. Under *Additional Optional Input Files*, add the *exhcens.txt* file (found in the studbook folder) to the *Census*. You may also add any of the *.fed* files (usually found in the SPARKS folder, but possibly in the studbook folder) to *Associations* and/or *.rgn* files to *Regions*.
7. Click on *Create*. Once PMx opens to the opening **Project Notes** screen, select *File > Save Project*.

PMx :: Create a new project

Demography Input File (Required)

☒ PRN

Female C:\SISdosbox\SPARKS\NA_Mal\FNA_MAL.PRN

Male C:\SISdosbox\SPARKS\NA_Mal\mNA_MAL.PRN

☐ CSV

☐ Moves

☒ Apply moves to both Demographic and Genetic views ☐ Apply moves to Demographic view only

Additional Optional Input Files

Census C:\SISdosbox\SPARKS\NA_Mal\EXHCENS.TXT

UDFs

Associations C:\SISdosbox\SPARKS\AZA.fed

Regions

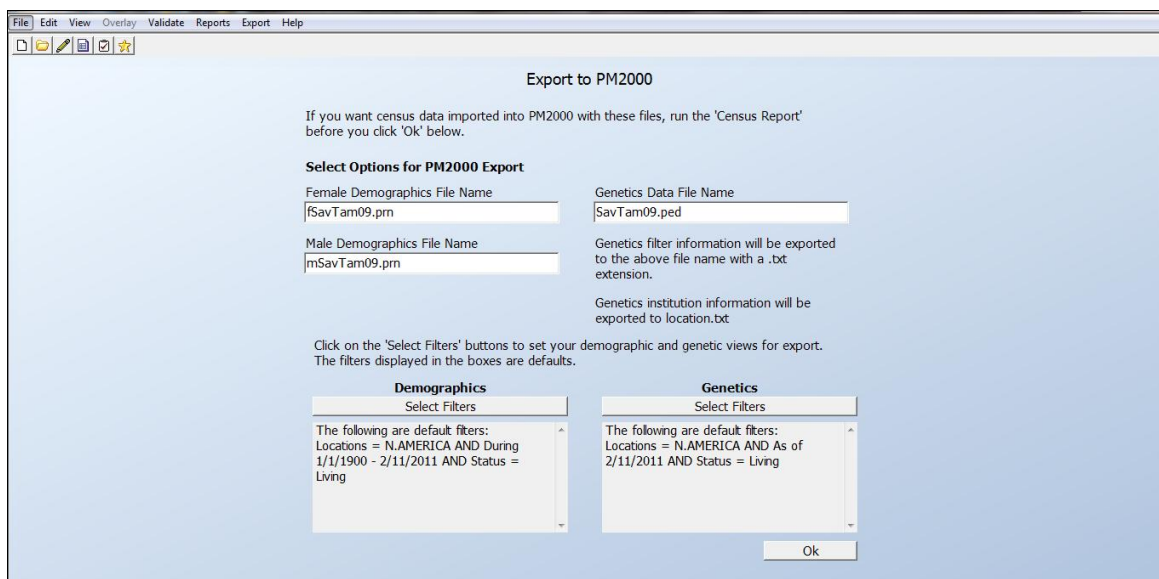
<< Back Cancel Create

Creating a Project from PopLink 2.1 or 1.3

There are two different types of PopLink exports, a Basic export and an Advanced export. The Advanced export allows greater analytical power in PMx demographic analyses (e.g., enables the user to change from yearly age classes to other divisions).

Basic Export from PopLink:

PopLink will create standard PM2000 and PMx export files (the same files are usable by both versions) from the studbook database. Data can be exported from the true studbook (e.g., SavTam09) or from a studbook with an analytical overlay applied (e.g., SavTam09 + Faust1). The database displayed at the top of the screen will indicate which database is being exported. Select the *PM2000 Export* from the Export drop-down menu, and this screen will be displayed:



The file names in the top three boxes are chosen based on the database name; these can be changed if desired, but do not change the extensions (.prn for demography files, .ped for genetics files).

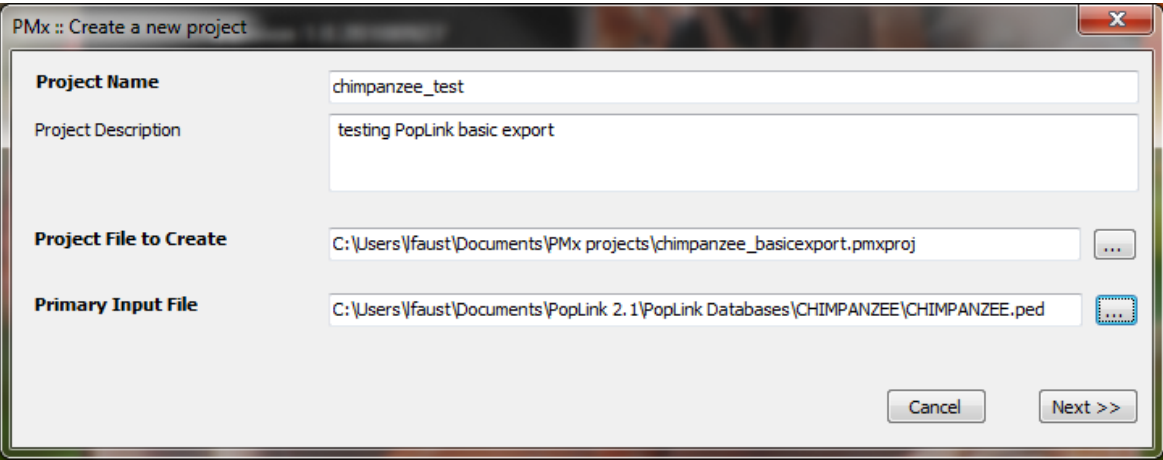
The *Demography filters* chosen will limit the studbook database to a specific population that will be used to calculate life table parameters (Mx, Qx, Lx, etc.). The chosen filters will be displayed in the filter box; change the default filters to the desired demographic window, which is generally the period of modern management for the species. Filters in addition to date and geographic windows can also be set. The *Genetic filters* are used to create the list of individuals that will be considered living individuals in the current population; PopLink exports this list of specimens and their pedigree information to PMx. If desired, change the default filters using the *Select Filters* button. After the desired filters have been set, click *OK* to create the export files.

PopLink can also export census data for graphing in PMx. To use this option, run the *Census Report* (*Reports > Census Report*) with the desired filters. Running the report automatically creates an *Exhcens.txt* file (no need to click on the *Export* button on the report).

PopLink places the PMx export files (.ped, .prn, and *Exhcens.txt*) in the studbook folder (e.g., C:\Documents and Settings\User Name\My Documents\PopLink 2.1\PopLink Databases\Studbook name in PopLink 2.1; C:\Program Files\PopLink 1.3\PopLink Databases\Studbook name in PopLink 1.3).

Basic Import into PMx:

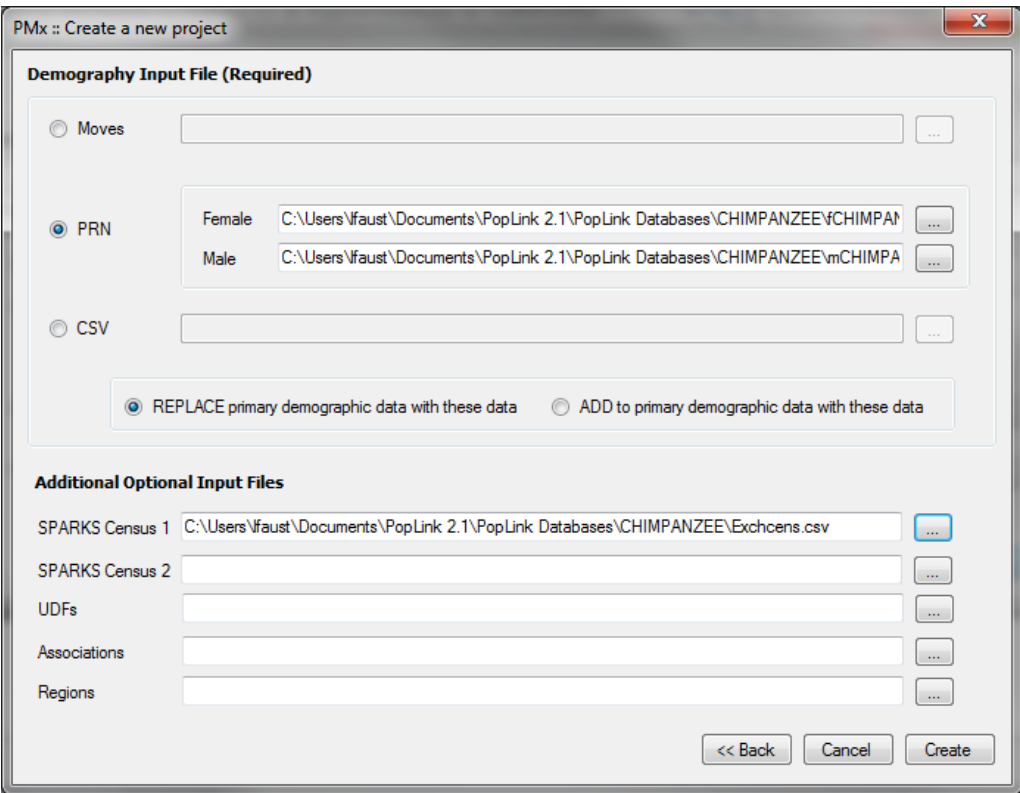
Open PMx, select *New Project*, and name it. The *Primary Input File* will be the .ped file in the studbook folder (*My Documents\PopLink 2.1\PopLink Databases\Studbook Name\Studbook Name.ped*):



The dialog box titled "PMx :: Create a new project" contains the following fields and buttons:

- Project Name:** chimpanzee_test
- Project Description:** testing PopLink basic export
- Project File to Create:** C:\Users\faust\Documents\PMx projects\chimpanzee_basicexport.pmxproj
- Primary Input File:** C:\Users\faust\Documents\PopLink 2.1\PopLink Databases\CHIMPANZEE\CHIMPANZEE.ped
- Buttons:** Cancel, Next >>

Click *Next*. On the next PMx import screen, enter the .prn files from the studbook folder, and also the *Exhcens.csv* file (optional) (note: screen format may be slightly different than shown below):



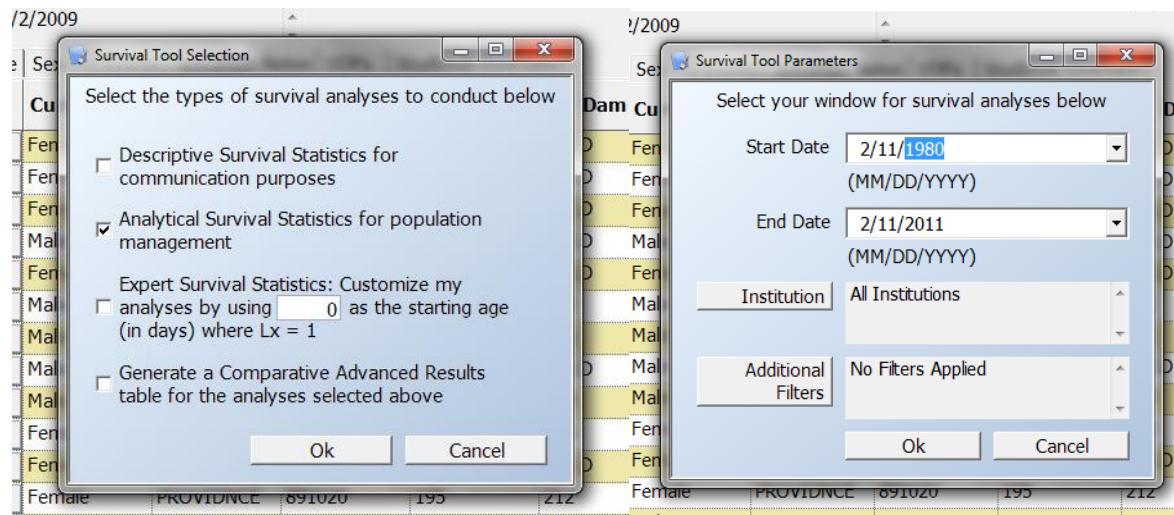
The dialog box titled "PMx :: Create a new project" shows the "Demography Input File (Required)" section. It includes the following options and fields:

- Demography Input File (Required):**
 - ☐ Moves
 - ☒ PRN
 - Female: C:\Users\faust\Documents\PopLink 2.1\PopLink Databases\CHIMPANZEE\CHIMPANZEE.prn
 - Male: C:\Users\faust\Documents\PopLink 2.1\PopLink Databases\CHIMPANZEE\CHIMPANZEE.prn
 - ☐ CSV
- REPLACE primary demographic data with these data** (selected) or **ADD to primary demographic data with these data**
- Additional Optional Input Files:**
 - SPARKS Census 1: C:\Users\faust\Documents\PopLink 2.1\PopLink Databases\CHIMPANZEE\Exhcens.csv
 - SPARKS Census 2:
 - UDFs:
 - Associations:
 - Regions:
- Buttons:** << Back, Cancel, Create

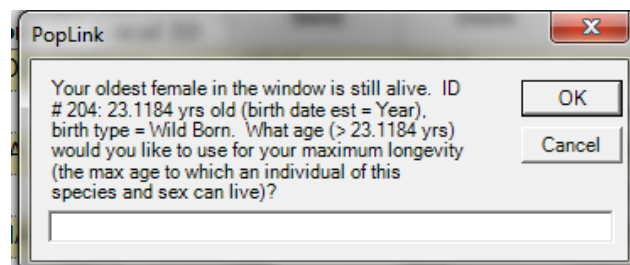
Advanced Export from PopLink:

Follow the directions above under Basic Export from PopLink to create the Genetic export and Census export files. To create the advanced Demographic export:

1. Run the *Survival Tool (Reports > Survival Tool)*, selecting the *Analytical Survival Statistics* option.
2. Set the appropriate filters for the export:



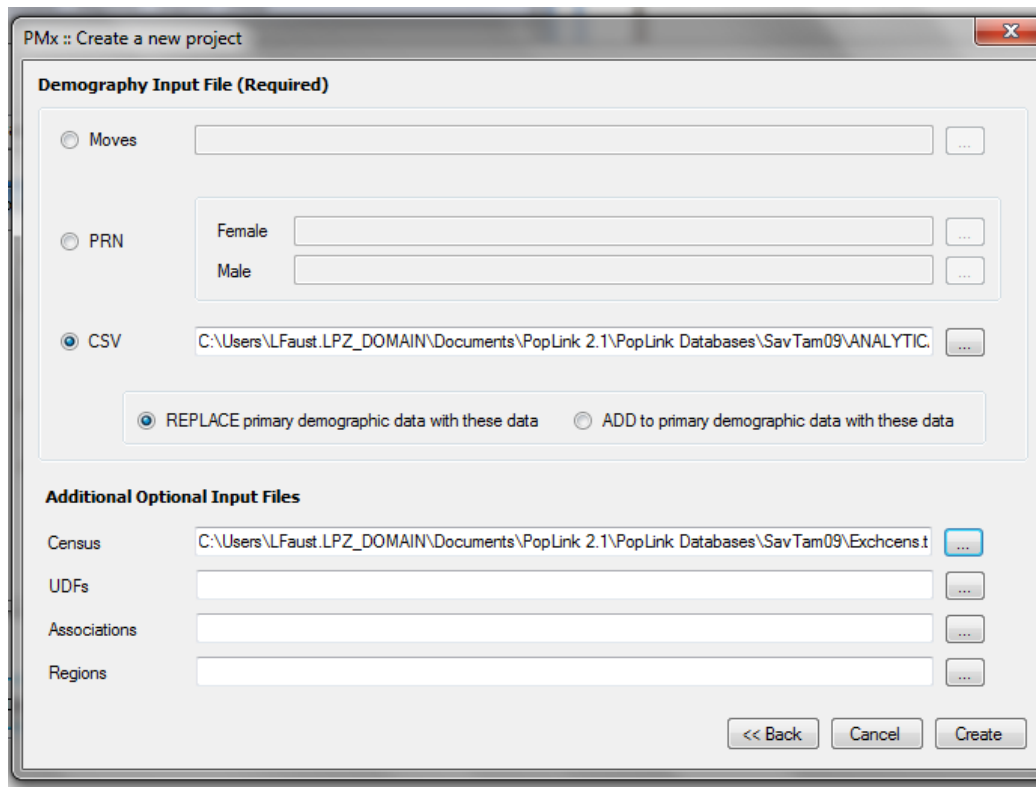
3. A pop-up box may appear indicating that the oldest individual in the demographic window is still alive and will provide information on this individual. Specify an age (greater than the age of the oldest living individual) to use as the maximum longevity and the end of the PMx life table for this sex. You may enter the age of this individual (rounded up to the next highest integer age). Alternately, if credible information is available that the species and sex can live to an older age, an older maximum longevity can be entered. For example, this might be appropriate if the population has not been maintained very long in captivity, has not had enough old individuals to represent the entire lifespan of the species, or if there are credible data from a field study or alternate captive population (either the same species or a related species) that can be used to make an estimate. Note: the maximum longevity can also be changed (by adding age classes to the PMx lifetable) through changing the *Demography Settings* in PMx.



4. When the *Analytical Survival Statistics Report* pops up, click the *Export* button in the upper right-hand corner. This will create a file called ANALYTICALSURVIVAL STATISTICS INCLUDING INDIVIDUALS TABLE.CSV that will be used in the demographic import into PMx.

Advanced Import into PMx:

Follow the same process described for the Basic Import, except for the *Demography Input File*, select the *Analytical Survival Statistics Included Individuals Table.csv* file from the studbook folder:

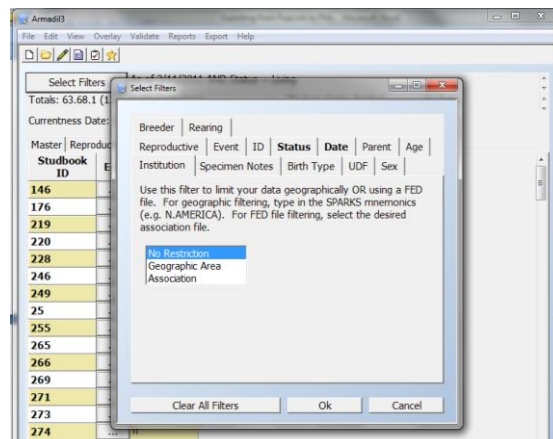


The image shows the 'PMx :: Create a new project' dialog box. It has a title bar with a close button. The main area is divided into two sections. The first section, 'Demography Input File (Required)', contains three radio buttons: 'Moves', 'PRN', and 'CSV'. The 'CSV' option is selected. To the right of the 'CSV' radio button is a text field containing the path 'C:\Users\LFaust.LPZ_DOMAIN\Documents\PopLink 2.1\PopLink Databases\SavTam09\ANALYTIC...' and a browse button (...). Below this, there are two radio buttons: 'REPLACE primary demographic data with these data' (selected) and 'ADD to primary demographic data with these data'. The second section, 'Additional Optional Input Files', contains four labels: 'Census', 'UDFs', 'Associations', and 'Regions'. Each label has a corresponding text field and a browse button (...). The 'Census' field contains the path 'C:\Users\LFaust.LPZ_DOMAIN\Documents\PopLink 2.1\PopLink Databases\SavTam09\Exchcens.t'. At the bottom right, there are three buttons: '<< Back', 'Cancel', and 'Create'.

Exporting Additional Files from PopLink: UDFs, Associations, Regions:

PMx can also display additional information about individuals. Files for *User Defined Fields* (UDFs), *Associations*, and *Regions* can be specified in the second *Create a New Project* screen in PMx, under *Additional Optional Input Files*.

UDF studbook data can be exported from PopLink 2.1. Click on the *Select Filters* button at the top-left main window, and click on the *Clear All Filters* button on the bottom left of the resulting pop-up window:



Go to the UDF tab in the main window. Select one of the cells, right-click, and select *Export to Excel*. This will create a file called *gc_UDF.csv* in the studbook folder (the file will automatically open in Excel; simply close the file and it will be saved in the appropriate format). When creating the PMx project, choose the UDF file on the second *Create a New Project* screen, under *Additional Optional Input Files*, and select the *gc_UDF.csv* file from the studbook folder.

To specify an association, select a **.fed* file under *Additional Optional Input Files*. In PopLink 2.1, these FED files are stored in *C:\Users\UserName\Documents\PopLink 2.1\Federation Files*. In PopLink 1.3, they are stored in *C:\Program Files\PopLink1.3\Federation Files*.

Creating a Project from other Data Sources

Although it is much easier to prepare the data files for use in PMx from the studbook programs SPARKS or PopLink, it is possible to create the required *Primary Input File* and optional other data files from databases maintained in other programs or, for example, from data in an Excel spreadsheet. The various formats of data files that can be read by PMx are provided in *Appendix D*.

Using Associations in PMx

Associations are used to represent national or regional zoo associations (such as EAZA, JAZA, AZA, ALPZA, etc.). SPARKS and PopLink provide **.fed* files for about 20 zoo associations, which are text files that list the ISIS mnemonic for each institution that is a current member of that association (as of the date that the *fed* file was created). These *fed* files are updated approximately annually and are available from ISIS. If an association *fed* file is attached in PMx, then this association will be listed in the *Association* column on the **Individual** tab for all individuals whose last *Location* was a member of that association. Although only one *fed* file can be attached during the creation of a project, additional multiple *fed* files can be added on the **Settings** tab in the **Genetics** section. Individuals can belong to more than one association, because institutions themselves can be members of more than one zoo association. Management sets can also be created automatically based on *Association*. *Caution:* Note that *Association* is accurate at the point in time that the *fed* file was created; since institutions move in and out of zoo association membership over time, the *Association* member list may not be accurate for historical (or future) data.

Using Regions in PMx

Regions are used in PMx to represent the geographic region in which the individual physically lives based on its last *Location*. This means that an individual cannot be in more than one region at a particular point in time.

SPARKS 1.6 exports data to PMx that include the *Country* and *Region* for each individual (based on last *Location* when the individual exited the filter window). The *Regions* used in this export are designated by country as follows:

- *North America* (Canada, Greenland, US, Bermuda)
- *Latin America* (from Mexico south through the Caribbean Islands, Central America and South America)
- *Europe* (including Russia, Armenia, Azerbaijan, Belarus, Estonia, Georgia, Kazakhstan, Kyrgyzstan, Latvia, Lithuania, Moldova, Tajikistan, Turkmenistan, Ukraine, Uzbekistan)
- *Africa* (all of Africa)

- *Middle East* (Bahrain, Iran, Iraq, Israel, Jordan, Kuwait, Lebanon, Oman, Qatar, Saudi, Syria, UAE, Yemen)
- *South Asia* (Afghanistan, Bangladesh, Bhutan, BIOT, India, Maldives, Nepal, Pakistan, Sri Lanka)
- *South East Asia* (Myanmar, Laos, Vietnam, Cambodia, Thailand, Malaysia, Singapore, Indonesia, Philippines)
- *East Asia* (China, Hong Kong, Macao, Taiwan, Japan, North Korea, South Korea, Mongolia)
- *Australasia* (Australia, New Zealand, Papua New Guinea, Fiji, New Caledonia, plus nearby island groups)

Designations for Asia and Middle East approximately follow the UN designations for these regions as depicted here:



For projects created from SPARKS 1.6 exports, the *Country* and *Region* will appear on the Individual tab even if no *rgn* file is attached. Management sets can be created automatically based on either *Country* or *Region*. If a different (custom) *Region* is desired than those outlined above, a custom *Region* file(s) can be created and attached. The format is similar to a *fed* file; it is a text file containing a list of ISIS mnemonics in that geographic region and is designated as a **.rgn* file.

Imports from SPARKS 1.5x or PopLink do not contain *Country* or *Region* information, and so these columns will appear blank in PMx unless a *rgn* file is attached. Like a custom *fed* file, a *rgn* file can be created fairly easily by editing (and renaming!) an existing *fed* file in a text editor. SPARKS offers an option (under the *Association* filter) to *Create* a comprehensive custom *fed* file that includes all *Locations* in the studbook, which can then be renamed, saved and edited into a custom *fed* or *rgn* file.

Caution: It is possible to attach multiple *rgn* files to a PMx project (one at creation and/or multiple files on the **Settings** tab in the **Genetics** section). However, since an individual can only physically be in one region at a time, if multiple region files are attached that are not mutually exclusive, then the last *rgn* file attached will take precedence (i.e., overwrite) previous regional designations for an individual. For example, if a complete Europe region file is attached first, and then a British Isles region file (containing a subset of European mnemonics specific to the British Isles) is subsequently attached, individuals at mainland European institutions will be listed as Europe under *Region*, while those in the British Isles will be listed as British under *Region*. If the order of attachment were reversed (i.e., *British.rgn* attached first and then *Europe.rgn*), individuals in the British Isles will be listed as Europe under *Region*.

Differences in Feature Availability: SPARKS and PopLink Exports

Most analyses and features of PMx are available using data exports from all versions of SPARKS and PopLink; however, there are some new features that are only available when using particular studbook keeping programs and versions for export. The additional features listed in the table below are not available using SPARKS 1.5x or PopLink 1.3, but are available with data exports from SPARKS 1.6x (and in some cases, with PopLink 2.1 using the Advanced option for demographic exports):

Feature	PopLink 2.1 (using Advanced export)	SPARKS 1.6x
Ability to change age class length	X	X
Ability to redefine early mortality	X	X
Ability to model continuous (vs seasonal pulse) reproduction	X	X
Detailed census data (i.e., captures, releases, imports, exports, stillbirths, LTFs)		X
Provides # past litters/ broods per individual		X
Ability to designate potential multiple parent IDs and probabilities		X
Calculation of both % Known and % Certain		X
Historical genetic analyses		X
Ability to import social groups		X
Country and geographic Region for individuals provided in Primary Input File		X

Opening an Existing Project

To open an existing PMx project, open PMx and click *Open Project*. PMx will automatically browse in the folder in which the last PMx project was saved. Navigate to the correct location containing the PMx project that you want to open (*.pmxproj), highlight the project file, and select *Open*.

Saving a Project

To save a PMx project, select *File* from the top menu bar and choose one of the following options:

Save Project: Automatically saves the project with the name chosen when the project was created (*.pmxproj) in the folder from which the data input files were chosen.

Save Project As: Allows the option to specify the name of the project file and/or location to which it will be saved.

Save Only Core Project: Similar to *Save Project*, but does not include detailed genetic calculations (kinship matrices); these can be very large files with large studbooks. If only the core project is saved, PMx will need to recalculate these matrices when the project and its *Genetic Details* are opened. The advantage to saving only the core project is to keep the size of the project file manageable and easy to email even for large studbooks.

Save Only Core Project As: Similar to *Save Project As*, but does not include the kinship matrices as indicated above.

PMx will also automatically ask if you want to save the project when you close the program.

PMx saves all files associated with a PMx project into one file, called **.pmxproj*. This file contains not only all of the PMx files but also the data files used to create the project (see *Appendix E* for more information about the files contained in the PMx project file). Therefore, PMx projects can be transferred easily with the transfer of this single file. Note, however, that as PMx is revised and updated, projects created with older versions may or may not be able to be opened in newer versions of PMx. Also, projects may not work properly when transferred to a computer with different regional settings than the computer on which the project was created.

Removing Temporary Files

When PMx runs, it creates temporary folders within the PMx program folder. These folders will have a name *TempNNN*, in which the *NNN* is a random number. If PMx is forced to exit without closing properly (e.g., if the program crashes with an error message), then the temporary folder may be left on the computer. These folders will be located within the Window TEMP location on the system and can be safely removed after PMx closes.

USING PMx

Primary Components of PMx

PMx has six primary sections: **Project Notes**, **Selection**, **Demography**, **Genetics**, **Goals**, and **Recommendations**. Each of these sections is described in detail in subsequent sections of this manual.

Across the bottom of the screen is the **Primary Population Status** footer, which displays the basic demographic and genetic statistics (*Current N*, *% Pedigree Known*, *Current Gene Diversity*, *Potential Gene Diversity*, and *Lambda*) for the selected population. These statistics are static and are not updated (i.e., not dynamic) if changes are made in ways other than through a new selection (e.g., dynamic pairings or culls are not reflected). This footer appears at the bottom of all primary-level screens (**Project Notes**, **Selection**, **Demography**, **Genetics**, **Goals**, and **Recommendations**) as a quick reference to the population status.

To open a section in PMx, click on its tab. It is not possible to have more than one section open at a time, because often changes made in one section will change the properties and values in another section. However, PMx stores much of the information from each section after it is first opened, so that the section can re-open much more quickly, updating only that information that needs to be updated. The **Demography** and **Genetics** sections will first open to a **Summary Statistics** window, from which a set of tabbed subsections are accessed from a *Details* button.

The **Project Notes** section is an unformatted text document, or 'clipboard'. When a project is created, some header information from the imported data files is transferred to the **Project Notes**. Buttons on other tabs allow the user to send some information and graphs to the **Project Notes**. Text can also be typed directly into the **Project Notes**. Users are strongly encouraged to make notes about the project; for example, any special assumptions made in the analyses should always be documented (otherwise it is almost certain that you will later forget what you did in your analyses). Project notes can be copied and pasted into Word documents or other editors.

When analyzing a pedigreed population and planning population management within PMx, the most logical sequence in which to work is to follow the order of the tabs. After creating the project, first examine the **Project Notes** to confirm that the imported data were what was intended. Then add to those Project Notes any additional documentation for the project. Next, the **Selection** section can be used to refine which individuals from the studbook are in or not in the analyzed and managed population. The **Demography** section would normally be visited next, to determine the demographic trends and prospects for the population. The **Genetics** section is then used to determine both the genetic health of the population and which pairings will be best to maintain that health. The **Goals** section can then be used to integrate demographic and genetic analyses to decide what long-term population goals can be achieved. Finally, the **Recommendations** section provides a table for documenting the decisions made about each individual. In actual use of PMx, the user will probably move back and forth between these sections – for example, to revisit demographic planning after the goals are refined – but it will often be useful to work initially through the sections in order. Even within the **Demography** and **Genetics** sections, the tabs are arranged in the order that most people will want to explore the data.

Working with Tables

Most of the features of tables within PMx are consistent from table to table. Although some features are disabled or not applicable to some tables, the primary features of working with tables in PMx are:

- Vertical and horizontal scroll bars will appear if they are needed for viewing parts of the table that do not fit in the window. Windows can be resized by clicking and dragging their edges.
- Column widths can be changed by clicking and dragging the dividing lines between columns.
- The rows can be sorted based on the data in any column by clicking on the column header. Clicking on the same header again will reverse the order of the sorting.
- Except for key initial columns (often, *UniqueID*) that are frozen (indicated by light shading), the order of columns can be changed by clicking and dragging.
- Right-clicking on the table will open a list of variables that can be displayed. Clicking to check a variable name will cause that variable to be added to the table. Unchecking a variable will remove it from the table. (Most tables have some key variables that are always displayed, whether or not the variable is checked in the list.)
- Changes to variables and column order will be saved with a project, so that tables will appear the same when the project is opened again.
- By selecting *Save PMx settings* in the *File* menu, the current table configuration can be saved so that it will be the default lay-out when new projects are created.
- Data within a table can be copied to the Windows clipboard for pasting into other programs using the standard highlighting, Ctrl-C (copy), and Ctrl-V (paste) Windows commands.
- Clicking on an *Export* button will open a dialog box for saving the table as a tab-delimited text (.txt) file, a comma-delimited .csv file, or as an Excel (.xls) file.
- Clicking on a *Filter* button will open a form for specifying the criteria on which the rows of the table can be filtered to a subset (see below).

Filtering a Table View

Rows on many tables can be filtered so that only a subset of individuals is displayed. Note, however, that filtering only subsets the individuals that are viewed and does not affect the calculations. It can be helpful to use a filter to create a subset of individuals that is then selected for another reason (e.g., to create a Management Set); in such cases, calculations will be based on those individuals that were selected. Some tables are filtered by default, but these filters can be changed. For example, *Males* on the **Pairing** tab will initially be filtered to living males, but unknown sex can be added if desired.

To filter the rows of a table, click on *Filter*. In the following window *Filter Display for Table*, select one of the three buttons either: 1) to display all individuals (no filter); 2) to set a single filter criterion; or 3) to set multiple filter criteria. In either case, the variable(s) to be used in the filter are selected from a drop-down list. Click on a row under *Column Name* to open this dropdown list. Then select the *Operator* (=, >, <, etc.) from its drop-down list. In this list, != means “not equal to”. Finally, specify the value to be compared to the variable. String variables are not case-sensitive. Logical variables can be compared to True or False (spelled out, but case-insensitive). When multiple criteria are set, you need to specify whether *Any* or *All* of the criteria need to be met.

In addition to specifying comparisons as criteria, you can add or remove any specific individuals from the table by highlighting those individuals in the lists at the bottom of the *Filter* window. These individual selections will be applied after (thus, overriding) the criteria above.

After specifying the desired filter criteria, click *OK* to accept those criteria and return to the table.

Filter Display for Table

☒ Do not filter the display of animals in this table

☐ Only show animals where AgeClass =

☐ Only show animals where All of the following are true:

Column Name	Op	Value

Highlight animals to add to the table:

- 313
- 317
- 338
- 342
- 377
- 383
- 386
- 389
- 390

Clear selection

Highlight animals to remove from the table:

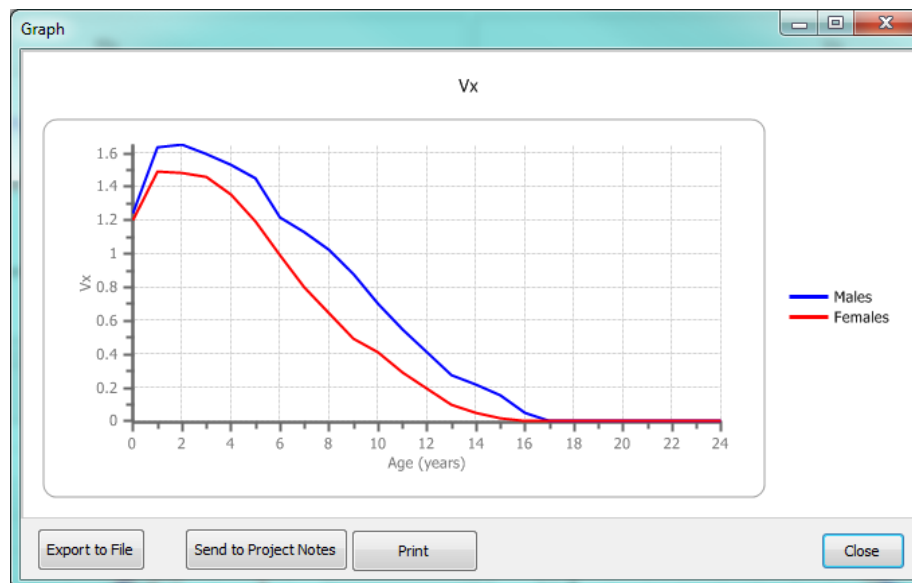
- 313
- 317
- 338
- 342
- 377
- 383
- 386
- 389
- 390

Clear selection

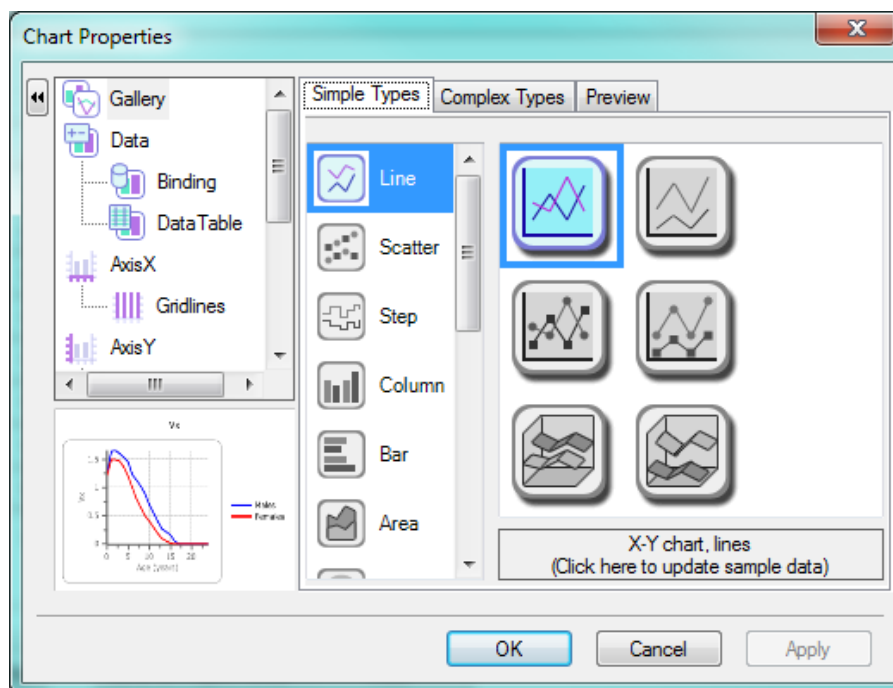
OK Cancel

Working with Graphs

Graphs displayed in PMx generally follow a common style (with some exceptions, such as the age pyramid graph). More details about using specific graphs are given in later sections of this manual, but a few words can be said here regarding the common features of PMx graphs. When a graph is displayed on a PMx tab window, it can be viewed larger and accessed for export by double-clicking on the graph to open a **Graph** window. Buttons on that window include options to *Export (to File)* the graph to a .png file, a format that can then be imported into other documents; to *Send to Project Notes* the graph, from where it can be copied and pasted into other documents; or to *Print* the graph. Exporting a graph will also recreate a .csv file containing the data used to create the graph, which can be imported into Excel.



Double-clicking on the graph in the **Graph** window will open up the **Chart Properties** window, where the features of the graph (and even the data points in it) can be edited before it is exported or printed.



Language Options and Regional Settings

PMx was first developed in English, with USA regional settings for data format. It is expected that the program will work correctly with other regional settings, with automatic adjustment to reading and displaying data in the local format (e.g., “1.00” in USA being the same as “1,00” in Germany, and in both cases meaning the number one). However, some data management programs that are used to prepare pedigree data for input into PMx may use region-specific data formats, causing problems in the transfer of data into PMx. In addition, differences in regional data formats may cause problems for transferring PMx projects to other computers that have regional settings different from the computer on which the PMx project was created.

PMx has a *Language* option on the main menu tool bar that can translate the text on the screens into languages other than English. At this time, translations into Japanese, Chinese (Mandarin) and Spanish are provided, but these are still being completed and tested. Other language translations will be included as options in the *Language* menu as volunteers provide the translated texts (contact PMx@vortex9.org if you want to offer to provide a translation). When the language is changed, not all labels within PMx screens will necessarily be translated immediately (e.g., some labels already set on the tabs may not be updated), but the text will appear in the last selected language when PMx is closed and then re-opened. If a translation is incomplete, text for which we do not yet have the translations will appear on the screens in English. Updates to PMx will include new and improved translations as they are received.

In addition, any user can edit the table of translated text (e.g., change to more local terminology) or provide an entirely new translation to a new language for their own personal use. The *PMxStrings.xls* file in the **PMx** program folder can be opened in Excel. The first three columns of the spreadsheet should not be edited. Subsequent columns are the translations that a user can edit. Changes can be made to an existing column, for example, to change Mexican Spanish to Argentinian Spanish, or to correct an error in a translated term, or entirely new columns can be created to add new languages to PMx. The first row of each column specifies the language to appear on the PMx Language menu. Do not use the same name as some prior column! The second row specifies the font to be used, and this can be important for languages that use alternative character sets. Note that a language may not display correctly on computers that have not installed that character set. Subsequent rows should be translations of the words in the English column. It is best if the translated texts are not much longer than the English texts, so that they will fit in the spaces on the PMx screens. A number of texts are repeated in multiple rows of the *PMxStrings* file. This is necessary because those texts are used in various places in the program (and translations similarly need to be repeated). If any rows are untranslated, the program will default to using the English term. After changes are made to *PMxStrings.xls*, those changes will be used in PMx the next time that the program is opened.

Getting Help

Support for users is not provided with the PMx software, beyond the information provided in this manual. (PMx is free; you get more than what you paid for!) Advisory groups of regional zoo associations (such as the AZA Small Population Management Advisory Group, and the EAZA European Population Management Advisory Group) will likely provide assistance with PMx to their members, but they are not responsible for the development and maintenance of PMx.

Within PMx, this manual is accessible from the *Help* menu on the main tool bar at the top of the PMx program window. In addition, from any location within the program, the manual can be opened at the section pertaining to the currently active part of PMx by hitting the F1 key.

Any reports of apparent bugs can be sent to PMx@vortex9.org, although no promise can be made that all such reports will receive responses or be investigated.

Upgrades

Upgrades to PMx will likely be released from time to time, either as minor fixes to bugs or as major upgrades with new features. There is no user registration for PMx, so users will not be notified automatically of the availability of such upgrades. The PMx website will have a list of significant bug fixes and new features provided with each new version. PMx will attempt to check for updates when opened if the computer is connected to the internet. Within the *Help* menu there is also an option to check the PMx website manually and download any upgrades more recent than the version running on your system. Attempts will be made to make all upgrades backward compatible to accept PMx project files created with prior versions, but no guarantee can be provided.

Cautions

PMx is distributed free of charge. It is provided without any promise of support. The primary developers of PMx and a large number of collaborating colleagues have attempted to provide the best, most current methods and tools to assist with the management of pedigreed populations. PMx is distributed with no guarantee that the methods perform as intended or described, that the computer code is without bugs that could influence results, or that the program is suitable for any particular purpose.

Acknowledgements

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SECTION 2: SELECTION SCREEN

Purpose

The **Selection** screen allows the user to fully define which individuals are included in the demographic and genetic population analyses. The individuals selected are used for both historical analyses as well as analysis of the current living population and therefore generally should include both living and dead individuals. Usually, the selected individuals comprise the population that is being managed demographically. Individuals may be excluded from demographic and/or genetic management because they are in other regions, or are held by private individuals or institutions that will not be participating in the cooperative breeding program, or due to behavioral, physiological, or husbandry reasons. Sometimes a different set of individuals (either a larger set or a subset) are believed to be a better representation of the demographic or genetic characteristics of the managed population.

There are two selection screens in PMx – the primary **Selection** screen on the main PMx window and another on the **Selection** tab in the **Genetics** module. The two screens operate in a similar manner with some minor differences (see the *Genetics Selection Tab* section of the manual for more information). The **Selection** tab is provided under **Genetics** for convenience so that the user can quickly modify the population for genetic analysis within the **Genetics** module.

*A good understanding of the **Selection** screen is crucial for successful and correct use of PMx. It is recommended to read the manual section for this screen completely before proceeding with analysis!*

How to Use This Tab

In many cases the user will have already used geographic, association, date span and/or other filters in the studbook database software (SPARKS, PopLink, etc.) when creating the export files for PMx in order to define which individuals should be included in the population analyses. If required, the **Selection** screen in PMx can be used to further refine the list of individuals that should be included in either demographic analyses, genetic analyses, or both.

Using the Selection Screen

The following information describes the **Selection** screen view when data are exported from SPARKS 1.6 or from PopLink (using the advanced Analytical Survival Statistics option); see subsequent information on differences using other studbook software exports and filters.

When the PMx project is first created the left-hand table shows the individuals in the *Selected Population* that will be included in the population analyses, based on the data exported from the studbook. In the right-hand table are those individuals *Not Selected* to be in the analyses. The total number of selected or unselected individuals (*Number Included/Not Included*) is displayed above each table. Individuals within each table can be sorted by any column by clicking on the column heading. Click again to sort in the reverse order. As with other tables in PMx, the table can be customized by changing the width and order of the columns, and by adding or deleting columns by right-clicking on the header. Many columns can be helpful in identifying individuals that should be excluded for either demographic and/or genetic analyses.

PM2000 users will notice an important difference between PM2000 and PMx imports. PM2000 only allows selection in the genetics section and only displays individuals living on the day chosen for genetic analysis. The PMx selection screen, on the other hand, allows selection for both demographic and

genetic analyses and shows both living and dead individuals, which allows PMx to conduct historical demographic and genetic calculations.

In PMx, the left-hand table with the *Selected Population* will contain the following individuals:

1. *Individuals already living in the population at the start of the date span selected for analysis*, including those individuals that may have left the population before the end of the analysis period by *Death*, *Lost-To-Follow up (LTF)*, *Release* or *Export*. These individuals contribute to the analyses from the start of the analysis date span to the end of the selected date span, or up until the date that they leave the population if they do so before the analysis end date.
2. *Individuals that enter the population at some point during the date span selected for analysis*, either by *Birth*, *Capture* or *Import*, including those individuals that leave the population before the end of the date span. These individuals contribute to the analyses beginning on the date they enter the population until the end date for analysis, or until they leave the population if this happens before the analysis end date.

The *Managed N* in the footer at the bottom of the screen represents the number of living individuals in the population currently selected for genetic analysis along with a summary of the genetic status of this population. Initially this population includes all individuals in the left-hand table (*Selected Population*) that are still alive at the end of the date span chosen for analysis, minus those individuals that were exported or released or became *Lost To Follow up* before the end of the analysis period (i.e., the individuals available for management at the end of the time period chosen for analysis).

PMx: okmantest1

File Language Help

Project Window Selection Demography Sources Data Recommendations

Selected Population Number Included = 414

UniqueID	Location	LocalID	HouseName	OtherID	Sex	Alive	AgeYrs
259	SD-WAP	102949	Mokolo	[]	Male	False	22
313	DALLAS	864685	Bambasa	[]	Female	False	25
157	PARIS ZOO	261079	Pablo	[]	Male	False	30
249	ANTWERP	M5758	Paprika	[]	Female	False	20
108	ROTTERDAM	101465	Mambuti	[]	Female	False	30
194	ROTTERDAM	101470	Lindi	[]	Female	False	24
219	BERLINZOO	900036	Aburo	[]	Male	False	27
283	DALLAS	823502	Fons	[]	Male	False	25
478	DISNEY AK	000211	Zenzelle	[0001DB]	Female	True	14
160	CHICAGOBR	21064	Fredricka	[]	Female	False	29
253	CHICAGOBR	22530	Mufuh	[]	Female	False	27
214	CHICAGOBR	22694	Uhuru	[]1688[]	Male	False	18

Export Import

Revert to originally imported data Update Selection

☒ Apply changes in Selection to Genetics ☒ Apply changes in Selection to Demography

Managed N = 170; % Pedigree Known = 100,0; Current Gene Diversity = 0,953; Potential Gene Diversity = 0,977; Lambda = 1,030

Not Selected Number Not Included = 299

UniqueID	Location	LocalID	HouseName	OtherID
60	EPULU		Mambasa	[]
52	EPULU		Nepoko	[]
155	DALLAS	001051	Viviane	[]145[]
154	DALLAS	600C74	Kopo	[]146[]
216	SD-WAP	102950	Kamina	[]
153	SANDIEGOZ	160217	Lisette	[]
152	SANDIEGOZ	004435	Kitambala	[]
68	SANDIEGOZ	004434	Bayahu	[]
172	COLO SPRG	74M012	Baruti	[]
69	PARIS ZOO	Z55165	Inumu	[]
35	PARIS ZOO	Z4911C	Dolo	[]
123	PARIS ZOO	Z57142	Ebola	[]

Export

Exactly which individuals are included in the *Managed N* when the PMx project is first created can be checked by sorting the *Selected Population* table by the column *Alive* and checking which individuals have *Alive = True* and *Gone = False*. The *Gone* column checks which individuals have left the population before the end of the date span analyzed through *Death*, *Lost To Follow up*, *Release* or *Export* – individuals that left the population are marked as *Gone = True*, while those that are still in the population at the end of the date span are marked as *Gone = False*. For example, an individual that was exported from the population (e.g., went to another zoo region) but is not dead would be marked as *Alive = True* and *Gone = True* and would not be included in the *Managed N*.

Project Notes Selection Demography Genetics Goals Recommendations

Selected Population Number Included = 137

UniqueID	Location	Local	HouseName	Sex	AgeYears	Alive	Gone
423	OKLAHOMA	7295	Malaika	[III] Female	9	True	False
432	YULEE	9300	Ingasu	[III] Female	9	True	False
437	OMAHA	1159	Kengo	[III] Male	8	True	False
438	ZOORASIA	1595	8	[IV] Female	8	True	True
447	DISNEY AK	9910	Jamal	[III] Male	7	True	False
452	YULEE	10M1	Nanoki	[0C] Male	7	True	False
453	COLUMBUS	2000	El Jewar	[0C] Male	7	True	False
457	YULEE	9500	Siri	[0C] Female	7	True	False
463	NY BRONX	9604	Hiari	[0C] Male	6	True	False
464	ZOORASIA	2	Kianga	[0C] Male	6	True	True
468	ZOORASIA	3	Layla	[0C] Female	6	True	True
478	DISNEY AK	0002	Zenzelle	[0C] Female	5	True	False
481	NY BRONX	9710	Kweli	[III] Female	5	True	False

Not Selected Number Not Included = 576

UniqueID	Location	LocalID	HouseName	OtherID
1	ANTWERP		Buta	[III]
2	ANTWERP		Congo I	[III]
3	ANTWERP		Tele	[III]
4	ANTWERP		Kitoko	[III]
5	ANTWERP		Kadanga	[III]
6	LONDON RP		Congo II	[III]
7	ANTWERP		Nn	[III]
8	ANTWERP		Roubi	[III]
9	LONDON RP		Buta	[III]
10	NY BRONX	371618	Congo	[III]
11	PARIS ZOO		Nn	[III]
12	KISAN OKA		Epulu	[III]

Export Import

Revert to originally imported data Update Selection

☒ Apply changes in Selection to Genetics ☒ Apply changes in Selection to Demography

Managed N = 45; % Pedigree Known = 100.0; Current Gene Diversity = 0.931; Potential Gene Diversity = 0.953; Lambda = 1.051

Additional changes to the *Selected Population* can be made on this screen. First decide if the new *Selected Population* will apply to the demographic analyses and/or to the genetic analyses. Specify which analyses should use the new *Selected Population* by checking one or both of the boxes *Apply changes in Selection to Genetics* and *Apply changes in Selection to Demography* at the bottom right of the screen. Different selections can be applied in a series – for example, by making a selection and applying it to demography, and then making a different selection and applying it to genetics.

Next, create a new *Selected Population* by highlighting the individual(s) on the appropriate table. Use the *Shift* or *Ctrl* keys to highlight several individuals within one table at the same time if desired. Then use the *→* and *←* buttons to move the highlighted individuals to the other table (from left to right to remove them from the *Selected Population*, and right to left to add them to the *Selected Population*). Once all individuals have been moved to create the desired *Selected Population*, click on the *Update Selection* button at the bottom of the screen to apply the new selection to all of the relevant analyses in the **Demography** and/or **Genetics** sections of PMx. If this step is overlooked, PMx will display the message “*Would you like to update to your new selection?*” as soon as the **Demography** or **Genetics** tab (whichever is affected by the change in selection) is accessed.

NOTE: The correct *Apply changes* box(es) must be checked before changes to the *Selected Population* are made (i.e., before individuals are moved from one table to the other); otherwise, the different selections may not be saved when the PMx project is closed and reopened.

NOTE: In contrast to genetic analysis in PM2000, for genetic analysis in PMx it is not necessary or even generally useful to restrict the selection to the currently living individuals in the population. PMx will automatically only use individuals living in the population at the end of the analysis date span analyzed to calculate the genetic and demographic characteristic of the current population.

If different selections have been made for demographic and genetic analyses, either selection can be viewed by checking the appropriate *Apply changes* box. Checking the *Apply to Demography* box only will display the demographic *Selected Population* on the left; checking the *Apply to Genetics* box (whether or not the *Apply to Demography* box is checked) will display the genetic *Selected Population* on the left. Each table (*Selected Population* or *Not Selected*) may be exported at any time using the relevant *Export* button underneath the table and saved as a .txt, .csv, or .xls file.

To return to the originally imported selection, click on the *Revert to originally imported data* button and then on *Update Selection* button. The original data selection will be applied to the demographic and/or genetic analyses depending on which box(es) *Apply changes* box(es) are checked.

NOTE: Reverting to the original data will reset modifications made in the project – for example, all *Management Sets* will be deleted. Use this button with caution.

For SPARKS 1.5 and PopLink (basic demographic) exports:

If the studbook data export filters are set for a “living today” setting rather than a historical genetic filter as recommended in *Section 1*, then only living animals may appear in the *Selected Population* table (left side of the **Selection** tab screen) and no historical genetic analyses will be available. Using a historical date span for the genetic export is not recommended, as it will include all individuals that were ever in the geographic or association filter, even if they have since left the region or association but are still living or are now *Lost-to-Follow up*.

The historical population for demographic analysis cannot be changed in PMx when it uses *.prn files imported from SPARKS 1.5 or PopLink basic exports. These files contain summary demographic information rather than raw data and therefore limit the manipulations that can be done in PMx. However, it is still possible to modify the demographic selection for living individuals, which affects the age distribution and starting population for projections. Such modifications will not change the life table data.

For maximum flexibility and analytical capability, it is recommended that you use either SPARKS 1.6 or PopLink with advanced demographic exports.

Deciding How and Where to Create the Selection for Analysis

There are several stages at which the population can be filtered for demographic and genetic analysis for the historical and current population. These include setting filters in SPARKS or PopLink for exporting studbook data to PMx, the main **Selection** screen in PMx, the **Selection** tab within the **Genetics** module, and on the **Culling** tab within **Genetics**. Each of these methods has consequences for the analysis results, and the chosen selection process may differ depending upon the characteristics of the population and the analysis results desired. The studbook software version used for export limits some of these options. The following may be a useful sequence of events to follow when creating a project:

1. *Set the necessary filters in SPARKS or PopLink before exporting studbook data to PMx.*
Set the studbook export filters to define the population that should be analyzed as closely as possible. This typically involves setting a filter that restricts location (e.g., geographic or association filter) and restricts data span to that which represent current husbandry or management (also see *Section 1* on creating PMx projects).
For example:
 - All individuals in Europe (geographic filter) from 1 Jan 1985 to today; or
 - All individuals in JAZA (Association filter) from 1 Jan 1990 to 1 Jan 2009

SPARKS 1.6 combines demographic and genetic exports into one file using the same filter criteria. The exported data includes information on when each individual entered and/or left the data span/population, allowing for historical analysis of both demographic and genetic data. PMx automatically determines which individuals are still living (*Alive* = true) and in the *Selected Population* (*Gone* = false) for results calculated on the current living population, such as the *Age Distribution* or current *Gene Diversity*.

SPARKS 1.5 and PopLink currently do not export information on when individuals enter and leave the population (if other than by birth/capture and death). Therefore it is necessary to set export filters for genetic analysis separately in these studbook programs to include only those individuals currently living in the population. In this case PMx will not report historical genetic results (see *Section 1* of the manual for information on setting export filters).

Setting the proper filters when exporting data from the studbook will result in a table of selected individuals in PMx (left table) comprised of all individuals exported for genetic analysis, which is either all individuals that were ever in the defined population anytime during the defined data span (SPARKS 1.6) or all living individuals in the defined population (SPARKS 1.5 or PopLink). The user then needs to decide if particular individuals/institutions should further be removed from the demographic and/or genetic analyses for other reasons.

2. *In PMx, deselect any additional individuals that need to be removed from all analyses (BOTH genetic and demographic analyses) – SPARKS 1. 6 and PopLink (advanced export) only.*

There may be a number of reasons why the user may want to remove additional individuals from both the genetic and demographic analyses. For example, there may be a particular individual in an institution that is used only for education purposes that the breeding program coordinator does not need to manage, that does not occupy cage space designated for the managed population, and whose genetic and demographic information is not important/desired in the analysis. It may be easier to remove this individual from the selection in PMx rather than set export filters in the studbook software so as not to include it in the export files. Another example might be that data were exported for a particular geographic region or zoo association, but there may be a reason to exclude individuals from a particular institution (e.g., private facility or dealer).

To remove individuals from both genetic and demographic analyses, deselect the individuals in the **Selection** tab in PMx while both the boxes for *Apply changes in Selection to Genetics* and *Apply changes in Selection to Demography* are checked. Remember to click the *Update Selection* button for any changes in selection to take effect. For SPARKS 1.5 or PopLink (basic) exports, the demographic selection used to calculate the life tables is determined within those programs and cannot be modified in PMx; therefore, any selection changes applied to demography in PMx will change the individuals in the age distribution and in the starting population for projections but will not change the data underlying the life table calculations..

3. *Remove individuals that can never breed again from genetic analyses.*

It is generally recommended to remove living individuals that can never breed or will never be bred again (e.g., post reproductive, sterilized, poor health, hybrid) from the genetic mean kinship calculations, as these individuals can no longer pass on their genetic material to the next generation and their inclusion influences the mean kinship values of other individuals in the population. However, these non-reproductive individuals may occupy cage space and need to be managed in other ways. In addition, their demographic information is valuable. Managers therefore often chose to include these individuals in the demographic analysis but to exclude them from genetic analysis. There are two options for removing these individuals from the analysis, and each method has its own set of consequences. Different people generally prefer

different methods and one is not more correct than the other, as long as the user is aware of how to interpret the results.

Option 1: Remove permanent non-breeders in the **Selection** screen, either on the main **Selection** screen or on the **Selection** tab within the Genetics module.

Uncheck the box *Apply changes in Selection to Demography* and make sure that the box *Apply changes in Selection to Genetics* is checked so that the selection will only be applied to the genetic calculations. Deselect the non-reproductive individuals by moving them to the table on the right, and click the *Update Selection* button. These individuals now are not counted in the genetic calculations but do appear in the age pyramid, population projections, and other demographic analysis.

NOTE: Only remove individuals that can definitely never breed again; do not remove contracepted or pre-reproductive individuals, those with temporary health problems, or other individuals that still hold the potential to breed later.

Consequences:

- The *Managed N* and genetic information in the PMx main footer will display the information for the subset of the population used for genetic analyses, not for the total living managed population.
- When making pairings under the **Pairing** tab, the displayed change in *GD* resulting from the pairings is the change compared to the *GD* in the subset of the current population used for genetic analysis, rather than the *GD* of the entire living population being managed.
- The **Recommendations** table will only include rows for the genetically managed individuals, and those individuals excluded from the genetic analysis may need to be manually added to the table if recommendations are to be included for these individuals.
- The 'unselected' individuals excluded from genetic analyses in this way are also removed from the historical genetic analyses for their entire lifetime (even if earlier in their lifetime they were capable of reproducing and should 'legitimately' contribute to the genetic statistics of the population at that time).
- The calculation of current effective population size (*Ne*) and *Ne/N* will be misleading, as it will not include these individuals. Living individuals that bred in the past but are now sterilized or post-reproductive will not contribute to the tally of breeders in the current population, on which the calculation of *Ne* is based.

Option 2: Remove permanent non-breeders in the **Culling** tab in the **Genetics** module of PMx.

Rather than deselecting non-reproductive individuals on one of the **Selection** screens, it is possible to exclude them from genetic analyses by culling them on the **Culling** tab in the **Genetics** module.

Consequences:

- The *Managed N* and genetic information in the PMx main footer will display the information for the total living population being managed (including the individuals that can never breed again). However, within the detailed **Genetic** module, the *Dynamic Population Variables* will display the information for the population with culled animals removed and with any chosen pairings having bred.

- When making pairings under the **Pairing** tab, the displayed change in *GD* resulting from the pairings is the change relative to the *Dynamic* value, which includes the effects of any culls (and pairs) already executed, for the entire living population being managed.
- The **Recommendations** table will include rows for all individuals in the management program, including the non-reproductive ones.
- The ‘unselected’ individuals excluded from genetic analyses in this way count toward the historical genetic analyses over their entire lifetime (even if they are already non-reproductive for a number of years)
- The *Ne* and *Ne/N* calculations will accurately reflect the number of past breeders in the population, even if the individuals are no longer capable of breeding in the future.

Terms and Concepts

Selected Population: Those individuals that are included in a particular analysis. The *Selected Population* for genetic analyses may be the same or different as the *Selected Population* for demographic analyses.

Managed N: Number of living individuals in the *Selected Population* for genetic analyses. This may or may not represent all living individuals in the population that need to be managed in terms of space, social groups, and other non-breeding considerations.

New Features

- PMx provides the option to exclude individuals from demographic analyses as well as genetic analyses (with SPARKS 1.6 and PopLink (advanced) exports); PM2000 only offered a selection screen in the genetics section.
- The selection screen in the genetic section of PM2000 only showed individuals living on the day chosen for genetic analysis. The PMx selection shows both living and relevant dead individuals (for SPARKS 1.6 and PopLink (advanced) exports), which allows PMx to conduct more precise historical calculations for both demographics and genetic analyses.

Helpful Hints

- Sorting the table first by *Gone* and then by a relevant variable such as *Age*, *ReproStatus*, *Known*, *Location*, or appropriate *UDF* can be useful to quickly identify living individuals to exclude from the genetically managed population.
- If changes are made to the *Selected Population*, it is recommended to document these changes in the **Project Notes**; otherwise it is easy to forget why some individuals were included and others excluded.

Cautions

- A good understanding of the **Selection** option is crucial for successful and correct use of PMx. It is recommended to read the manual section for this tab completely before proceeding with analysis.
- Some results may be misleading, depending upon how and where filters and selections are applied to the population data.
- The membership of regional zoo *Associations* is dynamic and changes over time. PMx does not have access to this information and therefore treats the *Association* list as static and equal to the list of institutions in the imported *.fed* file for that *Association*. For example, if an institution was a past member of an *Association* but recently left the *Association*, individuals at this institution in the past (when it was part of the *Association*) will not be included in the historical analyses.

- The current version of PMx will save the separate selections for demography and genetics, but only if the correct boxes (*Apply changes to ...*) are checked/unchecked before highlighting individuals and moving them from one table to the other. If individuals are moved and then different boxes are checked before clicking *Update Selection*, this new selection will not be saved.
- When making changes in selections it is recommended to carefully check the total *Number Included* above the *Selected Population* table, the *Managed N* in the footer, and other variables to confirm that the correct subset of individuals is being used.

SECTION 3: DEMOGRAPHY MODULE

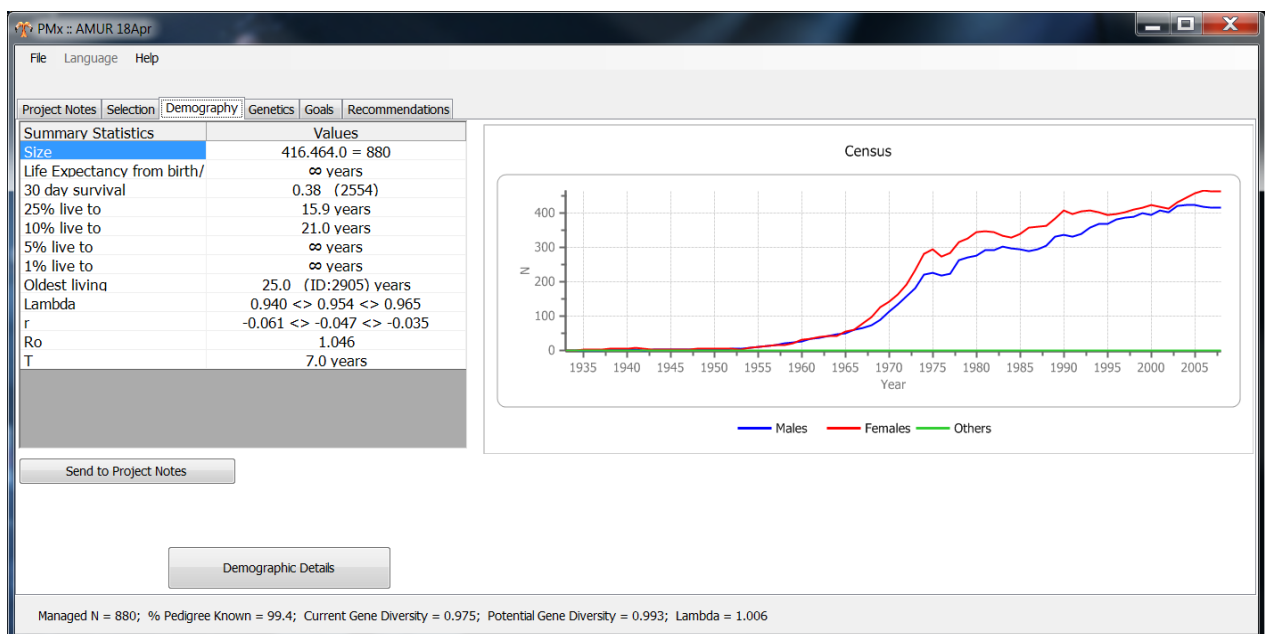
DEMOGRAPHY SUMMARY STATISTICS SCREEN

Purpose

The main **Demography Summary Statistics** screen provides basic summary statistics for the population as defined on the **Selection** tab. It includes a census graph for males, females, and individuals of unknown sex as well as population demographic values.

How to Use This Tab

The tabular information on the left side of the screen is based upon the selected population. If the individuals in the selected population are changed on the **Selection** tab and the box *Apply Updated Selection to Demography* is checked, this **Summary** tab as well as other demography values will be updated.



The following information is provided on this tab:

- Size:** Current size of the selected population (males.females.unknown sex = total).
- Life Expectancy:** Average life expectancy at birth/hatch, averaged between males and females. Will display ∞ if the oldest animal(s) ever existing is still living.
- 30 day survival:** Weighted average 30-day survival of males, females and unknown sex individuals, where weights are the sample sizes. Total sample size given in parentheses ().
- [25%] live to:** Based on an average between males and females, the age at which survivorship (L_x) reaches 0.25, 0.10, 0.05, and 0.01, respectively for 25%, 10%, 5%, and 1%. Some fields may display ∞ if the oldest animal(s) ever is still living.
- Oldest living:** The oldest currently living animal (displays age and *UniqueID* or *n* if more than one individual lives to that age).

<i>Lambda</i> (λ):	The proportional change in population size from one year to the next based on life table calculations (expected lambda), averaged for males and females. Lambda > 1 for increasing populations; lambda < 1 for declining populations.
<i>r</i> :	Instantaneous rate of change of the population, averaged for males and females. If $r > 0$, the population is increasing; if $r < 0$, it is decreasing.
<i>Ro</i> :	Net reproductive rate, which is the rate of change per generation (average number of offspring that an individual will produce in its lifetime), averaged for males and females. $Ro > 1$ for increasing populations and $Ro < 1$ for declining populations.
<i>T</i> :	Mean generation time (averaged for males and females), which is the average age of reproduction (production of offspring). It is also the average time from reproduction in one generation to reproduction in the next generation. T is <i>not</i> the age of first reproduction.

Once stochastic projections are run, the averages and bracketed *Confidence Intervals* are shown. Default setting for the confidence intervals is 95% (CI % may be changed on the demographic **Settings** tab).

Click on *Send to Project Notes* to copy the table data to the **Project Notes** tab. Double-click on the graph for options to print the graph, export it to a file, or send it to the **Project Notes** tab.

Click on the *Demographic Details* tab to open the full **Demography** section of PMx, an expansive demography module that includes tabs for more complex demography overview information, male and female life tables, age distribution and census graphs, population projections, reproductive planning, supplementation and removal (harvesting) schemes, and pre-set and user-defined demographic graphs. Options are also available to customize many program settings for analyzing the demographic data.

Helpful Hints

- Be sure to indicate a *Census File* when creating the project in order to display a census graph.

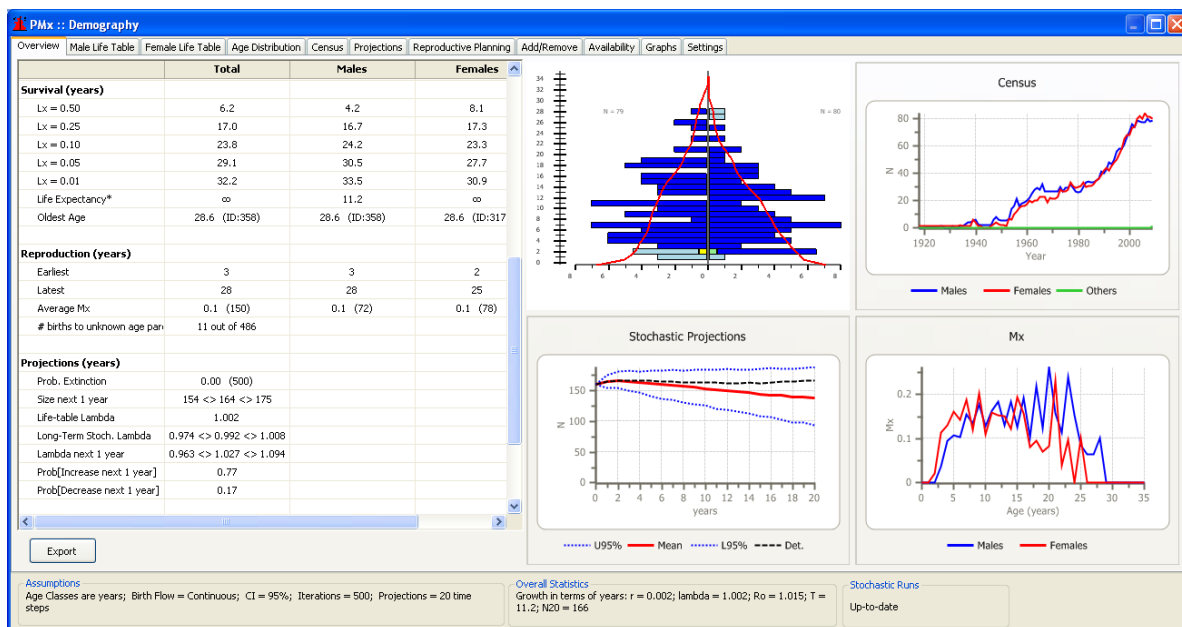
DEMOGRAPHY OVERVIEW TAB

Purpose

The **Demography Overview** tab provides more detailed demographic information for the current population as defined on the **Selection** tab (when the box *Apply Updated Selection to Demography* is checked). This includes total number of individuals by sex and reproductive status; population growth parameters; mortality rates; survival data; reproduction data; stochastic projection results; and impact of current age/sex structure.

How to Use This Tab

This tab is accessed from the *Demographic Details* button on the **Demography Summary Statistics** screen. The table on the left side of the screen provides a number of demographic statistics pertaining to the population. Values are provided for the *Total* population and also by sex (when appropriate). The four graphs on the right are repeated from the **Age Distribution**, **Census**, **Projections** and **Graphs** tabs (see the manual sections for these tabs for further explanation). If individuals are added to or removed from the *Selected Population* on the **Selection** tab, and the box *Apply Updated Selection to Demography* is checked, these statistics will be updated to reflect the new selection.



Totals

This section gives the number of living individuals in the current selected population (i.e., living as of the Analysis Date). Total counts, as well as counts broken down by sex, are listed for the following categories:

Pre Reproductive: Number of living individuals not yet of breeding age, defined by those individuals in the early age class(es) for which $Mx = 0$ (in the *Model Data* on the **Life Table** tab).

Breeding Age: Number of breeding age individuals, defined by those individuals in age classes where $Mx > 0$.

Post Reproductive: Number of living individuals considered to be no longer capable of breeding, defined by those individuals in older age classes where $Mx = 0$.

<i>Proven Breeder:</i>	Number of living individuals that have bred at least once in their lives, regardless of whether their offspring are still living and/or in the current population.
<i>Of breeding age:</i>	A subset of the above (proven breeders) that are still of breeding age (i.e., not yet post reproductive).
<i>Contracepted:</i>	Number of living individuals that are listed as <i>Contracepted</i> in the studbook database as of the end of the export date window.
<i>Sterilized:</i>	Number of living individuals that are listed as permanently <i>Sterilized</i> in the studbook database as of the end of the export date window.
<i>Fertile:</i>	Number of living individuals that are presumed capable of breeding (not listed as <i>Contracepted</i> or <i>Sterile</i> in the studbook database export).

Institutions

Provides the number of institutions (*Locations*) represented by the selected living population.

Life Table Summary

These values are based on life table calculations from demographic data of those individuals (living and dead) in the *Selected Population* on the **Selection** tab (for which the box *Apply Updated Selection to Demography* is checked), and is based on the date window (and any other filters, such as geographic or association filters) for the exported studbook data. Initially, deterministic values are displayed based on life table information. Once stochastic projections are run, several values are displayed in the center of the column and are bracketed by *Confidence Intervals*, defaulted to 95% (CI % may be changed on the demographic **Settings** tab).

<i>r:</i>	Instantaneous rate of change of the population, averaged for males and females. If $r > 0$, the population is increasing; if $r < 0$, it is decreasing.
<i>Lambda (λ):</i>	The proportional change in population size from one year to the next based on life table calculations (expected lambda), averaged for males and females. $\lambda > 1$ for increasing populations; $\lambda < 1$ for declining populations.
<i>T:</i>	Mean generation time (averaged for males and females), which is the average age of reproduction (production of offspring). It is also the average time from reproduction in one generation to reproduction in the next generation. <i>T</i> is <i>not</i> the age of first reproduction.
<i>Ro:</i>	Net reproductive rate, which is the rate of change per generation (average number of offspring that an individual will produce in its lifetime), averaged for males and females. $Ro > 1$ for increasing populations and $Ro < 1$ for declining populations.
<i>N20 (time step):</i>	A projection of how many individuals will exist in 20 time steps if current trends continue. Default <i>time step</i> is one year, but this can be changed in the Settings tab.

Mortality

Mortality (proportion of individuals that died during an age class) is given, with sample size provided in parentheses ().

<i>30 Day:</i>	Proportion of individuals that die within 30 days of birth or hatch. The length of time defined as early mortality may be changed on the demographic Settings tab.
<i>0 Age Class:</i>	Proportion of individuals that die during the first age class.
<i>Avg. Pre-Repro:</i>	Average of mortalities for all <i>Pre-Reproductive</i> age classes, where $Mx = 0$.
<i>Avg. Repro:</i>	Average of mortalities for all reproductive (<i>Breeding Age</i>) age classes, where $Mx > 0$.
<i>Avg. Post-Repro:</i>	Average of mortalities for all <i>Post-Reproductive</i> age classes, where Mx returns to 0.

Survival (time step)

Survival (L_x) of the selected population during the exported date window (and other filters).

$L_x = 0.50, 0.25$, etc: The age to which various proportions of the population survive (from 50% to 1%).

Life Expectancy: Average life expectancy at birth. Will display ∞ if the oldest animal(s) ever existing is still living.

Oldest Living: Oldest living individual (will display *UniqueID* if only a single individual, or n if more than one individual).

Reproduction (time step)

Reproductive summary of the selected population during the exported date window (and other filters).

Earliest: Age of earliest recorded reproduction in the selected population

Latest: Age of latest recorded reproduction in the selected population

Average M_x : Average overall reproductive rate M_x for age classes in which $M_x > 0$.

births to unknown age parents: Given in relation to all births.

Projections (time step)

Results of the stochastic projections (once they have been run).

Prob. Extinction: Probability that the population will go to zero (measured as the proportion of stochastic simulations in which the population goes to 0).

Size next 1 (time step): Projected size of the population, based on stochastic projections, after 1 time step (mean $\pm$ CIs).

Life-table Lambda: Growth rate based on the (deterministic) life table calculations.

Long-Term Stoch. Lambda: Growth rate based on the stochastic projection calculations (including CIs).

Lambda next 1 (time step): Growth rate in the next time step based on stochastic projections.

Prob[Increase next 1 (time step)]: Probability that the population will increase in the next time step, based on the stochastic projections.

Prob[Decrease next 1 (time step)]: Probability that the population will decrease in the next time step, based on the stochastic projections.

Age Structure Impact

Life table lambda is based on the exact demographic values in the male and female life tables, and do not take the actual population age and sex structure into consideration. However, deviations of the age and sex structure from a stable age distribution (SAD) will cause the short-term population growth rate to vary from the deterministic life table lambda. PMx compares the average stochastic lambda for the next two time intervals (S) to the life table lambda (L) and reports on the *Status* of the potential impact of this deviation from SAD. One of five *Status* messages is displayed:

Okay:

Life table and stochastic lambdas are in the same direction (both positive or both negative), the two lambdas differ by less than 2%, and there is less than 10% chance that the stochastic lambda (S) will be in a different direction than the life table lambda.

Actual growth rate deviates moderately from predicted growth rate:

Growth is in the same direction, but stochastic lambda deviates from life table lambda by 2-5%.

Actual growth rate deviates significantly from predicted growth rate:

Growth is in the same direction, but stochastic lambda deviates from life table lambda > 5%.

Moderate chance that the population will (increase, decrease) instead of (decrease, increase) as predicted:

There is a 10-20% change that stochastic lambda is in a different direction than life table lambda.

Significant chance that the population will (increase, decrease) instead of (decrease, increase) as predicted:

There is a > 20% change that stochastic lambda is in a different direction than life table lambda.

Demographic Footer

The footer across the bottom of the **Demography Overview** tab contains reminders of many of the variables that affect the demography (*Assumptions*); many of these assumptions can be changed on the demographic **Settings** tab. Also displayed are a few demographic *Overall Statistics* (*r*, *lambda*, *Ro*, *T*, projected *N*) as well as the status of the *Stochastic Runs* (*Outdated* or *Up-to-date*). This footer is displayed at the bottom of all **Demography** section tabs.

Cautions

- The age classes to be considered as Pre Reproductive, Breeding Age, and Post Reproductive are based upon past reproduction as indicated in the calculate *Mx* values for each sex in the life tables. It is possible that the population may simply not have bred at those ages yet; this is especially true if the overall population is relatively young or has not been in captivity long. Revision of the *Model Data* to *Mx* > 0 in early or late age classes may be needed to more appropriately define the biological reproductive lifespan for the species.
- The reproductive status of individuals (*Fertile*, *Contracepted*, *Sterilized*) is based on the designation of these individuals in the exported studbook database. If individuals are not listed as *Contracepted* or *Sterilized* in the studbook, they will appear as *Fertile* in PMx by default, which may or may not be accurate.
- Be sure to rerun the *Stochastic Projections* after making any changes in the *Model Data* or demographic *Settings*.

LIFE TABLES TABS

Purpose

These two tabs (**Male Life Table** and **Female Life Table**) provide the user with separate male and female life tables that provide the average survival and reproductive rates for the time period (view) for the data imported into PMx. The life tables allow for visualization of the demographic history of the chosen population.

How to Use This Tab

Life tables are created for males and females using life history data from all individuals in the selected time frame when data are exported from PopLink or SPARKS.

PMx :: NA MAL 25Mar :: Demography

Overview Male Life Table **Female Life Table** Age Distribution Census Projections Reproductive Planning Add/Remove Availability Graphs Settings

Females: Actual Data

Age (years)	Px	Mid Px	Qx	Risk Qx	Lx	Mid Lx	Mx	Risk Mx	Ex	Vx	Cx
0	0.93	0.96	0.07	32.4	1.00	0.96	0.00	32.4	15.35	1.04	0.10
1	1.00	1.00	0.00	31.0	0.93	0.93	0.00	31.0	14.92	1.15	0.09
2	1.00	0.99	0.00	30.8	0.93	0.93	0.00	30.8	13.92	1.22	0.09
3	0.98	0.98	0.02	26.4	0.93	0.92	0.14	26.4	13.06	1.31	0.08
4	0.98	0.99	0.02	25.2	0.91	0.90	0.36	25.2	12.30	1.26	0.07
5	1.00	1.00	0.00	25.0	0.89	0.89	0.15	25.0	11.40	0.97	0.07
6	1.00	0.96	0.00	24.3	0.89	0.89	0.29	24.3	10.40	0.87	0.07
7	0.92	0.96	0.08	21.8	0.89	0.85	0.14	21.8	9.81	0.65	0.06
8	1.00	0.97	0.00	20.7	0.82	0.82	0.29	20.7	9.21	0.57	0.05
9	0.95	0.94	0.05	18.8	0.82	0.79	0.00	18.8	8.43	0.30	0.05
10	0.94	0.93	0.06	14.3	0.77	0.75	0.18	14.3	7.89	0.34	0.04
11	0.92	0.96	0.08	9.6	0.73	0.70	0.00	9.6	7.40	0.18	0.04
12	1.00	1.00	0.00	8.0	0.67	0.67	0.20	8.0	6.67	0.20	0.03
13	1.00	0.92	0.00	8.0	0.67	0.67	0.00	8.0	5.67	0.00	0.03
14	0.83	0.91	0.17	6.8	0.67	0.61	0.00	6.8	5.09	0.00	0.03
15	1.00	1.00	0.00	4.4	0.56	0.56	0.00	4.4	4.50	0.00	0.02
16	1.00	1.00	0.00	4.0	0.56	0.56	0.00	4.0	3.50	0.00	0.02
17	1.00	1.00	0.00	4.0	0.56	0.56	0.00	4.0	2.50	0.00	0.02
18	1.00	0.50	0.00	4.0	0.56	0.56	0.00	4.0	1.50	0.00	0.02
19	0.00	0.00	1.00	0.0	0.56	0.28	0.00	0.0	1.00	0.00	0.01
20	0.00	0.00	1.00	0.0	0.00	0.00	0.00	0.0	0.00	0.00	0.00
21	0.00	0.00	1.00	0.0	0.00	0.00	0.00	0.0	0.00	0.00	0.00

Females: Model Data

Age (years)	Px	Mid Px	Qx	Risk Qx	Lx	Mid Lx	Mx	Risk Mx	Ex	Vx	Cx
0	0.93	0.96	0.07	32.4	1.00	0.96	0.00	32.4	15.35	1.04	0.10
1	1.00	1.00	0.00	31.0	0.93	0.93	0.00	31.0	14.92	1.15	0.09
2	1.00	0.99	0.00	30.8	0.93	0.93	0.00	30.8	13.92	1.22	0.09
3	0.98	0.98	0.02	26.4	0.93	0.92	0.14	26.4	13.06	1.31	0.08
4	0.98	0.99	0.02	25.2	0.91	0.90	0.36	25.2	12.30	1.26	0.07
5	1.00	1.00	0.00	25.0	0.89	0.89	0.15	25.0	11.40	0.97	0.07
6	1.00	0.96	0.00	24.3	0.89	0.89	0.29	24.3	10.40	0.87	0.07
7	0.92	0.96	0.08	21.8	0.89	0.85	0.14	21.8	9.81	0.65	0.06
8	1.00	0.97	0.00	20.7	0.82	0.82	0.29	20.7	9.21	0.57	0.05
9	0.95	0.94	0.05	18.8	0.82	0.79	0.00	18.8	8.43	0.30	0.05
10	0.94	0.93	0.06	14.3	0.77	0.75	0.18	14.3	7.89	0.34	0.04
11	0.92	0.96	0.08	9.6	0.73	0.70	0.00	9.6	7.40	0.18	0.04
12	1.00	1.00	0.00	8.0	0.67	0.67	0.20	8.0	6.67	0.20	0.03
13	1.00	0.92	0.00	8.0	0.67	0.67	0.00	8.0	5.67	0.00	0.03
14	0.83	0.91	0.17	6.8	0.67	0.61	0.00	6.8	5.09	0.00	0.03
15	1.00	1.00	0.00	4.4	0.56	0.56	0.00	4.4	4.50	0.00	0.02
16	1.00	1.00	0.00	4.0	0.56	0.56	0.00	4.0	3.50	0.00	0.02
17	1.00	1.00	0.00	4.0	0.56	0.56	0.00	4.0	2.50	0.00	0.02
18	1.00	0.50	0.00	4.0	0.56	0.56	0.00	4.0	1.50	0.00	0.02
19	0.00	0.00	1.00	0.0	0.56	0.28	0.00	0.0	1.00	0.00	0.01
20	0.00	0.00	1.00	0.0	0.00	0.00	0.00	0.0	0.00	0.00	0.00
21	0.00	0.00	1.00	0.0	0.00	0.00	0.00	0.0	0.00	0.00	0.00

Growth in terms of years: $r = 0.060$; $\lambda = 1.062$; $R_0 = 1.447$; $T = 6.1$; $N_{20} = 60$

Export Reset Smooth Table has been smoothed 0 times

Settings
Age Classes are years; Birth Flow = Continuous; CI = is95; Iterations = 500;
Projections = 20 time steps

Overall Statistics
Growth in terms of years: $r = 0.078$; $\lambda = 1.081$;
 $R_0 = 2.089$; $T = 8.3$; $N_{20} = 114$

Stochastic Runs
Outdated

On the left side of the screen is the *Actual Data* life table, which represents the true demographic rates imported into PMx and cannot be modified. On the right side of the screen is the *Model Data* life table. Initially both life tables display the same data; however, the *Model Data* life table can be manually altered or smoothed. Editable values in the *Model Data* life table are highlighted in gray and bolded (P_x , Q_x , and M_x). Once any of these values is altered PMx will automatically update the other values affected by the change, both in the *Model Data* table and also for other parameters such as λ and T in the **Demographic** footer at the bottom of the screen.

The *Smooth* button is located below the *Model Data* life table with a count of the number of times the table has been smoothed. Smoothing data can help to remove sharp dips and peaks within a data series. Each time the life table is smoothed, the P_x , Q_x , and M_x values are replaced with the median of that value, the preceding value, and the following value. The object of smoothing is to derive a P_x , Q_x , and

M_x curve that reflects the characteristics of the population as accurately as possible. Poor data quantity (small sample sizes) and quality can be a problem in many studbooks. The smoothing tool can provide more reasonable estimates of life table rates. However, care should be taken when smoothing data, as smoothing can often lead to unreasonable values in the life tables. Life tables should be examined for any smoothing anomalies when using this tool.

If the model data have been modified, the Life Table tab label will indicate this with “***”. *Stochastic Runs* will be labeled in red as **Outdated** in the lower right corner in the **Demographic** footer (see **Projections** tab for details). *Model Data* can be reset to the *Actual Data* at any time by clicking the *Reset* button under the *Model Data* life table.

When altering the life tables in any way, users should:

- Compare the *Actual Data* vs. *Model Data* life tables for all values.
- Check for reproduction in pre- and post-reproductive age classes. These may be outliers.
- Use knowledge of the species’ biology, husbandry, and management to modify the M_x values as needed.
- Check for modifications that significantly change the lambda or generation length.

When satisfied with the life tables, users can export either the *Actual* or *Model* life table to a text (*.txt), CVS (*.csv), or Excel file (*.xls) by clicking the *Export* button under the life table.

Below the *Actual Data* and *Model Data* life tables, PMx also calculates the population growth rate (r and λ) for a stable population under these conditions as well as net reproductive rate (R_0), generation time (T) and the projected number of males or females (N) for the specified projection time period (default = 20 years). All of these values are calculated independently for males and females.

Default assumptions are listed at the bottom left corner of the screen in the **Demographic** footer. These settings may all be changed on the **Settings** tab, which includes options for handling unassigned births, changing the proportion of unknown sex individuals, and dealing with multiple possible parents (see **Demography Settings** tab section for more details).

The **Settings** tab in Demography allows the user to:

- Change the birth flow (default = continuous).
- Change the length of the age classes (default = 1 year).
- Change the defined period to calculate early mortality (default = 30 days).
- Change the distribution of *Unassigned M_x* (default = in proportion to known).
- Add additional age classes to the bottom of the life table.
- Change the sex assignments to births (default = each birth is 0.5 male and 0.5 female).
- Change the sex assignment of unknown sex individuals (default = 0.5 male).
- Change the assignment of multiple parents (default = most likely parent is used for calculations if *UniqueIDs* have been exported; otherwise MULT is treated as Unknown).
- Change the time interval for reporting results (default = years) to days, weeks, months or decades. This changes *only* how population growth (λ , r) and generation length (T) are reported: these rates are relative to the interval chosen here. This setting does *not* change age class length. See **Projections** tab and **Settings** tab sections for more information.
- Change the birth sex ratio for projections (default = 0.50 male).

Terms and Concepts (see Appendix B for complete definitions)

Survival Rate (Px): The probability that an animal that is alive at age class x will survive to age $x + 1$.

Mid Px: The probability that an individual survives to the mid-point of age class x .

Mortality Rate (Qx): The proportion of individuals that die during an age class. This number is calculated from the number of animals that die during an age class divided by the number of animals that were alive at the beginning of that age class (the number of animals at risk).

Risk Qx: The number of animals that are alive during an age class. This is the sample size from which Qx is calculated. *Risk Qx* values are used to calculate mortality (Qx) by dividing the number of deaths that occurred during an age class by the total number of animals at risk of dying during that age class.

Survivorship (Lx): The probability that a new individual (e.g., age 0) will be alive at age x . Survivorship is a cumulative measure that represents the proportion of individuals that survive from birth to the beginning of a specific age class (i.e., the survivorship of age class 5 is influenced by all of the survival rates in the age classes from birth until age class 5).

Mid Lx: The proportion of individuals surviving to the mid-point of age class x .

Fecundity (Mx): The average number of same-sex young born to individuals in that age class. For each offspring, each parent gets 0.5 of the birth attributed to him/her.

Risk Mx: The number of animals that are alive during an age class. This is the sample size from which Mx is calculated. *Risk Mx* values are used to calculate fecundity (Mx) by dividing the number of births that occurred during an age class by the total number of animals at risk of reproducing during that age class.

Life Expectancy (Ex): The average number of additional years an individual in age class x can expect to live.

Reproductive Value (Vx): The expected number of offspring produced in this year and in future years by an animal in age class x .

Cx : The proportion of that sex that would be age x in a stable population.

r : Instantaneous rate of growth, calculated from the life table.

Lambda (λ) or Population Growth Rate: The proportional change in population size from one year to the next.

Net Reproductive Rate (Ro): Rate of change per generation.

Generation time (T): The time elapsing from reproduction in one generation to the time the next generation reproduces; also the average age of reproduction.

New Features

PMx provides greater flexibility in analyzing different species life histories, such as species with particularly short or long life spans. PMx provides the ability: to change the length of age classes; to add age classes; to define the time period for “early mortality” calculations; to model continuous or pulse reproduction; and to assign the sex of births based on actual sex or a fixed proportion. Several parameters (*Px midpoint*, *Lx midpoint*, *Ex*, *Vx*, *Cx*) have been added to the life tables.

Helpful Hints

- Always review the sample sizes of the age classes. If an age class has a sample size of fewer than 30 individuals, these rates should be viewed with caution.
- Px , Qx , and Mx can be modified to allow other demographic characteristics to be modeled.
- Standard graphs in the demographic **Graphs** tab reflect the data in the *Model Data* life tables; check these graphs to see if smoothing is necessary.

Cautions

- *Model data* currently are not saved with a PMx project; rather, *Model Data* default back to *Actual Data* when a saved project is reopened. This will affect projections, reproductive planning, and other similar demographic calculations. Be sure to export and save *Model Data* files so that these values can be recreated. Future versions of PMx may provide the ability to import model data files.
- Individuals with unknown birth date estimates are not used in any life table calculations, as the individual's age cannot be calculated. If possible, make sure all individuals in the population have birth date estimates prior to exporting to PMx in order to ensure these individuals are included in the life tables.
- Individuals with birth date age estimates will have their entered birth date used in calculations (i.e., the estimation range is ignored, and the entered date is used).
- Individuals of unknown sex are distributed as 0.5 male and 0.5 female throughout the life table calculations.
- The default when adding births into the life tables is to treat each birth as 50% male and 50% female. If the population has a sex bias the user may want to consider using the *Use Actual Sex* option on the **Settings** tab.
- Caution should be used with the *Smooth* tool, as too much alteration of data may misrepresent or alter trends within the life tables.
- Reproduction in the first age class typically will be overestimated, since PMx uses the N at the midpoint of the interval, while reproduction likely occurs near the end when few individuals are alive. To avoid this bias, PMx will automatically convert the age class length to a shorter time interval (e.g., month instead of year) when reproduction occurs in the first age class. Age class length can be changed on the **Settings** tab.

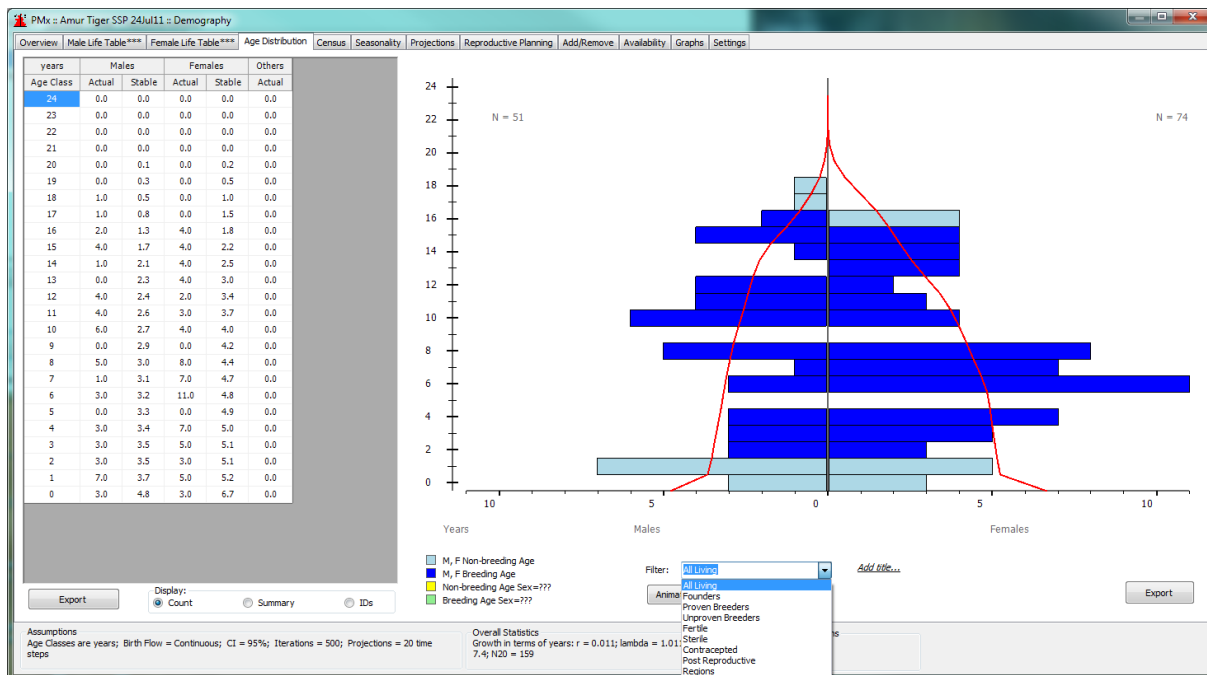
AGE DISTRIBUTION TAB

Purpose

This tab provides the user with the population's age structure data and graph, and also allows the user to project and visualize changes in the age distribution into the future.

How to Use This Tab

To the right of the screen, the **Age Distribution** graph shows the number males (on left) and females (on right) in different age classes (Y-axis). Each horizontal bar represents one age class (default age class = one year). The total number (N) of males and females is given on the figure at the top left and right corners respectively. The light blue color indicates those individuals that are out of the range of $Mx > 0$ and thus considered to be non-reproductive (immatures at the bottom of the distribution, post-reproductive individuals at the top). Unknown sex animals of breeding age are indicated in green; unknown sex animals of non-breeding age appear in yellow. Unknown aged animals are not shown.



The default view for the age pyramid is the living population, indicated as *All Living* in the drop-down menu beneath the figure. These are all individuals in the selected population that were living as of the Analysis Date, according to their age on that date. Other views (subsets of *All Living*) that can be selected from this drop-down menu are *Founders*, *Proven Breeders*, *Unproven Breeders*, *Fertile*, *Sterile*, *Contracepted* and *Post Reproductive*, and are determined as follows:

Founders. Displays all living genetic founders.

Proven Breeders. Displays sexually mature individuals that have produced offspring in the past.

Unproven Breeders. Displays sexually mature individuals that have not yet produced offspring.

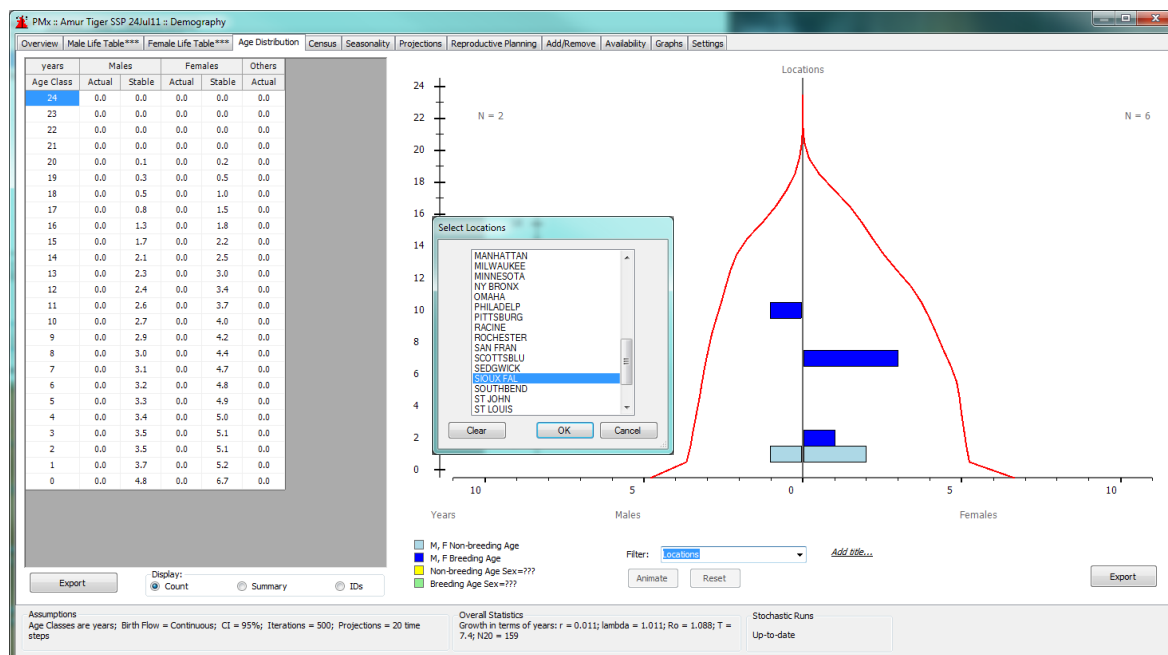
Fertile. Displays all individuals that are *not* characterized as *Sterile* or *Contracepted* in the imported studbook data.

Sterile. Displays all individuals that are characterized as *Sterile* in the imported studbook data.

Contracepted. Displays all individuals that are characterized as *Contracepted* in the imported studbook data. Currently, individuals marked as *Contracepted* in SPARKS may show up as ½ of a male and ½ of a female on the age distribution.

Post Reproductive. Displays all sexually mature individuals in age classes for which *Mx* has again dropped to 0 (i.e., no reproductive occurs at or after this age, based on *Life Table Model Data* for that sex).

The Filter drop down menu also provided the option to display age pyramids for a specific *Region*, *Association*, *Country*, or *Location*:



A title can be added above the age pyramid using the Add title ... button.

The table on the left side of the screen provides the data from which the age distribution graph is created. This table can be displayed by *Counts* (default), *Summary* and *IDs*; the display can be changed underneath the table:

Counts. Displays the actual numbers (Actual) and the numbers expected for a stable age distribution (Stable) for males, females and other sex types. A stable age distribution is the number of animals that would be expected in each age and sex class if the life table rates had been constant over time (indicated by the red lines on the graph).

Summary. Displays the total N for males, females and unknowns, as well as a breakdown of these totals to known and unknown age animals.

IDs: Displays a variation of the age distribution figure indicating each animal by their *UniqueID*. Clicking on one of these IDs in the table will provide a button  that will open a window with summary information on this specimen.

The *Animate* button uses the demographic assumptions and overall statistics (outlined in the footer at the bottom of the page, and as seen in the other PMx demography tabs) to animate the projected changes in the age distribution over time (default projection = 20 years). The *Animate* feature works only when viewing the graph of the total living animals (filter = *Alive*). The *Reset* button will reset the graph back to the original age distribution for the selected population.

Both the data table and the age distribution graph can be exported by clicking on the *Export* buttons.

Terms and Concepts

Age distribution: A two-way classification showing the numbers or percentages of individuals in various age and sex classes.

Founder: An individual obtained from a source population (often the wild) that has no known relationship to any individuals in the derived population (except for its own descendants).

New Features

- *Animate* button: Animates the projected changes (under assumed and current statistics, outlined in footer of page) in the age distribution of the total living population over time.
- Ability to view the age distribution of selected subsets of the population (e.g., proven breeders, by location).
- Tabular data can be viewed as Counts, Summary or IDs; only Counts were provided in PM2000.

Helpful Hints

Take a look at the age distribution:

- Are there any impossibly old animals? (if so, check your studbook data as these may be errors).
- Does the age structure show a baby boom or is it top- or bottom-heavy?
- Are there enough animals in breeding age classes to provide the desired amount of reproduction?
- Are unproven breeders aging, indicating a possible loss of breeding potential?
- How does the actual age distribution compare to the stable age distribution? If they are quite different, then population growth may behave quite differently in the future than it has in the past.

Cautions

The various age structure filters/views will only be as good as the studbook data.

- Example 1: A population that has a large portion of its pedigree recorded as unknown in the studbook may show very few proven breeders.
- Example 2: If contracepted animals are not recorded in the studbook, they will not be displayed on the graph.
- Example 3: If there are few reproductive data available (because the population has not been in zoos for very long, or parentage is not always recorded), the *Post Reproductive* view or the non-reproductive animals (indicated in a light blue on the graph) may not be correct.

CENSUS TAB

Purpose

The **Census** tab provides both numerical and graphical information on population size over time, including by sex and by origin (wild-caught vs. captive-born individuals).

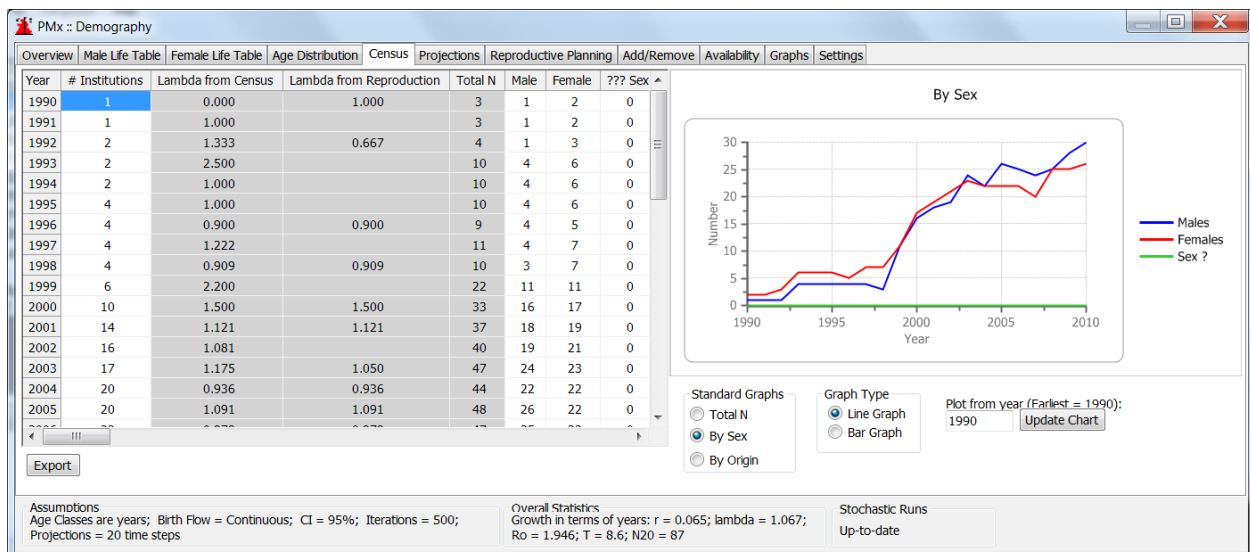
How to Use This Tab

The left side of the **Census** screen provides historical data on individual counts over time based on the imported studbook data and filters. Total population counts (and # institutions holding these individuals) are given as of 31 December of each year; these totals are also broken down by sex (males, females, unknown sex) and by origin (wild born, captive born, origin unknown). Yearly lambdas are provided based on census numbers (*Lambda from Census*), which includes changes in population size due to all sources (e.g., captures, imports, releases, exports), and also lambdas based on the life tables (*Lambda from Reproduction*), which take only births and deaths into account.

PMx projects created using census data from SPARKS 1.6 display additional information on the number of captures, births, stillbirths, releases, deaths, LTFs (lost-to-follow up), imports, and exports occurring during each year. Sex ratio (both as % males and #M:#F) is also provided.

These tabular data are not alterable. Use the *Export* button under the table to save the table as a *.txt, *.csv or *.xls file.

The right side of the screen displays a census graph. The default graph is a line graph of the total population size. The buttons below the graph allow the graph to be revised to display results by sex or by origin, and as a line or bar graph. The beginning date to be plotted can be changed (by typing in the first year to plot and clicking *Update Chart*), but PMx will not accept a date earlier than the exported data. Click on the '<<' button to reset date to earliest date. The graph can be exported by double-clicking on the graph and selecting either *Export to File* or *Send to Report*. Graphs of additional census data information are available under *Custom > Census* graphs on the **Graphs** tab in the **Demography** section.



New Features

This feature operates in a similar manner as the Census tab in PM2000; additional new features include:

- Ability to modify the starting year
- Ability to display the census as a bar graph
- Ability to view and graph additional events (e.g., captures, exports) over time
- Ability to graph sex ratio (for census population and at birth) over time
- Ability to view and graph both types of lambda over time

Helpful Hints

- SPARKS will only export census data up through the currentness date for the studbook. Be sure that the currentness date is correct to get complete available census information.

SEASONALITY TAB

Purpose

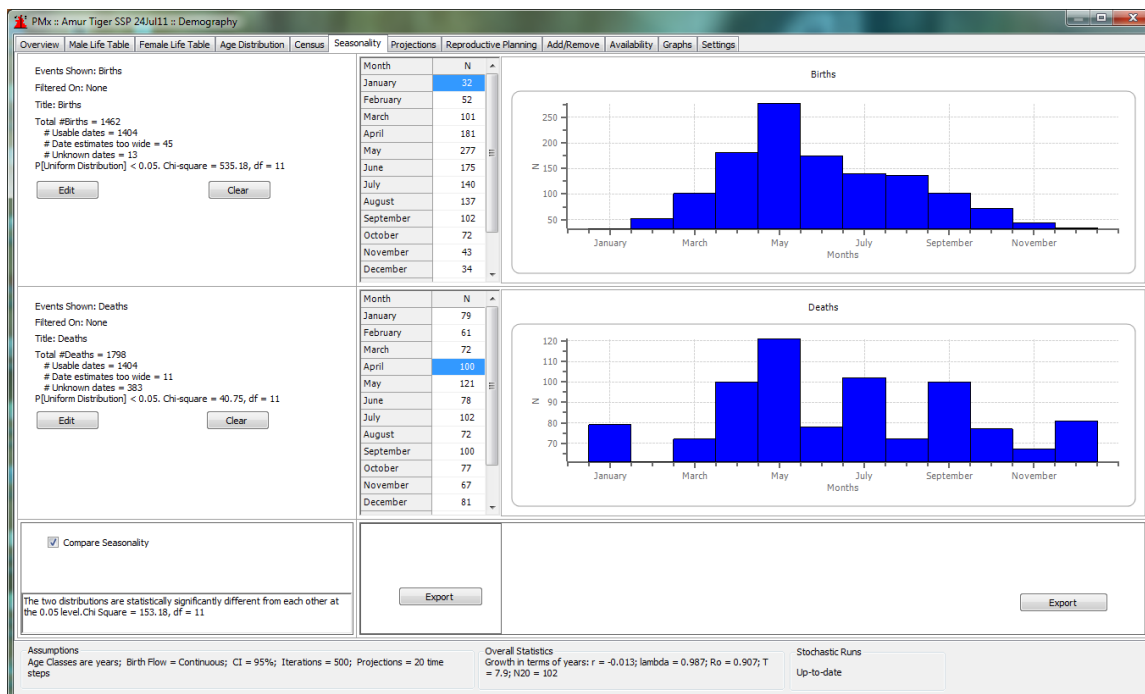
The Seasonality tab provides seasonal birth and death data (by month) and a statistical evaluation regarding whether these monthly trends differ significantly from a uniform pattern across the year. These data may help to inform population planning as well as suggest whether Pulse vs Continuous birth flow is a more appropriate choice on the demography **Settings** tab for this population.

How to Use This Tab

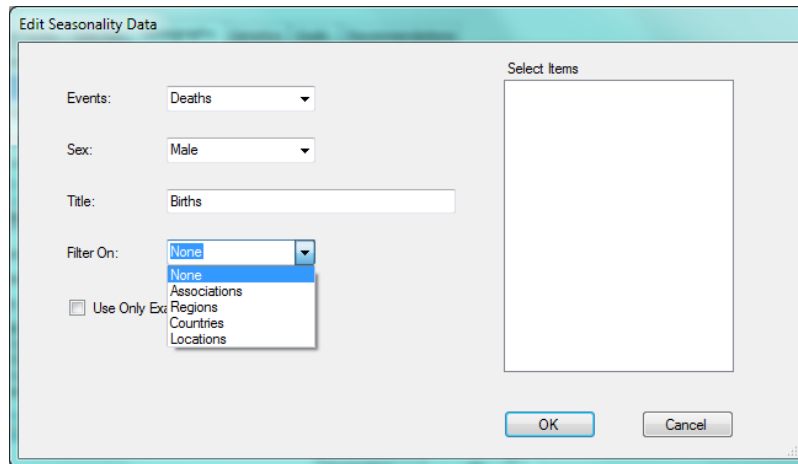
The default view displays birth data on the top section of the tab and death data on the second section underneath. The right side of the screen displays a histogram of number of events (births or deaths) per month; a table giving these frequencies are displayed to the left of each histogram. These tables can be exported as *.txt*, *.csv* or *.xls* files using the *Export* button below them; similarly, the graphs can be exported as *.png* files.

The left section of the tab specifies the data used for these analyses. The total (default) sample size is given for birth and deaths and then is divided into the number of events used in the tables and graphs (*# Usable dates*), the number of events omitted from the analyses due to date span estimates to the year or greater (*# Date estimates too wide*), and the number of events with *Unknown dates* (also removed from the analyses).

PMx conducts a Chi-square statistical test on each distribution to determine the probability that the observed data would occur by chance. Generally, if the $P[\text{Uniform Distribution}] < 0.05$, this indicates a non-random pattern of event distribution across months. If the distribution shows a strong peak and the analysis is statistically significant (i.e., $P[\text{Uniform Distribution}] < 0.05$), the user might consider choosing a *Pulse* birth flow on the demographic **Settings** tab.



PMx currently provides a few options for changing (filtering) the data used in each of the two analyses. Clicking the *Edit* button brings up a window of options for the table and graph to the right. Both births and deaths can be filtered by sex. In addition, deaths can be filtered by *Association*, *Region*, *Country* and *Location* of death (hopefully this option will be available for births as well in a future version of PMx). There is also an option to *Use Only Exact Dates*, omitting estimated dates from the analysis. A title can be provided for each graph.



Filters can be used to specify and compare two distributions: for example, the seasonality of births for males vs. female births can be compared by selecting Births for both distributions, and filtering each by a different sex. The *Compare Seasonality* check box in the lower left will perform a Chi-square statistical test to compare whether or not these two distributions are significantly different from each other.

Terms and Concepts

Chi-square: A statistical test that compares a distribution of observed frequency data to that expected based on a particular hypothesis (e.g., that there is no pattern in frequency, or that two distributions are the same), and estimates the statistical probability based on sample size (see a statistical reference or text for more detailed and precise information).

New Features

This is a new feature—seasonality data and analyses are not provided in PM2000.

Helpful Hints

- Remember to change the *Title* of the histogram when you change the *Events*, *Sex* and/or *Filter*.

PROJECTIONS TAB

Purpose

The **Projections** tab provides an estimation of future population size (total N, # males, # females) given the model life table demographic rates applied to the actual current age and sex distribution. Both deterministic and stochastic projections are provided, as well as a deterministic projection based on a starting stable age distribution. Projections can also be generated for non-breeding populations.

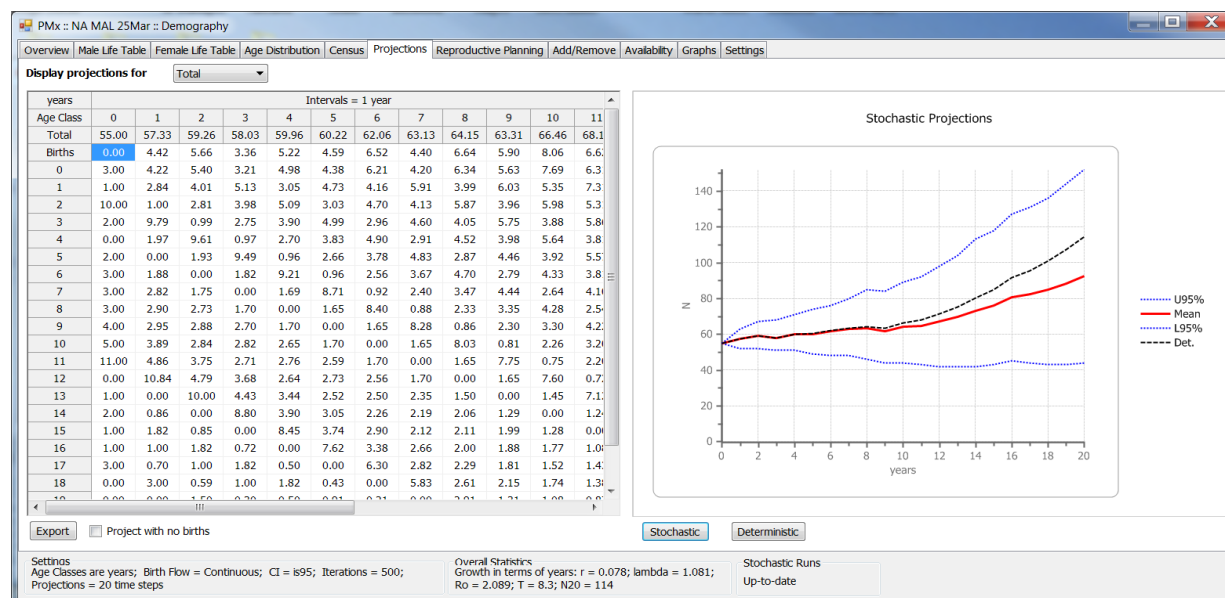
Actual vs Stable. The difference between the actual and stable projections demonstrates the impact of the current age structure. For example, if there are relatively few individuals of breeding age (as compared to a stable age distribution), growth will be lower and the population might even decrease in size. The impact of non-stable age distribution modulates and lessens over time as the age structure approaches a stable distribution.

Deterministic vs Stochastic. Life table rates represent average rates over a period of time and across individuals. In reality, reproduction and survival varies for each individual – these chance (stochastic) variations tend to ‘even out’ in large populations but can have an impact on small populations. These impacts accumulate over time, producing more variation (more uncertainty) in projected N over time. The mean stochastic projection provides a more realistic projection by incorporating these effects; variation around this mean is provided (as confidence intervals – CIs), which can be helpful in conveying the range of projected future population size.

Non-Breeding Populations (No Births option). PMx provides the option to easily project population size given no reproduction. This is useful for estimating population size and decline for populations being ‘phased out’ and managed ‘to extinction’ through attrition (i.e., no reproduction, normal survival).

How to Use This Tab

The table on the left provides the numerical projections for each interval over time; these projections are depicted on the graph on the right. Default projection settings are for 20 years using one-year intervals. The number of time intervals projected can be changed on the demographic **Settings** tab.

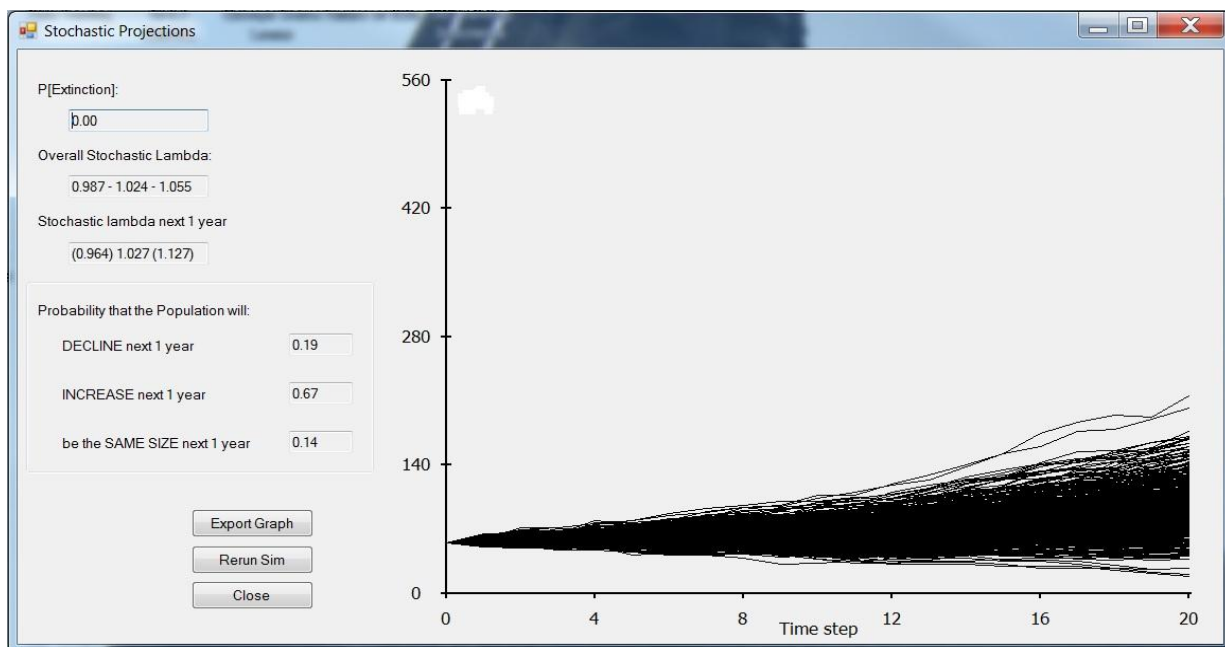


The initial projection displayed is deterministic for the total population (and possibly also stochastic, depending upon version of PMx used). Projections can be viewed for males and females separately using the pull-down menu above the table. Projections can be toggled between reproducing and non-reproducing populations using the check box below the table. The table data can be exported to .txt, .xls or .csv files using the *Export* button below the table. Double-clicking on the graph provides options for exporting the graph (as a .png file) or sending it to the report.

Depending upon the version of PMx that you are using, the stochastic projections may have been run automatically or may need to be run before the results can be viewed. The word **Outdated** will appear in the lower right either if stochastic projections have not been run, or if relevant data have been changed in PMx that could affect these projections and indicating that the stochastic projection should be run again. This will change to *Up-to-date* once stochastic projections have been run. Use the *Stochastic* button below the graph to run stochastic simulations of future population trends. This will open a new window that displays a line for each simulation of the population over time. The default settings run 500 iterations. Use the *Export* button to export the graph, the *Rerun Sim* button to run a new set of iterations, and the *Close* button to close this window. Numerical results provided in this window include:

- Probability of population extinction $P[\text{Extinction}]$ over the projected time period
- Mean stochastic lambda over the projected time period (and CIs)
- Mean stochastic lambda for the next year (and CIs)
- Probability that the population will Decline, Increase or be the Same Size in the next year (as defined by the proportion of simulations for each case)

Because these results are stochastic, the values will vary if the stochastic projection is re-run, although these differences should be slight if a large number of iterations are run.



Because stochastic projections incorporate the effects of skewed sex ratio, it is important to set the correct ratio of female mates to males in the **Settings** tab. The default setting is based on the relative average reproductive rates of males and females. In species in which a single male can breed with multiple females during the same breeding season (year), such as herd species, this number will be greater than 1.0. It is important to set this parameter to the appropriate value; otherwise, the stochastic projections may be erroneously pessimistic for a female-biased population (as PMx will leave some females unbred due to the apparent shortage of male mates).

The screenshot shows the PMx software interface for the 'Amur Tiger SSP 24Jul11' project, specifically the 'Demography' tab. The 'Settings' sub-tab is selected and highlighted with a red circle. The interface contains several configuration options:

- Birth Flow:** Radio buttons for 'Pulse' and 'Continuous' (selected).
- Age Classes:** A dropdown menu set to '1' and a unit dropdown set to 'years'.
- For early mortality use:** A text input set to '30' and a unit dropdown set to 'days'.
- Distribute Unassigned Mx:** Radio buttons for 'In prop. to known' (selected) and 'Exclude'.
- Add:** A text input set to '2' and a label 'age classes to life tables'.
- Assign sex to births in Life Table:** Radio buttons for 'Use actual sex' and 'Treat each birth as:' (selected), with a text input set to '0.50' and a dropdown set to 'male'.
- When calculating Life Table, Unknown sex are:** A text input set to '0.50' and a dropdown set to 'male'.
- Multiple Parents:** A dropdown menu set to 'Most Likely'.
- Report results using time unit as:** A dropdown menu set to 'years'.
- Project for:** A text input set to '20' and a label 'time steps'.
- Number of Iterations for simulations:** A text input set to '500'.
- Select Confidence Interval:** Radio buttons for '95%' (selected), '90%', '75%', and '68%'.
- Stochastic Projections:** A section highlighted with a red circle, containing 'Maximum # Females bred per Male:' set to '1' and '(Ratio of Male/Female Mx = 1.05)'.
- For projections, births are treated as:** A text input set to '0.50' and a dropdown set to 'male'.

At the bottom, there are buttons for 'Defaults' and 'OK'. A status bar at the very bottom displays 'Assumptions' (Age Classes are years; Birth Flow = Continuous; CI = 95%; Iterations = 500; Projections = 20 time steps), 'Overall Statistics' (Growth in terms of years: $r = -0.013$; $\lambda = 0.987$; $R_0 = 0.907$; $T = 7.9$; $N_{20} = 102$), and 'Stochastic Runs' (Up-to-date).

The **Settings** tab in Demography allows the user to:

- Change the number of iterations (default = 500; maximum = 1000).
- Change the time interval for reporting results (default = years) to days, weeks, months or decades. This changes *only* how population growth (λ , r) are reported: the rates are relative to the interval chosen here.
- Change the number of time intervals to project into the future (default = 20; maximum = 100).
- Change the birth sex ratio for projections (default = 0.50 male).
- Change the confidence interval for stochastic projections (default = 95%).
- Change the maximum number of females that breed with each breeding male (default = 1). PMx uses this number in stochastic projections to account for limited availability of breeding males in female-biased populations.
- **Note:** Changing the age class length on the **Settings** tab (from the default = 1 year) also affects projections, as the length of the time interval used for projections = age class length. For example, if age class = 1 month and the projections are for 20 time intervals into the future, the projection will be for 20 months, not 20 years; in this scenario, if a 20-year projection is desired, then projections would need to be run for 240 time intervals. See **Life Tables** tab and **Demography Settings** tab sections for more information.

Terms and Concepts

Stable age distribution (SAD): The proportional distribution of individuals across age classes that would result from the realization of the exact life table demographic rates (P_x and M_x). If these rates remain constant and exact, the population will grow (or decline) at a constant rate into the future.

Deterministic: Deterministic means predictable with no variation, or 'determined'. In deterministic calculation, exact values are applied to formulas that define relationships (e.g., first year mortality will always be 24%). Since there is no variation in input values, the result will always be the same.

Stochastic: Stochastic means variable due to chance or based on probabilities. In stochastic calculations, input values are based on probabilities (e.g., every individual has a 24% chance of not surviving its first year). Actual values used in the calculations will vary with each application and so the result will be variable.

Iteration: A single stochastic simulation of the population over the specified time period. Because events in a stochastic simulation are based on probabilities, the outcome of each iteration will be different; therefore, many iterations should be run to accurately estimate results.

Confidence interval (CI): This defines the range of values (upper and lower limits) that the parameter (in this case, mean population size) will take in relation to a specific level of likelihood. For example, a 95% CI means that 95% of the simulations result in values between the lower and upper limits.

P[Extinction]: Probability that the population will go to zero (measured as the proportion of stochastic simulations in which the population goes to 0).

New Features

Stochastic projections. While PM2000 provides deterministic population projections, PMx provides both deterministic and stochastic projections. Deterministic projections are derived from applying P_x and M_x values to the total N of individuals in each age-sex class. For stochastic projections, each individual has a probability of surviving each age class based on P_x . M_x is applied only to females and takes into account the availability of breeding males. Stochastic projections are more realistic, as the impact of small population size, skewed sex ratio and other chance events are incorporated, and provides a range of probable outcomes rather than a fixed number.

Projections with no reproduction. PMx provides the option to easily project the impact of halting reproduction in a population (useful in projecting decline in populations being managed to extinction).

Age structure status ratings. Once stochastic projections are run, PMx compares the stochastic growth rate (λ) for the next year to the deterministic growth rate (life table λ) and provides a warning if either:

- 1) the actual (stochastic) growth rate deviates substantially from the predicted (deterministic) growth rate (e.g., the population will grow much more slowly); or:
- 2) there is a moderate or significant chance that the direction of actual growth (increase vs. decrease) will be different than the direction predicted (e.g., the population will decline instead of increase).

This information can be found at the bottom of the table on the **Overview tab** in Demography once stochastic projections have been run. See **Demography Overview** in this manual for more information.

Helpful Hints

- Do not interrupt stochastic simulations but allow PMx to complete simulation runs before proceeding with other computer functions.
- Do not forget to rerun the stochastic projections if you change relevant data.
- Do not forget to change the “Maximum # females bred per male” value on the **Settings** tab if males are bred to more than one female each year.

Cautions

- The precision of stochastic projections is dependent upon the number of iterations. Running only a few iterations can give misleading results.
- Deterministic projections do not take into account the potential limitation of mates due to a skewed sex ratio. Actual growth may be lower than projected deterministically especially in monogamous species if the sex ratio is uneven or in polygamous species if there are significant fewer individuals of the limiting sex (typically females).
- Inbreeding depression is not explicitly incorporated into projections, although past inbreeding effects will be represented in the historical demographic rates. Demographic rates may change if inbreeding accumulates in the population.
- Remember that changes to *Model Data* are not saved with a project. If a saved PMx project is reopened, the *Actual Data* values will be used for the *Model Data* and therefore for projections. Smoothing and/or other desired changes to the *Model Data* will need to be re-entered.

Case Study: Generic tigers

The AZA Tiger Species Survival Plan manages tigers of known pedigree and taxonomy (Amur, Sumatran and Malayan tiger subspecies) within limited capacity. About 25% of tigers in AZA institutions, however, are of unknown origin, are likely subspecific hybrids, and are being managed as a non-breeding population to free up space for pedigreed tigers. Projection of the rate of decline of this generic tiger population through natural mortality allows species managers to anticipate available space for expanding the managed tiger populations and to plan accordingly to meet both institutional exhibit and population needs.

REPRODUCTIVE PLANNING TAB

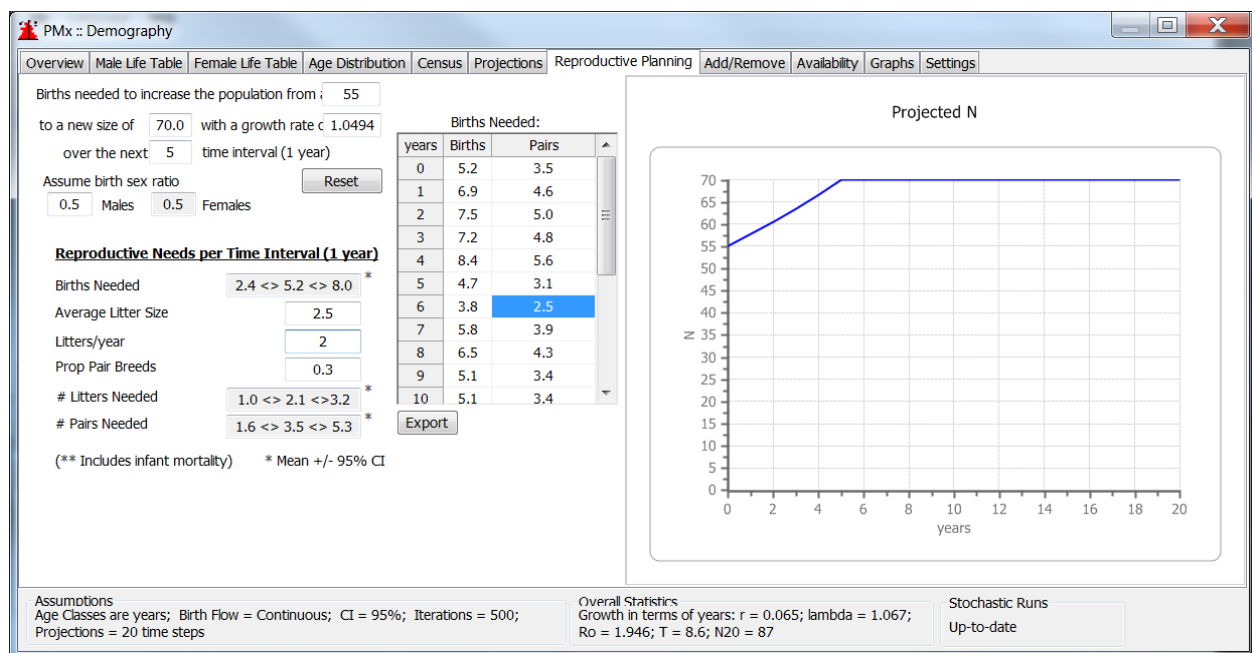
Purpose

The **Reproductive Planning** tab can be used to determine how many births and litters (or culls) are needed to reach a desired target population size or growth rate over a specified time period.

How to Use This Tab

The upper left corner of this tab provides four variables that interact to specify a particular population goal: starting population size, target population size, desired growth rate, and time period in which to achieve this goal. Modifying any one of these variables and then clicking in another field will cause PMx to recalculate the number of births needed each year to achieve this goal. When recalculating, PMx holds the starting population size and time period constant; however, if either the target population size or desired annual growth rate are modified, PMx will adjust the other of these two variables to accommodate this change. Birth sex ratio can also be changed (default = 50:50).

To simply maintain population size (a zero-population growth management plan), set the target size at the current size and lambda will change to 1.0. The number of births needed will be only that number needed to replace expected deaths. If the goal is to decrease the population size, *Births Needed* may show negative numbers. This reflects the number of individuals that must be removed from the population to cause the population to decline to the target size. The *Reset* button will restore the default values (which provide births and pairs needed in the next year in the current population to achieve the historic lambda, shown in the *Overall Statistics* in the footer of the screen). The graph on the right side of the tab displays the projected growth and stabilization of the population based upon the exact achievement of this growth rate and target population size.



The *Births Needed* table in the center of the tab show how many births are needed in the next year and each subsequent year to grow (or reduce) and maintain the population at the target size. The demographic rates from the *Model Data* life tables are applied to the age and sex distribution of the

current population to make these calculations. These calculations take into consideration the neonatal mortality rates, so the number of *Births Needed* represents the actual projected number of births needed as opposed to the number of surviving births. The *Pairs* column in the table displays the estimated number of pairs needed each year; this calculation takes into consideration the probability that a pair will breed and number of litters produced per year (see further discussion below).

The *Reproductive Needs per Time Interval* section on the lower left side of the screen can be used to translate the number of births needed into an estimation of the number of litters and breeding pairs. As a general rule, boxes with white-colored background may be changed by the user. Note that the default values are not population-specific (e.g., default litter size equals 1 for all populations). Boxes with shaded background show resulting calculated values. Calculated values are all given as a range (mean $\pm$ 95% Confidence Interval).

Enter the average litter (clutch) size for this population (often reported in the studbook software); this will allow PMx to estimate how many litters need to be produced next year to meet the goal. This often is not the same, however, as the number of breeding pairs that are needed. Two additional factors affect the number of pairs needed – the probability that a recommended pair breeds (i.e., produces a litter) and the number of litters produced during the year by each pair. The **Reproductive Planning** tab only allows for a single (average) probability of breeding to be entered to represent the success rate of all pairs; however, different probabilities of breeding can be attributed to specific pairs on the **Pairing** tab in the **Genetics** section. Use your experience and knowledge of the biology, husbandry, and behavior as well as knowledge of the individuals in the population to estimate the overall probability that each pair will breed. Probabilities < 1 will result in the need for more recommended breeding pairs.

Another factor that affects the number of pairs needed is the number of litters produced per year per pair. Many species produced only one litter per year; for species that can produce more than one litter per year, entering a number > 1 for *Litters/year* will cause PMx to calculate the minimum number of pairs needed. This assumes that each pair will be recommended to produce this number of litters; in many cases, there may be genetic or other reasons why managers may decide not to produce multiple litters from the same pair within one year but distribute the same number of litters among a large number of pairs.

The reproductive plan can be saved to a file using the 'Export' button. The graph also can be exported, sent to the **Project Notes** or printed by double-clicking on the graph.

Terms and Concepts

Population Growth Rate, or Lambda (λ): The proportional change in population size from one year to the next. A lambda of 1.11 means a 11% per year increase; lambda of 0.97 means a 3% decline in size per year.

New Features

- Ability to specify multiple litters per year.
- Provides the number of litters needed in the next year.
- Provides the confidence interval ranges for number of births, litters and pairs needed for the next year.

Helpful Hints

- Remember that the results of each reproductive plan are only calculated after clicking on another field.
- In many cases in population planning, using this screen for determining the number of pairs needed may not be a useful or accurate tool. For most populations it is necessary to assess the probability of each pair breeding on a case-by-case basis, and a general value for probability of breeding cannot be determined for the population. For example, an older pair who has been together for some time but has had no breeding success will have a lower probability of breeding than a proven breeding pair currently at peak reproductive age. For this reason *Births Needed* may be the most useful calculation. This can be compared to *# Offspring Expected* on the **Pairing** tab as a series of breeding pairs are created with different estimated probabilities of success.
- Always keep in mind what is realistic for the population when reproductive planning:
 - Are there enough animals in breeding age classes to provide the desired amount of reproduction?
 - Is there enough space available to hold that many offspring in a year's time?
 - Approximately how many offspring has this population produced annually historically?
 - On how basis was the target population size chosen?

Cautions

- As noted above, the calculations take neonatal mortality rates into consideration, so the results indicate the number of births needed as opposed to the number of surviving births.
- The default current population size may change before and after genetic analyses are conducted. Example, if animals are unselected for the genetic analyses, the default value for the current population size on the **Reproductive Planning** tab will reflect the new smaller size.
- Remember that changes to *Model Data* are not saved with a project. If a saved PMx project is reopened, the *Actual Data* values will be used for the *Model Data* and therefore for projections of needed births to achieve a particular growth rate. Smoothing and/or other desired changes to the *Model Data* will need to be re-entered.

ADD / REMOVE TAB

Purpose

The **Add/Remove** tab allows the user to define population management plans that include the addition of new individuals to the population and/or the removal of individuals from the population over a projected future time period and to assess the demographic impacts of these plans on population size.

How to Use This Tab

This tab is divided into three sections:

- Left section provides the ability to create, enable, disable or delete one or multiple supplementation or removal plans;
- Center table displays the tabular results (number of individuals added and/or removed) of the enabled plans over the projected time period; and
- Right section displays the projected population size (top) and the projected number of individuals added or removed (bottom) under the enabled plans over the projected time period.

To create a new plan, click on *Add Plan* to open the *Define a Supplementation or Removal Plan* window:

1. The table on the left shows the current number of individuals in each age and sex class. Two columns are provided (one for *Males*, one for *Females*) to specify the individuals to add or remove for each interval in which the plan will be applied. Values can be entered as the *Number* of individuals in each age and sex class to add or remove; or as the *Proportion* of each age and sex class to add or remove. Enter positive numbers to *Add* numbers, and negative numbers to *Remove* individuals.
2. Next, move to the right side of the screen to define the application of these additions and removals. Begin by entering a *Name* for the plan.
3. Enter the specific year (time interval) at which the plan should start (*Start time*). This is the first time interval at which the first individuals will be added or removed.
4. Enter the specific year (time interval) at which the plan should end (*End time*). This is the last time interval during which individuals will be added or removed.
5. Enter the *time interval* at which individuals will be added or removed.
6. The above three values – *Start time*, *End time*, and *every X time interval* – determine those time intervals during which individuals will be added and/or removed from the population. For example, if *Start time* = 2, *End time* = 20, and *time interval* = 5, then individuals specified in the table will be added and/or removed in time intervals 2, 7, 12, and 17.
7. Specify whether the values entered in the table on the left are given in terms of *Numbers* of individuals or *Proportions* of individuals within the age-sex class (see below for further discussion).
8. Check *Effect Reproductive Planning?* to incorporate the plan into the calculations on the **Reproductive Planning** tab to estimate the number of births needed to meet population goals.
9. The *Enable* box is checked by default; uncheck this box to disable the plan.
10. Click *Save* to save the plan and close this window (or *Clear* to return to the default values of zero).

Define a Supplementation or Removal Plan

Enter Numbers or Proportions
+ values imply Supplementation
- values imply Removals

years	Available	Available	Add/Remove	Add/Remove
Age Class	Males	Females	Males	Females
0	0	0	0	0
1	2	2	0	0
2	4	0	0	0
3	3	5	0	0
4	0	0	-2	-2
5	2	0	0	0
6	2	1	0	0
7	2	1	0	0
8	1	2	0	0
9	1	1	0	0
10	4	3	0	0
11	4	4	0	0
12	3	0	0	0
13	1	0	0	0
14	0	2	0	0

Name (Required):
Plan 2

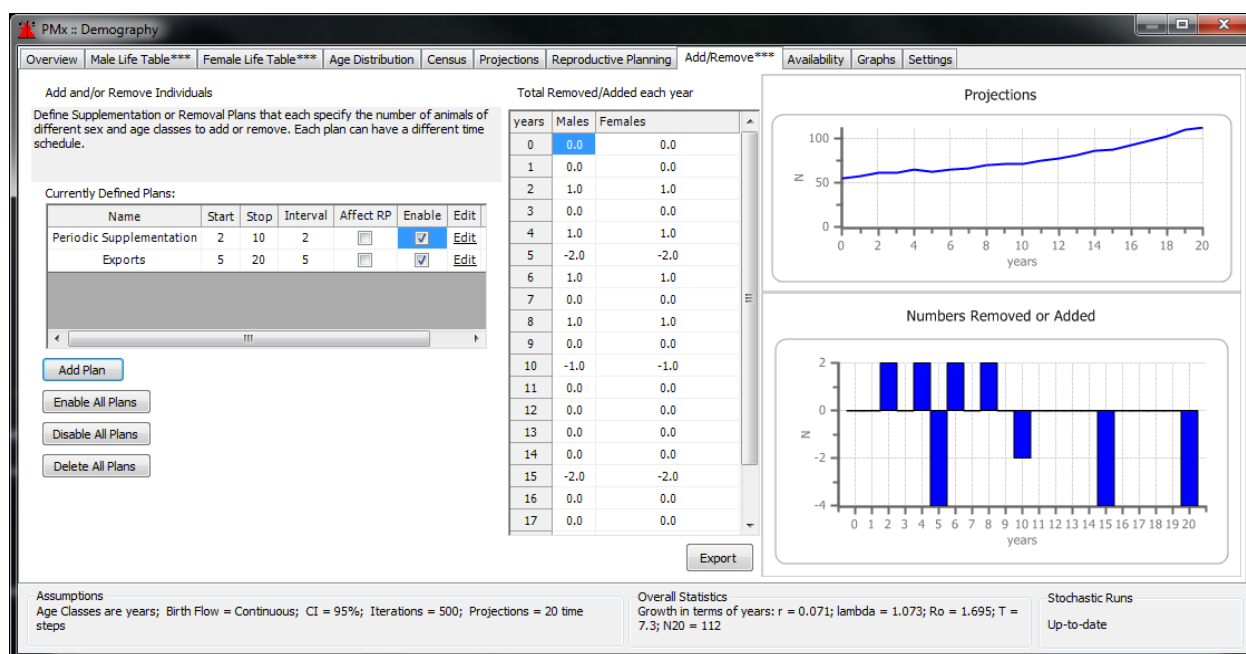
Time Intervals = 1 year
Start time: 5
End time: 20 Max = 20
Every 5 time interval

Values are:
☒ Numbers
☐ Proportions

☐ Effect Reproductive Planning?
☒ Enable

Save Clear Cancel

Each created plan will be displayed as a row in the table on the left side of the **Add/Remove** tab. Check boxes are provided here to easily apply or not apply the plan to reproductive planning (*Affect RP*) or to enable or disable the plan (*Enable*). Other modifications to the plan can be made by clicking *Edit* to open the *Define a Supplementation or Removal Plan* window. Individual plans can also be deleted at the end of the row using the *Delete* button. Multiple plans can be added and applied separately or in combination. Buttons are provided to *Enable All Plans*, *Disable All Plans*, or *Delete All Plans*.



The center table on the **Add/Remove** tab displays the total number of males and females added or removed each year (time interval) in the future (with all age classes grouped for each sex). Additions and removals in the same year are combined to display the net change in N. If insufficient individuals are available in the specified age and sex class to meet the removal plan, then removals will be incomplete for that time interval (e.g., if the plan calls to remove 4 six-year old males and only 3 males are projected to be in that age class in that time interval, then 3 will be removed, and no additional males will be taken from other age classes or from other time intervals). The *Export* button can be used to export this table.

The *Projections* graph at the top right corner of the tab displays the projected population size over time. The *Numbers Removed or Added* graph in the lower right displays the projected additions (above the zero baseline) and removals (below the baseline) over time; these are a visual representation of the numbers in the center table.

New Features

The **Add/Remove** tab is a new feature and was not available in PM2000. It incorporates aspects of the Supplementation and Harvest features available in the Vortex population simulation program.

Helpful Hints

- Be sure to enter **NEGATIVE** numbers for removing individuals.
- Use the **Availability** tab instead to assess the ability of the population to provide individuals available for removal while maintaining certain population goals (either target N or target lambda).
- Be aware that these plans do not affect the genetics of the population; supplementation is evaluated as an increase in numbers, not as the addition of new genetic founders. Likewise, the removal of individuals does not lead to increased inbreeding. To assess the genetic benefits of adding new founders, use the **Goals** section of PMx.

Cautions

- Be alert for incomplete removals due to insufficient availability when specifying *numbers* of individuals for removal.
- Remember that changes to *Model Data* are not saved with a project. If a saved PMx project is reopened, the *Actual Data* values will be used for the *Model Data* and therefore for projections. Smoothing and/or other desired changes to the *Model Data* will need to be re-entered.

AVAILABILITY TAB

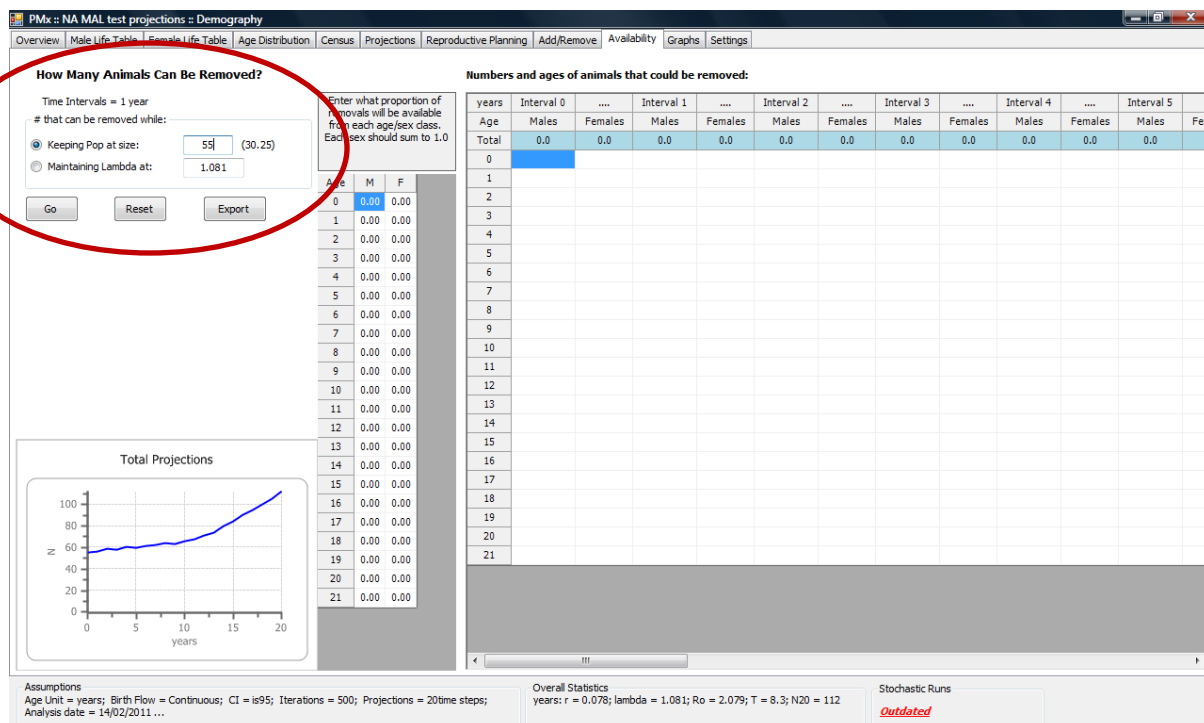
Purpose

The **Availability** tab allows the user to explore the number of individuals that can be removed from the population while maintaining it at constant size or growth rate. The user sets the age class(es) and sex(es) from which animals are removed. This tool is particularly useful in the design of release programs or other situations in which the managed population will be required to produce a harvest.

How to Use This Tab

The **Availability** tab is pre-filled with the current population size and growth rate. These are located in the top left corner of the screen.

Choose a population goal by setting either a constant population size OR a constant growth rate. Click the relevant button and adjust the number in the corresponding box to match the population goal. For example, to grow the population by 10% each year (in addition to any individuals that are removed), click the *Maintaining Lambda at* button and enter 1.10 in the box. To have the population remain at its current size, click the *Keeping Pop at size* button and enter the current population size in the adjacent box (note that you can also achieve this result by clicking the *Maintaining Lambda at* button and entering 1.00 in the adjacent box).



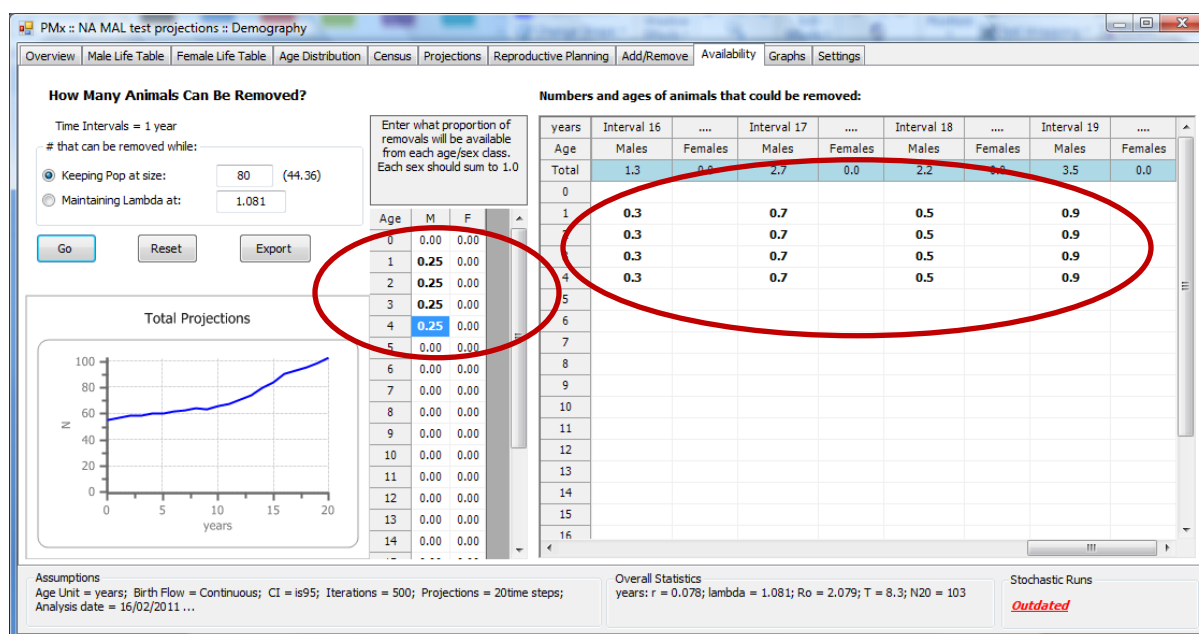
Next, go to the table labeled: *Enter what proportion of removals will be available from each age/sex class. Each sex should sum to 1.0.*

Decide which sexes and age classes are available and/or preferred for removal, and what proportion of the total removals should be made up of each available sex/age class. Enter these figures into the table,

making sure that each column (i.e., proportions for each sex) sums to 1.0. It is possible to set removals for only one sex; in that case, leave the proportions in the column for the other sex at 0.00.

Click on the *Go* button. The table on the far right will show the number of individuals that are projected to be available for removal, in each of the specified sex/age classes, at each interval (e.g., each year), for the time period considered (same as the setting for all projections) while meeting the goals set at the upper left side of the screen. The total number of individuals (across age classes) of each sex available for removal are shown in the blue row at the top of the table. This table can be exported to .txt, .csv and .xls formats by clicking on the *Export* button.

In the example shown below, the population has been set to increase from 55 to 80 individuals. Removals are set to consist only of males, and are to be split equally across the 1, 2, 3 and 4 year old age classes (i.e., 25% from each class). The results indicate that no animals are available for harvest until year 16, when the population has reached its target of 80 individuals. Beyond that the population is able to provide 1-3 males per year across all age classes.



The graph shown in the lower left corner provides deterministic projections for the population over the time frame considered. Each time a new removal schedule is entered by clicking on the *Go* button, the *Total Projections* are modified accordingly.

Clicking on the *Reset* button resets the harvest to zero and the population size, growth rate and population total projections to those of the current population.

Terms and Concepts

Lambda: Annual growth rate – the number you multiply the current population size by to project the size in one year (one time interval). For example, lambda = 1.10 would confer 10% annual growth, lambda = 1.00 confers zero growth, and lambda = 0.95 leads to 5% decline in one year.

New Features

The **Availability tab** is a new feature and was not available in PM2000.

Cautions

- Note that the numbers of individuals potentially available for removal are not displayed as integers (i.e., whole individuals). Be careful if rounding up, as this may lead to overharvest.
- PMx uses the current age structure and life tables to calculate the availability of animals for removal. A change in the underlying demographic rates, or a dramatic change to the age structure, will alter future harvest capability.
- Remember that changes to *Model Data* are not saved with a project. If a saved PMx project is reopened, the *Actual Data* values will be used for the *Model Data*. Smoothing and/or other desired changes to the *Model Data* will need to be re-entered.

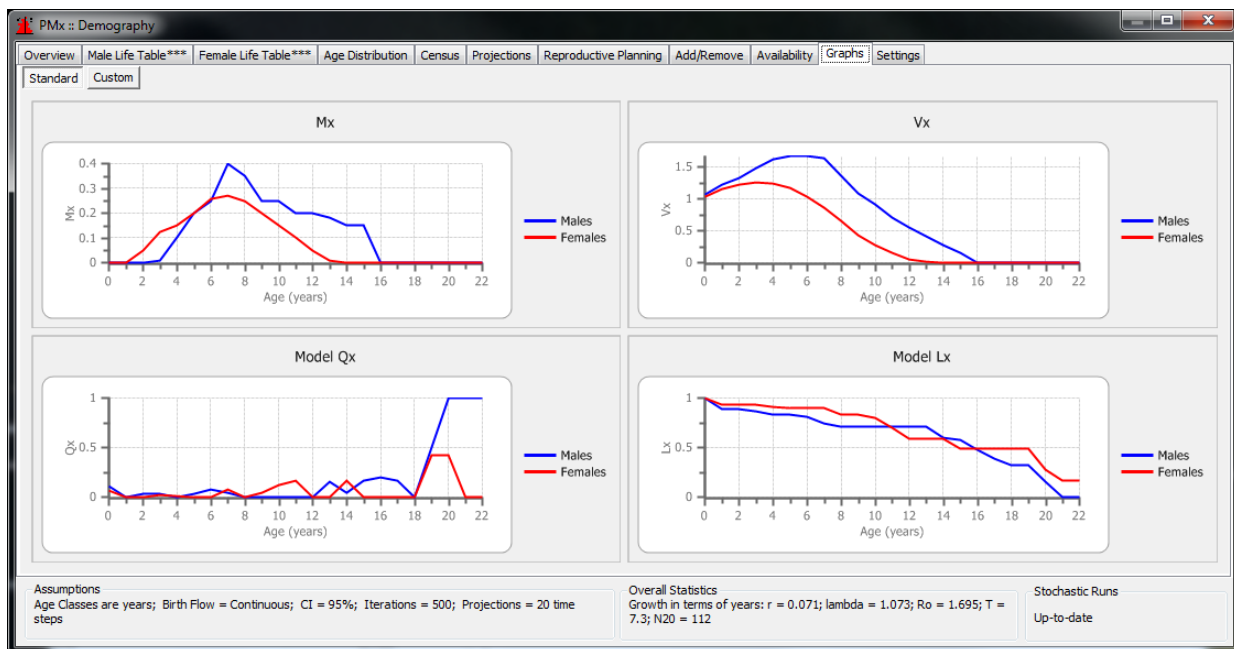
GRAPHS TAB (Demography)

Purpose

The demographic **Graphs** tab provides the user with graphical representation of basic *Model Data* life table values (*Standard*) as well as options to graph all life table and census table values (*Custom*).

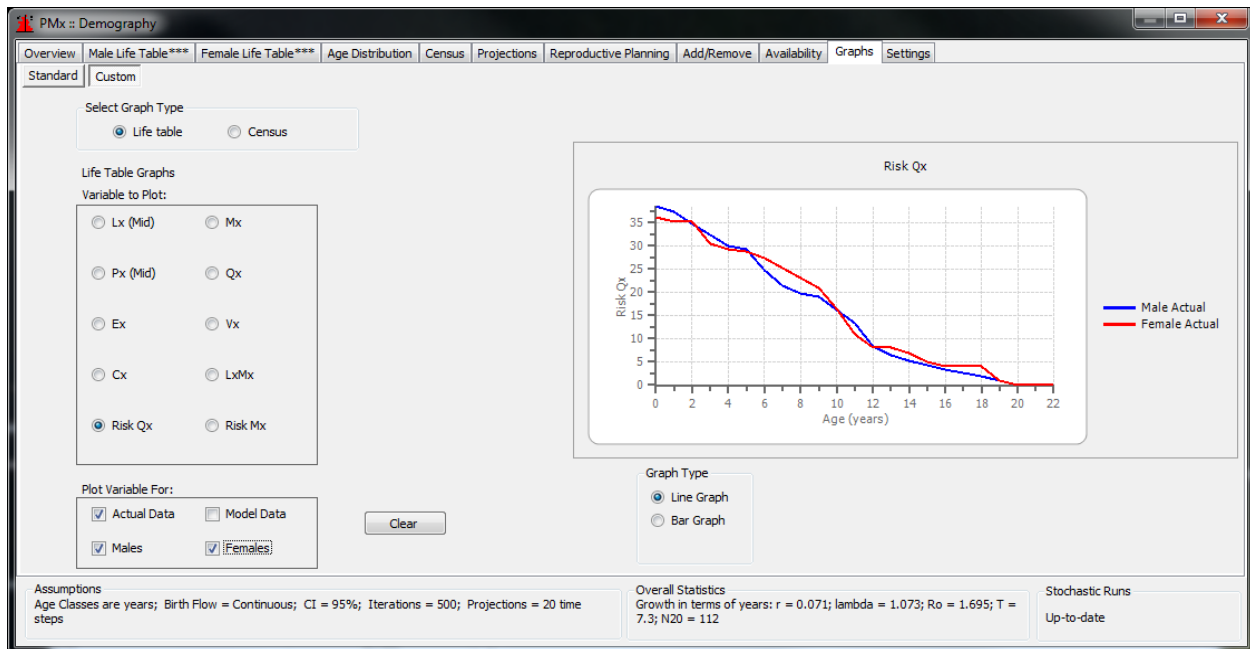
How to Use This Tab

Standard Graphs. Data for the four *Standard* graphs (*Mx*, *Vx*, *Qx*, *Lx*) are taken from the *Model Data* life table on the **Life Table** tabs. Any alteration or smoothing of data in the *Model Data* life tables will automatically be updated in the relevant graphs. Peaks and dips in the graphs may be removed or smoothed by altering life table data (see **Life Table** tab for more information). Double-clicking on a graph allows the user to print the graph, export the graph to a .png file, or send the graph to the report. Graphs sent to the report can be found on the **Project Notes** tab.



Custom Graphs (Life Table). This screen allows the user to create custom graphs from life table data.

- Select *Life table* in the upper left box.
- Next, select one of the 10 variables under *Variable to Plot* in the center left box (one box must be checked).
- Select whether to plot *Actual* and/or *Model* life table data (at least one of these boxes must be checked) in the lower left box.
- Select whether to plot data for *Males* and/or *Females* (at least one of these boxes must be checked) in the lower left box.
- Select whether to plot as a *Line* or *Bar* graph under the graph.
- The resulting graph will be displayed on the right. Double-clicking on the graph will provide options to print, export, or send the graph to the report.



Custom Graphs (Census). This screen allows the user to create custom graphs from census data. Available options will be dependent upon the data exported from the studbook program; currently, many options are only available via exports from SPARKS 1.6.

- Select *Census* in the upper left box.
- Next, select at least one of the 16 variables under *Variable(s) to Plot* in the two center left boxes. Multiple boxes can be checked; however, some variables cannot be plotted together, as they require different y-axes. Most variables are based on counts and can be plotted together. Exceptions are: *Sex Ratio* (% males) and *Birth Sex Ratio*, which can be plotted together but not in combination with other variables; and the two measures of *Lambda*, which can be plotted together but not in combination with other variables.
- Select whether to plot data for *Total* (all individuals), *Males*, *Females*, and/or *??? Sex* (unsexed) in the lower left box. These boxes are ignored for the following variables: *# institutions*; *Sex Ratio*; *Birth Sex Ratio*; *Lambda N*; and *Lambda Repro*.
- Select whether to plot as a *Line* or *Bar* graph under the graph. *Sex Ratio* and *Lambda* are more logical as line graphs.
- Revise the earliest date to plot, if desired, and click *Update*.
- The resulting graph will be displayed on the right. Double-clicking on the graph will provide options to print, export, or send the graph to the report.

Click *Clear* to uncheck all boxes and clear the *Custom* graph.

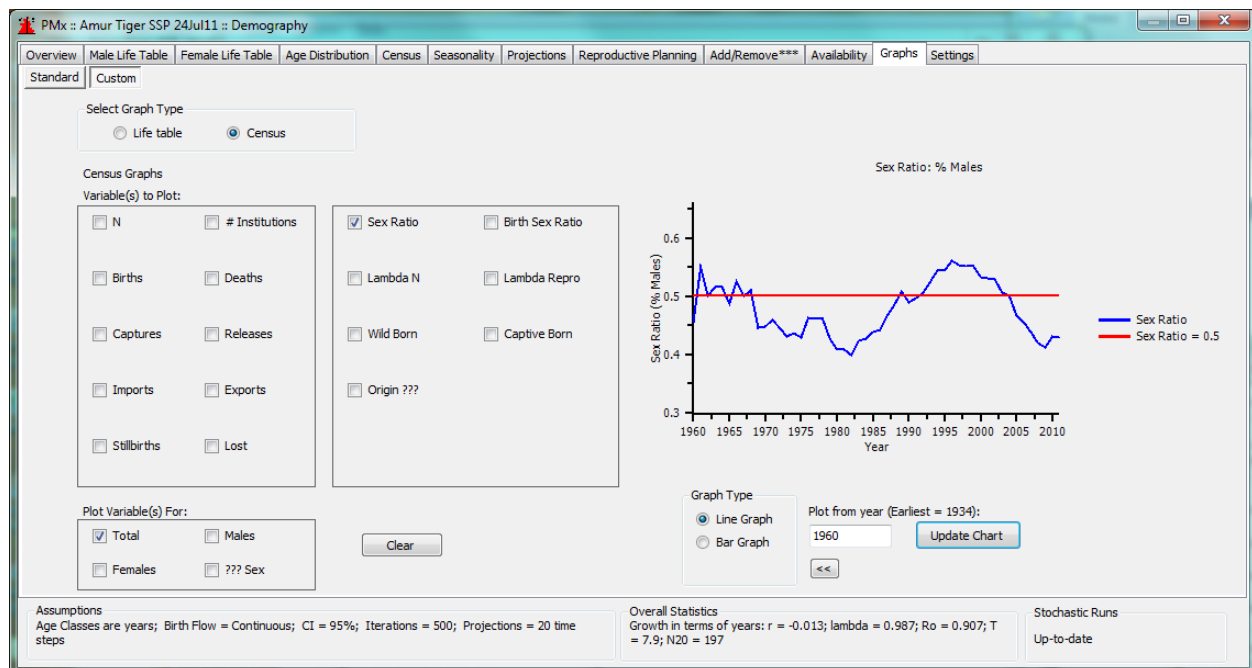
Terms and Concepts

Mid Lx (mid): Survivorship, or the proportion of individuals surviving from birth to the mid-point of age class x .

Px (mid): Survival, or the proportion of individuals which survive from the beginning of age class x to the mid-point of age class $x+1$.

Mx: Fecundity, or the average number of offspring born to individuals in that age class.

Qx: Mortality, or the probability that an individual of age x dies during age class x .



Ex: Life expectancy, or the average number of additional years an individual in age class x can expect to live.

Vx: Reproductive value, or the expected number of offspring produced this year and in future years by an animal of age x .

Cx: Proportion of population expected for this age and sex class under a stable age distribution.

Risk Qx: Number of individuals at risk of dying during that age class (sample size for Qx).

Risk Mx: Number of individuals at risk of reproducing during that age class (sample size for Mx).

Lambda: Proportional change in population size from one year to the next. Lambda N is based on observed changes in population size due to all causes; Lambda Repro is based on population changes due to births and deaths only.

New Features

PMx greatly increases the variables that can be plotted over time. Notable new variables include # Institutions, Sex Ratio, Lambda N and Lambda Repro under Custom Census graphs.

Helpful Hints

- If the model data have not been altered, the *Model* line(s) will overwrite the *Actual* data line(s), making it appear as if the actual data are not being plotted.
- Ex (life expectancy) cannot be calculated if the life table is infinite (i.e., L_x does not go to zero).
- Plotting both *Lambda N* and *Lambda Repro* on the same graph can illustrate the impact of managerial (captures, imports, releases, exports) vs biological (births and deaths) events on population size and trends.
- If both the *N* and "*# Institutions*" boxes are checked, you will be given the option of using a combined line (for *N*) and bar (for *# Institutions*) graph.

SETTINGS TAB (Demography)

Purpose

The **Settings** tab allows the user to customize settings for demographic planning – specifically, it provides the ability to modify the way in which some life table calculations are made, to change the length of the time interval used for calculations (to something different than one year), and to set factors related to population projections. Information about these options can also be found on the **Life Tables** tab and **Projections** tab.

How to Use This Tab

In general, options in the left column relate primarily to life table settings. Settings for projections can be found in the right column. After changing any of the values, click *OK* to apply these changes. The tab label will display “****” to indicate that changes from the default values have been made, and the *Stochastic Runs* box in the lower right corner will change to **Outdated**, indicating the need to rerun the stochastic projections with these new settings. Clicking *Defaults* will return the settings to the default values.

Setting options are listed below:

Birth flow: (default = continuous)

Select birth flow as *Continuous* (reproduction throughout the year) or *Pulse* (seasonal breeders). Continuous birth flow applies the *Mx* values to the number of individuals in the age class after 50% of the mortality for that age class has occurred. Pulse birth flow applies *Mx* values to all individuals entering the age class (essentially simulating all births occurring on the same day each year).

Age class length: (default = 1 year)

Change the length of the age class in the life tables. This can be changed to a particular number of days, weeks, months, years or decades, and may be useful for species with particularly short or long lifespans. Changing the age class length also affects projections, as the length of the time interval used for projections = age class length (see **Projects** tab for more information).

Early mortality definition: (default = 30 days)

Change the length of time used to calculate early mortality displayed on the demography **Overview** tab.

Unassigned Mx: (default = in proportion to known)

Determine if births to unknown age parents contribute to *Mx* in proportion to the *Mx* rates of individuals of known age (default), or are excluded from the life table calculations.

Add age classes:

Add additional age classes to the bottom of the life tables (for both sexes). Additional age classes will be of the same length as the original ones. This is useful, for example, when the oldest recorded individual is still living.

Assign sex to births: (default = each birth is 0.5 male, 0.5 female)

Determine if each birth is considered as part male/part female (i.e., contributes to *Mx* of both parents) or if the actual sex of each birth is used in *Mx* calculations (i.e., contributes only to *Mx* of the same sex parent).

Unknown sex: (default = 0.50 male)

Set the proportion of male:female to attribute to individuals of unknown sex.

Multiple parents: (default = Most Likely)

Change the assignment of parentage when there are multiple possible parents. Options are:

Most Likely = assign parentage to the individual with the highest probability of being the parent for demographic calculations (*Mx*).

Treat Mult as Unknown = change any sire or dam indicated by MULT to UNK (unknown individual) for *Mx* calculations.

Use Probabilities = assign a proportion of the offspring to each identified possible parent based on the probabilities given in the studbook database.

Note that these options currently only apply to exports from SPARKS 1.6x and only when MULT parents are explicitly identified with probabilities assigned. For other studbook exports, MULTs are treated as UNKs unless the .csv or .ped file is manually edited to include possible parents and their probabilities. This setting will be ignored by PMx if there are no MULTs in the data, even if the option appears active.

Note: Currently these three options are named differently in the Demography and Genetics **Settings**; however, they represent the same three methods of dealing with multiple parents and probabilities.

Future versions of PMx will use the same labels; until then:

<u>Demography setting</u>		<u>Genetics setting</u>
<i>Use Probabilities</i>	=	<i>Probabilistic Parents</i>
<i>Most Likely</i>	=	<i>Most Likely Parents</i>
<i>Treat Mult as Unknown</i>	=	<i>Omit Uncertain Parents</i>

Note that the default setting for *Demography* is different than the default setting for *Genetics*.

Time unit for results: (default = years)

Change the time interval for reporting results (default = years) to days, weeks, months or decades. This changes *only* how population growth (λ , r) is reported: the rates are relative to the interval chosen here. This setting does *not* change the age class length.

Length of projections: (default = 20 time steps)

Change the number of time intervals to project into the future (maximum = 100). This applies to deterministic projections, stochastic projections, age distribution projections, reproductive planning, add/remove plans, and availability projections.

Number of iterations: (default = 500)

Change the number of iterations (maximum = 1000).

Confidence interval: (default = 95%)

Change the confidence interval for stochastic projections (options are 95%, 90%, 75%, and 68%).

Maximum # females bred per male: (default = determined by relative values of average reproduction of males and females)

Change the average number of females that breed with each breeding male. PMx uses this number in stochastic projections to account for limited availability of breeding males in female-biased populations.

Birth ratio for projections: (default = 0.50 male)

Birth ratio used for all projections.

Terms and Concepts

Mx (fecundity): Average number of offspring born to individuals in that age class.

Iteration: A single stochastic simulation of the population over the specified time period. Because events in a stochastic simulation are based on probabilities, the outcome of each iteration will be different; therefore, many iterations should be run to accurately estimate results.

Confidence interval (CI): This defines the range of values (upper and lower limits) that the parameter (in this case, mean population size) will take in relation to a specific level of likelihood. For example, a 95% CI means that 95% of the simulations result in values between the lower and upper limits.

New Features

Many of the setting options on this tab were not available in PM2000. The ability to change age class length and other life table settings allow for greater flexibility in modeling different life histories. The ability to run stochastic population projections provides more realistic estimates of future population trends. The addition of these options will improve demographic planning for managed populations.

Helpful Hints

- Be sure to adjust the maximum number of females per breeding male as appropriate; otherwise, stochastic projections will be misleading, especially for polygynous species.
- Consider shortening age classes for short-lived species (e.g., small rodents), especially if reproduction occurs within the first year.
- Check the settings before and after reviewing the life tables. Depending on the species, alteration of the default settings may provide more accurate interpretation of the data.
- Remember to rerun the stochastic projections after making changes to the demographic settings.

SECTION 4: GENETICS MODULE

GENETICS SUMMARY STATISTICS SCREEN

Purpose

The main **Genetics Summary Statistics** screen provides current and historical summary statistics for the selected, living population as defined on the **Selection** tab. Once the genetic analysis has been completed (by going into and then closing *Genetic Details*), this screen will display a graph that includes a historical census (in red) and gene diversity over time (in blue).

How to Use This Tab

The tabular information on the left side of the screen is based upon the selected population. If the individuals in the selected population are changed on the **Selection** tab and the box *Apply Updated Selection to Genetics* is checked, this **Summary** tab as well as other genetic values will be updated. The following information is provided on this tab:

Founders: PMx considers a founder to be an animal with Wild/Wild parentage that has living descendants in the selected population. A broader definition of the term is an individual obtained from a source population (often the wild) that has no known relationship to any individuals in the derived population except for its own descendants. Founders are often wild-caught, but for some regional populations animals imported from another, unrelated captive population might be considered founders as well. If an unrelated, living animal has no descendants, that animal is considered to be a potential founder until it contributes progeny to the captive population (then it becomes a true founder).

Living Animals: The number of living animals in the currently selected population.

Living Descendants: The number of living animals descended from founders. This may be a fractional number because PMx normally excludes all animals with unknown parents from genetic analyses, and includes only those parts of individuals that can be traced back to known founders. For example, an animal with a known dam but an unknown sire will be tallied as half an animal in genetic analyses unless otherwise specified under the *Settings* tab.

% Ancestry Known: The percentage of the living individuals' pedigree that can be traced back to known founders, either through positive identification of all ancestors or all *possible* ancestors. Thus, 100% *Known* individuals can have completely identified ancestors, or can have MULTs (multiple possible parents) in their pedigree *provided* that the identity of all possible parents is specified in the *Sire* and/or *Dam* fields in the database.

% Ancestry Certain: The percentage of the living individuals' pedigree that can be completely identified (exact identity of both parents is known) and traceable back to known founders. Individuals that are 100% *Certain* do not have any MULTs or UNKs in their pedigree. *Certainty* represents a higher degree of knowledge than *Known* and therefore is always less than or equal to *Known*.

Gene Diversity: Proportional gene diversity (as a proportion of the source population) is the probability that two alleles from the same locus sampled at random from the population are not identical by descent from a common ancestor. Gene diversity is the heterozygosity of founder alleles ($= 1 - \text{inbreeding}$) expected in progeny produced by random mating.

Gene Value: Gene value is the gene diversity of the living individuals weighted for the reproductive value of individuals. Gene value is the heterozygosity of founder alleles expected in progeny produced by random mating and if each individual were to produce the number of offspring expected from its age-based reproductive value.

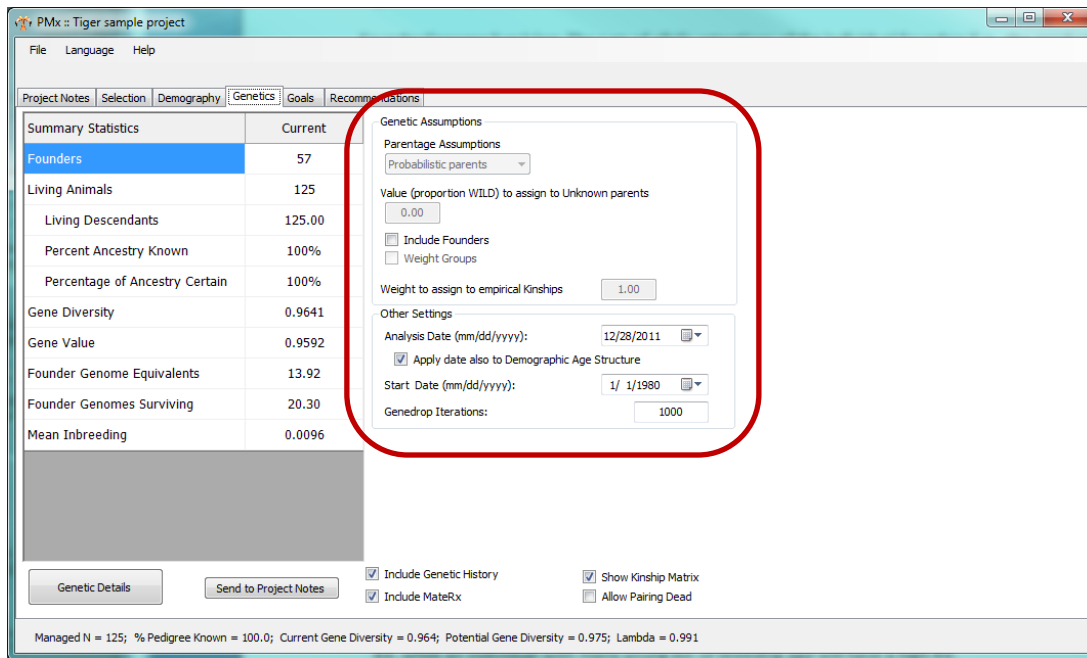
Founder Genome Equivalents: The number of unrelated individuals (founders) that would represent the same amount of gene diversity as does the population of currently living individuals. A population's *FGE* becomes smaller than the actual number of population founders over time, as founder representations vary and gene diversity is lost from the population.

Founder Genomes Surviving: The sum of allelic retentions of the individual founders (i.e., the product of the mean *allelic retention* and the *number of founders*).

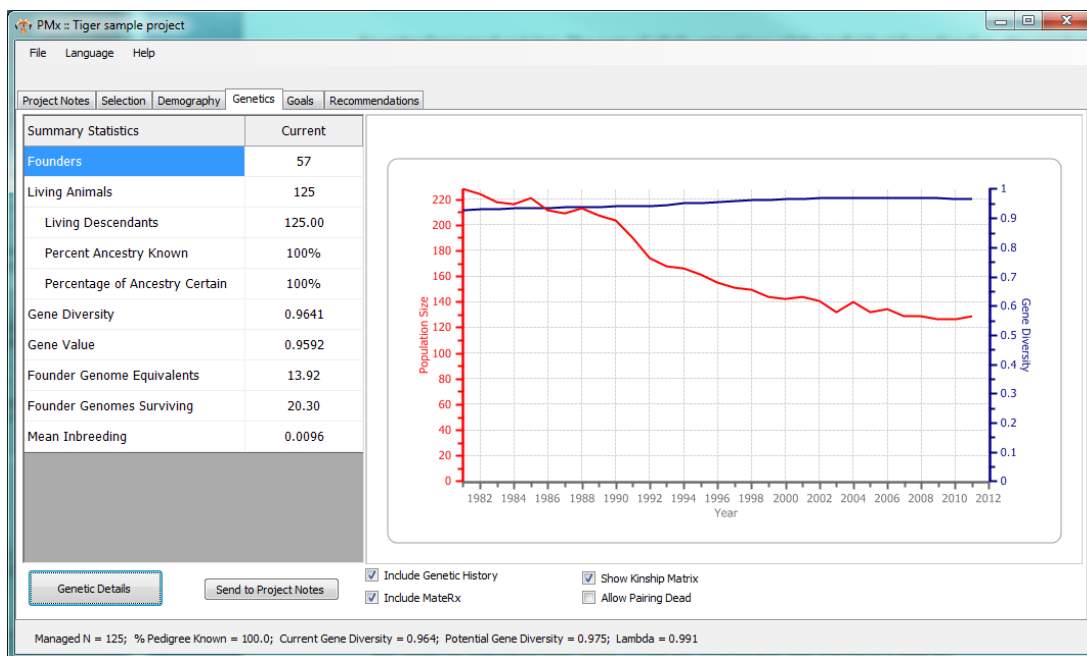
Mean Inbreeding: The average of the inbreeding coefficients among the living individuals, weighted by the % known for each individual. The mean inbreeding coefficient of a population will be the proportional decrease in observed heterozygosity relative to the expected heterozygosity of the founder population.

When the **Genetics** Screen is first opened, the right side will display options to change the *Genetic Assumptions* and *Other Settings* related to the genetic analysis. These options are also available on the Genetics **Settings** tab (under *Genetic Details*), but are duplicated on this screen for convenience (see the manual section on Genetic **Settings** for detailed explanations of these options):

- *Parentage Assumptions:* Default is *Probabilistic parents* (applicable to datasets with MULT parents).
- *Value (proportion WILD) to assign to Unknown parents:* Default is zero (applicable to datasets with UNKnown parents).
- *Include Founders:* Checkbox to include founders (rather than just the captive-born population) into the genetic calculations.
- *Weight Groups:* Applicable to datasets with groups.
- *Weight to assign to empirical Kinships:* Default is 1.00 (applicable to datasets with imported empirical kinships).
- *Analysis Date:* End date of the analysis. Default is the end of the export filter window and typically is the date of export unless otherwise specified.
- *Apply date also to Demographic Age Structure:* Checkbox to apply the above *Analysis Date* to the demographic analysis as well as genetic analysis; default is yes.
- *Start Date:* Starting date of the analysis. Default is the starting date of the export filter window.
- *Gene drop Iterations:* Number of iterations that the gene drop simulation is run. Default = 1000.



Click on the *Genetic Details* tab to open the full **Genetic** section of PMx, an expansive genetics module that includes tabs for more complex genetic overview information, detailed information on all individuals in the selection, founder information, kinship matrix, pairwise information (similar to the MateRx software program), pairing and culling options, management sets (similar to MetaMK), and pre-set and user-defined genetic graphs. Options are also available to customize many program settings for analyzing the genetic data and for making a new selection for genetic analysis. Once the user exits the **Genetics** module and returns to this **Summary Statistics** Screen, the genetic settings will be replaced with a graph depicting the population size over time (red line) and gene diversity over time (blue line).



After clicking on *Genetic Details*, be patient. Some of these detailed analyses can be quite time consuming to calculate, and it may take awhile for the **Genetics** module to open. The larger the dataset, the longer the calculations will take to display. The user can reduce the calculation time by turning off some of the more time intensive calculations using these check boxes at the bottom of the screen:

- *Include Genetic History*: Turns historical genetic calculations on and off.
- *Include MateRx*: Turns the pairwise display calculations on and off (see ***Pairwise Info Tab*** section)
- *Show Kinship Matrix*: Turns the kinship matrix display calculations on and off (see ***Kinship Matrix Tab*** section)

The default setting is for these calculations to be activated for smaller datasets (studbooks with fewer than N = 1000 individuals in the selected population). When datasets become large, these settings will turn off automatically as a default setting. These calculations require pairwise calculations, which can become a very large number of calculations as the number of individuals in the dataset increases. The default settings can be changed by checking or unchecking any of the boxes as desirable.

An additional check box *Allow Pairing Dead* is provided to allow the pairing of dead individuals. This is useful, for example, when assisted reproduction with cryopreserved gametes may be used in some of the pairing recommendations. The default setting is for this option to be turned off to speed up PMx processing. Checking this box will allow dead individuals to be added to the **Pairing** and **Management Set** Tabs if the filter is modified to include them. Dead individuals will not be included in the genetic status calculations on the living population (e.g., GD, MKs of living individuals). This option will require a historical genetic export.

Click on *Send to Project Notes* to copy the table data to the **Project Notes** tab. Double-click on the graph for options to print the graph, export it to a file, or send it to the **Project Notes** tab.

New Features

Several of the genetic statistics are new in PMx, such as *Percent Ancestry Certain*, as well as some of the settings and assumptions, such as the ability to use multiple parent data.

Helpful Hints

- If data in some of the tabs are not available (e.g., kinship matrix), check to see if the check boxes on this screen defaulted to Off due to the size of the dataset.
- An Appendix detailing how to use PMx genetic tools for genome resource banking (including identification of individuals to bank given certain GRB goals, and strategies for using these samples by pairing dead individuals) is being developed for inclusion in a future edition of this manual.

Cautions

- If the *Analysis Date* is set to some date other than the date on which the studbook data were exported, the *Location* for each individual will not change to match the new *Analysis Date* but will reflect the *Location* of the individual at the end of the export filter window. This is because SPARKS and PopLink currently only export the last *Location* (in the filter window) to PMx; PMx does not have the ability to track moves over an individual's lifetime.

GENETICS OVERVIEW TAB

Purpose

The **Genetics Overview** tab provides more detailed genetic information for the current and historical population as defined on the **Selection** tab (when the box *Apply Updated Selection to Genetics* is checked). This includes the number of living animals, living descendants, founders, potential founders, percent ancestry known and certain, gene diversity and gene value, population mean kinship, founder genome equivalents, founder genomes surviving, mean inbreeding, current and historical mean Ne, and Ne/N. Projected values of select variables are also given based on management recommendations (hypothetical offspring from recommended breeding pairs and the impact of recommended culls).

How to Use This Tab

This tab is accessed from the *Genetics Details* button on the **Genetics Summary Statistics** screen. The table on the left side of the screen provides a number of genetic statistics pertaining to the *Current* population. Values in the *Dynamic* column incorporate the effect of hypothetical offspring produced by recommended breeding pairs as well as the removal of individuals recommended to be culled. The remaining columns provide annual genetic values for the historical population during the selected filter window for analysis. If individuals are added to or removed from the *Selected Population* on the **Selection** tab, and the box *Apply Updated Selection to Genetics* is checked, these statistics will be updated to reflect the new selection. Click the *Export* button to export the data as a .txt, .csv or .xls file.

		Current	Dynamic	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008
Founders		57		40	40	42	45	45	47	49	51	51	58	58	58	58	58	58	58	58
Potential (additional)		0																		
Living Animals																				
N Individuals		125	143.00	174	168	166	161	155	151	149	144	142	144	141	132	140	132	134	129	129
Living Descendants		125.00	143.00	174.00	168.00	166.00	161.00	155.00	151.00	149.00	144.00	142.00	144.00	141.00	132.00	140.00	132.00	134.00	129.00	129.00
% Ancestry Known		100%	100%	100%	100%	100%	100%	100%	100%	100%	100%	100%	100%	100%	100%	100%	100%	100%	100%	100%
% Ancestry Certain		100%	100%	100%	100%	100%	100%	100%	100%	100%	100%	100%	100%	100%	100%	100%	100%	100%	100%	100%
Gene Diversity																				
Based on Kinship Matrix		0.9641	0.9645	0.9411	0.9449	0.9502	0.9525	0.9541	0.9566	0.9600	0.9624	0.9636	0.9660	0.9680	0.9677	0.9681	0.9679	0.9678	0.9683	0.9677
Based on Gene Drop		0.9642																		
Potential		0.9754																		
Gene Value		0.9592	0.9600	0.9323	0.9375	0.9404	0.9419	0.9416	0.9437	0.9448	0.9466	0.9360	0.9438	0.9499	0.9478	0.9578	0.9585	0.9588	0.9609	0.9620
Population Mean Kinship		0.0359	0.0355	0.0589	0.0551	0.0498	0.0475	0.0459	0.0434	0.0400	0.0376	0.0364	0.0340	0.0320	0.0323	0.0319	0.0321	0.0322	0.0317	0.0323
Founder Genome Equivalents																				
Based on Kinship Matrix		13.92	14.08	8.49	9.07	10.04	10.53	10.89	11.52	12.51	13.31	13.74	14.71	15.60	15.49	15.65	15.57	15.52	15.75	15.46
Based on Gene Drop		13.98																		
Potential		20.34																		
Founder Genomes Surviving		20.34																		
Mean Inbreeding		0.0096	0.0171	0.0606	0.0535	0.0492	0.0457	0.0411	0.0349	0.0325	0.0301	0.0299	0.0223	0.0186	0.0187	0.0156	0.0158	0.0144	0.0141	0.0093
Mean Ne		72.99																		
Over Generations:		4.04																		
Current Ne		38.40																		
Based on Breeding Males:		16.0																		
and Breeding Females:		24.0																		
Ne/N		0.3072																		

Export

Assumptions:
Do Not Include Founders; Unknown Weight = 0.00

Dynamic Population Variables
GD = 0.9645; GV = 0.9600; MK = 0.0359; % Known = 100%; N = 143.0

The following information is provided on this tab (see *Appendix B – Glossary* for detailed definitions):

<i>Founders:</i>	Number of founders that have contributed to the selected living population.
<i>Potential (fdrs):</i>	Number of potential founders (living individuals that have no living relatives in the population but have the potential to reproduce and contribute to the population).
<i>N Individuals:</i>	Number of living animals in the currently selected population for genetic analysis.
<i>L. Descendants:</i>	Number of living animals descended from founders.
<i>% Anc. Known:</i>	Percent of the living individuals' pedigree that can be traced to a group of founders.
<i>% Anc. Certain:</i>	Percent of the living individuals' pedigree that can be traced back to specific founders.
<i>Gene Diversity:</i>	Gene diversity (GD) in the current living population (as a proportion of the source population). PMx calculates GD in two ways:
<i>(Kinship Matrix):</i>	Gene diversity calculated from the kinship matrix as $1 - \overline{mk}$, where $\overline{mk}$ is the average mean kinship in the population.
<i>(Gene Drop):</i>	Gene diversity (GD) calculated from gene drop simulations. Each founder is assigned two unique alleles that pass stochastically through the pedigree. Final GD is calculated from the final distribution of alleles and is based on the number of alleles and the evenness of allele frequencies.
<i>Potential (GD):</i>	Potential GD of the population if optimal reproduction of potential founders were to be achieved (calculated as $1 - (1/2FGE_{\text{potential}})$, where $FGE_{\text{potential}}$ is the population's potential founder genome equivalent).
<i>Gene Value:</i>	Gene value of the current living population and is the gene diversity of the population weighted for the reproductive value of individuals.
<i>Pop. Mean Kinship:</i>	Average mean kinship value of individuals in the current living population.
<i>Founder Genome Equivalents:</i>	Number of unrelated individuals (founders) that would represent the same amount of gene diversity as does the population of currently living individuals. PMx gives FGEs calculated from the kinship matrix and also gene drop simulations.
<i>Potential (FGE):</i>	Maximum FGE that can be attained (if all founder allele retentions are set to their potential retention). Provides an upper limit to what might be achieved through perfect genetic management but is not usually realistically achievable.
<i>FG Surviving:</i>	Sum of allelic retentions of the individual founders (i.e., the product of the mean allelic retention and the number of founders).
<i>Mean Inbreeding:</i>	The average of the inbreeding coefficients among the living individuals.
<i>Mean Ne:</i>	Average effective population size of the selected population over the analysis time span. Given in relation to the number of <i>Generations</i> over which <i>Ne</i> is calculated.
<i>Current Ne:</i>	Effective population size of the selected living population, based on the number of living males and females that have produced offspring.
<i>Ne/N:</i>	Ratio of the effective population size to census size of living, captive-born individuals.

Genetic Footer

The footer across the bottom of the **Genetic Overview** tab contains reminders of the *Assumptions* with respect to the genetic analysis; these assumptions can be changed on the genetics **Settings** tab. Also displayed are a few genetic *Dynamic Population Variables* (*GD*, *GV*, *population MK*, *% Known*, *N*), which are updated as *Selected Pairs* and *Selected Culls* are added to or removed from the analysis. This footer is displayed at the bottom of all **Genetic** section tabs.

Cautions

- Individuals that are toggled out of the selected population on the **Selection** tab for genetic analysis will not be included in either the current or historical genetic calculations.
- Since historical genetic values are based on the individuals in the current selected population for the genetic analysis, they may not accurately reflect the actual genetic status of the population at those points in the past. For example, individuals that were excluded from the genetic analysis because they are currently sterilized or post-reproductive (permanent non-breeders) will not be tallied in the historical genetic values, even if they were part of the managed population in the past.
- The *Current Ne* (and therefore *Ne/N*) may be underestimated if living individuals (such as permanent non-breeders) are removed from the genetic analysis on the **Selection** tab, if these individuals reproduced in the past. A more accurate calculation for *Current Ne* and *Ne/N* can be obtained by noting these values before removing any living individuals for the genetic analysis.

FOUNDERS TAB

Purpose

The **Founders** tab shows a list of all founders and several statistics about their genetic contributions to the living captive-born population (based on the selected population).

How to Use This Tab

When opening this tab, the default sorting of founders is by *Unique ID*. As in most other tables in PMx, the table can be sorted by any of the headings by clicking on the column heading, and the individuals listed in the table can be filtered by clicking on the *Filter* button in the lower right-hand corner.

UniqueID	Sex	Age	Alive	Representation	Contribution	Allele Retention	Potential Retention	Descendants
2449	Female	3	False	0.0105	1.3125	0.2170	0.2170	21.0
2448	Male	3	False	0.0105	1.3125	0.2070	0.2070	21.0
2458	Female	12	False	0.0118	1.4688	0.2535	0.2535	33.0
2457	Male	14	False	0.0203	2.5313	0.3995	0.3995	33.0
2460	Female	11	False	0.0075	0.9375	0.1620	0.1620	31.0
2459	Male	11	False	0.0075	0.9375	0.1740	0.1740	31.0
2462	Female	5	False	0.0085	1.0625	0.1925	0.1925	33.0
2461	Male	3	False	0.0085	1.0625	0.2020	0.2020	33.0
790	Female	12	False	0.0228	2.8438	0.3400	0.3400	43.0
924	Female	13	False	0.0134	1.6719	0.2315	0.2315	50.0
923	Male	12	False	0.0134	1.6719	0.2180	0.2180	50.0
3060	Male	17	False	0.0455	5.6875	0.7045	0.7045	43.0
WILD2	Female	U	False	0.0475	5.9375	0.7430	0.7430	46.0
WILD1	Male	U	False	0.0475	5.9375	0.7305	0.7305	46.0
2222	Female	16	False	0.0205	2.5625	0.3290	0.3290	26.0
WILD4	Female	U	False	0.0320	4.0000	0.7340	0.7340	18.0
WILD3	Male	U	False	0.0320	4.0000	0.7480	0.7480	18.0
3501	Female	17	False	0.0300	3.7500	0.4925	0.4925	27.0
2453	Female	4	False	0.0180	2.2500	0.5000	0.5000	10.0

Export Filter

Assumptions: Do Not Include Founders; Unknown Weight = 0.00

Dynamic Population Variables: GD = 0.9645; GV = 0.9600; MK = 0.0359; % Known = 100%; N = 143.0

The genetic contribution of each founder is described using the following five variables:

- Representation:** Proportion of the genes in the descendant population that derives from that founder (i.e., proportional *Founder Contribution*).
- Contribution:** Number of copies of a founder's genome that are present in the living descendants. Each offspring contributes 0.5, each grand-offspring contributes 0.25, etc.
- Allele Retention:** Probability that a random gene in a founder individual exists in at least one individual in the living, descendant population.
- Potential Retention:** Proportion of genes present in a founder that have the potential to be incorporated in the descendant population. If the individual is a potential founder or is still living, its potential retention is 1.00. For dead founders, potential retention will be the same as the *Allele Retention* for that founder.
- Descendants:** Number of descendants in the selected living population.

If UNKnown parents are to be considered as WILD (at least in part, see Genetics **Settings**), then the founders who have UNK x UNK for their parents will be tagged with a 'U' after their *UniqueID* in the table. If UNK parents are to be excluded from calculations, then individuals with UNK x UNK parents will not be listed in the founder table.

Founders with a *Unique ID* of *MateOfxxx* (in which xxx is the *Unique ID* of another individual) are hypothetical (or “pseudo”) individuals that were created by PMx in order to complete the pedigree. These individuals are the UNKNOWN parents of individuals whose other parent is xxx. For example, if an individual has the following parents – dam with *Unique ID* = 123 and the sire is unknown, then an individual would be created called “MateOf123” to represent the sire (and the parents of this individual would be UNK). An exception to this occurs if the dam is herself wild-caught. In that case, it is assumed that the dam was pregnant when captured, and the sire “MateOfxxx” is given parents as WILD.

The *Change* button at the bottom center allows the user to change the genetic assumptions related to the founders of the population. Checking the *Include Founders* box will include the founders in all genetic analyses. Normally, wild-caught or imported founders are not included in tallies of the genetic population status (*GD*, *GV*, and *FGE*); the default is for genetic calculations to include only the descendant individuals (see the **Genetic Settings manual section** for detailed information about these options).

The founder table can be exported from PMx (and saved as a *.txt*, *.csv* or *.xls* file) by clicking the *Export* button at the bottom left of the screen.

New Features

PMx provides greater flexibility in assigning the proportion of UNKNOWN parentage to be considered as WILD (PM2000 only provided options to treat UNKNOWN parents as 100% or 0% WILD). PMx also has the ability to incorporate MULT parental assumptions.

Helpful Hints

- Sort the founder list by the *Alive* column in order to identify any living founders. Living founders should generally be given preference in breeding over non-founders that have similar (or larger) mean kinships.
- Add the column *MyDescendants* to display a list of the first 25 descendants of each founder, which can be useful to identify descendants of underrepresented founders or those of lineages of particular interest.

INDIVIDUALS TAB

Purpose

The **Individuals** tab is used to display all of the specific information that is either imported for an individual or group, or accrues as various analyses are run. Subsets of this information are utilized on many other screens, but by default, all possible information is displayed here.

More details on Groups will be added as they are developed.

How to Use This Tab

Upon opening the tab, all of the information currently available for each individual or entity (i.e., group) in the selected population will be displayed (i.e., data are unfiltered). A short description of most variables can be viewed by placing the cursor on either the header label or on a cell in that column for one of the individuals. More detailed descriptions of each variable can be found in *Appendix A*.

This table can be modified as follows:

- Right-click on the header line and a menu of all variables will appear. By default, all are checked. Unchecking any variable will remove that column from the display. This does not remove the data from the project, just from the current table view. Any variable can be added back to the table at any time by right-clicking on the header and checking the box.
- Columns may be moved from one position to another by clicking on the header for a particular column and dragging it to the desired position.
- The overall data may be sorted by clicking on any header. As all of the information is treated as text, information will be ordered by characters, then numbers, then letters. Data may be sorted in ascending or descending order by clicking repeatedly on the header.
- Individuals can be marked using different colors in the *Flags* column, which can then be used for sorting.

UniqueID	Location	LocalID	HouseName	OtherID	Sex	Known	Certainty	BirthDate	BirthDateEst	Alive	Death
251	DORMUND	US2544	KAKA	[] [] []	Female	U.9375	U.9375	2006-10-06	Exact	True	--
252	TAIPING	ZT0238	DURGA	[] [] []	Female	1.0000	1.0000	1999-10-02	Exact	True	--
253	TAIPING	ZT0178	DINA	[] [] []	Male	0.9375	0.9375	2000-09-27	Exact	True	--
254	TAIPING	ZT0278	GAYA	[00-01BC-86B8][] []	Female	0.9375	0.9375	2000-09-27	Exact	True	--
255	TAIPING	ZT0277	YANI	[00-01E7-23BE][] []	Female	0.9375	0.9375	2000-09-27	Exact	True	--
257	HALLE	207305	SIRIUS	[968000004754586][] []	Male	0.9375	0.9375	2007-10-02	Exact	True	--
258	BERLIN TP	---	TAREK	[968000004262588][] []	Male	0.9375	0.9375	2007-10-02	Exact	True	--
259	HALLE	207307	JOHANN	[968000004765399][] []	Male	0.9375	0.9375	2007-10-02	Exact	True	--
260	SEDGWICK	12427	MALIK	[] [] []	Male	1.0000	1.0000	2007-07-30	Exact	True	--
261	SEDGWICK	12428	HAKIM	[] [] []	Male	1.0000	1.0000	2007-07-30	Exact	True	--
266	MELAKA	ZM1490	CHIKO	[] [] []	Male	1.0000	1.0000	2008-10-14	Exact	True	--
267	LANGK E A	---	CHIKI	[] [] []	Female	1.0000	1.0000	2008-10-14	Exact	True	--
269	MELAKA	---	---	[] [] []	Male	1.0000	1.0000	2008-10-14	Exact	False	2008-
270	MELAKA	---	---	[] [] []	Unknow	1.0000	1.0000	2008-10-14	Exact	False	2008-
271	MELAKA	---	NICOLE	[] [] []	Female	1.0000	1.0000	2008-02-07	Exact	False	2008-

Some columns include multiple pieces of information. Clicking on one of the individual data cells in the column will display a  button. Click on this button to open a box that displays each piece of data. This applies to *OtherID*, *Sire*, *Dam*, *SireProb*, *DamProb*, *Offspring*, *PriorMates*, *ReproYears*, *MyFounders*, *MyFounderContribs*, *UDFs*, *DemMoves*, and *GenMoves*.

It is possible to edit some of the data directly in this table rather than having to import a new dataset. For example, the *Sex* or *House Name* of an individual can be changed in this table. Other data fields, such as the mean kinship value of an individual, cannot be edited. Clicking on one of these cells will display the message: “*This variable cannot be edited*”. Once changes have been made, clicking on another tab will bring up two messages: “*Would you like to update Genetics to include your data changes?*” and “*Would you like to update Demography to include your data changes?*” Click Yes to apply these changes to the respective analyses.

Click the *Export* button to create a copy of the currently visible data as a text file (.txt), Excel file (.xls), or a comma-delimited file (.csv). The text file may be opened with NotePad, BlocNotes, WordPad, Word or any other word-processing software. Changes made to these files will not be appear in PMx.

The *Update Table* button will import information available as a result of activity on other tabs or screens. **Pairing** and **Culling** tab choices in the **Genetics** section, *Reproductive Goals* and information from the **Recommendations** screen will accrue to the appropriate columns in the **Individual** table.

Terms and Concepts

See *Appendix A* for a complete list of *Individual Variables* and definitions.

New Features

The **Individuals** tab provides much more detailed information about each individual (about 4x as many variables as were available in PM2000). This reduces the need to go back to the studbook data during data analysis and masterplanning, as much of the commonly needed information is now exported to and is available in PMx directly.

Helpful Hints

- This table contains a large amount of data on historical and currently living individuals (i.e., all individuals in the export filter). The sorting and filtering functionalities available in PMx can be used to quickly summarize information and answer questions about the population, current and historical, and to identify subsets of individuals with specific characteristics of interest.

Cautions

- The ability to edit data within PMx is a double-edged sword. Greater flexibility and convenience also come with increased opportunities for error, so edit with caution. Remember that changes made in PMx will not translate back to the original studbook data. Any revisions in the true data also need to be made directly in the studbook data (e.g., within SPARKS or PopLink).

KINSHIP MATRIX TAB

Purpose

The **Kinship Matrix** tab displays the kinship values between every pair of living individuals in the selected population. The kinship value between any two individuals is also equal to the inbreeding coefficient of any offspring that are produced by mating between these two individuals. Most of the additional genetic analyses can be calculated from this table of kinship values.

How to Use This Tab

To quickly calculate the kinship between any two individuals, enter the two *Unique IDs* in the open boxes on the left of the screen and click *Calculate*. This will return the *Kinship* value between the pair.

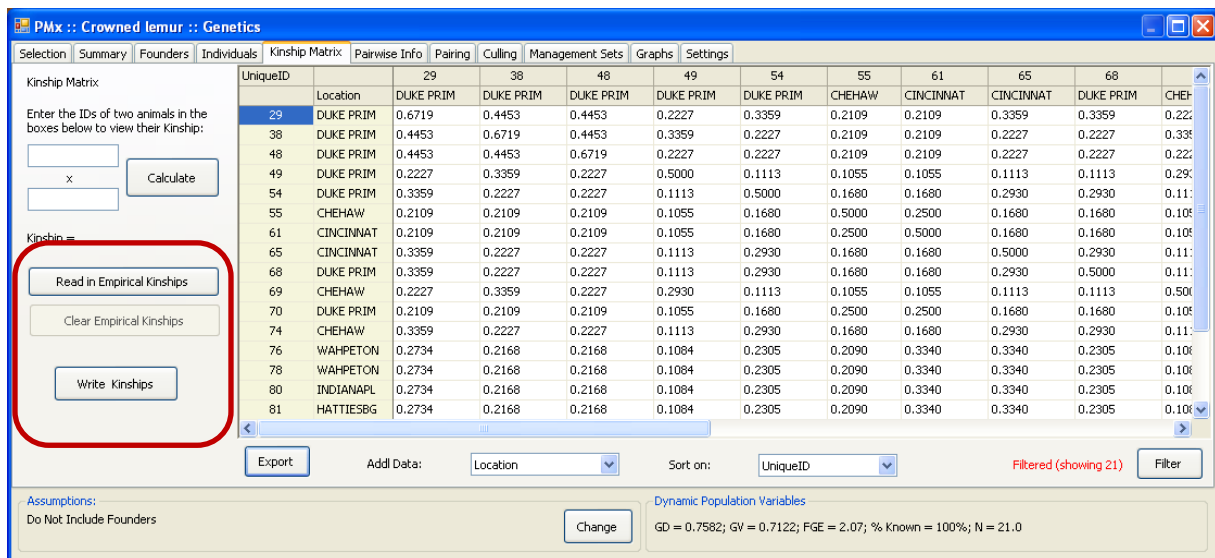
UniqueID	Location	29	38	48	49	54	55	61	65	68	69	70	74	76	78	80	81
29	DUKE PRIM	0.6719	0.4453	0.4453	0.2227	0.3359	0.2109	0.2109	0.3359	0.3359	0.2227	0.2227	0.2227	0.2227	0.2227	0.2227	0.2227
38	DUKE PRIM	0.4453	0.6719	0.4453	0.3359	0.2227	0.2109	0.2109	0.2227	0.2227	0.2227	0.2227	0.2227	0.2227	0.2227	0.2227	0.2227
48	DUKE PRIM	0.4453	0.4453	0.6719	0.2227	0.2227	0.2109	0.2109	0.2227	0.2227	0.2227	0.2227	0.2227	0.2227	0.2227	0.2227	0.2227
49	DUKE PRIM	0.2227	0.3359	0.2227	0.5000	0.1113	0.1055	0.1055	0.1113	0.1113	0.2930	0.2930	0.2930	0.2930	0.2930	0.2930	0.2930
54	DUKE PRIM	0.3359	0.2227	0.2227	0.1113	0.5000	0.1680	0.1680	0.2930	0.2930	0.2930	0.2930	0.2930	0.2930	0.2930	0.2930	0.2930
55	CHEHAW	0.2109	0.2109	0.2109	0.1055	0.1680	0.5000	0.2500	0.1680	0.1680	0.1680	0.1680	0.1680	0.1680	0.1680	0.1680	0.1680
61	CINCINNAT	0.2109	0.2109	0.2109	0.1055	0.1680	0.2500	0.5000	0.1680	0.1680	0.1680	0.1680	0.1680	0.1680	0.1680	0.1680	0.1680
65	CINCINNAT	0.3359	0.2227	0.2227	0.1113	0.2930	0.1680	0.1680	0.5000	0.2930	0.2930	0.2930	0.2930	0.2930	0.2930	0.2930	0.2930
68	DUKE PRIM	0.3359	0.2227	0.2227	0.1113	0.2930	0.1680	0.1680	0.2930	0.5000	0.2930	0.2930	0.2930	0.2930	0.2930	0.2930	0.2930
69	CHEHAW	0.2227	0.3359	0.2227	0.2930	0.1113	0.1055	0.1055	0.1113	0.1113	0.1113	0.1113	0.1113	0.1113	0.1113	0.1113	0.1113
70	DUKE PRIM	0.2109	0.2109	0.2109	0.1055	0.1680	0.2500	0.2500	0.1680	0.1680	0.1680	0.1680	0.1680	0.1680	0.1680	0.1680	0.1680
74	CHEHAW	0.3359	0.2227	0.2227	0.1113	0.2930	0.1680	0.1680	0.2930	0.2930	0.2930	0.2930	0.2930	0.2930	0.2930	0.2930	0.2930
76	WAHPETON	0.2734	0.2168	0.2168	0.1084	0.2305	0.2090	0.3340	0.3340	0.3340	0.2305	0.2305	0.2305	0.2305	0.2305	0.2305	0.2305
78	WAHPETON	0.2734	0.2168	0.2168	0.1084	0.2305	0.2090	0.3340	0.3340	0.3340	0.2305	0.2305	0.2305	0.2305	0.2305	0.2305	0.2305
80	INDIANAPL	0.2734	0.2168	0.2168	0.1084	0.2305	0.2090	0.3340	0.3340	0.3340	0.2305	0.2305	0.2305	0.2305	0.2305	0.2305	0.2305
81	HATTIESBG	0.2734	0.2168	0.2168	0.1084	0.2305	0.2090	0.3340	0.3340	0.3340	0.2305	0.2305	0.2305	0.2305	0.2305	0.2305	0.2305

On each axis in the main kinship matrix, one additional column of data can be displayed following the *Unique ID*. The default variable displayed is *Location*. Use the *Add Data* pull-down menu at the bottom of the screen to choose a different variable to be displayed.

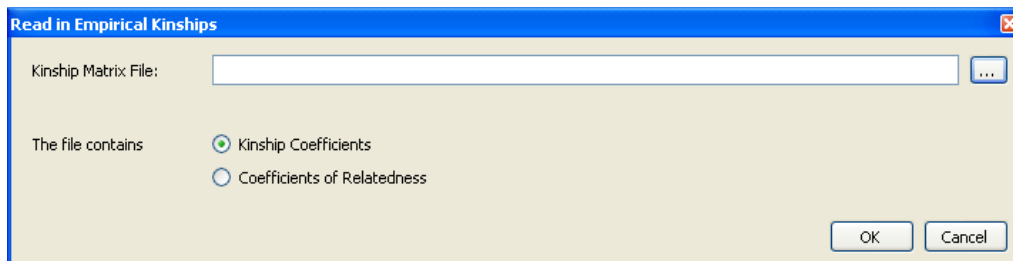
Unique ID is the default order of individuals. The *Sort on* pull-down menu at the bottom of the screen can be used to choose a different variable for sorting individuals.

As in the other **Genetic** tabs, the individuals displayed in the kinship matrix can be filtered to display a particular subset of individuals by clicking on *Filter* in the lower right-hand corner of the screen.

To include kinship coefficient data that were calculated from a data source different from the pedigree analysis (e.g., molecular data from microsatellite analyses), click the *Read in Empirical Kinships* button. This option allows the user to specify a matrix of relatedness or kinships among pairs of individuals. For example, this method can be used to define kinships among founders, rather than using the default assumption that founders are not related. Founder kinships may be available because of known familial relationships (such as a clutch or littermates) or from molecular genetic evidence that indicates close kinship among some founders.



A window will open that provides the option to attach a kinship matrix text file that contains either kinship coefficients between any two individuals, or coefficients of relatedness. Kinships are symmetrical, by definition, but the imported file of empirical kinships only needs to contain the diagonal values and the below-diagonal values. Values can be included that are nonsensical from a genetics standpoint (for example, true kinships must range from 0 to 1), but PMx will accept any numerical values that are provided.



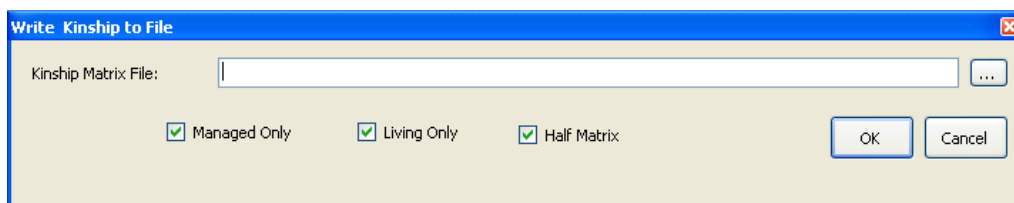
Example of a *Kinship Matrix File* (text in bold NOT entered):

123					} List of individuals with kinships to be specified
124					
201					
202					
300					
0.50	0.56	0.57	0.87	0.50	} Kinship (f_{xy}) matrix
0.56	0.50	0.66	0.50	0.45	
0.57	0.66	0.53	0.38	0.55	
0.87	0.50	0.38	0.50	0.90	
0.50	0.45	0.55	0.90	0.60	

Empirical kinship data can be weighted differently from the data calculated from the pedigree. Click the *Change* button in the *Assumptions* section at the bottom of the screen to open the *Genetic Assumptions* box, and change *Weight to assign to empirical kinships* (the value must be between 0 and 1). This box will only be accessible if empirical data has been imported. Weights can also be changed on the Genetics **Settings** Tab.

Clicking the *Clear Empirical Kinships* button will reset the matrix to the original data calculated from the pedigree file.

To export the kinship matrix, click the *Write Kinships* button on the lower left-hand corner of the screen. A box will appear that allows the user to specify which individuals to include – the managed individuals only (i.e., the selected population for genetic analysis chosen on the **Selection** screen), the living individuals only, and/or the entire (half) matrix. The kinship matrix can also be saved as a .txt, .csv, or .xls file by clicking the *Export* button at the bottom of the screen.



Terms and Concepts

Kinship value (KV): The weighted mean kinship of an individual, with the weights being the reproductive values of each of the kin. The mean kinship value of a population predicts the loss of gene diversity expected in the subsequent generation if all animals were to mate randomly and all were to produce the numbers of offspring expected for animals of their age.

Coefficient of relatedness (r): The probability that at a given locus, an allele sampled from one individual is identical by descent to at least one of the alleles at that locus in a second individual. In a population with no inbreeding, *r* is two times kinship.

Inbreeding coefficient (F): Probability that the two alleles at a genetic locus are identical by descent from an ancestor common to both parents.

New Features

The ability to include empirical kinships is more streamlined than in PM2000 and the file is easier to import and integrate into the data analysis. The user also has the option of using a weighted mean of the empirical kinships and the kinships originally calculated from the pedigree (see Genetics **Settings**).

Helpful Hints

If adding empirical data, be sure that the text file is in the correct format, and only includes the *Unique ID*, or studbook number, of each individual, followed by the kinship matrix with no additional text or characters. If the input file is incorrect, an error will cause the program to close.

Cautions

Empirical kinship data should only be included after discussions with a population management advisor. Kinships and coefficients of relatedness calculated from pedigree analysis and genetic analysis will not necessarily be the same because they are based on different values and using different methods.

PAIRWISE INFO TAB

Purpose

The **Pairwise Info** tab provides information about all possible male – female pairs in the selected living population. This information can be used to categorize the relative suitability of pairs for breeding. This tab incorporates much of the functionality available in the MateRx DOS-based software program.

How to Use This Tab

This tab displays a matrix of *Males* (rows) and *Females* (columns) for the selected living population. Numerous variables can be displayed in the table, which can be sorted, filtered and exported.

About the Mate Suitability Index (MSI)

The default value in the table is the *MSI* (Mate Suitability Index) value for each male –female pair. *MSI* is a composite score that integrates four genetic components into a single index:

1. Delta GD (dGD): Change in gene diversity (GD) of the population if one offspring is produced by the pair. Positive dGD increases the GD of the population, while negative dGD decreases GD.
2. Differences in MK values (MKDiff): Difference in the genetic value (mean kinship value) of the male and female. Breeding a pair with a large MKDiff is detrimental because it combines under-represented and over-represented genetic lines.
3. Inbreeding coefficient (F): Inbreeding coefficient of any offspring resulting from the pair (i.e., the kinship value for the pair). Inbreeding is considered to be detrimental to the fitness of the resulting offspring.
4. Unknown ancestry: The amount of unknown ancestry in the male and female. Incomplete pedigree information means that the genetic value and relatedness of a pair cannot be accurately calculated.

These variables are combined using a default set of definitions (that can be modified on the genetic **Settings** tab) to assign a *MSI* score of 1 to 6 for each pair, which can be thought of as follows:

- 1 = very beneficial (genetically) to the population
- 2 = moderately beneficial
- 3 = slightly beneficial
- 4 = slightly detrimental
- 5 = detrimental, should only be used if demographically necessary
- 6 = very detrimental (should be considered only if demographic considerations override preservation of genetic diversity)
- “-“ = very highly detrimental (should not be paired, due to high level of kinship of pair)

The *View MateRx settings* button and the demographic **Settings** tab give more detailed information regarding how the *MSI* values are calculated, and also allow these settings to be modified (also see the MateRx documentation (Ballou *et al.* 1999) for more information on MateRx and these calculations).

Using Pairwise Info

The default table of *MSI* values for pairs can be used to quickly assess the relative genetic value of a pair, subset of pairs, potential mates for one individual, and many other valuable data when making breeding recommendations. This can be especially helpful to quickly explore options for pairing individuals at one facility that houses numerous individuals of each sex or to quickly identify an alternative suitable mate if a recommended breeding fails.

Other variables besides *MSI* can be displayed in the table by using the pull-down menu for *Data to display* to the left of the table; additional variables are *eMSI*, *DeltaGD*, *MKDiff*, *F*, *Known*, and *Ranks* (the individual rankings for *dGD*, *MKDiff* and *F*, in that order, used to calculate the *MSI*). The value for any of these variables for a particular male - female pair can be quickly viewed by entering the *UniqueID* for each of the two individuals in the boxes on the left and clicking the *Calculate* button.

The table lists the *UniqueID* of each male (rows) and female (columns), followed by an additional row or column. The default for this additional variable is *Location*; however, other variables (such as *House Name* or *Age*) can be selected by using the pull-down menu for *Addl Data* at the bottom of the screen.

Individuals are sorted by *UniqueID* as a default setting; this can be changed for rows and/or columns using the pull-down menus for *Sort Rows on* and *Sort Cols on* at the bottom of the screen. Use the *Filter* to subset the data, for example, to view only reproductive age individuals, or individuals at only one *Location* or small number of *Locations*.

Data in the table can be updated (*Dynamic*) based on *Selected Pairs* and *Selected Culls* by clicking the *Update Table with Pairs and Culls* button on the left.

The displayed table can be exported using the *Export* button and saved as a *.txt*, *.csv* or *.xls* file.

The screenshot shows the PMx software interface for the 'Amur Tiger Sample Project :: Genetics'. The 'Pairwise Info Matrix' tab is active. On the left, a sidebar contains a 'Data to display:' dropdown set to 'MSI', input fields for '4073' and '5286' with a 'Calculate' button, and an 'Update Table with Pairs and Culls' button. The main area displays a table with 'UniqueID' and 'Males V' as headers, followed by columns for various locations (PITTSBURG, COLUMBUS, MANHATTAN, etc.) and a final column for 'Location'. The bottom of the interface features an 'Export' button, 'Addl Data:' dropdown (circled in red), 'Sort Rows on:' and 'Sort Cols on:' dropdowns (both set to 'MK'), and a 'Filter' button. A status bar at the bottom shows 'Assumptions: Do Not Include Founders; Unknown Weight = 0.00' and 'Dynamic Population Variables: GD = 0.9645; GV = 0.9600; MK = 0.0359; % Known = 100%; N = 143.0'.

Terms and Concepts

MSI: *Mate Suitability Index (MSI)* is a numerical genetic assessment of a male-female pair that incorporates several variables into one ranking (*MSI* range is 1 to 7, with 1 being the most genetically beneficial).

eMSI: *MSI* score that includes the extension (fractional value after the integer).

DeltaGD: Net change in gene diversity of the population if the pair produced one surviving offspring.

MKDiff: Net difference in the mean kinship (MK) values for the male and female.

New Features

The **Pairwise tab** is a new feature and was not available in PM2000. It essentially incorporates the DOS-based software program MateRx functionality into PMx.

Helpful Hints

- Filters can only be used for the variables in the row and column “headers” – i.e., *UniqueID* and *Addl Data* variable. Once the table is filtered, the *Addl Data* variable can be changed without affecting the filter. For example, to get a table for only reproductive age individuals with their locations, set *Addl Data* to *AgeYears*, use the *Filter* button to restrict the table to only breeding age individuals, and then change *Addl Data* to *Location*.
- Sorting the rows and columns by *MK* will position the most genetically valuable individuals in the upper left of the table (and the most detrimental in the lower right).
- Import the matrix into Excel or similar program and use the Autofilter or other Excel functions to quickly identify the range of *MSI* options and best potential mates for females.
- If the table on the **Pairwise Info** tab is empty, be sure that the *Include MateRx* box is checked on the **Genetics Summary Statistics** screen.
- PMx applies a threshold level of inbreeding to determine *MSI* = “-” (do not breed this pair). The default threshold is $F = 0.125$, but will be set higher for populations in which the average $F > 0.125$. The threshold set automatically by PMx for a particular dataset is given to the left of the table as (*No Way for $F = 0.125$*). Click on *View MaterRx settings* for more information or to modify *MSI* definition settings.
- Modifying the *MateRx settings* will cause PMx to recalculate the **Pairwise Info** table and may reset the *Filter*, *Sort on* variables and *Addl Data* variable to the default settings.
- Dead individuals currently cannot be added to the **Pairwise Info** table.

Cautions

- *MSI* scores may not be suitable to use for managing every captive population. Be cautious when using this feature for managing populations with unusual histories or structures (few founders, very small *N*, large amount of unknown pedigree, high levels of inbreeding).

PAIRING TAB

Purpose

The **Pairing** tab provides detailed information on the impact of breeding specific pairs on the genetic status of the population. Recommended breeding pairs can be documented and their cumulative impact (given a certain probability of success) incorporated dynamically into PMx genetic calculations.

How to Use This Tab

The default setting is for all males to be displayed in the left table and all females in the right table (with unsexed individuals omitted from both tables). These settings can be changed using the *Filter* button, although the table labels (*Males*, *Females*) will not change. The default columns for each table are: *UniqueID*, *MKdynamic*, *Rank*, *KVdynamic*, *Known*, *AgeYears*, *Location*, *ReproStatus*, *F Result*, and *MSI*. As with most tables in PMx, the variables displayed can be customized by right-clicking on the header and adding and/or removing variables. Note that the variables *UniqueID*, *MKdynamic*, *KVdynamic*, *Rank* and *F Result* are required and cannot be deleted. Data can be sorted by clicking on the column header.

The *Results* table in the upper right corner displays information regarding the pair of individuals highlighted (blue rows) in the two tables. The top right gives information about the pair (inbreeding coefficient *F* of the offspring, and the *MSI* score for the pair). The rest of the table gives the new values (and net change) for *Gene Diversity*, *Gene Value*, *Founder Genome Equivalents (FGE)*, and *Percent* (of pedigree) *Known* if that pair produces surviving offspring (*# Offspring* produced by a pair can be changed from the default value of one in the field below the table). The blue columns in the *Males* and *Females* tables give the *F* (of resulting offspring) and *MSI* score for all possible mates of the individual highlighted in blue in the other table. The *MSI* column can be changed to display other variables (*eMSI*, *DeltaGD*, *MKDiff*, or *Ranks*) instead of *MSI* using the *Pairwise data to display* button at the top of the screen.

In this example, male 4193 and female 4074 are highlighted (blue rows). The resulting *F* for this pair is 0.0718 and *MSI* is 4, as seen in the blue columns on these rows and also in the *Results* table. The values for *F* and *MSI* in the blue columns for other females give the *F* and *MSI* for each of those respective females when paired with male 4193, allowing a quick “at a glance” assessment of the range of values across potential mates. Likewise, the *F* and *MSI* values given for the other males are in relation to pairing with female 4074.

PMx :: Amur Tiger Sample Project :: Genetics

Overview | Founders | Individuals | Kinship Matrix | Pairwise Info | **Pairing** | Culling | Management Sets | Graphs | Settings | Selection

Pairwise data to display: MSI

Males

UniqueID	MKdyn	Rank	KVdyn	Location	AgeY	F Result	MSI
4203	0.0240	1	0.0283	OMAHA	15	0	4
5049	0.0264	2	0.0335	INDIANAPL	5	0	2
4193	0.0270	4	0.0199	MANHATTAN	16	0.0718	4
4071	0.0270	3	0.0233	COLUMBIA	17	0.2573	7
3640	0.0272	5	0.0223	NY BRONX	22	0.0093	2
4491	0.0276	6	0.0203	DES MOINE	13	0	3
4490	0.0276	7	0.0203	DETROIT	13	0	3
4499	0.0276	8	0.0208	CHICAGOLP	11	0	3
4541	0.0283	9	0.0280	LOUISVILL	11	0.0077	3
5286	0.0292	10	0.0370	COLO SPRG	3	0	1
4755	0.0321	11	0.0363	COLUMBUS	8	0	2
4586	0.0341	13	0.0381	CALGARY	10	0	4
4168	0.0341	12	0.0359	CHICAGOBR	17	0.0336	4
4304	0.0341	14	0.0277	NY BRONX	14	0.0266	4
4825	0.0347	15	0.0356	RACINE	8	0.0142	6
4748	0.0356	16	0.0359	CLEVELAND	8	0.0134	6

Filtered (showing 49) Filter Export

Females

UniqueID	MKdyn	Rank	KVdyn	Location	AgeY	F Result	MSI
4407	0.0215	1	0.0277	PITTSBURG	13	0	4
4074	0.0244	2	0.0191	MANHATTAN	17	0.0718	4
4983	0.0247	4	0.0247	COLUMBUS	7	0.0202	4
4984	0.0247	3	0.0247	MINNESOTA	7	0.0202	4
4073	0.0259	5	0.0215	COLO SPRG	17	0.0718	4
4542	0.0262	6	0.0244	SYRACUSE	11	0.0085	2
5050	0.0264	7	0.0330	COLUMBUS	5	0	4
4828	0.0265	8	0.0237	INDIANAPL	8	0.0234	4
4916	0.0270	9	0.0260	BRIDGEPT	7	0.0376	4
4194	0.0270	10	0.0198	RACINE	16	0.2539	7
4500	0.0276	11	0.0203	SAN FRAN	11	0	2
4501	0.0276	12	0.0203	ST PAUL	11	0	2
4413	0.0285	13	0.0251	DES MOINE	14	0.0156	3
4195	0.0287	14	0.0223	CHICAGOBR	16	0.2539	7
4412	0.0300	15	0.0265	MADISON	14	0.0156	3

Filtered (showing 74) Filter

Results

	New Value	Change
Offspring F and Pair MSI	0.0718	4.3178
Gene Diversity	0.9646	0.0001
Gene Value	0.9605	0.0003
FGE	14.1414	0.0438
Percent Known	1.0000	0.0000

Success: 0.4 # Offspring: 2.5 Accept Auto

Selected Pairs

Sire	Dam	F	Success	Offspring	Location	Notes
5456	5200	0.0274	0.3500	2.5		
5341	4970	0.0000	0.6000	2.5		
5464	4969	0.0625	0.4000	2.5		
5286	5287	0.0000	0.2500	2.5		

Pairs = 18; # Offspring attempted = 45
Offspring expected = 19.13

Export Remove Remove All

Assumptions:
Do Not Include Founders; Unknown Weight = 0.00

Dynamic Population Variables
GD = 0.9645; GV = 0.9601; MK = 0.0359; % Known = 100%; N = 144.1

Change

Once a pair has been highlighted for breeding, enter the estimated probability of success for that pair (range is 0 to 1) in the *Success* field. Enter the *# Offspring* attempted for this breeding (e.g., mean litter size x number of litters). The default for both variables is 1 (i.e., 100% chance of producing 1 offspring). These variables can be different for each pair, allowing for different expected breeding success rates for different pairs (e.g., due to health, age, needed transfers, etc.). Click on the *Accept* button to accept a highlighted pair. This will add the pair to the *Selected Pairs* table on the right. Breeding *Location* and other *Notes* about the recommendation can be entered into this table. After each pair is selected, the measures of genetic value of the remaining animals and the *Dynamic Population Variables* will be updated (PMx does this by adding the number of offspring indicated to the population and recalculating all genetic variables). The section below the *Selected Pairs* table will display a cumulative total of the *# Pairs* recommended, *# Offspring Attempted*, and *# Offspring Expected* (based on the indicated *Success*).

Setting the *Success* variable to 0 is equivalent to the “Pair Only” option in PM2000, and is the same as the *Static MK* method that is available in the *Auto Pair* tool (see below). With that setting, no offspring are expected and the genetic calculations for the population will not be updated.

The *UniqueID* of individuals that have been added to the *Selected Pairs* will be highlighted blue on the *Males* and *Females* tables for easy identification of individuals that have already been selected for breeding. Check the *Do not show Paired* box in the upper right corner to remove these individuals from the tables. Checking this box does not affect the genetic calculations; it only visually removes them from the displayed table so that the list of remaining unpaired individuals is more clearly visible and shorter. Checking and unchecking this box will toggle these individuals in and out of the display but does not affect the genetic calculations.

The screenshot displays the PMx software interface for the 'Amur Tiger Sample Project :: Genetics'. The 'Pairing' tab is active, showing 'Males' and 'Females' tables with columns for UniqueID, MKdyn, Rank, KVdyn, Location, AgeY, F Result, and MSI. The 'Selected Pairs' table on the right lists pairs with columns for Sire, Dam, F, Success, Offspring, Location, and Notes. A 'Results' section at the top right shows 'Offspring F and Pair MSI' and 'Gene Diversity'. A red circle highlights the 'Do not show Paired' checkbox. Another red circle highlights the 'Accept' and 'Auto' buttons. The bottom of the interface shows 'Assumptions' (Do Not Include Founders; Unknown Weight = 0.00) and 'Dynamic Population Variables' (GD = 0.9645; GV = 0.9601; MK = 0.0359; % Known = 100%; N = 144.1).

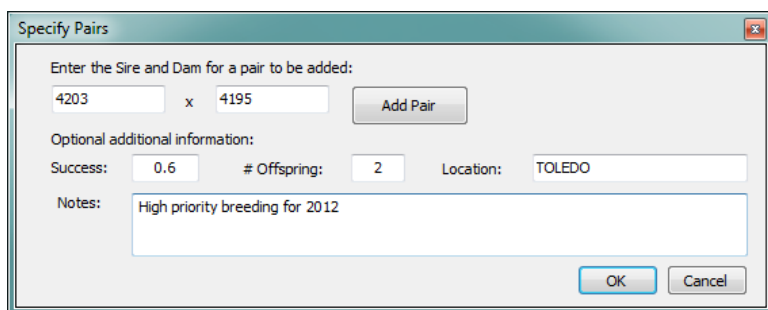
The *Remove* button below the *Selected Pairs* table will ‘unpair’ the highlight pair, remove their hypothetical offspring, recalculate all genetic values, and remove the pairing from the *Selected Pairs* table. *Remove All* will remove all pairs. In both instances, the genetic calculations will reflect these changes. Due to programming limitations PMx may not remove the blue highlighting from the *UniqueID* even though an individual no longer is recommended to breed.

The *Export* buttons below the *Males* and *Females* tables and the *Selected Pairs* table can be used to save these tables as .txt (and in some cases, also .csv or .xls) files.

Other Options on the Pairing Tab

Specify Pairs

This button at the top of the screen allows the user to type in specific pairs recommended for breeding, as an alternative to selecting them from the tables. This method also allows the pairing of dead animals, even if the *Allowing Pairing Dead* option is not checked on the main Genetics **Summary Statistics** screen. After entering the pertinent information, click *OK* to exit the window, or click *Add Pair* to accept this pair and add additional pairs. PMx does not check the sex of individuals and will allow a female x male pairing as well as same sex pairings. Be careful to enter the male *UniqueID* first and the female second in order to have the correct *UniqueIDs* displayed under *Sire* and *Dam* in the *Selected Pairs* table. If this method is used to select pairs, PMx may not highlight in blue the *UniqueIDs* of selected individuals in the *Male* and *Female* tables to indicate that they have been selected for breeding already.



The 'Specify Pairs' dialog box is used to manually add breeding pairs. It contains the following fields and controls:

- Enter the Sire and Dam for a pair to be added:** Two text input fields with values '4203' and '4195', separated by an 'x' symbol. An 'Add Pair' button is to the right.
- Optional additional information:**
 - Success:** A text input field with the value '0.6'.
 - # Offspring:** A text input field with the value '2'.
 - Location:** A text input field with the value 'TOLEDO'.
 - Notes:** A large text area containing the text 'High priority breeding for 2012'.
- Buttons:** 'OK' and 'Cancel' buttons at the bottom right.

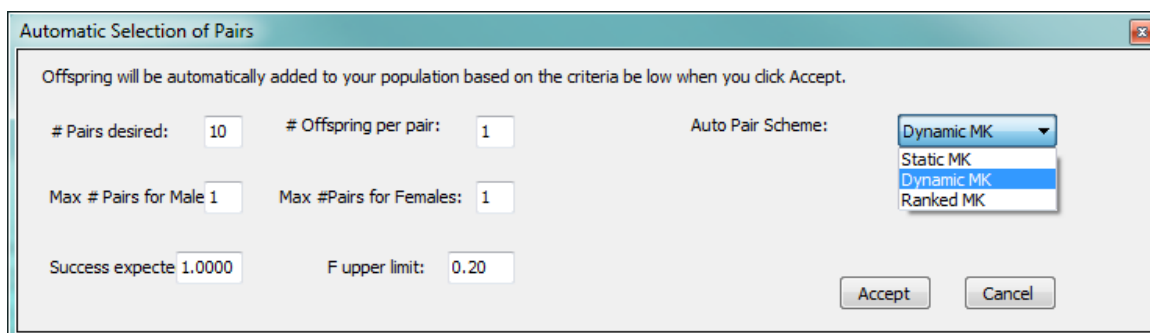
Read Pair File

Click on this button at the top of the screen to import a previously created list of breeding pairs. This file can be generated using the *Export* button in PMx or can be created manually. The imported file should be a text file that can have semi-colon, colon or tab delimiters (but not commas) between fields (see *Appendix D* for more information on input file format).

Auto

Located above the *Selected Pairs* table is the *Auto* pair button, which will automatically generate the optimal genetic pairs, based on the following specifications:

- *# Pairs desired* (default = 10)
- *# Offspring per pair* (default = 1)
- *Maximum # Pairs for Males* and *Maximum # Pairs for Females* (default = 1)
- Probability of reproductive success for each pair (*Success expected*) (default = 1.0000)
- Maximum allowable level of inbreeding (*F upper limit*) (default = 0.20)
- *Auto Pair Scheme* for creating pairs (either *Static MK*, *Dynamic MK*, or *Ranked MK*).



The 'Automatic Selection of Pairs' dialog box allows users to set criteria for automatic pair selection. It includes the following fields and controls:

- Offspring will be automatically added to your population based on the criteria be low when you click Accept.**
- # Pairs desired:** Text input field with value '10'.
- # Offspring per pair:** Text input field with value '1'.
- Auto Pair Scheme:** A dropdown menu with options: 'Dynamic MK' (selected), 'Static MK', 'Dynamic MK', and 'Ranked MK'.
- Max # Pairs for Male:** Text input field with value '1'.
- Max # Pairs for Females:** Text input field with value '1'.
- Success expected:** Text input field with value '1.0000'.
- F upper limit:** Text input field with value '0.20'.
- Buttons:** 'Accept' and 'Cancel' buttons at the bottom right.

- Static MK:* This breeding scheme creates pairs by attempting to pair the next available male with the lowest *MK* value with the next available female with the lowest *MK* value (within the limits set by maximum allowable F and maximum # of mates). This process is repeated until the desired number of pairs has been reached. The *MK* of all individuals and the genetic calculations remain static (no hypothetical offspring are created). This option may be considered for populations with a low breeding success rate.
- Dynamic MK:* This breeding scheme is similar to *Static MK* with one exception: after each pair is selected, the genetic calculations are updated to reflect the expected number of offspring from that pair, meaning that the *MK* of an individual is dynamic and increases as its relatives reproduce successfully. This option is a good scheme for populations with a good probability of success for pairs.
- Ranked MK:* This breeding scheme goes through the entire list of possible breeding pairs, uses iterative culling to remove the worst options (based on *MK*) from the list, and then recommends that the last remaining male and female as a pair, repeating this process until the desired number of pairs are selected. This option is a good scheme for populations that get one opportunity for breeding and then die (i.e., use for discreet generations, reintroductions), or at least have relatively little overlap of generations.

Repro Goals

This button at the top of the screen estimates the lifetime reproductive goals for the currently living individuals in the population. *This is a new tool that has not yet been extensively tested. Only use if you are familiar with the underlying algorithms in this tool.*

This tool projects the number of offspring that each currently living individual is expected to be recommended to produce over its lifetime, if everything were to happen perfectly as planned (e.g., survival and reproduction is predictable and realized according to the life-table data) in order to replace the entire living population with the entire next generation. **WARNING:** this tool indicates the number of offspring to produce over an individual's lifespan, not just in the next year. This should be considered as an approximate benchmark to identify which individuals may be recommended for the most reproduction over their lifetime and, conversely, which individuals are unlikely to ever receive a breeding recommendation.

The algorithm first uses dynamic *MK* pairing to produce enough offspring from the genetically top-ranked males and females to increase the population to the user-entered *Limit*. Then the algorithm uses *Auto Cull* to remove the least valuable animals from the current generation until the population returns to the *Target N* again. The algorithm goes back and forth between the *dynamic MK* pairing and *Auto Cull* until the entire next generation is created and the entire current generation has been culled (see *Appendix F* for more information). To calculate *Life Time Reproductive Goals*, specify:

- Target N:* The target population size in the next generation (default = current population size).
- Limit:* The maximum population size allowed (default value = current population size + 20).

Max Pairs (Male/Female) If *Vx Multiplier* box is **not** checked: Enter the maximum number of times that each male/female is allowed to reproduce (i.e., the number of offspring each individual is allowed to produce, as PMx assumes that each reproductive event produces only one offspring).
 If *Vx Multiplier* box is checked: PMx uses the numbers entered for *Max Pairs* as multipliers of the *Vx* (demographic reproductive value, based on the individual's sex and age) to determine the maximum number of times each male/female will be allowed to reproduce in the calculations of the lifetime reproductive goals (e.g., PMx assumes post-reproductive individuals can no longer reproduce and young animals will have the highest reproduction). **Caution:** Be sure to check *Vx* values in the life tables found in **Demography** section before using this tool. If *Vx* values are considered unreliable as indicators of future reproductive success, consider not checking the *Vx Multiplier* box; otherwise the results from this tool may be inaccurate for this population. In addition, be aware that it might be normal for the maximum reproduction that can be obtained from an individual to be several-fold to many-fold greater than the *Vx* estimated from the life table based on past management conditions.

Once these variables have been specified, click the *Calculate* button to calculate the *Reproductive Goals* for each individual and the *Resulting GD* for the population in the next generation if all reproductive goals are perfectly reached (i.e., if everything happens as ideally as possible). This value of *GD* could be used in goal setting because it calculates a more realistic upper limit of gene diversity, given the currently living animals in the population (i.e., indicates what is biologically possible), than *GD* calculated from *Potential Founder Genome Equivalents* that is given on the Genetic **Overview** tab. However, this may still be an unrealistically high projection for the population *GD*, depending on management constraints, reproductive success, or just bad luck. Click on the *Accept* button to add the calculated *Repro Goals* to the data for each individual. This column can be added to many of the tables in PMx.

Life Time Reproductive Goals

Target N: 150 Max Pairs for Male: 3 Max Pairs for Female: 3 Limit: 170 ☒ Vx Multiplier

Resulting GD = 0.9598 **Calculate**

UniqueID	Sex	Location	Repro Goals
5200	Female	MINNESOTA	4
5203	Female	BILLINGS	4
5204	Female	BILLINGS	4
5205	Female	PHILADELPHIA	4
5206	Male	ERIE	3
5207	Female	BUFFALO	0
5219	Male	GRANBY	5
5221	Male	TORONTO	5
5286	Male	COLO SPRG	5
5287	Female	COLO SPRG	5
5341	Male	SEDGWICK	4
5342	Female	ST LOUIS	2
5343	Female	INDIANAPOLIS	5

Note: Lifetime reproduction goals are NOT recommendations for pairings for next year and the optimal allocation of animals to pairings will change over time due to uncontrolled births and deaths.

Accept **Cancel**

Assumptions

Some of the assumptions made by PMx for genetic analyses can be modified by clicking the *Change* button at the bottom of the screen. These include parental assumptions regarding multiple possible parents, proportion of WILD to assign to UNK parents, including founders in the analysis, assigning weights to groups, and assigning weights to empirical kinships. Be cautious in changing any of these settings unless the population has special analysis needs and you are very familiar with how the genetic analyses are calculated. All of these options can also be found in the Genetics **Settings** tab, so changing them in one location will also change them in the other (see **Genetics Settings** tab section for more information).

Terms and Concepts

See the **Genetics Summary Statistics** screen, **Genetic Overview** tab, and **Pairwise Info** tab sections and the *Appendix B - Glossary* for definitions of the variables on this tab.

New Features

- New ways to incorporate multiple potential parents into the genetic analysis.
- New ways to deal with animals with unknown parentage.
- User can add or remove more variables from the male and female tables and customize them for the needs of a particular managed population.
- The relative suitability of many potential mates can be seen simultaneously on the tables.
- Paired individuals can be visibly removed from the tables to see “who is left to pair”.
- User can incorporate likelihood of reproductive success for each recommended breeding pair.
- User can indicate the number of offspring recommended for each breeding pair.
- PMx calculates the cumulative expected number of offspring.
- Lifetime reproductive goals can be estimated.
- Optimal breeding pairs can be automatically calculated.

Helpful Hints

- PMx automatically uses a dynamic MK list (i.e., genetic calculations are revised after each pair is selected). For pairing using a static MK list, enter ‘0’ for *Success* for each pair (note that the *# Offspring expected* then will not be calculated).
- Use *ReproGoals* to help estimate how close intensive management might allow the population to approach the *Potential GD*.
- A powerful addition to this tab is the ability to add variables to the tables that are especially relevant to the species or population. For some populations, these might include *Rearing type*, *Prior Mates*, past *ReproYears*, etc. Since space is limited in these tables to display multiple columns, less useful columns can be removed or, if they are fixed, can be “hidden” by pulling the right edge of the column to the left to reduce its width.
- To view dead individuals on the **Pairing** tables, make sure that the *Allow Pairing Dead* check box is checked on the main **Genetics Summary Statistics** screen, and change the table filters to include dead individuals.
- *AutoPair* and *ReproGoals* create pairs from only the individuals on the displayed filter view.

Cautions

Only use *Repro Goals* if you are very familiar with the underlying algorithms. This is a new tool that has not yet been extensively tested for its best uses in population management.

CULLING TAB

Purpose

The **Culling** tab allows the identification of those individuals that are genetically overrepresented in the population, and provides the ability to assess the effect of removing individuals on the genetic status of the population. Individuals may be removed (culled) to promote genetic management (surplus animals) or to identify individuals that are not valuable in this population but may be good for use in release programs or for export to other regional populations. The **Culling** tab may also be used to deselect individuals from the genetic analysis that for whatever reason can never breed again and should therefore be removed from the mean kinship calculations before pairing decisions are made. See the *Section 2* of the manual for a description of the consequences of removing non-reproductive individuals using the **Culling** tab rather than the **Selection** screens.

How to Use This Tab

All living individuals in the selected population for genetic analyses are listed in the *Current Population* table on the left side of the screen. As with other PMx tables, clicking on the appropriate column heading will sort the individuals by that variable, and right-clicking on the header opens the full list of variables that can be added to or deleted from the table.

The *dGD* column (in blue) shows the change in the population's gene diversity that would result if that individual were removed from the population. A negative value for *dGD* means that the population's overall gene diversity would decrease if that individual were to be removed (indicating a genetically valuable individual); a positive *dGD* indicates a genetically overrepresented individual whose removal would increase the gene diversity of the population. This column can be sorted to quickly identify the most overrepresented (i.e., least genetically valuable) individuals in the population.

PMx :: Amur Tiger Sample Project :: Genetics

Overview Founders Individuals Kinship Matrix Pairwise Info Pairing **Culling** Management Sets Graphs Settings Selection

Current Population

UniqueID	Sex	MKdynamic	KVdynamic	Location	Known	F	AgeYears	ReproStatus	dGD
4203	Male	0.0230	0.0266	OMAHA	1.0000	0.0000	15	Fertile	-0.0002
4407	Female	0.0219	0.0280	PITTSBURG	1.0000	0.0000	13	Fertile	-0.0002
4983	Female	0.0250	0.0249	COLUMBUS	1.0000	0.0313	7	Fertile	-0.0002
4984	Female	0.0250	0.0249	MINNESOTA	1.0000	0.0313	7	Fertile	-0.0002
5049	Male	0.0260	0.0326	INDIANAPL	1.0000	0.0000	5	Fertile	-0.0002
5050	Female	0.0260	0.0321	COLUMBUS	1.0000	0.0000	5	Fertile	-0.0002
4071	Male	0.0238	0.0233	COLUMBIA	1.0000	0.0146	17	Fertile	-0.0002
4193	Male	0.0263	0.0198	MANHATTAN	1.0000	0.0078	16	Fertile	-0.0002
4194	Female	0.0263	0.0197	RACINE	1.0000	0.0078	16	Fertile	-0.0002
3640	Male	0.0270	0.0217	NY BRONX	1.0000	0.0000	22	Fertile	-0.0002
4045	Female	0.0331	0.0250	NY BRONX	1.0000	0.0000	18	Fertile	-0.0001
4195	Female	0.0281	0.0223	CHICAGOBR	1.0000	0.0078	16	Fertile	-0.0001
4319	Female	0.0318	0.0289	GRANBY	1.0000	0.0000	14	Fertile	-0.0001
4412	Female	0.0306	0.0270	MADISON	1.0000	0.0000	14	Fertile	-0.0001

Export Read Cull File Unfiltered (showing 125) Filter

Assumptions: Do Not Include Founders; Unknown Weight = 0.00 Change

Dynamic Population Variables: GD = 0.9641; GV = 0.9600; MK = 0.0359; % Known = 100%; N = 141.0

Results

	New Value	Change
Gene Diversity	0.9639	-0.0002
Gene Value	0.9600	0.0000
FGE	13.8543	-0.0804
Percent Known	1.0000	0.0000

Selected Culls

UniqueID	Location
4073	COLO SPRG
4074	MANHATTAN

Cull Animal Auto

Export Reverse Cull Remove All

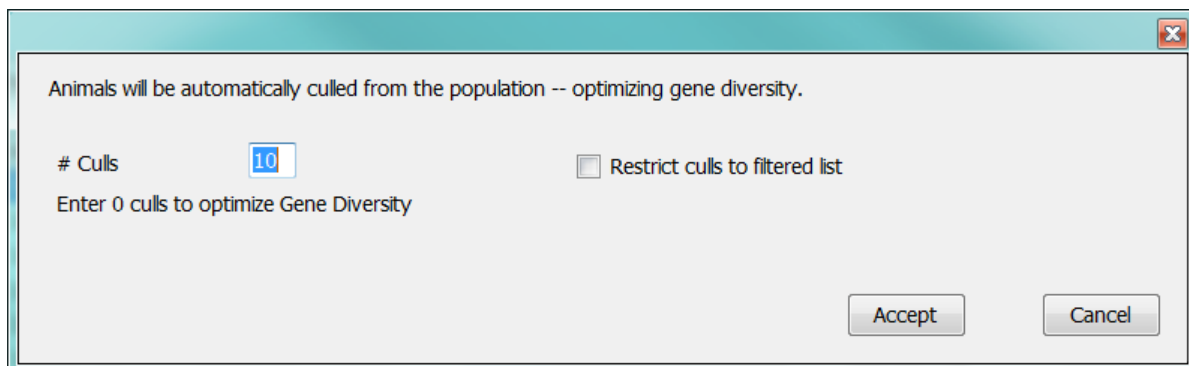
☐ Apply culls to demography

The *Results* table on the right displays the effect of removing the individual highlighted (blue row) in the *Current Population* table. The table reports the *New Values* for *Gene Diversity*, *Gene Value*, *Founder Genome Equivalents (FGE)*, and *Percent Known*, as well as the net *Change* in value for each variable, if the individual were culled (removed) from the managed population.

Clicking on the *Cull Animal* button (underneath the *Results* box) will simulate removal of the individual from the population. The culled individual will be displayed in the *Selected Culls* box on the bottom right side of the screen and the population's genetic statistics will be updated in the *Results* box and other screens under *Dynamic Variables*. Culling will also impact the genetic values of other individuals. To "un-cull" an individual, click on the individual in the *Selected Culls* box so that it is highlighted, then click on the *Reverse Cull* button. This will add the individual back to the list, update the population's genetic statistics in the *Results* box, and update the measures of genetic value of the other individuals in the list. All *Selected Culls* can be reversed using the *Remove All* button. Culled individuals can also be removed from the *Age Distribution*, *Projections* and other demographic screens and calculations by checking the *Apply culls to demography* box before individuals are culled.

The *Current Population* table and list of *Selected Culls* can be exported using the *Export* buttons under each respective section. If the *Selected Culls* box is exported, a *Cull File* will be created (see below). As with most PMx tables, the list of individuals displayed in the *Current Population* table can be filtered using the *Filter* button.

Auto button: This feature can be used to identify the best x number of individuals for culling so that the overall population gene diversity is optimized. Clicking the *Auto* button will open the *Auto Cull* window. Enter the number of individuals to be culled (default value is 10). Click *Accept*. The optimal x individuals to be culled will now appear in the *Selected Culls* box and all genetic calculations will be updated. Entering 0 for the # *Culls* will cause PMx to cull until *GD* is maximized. Check the *Restrict culls to filtered list* box to limit *Autocull* to only those individuals displayed (e.g., one sex, older individuals).



Read Cull File button: This feature will read in a previously created list of individuals to be culled. Clicking on the *Read Cull File* button will open the *Read in Cull List* window. Navigate to and select the file containing the lists of individuals to be culled, and click *OK*. The *Cull File* can be created in two different ways. It is created if the *Selected Culls* box is exported, and later, if necessary, these individuals may be added or removed manually from the list. Alternatively, a cull file can be created manually as a text file listing the individuals to be culled, with one individual *UniqueID* per line.

New Features

The ability to automatically generate a list of optimal individuals to cull (*Auto cull*) is new to PMx.

Cautions

The default column widths may hide some details, particularly in the *dGD* column. Unless the column is stretched wider, it may not initially display the minus signs for the negative values.

MANAGEMENT SETS TAB

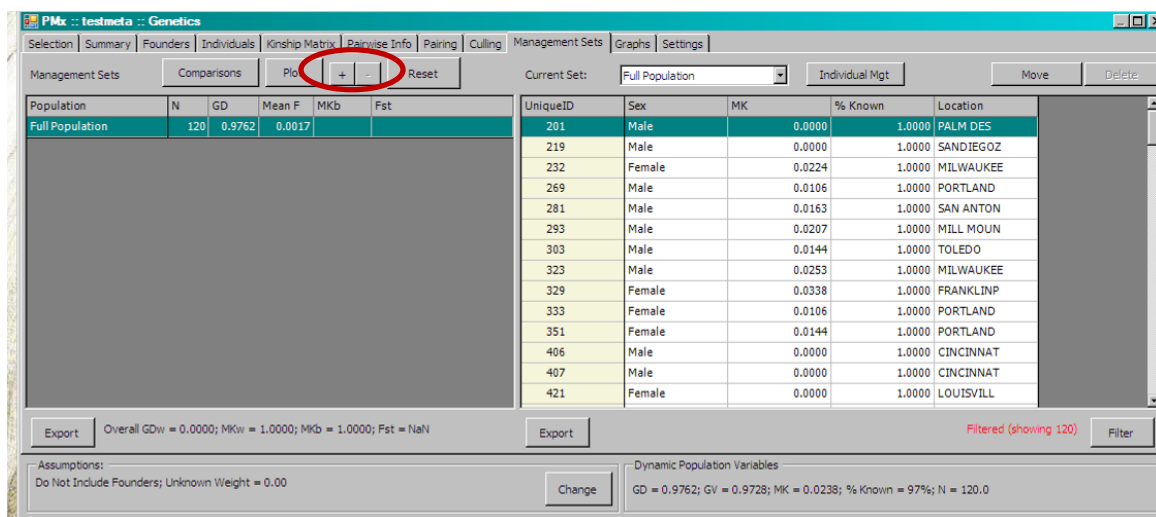
Purpose

The **Management Sets** tab is used to divide a studbook population into subpopulations, or *Management Sets*, and to examine the genetic divergence and similarities between subpopulations as well as to test the genetic effects of the movement of individuals among these subpopulations. These subpopulations could represent population subsets such as:

- large herds or flocks within a managed population;
- operational distinctions, such as education specimens vs. breeding specimens within a population;
- separately managed regions within a global population;
- animals managed within a zoo association vs. outside of a zoo association; or
- captive and wild populations within a reintroduction program.

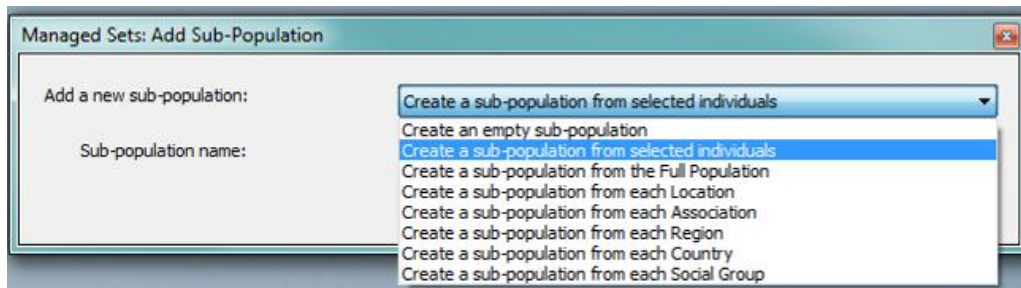
How to Use This Tab

Upon opening this tab, a list of management sets is displayed on the left and a list of individuals on the right under *Current Set*. Above the list of management sets, PMx provides access to the *Full Population*, which includes all individuals in the population as selected in the **Selection** tab.



Management sets can be created by the user as subpopulations. Certain types of sub-populations can be automatically created using the “+” button. This option can create subpopulations based on *Location*, *Association*, *Region*, *Country*, *Social Group*, or a management set that includes the *Full Population*. *Association* or *Region* files must have been imported into PMx when the project was created or can be added using the Genetic **Settings** tab. *Regions* and *Countries* (based on *Location*) are automatically imported from SPARKS 1.6 exported data (see *Section 1 on Using PMx* for more information on *Regions*).

Subpopulations can also be created by manually selecting individuals. To do this, use the *Ctrl* and/or *Shift* keys to right-click and highlight all of the individuals that are to be grouped as a subpopulation. With these individuals highlighted, click the “+” button and select *Create a subpopulation from selected individuals*. Name the subpopulation and click *OK*. Empty subpopulations can also be created (e.g., wild habitat into which captive individuals will be reintroduced).



Subpopulations can also be removed. Highlight the subpopulation on the list of *Management Sets* and click the “-” button to remove the selected subpopulation. Clicking the *Reset* button will remove all of the subpopulations.

Once created, individual subpopulations can be selected and viewed by using the drop-down list for *Current Set*. Clicking on a *Management Set* in the table on the left will also open that subpopulation as the *Current Set* on the right. Like most tables in PMx, the *Management Sets* and *Current Set* tables can be saved as .txt, .csv or .xls files using the *Export* button.

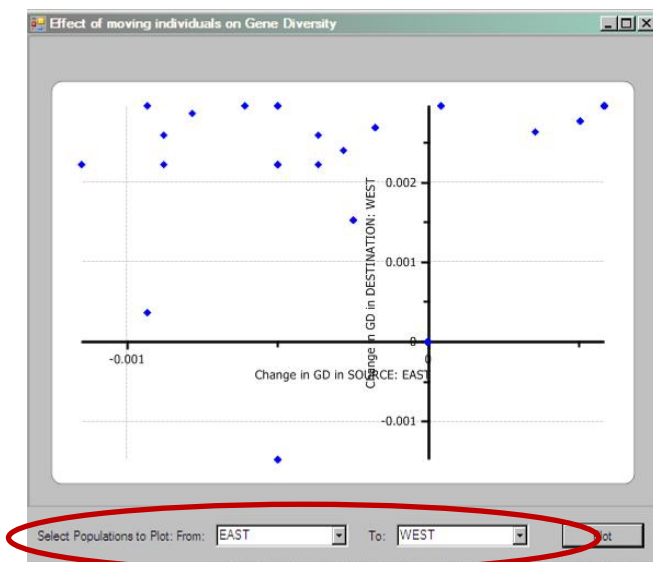
Population	N	GD	Mean F	MKb	Fst
Full Population	346	0.9478	0.0656		
Austral	53	0.8709	0.0862		
EastAsi	11	0.8675	0.0762	0.0779	0.0165
Europe	104	0.8781	0.0777	0.0937	0.0149
NorthAm	71	0.9022	0.0394	0.0507	0.0310
SEAsia	106	0.9264	0.0563	0.0071	0.0388

Overall GDw = 0.8972; MKw = 0.1028; MKb = 0.0353; Fst = 0.0535

Summary information for each subpopulation (N , GD , $Mean F$) is given in the table on the left, along with information on the relationships of these subpopulations (MKb , Fst) to the one selected as the *Current Set*. Summary statistics describing the average relationships among all subpopulations (GDw , MKw , MKb , Fst) are displayed in the lower left of the window under the list of *Management Sets*. Click the *Comparisons* button to show a matrix indicating the Fst (in blue) and MKb (in pink) between each pair of subpopulations. This table can be saved as a .txt, .csv or .xls file using the *Export* button.

Population	N	GD		Austral	EastAsi	Europe	NorthAm	SEAsia
Austral	53	0.8709						
EastAsi	11	0.8675		0.0779				
Europe	104	0.8781		0.0165	0.0067			
NorthAm	71	0.9022		0.0149	0.0102	0.0345		
SEAsia	106	0.9264		0.0388	0.0126	0.0503	0.0332	

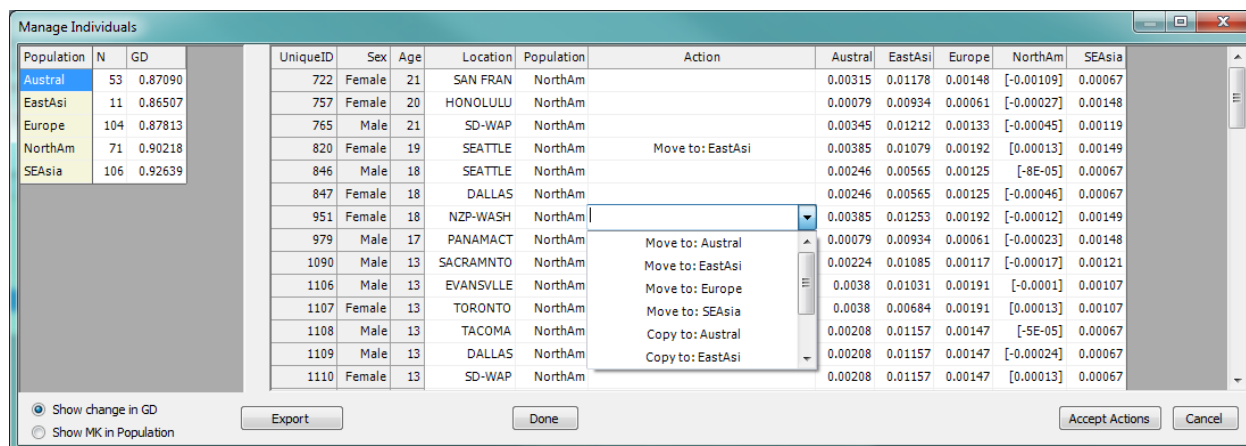
Click the *Plot* button above the *Management Sets* table to produce a plot indicating the effect (change in gene diversity) of moving any single individual from one subpopulation to another. The impact on the source population is given on the horizontal x-axis, while the impact on the destination population is given on the vertical y-axis. The subpopulations and direction of the transfer can be selected at the bottom of the window; click the *Plot* button to redraw the plot for the new subpopulations. The sample plot below shows that transfer of the majority of individuals, if moved from the EAST subpopulation to the WEST subpopulation, would reduce *GD* in the EAST subpopulation while increasing *GD* in the WEST subpopulation. The preferred genetic situation would be to transfer individuals whose transfer would result in an increase in *GD* for both the source and destination subpopulations. These are the individuals located in the upper right corner of the plot. Transfer of individuals in the lower left corner of the plot should be avoided, as this causes a decrease in gene diversity in both populations.



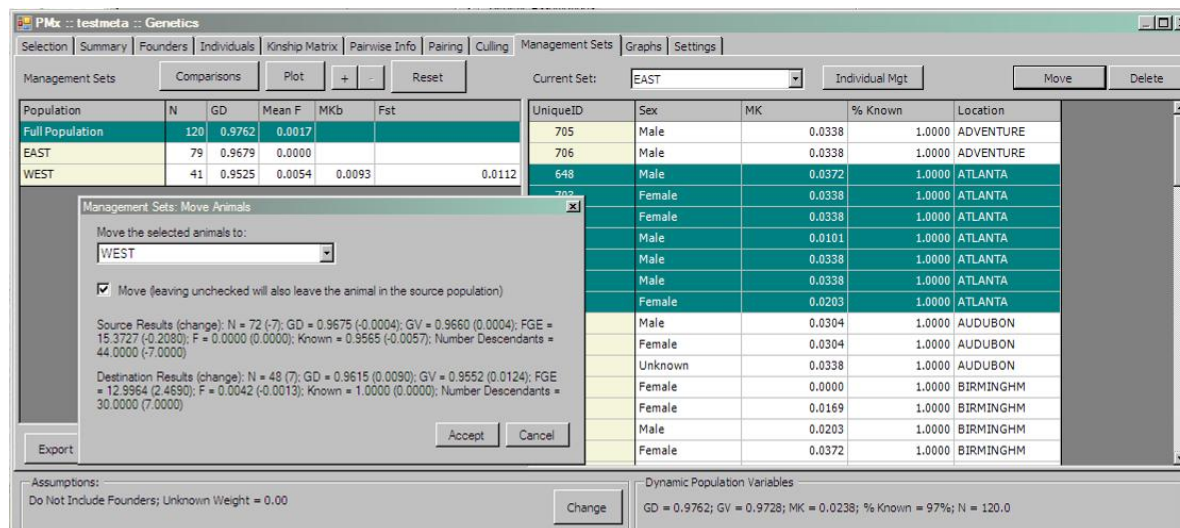
PMx provides two methods for exploring the genetic impact of moving specific individuals between subpopulations and for making these transfers within the program in order to evaluate the cumulative impacts of multiple moves.

Individual Mgt: Set the *Current Set* to the desired source population. Click the *Individual Mgt* button above the *Current Set* table to open a table containing all of the individuals in the *Current Set* (source population). Unlike most PMx tables, the column variables cannot be modified but are set to *UniqueID*, *Sex*, *Age*, *Location* and (sub)*Population*. Also displayed is the change in *GD* (or *MK*, if selected in lower left corner) to the source [in brackets] and destination (without brackets) subpopulations if that individual alone were to be moved to that subpopulation. Click on the column header to sort by any column (e.g., change in *GD* in the source population).

Use the pull-down menu in the *Action* column for a specific individual to simulate the transfer of the individual to another subpopulation. Multiple transfers can be designated to multiple subpopulations from this source subpopulation. Clicking on the *Accept Actions* button will transfer these individuals to the designated destination subpopulations and recalculate all of the individual and population statistics. The new *N* and *GD* of each subpopulation will be displayed in the upper left corner of this window. Selecting *Copy to* (instead of *Move to*) will place the individual in both subpopulations (copying it to the destination subpopulation while leaving it in the source population) (e.g., transfer of gametes).



Move button: To test the transfer of individuals or groups of individuals without completing the moves, use the *Move* button in the upper right corner of the main **Management Sets** window. Set the *Current Set* to the desired source subpopulation. Select an individual or group of individuals to move between subpopulations by highlighting them using *Ctrl* or *Shift*/right click keys. Then click the *Move* button. A pop-up window will appear. Indicate the destination subpopulation. Detailed results of the transfer on the source and recipient subpopulations will appear in the pop-up window. If the *Move* check box is selected, the individual will be moved; if the box is unchecked, then the individual will be left in the source subpopulation and copied to the destination subpopulation. Clicking the *Accept* button will cause the individual(s) to be moved or copied. Clicking *Cancel* will cause the individual(s) to remain in the source subpopulation.



Delete button: The Delete button in the upper right corner of the main window can be used to delete the highlighted individual(s) from the Current Set.

Terms and Concepts

Subpopulation: Any group of individuals selected from the *Full Population* or from another subpopulation. Subpopulations do not have to be mutually exclusive or exhaustive.

(pairwise) MKb: Mean kinship between a pair of subpopulations; the mean of all pairwise kinships, for all combinations of an individual from subpopulation 1 with an individual from subpopulation 2. See cautions below.

(pairwise) Fst: A measure of the genetic divergence between two subpopulations. Technically defined as the proportion of the genetic variance of the combined pair of subpopulations that is due to the genetic differences between the subpopulations. Equivalently, the extra genetic variance contained in the combined pair of subpopulations over the mean genetic variance within each subpopulation, expressed as a proportion of the total genetic variance in the combined set. Note that genetic variance is proportional to GD , so $Fst = GDb / GDt$, and since $GD = 1 - MK$ for any population, $Fst = (1 - MKb) / (1 - MKt)$. See cautions below.

Full Population: The selected living population.

Full Population statistics:

GDw: The weighted mean GD within subpopulations, with each within-subpopulation GD being obtained as $1 - MK$ (including only kinships between individuals in that subpopulation), and the mean across subpopulations being weighted by the number pairwise kinships within each subpopulation (N^2 , in which N is the number of living, captive-born animals in the subpopulation).

MKw: The overall mean of all kinships between two individuals that are in the same subpopulation. This will be the same as a weighted mean of the MKw values for the subpopulations, with the weightings being the number of pairwise kinships in the subpopulations.

MKb: The overall mean of all pairwise kinships between individuals in different subpopulations. This will be the same as the weighted mean of all the pairwise MKb values, with the weights being the number of kinships included in the MKb value for each pair of subpopulations.

Fst: A measure of the overall amount of genetic divergence among subpopulations. Measured as the proportion of the GD of the total population (GDt , the sum of all defined subpopulations) that consists of variance between subpopulations. Defined as $Fst = GDb / GDt = (GDt - GDw) / GDt$, with each GD calculated as $1 - MK$ for its parallel MK , and with the means across subpopulations weighted by the number of kinships that are included in each calculation. Thus, the Fst for the overall set of subpopulations will be more heavily influenced by the divergence among the larger subpopulations, and is not simply the average of all pairwise Fst values. [Note that there are other formulations of Fst that do weight each subpopulation equally, regardless of its size.]

New Features

This feature is comparable to the META-MK software previously available from Jonathan Ballou (2006).

Helpful Hints

- The *Filter* button can be used to refine the view of the *Full Population* or other subpopulation selected as the *Current Set*. However this does not alter the contents of the *Current Set*. Metrics are not recalculated based on filter settings and still reflect the pre-filtered population. The filter simply creates smaller views of the population. For example, it can be useful to limit the *Current Set* view to show only those individuals that meet certain criteria for transfer (e.g., females over 3 years of age).
- It can be useful to add a column to the *Current Set* table to indicate the management set(s) to which each individual belongs. This can be done by right-clicking on the column header and adding the *Management Sets* column. This individual variable can also be added to other PMx tables.
- If the *Selected Population* is reset by clicking the *Revert to originally imported data* button on the main **Selection** screen, all *Management Sets* will be deleted.
- Individual *MK* values reported in **Management Set** tab are the *MK* value calculated with respect to the *Full Population*, not for the subpopulation defined by the *Management Set*.

Cautions

Fst and *MKb* are contextual metrics in this application; the values sometimes reflect the pairwise relationship between two subpopulations and sometimes represent a mean level of relationship (or, conversely, divergence) among the set of subpopulations being considered. In the *Comparisons* button, these values are reported between pairs of subpopulations. In the **Management Sets** tab, the values reported refer to relationships between the *Management Set* subpopulation in the list on the left of the screen and the *Current Set* selected on the right side of the screen. Selecting a different *Current Set* will cause values on the left side of the screen to be repopulated reflecting the relationship to the new *Current Set*.

Note that when the *Current Set* is selected on the right of the screen is *Full Population*, the values for *Fst* and *MKb* to each subpopulation on the left of the screen are not populated. To generate a true *Fst* (subpopulation to total population) and populate these fields, a subpopulation called *Total Population* should be created. This subpopulation should contain the same animals as in the *Full Population*. Once the *Total Population* is created and selected as the *Current Set*, *Fst* and *MKb* between each subpopulation and the *Full Population* can be determined.

GRAPHS TAB (Genetics)

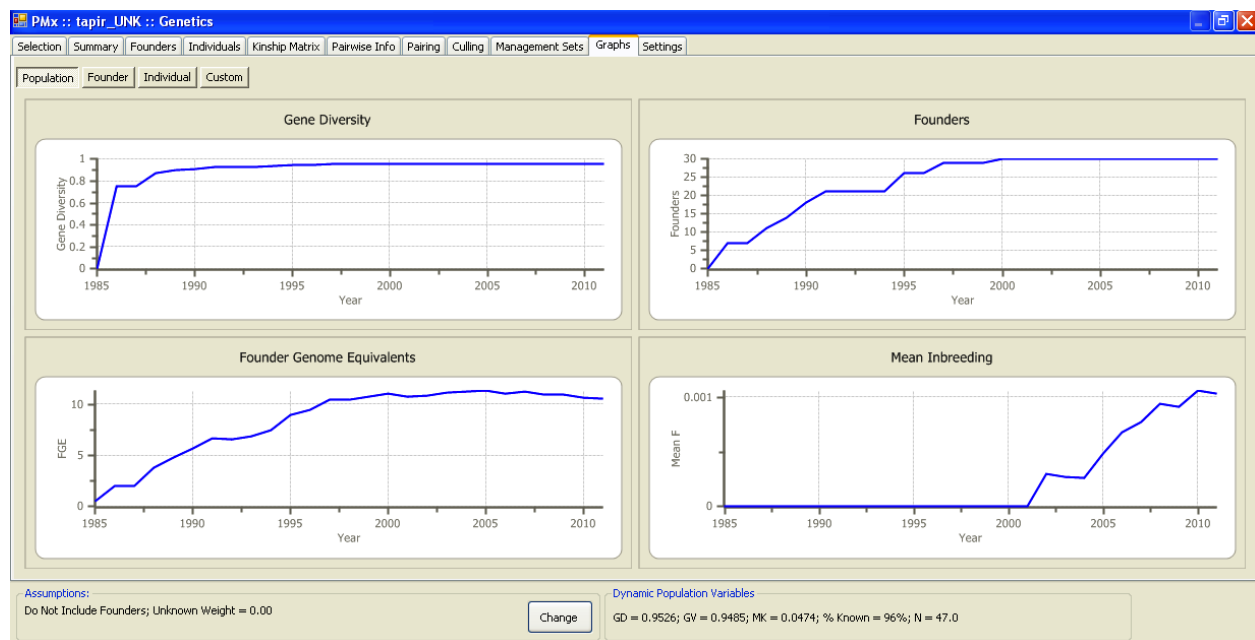
Purpose

The genetics **Graphs** tab provides a visual representation of the genetic summaries of the project data. Four different categories of graphs are available on this tab. *Population* graphs show how the genetic status of the population has changed over time. An assessment of how well founders are represented in the population can be made using the *Founder* graphs. *Individual* graphs show the degree of inbreeding and kinship among selected individuals. In addition, the *Custom* graph button provides the flexibility to customize the genetic graphs for founders, individuals, and populations.

How to Use This Tab

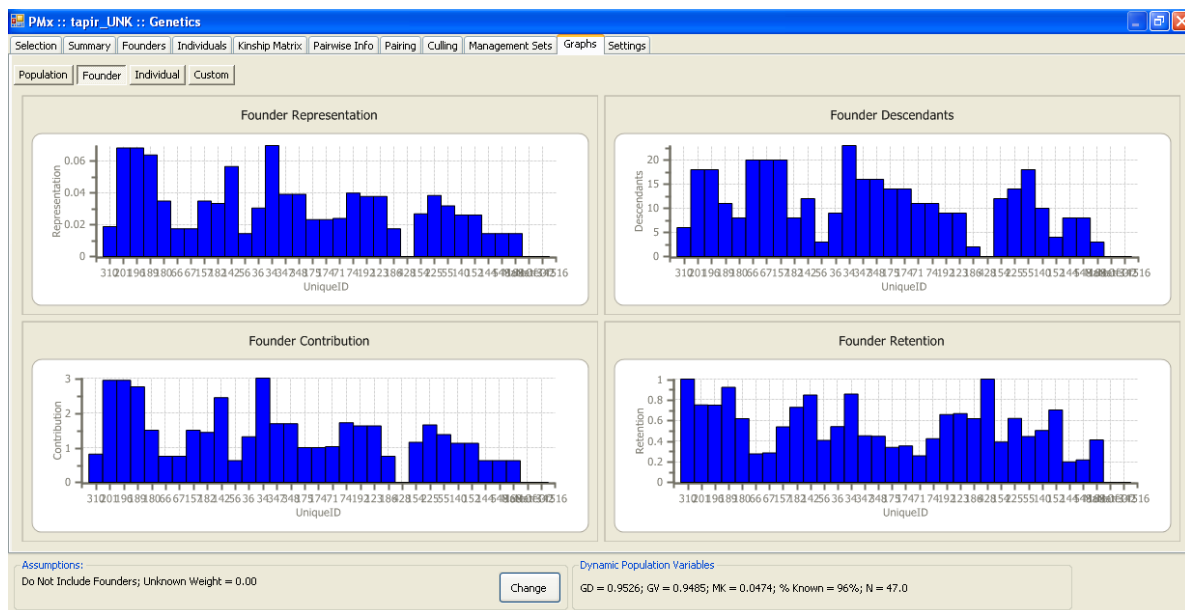
The buttons at the top left corner of the screen can be used to assess *Population*, *Founder*, *Individual* or *Custom* graphs. Double-clicking any graph opens a new window that allows the graph to be exported as a .png file, printed or sent to the *Project Notes*.

Population Graphs. These four graphs show how *Gene Diversity*, number of *Founders*, *Founder Genome Equivalents*, and *Mean Inbreeding* have changed over the window of time specified in the **Settings** tab. Note: These values are based only on those individuals that are included in the selected population on the **Selection** screen for genetic analysis. This may or may not reflect the actual historical managed population over time. For example, if current living post-reproductive individuals are removed from the genetic analysis, these individuals will not be included in the historical genetic analyses even during their early and reproductive years (see *Section 2 – Selection screen* for more discussion on this topic).

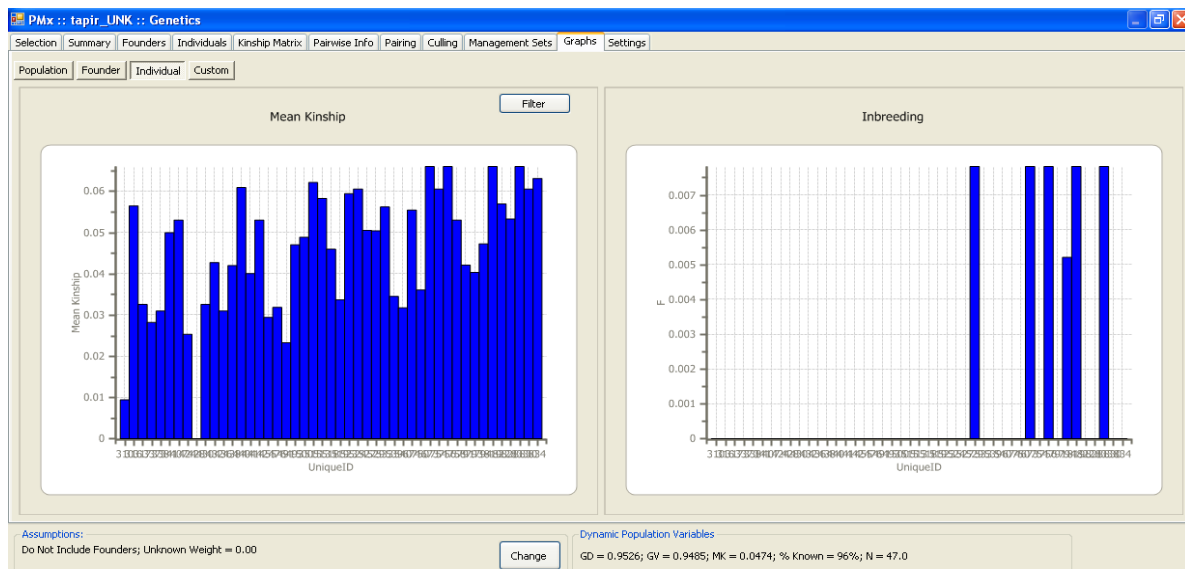


Founder Graphs. This screen shows histogram plots displayed one of four measures for each founder:

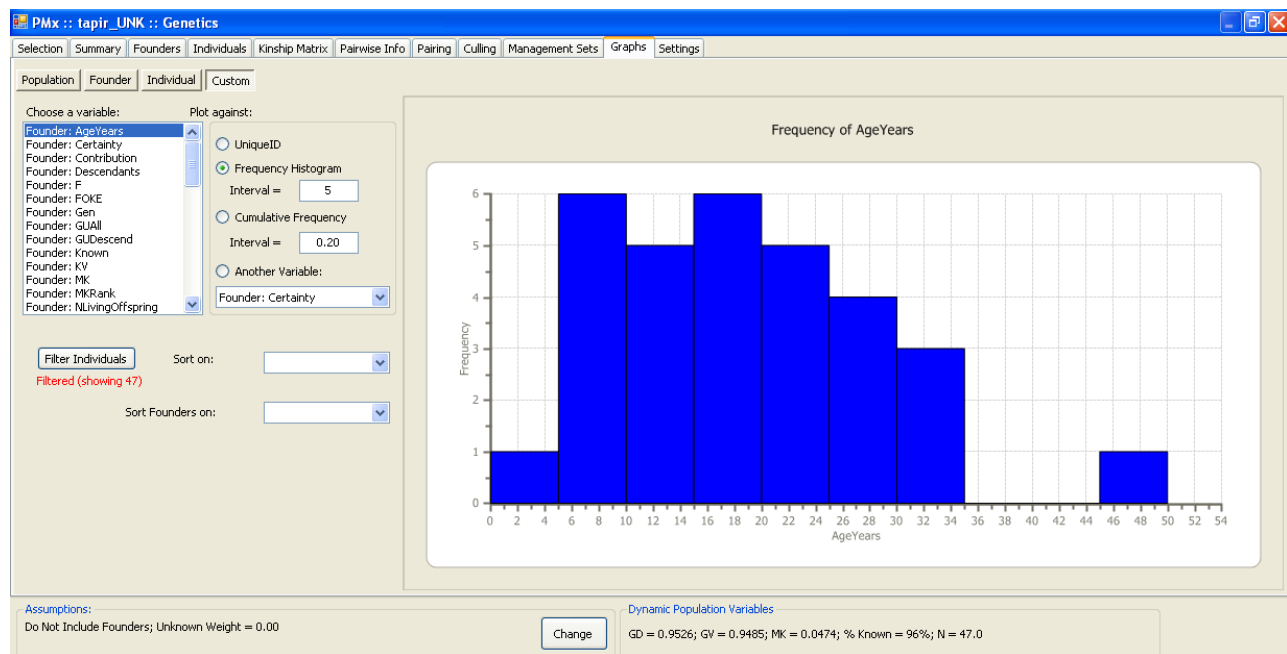
- *Representation* (number of copies of each founder's genes present in the living, descendant population)
- *Descendants* (number of living descendants)
- *Contribution* (proportion of the genes in the living descendant population that are derived from each founder)
- *Retention* (probability that each founder's alleles are still present in at least one living descendant)



Individual Graphs. Histograms are given for *Mean Kinship* and *Inbreeding* for each individual in the selected living population. Use the *Filter* button to specify the individuals to be graphed without affecting other genetic analyses or graphs.



Custom Graphs. The *Custom* graphs menu provides the capability to plot almost any data from the PMx project analyses. To create a graph, choose the graph category (*Population, Founder, Individual*) and the variable or genetic summary to graph. These variables may be plotted against another genetic variable, against individuals (*Unique IDs*), as a frequency histogram, or as a cumulative frequency. The *Frequency Histogram* and the *Cumulative Frequency* options allow the user to specify the interval for which data are combined and displayed. The *Filter Individuals* button can be used to change the specified individuals to be graphed. The *Sort on* and *Sort Founders on* pull-down menus can be used to change the order of the individuals on the x-axis when *Unique IDs* are used. For definitions of *Custom* graph variables, see the Summary, Overview, Founders and Individuals tab sections of the manual and the *Appendix B – Glossary*.



Terms and Concepts

See *Appendix B – Glossary* for definitions of genetic terms used on this tab.

Helpful Hints

- If the labels on the graph axes are bunched together, double-clicking on the graph and dragging the corner of the graph to increase its size will spread out the labels.
- Export the historical genetic *Population* graphs before excluding post-reproductive, sterilized or other permanent non-breeders from the genetic analysis on the **Selection** screen in order to include them in the genetic calculations.

Cautions

While it is possible to create a large number of different graphs with *Custom* graphs, be aware that many of these would be relatively meaningless or very hard to interpret. Pay attention to the graph settings in order to create a useful graph.

SETTINGS TAB (Genetics)

Purpose

The **Settings** tab in the **Genetics** module allows the user to customize settings for genetic assumptions and analyses – specifically, it provides the ability to modify the way in which multiple and unknown parents are treated in the pedigree analysis, how founders are treated, and how *MSI* values are calculated. This tab also provides options to change the analysis date window (start and end dates) and allows the user to attach optional additional files after the project has been created.

How to Use This Tab

This tab is divided into three sections. The left column provides options for modifying the *Genetic Assumptions* in the data analysis and for setting the *Analysis Date*. The center column provides options to modify the *MateRx Settings* that contain the definitions and rules used in calculating *MSI* for the **Pairwise Info** tab. The right column can be used to attach and read in *Additional Data Files* after the project has been created. After changing any options, click *Implement changes* to apply these changes.

Genetic Assumptions

These options are also available on the **Summary Statistics** screen before *Genetic Details* is opened.

Parentage Assumptions: Changes the assignment of parentage when there are multiple possible parents. Default setting is *Probabilistic parents*. Options are:

- Probabilistic parents:** Assign a proportion of the offspring to each identified possible parent based on the probabilities given in the studbook database.
- Most likely parents:** Assign parentage to the individual with the highest probability of being the parent for genetic calculations. In case of ties, the first one listed is used.
- Omit uncertain parents:** Change any sire or dam indicated by MULT to UNK (unknown individual).

Note that these options currently only apply to exports from SPARKS 1.6 and only when MULT parents are explicitly identified with probabilities assigned. For other data exports, MULTs are treated as UNKS unless the .csv or .ped file is manually edited to include possible parents and their probabilities.

Value (proportion WILD) to assign to Unknown parents: Assigns a portion of the pedigree of an unknown (UNK) individual as being an unrelated founder (WILD). Default value is zero. This option is available only if there are UNKnown parents in the database.

0 = do not include individuals with unknown parents in genetic calculations

0.5 = treat individuals with unknown parents as $\frac{1}{2}$ unknown and $\frac{1}{2}$ wild

1.0 = treat all animals with unknown parents as having wild parents

The optimal value to use here depends on the amount of unknownness in the population's pedigree. If the population has a mostly unknown pedigree, then it may be better to use a higher value here. If the population has only a small amount of unknownness in the pedigree, then it may be better to use a lower value here. The appropriate value may also be influenced by how likely it is that the unknown individuals are related to the rest of the population or not.

Include Founders: Choose whether or not to include the founders in the genetic summaries of population genetic status and measures of genetic value of individuals. The default setting for genetic statistics is to include only the descendent individuals but to exclude wild-caught founders. Note that by including the founders, the kinship calculations are not affected.

Weight Groups: Allows large groups to be weighted when calculating the population statistics. Group data must be entered into a .ped file (or possibly a file from ZIMS in the future). Do not use this tool unless you are familiar with it.

Weight to assign to empirical Kinships: Provides the option to integrate empirical data with estimated kinships among founders (e.g., molecular data) into PMx and to specify how much to weight these empirical data. Weighting depends on the level of confidence in the molecular results and can be done by entering a value between 0 and 1, in which:

0 = do not use empirical data; use only original pedigree calculations

0.5 = use a split between empirical and pedigree data (e.g., if empirical data says kinship = 0.3 and pedigree data says kinship = 0.1, then PMx will use 0.2)

1.0 = use empirical data for those kinships entered by importing a file of empirical kinships, rather than a kinship calculated from the pedigree(default value)

The optimal value to use here depends on the uncertainty (standard error) around the empirical data. If there is a smaller standard of error, then higher weight should be given to the data. If there is a larger standard of error, then a lower weight should be given to the data. However, more research is needed on this. This box will only be accessible if empirical kinships have been imported.

Other Settings

Analysis Date: Date that defines the end of the analysis window. This is the ending date for the genetic historical calculations. This date also defines the "current" population; the genetic status of the "living" population is calculated with respect to this date. Default date is the end of the date window for the exported data. Checking the *Apply date also to Demographic Age Structure* box will apply the new date to all historical and current demographic calculations (default setting).

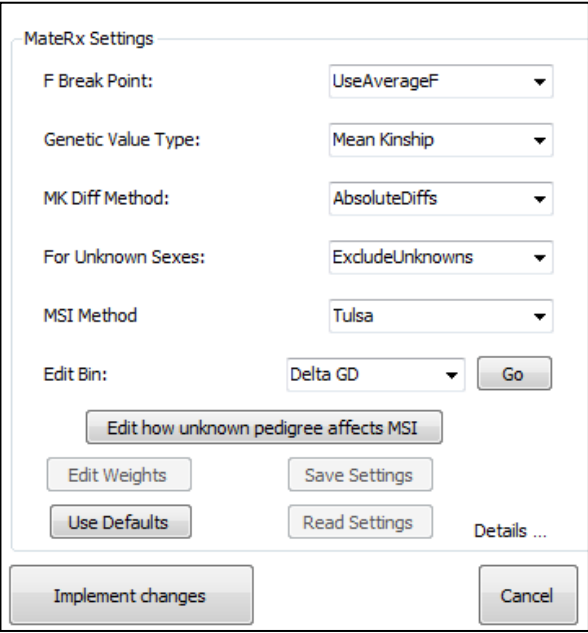
Start Date: Date that defines the beginning of the analysis window for historical genetic analyses (default is the start of the date window for the exported data).

Gene drop Iterations: Number of iterations for gene drop simulations (default = 1000). More iterations will provide more precise results, but usually 1000 is sufficient for most purposes.

MateRx Settings

These settings apply to how MSI scores and ranks are calculated for pairwise comparisons, and are accessible from both the genetic **Settings** tab and the **Pairwise Info** tab. These subscreens provide information on the characteristics of the population with respect to pairwise comparisons and also provide the ability to modify the definitions, weights and calculation method for computing *MSI* values.

MSI is a composite score that integrates four genetic components (*Delta GD*, *MKDiff*, *Inbreeding* and *Unknown*) into a single index. These variables are combined using specific definitions (that can be modified) to assign a *MSI* score of 1 to 6 for each pair, with *MSI* of 1-3 being genetically beneficial and 4-6 being genetically detrimental to the population (and “-” indicating “No Way” pairs that should not be bred due to high kinship level of pair).



MateRx Settings

F Break Point: UseAverageF

Genetic Value Type: Mean Kinship

MK Diff Method: AbsoluteDiffs

For Unknown Sexes: ExcludeUnknowns

MSI Method: Tulsa

Edit Bin: Delta GD Go

Edit how unknown pedigree affects MSI

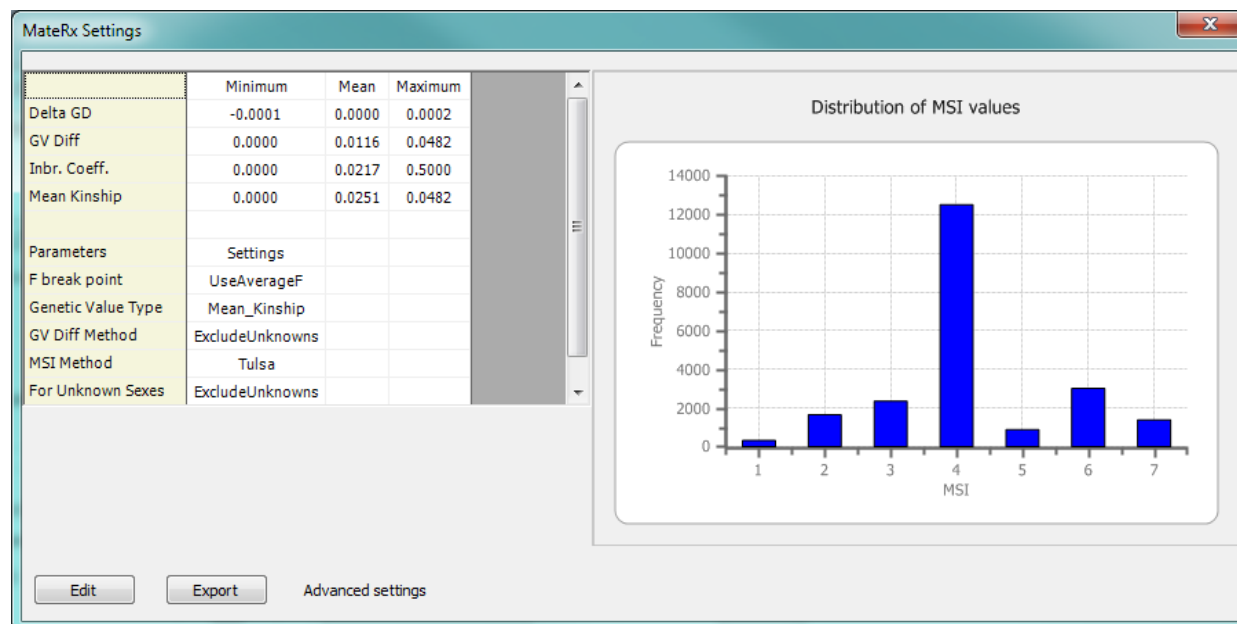
Edit Weights Save Settings

Use Defaults Read Settings Details ...

Implement changes Cancel

Viewing MSI Information

Click on *Details* at the bottom center of this screen (or *View MateRx settings* on the **Pairwise Info** tab) to open a new window that give the *Minimum*, *Mean* and *Maximum* values for *Delta GD*, *GV Diff* (MK Diff), *Inbreeding Coefficient*, and *Mean Kinship* for all pairs in the population. Also given are the current settings for several factors related to the calculation of *MSI*, many of which can be changed on the **Settings** tab. Displayed on the right is a histogram of the *MSI* scores for all pairs in the population (see the **Pairwise Info** tab for further explanation of *MSI* and other variables). Click the *Export* button to save the table as a .txt file. Click the *Edit* button to return to the **Settings** tab.



Click on *Advanced settings*. The default view is to display *Bin data*, which shows how each variable is defined across the rankings of 1 to 6, referred to as *Bins*. Each variable has a value that sets the *Break Point* between *Beneficial* and *Detrimental* pairings with respect to that variable. The variables *Inbreeding Coefficient* and *Unknown Pedigree* also define values as *No Way* points (individuals are too related and/or too much of the pedigree is unknown to make a meaningful assessment). The *Bins* for each variable – *Delta Gene Diversity*, *Difference in GV*, *Inbreeding Coefficient* and *Unknown Pedigree* – are defined in terms of:

- **Percentiles:** Percent of the range of values that fall into that bin (e.g., 33% indicates that the bin contains pairs with values in the first third of the range).
- **Value:** Value that defines the lower limit (starting point) of that bin.
- **#:** Number of total pairings that fall into that bin.
- **%:** Percent of total pairings that fall into that bin.

	Beneficial 1	Beneficial 2	Beneficial 3	Break Point	Detrimental 4	Detrimental 5	Detrimental 6	No Way
Delta Gene Diversity								
Percentiles	0.33	0.67	1.00		0.33	0.67	1.00	
Value	0.00013	0.00006	0.00000	0.00000	-0.00005	-0.00009	-0.00014	-1.00000
#	430	3241	7657		6923	2329	199	
%	0.02	0.16	0.37		0.33	0.11	0.01	
Difference in GV								
Percentiles	0.33	0.67	1.00		0.33	0.67	1.00	
Value	0.00398	0.00796	0.01193	0.01193	0.02402	0.03610	0.04818	1.00000
#	4708	4171	3438		5849	2231	382	
%	0.23	0.20	0.17		0.28	0.11	0.02	
Inbr. Coefficient								
Percentiles	0.00	0.50	1.00		0.33	0.67	1.00	
Value	0.00000	0.00632	0.01264	0.01264	0.04989	0.08713	0.12438	0.12500
#	13383	607	715		3873	1793	408	
%	0.60	0.03	0.03		0.17	0.08	0.02	
Unknown Pedigree								

At the bottom of the window, there is an 'Export' button and a 'Display:' section with two radio buttons: 'Bin data' (selected) and 'Individual data'.

At the bottom of the table (not visible in the above screenshot) is the total number of pairings that receive an *MSI* equal to ratings indicated by the name of the *Bin* (i.e., 1-6 and *No Way*). These *MSI* values are calculated from the four individual variable rankings using one of two methods. The default method is known as the *Tulsa* method and is based on a set of logic rules. An alternative is to use a *Weighted* method, in which weights can be assigned to the first three variables to determine the final *MSI* (see below).

Click the *Individual data* button at the bottom of the screen to view detailed information for each male-female pair. This table contains one row for each pair, the values for each of the four variables (*Delta GD*, *GV Diff*, *F*, and *% Known*), the bin rating for *dGD*, *GVDiff* and *F*, and the composite final *MSI* score as well as the *extended MSI*. This table can be sorted by clicking on the heading of any column. Both the Individual data table and Bin data table can be saved as an *.txt* file by clicking the *Export* button.

Sire	Dam	% Known	Delta GD	GV Diff	F	Rank GD	Rank Diff	Rank F	MSI	Ext. MSI
3640	4045	1.00	0.00005	0.00635	0.001	2	4	2	4	4.2286
3640	4073	1.00	0.00010	0.00062	0.009	2	1	3	2	2.1075
3640	4074	1.00	0.00011	0.00237	0.009	1	2	3	2	2.1204
3640	4148	1.00	0.00001	0.01212	0.126	3	5	7	7	7.7489
3640	4149	1.00	-0.00001	0.01474	0.126	4	5	7	7	7.8107
3640	4194	1.00	0.00009	0.00019	0.129	2	1	7	7	7.4765
3640	4195	1.00	0.00008	0.00194	0.129	2	1	7	7	7.5178
3640	4223	1.00	0.00001	0.01350	0.000	3	5	1	6	6.3928
3640	4252	1.00	0.00004	0.00876	0.005	3	4	2	4	4.2975
3640	4280	1.00	0.00003	0.00966	0.039	3	5	4	6	6.4228
3640	4294	1.00	-0.00001	0.01560	0.000	4	6	1	6	6.4424
3640	4305	1.00	0.00005	0.00751	0.001	3	4	2	4	4.2537
3640	4319	1.00	0.00006	0.00516	0.034	2	3	4	4	4.3007
3640	4407	1.00	0.00013	0.00512	0.000	1	4	1	4	4.1122
3640	4412	1.00	0.00007	0.00364	0.000	2	3	1	3	3.1601
3640	4413	1.00	0.00008	0.00211	0.000	2	2	1	2	2.1240
3640	4427	1.00	0.00006	0.00501	0.021	2	4	4	4	4.2581

Display: ☐ Bin data ☒ Individual data

Export

Defining Bins

The default definitions for the *Bins*, *Break Points* and *No Way* points are as follows:

Delta GD: The *break point* is "0" change in GD. Default values are set so that categories 1-3 each contain 33% of the range above the *break point* and categories 4-6 each contain 33% of the range below the *break point*. There is no *No Way* category.

GV Diff: The upper limit (top of *Bin 1*) is set at the best possible (i.e. smallest) *MK Diff* from a pairing. The lower limit (bottom of *Bin 6*) is set by the worst possible *MK Diff* from a pairing. The *break point* is the average *MK Diff* of all rated pairings. As above, default values are set so that categories 1-3 each contain 33% of the range above the *break point* and categories 4-6 each contain 33% of the range below the *break point*. There is no *No Way* category. Only the pairs with inbreeding coefficients less than the *No Way* point set for *F* are included here.

F: The upper limit is set at 0.00. The lower limit is set at 0.1249 (or a user defined level). The *break point* is the average *F* of all possible pairs. *Bin 1* is limited to *F* = 0.00. *Bins 2* and *3* are each 50% of the range between 0.00 and the *break point*. *Bins 4-6* are each 33% of the range between the *break point* and 0.1249 (or upper limit). The default *No Way* point is 0.125; however, this point is modified for inbred populations in which the average *F* is greater than 0.125, as follows:

If average *F* > 0.5, *No Way* = 1.0
 If average *F* > 0.25, *No Way* = 0.5
 If average *F* > 0.125, *No Way* = 0.25
 Otherwise, *No Way* = 0.125

It is possible to edit the bin definitions. On the genetics **Settings** tab, use the pull-down menu *for Edit Bin* to select the variable to edit, and click the *Go* button. This will open a window that allows the bin definitions to be modified, either by specifying *Values* (default) or *Percentiles*. The *Break Point* and *No Way* point can also be modified. The right side of the window provides a summary of the number of pairs that fall into each *Bin* based on the variable being edited (left column) and based on the composite *MSI* values using the definitions in this window. The box in the lower right corner gives the *Minimum*, *Mean* and *Maximum* values for the variable being edited for those pairs evaluated here (those above the *No Way* point for *F*) and for all possible pairs (*Global*).

The screenshot shows the 'Editing Delta_GD' window. At the top, there is a 'Select what to edit' section with three radio buttons: 'Percentiles' (selected), 'Values', and 'Break Point_No Way'. Below this are three main panels: 'Percentiles', 'Values', and 'Frequency'.

Percentiles Panel:

BIN	From	To
1	0.00	< x <= 0.50
2	0.50	< x <= 0.75
3	0.75	< x <= 1.00
4	0.00	< x <= 0.33
5	0.33	< x <= 0.67
6	0.67	< x <= 1.00
!!!		

Values Panel:

From	To
0.000161	>= x >= 0.000081
0.000081	> x >= 0.000040
0.000040	> x >= 0.000000 = (Break Point)
0.000000	> x >= -0.000040
-0.000040	> x >= -0.000082
-0.000082	> x >= -0.000122 = Max(No Way, min)
No Way Point=	-1.000000

Frequency Panel:

Delta_GD	MSI
108	51
252	82
685	84
937	1913
1043	357
270	740
0	331

At the bottom left, there are buttons: 'Validate Changes', 'Cancel', 'Restore Defaults', and 'Finished - Close'. Below these buttons, the text 'Values OK' is displayed in red. At the bottom right, there is a 'Statistics' box with the following data:

Statistics	Used in MateRx	Global
Min	-0.000122	-0.000123
Mean	-0.000021	-0.000023
Max	0.000161	0.000161

To edit a *bin*, choose *Percentiles*, *Values* or *Break Point No Way* in the *Select what to edit* box at the top of the window. The editable values will be highlighted and others grayed out. Make the desirable revisions and then click the *Validate Changes* button. PMx will check the values for validity and will return the message **Values OK** in the lower left if they are accepted; otherwise, PMx will return an error message, such as **MateRx Values Out of Sequence Try Again or Cancel**. The frequencies in the columns on the right will be updated if new definitions are accepted. Click the *Restore Defaults* button to reset to the default definitions for this variable and click *Validate Changes* again. Click the *Finished - Close* button to exit this window.

Calculating *MSI*

Tulsa method. The default method for combining the various bin rankings for *Delta GD*, *GV Diff* and *F* is referred to as the *Tulsa* method based on a set of rules by the MateRx software design team and other members of the AZA Small Population Management Advisory Group (SPMAG). First, each pair is assigned a rank of 1 to 6 for each of the factors (*Delta GD*, *GV Diff* and *F*). Their rank is 1 if the value for that pair falls in the first bin, 2 if the value falls in the second bin, etc. Thus, each pair will have three ranks (e.g., 1, 2, 1). These three ranks are then evaluated to derive a final *MSI* as follows:

If all ranks < 4:

- If ranks are 111, then *MSI* = 1; *MSI* = 2 for ranks of 222; *MSI* = 3 for ranks of 333
- If sum of ranks < 5, then *MSI* = 1 (i.e., 112, 121, 211); otherwise:
 - If sum of ranks < 6 or *GD* = 1, then *MSI* = 2 (i.e., 113, 131, 311, 122, 123, 132, 133)
 - All others are *MSI* = 3 (i.e., 223, 232, 233, 322, 323, 332)

For ranks with at least one 4:

- If *F* = 6 or *GV Diff* = 5 or 6, then *MSI* = 6; otherwise:
 - If *GD* = 1, 2, 3 or 4, then *MSI* = 4
 - If *GD* = 6, then *MSI* = 5
 - If *GD* = 5 and *F* = 5, then *MSI* = 5
 - If *GD* = 5 and *F* < 5, then *MSI* = 4

These three genetic components are based on pedigree data. If there is an unknown parentage in the pedigree of an individual, PMx cannot calculate these measures accurately. Individuals with partially unknown pedigree will have these variables calculated using the known portion of the pedigree. The more uncertainty there is about the pedigree, the less valuable these estimates become. The general management strategy is to penalize individuals with high levels of partially unknown parentage.

PMx prorates the *MSI* value for varying levels of partially unknown parentage in the following way. The default settings are as follows. If the offspring of the pair has:

If unknown genome is $\leq 6.25\%$, there is no penalty on the *MSI*.

If unknown genome is $> 6.25\%$, the *MSI* pairing is 4 unless *MSI* is already 5 or 6.

If unknown genome is $> 12.5\%$, the *MSI* pairing is 5 unless *MSI* is already a 6.

If unknown genome is $> 25\%$, the *MSI* pairing is 6.

If unknown genome is $> 50\%$, the *MSI* pairing is *No Way*.

These rules for how unknown parentage affects the final *MSI* value can be revised by clicking the *Edit how unknown pedigree affects MSI* button. This opens a new window that allows the definitions to be modified for each bin in terms of % *Genome Unknown* and the *Impact* value of that bin designation. On the right is a choice of four methods for incorporating pedigree uncertainty into the *MSI* calculation:

- *MSI Minimum*: *MSI* values will be at least the *Impact* value (default method)
- *MSI Incremented*: *Impact* value is added to the current *MSI*
- *MSI Assigned*: *MSI* is changed to the *Impact* value
- *No Effect*: *MSI* is calculated ignoring the *Impact* of unknowns

As with the *Edit bin*, click *Validate and Save Changes* after changed the settings; clicking *Reset* will return the values and method to the default settings.

Weighted method. An alternative method for combining the variable rankings into a composite *MSI* value is to use quantitative weighting of the ranks for the three variables *Delta GD*, *GV Diff* and *F* as opposed to a set of logic rules such as the *Tulsa* method. The default *Weights* are equal between the three variables but can be modified by clicking the *Edit Weights* button in the lower center of the **Settings** tab. This window provides similar options for editing, validating and saving, and resetting the values as the *Edit bin* windows.

Setting the Overall MateRx Settings

The center section of the genetic **Settings** tab provides options for changing five general settings for calculating *MSI* values. These options are:

<i>F Break Point:</i>	Use Average F (default) Use Average MK
<i>Genetic Value Type:</i>	Mean Kinship (default) Kinship Value
<i>MK Diff Method:</i>	Absolute Diffs (default) Balanced Ranks
<i>For Unknown Sexes:</i>	Exclude Unknowns (default) Show as Male Show as Female Show as Both
<i>MSI Method:</i>	Tulsa (default) Weighted

Click on the *Use Defaults* button to reset all *MateRx Settings* to the default values and settings. The *Save Settings* and *Read Settings* buttons are not currently active but are intended for future use.

After making any changes under the *Genetic Assumptions*, *Other Setting* or *MateRx Settings*, click on the *Implement changes* button to apply these new settings.

Additional Data Files

These settings provide the option to import additional data files for use in the project. Multiple files can be added serially.

Associations are *.fed files that are text files that contain a list of institutional mnemonics representing the members of a particular regional zoo association. These are distributed with SPARKS and PopLink and reside in those program folders; however, these association lists are time-sensitive (as association membership changes) and so these files should be updated regularly. It is possible to modify or create new association lists by editing an existing .fed file or creating a new one. Once imported, the variable *Association* can be added to most PMx data tables and can be used to automatically create *Management Sets* on the **Management Sets** tab. PMx will assign associations to individuals based on its current (last) location, not based on historical association membership (also see *Section 1* of the manual).

Regions are *.rgn files that are text files that contain a list of institutional mnemonics representing institutions that reside in a particular geographic region. SPARKS 1.6 will automatically export *Region* for each individual (as well as *Country*); for other data exports, or to customize the definitions of regions, it is necessary to create an *.rgn file similar to a .fed file and attach it here. See *Section 1* of the manual for more information on *Regions*.

Optional specification of moves in and out of Genetic view provide more flexibility in determining when individuals move in and out of the selection for genetic analysis in order to more accurately assess historical genetic status of a population. Files can be imported that *Replace* or *Add Moves* to the existing imported data. This is an advanced option still under testing; more information on this feature will be available in a later version of this manual.

UDFs are *.udf files that are *User Defined Fields* that can be custom created to provide information on individuals specific to the needs of the data analysis or population planning (e.g., taxonomic information). *UDFs* can be read in during studbook exports (e.g., SPARKS 1.6), when the PMx project is created, or at a later point using the **Settings** tab. PMx gives the option to specify if the data in these files should be added to or should replace *UDF* data already imported for the individuals. Adding data will create new *UDF* fields while keeping any existing *UDF* data intact. Replacing *UDF* data will cause all existing *UDF* fields to be deleted and the new data inserted.

Read Empirical Kinships enables a file to be imported that specifies the kinship matrix different than that calculated from the pedigree (e.g., based on molecular data). See the **Kinship Matrix** section for more information on this option.

To add a file, click on the button to browse to and open the file. Then click *Read Files* to read in its contents. Once all files have been read, go to the **Individuals** tab and click on the *Update Table* button to insert the new data into the table.

Terms and Concepts

Iteration: A single stochastic simulation of the population over the specified time period. For gene drop, this means a simulation of which alleles (randomly) pass from parent to offspring through the recorded pedigree. Because events in a stochastic simulation are based on probabilities, the outcome of each iteration will be different; therefore, many iterations should be run to accurately estimate results.

DeltaGD: Net change in gene diversity of the population if the pair produced one surviving offspring.

GV Diff: Difference between the mean kinship values of the male and female in pairwise comparisons (or the difference between kinship values if *Kinship Value* is used instead of *Mean Kinship for Genetic Value Type*).

Inbreeding Coefficient (F): Probability that the two alleles at a genetic locus are identical by descent from an ancestor common to both parents.

% Unknown: Percent of the male's and female's genome that can be traced back to known founders.

Balanced Ranks: Difference between the MK (or KV) ranking within sex for the male and for the female.

eMSI: Extended MS. For each factor (*Delta GD*, *GV Diff* and *F*) a percentile is calculated as the percentile of the range that the factor's value falls within the bin. For example, if the *F* value for a pair falls 2/3 of the way between the lower value of that bin and the upper value of that bin, then its percentile is .67. The percentiles are then averaged (or weighted averaged) across the three factors, and this average is then appended to the *MSI* value in decimal format.

See the **Pairwise Info** tab for other MateRx-related definitions.

New Features

Most of the setting options on this tab were not available in PM2000, including more flexibility in dealing with multiple (MULT) and unknown (UNK) parents, specifying the zoo association or geographic region of an individual, revising individuals' moves in and out of the genetic window, and all settings for MateRx-type analysis.

Helpful Hints

- Check that your association *.fed* files are current before using them for inter-regional analysis.
- Use *Associations* to create your own management sub-groups of institutions.
- Be sure to click on *Read Files* after specifying additional data files; otherwise, the new data will not be read into PMx.

SELECTION TAB (Genetics)

Purpose

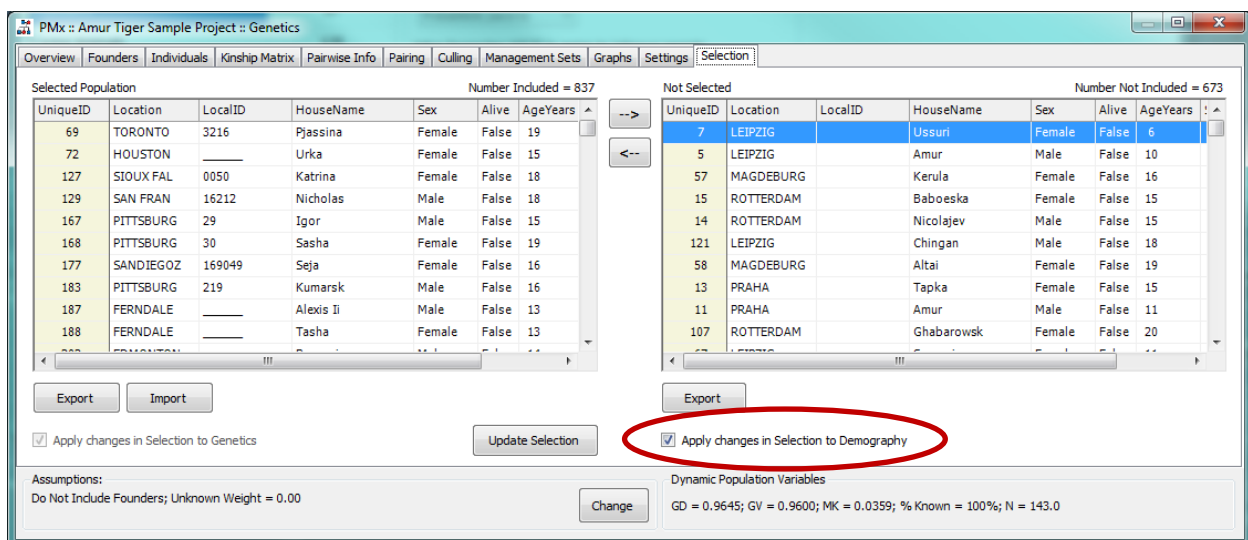
The **Selection** tab in the **Genetics** section can be used to define the potentially breeding population, i.e. only those animals to be included in the genetic analysis. This tab operates in a similar manner as the main **Selection** screen located outside of **Genetics** module; it is duplicated here for convenience to allow the user to be able to quickly modify the population for genetic analysis without having to close the **Genetics** module.

How to Use This Tab

This screen operates in a very similar manner as the primary Selection screen – refer to *Section 2* in this manual (Selection screen) for detailed information.

There are two differences in the **Selection** tab located under **Genetics**:

1. All changes in selection are automatically applied to the genetic calculations. There is an option to *Apply changes in Selection to Demography* that can be toggled on or off, but the application of changes to genetics is mandatory.
2. The main **Selection** screen provides the option to *Revert to originally imported data*. This option is not available here.



Helpful Hints/Cautions

See *Section 2 (Selection screen)* for helpful hints and cautions.

SECTION 5: GOALS SCREEN

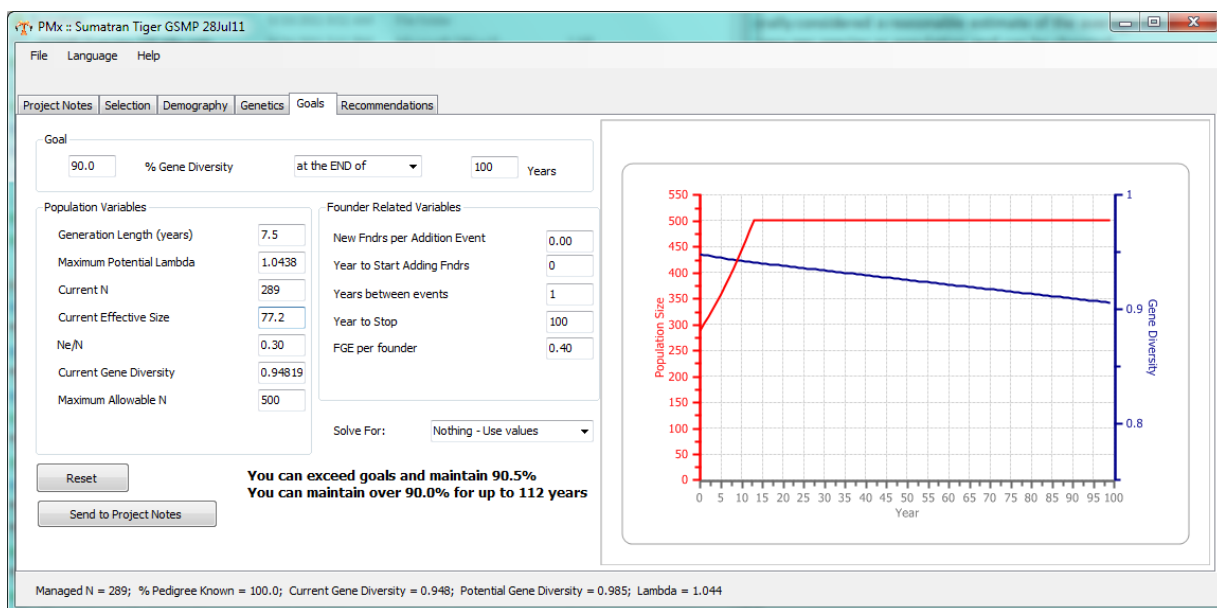
Purpose

The **Goals** Section of PMx provides deterministic projections for the retention of genetic diversity in the population over time given a particular set of biological and management conditions. Various options can be explored to assess how they perform in terms of meeting long-term genetic program goals.

How to Use This Section

The first step is to specify a genetic goal in terms of the amount of genetic diversity (GD) to be retained. Using the drop-down menu, this genetic *Goal* can be set as a minimum % gene diversity *at the END* of a specific number of years, or as a minimum % gene diversity to be retaining *DURING* the entire time span of the program. In the first scenario, GD may drop below the target level during the program and still meet the goal as long as the minimum GD is met on the final year of the program (e.g., by adding new founders near the end of the program). The default setting is to retain 90% of the wild gene diversity at the end of 100 years.

Once the *Goal* has been set, PMx will determine if this goal is achievable with the specified values for the *Population Variables*. PMx will retrieve information from various parts of the project to provide the default values for *Generation Length*, *Maximum Potential Lambda*, *Current N*, *Current Effective Size*, *Ne/N*, and *Current Gene Diversity*. *Maximum Allowable N* uses the *Current N* as the default setting. These values can be changed from the default values. PMx uses these values to project the change in population size and change in gene diversity over time. The results in relation to the *Goal* are displayed in bold at the bottom left of the page and will indicate either: a) this genetic goal can be achieved under current variable settings (and perhaps with even fewer animals or for a longer time period); or b) the genetic goal is not achievable, in which case PMx will indicate both how long the genetic goal can be maintained and also the projected genetic diversity at the end of the projected time period.

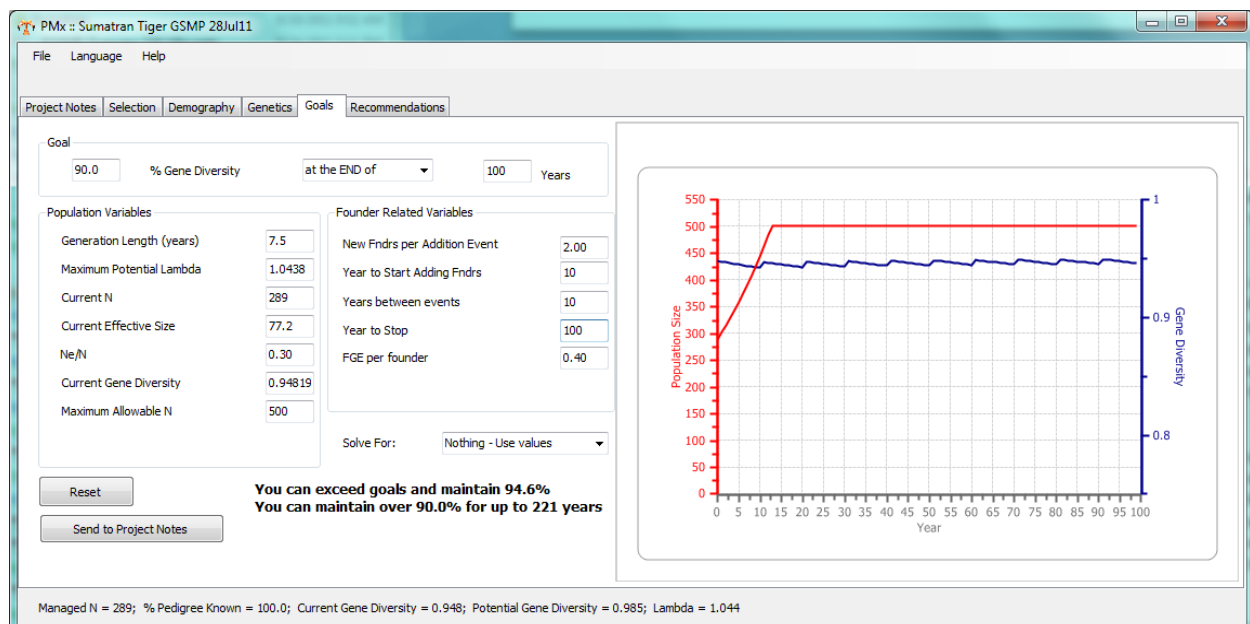


The graph on the right hand side of the page illustrates the modeled scenario, specifically the population size projection and the gene diversity retained over the specified time period specified in the *Goal*. Double-clicking on the graph will open it in a new window that allows the graph to be exported to file, sent to **Project Notes** or printed.

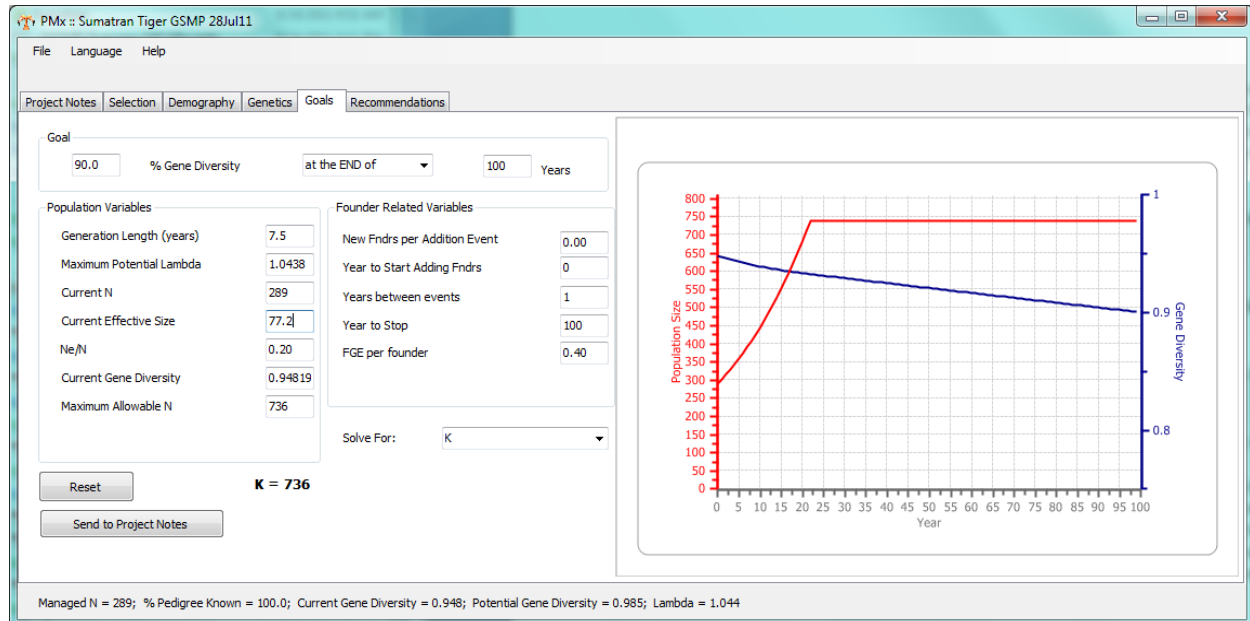
If the goal cannot be met, then the *Population Variables* may be changed to assess their effect on the population's long-term gene diversity. It is typical to start by increasing the *Maximum Allowable N* to a larger but reasonable number (5000 is the maximum value). Click on the graph on the right or in any other field to view the updated results. Changing variables such as *Lambda*, *Ne/N*, *Generation Length* and *Current Gene Diversity* (if potential gene diversity is substantially higher) to other reasonable values can be explored to get a sense for what may be achievable for the population. To return to the original default values, click on the *Reset* button on the bottom left of the page.

The second column allows for the addition of new founders to the population (the default setting is no additional founders). Under *Founder Related Variables* enter the number of founders that will be added for each importation (*New Fndrs per Addition Event*). Next indicate the *Year to Start Adding Founders*, the number of *Years between events* (importations), and the *Year to Stop* (i.e., the last year that founders will be added). The total number of founders added will be a product of the number of founders to be added each time and the number of addition events during the specified time period and intervals. These additions will be reflected on the graph as increases in gene diversity.

The actual genetic contribution of a new founder can be indicated by the *FGE per founder* parameter. The default for FGE per founder (Founder Genome Equivalents expected to be recruited per founder) is 0.4. This value is generally considered a reasonable estimate of the average FGE that would be recruited per founder but may vary per species or population and can be changed.



The *Solve For* drop-down menu allows the user to calculate the value of variable *X* required to meet the *Goal* given the other parameter values. For example, *Solve For: K* will cause PMx to calculate the population size required to meet the *Goal* at the top of the page. The *Solve For* feature can be used in conjunction with other adjustments to the *Population Variables* and *Founder Related Variables*.



The *Send to Project Notes* button will export the currently displayed management goal and strategy to the **Project Notes** screen.

Terms and Concepts

See **Demography** (Section 3) and **Glossary** (Appendix B) for explanations of the *Population Variables*.

New Features

The ability to set a minimum genetic goal to be maintained *During* a time period is now functional (this feature was disabled in PM2000).

Helpful Hints

- When using the *Solve For* feature, be sure to *Reset* the values before solving for a different variable.
- Although the retention of 90% gene diversity for 100 years is a standard goal for most managed populations, in some cases this is not achievable, and other goals (lower 90% and/or shorter time period) may be considered. For some populations, it might be reasonable to set the goal higher than 90% for 100 years. A large, well managed population with long generation length and/or with periodic addition of new founders may be able to retain 95% GD for 200 years.

Cautions

Remember to model only what is reasonable for the population. For example, it may not be possible to import founders on a regular basis, a higher growth rate may not be feasible for a highly male-biased population, or it may not be feasible to increase generation length if reproduction in older individuals is unreliable.

SECTION 6: RECOMMENDATIONS SCREEN

Purpose

The **Recommendations** section provides a table in which recommendations for individuals can be recorded and exported for reporting purposes. Recommendations can be generated automatically from selected pairs and culls in other parts of the program and/or can be entered manually, and can be exported as a table of recommendations for all individuals or a table with recommendations for each institution.

How to Use This Section

Typically the **Recommendations** section is used after demographic and genetic analyses have been completed. Click on the **Recommendations** section tab to view the recommendations table. Each individual represents a row in the table. Basic information such as *Location*, *Local ID*, *Sex*, and *AgeYears* are given for each individual; as with other tables in PMx, other columns can be added or deleted by right-clicking on the column header to customize the table.

PMx provides the following additional columns to specify the recommendation for each individual:

- Disposition: Indicates the recommended action regarding the physical placement of the individual. Default setting is *Hold* (remain at current location); alternate choices on the pull-down menu are: *Send To*, *Export*, *Receive From*, *Import From*, *Available*, *Other*, *Unknown*.
- New Location: Indicates the recommended destination of the individual if it is recommended to be moved (e.g., *Send To*, *Export*). Default setting is blank. The pull-down menu provides a list of ISIS mnemonics included in the data files used to create the PMx project; other location names can be manually typed into the cell (which is set to fill in from the list).
- Breeding: Indicates the recommended action regarding the breeding or placement of an individual in a social group. Default setting is *Do Not Breed*; alternate choices on the pull-down menu are: *Breed*, *Surplus [i.e., not needed in the managed population]*, *Social [i.e., to be kept with other animals for social reasons but not for breeding]*, *Other*, *Unknown*.
- With: Indicates the *Unique ID* of the recommended mate of the individual if recommended to breed; can take on alternate meanings (e.g., Group X, if *Breeding* = *Social*). Default setting is blank.
- # offspring: Indicates the recommended number of offspring from the individual with respect to the breeding recommendation. Default setting is blank. Fills automatically from **Pairing** tab.
- RecNotes: Provides a field for the user to add miscellaneous notes about the individual and/or detailed recommendations for that individual. Default setting is blank. Examples of entries include: "Excluded from genetic analysis", "Breed via AI", "Has contraceptive implant", "Priority breeder", "Include in research study", etc.

If pairs have been selected on the **Pairing** tab, these recommendations will be automatically transferred to the recommendations table for both the male and female. If an ISIS mnemonic is typed into the *Location* column in the *Selected Pairs* table on the **Pairing** tab, then the *Disposition* of any individual in that pair that is not at that location will be changed to *Send To* and the *New Location* will be filled in on the recommendations table. Recommended culling of individuals are also transferred to the recommendations table. The *Disposition* of any individuals that were selected to be culled on the **Culling** tab will be changed to *Available*. All of these entries can be manually altered.

UniqueID	Location	LocalID	Sex	AgeYears	Disposition	New Location	Breeding	With	# offspring	RecNotes
4809	BUFFALO	M04040	Female	8	Hold		DoNotBreed			
4813	DENVER	A03189	Male	8	Hold		DoNotBreed			
4815	LOUISVILL	102941	Female	8	Hold		DoNotBreed			
4825	RACINE		Male	8	SendTo	MINNESOTA	Breed	4930	2.5	
4826	SIOUX FAL	3872	Female	8	Hold		DoNotBreed			
4827	DETROIT	11141	Female	8	Hold		DoNotBreed			
4828	INDIANAPL	203030	Female	8	Hold		Breed	5049	2.5	
4831	TOLEDO	7182	Male	8	Hold		DoNotBreed			
4833	HOGLE	U03009	Female	8	Hold		DoNotBreed			
4916	BRIDGEPT	102028	Female	7	Hold		Breed	4973	2.5	
4929	SIOUX FAL	3104	Female	7	Hold		DoNotBreed			
4930	MINNESOTA	13238	Female	7	Hold		Breed	4825	2.5	
4965	DULUTH	100323	Male	6	Available		DoNotBreed			
4966	ROCHESTER	105412	Female	6	Hold		DoNotBreed			
4967	ROCHESTER	105413	Female	6	Hold		DoNotBreed			
4969	GLEN OAK	1419	Female	6	SendTo		DoNotBreed			
4970	GLEN OAK	1418	Female	6	Export		DoNotBreed			
4971	COLUMBIA	8854	Female	6	ReceiveFrom		DoNotBreed			
4973	BRIDGEPT	101646	Male	6	ImportFrom		Breed	4916	2.5	
4974	DENVER	A08410	Female	6	Available		DoNotBreed			
4975	LANSING	2926	Female	6	Other		DoNotBreed			
4983	COLUMBUS	206006	Female	7	Unknown		DoNotBreed			
4984	MINNESOTA	12317	Female	7	Hold		DoNotBreed			

Managed N = 125; % Pedigree Known = 100.0; Current Gene Diversity = 0.964; Potential Gene Diversity = 0.975; Lambda = 0.991

The *Clear all* button at the bottom of the screen will clear all recommendations to the default settings (*Hold*, *Do Not Breed*). The *Reset from Pairs and Culls* button will reset all recommendations to only those from the *Selected Pairs* and *Selected Culls* on the **Pairing** and **Culling** tabs; all other individuals will reset to the default settings.

The default set of individuals that are displayed in the recommendations table are usually the living individuals in the last *Selection* – more specifically, those for which *Gone* = false and *Selected* = true. This may or may not be the exact list of individuals desired. As with other tables in PMx, the *Filter* button can be used to modify the list of individuals included on the recommendations table, either by setting different filters or highlighting and *Adding* or *Removing* specific individuals. The *Reset to default filter* button will return the filter to the initial settings.

Filter Display for Table

☐ Do not filter the display of animals in this table

☐ Only show animals where

☒ Only show animals where All of the following are true:

Column Name	Op	Value
Gone	=	false
Selected	=	true

Highlight animals to add to the table:

1
2
3
5
7
11
13
14
15

Clear selection

Highlight animals to remove from the table:

1
2
3
5
7
11
13
14
15

Clear selection

Reset to default filter

OK Cancel

Exporting and Importing Files

The buttons at the bottom of the screen can be used to export and import data for the recommendations table. The *Export* button will create a *.txt file (as well as a *.csv file) of the recommendations table with individuals as lines (rows) similar to the format in PMx. This file can be opened in Word, Excel or other programs and used to generate reports regarding individual recommendations. The *Export Institutional Recs* button will create a *.txt file of the recommendations grouped by institution; for each institution that currently has or is recommended to receive an individual, recommendations are first listed for *Animals currently at the institution* (if any) and then recommendations are listed for *Animals planned to be moved to this institution* (if any), as seen in the example below. This file can also be opened in various programs to create a master plan report.

Animals currently at the institution:									
4562	MINNESOTA	10470	Male	11	Hold	DoNotBreed			
4930	MINNESOTA	13238	Female	7	Hold	Breed	4825	2.5	
4984	MINNESOTA	12317	Female	7	Hold	DoNotBreed			
5200	MINNESOTA	13204	Female	4	Hold	DoNotBreed			
Animals planned to be moved to this institution:									
4825	RACINE	_____	Male	8	SendTo MINNESOTA	Breed	4930	2.5	

The exported text file for individual recommendations (or any similarly formatted text file) can be imported into PMx to modify the recommendations table. There are two options: *Import Recs* will import the individual recommendations in the text file, replacing any existing recommendations in the table. The *Import List* button will import the individuals in the text file but will not overwrite the existing recommendations. New individuals that are added to the table via an imported file will have “(Not Selected)” added in the *RecNotes* field.

A common practice for some managers is to conduct the demographic analysis for a population, and then to exclude some individuals (e.g., sterile or post-reproductive individuals) from the genetic analysis through selection applied only to genetics (see **Selection** screen). This process will result in only those individuals used in the genetic analysis being included in the recommendations table, as the default filter is *Selected = true* (based on the last selection). In this case, excluded individuals can be added to the table using filtering options. An alternate, and often easier method, is to follow this process:

1. While using the Selection for demography (entire managed living population), go to the **Recommendations** screen and *Export* the table that includes all individuals in the management program.
2. Go to the **Selection** screen, make the new selection that is applied to genetics only (excluding permanent non-breeders and/or other individuals from the genetic analysis).
3. Make *Pairs* and *Culls* as appropriate.
4. Go to the **Recommendations** screen and choose *Import List*. Import the exported text file from the full (demographic selection) population.
5. The result should be that the recommended pairs and culls should remain unaffected, but that the excluded individuals are added to the Recommendations table. These individuals will show *(Not Selected)* in the *RecNotes* column, which can be modied (e.g., to “Excluded from genetic analysis”).

This process essentially duplicates the “Add Back Deselected Animals” function in PM2000.

New Features

This feature is similar to the recommendations section of the templated report in PM2000 but is available upfront in PMx and can be continually modified. PMx provides greater flexibility regarding the fields (columns) available in the table, and provides the option to import sets of recommendations.

Helpful Hints

- Sort the table by *UniqueID*, current *Location*, *Breeding*, or other desired order before export.
- When manually adding a *New Location*, it is recommended that the user enter the official ISIS mnemonic for that location when possible. Be careful to avoid spelling errors.
- Recommendations for institutions that do not currently have individuals (but are recommended to receive them) will be included at the end of the *Export Institutional Recs* file.
- If it is difficult to get the correct list of individuals in the table using the available filtering options, consider setting up a *UDF* or *Flag* for the relevant individuals that can be used as a filter. For example, *Flag* != ☐ (that is, *Flag* is not blank) will return all individuals that have been marked with a flag in the **Individuals** tab, regardless of the color of the flag.
- Export the Recommendations table after making changes to it (to save it intact). In some cases, making changes in PMx can cause the Recommendations table to also change (causing some individuals and/or recommendations to be deleted). If this occurs, the exported text file can be used to recreate the recommendations using *Import Recs*.

APPENDIX A. LIST AND DESCRIPTION OF INDIVIDUAL VARIABLES

Variables are listed in the default order that they appear on the **Individual** tab in the **Genetics** section. Although the variable descriptions below may refer to an individual for convenience, many of these variables can be applied to a group as well. Not all variables are exported by all studbook software versions; columns for unused variables are omitted in PMx.

UniqueID: The identifier used for a single individual or group throughout the project, typically the studbook number.

Location: The last location of the individual within the scope of the project. Usually the current or last location, indicated by the institution's ISIS mnemonic. If an individual left the scope of the project (e.g., was transferred outside the region or association), then *Location* may not reflect the current location.

LocalID: Identification number used by the institution indicated in the *Location* field. *LocalID* must be referenced in conjunction with *Location*.

HouseName: Often a familiar name used for an individual.

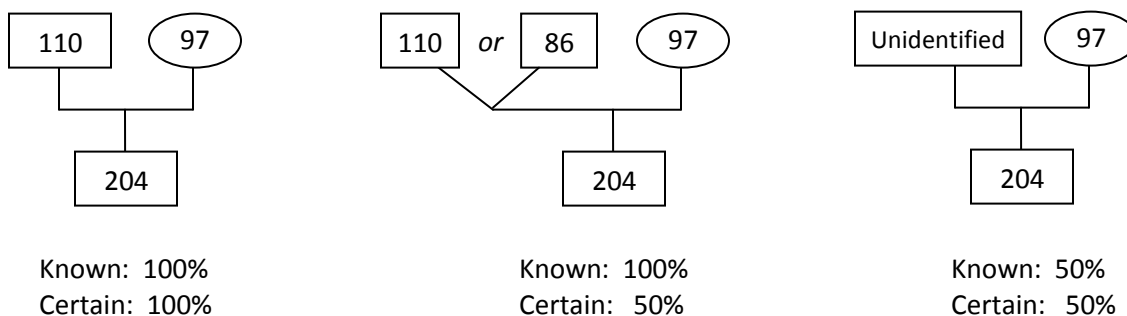
OtherID: Various identifiers, such as Transponder #, Tag/Band, Tattoo, and ColorPhase, in that order.

Sex: Options are Female, Male, Hermaphrodite, Abnormal, Asexual, Unknown. [Group terms to be determined at a later date.]

Known: Proportion of an individual's genome that is traceable to known founders, either through positive identification of all ancestors or all *possible* ancestors. Thus, 100% known individuals can have completely identified ancestors, or can have MULTs (multiple possible parents) in their pedigree *provided* that the identity of all possible parents is specified in the *Sire* and/or *Dam* fields in the database.

Certainty: Proportion of an individual's genome that is completely identified (exact identity of both parents are known) and traceable to known founders. Individuals that are 100% Certain do not have any MULTs or UNKs in their pedigree. *Certainty* represents a higher degree of knowledge than *Known* and therefore is always less than or equal to *Known*. Wild-caught founders (i.e., parents are WILD x WILD or WILD# x WILD#) are 100% known and certain; any UNK is unknown and uncertain.

To illustrate the distinction between *Known* and *Certainty*:



BirthDate: Date of birth (YYYY-MM-DD)

BirthDateEst: The resolution to which the *BirthDate* that can be estimated, if it is not a known date.

Alive: True if the individual is alive at the end of the date span defined by the project (i.e., data filter set in studbook for exporting files). The individual may or may not be living currently. For individuals that are Lost-to-Follow up, *Alive* = true (may or may not be living currently).

DeathDate: Date of individual's actual death (YYYY-MM-DD), even if this occurred outside of the project date span.

DeathDateEst: The resolution to which the *DeathDate* that can be estimated, if it is not a known date.

DeathCode: Codes for cause of death, specifying four parameters in this order: Circumstance, Carcass Disposition, Topographic, Etiological (optional). Individuals that are Lost-to-Follow up are indicated by "lft". Provided with SPARKS 1.6 exports.

Sire: *UniqueID* of sire (male parent) if known. Multiple possible sires may be listed if their *UniqueIDs* have been exported. Other options are: WILD if the animal is wild-caught; WILDx if the animal is wild-caught and has known siblings in the dataset (with "x" being a unique # or other identifier across siblings); UNK if sire is unknown; UNKx if sire is unknown and has known siblings; MATEOF<stud_id> will be constructed for the unknown mate of a known parent.

SireProb: Probabilities that the indicated sire(s) were indeed the actual sire(s), listed in the same order as under *Sire*.

Dam: *UniqueID* of dam (female parent) if known. See *Sire* above for additional options.

DamProb: Probabilities that the indicated dam(s) were indeed the actual dam(s), listed in the same order as under *Dam*.

Gen: Generation in captivity. Founding (wild-caught) individuals are considered to be generation 0. Offspring from two founding individuals are generation 1, and so on. Parents of an individual are often not of the same generation, in which case the average generation value for that individual will be the average of the values of each of its parents, plus one.

F (inbreeding coefficient): The probability that the two alleles at a genetic locus are identical by descent from an ancestor common to both parents. The mean inbreeding coefficient of a population will be the proportional decrease in observed heterozygosity relative to the expected heterozygosity of the founder population.

MK (mean kinship): Coefficient between an individual and all individuals (including itself) in the living, captive-born population. The mean kinship of a population is equal to the proportional loss of gene diversity of the descendant (captive-born) population relative to the founders and is also the mean inbreeding coefficient of progeny produced by random mating. Mean kinship is also the reciprocal of two times the founder genome equivalents: $MK = 1 / (2 * FGE)$. $MK = 1 - GD$.

MKRank: Ordered rank by mean kinship within sex. 1M = the top male (lowest MK value); 1F = top female in the list. In the case of ties in MK, individuals are assigned *MKRanks* in random order, i.e., if there are 4 individuals with MK = 0.1597, they will be assigned 4 consecutive MKRanks, but the 4th assigned is equivalent to the 1st assigned.

FOKE (First-Order Kin Equivalents): The number of first-order kin (siblings or offspring) that would contain the same number of copies of an individual's alleles (identical by descent) as are present in the entire captive-born population. Thus an offspring or sibling contributes 1 to FOKE; each grand-offspring contributes 0.5 to FOKE; each cousin contributes 0.25 to FOKE. $FOKE = 4 * N * MK$, in which N is the number of living animals in the captive population.

KV (Kinship Value): The weighted mean kinship of an individual, with the weights being the reproductive values (Vx) of each of the kin. The mean KV of a population predicts the loss of gene diversity expected in the subsequent generation if all individuals were to mate randomly and all were to produce the numbers of offspring expected for individuals of their age.

GUAll (Genome Uniqueness – All): The probability that a random allele from the individual is not present in any other living individual in the population, founders included (i.e., same allele descended from a common ancestor).

GUDescend (Genome Uniqueness – Descendants): The probability that a random allele from the individual is not present in any other living non-founder individual in the population (descendants).

ProbLoss: Probability that a random allele from the individual will be lost from the population in the next generation, because neither this individual nor any of its relatives pass on the allele to an offspring. Assumes that each individual will produce a number of future offspring equal to its reproductive value.

AgeDays: Age of individual in days based on the *Analysis Date* on the *Settings* tab (for living individuals) or age at death (for dead individuals). *AgeDays* for individuals lost-to-follow up is designated by "----".

AgeYears: Age of individual truncated to years based on the analysis date on the *Settings* tab (for living individuals) or age at death (for dead individuals). *AgeYears* for individuals lost-to-follow up is designated by "--".

AgeClass: Age class of the individual based on the age class length designated on the Demography *Settings* tab. *AgeClass* is the same as *AgeYears* for living individuals if age class length = one year. *AgeClass* for dead individuals is designated by "--").

Vx: The expected number of offspring produced this year and in each future year by this individual (based on its age and sex).

NOffspring: The number of offspring already produced by this individual (all offspring recorded in the studbook; not affected by date span of the project).

NLivingOffspring: The number of offspring already produced that are currently living.

NBroods: The number of litters/broods/clutches produced by this individual (based on birth dates only, without regard to identity of mate, and therefore a minimum estimate).

Rearing: Rearing situation of the individual recorded in the studbook; options are: Parent, Hand, Foster, Peer, Supplemental, Unknown, None, Colony/Group.

ReproGoals: A projection of the total desired number of future progeny for each individual, given the current genetic and demographic structure of the population and taking into account optimal matings and optimal removals of over-represented animals. Exact achievement of all reproductive goals and optimal removals would maximize gene diversity in the next generation.

Offspring: *UniqueIDs* of the individual's offspring.

PriorMates: *UniqueIDs* of the known mates involved in producing individual's offspring.

ReproYears: Years in which the individual produced offspring.

LastReproDate: Date of last known reproduction (date of birth of last offspring).

MyFounders: *UniqueIDs* of founders that are genetically represented in the individual.

MyFounderContribs: Proportion of each founder represented in the individual (in same order as *MyFounders*).

MyDescendants: *UniqueIDs* of the individual's descendants (up to the first 25).

Entity: Whether this "animal" represents an individual or a group.

Count: Number of individuals represented by this entity (count = 1 for an individual; count = group size for a group).

MatingType: Indicates the process by which the entity was created. Options are: Sexual, Clonal, Selfing, Merge (for groups), Split (for groups), Haploid, Other, Unknown.

ReproStatus: Current reproductive status of the individual. Options are: Fertile, Contracepted, Sterile, PostReproductive, Other, Unknown (based upon the status designated in the exported data; default = Fertile).

BirthType: Birth origin of the individual (Wild Born, Captive Born, Other, or Unknown).

Associations: Lists the current zoo association(s) for this individual, based on the last location of the individual and the zoo associations for which this institution is a member. The appropriate association *.fed file(s) must be specified either during data import or on the **Genetics Settings** tab.

Country: Lists the country of the last location for this individual (provided with SPARKS 1.6 exports).

Region: Lists the geographic region based on the last location of the individual. SPARKS 1.6 exports will provide this information automatically using the following regions: Europe, Africa, North America,

Latin America, Middle East, South Asia, Southeast Asia, East Asia, and Australasia. Regions can also be specified using *.rgn file(s).

ManagementSets: Lists the Management set(s) in which the individual is included. Imported from the **Management Sets** tab by use of the *Update Table* button.

SocialGroup: Social groupings as assigned at the Location (from SPARKS).

UDF1 – UDF7: User Defined Fields displayed using the actual UDF name_udf. Up to seven will be individually available.

UDFs: All UDFs (including the first seven) are combined into this column, with UDFs separated by “|”.

DemMoves: Displays the conditions for how the individual entered and left the project window. This will match *GenMoves* unless a separate *Moves* file is imported. Options for entering the project are: Capture, Birth, LeftEntry, Unknown. Options for leaving the project are: AliveOut, Lost, Release, Death.

GenMoves: Displays the conditions for how the individual entered and left the project window. Options for entering the project are: Capture, Birth, LeftEntry, Unknown. Options for leaving the project are: AliveOut, Lost, Release, Death.

Gone: True if the individual is not in the population at the end of the date span defined by the project. The individual may have left the project through death or transfer or be Lost-to-Follow up (*ltf*). Inverse of the variable *Alive*.

GoneDate: Date on which the individual left the population (if it left by some means other than death, such as by transfer, export or lost-to-follow up). This is the true exit date and is not restricted to the date span defined by the project. Individuals that are either alive at the end of the project or have died have a *GoneDate* of “--”.

Flag: Click the button to set a color flag for one or more individuals. Multiple sequential individuals can be flagged using the *Shift* key. Once flagged, individuals can be sorted or filtered by color, similar to a UDF.

Notes: Notes of any kind may be typed into the field.

Recommendation Information:

The following fields display information entered into the **Recommendations** tab. Click on the *Update Table* button on this tab to update these fields. Recommendations should be edited on the **Recommendations** tab and not on the **Individual** tab.

RecDisposition: Recommendation for the possible transfer of an individual. Options are: Hold, SendTo, Export, ReceiveFrom, ImportFrom, Available, Other, Unknown.

RecDestination: Location at which the individual is recommended to live in the future (either remain at the current location or be transferred to a different location).

RecBreed: Recommendation for this individual with respect to breeding. Standard options are: DoNotBreed, Breed, Surplus, Social, Other, Unknown.

Npairs: Number of pairings assigned to this individual in the breeding recommendations (count of entries in “With” field on the **Recommendations** tab).

RecMates: List of the *UniqueIDs* of mates assigned to this individual in the breeding recommendations (list of entries in “With” field on the **Recommendations** tab).

RecNotes: Notes about the breeding and transfer recommendations (RecNotes field on the **Recommendations** tab).

DemSelected: True if the individual is in the *Selected Population* for demographic analysis.

APPENDIX B. GLOSSARY OF TERMS

Demographic Terms

Age Distribution: A two-way classification showing the numbers or percentages of individuals in various age and sex classes in the population.

Fecundity (Mx): The average number of same-sexed young born to individuals in that age class. For each offspring, each parent gets 0.5 of the birth attributed to him/her. The fecundity rates provide information on the age of first, last, and maximum reproduction.

Instantaneous Rate of Change (r): The intrinsic rate of increase of a population per unit time, equal to the projected exponential rate of increase, averaged for males and females, as determined from the birth and death rates. If $r > 0$, the population is projected to increase; if $r < 0$, it is decreasing.

Life Expectancy (Ex): The average number of additional years an individual in age class x can expect to live.

Mean Generation Time (T): The average age of reproduction (production of offspring) averaged for males and females. It is also the average time from reproduction in one generation to reproduction in the next generation. T is *not* the age of first reproduction.

Mortality Rate (Qx): Probability that an individual of age x dies during time period. $Qx = 1 - Px$. This number is calculated from the number of individuals that die during an age class divided by the number of individuals that were alive at the beginning of the age class (i.e. "at risk").

Net Reproductive Rate (Ro): The rate of change per generation (average number of same-sex offspring that an individual will produce in its lifetime), averaged for males and females. $Ro > 1$ for increasing populations and $Ro < 1$ for declining populations.

Population Growth Rate (Lambda, λ): The proportional change in population size from one year to the next. Lambda can be based on life table calculations (the expected lambda) or from observed changes in population size from year to year. A lambda of 1.11 means an 11% per year increase; lambda of .97 means a 3% decline in size per year.

Reproductive Value (Vx): The expected number of same-sex offspring produced this year and in future years by an individual of age x .

Risk Qx/Risk Mx: The number of individuals that have lived during an age class. The number at risk is used to calculate Mx and Qx by dividing the number of births and deaths that occurred during an age class by the number of individuals at risk of dying and reproducing during that age class.

Stable Age Distribution (SAD): The proportional distribution of individuals across age classes that would result from the realization of the exact life table demographic rates (Px and Mx). If these rates remain constant and exact, the population will grow (or decline) at a constant rate into the future.

Survival, Age-Specific (Px): The probability that an individual that is alive at age class x will survive to age $x + 1$; is conditional on an individual being alive at the beginning of the time period. Alternatively, the proportion of individuals which survive from the beginning of one age class to the next.

Mid Px: The probability that an individual survives to the mid-point of age class x .

Survivorship, Age-Specific (Lx): The probability that a new individual (e.g., age 0) is alive at the *beginning* of age x . Alternatively, the proportion of individuals which survive from birth to the beginning of a specific age class.

Mid Lx: The proportion of individuals surviving to the mid-point of age class x .

Genetic Terms

Allele Retention: The probability that a gene contributed by a founder individual exists in at least one individual in the living, descendant population.

Coefficient of Relatedness (r): The probability that at a given locus, an allele sampled from one individual is identical by descent to at least one of the alleles at that locus in a second individual. In a population with no inbreeding, r is two times the kinship value.

Coefficient of Kinship, Kinship Coefficient, or Coefficient of Consanguinity (often symbolized f or k): The probability that at a given locus, an allele sampled from one individual is identical by descent to an allele sampled at random from that locus in a second individual.

Cull: Remove an individual from the managed population used for genetic analysis.

Effective Population Size (Ne): The size of a randomly mating population of constant size with equal sex ratio and a Poisson distribution of family sizes that would: a) result in the same mean rate of inbreeding as that observed in the population, or b) result in the same rate of random change in gene frequencies (genetic drift) as observed in the population. These two definitions are identical only if the population is demographically stable (because the rate of inbreeding depends on the distribution of alleles in the parental generation, whereas the rate of gene frequency drift is measured in the current generation).

First Order Kin Equivalents (FOKE): The number of first-order kin (siblings or offspring) that would contain the number of copies of an individual's alleles (identical by descent) as are present in the living, captive-born population. Thus an offspring or sib contributes 1 to FOKE; each grand-offspring contributes 1/2 to FOKE; each cousin contributes 1/4 to FOKE. $FOKE = 4 * N * MK$, in which N is the number of living individuals in the captive population.

Founder: An individual obtained from a source population (often the wild) that has no known relationship to any individuals in the derived population (except for its own descendants).

Founder Contribution: Number of copies of a founder's genome that are present in the living descendants. Each offspring contributes 0.5, each grand-offspring contributes 0.25, etc.

Founder Genome Equivalents (FGE): The number of wild-caught individuals (founders) that would produce the same amount of gene diversity as is present in the living, descendant population. The gene diversity of a population is $1 - 1 / (2 * FGE)$.

Founder Genome Surviving: The sum of allelic retentions of the individual founders (i.e., the product of the mean allelic retention and the number of founders).

Founder Representation: Proportion of the genes in the descendant population that derives from that founder (i.e., proportional Founder Contribution).

Gene Diversity (GD): The proportional gene diversity (as a proportion of the source population) is the probability that two alleles from the same locus sampled at random from the population are not identical by descent from a common ancestor. Gene diversity is calculated from allele frequencies, and is the heterozygosity expected in progeny produced by random mating, and if the population were in Hardy-Weinberg equilibrium.

Gene Value (GV): The gene diversity of the living individuals weighted for the reproductive value of individuals. Gene value is the heterozygosity expected in progeny produced by random mating, if the population were in Hardy-Weinberg equilibrium, and if each individual were to produce the number of offspring expected from its age-based reproductive value.

Genome Uniqueness (GU): Probability that an allele sampled at random from an individual is not present, identical by descent, in any other living individual in the population. GU-all is the genome uniqueness relative to the entire population. GU-Desc is the genome uniqueness relative to the living non-founder descendants.

Inbreeding Coefficient (F): Probability that the two alleles at a genetic locus are identical by descent from an ancestor common to both parents. An individual's inbreeding coefficient is equal to the kinship coefficient of its parents.

Kinship Value (KV): The weighted mean kinship of an individual, with the weights being the reproductive values of each of the kin. An individual with mostly old, nearly post-reproductive kin will have a low KV, while an individual with many young kin of breeding age will have a high KV.

Living Individuals: The number of living individuals in the currently selected population.

Living Descendants: The number of living individuals descended from population founders. This may be a fractional number because PMx normally excludes all individuals with unknown parents from genetic analyses, and includes only those parts of individuals that can be traced back to known founders. For example, an individual with a known dam but an unknown sire will be tallied as half an individual in genetic analyses unless otherwise specified under the **Settings** tab.

Mean Inbreeding: Mean inbreeding is the average of the inbreeding coefficients among the living individuals. The mean inbreeding coefficient of a population will be the proportional decrease in observed heterozygosity relative to the expected heterozygosity of the founder population.

Mean Kinship (MK): The mean kinship coefficient between an individual and all individuals (including itself) in the living, captive-born population. The mean kinship of a population is equal to the proportional loss of gene diversity of the descendant (captive-born) population relative to the founders and is also the mean inbreeding coefficient of progeny produced by random mating. Mean kinship is also the reciprocal of twice the founder genome equivalents: $MK = 1 / (2 * FGE)$. $MK = 1 - GD$.

MKb: Mean kinship between two populations; the mean of all pairwise kinships, for all combinations of an individual from population 1 with an individual from population 2.

% Pedigree Certain: The percentage of the living individual's pedigree that can be traced back to specific individual founders.

% Pedigree Known: Percent of an individual's genome that is traceable to known group of founders. Thus, if an individual has an UNK sire, the % Known = 50.

Potential Retention: The proportion of genes present in a founder that have the potential to be incorporated in the descendent population. If the individual is a potential founder or is still living, its potential retention is 1.00. Otherwise, for dead founders, potential retention will be the same as the Allele Retention for that founder.

Prob Lost: Probability that a random allele from the individual will be lost from the population in the next generation, because neither this individual nor any of its relatives pass on the allele to an offspring. Assumes that each individual will produce a number of future offspring equal to its reproductive value, V_x .

Modeling Terms

Confidence interval (CI): This defines the range of values (upper and lower limits) that the parameter (in this case, mean population size) will take in relation to a specific level of likelihood. For example, a 95% CI means that 95% of the simulations result in values between the lower and upper limits.

Deterministic: Deterministic means predictable with no variation, or 'determined'. In deterministic calculation, exact values are applied to formulas that define relationships (e.g, first year mortality will always be 24%). Since there is no variation in input values, the result will always be the same.

Iteration: A single stochastic simulation of the population over the specified time period. Because events in a stochastic simulation are based on probabilities, the outcome of each iteration will be different; therefore, many iterations should be run to accurately estimate results.

P[Extinction]: Probability that the population will go to zero (measured as the proportion of stochastic simulations in which the population goes to 0).

Stochastic: Stochastic means variable due to chance or based on probabilities. In stochastic calculations, input values are based on probabilities (e.g., every individual has a 24% chance of not surviving its first year). Actual values used in the calculations will vary with each application and so the result will be variable.

APPENDIX C. FREQUENTLY ASKED QUESTIONS

Questions occasionally come up about PMx during masterplanning or training courses. Here are some frequently asked questions (FAQs) regarding the use of PMx. We hope to continue to expand this section. If you have suggestions for additional FAQs, please send them to Kathy Traylor-Holzer (kathy@cbsg.org), and include the answer if you know it.

General

How can I add additional input files after I have already created the project?

Some files can be added after a project has been created – the association files (e.g., *.fed), region files (e.g., *.rgn), moves files (e.g., *.mov), and UDF files (e.g., *.udf) can be added on the **Genetics Settings** tab. Other files (e.g., census files) can only be added when creating a project.

When opening my PMx export files in Excel, the numbers are converted to text. How can I convert them back to numbers?

Text and comma-delimited files can be imported into Excel. Numbers exported to an Excel file will be converted as text (a small green triangle may appear in the upper left of the cell). To convert to numbers format in Excel 2007, select a range of cells and use the *Number Format* option to change the format of the cells to *Number*. In Excel 2003, use the following:

For one cell: Select the cell, click the button that appears, and click *Convert to Number*.

For a range of cells:

- In an empty cell, enter the number 1.
- Select the cell containing 1, and on the **Edit** menu, click *Copy*.
- Select the range of numbers stored as text that you want to convert.
- On the **Edit** menu, click *Paste Special*, then under **Operation**, click *Multiply*.
- Click *OK*.
- Delete the content of the cell entered in the first step.

An alternative method (which will convert all non-integers to numbers) is:

- Open the Excel worksheet.
 - Hit Ctrl-F to open the *Find and Replace* dialogue window.
 - Click on the *Replace* tab.
 - In the *Find what* box, type a period (if using American-style numbers) or a comma (if using European-style numbers).
 - Type the same character (period or comma) into the *Replace with* box.
 - Click on *Replace All*.
-

Demography

Why are there so many age classes on the age pyramid? And why so many points on the life table graphs?

Check the age class length to see if it is shorter than you expect or intend. A shorter age class means more age classes in the life tables, more points on the graphs, and more bars on the age pyramid. If your data included reproduction in the first age class, PMx may have automatically shortened age class length to avoid this problematic situation.

Why does PMx give me a message that Ex is not available for the life table?

In some studbook datasets, life expectancy (*Ex*) cannot be defined because the *Lx* value does not go to zero (i.e., the life table is infinite). In this case, *Ex* cannot be calculated or plotted.

Why is the Census tab blank? What does the message that the “census is not available” mean?

You must attach the correct census file in the second screen when creating a project. For SPARKS 1.5x or PopLink, this is the *exhcens.txt* file; if you exported from SPARKS 1.6, then the census input file is *pmxcens.csv*. You must run the Census Report in SPARKS 1.5x or PopLink to create the necessary *exhcens.txt* file (SPARKS 1.6x creates the *pmxcens.csv* file automatically during the PMx export).

Why does the stochastic projection for my population show a decline, while the deterministic projection shows positive population growth?

Stochastic projections incorporate additional factors not considered by deterministic projections. Skewed sex ratio, in particular, has no effect on deterministic projections, but can have a significant impact on stochastic projections. Monogamous species with skewed adult sex ratios will suffer from a limitation of mates, leaving unpaired (unbred) adults of the more common sex. For polygynous species (e.g., many herd species), too few females lead to a similar problem; however, fewer males is typically not a problem and in fact may be an intentional management strategy. For such species, it is important that the maximum number of females bred per male is set correctly on the **Demographic Settings** tab, so that female-biased populations are modeled correctly. Other factors, such as very small population size and resulting annual fluctuations in birth and death rates, also reduce population growth; these real life factors are incorporated into stochastic projections but are ignored in deterministic projections (see **Projection** Tab section for further explanation).

When I try to plot both actual and model data on a Custom Life Table graph in Demography, only the model data line shows on the graph. Why doesn't the actual data show up as well?

If the model data have not been changed, then the two lines will be the same and the model data line will overwrite (plot on top of) the actual data line.

Genetics

Should I remove the dead individuals from the Selected Population for the genetic analysis?

If the data were exported from SPARKS 1.6, then the dead individuals should be left in the selection for genetic analysis if they met the other criteria (e.g., region or association) for the population. SPARKS 1.6 exports information to PMx regarding the dates on which each individual entered and/or left the population based on the filter criteria so that dead individuals can be properly included in both historical and current population analyses. PMx will use only living individuals to calculate the genetic status of the current living population.

Why are the Kinship Matrix, Pairwise Info Matrix, and Population Graphs sometimes blank?

These matrices can be very large (e.g., the kinship matrix has about 1 million entries for a studbook with 1000 animals), and the writing of the values to the tables for display can therefore be very time intensive for large studbooks. To avoid very slow loading of PMx genetics, the default setting is to display these tables for small- to moderate-sized datasets, but not to show these tables if the selected set has > 1000 individuals. The user can choose to see any or all of these calculations by checking or unchecking the corresponding boxes at the bottom of the **Genetics Summary Statistics** page.

When using the Allow Pairing Dead individuals option, how are MKs and GD calculated?

The mean kinship (MK) of a dead individual is the mean kinship of that individual to the living population (i.e., does not include its kinship to itself). Population GD and the MKs of living individuals are calculated as normally based on the living population and do not include dead individuals.

Why don't my changes (e.g., ReproGoals, Management Sets, pairing and culling recommendations) show up in the Individual tab?

You must click on the *Update Table* button to add any changes made on other tabs.

Do Management Sets need to be mutually exclusive and exhaustive, or can individuals be in more than one management set?

Membership in one management set does not affect the membership in other management sets. Therefore, individuals can be in more than one management set (e.g., in 'EEP' and in 'Global Captive' populations). Individuals also do not need to be in any of the created management sets.

APPENDIX D. INPUT FILE FORMATS

General Issues

Every individual in the pedigree entered into PMx must have a unique identifier. This *UniqueID* can be the studbook number in a SPARKS or PopLink database, or the GAN (Global Accession Number) of ZIMS, or any other identifier that is uniquely assigned to each individual. The only other data fields that are mandatory for every individual are *Dam* (*Sire* is optional, because an asexual species might have no sires), *Selected* (a flag to indicate if an individual is to be included in the analysis), and *Alive* (a flag to indicate if an individual is alive).

Constraints on data fields

For data fields that are string variables, such as the *UniqueID*, *OtherIDs*, *Location*, and *UDFs* (user-defined fields), PMx places no limitations on the string length. The only characters that cannot be used within string variables are colon (':'), semi-colon (';'), and tab. Date fields in text files must be formatted as *yyyymmdd* (e.g., **20110315**), *yyyy-mm-dd*, or *mm/dd/yyyy* (e.g., **3/15/2011**). The first format is preferred, as it is less likely to cause confusion in regions with different data formats. Data fields that are true/false (Boolean) variables can be entered as any of **True**, **T**, **1**, **Y**, or **Yes** (all case insensitive), with all other values being interpreted as False. Extra spaces around fields are always removed. Thus, " **123**", "**123** ", and "**123**" will all be read as "**123**".

Data files that can be imported

PMx can read different kinds of information from a variety of data files, and several of the types of data file can be provided in any of several formats. The *Primary Input File* provides the pedigree information to PMx. It is the only file that is mandatory for creating a PMx project. Optional files include any of a number of forms of a *Demographic Input File*, and files to provide *Census* tallies, *UDF* data (user defined fields for specifying additional information about each individual), *Associations* (lists of institutions that are members of an association), or *Regions* (lists of institutions that are within a region that is defined geographically or otherwise). A *Location* file can provide address and contact information for each location with specimens. Within PMx **Genetics**, files can be specified to provide empirically determined kinships, lists of pre-determined pairings, or lists of pre-determined individuals to be culled. Many of these files are created automatically by studbook management programs such as SPARKS and PopLink, but the formats are specified below for users who wish to create or edit these files with other programs. Sample files in each format are provided in the PMx Installation.

Primary Input File

The *Primary Input File* can be obtained from a *Genetics Export* (as an *exchange.dbf* file) from SPARKS 1.5, from a *PMx Export* (as *exchange.csv*) from SPARKS 1.6, from the **.ped* file created by PM2000, from a **.ped* file exported by PopLink, or from a **.csv* file that could be created from an Excel data set or with a text editor. The required format for each of these files is described below. Note that the fields for pedigree records can be ordered differently than specified below, as long as a header line identifies the sequence used.

1. *Exchange.dbf* produced by *Genetics Export* from SPARKS 1.5

PMx will accept and translate the *exchange.dbf* file that is currently produced by SPARKS 1.5. This is perhaps not the preferred method, because PMx relies on an old MS-DOS program to do the translation from *exchange.dbf* to a **.ped* file (see format below).

Fields in the *exchange.dbf* are as follows. SPARKS labels some of these fields differently, but either the SPARKS labels or the field names below are acceptable. Those fields in brackets are ignored by PMx, and can be omitted:

ID; DamID; SireID; BirthDate; BirthDateEst; Sex; [ID]; [DID]; [SID]; [DateIn]; [InEst]; [DateOut]; [OutEst]; [6 ignored fields]; DeathDate; Location; Local ID; [InstCode]; SocialGroup; Selected (T/F); Dead (T/F); [14 ignored fields]; OtherID

Sex is coded as 0-7, with the following meanings:

0 = fertile female

1 = fertile male

2 = sterile male

3 = sterile female

4 = sterile unknown (or abnormal)

5 = fertile unknown

6 = contracepted male

7 = contracepted female

(any other code will be interpreted as unknown sex, with unknown fertility)

2. [exchange].csv created by translation of exchange.dbf

The *exchange.dbf* file created by SPARKS can be transformed into a *.csv or *.txt text file, for example through importing and then saving the data using Excel. An advantage to taking this extra step is that the text file can be easily edited to insert additional data fields that are not included in the *exchange.dbf* file created by SPARKS.

Although Excel commonly creates a .csv (comma separated values) file as one possible text format, PMx actually requires that the delimiter between fields NOT be a comma, so it may be necessary to use a text editor to replace all comma delimiters. The fields can be separated by a colon (':'), semi-colon (';'), or tab. Commas as field delimiters are not permitted by PMx, because they cause confusion when used with regional data formats in which the comma is the decimal delimiter.

The first line of the file is a header listing the exchange fields. It must be there.

The second line is an optional header that contains optional *UDF* labels, with the format:

UDFS: UDF1Label, UDF2Label, ...

Any number of comment lines can be inserted in the file if the comment lines are started with '*'.

The list of fields for each individual is the same as for the *exchange.dbf*, above, except that each line can be extended with any number of *UDFs*.

Special coding of *Sire* and *Dam* can be used to specify mating types other than sexual reproduction of a single diploid male with a single diploid female, and optional lines can be inserted after a record to further specify multiple possible sires or dams, move records, or *UDFs*. The formats for these special codes are the same as specified below for the *.ped* file.

3. **.ped* file created by either PM2000 or PopLink

The .ped file is a simple text file that is produced automatically when a PM2000 project is created or can be exported from PopLink. Like the *exchange.csv* file, above, it has the advantage that optional additional data can be inserted that are not automatically included in the exports from PM2000 or PopLink.

Comment lines starting with '*' will be skipped (except for special types of lines, as described below).

First line specifies the analysis date as:

Analysis date: 20091231

Next line is a header starting with "**Number of animals:**", and it will be skipped.

UDF labels can be optionally specified in a header line as:

UDFs: UDF1Label, UDF2Label, ...

Primary data record format (must be all on one line), with fields in the following order:

ID; SireID; DamID; Sex; Selected (T/F); Dead (T/F); Birth Date (blank if unknown); Death Date (blank if not dead or not known); Location; Local ID; Other ID

Any number of UDF fields can be appended to each data line.

Sex is coded as 0-7, interpreted as in SPARKS (see above).

A variety of optional further data on an individual can be provided following an individual's record, with lines starting with '*', as follows.

Records of moves of an individual into and out of the population can optionally be inserted immediately after a record, with the format:

***MOVE: DateIn; InEst; InType; DateOut; OutEst; OutType; Location; Notes**

The date fields coded as specified above.

Est (estimate) fields are coded as "**Exact**" (a blank or "**None**" is also treated as exact), "**U**" (for an unknown date), "**Y**" or "**Year**" (known only to year), "**M**" or "**Month**" (known only to month), or "**D**" or "**Day**", with each of Y, M, and D optionally followed by an integer to indicate the number of years, months, or days to which a date is known.

Currently accepted TypeIn values are: "**birth**", "**capture**", "**found**", "**import**", "**leftentry**", "**entry**".

Currently accepted TypeOut values are: "**death**", "**release**", "**lost**", "**export**", "**rightexit**", "**exit**", "**alive**".

Location and *Notes* are optional, and can be any text string.

Optional UDF records can be inserted after an individual, with format:

***UDF: UDF1value; UDF2value; ...**

(Note that UDFs can instead be provided as extra variables appended to the line of primary data for each individual.)

Optional specification of multiple or uncertain sires the line after an individual record:
(Note that there are several currently acceptable formats.)

***SIRE: sire1ID; prob1**

***SIRE: sire2ID; prob2**

with the *sireIDs* being the possible sires and *prob* being the probability (or proportional contribution) for a possible sire.

Or, equivalently,

***SIREs: sire1ID; sire2ID**

***SIREPROBS: prob1; prob2**

Note the difference between ***SIRE** (one sire per line, with its probability) and ***SIREs** (multiple sires, with probabilities on another line starting with ***SIREPROBS**).

If probabilities are not specified (in either style above), they are assumed to be equal across all possible sires.

Optional lines for specifying multiple possible dams follow the same formats (with ***DAM** rather than ***SIRE**).

Multiple possible parents of unknown sex can be entered similarly, with ***UNK**, ***UNKs**, and ***UNKPROBS**, in which case they will be assigned as both possible sires and possible dams, with probabilities in each case set to ½ the total probability that the animal was a parent of one kind or the other.

For *Individuals*, parentage probabilities are rescaled to add to 1.0 if sum > 1. If sum < 1, then the missing part is assigned to an UNK parent.

For *Groups*, if sum > 1, probabilities are assumed to be number of diploid genomes contributed by each sire or dam, and sum of *Probs* becomes the Group size. If sum < 1, then the missing part is assigned to an UNK parent, and Group size is set to 1.

Special codes for SireID and DamID:

WILD – animal is wild-caught (can also be **WLDx**, with x being a number)

UNK – animal otherwise has unknown parent (can also be coded as **NONE** or just left blank)

Note: if an animal is wild-caught, both parents should be listed as **WILD**, unless it is one of the forms of asexual or non-sexual reproduction (see below): **SPLIT, CLONE, SELF, HAPLOID, EXTRACT, MERGE**

If only one parent is **WILD** (and similarly with **UNK**) then that “wild” parent will be replaced by a pseudo-founder – an animal that is inserted into the pedigree and is itself a founder. The pseudo-founder is given the ID of “MateOf”+ID of the known parent.

An animal should not be given parents **WILD** x **UNK**, because PMx won’t know if it is WILD or UNK.

MULT (or **MULTx**, or **MLTx**, with x being a number) listed as a parent can be followed by lines specifying who are the possible sires or dams, with probabilities, using the format described above for “***SIREs**”, “***SIRE**”, “***DAMS**”, “***DAM**”, etc. If not followed by specification of the possible parents, **MULT** will be treated the same as **UNK**.

(If a single sire and dam are listed in the Individual record, and ***SIRE** or ***DAM** lines are also provided, **PMx** will ignore the ***SIRE** and ***DAM** lines.)

Any unrecognized *SireID* or *DamID* will be treated as a founder animal (inserted into the pedigree) with **UNK** x **UNK** parents.

Acceptable specifications of various Mating Types:

The mating type that created an offspring is assumed to be *Sexual* diploid individual if parents are each given as one of *SireID* or *DamID*, **UNK**, **WILD**, or **MULT** (including **MLTx**).

However, for other matings types (non-sexual reproduction or various forms of group formation), the “*SireID*” data field can be used to enter a special code to describe the mating type. If “*SireID*” is:

GROUP: Entity is assumed to be a *Group*, formed by a sexual merge, in which sum of contributions from sire side are scaled to equal sum of contributions from dam side. Sires contributing to this Group should be specified on subsequent lines of ***SIRE** and/or ***SIREs**. The contributions of these sires to the Group, if unequal, should be specified on ***SIRE** and/or ***SIREPROB** lines. Group size is the sum of the contributions, unless specified otherwise with **GROUPx** as the *SireID*, in which case x gives the total size of the new group, and contributions of parents are re-scaled to sum to x.

MERGE: Entity is assumed to be a *Group*, formed by a merge. Dam would normally be listed as **GROUP** or **MULT**, and the parents contributing to this merge should be specified on subsequent lines of ***DAM** and/or ***DAMS**. The contributions to the Merge, if unequal, should be specified on ***DAM** and/or ***DAMPROB** lines. A single *DamID* (other than **GROUP** or **MULT**) could be listed, in which case the “merge” would be the same as a clone of that dam.

SPLIT: Entity is assumed to be a *Group*, formed by a split. *DamID* can be a single entity (e.g., the group from which a split was made) or can be **GROUP** or **MULT** if there are multiple possible parents from which the split was made.

CLONE: Entity is a *Clone* of the Dam, and of the same *EntityType* as the Dam. If *DamID* is **MULT** or **GROUP**, then there were multiple possible parents from which the clone was made.

SELF: Entity is an *Individual* formed by selfing the Dam. If *DamID* is **MULT** or **GROUP**, then there were multiple possible parents from which the selfing occurred.

EXTRACT: Entity is an *Individual* formed by extracting an individual from the Dam (presumed normally to be a group entity). If *DamID* is **MULT** or **GROUP**, then there were multiple possible parents from which the extract occurred. If Dam is an Individual, then extract is the same as a clone. (Genetically, Clone, Split, and Extract all have the same consequences for kinships.)

HAPLOID: Entity is an *Individual* formed from a haploid gamete (possibly then duplicated to make a completely homozygous diploid individual) from the Dam. If *DamID* is **MULT** or **GROUP**, then there were multiple possible parents from which the gamete came.

Of the above special codes for *MatingTypes*, the only one that can be applied also to the Dam is **GROUP**. (The other codes in place of the *SireID* all imply that the set of possible parents will be specified in the Dam.) If *DamID* and *SireID* are both **GROUP** or **MULT**, then the reproduction was a sexual merge (see description above under *SireID* = **GROUP**). If any of **MERGE**, **SPLIT**, **CLONE**, **SELF**, **EXTRACT**, or **HAPLOID** are listed for the *DamID*, she will be treated as an UNK founder (unless an animal with that ID is actually in the studbook!).

4. [Exchange].csv created by a PMx export from SPARKS 1.6

SPARKS 1.6 exports the pedigree to PMx as a semi-colon delimited text file that contains more information than the data exported by SPARKS 1.5 or by PopLink. Although semi-colon delimiters are used to avoid confusion with numeric formats, the file must have a .csv extension so that PMx can recognize it as a SPARKS 1.6 export.

The first few lines of the file are headers, each beginning with '*'. These header lines are ignored by PMx.

Another header line provides the date window used in the export, with the following format:

* **Dates: 01/01/1970 <= 28/02/2011**

A mandatory header line lists the exchange fields, with format:

*
ID;ID;Sire;Dam;Sex;Selected;BirthType;ReproStatus;Living;DOB;DOBst;DOD;DODst;DeathCodes; Location;LocalID;Social;Program;Country;HouseName;Transpond;TagBand;Tattoo;ColorPhase;LitterSize; No_Litters;Litter_List; UDFs

[Note that this line specifies the sequence of data fields in all individual records, so it is critical that it be included and correct.]

The next line is an optional list of UDF labels:

* **UDFs: UDF1label; UDF2label; ...**

Several further header lines describe the format of lines that specify multiple possible parents, and move records. These lines begin with '*' and are ignored by PMx. Any number of comment lines can be inserted later in the file if started with '*'.

The data record for each individual must begin with "ID:"

Special coding of *Sire* and *Dam* can be used to specify mating types other than sexual reproduction of a single diploid male with a single diploid female, and optional lines can be inserted after a record to further specify multiple possible sires or dams, move records, or UDFs. The formats for these special codes can be the same as specified above for the .ped file, but additional formats are also accepted, as follows:

Multiple possible sires can be entered on lines following the animal, as described above in the *.ped format. These possible parent data can be entered on lines starting with "SIRE:", "SIRES:", and

"SIREPROBS:", rather than **"*SIRE:"**, **"*SIREs:"**, and **"*SIREPROBS:"**, but when the asterisk is omitted then the probabilities are taken to be percents (0 to 100) rather than proportions (0 to 1).

ISIRE: ID; sire1ID; prob1

ISIRE: ID; sire2ID; prob2

with the *sireIDs* being the possible sires and *prob* being the probability (or proportional contribution) for a possible sire, and the ID being the offspring for whom that possible sire is being assigned.

Or, equivalently,

ISIRES: ID; sire1ID; sire2ID

ISIREPROBS: ID; prob1; prob2

The ISIRE lines can be preceded with **'***, as in ***ISIRE:**

And similarly for DAMS.

If possible sires or dams for an animal are listed several times in a file, then those sets of possible parents are collectively considered to be the possible parents of the animal.

An advantage of this format, in which the ID of the offspring is listed, is that the lines with these parentage data do not have to follow immediately after the offspring in the pedigree file, but can instead be inserted anywhere within the file. For example, the records listing the possible parents can all be inserted at the bottom of the pedigree file.

If a parent of an animal is listed as **MULT1, MULT2, ...**, or **GROUP1, GROUP2, ...** then another alternative to listing the possible parents on the subsequent data line is to give later in the file the animals that comprise that MULT (or GROUP), with data lines in the following format:

ID: MULT1

***SIRE: 123; 0.50**

***SIRE: 124; 0.50**

Or, equivalently

ID: MULT1

***SIREs: 123; 124**

***SIREPROBS: 0.50; 0.50**

And similarly with *Dam* instead of *Sire* for multiple possible dams, and the *Sire* and *Dam* labels can be preceded (or not) by an **'***.

The initial **ID** tag can be any of **ID**, **INDIVIDUAL**, **MULT**, or **GROUP**, or any of these preceded by an **'***.

The advantage of using this format to specify which animals are included in a MULTx parent (with 'x' being a number) is that a number of animals with the same set of possible parents can be assigned MULTx as the parent and then only once in the file do the parents in that MULTx set need to be identified.

The *exchange.csv* file can also contain move records, as described above for the **.ped* file format, except that the leading MOVE tag does not start with an **'***, e.g.,

MOVE: 2;19790101;Y;capture;19810520; ;death;

5. Lineage pedigree format

PMx can read the *Primary Input File* as a Lineage (reference) pedigree file, with the extension *.txt*. The first few lines are skipped headers; lines starting with '#' or '*'

Record format:

**ID,Dam,Sire,Sex,Selected,Living,Age,Vx,Location,Generation,Known,#Progeny,
Inbreeding,MK,KV,GU_all,GU_desc,PrLoss,[UDFs, ...]**

Note that females are coded as 1, males as 0. (Opposite from SPARKS and *.ped* coding of the sexes.)

The data fields after *Location* and *Vx* are not actually read by PMx, and only they need to be there at all if optional *UDFs* are added to the end of the line. PMx will allow *DAM, *SIRE, *UDF, and *MOVE lines in the Lineage file, just as it does with the *.ped* file (see above).

Demography Input Files

The table below shows the types of input files that can be imported for demographic components of PMx, the software that creates them, how they are created, and their content.

File Type	Created Using	Created by	Contents/Uses
*.prn	SPARKS 1.56, 1.6 or PopLink	In SPARKS: Under <i>Analysis</i> , <i>Exporting a Demography Export</i> for a given filter condition. In PopLink, by <i>Exporting to PM2000</i> for a given filter condition Both <i>prn</i> files (male, female) will be in either the SPARKS folder, or the PopLink Database Folder	Creates a male and female annual age-class life-table. Age-class lengths cannot be modified as the export consists of an already-calculated life-table, not raw data.
Exchange.csv	SPARKS 1.6	Under <i>Analysis</i> , <i>Export to PMx</i> for a given filter condition. File will be in the SPARKS studbook folder	Provides the raw data for PMx to calculate male and female life-tables. Since the raw data are included, users can modify the age class width to different time lengths.
ANALYTICAL SURVIVAL STATISTICS INCLUDED INDIVIDUALS TABLE.csv	PopLink	1. Under <i>Reports</i> Menu, select " <i>Survival Tool</i> ". Check " <i>Analytical Survival Statistics for Population Management</i> ". 2. Set desired filter. 3. With " <i>Analytical Survival Statistics Report</i> ", click on the " <i>Included Individuals Table</i> ". 4. Select <i>Export</i> . 5. File will be in the PopLink Database Folder.	Provides the raw data for PMx to calculate male and female life-tables. Since the raw data are included, users can modify the age class width to different time lengths.
*.mov	No software currently produces this file	Manually	Provides information on every move into and out of the population by any individual. Provides the raw data to calculate male and female life tables.
*.ped	None	Manually	For a <i>ped</i> file to be used, it must contain MOVE information as specified above. While a <i>ped</i> file is created by PM2000, PopLink, and PMx (but only after successfully creating a project), none of these formats currently generates <i>ped</i> files with the MOVE information.

The formats of these file types follow:

1. *.prn Formats

PopLink and SPARKS both can export a life-table for import to PMx. These are not the preferred import files for demography, as they do not let the user define their own age classes. There needs to be one PRN file for the males, and another for the females. These files can be produced as .txt files manually if life-table information is available from another source. Format of file is as follows:

Line 1 : Header = "Studbook Data for:" Not used for any purpose.
Line 2: Common name
Line 3: Latin name
Line 4: Sex
Line 5: "Data exported on: mm/dd/yyyy"
Line 6: "Data compiled by: name"
Line 7: "Contact info: address"
Line 8: "Data current thru: mm/dd/yyyy"
Line 9: "Scope of data: international, regional, etc"
Line 10: Header
Line 11: blank
Line 12: beginning of data in following format:
Space, number alive, space, Qx, space, Mx, space, Age class format" x – x+1", space, sample size for Qx, space, sample size for Mx
Line 12 – n: repeat data for each age class until no more animals at risk
// Data are followed by a blank line
Next line: "Filter conditions in effect:"
// All following lines are optional:
// Any additional lines will be interpreted as additional filter information
// For example:
Next line optional: "During mm/dd/yyyy – mm/dd/yyyy"
Next line optional: "Status = status"

// Sample file:

Studbook Data for: (Check after data for filter conditions.)
CALIFORNIA CONDOR
GYMNOGYPS CALIFORNIANUS
female
Data exported on: 20 Apr 2010
Data compiled by: Michael Mace
Contact info:
Data current thru: 18 Dec 2008
Scope of data: International - North America (HOST Zoological Society of San Diego)
Number Alive / Qx / Mx / Age Class / Sample Size (Qx) / Sample Size (Mx) /

10.000 0.150 0.000 0- 1 268.6 218.4
8.000 0.060 0.000 1- 2 164.7 151.1
8.000 0.130 0.000 2- 3 120.1 109.1
// etc, etc, etc
0.000 0.000 0.000 44-45 0.0 0.0
0.000 0.000 0.000 45-46 0.0 0.0

Filter conditions in effect:
During 1/1/1990 – 3/23/2010
// End of sample file

Note: Data are fixed format space delimited.

2. Exchange.csv Formats

This is the same format as specified above [Exchange].csv created by a PMx export from SPARKS 1.6]

3. Analytical Survival Statistics Included Individuals Table.csv Formats

For every animal that has been in the population under conditions that match the set filter (e.g., alive between 1/1/1990 and 1/1/2011 in North America) needs to have a record for every time it entered the filter. Each record needs to have the entry information (date, type, age) and then the exit information associated with that entry (still alive, died, exported).

Animals with unknown birth, entry or exit dates are not to be included.

Line 1: Header: "Studbook ID, Sex, Birth Type, Birth Date, Birth Date Est. ,Entry Date, Entry Date Est., Entry Age (In Days) ,Entry Method, Exit Date, Exit Date Est., Exit Age (In Days),Exit Method, Censored/Complete"

Lines 2 to n: data with the following format, fields separated by ", ":

Studbook ID:	Up to 6 characters long
Sex:	"Male", "Female", "Unknown"
Birth Type:	"Wild Born", "Captive Born", "Unknown"
Birth Date	"MM/DD/YYYY"
Birth Date Est	"None", "Month", "Year", "+/- x Years"
Entry Date:	"MM/DD/YYYY"
Entry Date Est:	"None", "Month", "Year", "+/- x Years"
Entry Age:	"XXX"
Entry Method:	"alive at start of window" "born into window" "imported into window"
Exit Date:	"MM/DD/YYYY"
Exit Date Est:	"None", "Month", "Year", "+/- x Years"
Exit Age:	XXX
Exit Method:	"died" "LTF" "alive at end of window" "exported out of window"
Censored/Complete:	"Complete" if animal died or alive "Censored" if animal exported or LTF

//Sample format:

```
Studbook ID,Sex,Birth Type,Birth Date,Birth Date Est.,Entry Date,Entry Date Est.,Entry Age (In Days),Entry  
Method,Exit Date,Exit Date Est.,Exit Age (In Days),Exit Method,Censored/Complete  
1,Male,Captive Born,9/19/1974,None,1/1/1990,None,5583,alive at start of  
window,5/22/1993,None,6820,died,complete  
2,Male,Captive Born,10/19/1980,None,1/1/1990,None,3361,alive at start of  
window,4/22/1996,None,5664,died,complete  
4,Male,Captive Born,11/8/1981,None,1/1/1990,None,2976,alive at start of  
window,1/2/2001,Year,6995,died,complete  
15,Male,Captive Born,10/18/1983,None,1/1/1990,None,2267,alive at start of  
window,12/3/2003,None,7351,died,complete  
23,Male,Captive Born,10/11/1984,None,1/1/1990,None,1908,alive at start of  
window,3/28/1990,None,1994,died,complete
```

4. MOVE file Formats

There should be a record for every instance an individual entered the filter window. PMx will normally expect such files to have extension *.mov*, but they can be any text file.

Skips comment lines starting with '*'

Record format:

ID ; DateIn; InEst; InType; DateOut; OutEst; OutType; Location; Notes

Formats for the dates, move types, and date estimates are the same as specified above for the *MOVE records that can be inserted into a *.ped* file. *Location* and *Notes* are optional.

5. *.ped Formats

To be used for demography, the *.ped* file must contain MOVE information. See above for format of the *.ped* file with MOVE information.

Census File Formats

The table below shows the types of input files that can be optionally imported to generate Census content in PMx, the software that creates them, how they are created, and their content.

File Type	Created Using	Created by	Contents/Uses
<i>exhcens.txt</i>	SPARKS 1.56 and PopLink	<u>In SPARKS</u> : Under <i>Analysis</i> , run a <i>Census Report</i> . This file will automatically be created and reside in the SPARKS studbook folder. <u>In PopLink</u> run "Census Report" under "Reports". File will be created in the PopLink Database folder	Year by year counts of number of males, females, unknown sex, and number of wild born, captive born and origin uncertain individuals.
<i>PMxCensus.csv</i>	SPARKS 1.6	In SPARKS: This file is created automatically along with the primary input field <i>exchange.csv</i> (under <i>Analysis</i> , <i>Export to PMx</i>) and will reside in the SPARKS studbook folder.	Like <i>exhcens.txt</i> from SPARKS 1.56, but with additional content.

The formats of these file types follow:

1. Exhcens.txt format

Starts with a blank line. Here '.' represents spaces. The variables just need to be separated by spaces; the number of spaces does not matter. Spaces before the first column are expected. The exact name of the variables in the header line (actually line 3) can vary, but there can be no spaces within a variable name. The order must be maintained as:

Order Content

1	Year
2	Total alive
3	Male alive
4	Female alive
5	Unknown Sex alive
6	Total alive
7	Wildborn alive
8	Captive born alive
9	Origin unknown alive

(Note that *Total_Alive* is repeated twice – that is the format output by SPARKS 1.56 and PopLink.)

Sample file:

. (blank)

HUMBOLDT.PENGUIN,.SPHENISCUS.HUMBOLDTI

..Year...Tot_sex.....Male....Female...Unk_sex..Tot_born..Wildborn.....Capt.....Unk

..1962.....7.....1.....2.....4.....7.....4.....3.....0
 ..1963.....7.....1.....2.....4.....7.....4.....3.....0
 ..1964.....7.....1.....2.....4.....7.....4.....3.....0
 ..1965.....9.....2.....3.....4.....9.....6.....3.....0
 ..1966.....9.....2.....3.....4.....9.....6.....3.....0
 ..1967.....16.....7.....4.....5.....16.....13.....3.....0
 ..1968.....16.....7.....4.....5.....16.....13.....3.....0

Etc...

2. PMxCensus.csv format

This should be a semi-colon separated file.

Line 1: is blank.

Line 2: "*" followed by species name. This line is not used for anything.

Line 3: "*" followed by variable names, not used for anything, but data are expected to be in this order for each record.

Variables need to be in this order, separated by ";", names of variables are irrelevant.

Order Content

1	Year
2	Total alive
3	Male alive
4	Female alive
5	??? Sex alive
6	Total alive
7	Wildborn alive
8	Captive born alive
9	Origin ? alive
10	Males captured

Order Content

11	Females captured
12	??? Sex captured
13	Male born
14	Females born
15	??? Sex born
16	Males stillborn
17	Females stillborn
18	??? Sex stillborn
19	Males released
20	Females released

Order Content

21	??? Sex released
22	Males died
23	Females died
24	??? Sex died
25	Males imported
26	Females imported
27	??? Sex reported
28	Males exported
29	Females exported
30	??? Sex exported

(blank)

*AMUR (SIBERIAN) TIGER, PANTHERA TIGRIS ALTAICA

*Year;Tot_sex;Male;Female;Unk_sex;Tot_born;Wildborn;Capt;Unk_born;Captures_M;Captures_F;Captures_U; Births_M;Births_F;Births_U;Stillb_M;Stillb_F;Stillb_U;Releases_M;Releases_F;Releases_U;Deaths_M;Deaths_F; Deaths_U;LTFS_M;LTFS_F;LTFS_U;Imports_M;Imports_F;Imports_U;Exports_M;Exports_F;Exports_U;

[illegible]

Other Optional Input Files

UDFs Input File

UDFs can be provided within a separate file, rather than or in addition to being included within the primary input file.

First line must be UDF labels: “UDFs: UDF1label, UDF2label, ...”, but there does not have to be a label for every UDF (and there can be extra labels for UDFs never entered for any animals). Any label of “*STUD_ID*” will be skipped, which allows this file to be created by converting the SPARKS *udf.dbf* file into a .csv file.

Comment lines starting with '*' will be ignored.

Record format:

ID; UDF1value; UDF2value; ...

Note that UDFs are stored as strings, even if they have a numerical format.

Association Input File

This can be a text file with any name, although PMx will specifically look for files with extension *.fed*. The file should be just a list of MNEMONICS, one per line, of all *Locations* that are to be considered part of that association. The *Association(s)* for each animal will be listed in PMx as a label that is the filename, minus the *.fed* extension. Multiple *.fed* files can be read, and an animal can be listed as being within more than one *Association* (e.g., *.fed* files might be used to read “AZA”, “CAZA”, “WAZA”, and even “FRIENDSOFJON”.)

Region Input File

This can be any text file, although PMx will specifically look for files with extension *.rgn*. The file should be just a list of MNEMONICS, one per line, of all *Locations* that are part of that *region*. The *Region* for each individual will be listed in PMx as the filename, minus the *.rgn* extension. Multiple *.rgn* files can be read, but each individual will be listed as within only the last of the regions in which it was a member.

Locations File

When SPARKS or PopLink creates an export for PM2000 or PMx, it also creates a *Location.txt* file that lists contact information for each institution that is listed as a holder of the animals. The format of this file is highly specific, with the spacing being critical. (No delimiters can be used, because it would be impossible to know if those delimiters might, for example, be included in the address information for a location.) These location data are used only in the labels displayed in the Recommendations reports.

It is not recommended that users try to edit this file. The format is a line per location, with the following data:

MNEMONIC	characters 1-9
INSTCODE	characters 10-18
INSTITUTION	characters 19-58
ADDRESS	characters 59-92
CITY	characters 93-112
STATE	characters 113-132
COUNTRY	characters 133-152
MAILCODE	characters 153-162
PHONE	characters 163-182
FAX	characters 183-202
EMAIL	characters 203-237
CONTACT	characters 238-end of line

Kinships File

Empirically determined kinships can be read in from a text file, in which case PMx can replace the kinships calculated from the pedigree for those pairs of animals with the ones read from the file. These kinships might be determined from DNA analyses, or from knowledge of familial relationships, or in any other way. Normally, the file will have extension *.kin*, but any extension is accepted. The format of the file is that the initial lines list, one per animal, the IDs of the animals in the empirical kinship matrix. Subsequent lines give the kinships, although only the lower half (and the diagonal) of the matrix are required. Values are separated by tab, space, ':', or ';'. A value of -1 is a code for a missing value, in which case PMx will assign the kinship calculated from the pedigree for that pair.

```
12
25
31
522
0.50
0.10 0.50
0.00 0.10 0.55
0.25 0.00 0.25 0.45
```

The file can instead provide the coefficients of relatedness, in which case it would normally have the extension *.rel* (but can have any extension). If PMx is told that the file contains relatedness values, then each value will be divided by two to obtain the kinship.

Pairing File

A set of pairs can be specified within a file, for later reading into PMx. The first line is a header that will be skipped. If the header contains 'F' as its third specified variable, then the reading of the data lines will assume that the inbreeding of the pairing is included. Otherwise, it is assumed that F is not included in each row of the file.

The subsequent lines list, one per line, the pairings, with variables separated by ':', ';', or tab. The field delimiter cannot be a comma, because that would cause misreading of numeric data in many regional data formats.

The *SireID* and *DamID* must be listed as the first two variables. 'F', if included in the header, is given next, followed by the probability of success, the number of offspring to be produced, the location of the pairing, and any notes. However, any line can be truncated at any variable after the *SireID* and *DamID*, in which case the missing values will be assigned as probability = 1.0, #offspring = 1, location and notes both blank. (The inbreeding coefficient is ignored, as PMx will calculate the inbreeding for the pair.)

For example:

Sire	Dam	F	Success	Offspring	Location	Notes
391	390	0.0000	0.8000	4	CHICAGOBR	High priority!
412	417	0.1016	1.0000	1	LONDONRP	Nice animals
437	425	0.1016	0.2500	1	ST LOUIS	Mean

Culling File

A set of animals to be culled from the population can be specified within a file, for later reading into PMx.

The first line can be an optional header with "*UniqueID, Location*" (or anything that starts with "*UniqueID*"), and it will be skipped. The subsequent lines list, one per line, the IDs to be culled. These can be optionally followed by Location or any other information, separated from the ID by ':', ';', or tab.

For example:

UniqueID	Location
317	DALLAS
338	SAN ANTON
377	COLO SPRG

APPENDIX E. PMX OUTPUT FILES

Most of the work with PMx is interactive, assessing population status via analyses shown on screens and working through demographic and genetic decisions to obtain population management goals. Tables, graphs, and final recommendations can be exported in various formats to facilitate the documentation and dissemination of management plans. However, hidden within the *.*pmxproj* file that is created when PMx saves a project are a number of files that contain output that sometimes will be useful. The *.pmxproj* file is actually a compressed (zipped) file that uses the standard file compression format. Therefore, access to the contents of the file requires only the following few steps:

- Make a copy of the file (so that the PMx project itself is not damaged).
- Rename the copy, changing the extension to .zip (e.g., *lions.pmxproj* becomes *lions.zip*).
- Extract any files of interest from the .zip file, using any of the standard programs (e.g., PKZip, or Windows 7 Explorer).

Pmxproj File Contents

The *.pmxproj* file contains:

- Copies of all input files that were used to create the PMx project (e.g., the *.ped* or *.csv* primary input file; *.prn* or *.csv* or *.txt* files with demographic and census input; and additional files such as *.fed* and *.rgn* files).
- Various *.csv* files that contain tables of demographic results, such as the life tables and population projections.
- Six files with the calculated kinship matrices for each possible combination of genetic assumptions. These files are stored in binary (*.bin*) format, and will be readable only via programs able to read this format (i.e., the files will not be readable in a text editor). For studbooks that have no unknown or uncertain parents, several or all of these kinship files will be exact copies, because the genetic assumptions will have no effect on the kinship calculations.
- A *.pmi* file that contains the full list of the individual data (as can be viewed on the **Individual** tab of **Genetics**), and a *.pop* file that has a smaller set of core information about each individual. These files are semi-colon delimited, so they can be easily opened in Excel or other programs.
- A *.rep* file that contains, as a formatted text file, a table of the founder contributions to each individual in the descendant population.
- The **Project Notes** saved as a *Report.rtf* file, so that they can be imported into Word or other text editing programs.
- The **Recommendations** table saved as a tab-delimited *RecFile.txt* file that can be imported into Excel or other programs.
- A *PMxProject.xml* file that contains, in xml format (readable by Internet Explorer and other programs) the core information that defines the project.

It is highly recommended that the files within the original *.pmxproj* file (as opposed to a copy) not be edited, because the formats of some of the files are highly specific and any changes might make the PMx project unreadable by PMx. Because all of the files needed by PMx are included within the *.pmxproj* file, a project can be transferred to another folder or to another computer by simply copying the *.pmxproj* file. Moreover, because copies of all input files that were used to create a Project are stored within the *.pmxproj* file, those original data are archived with the project and can be used to revert to the originally imported data (via a button on the **Selection** tab) if it becomes necessary to discard all modifications made within PMx to the selected population.

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