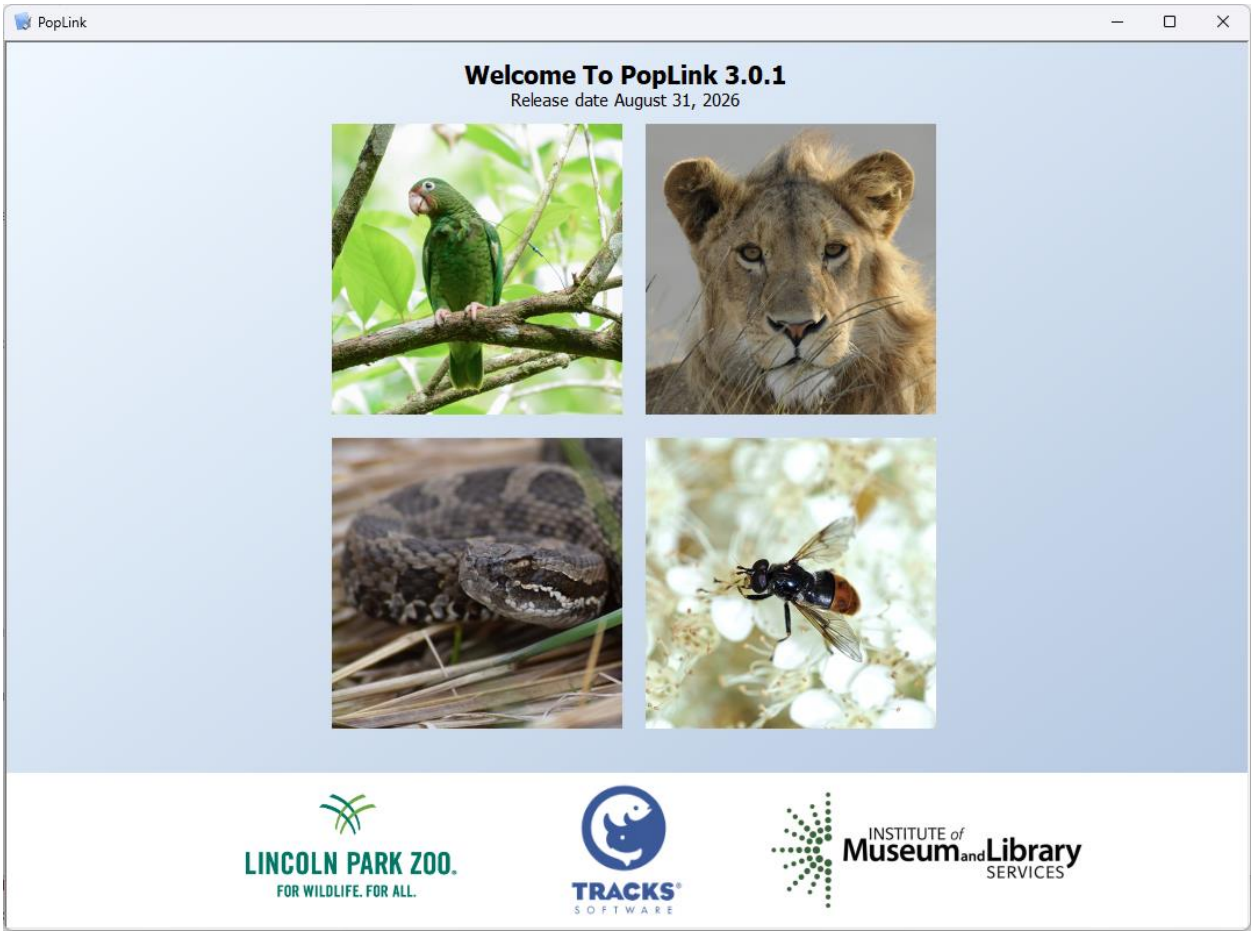

PopLink Version 3.0.1
User's Manual

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The software and the manual are not guaranteed to be free of bugs and errors and are provided to you on an "as is" basis without any warranty of any kind. The user is responsible for insuring that the application of PopLink is appropriate to the problem at hand.

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Chapter 1: INTRODUCTION and OVERVIEW

1.1 WELCOME to POPLINK 3.0!

PopLink 3.0 is a major update that expands PopLink's capabilities beyond traditional zoo and aquarium studbook management and introduces features specifically designed for researchers and managers tracking wildlife populations in the field. In addition to storing and analyzing population data, PopLink 3.0 now enables you to:

- Import spreadsheet data to quickly create new studbooks or add individuals to existing populations.
- Track resighting data (i.e. detections over time of marked individuals).
- Track reproductive efforts across breeding attempts, recording data on important reproductive milestones before successful offspring are recorded in the studbook.
- Import User Defined Field (UDF) data to efficiently create and update custom fields.

These new features make it easier to collect, organize, and analyze data from a wide range of wildlife monitoring and conservation programs.

How can maintaining a database in PopLink 3.0 help your population?

Wildlife biologists have long recognized the value in marking individuals, and data on resightings of marked or known individuals allow researchers to estimate a population's abundance, growth rates, survival and reproductive rates, and more. Increasingly, researchers have also recognized the value of maintaining comprehensive records for entire populations, including demographic, pedigree, and reproductive information. These populations span the management spectrum from *ex situ* breeding programs, to conservation translocation efforts like the Puerto Rican Parrot Recovery Program with individuals managed both *in situ* and *ex situ*, to herds of plains bison roaming fenced pastures that encompass thousands of acres, to intensively monitored free-ranging populations like the lions of the Ngorongoro Crater.

By tracking individuals, their life history events, and their relationships through time, researchers and managers can address a wide variety of conservation and management questions. For example, these data can be used to:

- Identify the most appropriate animals to breed or release in conservation translocation programs (Faust et al., 2024)
- Identify breeding pairs to receive *ex situ* born offspring for cross fostering (Gese et al., 2018)
- Quantify immigration rates and the impact of immigration on population growth (Summers et al., 2024)
- Track individual inbreeding levels, and test for the possibility of an inbreeding purge (Kennedy et al., 2014)
- Identify individuals to remove from a population to maintain genetic diversity (Giglio et al., 2018)
- Understand a disease inheritance mechanism and manage it (Ralls et al., 2000)
- Identify candidates for genome sequencing (Galla et al., 2022)
- Build a population viability analyses model that evaluates the genetic and demographic health of *ex situ* and *in situ* recovery populations (Faust et al., 2024)

PopLink 3.0 provides a centralized platform for storing, managing, and organizing the demographic, reproductive, resighting, and pedigree data that make these analyses possible.

While PopLink 3.0 now supports a wider range of wildlife monitoring and conservation applications, its origins are in the management of studbook populations within zoos and aquariums. As a result, the terminology and examples throughout this manual reflect that history, even when the software can be applied to free-ranging wildlife populations. In addition, there may be unique situations you're trying to include in your monitoring dataset that could be configured in multiple ways within PopLink, and setting your data structure up correctly at the beginning can be important. **We are happy to brainstorm with you on how to apply this tool to your conservation program - if you have questions, please contact us at** software@lpzoo.org.

1.2 INTRODUCTION TO POPLINK

PopLink is a computer program designed to help maintain, analyze, and export the data of an individually monitored population that are relevant to its genetic and demographic management. This software can be useful to **studbook keepers**, the individuals responsible for tracking and maintaining the data relevant to an individual species, **conservation program managers,** who are interested in analyzing trends for their population over time, and to **population biologists,** the individuals responsible for analyzing the data for use in genetic and demographic analyses upon which management decisions are based.

PopLink was designed to give users the ability to:

- Securely store their population data in a structured database
- Assist with data management and manipulation (fixing errors, appropriately documenting studbook changes, prioritizing data clean-up)
- Assist with analytical assumption making for the purposes of population management
- Import and compare data from multiple sources (other PopLink studbooks, CSV files)
- Export data to software used in population management (PMx)

1.2.1 How to Use This Manual

In the manual, look out for this icon:

NOTE: There will be special reminders here that will alert you to important points or explain confusing concepts.

1.2.2 Program Information

If you have any comments, questions, bugs, or compliments to report about PopLink, please contact us directly at software@lpzoo.org. While we have minimal resources for ongoing development, we still attempt to fix critical run-time errors.

The latest version of the PopLink program and the manual will be accessible via the website https://www.poplink-download.org. When downloading directly from the website, you'll be asked to register which will enable us to notify you about future versions. You can also email software@lpzoo.org to be added to the mailing list to receive updates about new PopLink releases.

1.2.3 System Requirements

Hardware

Minimum system requirements: 2 GB free hard drive space, 4 GB RAM

Operating System:

PopLink 3.0 is compatible with Windows 10 and 11 or Windows Server 2016 or later. Although primarily developed for PCs, it has been successfully run on Macs using Boot Camp or Parallels, which require a version of the Windows operating system before PopLink can be installed (following normal installation instructions).

1.2.4 Getting Help in PopLink

There are three mechanisms to help while you're working with PopLink:

1. The manual, which can be downloaded from the website or opened through the Help menu in the software.
2. On-screen help text: If you hover over icons, tool tips will appear describing the function of a particular icon.
3. If you have specific questions that are not addressed in the manual, you can contact us at software@lpzoo.org.

1.3 BACKGROUND ON STUDBOOKS

1.3.1 What is a Studbook?

A studbook is a true record of the history of a population. The "population" in question includes all or some of the individuals of a given species in a defined geographic area, which is typically defined when the studbook is initiated. The studbook includes key events (birth dates, death dates, transfers between locations), parentage, and any other relevant information about the animals (e.g., house names, behavioral notes, etc.). The entire history of each individual is traced in a studbook as much as possible. Taken together, these collective histories describe the population's genetic and demographic identity.

1.3.2 Why Keep Studbooks?

Studbooks are primarily used for monitoring and managing populations; without studbooks, it would be virtually impossible to manage populations scientifically. In the zoological associations of the world, such as the Association of Zoos and Aquariums (AZA), managed programs like the Species Survival Plans® (SSP) use studbooks to demographically and genetically manage animals of a particular species at participating institutions as a single population.

Studbook datasets provide accurate, up-to-date information in a standardized format; this standardized format enables detailed genetic and demographic analyses. For example, studbooks can be used to gain basic information about the current status of a population (numbers of individuals, genetic health, etc.), to help make decisions about which animals to breed based on the best genetic pairings, and to help assess whether a population is stable, increasing, or decreasing in numbers. In addition, these datasets can be crucial repositories for the history of a population and its monitored data, enabling easy transfer of records over time between program managers, scientists, and anyone else who needs to utilize the population's data.

1.3.3 What is a Studbook Keeper?

A studbook keeper is the individual who compiles and maintains a population's studbook, researching and tracking the pedigree and demographic data on a group of animals. In managed populations in zoos and aquariums, much of this job involves ferreting out the "truth" from multiple versions of an animal's record, and the studbook keeper is the only person focused on this pursuit from a population-level focus rather than an institution-level focus, for populations that are held across many different facilities. The studbook keeper is often also the "species expert" who knows the data history, the history of the population being monitored, the species' biology, and the necessary information for appropriate population management. The studbook keeper is also responsible for maintaining data quality, which is critical to the effectiveness of management decisions. Genetic and demographic recommendations for population management are only as good as the data upon which they are based; thus, inconsistencies and errors in studbooks can compromise the desired effects of even the best management plans.

1.3.4 What Data Are Included in a Studbook?

A studbook tracks the movement of each animal for its entire life, starting with the date of capture or date of birth (known or estimated), and ending with the date of death or the date at which the animal leaves the focal population (or is lost-to-follow-up). In addition, the studbook should also include information on parentage, sex, origin, cause of death (if known), house name, transponder number, band or tattoo number, and any other information that will assist in tracking individual animals.

Studbooks are limited in scope in several ways:

1) **Taxonomic Scope**
   In general, the taxonomic scope of a studbook is a species or subspecies; you may want to think carefully about splitting subspecies into separate studbooks vs. maintaining them all in a single studbook. If all subspecies are included in a single database, each subspecies can be identified with a User Defined Field (UDF; *see section 4.10* on how to use and create UDFs). Because a UDF allows sorting and selection of animals for reports and analyses, in most cases it is best to create a single database for all subspecies. For species with uncertain taxonomy (i.e., they might change as more information is accumulated), a single database will accommodate addition or loss of taxa.

2) **Geographic Scope**
Studbooks in zoos and aquariums are typically at the regional (i.e. AZA, EAZA) or global level. Studbooks for other populations will have geographic scopes defined by the population the studbook keeper is interested in managing or is closely monitoring. Generally, for studbooks for *ex situ* populations it is important that the studbook trace and record each animal's pedigree back to wild-caught animals, if possible. This means that a regional studbook keeper does not stop at the regional boundaries when collecting data. The regional studbook keeper should enter all captive ancestors of animals that have lived or are living in the region regardless of where those ancestors now live or have ever lived. Complete pedigrees are essential to reliable genetic analyses; incomplete pedigrees hamper genetic analyses and must be "completed" via hypothetical ancestors and/or assumptions that are often little more than good guesses (see Chapter 9 on assumptions in studbooks). If relationships between wild-caught founders are known, or if a studbook is being used to monitor a wild population and relationships are known, that information should be incorporated into the studbook as much as possible.

3) **Temporal Scope**
Zoo records for some species go back into the 1800s. Although many animals do not reproduce successfully when a population is first started, their records may be valuable for demographic analyses (i.e., age-specific mortality). Thus, every effort should be made to include as many animals as possible. With large datasets, studbook keepers often start with living individuals and their dead relatives, and then add historic records (of animals that did not reproduce or whose family lines died out) gradually over time. Studbook keepers should not limit temporal scope because of perceived, or real, changes in husbandry or management. No animal should be excluded from a studbook because it lived under "outmoded" management and husbandry regimes. There are a few cases in which entering all animals within the scope given above may be unrealistic and represent an inordinate amount of work without a corresponding benefit; such cases should be carefully considered to ensure that reducing the data entered will not limit the utility of the studbook as a record of a population or in analysis.

4) **Institutional Scope**
Any and all institutions that can be verified as holding or having held animals should be included in the studbook. For zoo populations, this means that inclusion of data from an institution should not be contingent on whether it is a member of a particular regional association; if an institution provides data to the studbook keeper, it should be included in the studbook, provided it can be verified. When a reliable source reports an animal's transfer to an institution that does not respond to the studbook keeper's requests for information, the transfer should be entered and the animal should be designated as lost-to-follow-up at the receiving institution (*see section 4.7.2* on how to enter lost-to-follow-up).

1.3.5 History of Studbook Software

Computerized studbook datasets have been used by zoos and aquariums for management of their populations, and studbook keepers have used a variety of software to do so. Because there are still references within PopLink to some of these, we will briefly highlight them:

- SPARKS (**Small Population Analysis and Record Keeping System**) (ISIS, 2002): developed by International Species Information System (ISIS), now obsolete
- **PopLink** (Faust et al., 2026): developed by Lincoln Park Zoo to initially serve as a bridge between SPARKS and ZIMS (versions 1.0-2.5), and eventually modified to make it more applicable to conservation and research projects (version 3.0)
- ZIMS for Studbooks (**Zoological Information Management System)** (Species360 Zoological Information Management System, 2026)**:** developed by Species360 (formerly ISIS), this is an online, centralized (i.e. multi-institution/multi-user), real-time record-keeping system used by the zoo and aquarium community.

Note that some conservation projects that have an affiliation with a zoo or aquarium use ZIMS as their studbook keeping solution. Exploring the features of both ZIMS and PopLink may be beneficial before you decide which system to use.

Chapter 2: GETTING STARTED IN POPLINK

2.1 INSTALLATION OF POPLINK

PopLink is available for download at **https://www.poplink-download.org**

SQLLocalDB is required to run PopLink; this installs automatically within the setup of PopLink.

To install PopLink, you must have administrator privileges. If you don't have administrative privileges, have an administrator install for you (see instructions in the InstallReadMe file). If you are an administrator,

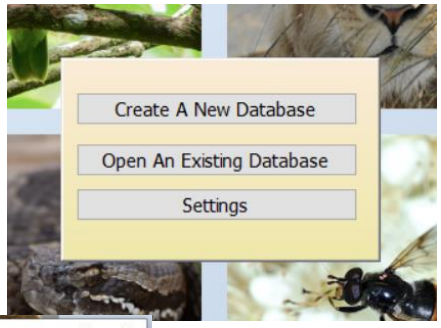
1. Download the PopLink Installer file and save it to your computer
2. Use Windows Explorer to navigate to the downloaded file (PopLinkInstaller%DATE%.exe) and double click on the file to start installation
3. Download the InstallReadMe file and follow the instructions

Once you've completed these steps, the installation automatically puts a PopLink shortcut on your desktop and you're ready to start PopLink. If you have a previously installed version of PopLink (any 2.x version), PopLink 3.0 will automatically move your studbook folders.

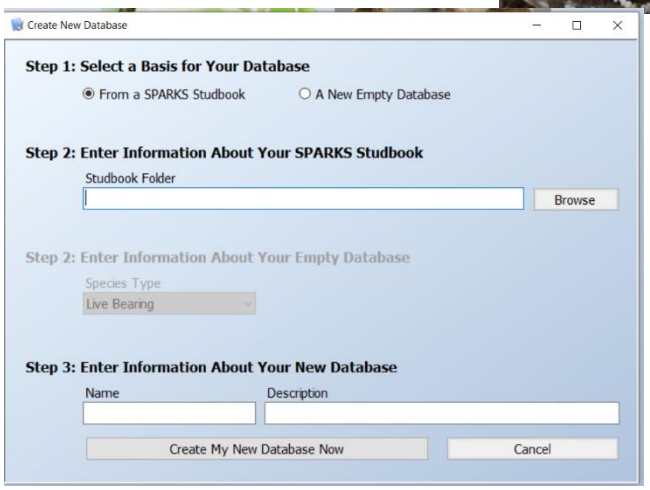
PopLink stores data in a SQL database, and "power users" who are interested in accessing and analyzing their data outside of PopLink can do so using SQL server Management Studio, which can be used to view, export, and run customized queries on the underlying database tables created by PopLink. For instructions see Appendix 2.

2.2 LAUNCHING POPLINK – USER LOGIN

When you click on the PopLink shortcut placed on your desktop during installation, the program will prompt you to login with a User ID. This can be anything (your full name, your initials, etc.), and PopLink will remember this user ID the next time you log into the program. This ID is used to track the user who made changes to the studbook database, exported data, ran reports, etc. After logging in, you have three options to choose from:



2.3 CREATING A NEW POPLINK DATABASE



New databases are created in PopLink in two ways[1]:

1. importing the desired data from an existing SPARKS studbook;
2. creating a new "empty" database within PopLink.

Under "Step 2" you can navigate to the folder with a SPARKS studbook, or for an empty PopLink database, specify whether the species is live bearing or egg laying.

Under "Step 3", enter

1. **a name** for your PopLink database. If you're importing from SPARKS the default name will be the existing file's name, which you can edit. PopLink has no character length limitations on file name, but does not allow your studbook name to start with a number or include dashes "-", spaces, slashes "\", or other restricted characters. The program may prompt you to choose a new name if your studbook name has invalid characters.
2. **a text description (**optional**)** of your new database; this is a good place to record details about the purpose of the database (e.g. "this is a database used in the June 2026 planning meeting at Lincoln Park Zoo").

When these steps are completed, click on "Create My New Database Now" to proceed.

2.4 OPENING AN EXISTING POPLINK DATABASE

Any studbooks that you've previously opened in PopLink are accessible through the Open an Existing Database button. The resulting table includes a list of all databases ordered by the last time they were modified (columns are sortable). Highlight a database and select "Open Database" at the bottom to open or "Delete Database" to remove a database from your folder.

Studbook databases created in previous versions of PopLink can be read by PopLink 3.0 and should have been automatically moved into this folder. If they are missing, please see the following section about "Changing File Storage Locations".

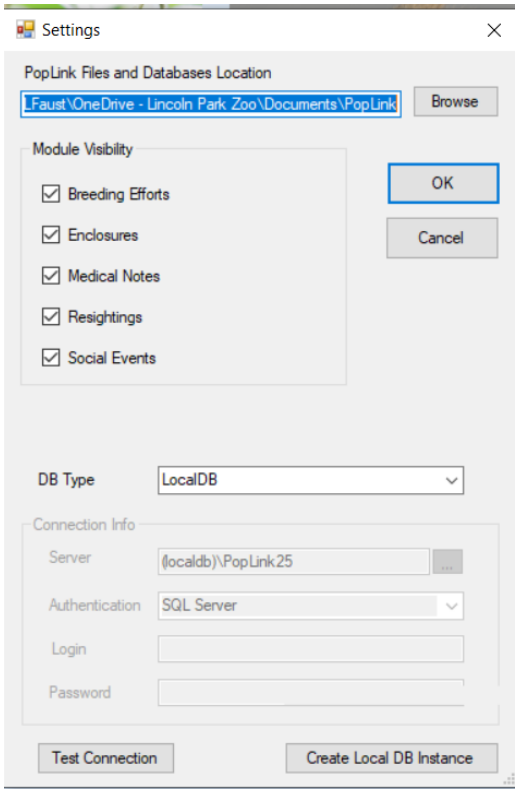
If your studbooks from previous versions of PopLink violate any of PopLink 3.0's naming restrictions, including starting with numbers or incorporating spaces, dashes, slashes, or other restricted characters, the program will prompt you that your studbook name is invalid. If this error message appears, use Windows Explorer to navigate to My Documents\PopLink\PopLink Databases and rename the studbook folder with a name that does not violate SQL naming restrictions. You can then open the studbook through the Open Databases dialogue box.

2.5 SETTINGS

The Settings pop-up allows you to specify your file location storage, allows you to turn additional data modules on/off, and has some technical information sometimes required for trouble-shooting installation problems.

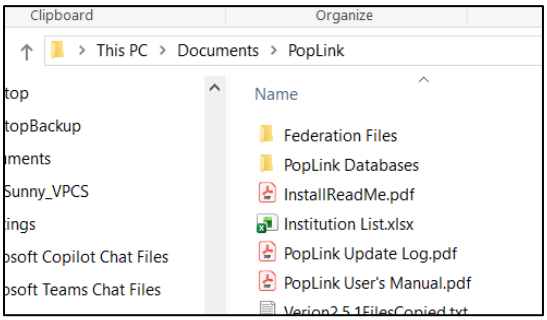
The Settings box is not studbook specific – any settings you specify are applied across any studbook you might open.

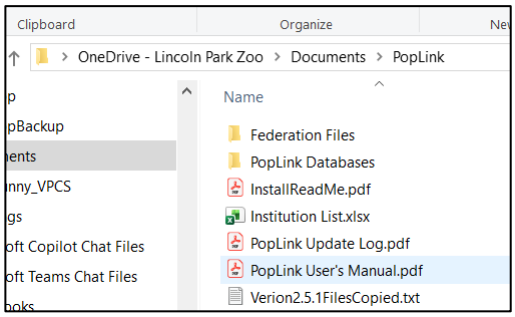
[1] While it is not included in PopLink's main import functionality, staff at Lincoln Park Zoo have the capacity to translate ZIMS databases into PopLink format. Contact software@lpzoo.org for more details.



2.5.1 PopLink Files and Databases Storage Location

PopLink's default location is in your My Documents folder (sometimes synced onto a OneDrive folder depending on your organization's and computer's setup):





2.5.2 Changing File Storage Locations

Changing file storage locations should not be done frequently – the simplest setup for you as a studbook keeper and us when we need to assist you is to leave your PopLink files stored in the default location of C:\My Documents\PopLink (which can also be described with the address C:\Users\User Name\Documents\PopLink depending on your Operating System). As many organizations have this location also synced with OneDrive or another service, the setup may be slightly different on your default installation. Changing this default location will typically not be necessary. If there is the need to move the location, you can use this Settings option to store it elsewhere on your C: drive (we suggest creating a new folder called C:\PopLink and browsing to that in the address box).

NOTE: When changing the location of your PopLink folder, all the associated files will be moved and then the files in the previous location will be *deleted*. Consequently, if you've changed the location in the past but want to set it back to the "default" of My Documents, you'll need to manually create a new folder titled PopLink in your My Documents folder (hit Browse and then use the "Make New Folder" option) and select that folder as your new location. When creating a new folder, highlight the desired location (i.e. My Documents) before selecting Make New Folder option. Make sure that when you use the "database location" box you're pointing to a main PopLink folder, not your PopLink databases folder, to avoid confusing folder imbedding.

2.5.3 Module Visibility

The Module Visibility feature allows you to show or hide any of the optional modules (Breeding Efforts, Enclosures, Medical Notes, Resightings, Social Events). When selected, the module's data tables will be visible and editable within PopLink and the associated reports will show up in the Reports menu. When unchecked, the module and its reports are hidden. No data are deleted or lost when a module is hidden; when toggled back on, all the data previously entered will still be present. As a default, all extra modules are unselected and not shown. Once selected, those settings will remain every time you open any studbook.

Note that the Settings functionality can also be accessed from the Edit dropdown menu, although you cannot change the file storage location while you have a database in PopLink open.

2.5.4 Advanced Settings

The advanced settings at the bottom were added to better handle different instances of SQL. The default setting for PopLink in DB Type of the Advanced settings is "LocalDB". "Existing SQL Express" along with the server name "(localdb)\PopLink25" and user login and password is for users with an existing copy of Microsoft SQL installed on their computer or network. "Existing SQL Server" along with the server name "(localdb)\PopLink25" and user login and password is for users with an existing copy of the full version of SQL Server already installed.

2.6 SAVING, BACKING-UP, MOVING, DELETING AND ACCESSING POPLINK DATABASES

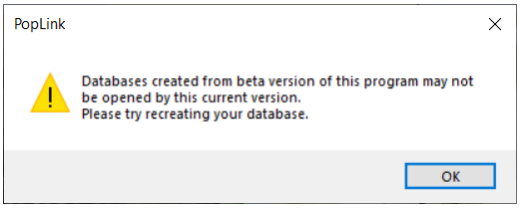
PopLink automatically saves any database you are working in; you never have to formally save your studbook while you are working on it or before exiting.

It is a very good idea to create backups of your database in external secure locations (in case of computer crash) or archiving versions over time in case of file corruption or data entry errors. The easiest way to create a backup (e.g. a copy) of your database is to use the "Backup Database" menu option under the File drop-down menu. The default backup location places the database in a folder on your desktop; this folder can then be zipped and emailed, moved to a network folder, etc.

You can move your PopLink databases using Windows Explorer by locating the studbook you want to move in C:\My Documents\PopLink\PopLink Databases. To move the studbook(s), copy and paste the studbook's folder between one computer's PopLink Databases folder and the other.

A quick way to just move the database and not all the associated files (reports, import files, etc.) can also be to copy the data.bin file from your studbook folder – this is a compressed data format that can typically easily be attached to an email. Just remember that any associated information with the studbook (archived files with data import, copies of reports that have been run and exported, data exports) will not be moved with this technique. You can paste the data.bin into a new folder you create within My Documents\PopLink\PopLink Databases and open it like any of your other studbooks through Open Existing Databases.

To delete a database, use the Delete function in the Open Database dialogue box. If you end up deleting a database through Windows Explorer, follow the instructions in Appendix 2, Deleting a Database to remove it from SQL Server as well.



If you ever get this error message, be reassured that your database is openable and PopLink may just be having a slight challenge with its SQL connection. To deal with this error message, 1) go to your studbook folder (My Documents\PopLink\PopLink Databases), 2) create a new, empty folder and give it a unique name for your studbook, 3) navigate in the same PopLink Databases folder to the studbook you were unable to open and copy the data.bin file, 4) paste the data.bin file into the new studbook folder you just created, 5) open it as normal through the Open Existing Databases dialogue box.

2.7 CHECKLIST FOR STUDBOOK KEEPERS STARTING A STUDBOOK

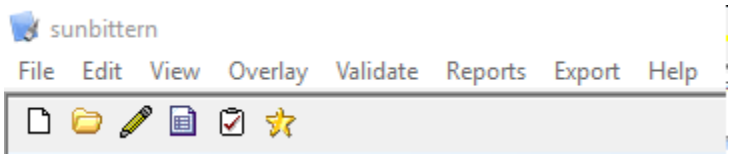
When you start using PopLink, there are a few important steps:

1) If you have any questions about how to best store or design your studbook configuration, discuss them with a population biology advisor (including contacting the PopLink creators at software@lpzoo.org), as there may be multiple ways to track information important to your population. This might include:
    a. Defining the "extra" user defined fields (UDFs) that you want to track for your population
    b. Adding any extra Locations that might not be part of PopLink's main Locations List
    c. Deciding whether you're going to use the extra data modules and how they should be configured
    d. Deciding on important data conventions you may use across your dataset and document in your Studbook Overview
2) To get your animals into your studbook you can,
    a. Enter your population's data directly (see Chapter 4) or
    b. Import your core population data and make edits to the imported records to provide additional information on the animals (see section 4.8)
3) If desired, you can also import additional data into your studbook to streamline data entry, including UDF data and data in the Breeding Efforts and Resightings modules (see Chapter 4)
4) After you've gotten some or all of your data into PopLink, run PopLink data validation and address errors as appropriate (see Chapter 6)

Chapter 3: VIEWING AND MANAGING DATA IN POPLINK

3.1 ORIENTATION

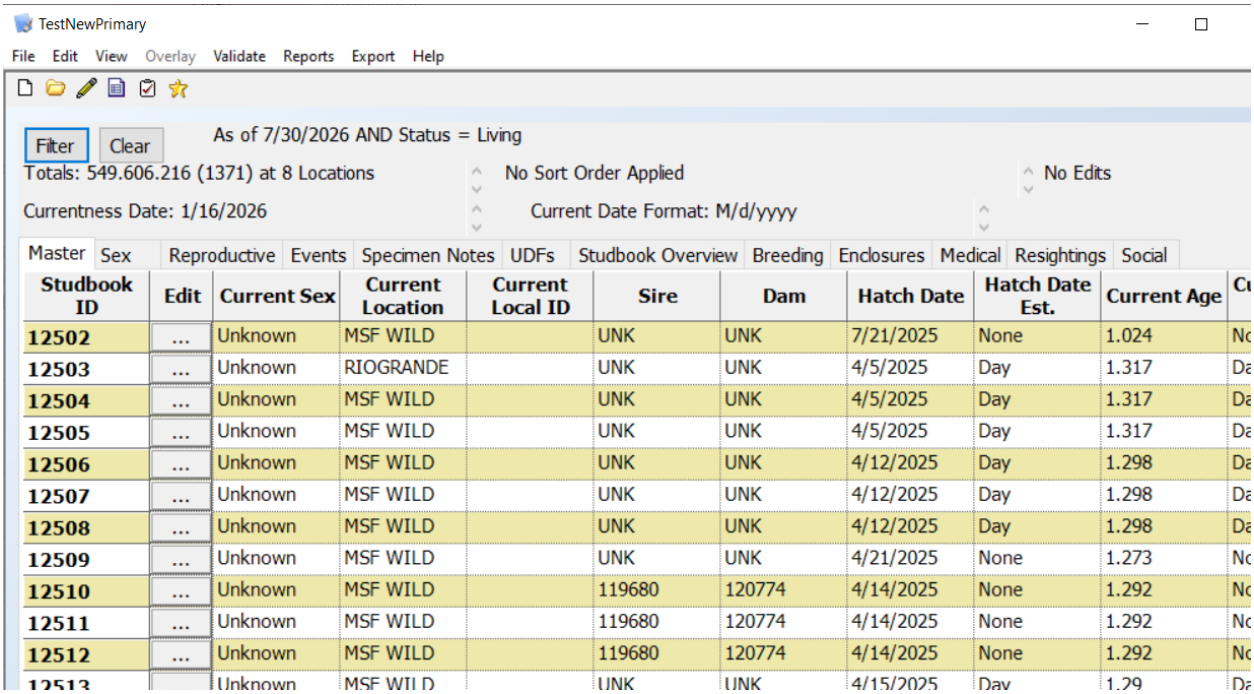
Once a database has been created and opened, PopLink will open its main program window; important program functions can be found in the upper left-hand corner:



PopLink displays the studbook name in the upper left-hand corner of the window. The eight pull-down menus directly below the blue bar can be used to navigate throughout the program. The shortcut buttons below the menu functions can be used to (in order from left to right): Create a New Studbook, Open an Existing Studbook, Edit an Animal's Record, View Data (i.e., jump to the studbook viewer), Run Data Validation, or View an Animal Report.

3.2 STUDBOOK VIEWER

Once a database has been created and opened, PopLink will display the Master data table in the Studbook Viewer window:



Studbook ID	Edit	Current Sex	Current Location	Current Local ID	Sire	Dam	Hatch Date	Hatch Date Est.	Current Age	Cu
12502	...	Unknown	MSF WILD		UNK	UNK	7/21/2025	None	1.024	No
12503	...	Unknown	RIOGRANDE		UNK	UNK	4/5/2025	Day	1.317	Da
12504	...	Unknown	MSF WILD		UNK	UNK	4/5/2025	Day	1.317	Da
12505	...	Unknown	MSF WILD		UNK	UNK	4/5/2025	Day	1.317	Da
12506	...	Unknown	MSF WILD		UNK	UNK	4/12/2025	Day	1.298	Da
12507	...	Unknown	MSF WILD		UNK	UNK	4/12/2025	Day	1.298	Da
12508	...	Unknown	MSF WILD		UNK	UNK	4/12/2025	Day	1.298	Da
12509	...	Unknown	MSF WILD		UNK	UNK	4/21/2025	None	1.273	No
12510	...	Unknown	MSF WILD		119680	120774	4/14/2025	None	1.292	No
12511	...	Unknown	MSF WILD		119680	120774	4/14/2025	None	1.292	No
12512	...	Unknown	MSF WILD		119680	120774	4/14/2025	None	1.292	No
12513		Unknown	MSF WILD		UNK	UNK	4/15/2025	Day	1.29	Da

In addition, you can six different data tables accessible via tabs: Master, Sex, Reproductive, Events, Specimen Notes, User Defined Fields (UDFs), and the Studbook Overview. In addition, if you opted to show them using the Settings pop-up, you will also see the Social, Enclosures, Medical, Breeding, and Resightings tables. These tables can be returned to from any other screen by selecting "Translated Data" from the "View" drop-down menu or clicking on "View Data" shortcut button.

Above the data, PopLink reports 1) what filters are being applied to the data (see Chapter 5 for more details on filters), 2) the total numbers of individuals in the current filtered data, denoted as Males.Females.Unknown/Other (Total), 3) the total number of locations for animals in the current filtered data, 4) whether the table has been sorted

from its original order, 5) which animals have been edited in the current session, 6) the currentness date for the studbook, and 7) the current date format used by PopLink (based on your computer's settings)

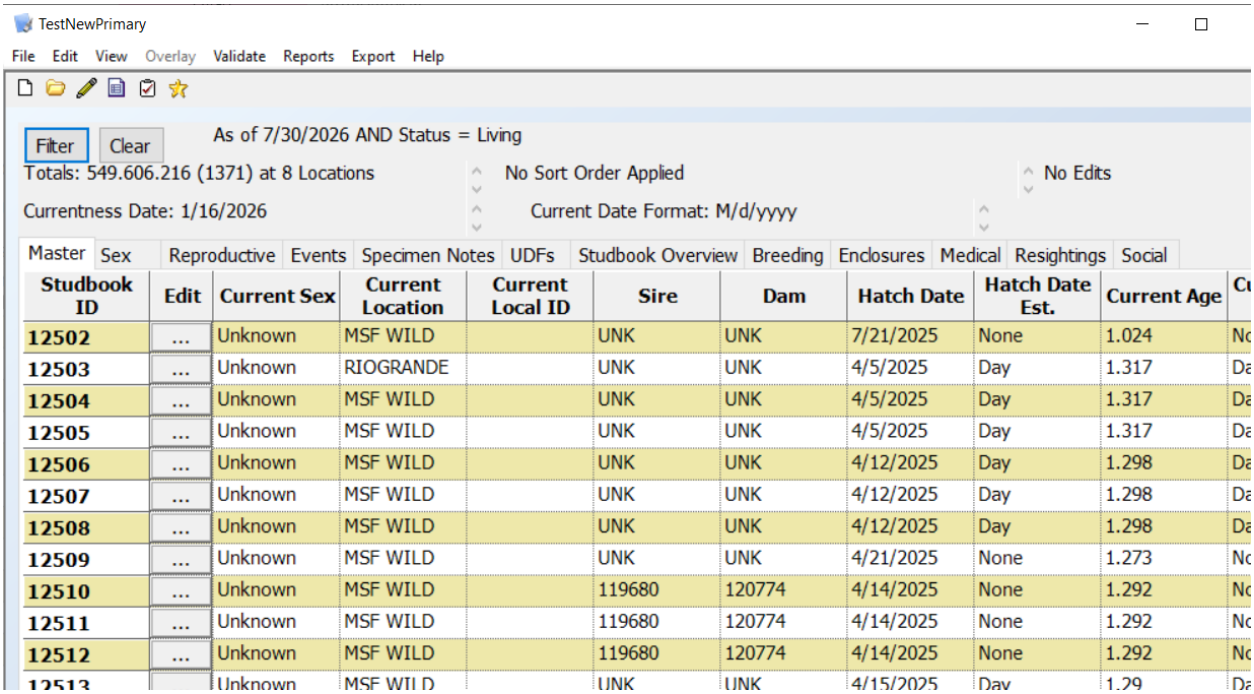
NOTE: In any data table and most reports, double-clicking on an animal's Studbook ID will pop up an Individual Animal Report which displays the entire record for that individual.

Edits can be made to an animal's record by clicking on the Edit button directly to the right of its Studbook ID button or on the Individual Animal report (for more details, see Chapter 4).

In most data tables (including those displayed in reports), you can right-click anywhere in the table and select "Export to Excel", which will automatically pop-up a spreadsheet version

Data in the Studbook Viewer can be sorted by clicking on the column headers at the top of any field. By default, entries are displayed in ascending numerical order of Studbook ID. Clicking once on a column header will sort the entries in ascending order; clicking again will sort the entries in descending order. Fields with both numeric and alphabetic entries will sort numeric entries before alphabetic entries. When a field is selected for sorting, its button will have an arrow indicating whether the sorting is in ascending or descending order. **Note that data can only be sorted by one column at a time; no "double-sorting" occurs.**

3.3 MASTER DATA TABLE



Studbook ID	Edit	Current Sex	Current Location	Current Local ID	Sire	Dam	Hatch Date	Hatch Date Est.	Current Age	Cu
12502	...	Unknown	MSF WILD		UNK	UNK	7/21/2025	None	1.024	No
12503	...	Unknown	RIOGRANDE		UNK	UNK	4/5/2025	Day	1.317	Da
12504	...	Unknown	MSF WILD		UNK	UNK	4/5/2025	Day	1.317	Da
12505	...	Unknown	MSF WILD		UNK	UNK	4/5/2025	Day	1.317	Da
12506	...	Unknown	MSF WILD		UNK	UNK	4/12/2025	Day	1.298	Da
12507	...	Unknown	MSF WILD		UNK	UNK	4/12/2025	Day	1.298	Da
12508	...	Unknown	MSF WILD		UNK	UNK	4/12/2025	Day	1.298	Da
12509	...	Unknown	MSF WILD		UNK	UNK	4/21/2025	None	1.273	No
12510	...	Unknown	MSF WILD		119680	120774	4/14/2025	None	1.292	No
12511	...	Unknown	MSF WILD		119680	120774	4/14/2025	None	1.292	No
12512	...	Unknown	MSF WILD		119680	120774	4/14/2025	None	1.292	No
12513		Unknown	MSF WILD		UNK	UNK	4/15/2025	Day	1.29	Da

The Master data table summarizes basic information on the animals in the studbook database. Some of the fields in this table (Studbook ID, Sire, Dam, Birth Type, Birth Date, Birth Date Estimate, Rearing, Owner) are based on data entered directly into the Master table; all other fields (Estimated Conception Date, Current Sex, Current Reproductive, Current Status, Current Location, Current Age, Current Age Est., Current House Name, Current Local ID, Last Resighting and Current Enclosure) are based on data entered into the other tables in your dataset (e.g. the Sex table, the Events table, and the Enclosures and Resightings tables if they are shown, etc.).

For more details on how to enter data into specific Master Data Table fields, see Chapter 4. A few notes on how PopLink fills in specific fields:

3.3.1 Estimated Conception Date

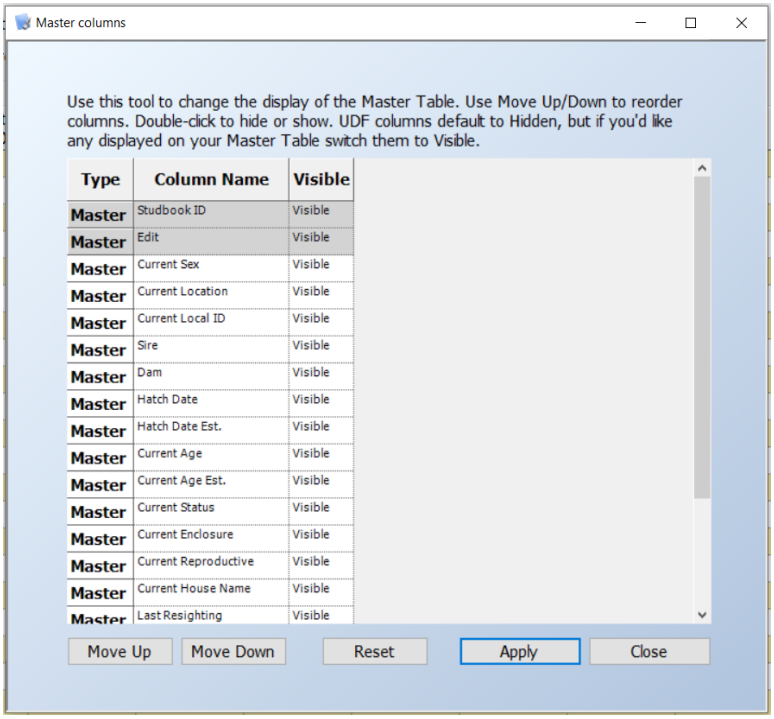
PopLink reports the estimated conception date to aid population managers in their attempt to identify unknown parentage. The conception date is calculated based on that animal's birthdate (and estimate) and the gestation period entered during studbook creation (which can be edited in the Studbook Overview Data Table). This date should be viewed as a general guide of when conception may have taken place and will have the same date estimator (i.e. the same level of certainty) as the birthdate's estimator.

3.3.2 All "Current" Fields

These fields (e.g., "Current Sex," "Current Location") display the **current** (for living individuals) or **last** (for dead, lost-to-follow-up, or released individuals) information for any given field. Note that, if you set an As Of date filter (see Chapter 5 for more details), these fields do not reflect the "current" status as of that date, but the current status as of today's date. If an animal has a completely unknown birthdate, age cannot be calculated and the Current Age field will display "---". The "Current Enclosure" field is based on data in the Enclosures table if relevant records exist for an individual (these data are optional and may not be tracked in all studbooks). If there are no relevant enclosure records, this field will display "Not Reported"; if an animal has some Enclosure records but none are current/last, this field will display "None Current".

3.3.3 Edit → Master Display Fields

If you'd like to change the order of fields displayed in the Master table or hide some fields that are not relevant to your studbook, you can do so in the Edit menu by selecting Master Display Fields. In the dialogue box, you can toggle fields from visible to hidden (and back) by double clicking on them. Reorder fields using Move Up/Down and hit Apply. Your setup will be saved and shown the next time you open your studbook.



3.4 SEX DATA TABLE

Filter Clear As of 7/30/2026 AND Status = Living
Totals: 551.609.364 (1524) at 8 Locations Sorted by: Studbook ID Ascending
Currentness Date: 1/30/2026 Current Date Format: M/d/yyyy

Master | Sex | Reproductive | Events | Specimen Notes | UDFs | Studbook Overview | Breeding | E

Studbook ID	Edit	Sex	Event Date	Event Date Est.	Current House Nam
12502	...	Unknown	7/21/2025	None	
12502	...	Female	8/30/2025	None	
12503	...	Unknown	4/5/2025	None	
12504	...	Male	4/5/2025	Day	
12505	...	Unknown	7/21/2025	None	
12506	...	Abnormal	7/21/2025	None	
12507	...	Unknown	7/21/2025	Unknown	
12508	...	Unknown	4/12/2025	Day	

The Sex data table displays all sex events of each animal, including the recorded Sex, the Event Date for when sex was determined, and the Event Date Estimate. PopLink recognizes five different possibilities for Sex status: Female, Male, Unknown, Abnormal, and Hermaphrodite.

The sex of an animal in PopLink is treated as an event stream rather than a constant state, since the sex status of an individual can change during its life. Many animals may only have a single entry in the Sex Data Table (i.e. animals could be reliably sexed from birth); however, animals that are not sexually dimorphic or where sex is not easily identifiable at birth could initially be classified as Unknown until genetic testing or reproductive maturity confirms the sex. In a case where an animal's sex is initially unknown or misidentified, an animal would have multiple entries in the sex data table. For example, in the table above animal 12502 was unsexed at birth and was determined to be female after genetic testing on 8/30/2025. Treating sex as an event stream also enables PopLink to accommodate species where sex can change over their lifetimes.

3.5 REPRODUCTIVE DATA TABLE

Filter Clear As of 7/30/2026 AND Status = Living
Totals: 551.609.364 (1524) at 8 Locations No Sort Order Applied
Currentness Date: 1/30/2026 Current Date Format: M/d/yyyy

Master | Sex | Reproductive | Events | Specimen Notes | UDFs | Studbook Overview | Breeding | Enclosur

Studbook ID	Edit	Reproductive	Event Date	Event Date Est.	Current House Nam
12502	...	Not Contracepted	7/21/2025	None	
12502	...	Neutered/Sterile	7/30/2026	None	
12503	...	Not Contracepted	4/5/2025	None	
12504	...	Not Contracepted	4/5/2025	Day	
12505	...	Not Contracepted	7/21/2025	None	
12506	...	Not Contracepted	7/21/2025	None	
12507	...	Not Contracepted	7/21/2025	None	
12508	...	Not Contracepted	4/12/2025	Day	

The Reproductive Data table can be used to track changes in the reproductive status of individual animals. It displays all reproductive status events of each animal, including the Reproductive Status, the Event Date for when reproductive status was assessed, and the Event Date Estimate. PopLink recognizes three different possibilities for Reproductive status: Not Contracepted, Contracepted, and Neutered/Sterile.

Like Sex, reproductive status is treated as an event stream rather than a constant state in PopLink because it can change throughout an animal's life. Most animals will be entered with a not contracepted status at birth, but throughout their lives could be placed on and removed from contraception multiple times.

3.6 EVENTS DATA TABLE

Filter Clear As of 7/30/2026 AND Status = Living

Totals: 551.609.364 (1524) at 8 Locations No Sort Order Applied

Currentness Date: 1/30/2026 Current Date Format: M/d/yyyy

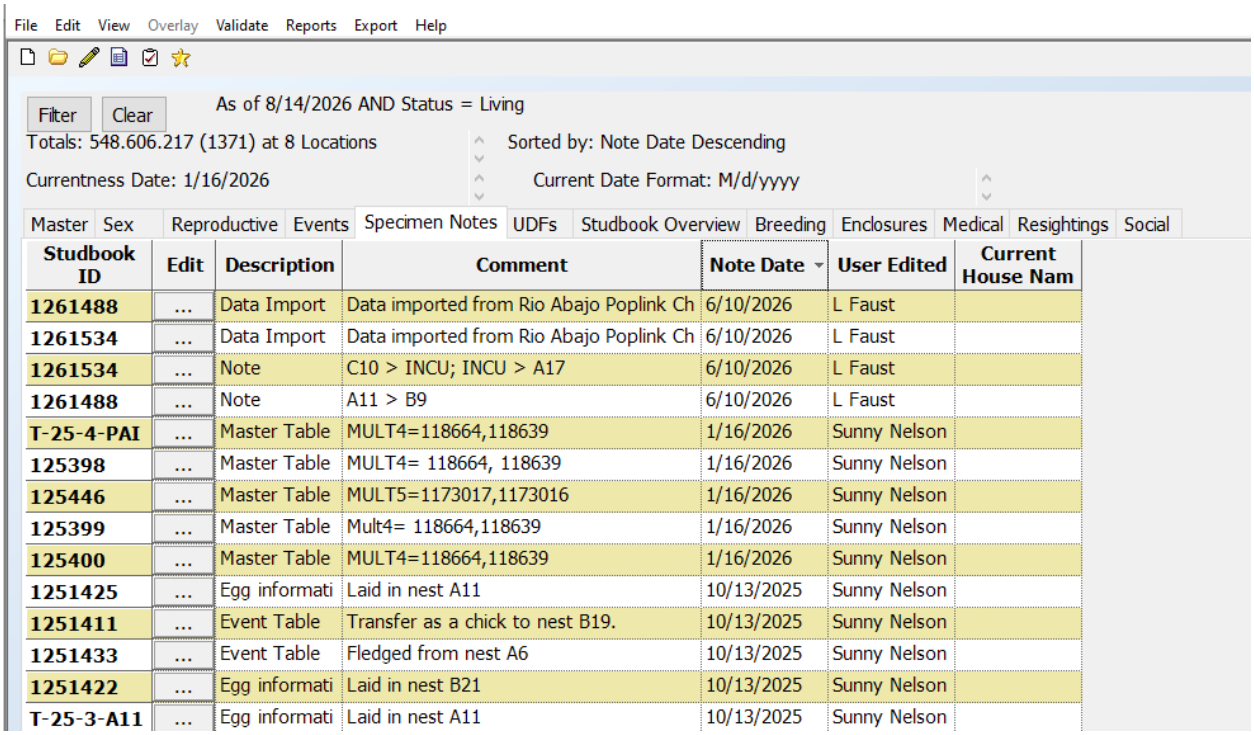
Master Sex Reproductive Events Specimen Notes UDFs Studbook Overview Breeding Enclosures Medical Resightings Social

Studbook ID	Edit	Transaction Code	Location	Local ID	Transaction Date	Transaction Date Est.	Current House Nam
100201	...	Hatch	RIOGRANDE	100201	7/2/2000	Year	
100201	...	Transfer	EY WILD	100201	7/3/2000	Year	
100203	...	Hatch	RIOGRANDE	100203	7/2/2000	Year	
100203	...	Transfer	EY WILD	100203	5/18/2001	None	
100207	...	Hatch	RIOGRANDE	Quebrado	4/6/2000	None	
100209	...	Hatch	RIOGRANDE	100209	4/11/2000	None	
100209	...	Transfer	ARECIBO		2/1/2001	None	
100209	...	Transfer	MARICAO		12/14/2021	None	
100209	...	Transfer	RIOGRANDE	NONE	2/27/2024	None	
100209	...	Transfer	MARICAO	NONE	3/27/2024	None	
100210	...	Hatch	ARECIBO	100210	5/9/2000	None	
100211	...	Hatch	RIOGRANDE	100211	7/2/2000	Year	

The Events Data Table lists, in chronological order by animal, all events that have occurred for each animal in the dataset. Information in the Events data table includes **Transaction Code** (i.e., "Event type"), **Location** (of the transaction), **Local ID** (of the animal, when included), **Transaction Date**, and **Transaction Date Estimate**. PopLink recognizes eight different Event types: Captive Birth, Wild Capture, Transfer (to another location), Release (into the wild), Recapture (from the wild), Death, Go LTF (Lost-to-Follow-Up), and Return From LTF.

Note that when data are filtered (see Chapter 5), if an animal fits into a given filter (e.g. living in between 1/1/1990 and 1/1/2026), all of that animal's events will be displayed in this table, even if the events occurred outside the filter date range.

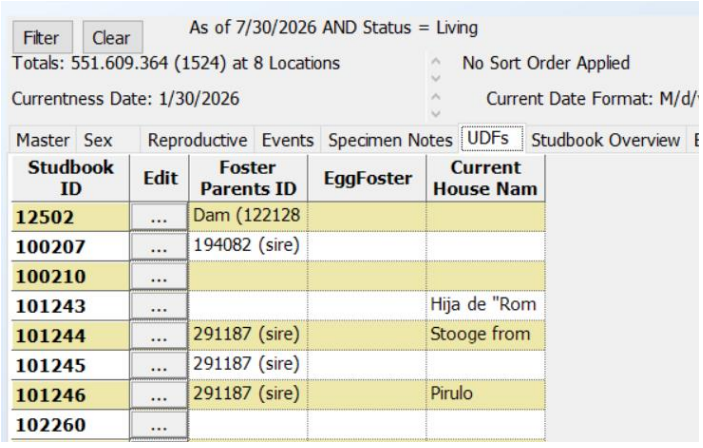
3.7 SPECIMEN NOTES DATA TABLE



Studbook ID	Edit	Description	Comment	Note Date	User Edited	Current House Nam
1261488	...	Data Import	Data imported from Rio Abajo Poplink Ch	6/10/2026	L Faust	
1261534	...	Data Import	Data imported from Rio Abajo Poplink Ch	6/10/2026	L Faust	
1261534	...	Note	C10 > INCU; INCU > A17	6/10/2026	L Faust	
1261488	...	Note	A11 > B9	6/10/2026	L Faust	
T-25-4-PAI	...	Master Table	MULT4=118664,118639	1/16/2026	Sunny Nelson	
125398	...	Master Table	MULT4= 118664, 118639	1/16/2026	Sunny Nelson	
125446	...	Master Table	MULT5=1173017,1173016	1/16/2026	Sunny Nelson	
125399	...	Master Table	Mult4= 118664,118639	1/16/2026	Sunny Nelson	
125400	...	Master Table	MULT4=118664,118639	1/16/2026	Sunny Nelson	
1251425	...	Egg informati	Laid in nest A11	10/13/2025	Sunny Nelson	
1251411	...	Event Table	Transfer as a chick to nest B19.	10/13/2025	Sunny Nelson	
1251433	...	Event Table	Fledged from nest A6	10/13/2025	Sunny Nelson	
1251422	...	Egg informati	Laid in nest B21	10/13/2025	Sunny Nelson	
T-25-3-A11	...	Egg informati	Laid in nest A11	10/13/2025	Sunny Nelson	

The Specimen Notes Table is used to record important text information about specific animals as text notes. A given animal may have no Notes (and will therefore not show up in this table) or one or more Notes. The **Description** displays the type of note (based on pre-existing note types). The **Comment** field is a text box of unlimited length. The **Note Date** field can be edited by the user to reflect the relevant date for each animal note and the **User Edited** field gives the source of the comment. For changes PopLink makes to the data during importation (e.g. separating sex and reproductive status), the description will display 'PopLink Assumption Note', comments will explain the changes in the translated data, and the user will be whomever was logged into PopLink when the database was created.

3.8 USER DEFINED FIELDS DATA TABLE



Studbook ID	Edit	Foster Parents ID	EggFoster	Current House Nam
12502	...	Dam (122128		
100207	...	194082 (sire)		
100210	...			
101243	...			Hija de "Rom
101244	...	291187 (sire)		Stooge from
101245	...	291187 (sire)		
101246	...	291187 (sire)		Pirulo
102260	...			

The User Defined Fields (UDF) Table contains any UDFs created for the population. UDFs allow the studbook keeper great flexibility to track things important to their population, or to define subsets of the population to analyze or filter. UDFs can be used to identify subspecies, color phases, hybrids, chromosome type, IDs of related individuals (mates, foster parents, etc.), disease status, or any other trait that can be tracked as a single field per animal. With

a UDF the user can define a specific subset of the data for analysis. For example, once identified with a UDF, the studbook keeper can analyze just one subspecies out of the entire studbook database. Use of several UDFs simultaneously will allow a creative studbook keeper to divide the database into a wide range of subsets for analysis.

Some UDFs will remain constant over an animal's entire lifespan. Subspecies would usually be such a UDF, unless the animal was misidentified or the subspecies definition was to change. However, some UDFs may change with time (e.g., nonproven parent to proven parent). When using UDFs, it is extremely important to keep them up to date if their status changes. It is best to avoid adding UDFs that will change frequently unless they are very important; the UDF is only as useful as the studbook keeper's ability to keep it up-to-date.

3.9 STUDBOOK OVERVIEW

Master | Sex | Reproductive | Events | Specimen Notes | UDFs | Studbook Overview | Breeding | Enclosures | Medical | Resightings | Social

Name	Edit	Value
PopLink Version		3.0.1
Studbook Description	...	January 2026 updates for LF
Studbook Keeper	...	Sunny Nelson
Studbook Keeper Location	...	Sunny Nelson
Studbook Keeper Email	...	snelson@lpzoo.org
Studbook Scope	...	Puerto Rican Aviaries
Class	...	Aves
Order	...	Psittaciformes
Family	...	Psittacidae
Scientific Name	...	Amazona Vittata
Common Name	...	PUERTO RICAN PARROT
	...	POPLINK STUDBOOK CONVENTIONS FOR THE PUERTO RICAN PARROT LOCATIONS USFW PRPR = El Yunque captive population - Iguaca Aviary (formerly Luquillo Aviary); 3-letter acronym = EYC EL YUNQUE = El Yunque National Forest wild population; EYW ARECIBO = Rio Abajo captive population - José L. Vivaldi Memorial Aviary; RAC

The Studbook Overview contains data on your database's history and status. Any fields that are editable are denoted with an "Edit" button. The **Species Notes** field is an important place to document essential information about your studbook's conventions, history, problems or data errors, or other essential information. The format of *Species Notes* is text, which allows for complex and detailed explanations. Because the information in *Species Notes* travels with the studbook database, it helps interpretation of the data by population managers, future studbook keepers, and others who may work with the dataset. Every major assumption and every convention should be documented in this section.

3.10 BREEDING EFFORTS TABLE

Master | Sex | Reproductive | Events | Specimen Notes | UDFs | Studbook Overview | Breeding | Enclosures | Medical | Resightings | Social

Edit	Breeding Individuals	Breeding Location	Breeding Location Discovery Date	Breed Start Date	Start Date Est.	Breed End Date	End Date Est.	Pregnancy Confirmed
...	190,191	Room 1	7/5/2024	7/1/2024		7/30/2024		7/15/2024
...	143,149	Room 2	7/3/2025	7/1/2025		7/30/2025		7/15/2025
...	185,186	Room 1	7/8/2026	7/1/2026		7/30/2026		7/25/2026

Historically, it has been difficult to get a complete picture of breeding activity using studbook data alone. While we can see that a pair produced offspring (as long as those offspring were assigned a studbook ID), we are missing additional information of the broader breeding story, and many important details were not historically captured in studbook data. The data in the Breeding Efforts Table helps fill in these gaps, allowing users to build a more complete understanding of breeding outcomes by helping to answer questions like: What proportion of a population's reproductive-aged animals were attempting to breed? How long was a pair given physical access to each other during the breeding season? If a pair did not produce living offspring, did they produce eggs, and were any of those eggs fertile? Do pairs produce more offspring when using a specific nest box or breeding enclosure? The Breeding Efforts table contains different fields for egg-laying and live-bearing taxa. For more information on the data and data conventions specific to the Breeding Efforts module, please see *section 4.15*. **This module is optional and can be hidden/shown using the Settings option from the Edit menu.**

NOTE: Because breeding effort events by definition involve multiple individuals, this table is *event-based* rather than individual-based like the rest of the data tables. In the Breeding data table, there are multiple Studbook IDs on the far left of the table, and the event will be shown in all included individual's records. When you select the edit button for a specific event from the Breeding data table, the edit data screen that appears will be for the anchor animal. The event can also be edited through any of the Breeding Individual's records. When edited, an event will be updated in all animals' records.

3.11 ENCLOSURES DATA TABLE

Master | Sex | Reproductive | Events | Specimen Notes | UDFs | Social | Enclosures | Medical | Studbook Overview

Studbook ID	Edit	Enclosure Name	Enter Date	Enter Date Est.	Exit Date	Exit Date Est.	Comment
64	...	Holding 1 (CHICAGOLP)	1/1/2005	None	3/23/2009	None	
64	...	Exhibit B (CHICAGOLP)	3/23/2009	None		None	moved for breeding intro
70	...	Holding 2 (CHICAGOLP)	1/1/2010	None	5/12/2010	None	
70	...	Exhibit A (CHICAGOLP)	5/12/2010	None		None	
73	...	Exhibit C (CHICAGOLP)	7/12/2010	None		None	

The Enclosure Data Table allows you to track the enclosure, and thus social group history, of the animals within your studbook. These data help to answer questions such as "what enclosures has Animal #23 lived in over their life?", "who have they lived with", and "who are they living with now?". The implications of these data are far reaching – from gauging the social aptitude of an individual to tracing possible disease contacts. If maintained consistently for a studbook or even a subset of a studbook (e.g. a single institution with a large portion of the population), it can contain a wealth of useful information. Some programs have also used this module with animals in the wild to track as they transition between social groups rather than physical enclosures. **This module is optional and can be hidden/shown using the Settings option from the Edit menu.**

Information in the Enclosure Data Table includes the **Enclosure Name,** which is pre-defined using the User Defined Enclosures functionality (*see section 4.13*). **Enter dates, Exit dates**, **Date Estimates,** and any desired **Comments** on the specifics of the move into the enclosure. Each individual can have multiple Enclosure records over its lifetime.

3.12 MEDICAL TABLE

Master | Sex | Reproductive | Events | Specimen Notes | UDFs | Social | Enclosures | Medical | Studbook Overview

Studbook ID	Edit	Category	Type	Value	Unit of Measure	Start Date	End Date	Observer	Comment
716	...	Diagnostics	Culture	.	.	1/1/1995	.	tg	rectal culture collected during routine
716	...	General Medic	.	.	.	1/1/1998	.	tg	regurgitation commonly seen, vet say
716	...	Medical Alert	Permanent	.	.	1/1/2003	.	tg	ALLERGY - peanuts (no peanut butter
716	...	Medical Proced	Medical Exam	.	.	1/1/2005	.	tg	yearly physical: weight, blood, culture
716	...	Medication	Vaccine	200	Milligram(s	1/1/2005	.	tg	VACCINE - flu shot delivered during y
716	...	Weight	.	110	Pound(s)	1/1/2005	.	tg	weight at yearly physical

The Medical Data Table allows you to track important medical records for individuals. This is not meant to be a replacement for a full medical record-keeping system but can be a useful tool in tracking major events in an animal's health, as well as medical information relevant to population management and daily care, and may be useful for studbook keepers who don't have access to more robust paid veterinary records systems. Having this type of information easily accessible can facilitate timely answers for health-related questions and medical emergencies. **This module is optional and can be hidden/shown using the Settings option from the Edit menu.**

Information in the Medical Data Table is organized by **Category,** which describes one of eight different kinds of medical notes (Clinical Sign, Diagnostics, Disease Status, General Medical Note, Medical Alert, Medical Procedure, Medication, and Weight). The **Type** field gives more details specific to each Category. The **Value**, **Unit of Measurement** and **End Date** only appear for specific note Categories and only appear as options when appropriate. The **Start Date**, **Observer**, and **Comment** appear for every note Category and Type. Each individual can have multiple Medical records over its lifetime.

3.13 RESIGHTINGS TABLE

Master | Sex | Reproductive | Events | Specimen Notes | UDFs | Studbook Overview | Breeding | Enclosures | Medical | Resightings | Social

Studbook ID	Edit	Resighting Date	Site #	Resighting Notes
185	...	5/22/2026	6	Ear tag damaged
185	...	6/15/2026	4	With dominant male

Regular monitoring of free-ranging animals is essential for assessing a population's demographic status. The ability to identify individual animals based on unique features (e.g., tiger stripe patterns) or human-applied markers (ear tags, bands, VHF collar, etc.), enables the tracking of resightings in the field. Data stored in the Resightings Table allow users to efficiently enter, store, view and export sightings data for individual studbook animals. For more information on the data and data conventions specific to the Resightings module, please *see section 4.16*. **This module is optional and can be hidden/shown using the Settings option from the Edit menu.**

3.15 SOCIAL DATA TABLE

Master | Sex | Reproductive | Events | Specimen Notes | UDFs | Social | Enclosures | Medical | Studbook Overview

Edit	Event	Event Date	Date Est.	Outcome	Comment	Related Specimen		
...	Altercation	2/6/2012	None	-	spat over treats las	976	1129	
...	Breeding Inte	3/20/2012	None	+	Solicited Hank, suc	716	979	
...	Introduction -	1/1/1996	None	+	prosocial grooming	185	304	1029

The Social Data Table allows you to track the social interactions for individuals within your studbook, if desired. This module enables tracking over time of major social events, which individuals are involved, and the event's general outcomes. These types of data can be useful when trying to answer questions like: "have these two individuals been

introduced before?", or "are they behaviorally compatible?". This module can also be helpful when tracking breeding compatibility and competency if it is consistently used to record breeding behavior and outcomes. This can help answer questions such as: "who has this individual shown breeding behaviors towards?", "how closely is this pair bonded," or "at what age did an individual first start exhibiting breeding behaviors?". **This module is optional and can be hidden/shown using the Settings option from the Edit menu.**

Information in the Social Data Table includes the **Event,** which includes six event types: Introduction (visual, physical/restricted, and full), Altercation, Breeding Interaction, Prosocial, and Other. For each event, you also track the **Event Date**, **Date Estimate, Outcome** (+, -, or 0 for neutral), and any desired **Comment** on the specifics of the event. In addition, it lists the **Related Specimens** who were involved in the event. Clicking on each Related Specimen will pop-up an individual's Animal Report.

The way event types are used may vary from studbook to studbook depending on the important social interactions and behaviors of a species; if tracking and analyzing these data, be sure to be consistent within your studbook and record your conventions in the Studbook Overview Notes section.

NOTE: Because social events by definition involve multiple individuals, the Social table is *event-based* rather than individual-based like the rest of the data tables. In the Social data table, there is no Studbook ID on the far left of the table; instead, each row represents a unique social event that encompasses multiple animals. Each event is anchored in the individual animal's record in which the event was originally created. When you select the edit button for a specific social event from the Social data table, the edit data screen that appears will be for the anchor animal. The event can also be edited through any of the Related Specimens' records. When edited, a Social event will be updated in all Related Specimens' records.

3.16 OTHER DATA TABLES STORED IN POPLINK

In addition to the main data tables that comprise your studbook database, PopLink stores some additional Data Tables:

1. ***Location List***
   In the File pull-down Menu, you can select the option to look at the complete Location List, which is based on the most recent location list from Species360 (current as of January 2026). It contains names, addresses, and contact information for all locations with mnemonics (character code for each institution of up to 9 characters).

   Although this location list is easily viewed in PopLink, the current version does not include a search function to easily look up mnemonics or other location data, and the table is slow to load. We've included it as an *Institution List.xls* file in your PopLink folder (unless otherwise specified, found as a default in My Documents\PopLink), which you can open in Excel and easily search using the "Find" function (Ctrl-F).

2. ***Deleted Translated Data Table***
   In the View pull-down Menu, you can select the option to view tables of any information that you deleted during past editing. For more information on this table, *see section 4.17.1*.

3. ***User-Defined Locations Table***
   In the View or Edit pull-down Menus, you can select the option to view a table of User-Defined Locations. For more information on this table, *see section 4.7.3*.

4. ***User-Defined Fields Table***

In the Edit pull-down Menu, you can select the option to view a table of User-Defined Fields. For more information on this table, *see section 4.10*.

5. ***User Defined Enclosures Data Table***
   In the Edit pull-down Menu, you can select the option to view a table of User-Defined Enclosures. For more information on this table, *see section 4.13*.

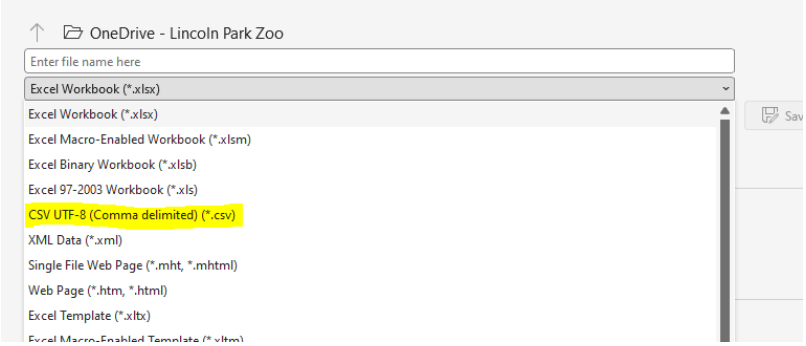
6. ***Resightings Fields***
   In the Edit pull-down Menu, you can select the option to view a table of Resighting Fields. For more information on this table, *see section 4.16.2*.

Chapter 4: ENTERING, IMPORTING, and EDITING DATA IN POPLINK

4.1 OVERVIEW

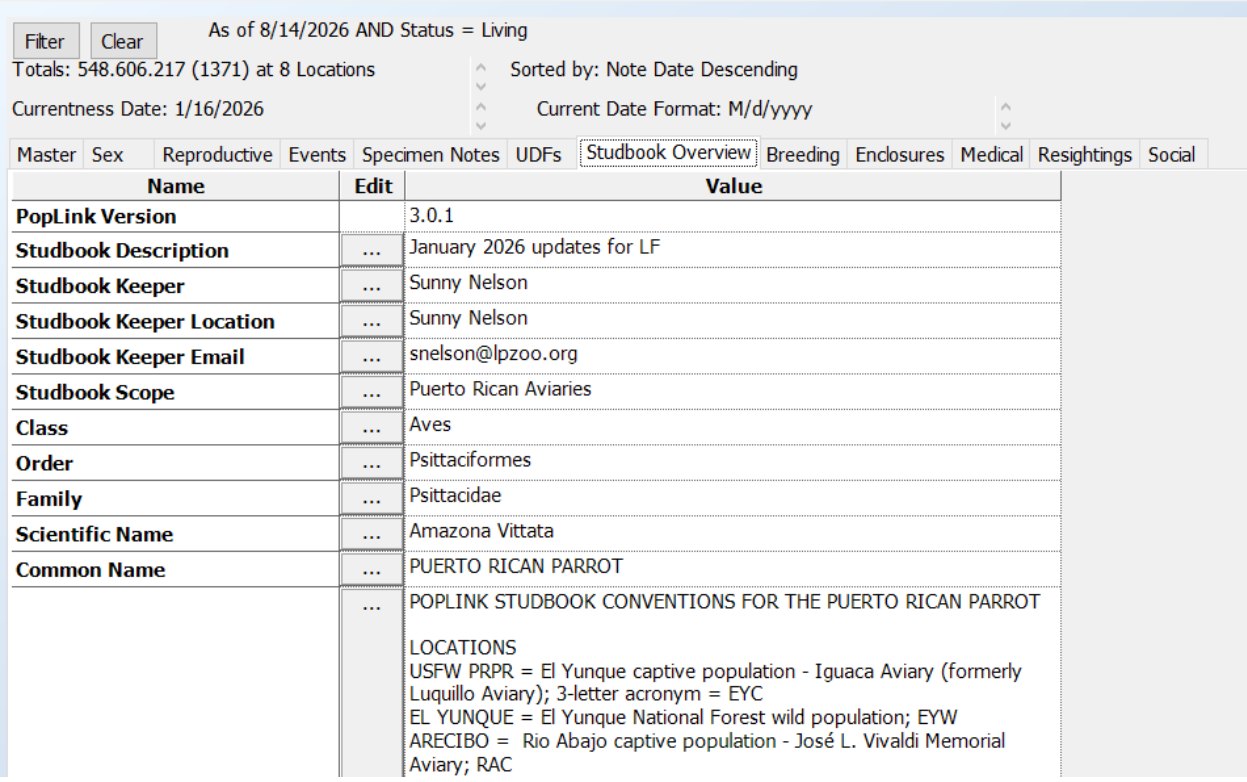
Managed populations are constantly fluctuating as individuals are born, die, and move between locations. Studbook databases evolve along with such changes, as well as with a studbook keeper's understanding of the population's history. To effectively manage populations, all such changes must be recorded accurately and promptly in the studbook database.

PopLink allows for two methods for getting data into a studbook: by entering it directly via the program's Add/Edit routines, or importing data from CSV files, specifically for Core Animal Data, Breeding Effort Data, UDF Data, and Resightings Data. To create CSV files for import, you can first edit files in Microsoft Excel and then save them (Save As) a .csv format. There are typically multiple options in the drop-down; the screen cap is one example, but any of the formats with .csv should be able to be imported. CSV UTF-8 supports international characters, symbols, etc. CSV (Comma delimited) drops all special characters, making some imported data look garbled. Note that when you save as a .csv, **only a single sheet** (the first tab) is saved.



4.2 ENTERING/EDITING DATA IN THE STUDBOOK OVERVIEW TABLE

In the Studbook Overview Table, you can edit any of the general fields associated with your studbook and add details about studbook-wide conventions in the Species Notes field. For more details on the types of information that should be recorded in Species Notes, *see section 3.9*.



Note that changing the **Species Type** field (i.e., Egg Laying or Live Bearing) after studbook creation has studbook-wide consequences. When **Species Type** is switched, the display language throughout PopLink (e.g. column headers, data labels on data entry forms, etc.) will change to match the new Species Type (Egg Laying or Live Bearing). The language within all existing animal records also updates as appropriate (e.g. a Birth event is changed to a Hatch event) and any future records conform to the current Species Type.

4.3 ENTERING A NEW ANIMAL

To add a new animal to your dataset, select the "New Specimen" option from the Edit pull-down menu. This will produce an animal editor pop-up window with tabs for editing relevant information from each data table. For new animals, the data fields will be blank. To successfully enter data for a new individual, you will have to fill in data in the Master, Sex, Reproductive, and Events Tables; Specimen Notes, UDFs, and any of the extra module tables are optional.

Note that there are mandatory fields that must be completed to have a valid animal record; if you have skipped one of those fields, PopLink will pop-up a reminder before you exit the animal editor. Typically, if you make any edits or entry on a screen, you have to "Apply Changes" before you can click OK and close the window, or click one of the top tabs to move on to the next data entry screen.

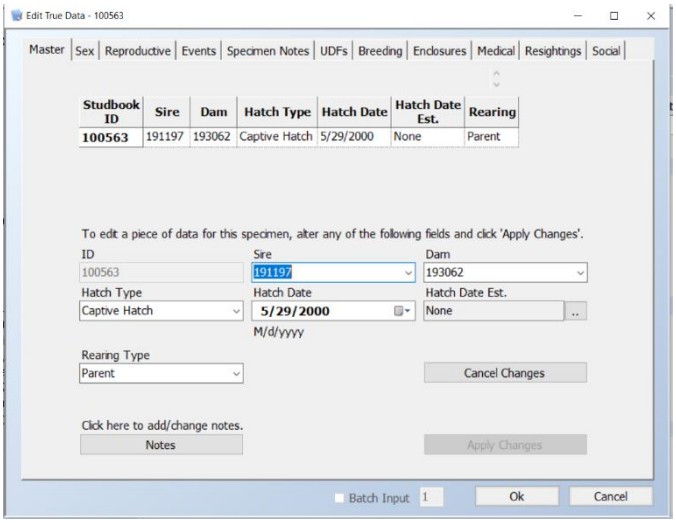
4.4 EDITING AN INDIVIDUAL ANIMAL'S DATA

To edit an existing animal, use the "Edit" button located to the right of an animal's Studbook ID, the "Edit Animal" option in the Edit pull-down menu, or the "Edit Animal" button in the Individual Animal Report. An animal editor

window with tabs for editing relevant information from each data table will pop up. For existing animals, the existing data will be displayed at the top of the screen, and the editable fields will be displayed below.

As the animal editor for editing existing data and entering data for a new animal is the same, we will describe both processes together for each data table.

4.5 ENTERING/EDITING MASTER DATA



Under the Master tab, you may use pull-down boxes or directly enter text to edit information in the following fields:

4.5.1 Studbook ID

When editing an existing animal, the studbook ID will not be editable. If an existing studbook animal needs to be renumbered for some reason (e.g. an animal with a temporary number needs to be assigned a permanent number), that can be done via the Edit→Renumber Animal menu option; *see section 4.18.2* for more details.

When adding a new animal, PopLink will automatically find the highest studbook number in your studbook and assign the next sequential studbook number to the new animal. You should only alter this pre-assigned number under specific circumstances (e.g. if the animal needs a temporary number). If you need to see the highest studbook or temporary number, you can easily do that by sorting the unfiltered Master Table by studbook number.

The primary purpose of the studbook identification number (studbook ID) is to provide a unique identifier for every animal. Once an animal is published with a permanent studbook number, that number should never be changed. The studbook numbering system used by the studbook keeper should be as simple as possible. The studbook is meant to continue beyond the studbook keeper and simplicity will help ensure that it can be interpreted now and will remain useful into the future.

Embedded coding or complicated numbering systems, such as those indicating year of birth, collection date, or initial location, are not typically recommended for the studbook ID; there are other fields within the studbook that record this information. Few individuals besides the initial studbook keeper will understand the system correctly and confusion will increase with time.

Numbers need not be sequential according to birth or capture date. Letters and leading zeros should not be used in the permanent studbook numbers. Letters can be used to designate temporary studbook numbers: a typical convention for zoo populations is to use a "T" to designate temporary studbook numbers. The "T" numbers should be unique and never reused, even after they have been changed to a permanent number. When "T" numbers are

replaced with permanent numbers, the former "T" number should always be entered into the Specimen Notes table as an "Old Studbook Number" note (this is not done automatically by PopLink). Leading zeros should not be used because much of the existing software may have problems recognizing "001," "01," and "1" as different studbook IDs.

4.5.2 Sire/Dam

Use the Sire/Dam fields to enter parentage information either using the pull-down list or typing directly into the field. The Sire pull-down list includes all males in the studbook, as well as generics (WILD, UNK, MULT). If entering an option that is not in the list, double-check that the studbook ID is included in the studbook and is a Male. The Dam field is identical to Sire, except the pull-down lists all females in the studbook. **Every entry in the dam or sire field should either match the studbook number of an animal in the studbook or be *WILD* (or *WILD1, WILD2,* etc.), *UNK* (or *UNK1, UNK2*, etc.), or *MULT* (or *MULT1, MULT2*, etc.)**. There are a few different "types" of sires and dams a studbook keeper may encounter:

1. Dam and Sire Known: In the simplest case, the dam and sire are known, are already in the studbook, and can be entered by typing in the correct studbook ID for each.

2. Wild-Caught Animals: If an animal is wild-origin and nothing further is known about its ancestors, then enter *WILD* for dam ID and sire ID. Genetic analyses using studbook data assume that any parent recorded as *WILD* is unique: it is the parent of that animal only and is unrelated to all animals in the studbook except those who descend from that one offspring. If more pedigree information is known in a wild population either via close monitoring or via genetic sequencing, you could incorporate those relationships into the studbook data or later in the analytical stage. Consult with a population biologist if you have questions on how to incorporate more detailed data into your studbook, as it can influence how valuable individuals look in subsequent genetic analysis.

3. Dam and/or Sire Are Known but Not in Studbook: Things are more difficult if the parents are known but are not yet in the studbook. This can happen if the parents are in the international studbook or in a regional studbook for a different region. It can also happen if a birth or hatch is reported for parents whose have never been recorded in any studbook before. If the parents are in another studbook (international or another region), then those parents should be assigned regional numbers and added to the studbook. All ancestors of those newly identified parents should be given studbook numbers and entered in the studbook, tracing back the ancestors of each animal back to wild (i.e., to animals with dam and sire listed as *WILD*), or to animals of unknown origin. If the dam and/or sire is not yet in any studbook, but some information is available on them, then they should be assigned studbook numbers and added to the studbook. If the current status of those parents (living or dead) is uncertain, the parents (in the new studbook entries just made for them) should be recorded as lost-to-follow-up (*see section 4.7.2* on lost-to-follow-up). Those new parents should be given dams and sires (i.e., the grand-parents of the original animal that started all this mess) of

WILD if the parents are from a game ranch, a breeder that likely got his or her animals from the wild, or another source that is unrelated to the rest of the population and probably from the wild

or

UNK if they probably are (or were) animals in the studbook population, but there is no information on who they were.

If names or ID numbers exist for the dam and/or sire, but nothing else is known about them, it is tempting (and easy) to enter those names in the Dam and Sire fields (because this would avoid creating studbook records for the newly discovered dam and sire). Any Dams/Sires without their own individual studbook record are treated as Unknown parents. Therefore, a studbook record should be created for each parent, making it explicit what is and is not known about them.

4. Dam and Sire Are Unknown: If truly nothing is known about the parents of an animal, then dam and sire should be entered as *UNK*. One parent might be known but the other parent is unknown

(perhaps the dam in a multi-male, multi-female social group, or perhaps the sire in a herd with one breeding male). In this case, enter the studbook number of the known parent and enter *UNK* for the unknown parent. Just as with *WILD*, genetic analyses will assume that each *UNK* parent is unique (i.e., unrelated to all others in the studbook).

Entering *UNK* for a parent should be the last recourse of a frustrated studbook keeper. Unknowns cause real problems for genetic analyses, demographic analyses, and even documentation of the legal status of an animal. When a dam or sire is *UNK*, it means there is no clue as to whether the animal is captive-born or wild-caught, if it is inbred, who its relatives are in the population, or if it is a valuable breeder. The historical record of the population and all management decisions based on that record are compromised when animals are recorded with either one or both parents as *UNK*. However, if the parents truly are unknown, there is no other option but to enter *UNK*. Analytical assumptions can be made later so that these animals can be utilized in genetic and demographic analyses (see Chapter 9 for more details).

5. There is some information on relationships, but the dam and sire are not explicitly known: Sometimes, there is some information about the likely parentage, but the identity of the dam or sire is uncertain. It would be a shame to throw away some of this information. One such case arises when litter mates or nest mates or egg-mass mates can be identified, but parents are unknown. If the animals are wild-born, you can enter *WILD1* and *WILD2* for the parents of each sibling (or *WILD3* and *WILD4*, etc., if the earlier *WILD_* numbers have already been used). Genetic analyses will then correctly use the knowledge that these animals are siblings that came from a single pair in the wild. If a pregnant or gravid female is brought into captivity, then the studbook number of the dam would be recorded while the sire would be listed as *WILD#*.

A similar situation can arise when a litter (or clutch or brood) is conceived and born (or hatched) in captivity, but the dam and/or sire is unknown. In this case, the unknown parent(s) should be entered as *UNK1* (and/or *UNK2*, etc.). This will show that the siblings have the same parents but also indicate that it is not known who those parents are. When multiple offspring have *UNK1* as a parent, genetic analyses will assume that *UNK1* is an animal who was a parent to each of those offspring (but a parent to no one else in the studbook). Thus, while animals with *UNK* for parents are assumed to be unrelated (each *UNK* is unique), animals with *UNK1* and *UNK2* for parents are assumed to be siblings.

Occasionally, such as when animals are housed in large social groups, when multiple males are rotated through an enclosure with a female, or when artificial insemination is done with semen pooled from multiple males, it might be possible to specify that the sire or dam is one of several known individuals. In these cases, enter *MULT* (or *MULT1*, *MULT2*, etc., if earlier *MULT_* were already used) is used to indicate that any one of several males (or females) could have been the sire or dam. The possible sires or dams for *MULT* must be recorded in a Special Data field.

Analytical software like PMx is able to read in the multiple potential parents assigned to a MULT and incorporate those parents into genetic and demographic analysis. This means that tracking the MULTs within your studbook is a critical step in facilitating the management of your population. For instructions on exporting MULT parents from PopLink to PMx, please *see section 7.1.1*.

In summary, the key is to enter everything known about the pedigree of each animal in the studbook. When it is necessary to make assumptions about some tricky or unusual parentage determinations, those assumptions should be documented clearly in a Specimen Notes field. Remember, the computer files are the only permanent records of the studbook knowledge. A studbook keeper's scribbled notes and recollections of what was done and why, will soon be lost. Any information worth knowing should be in the studbook.

4.5.4 Birth/Hatch Type

Use the pull-down menu to select captive born/hatch, wild born/hatch, or unknown. You should not enter free text into this field. Note that "Birth Type" is equivalent to "Origin" of an animal.

This data field is important because, along with the Dam and Sire fields, it can be used to help decide which animals are likely to carry unique genetic information. The options for this data field are straightforward. If the animal was collected from the wild its birth type should be entered as *WILD BORN/HATCH*. The birth event should be interpreted as physical separateness from a parent or parents. Therefore, an immature animal collected with a parent would be *WILD BORN/HATCH*, while an animal born to a pregnant female collected from the wild would be *CAPTIVE BORN/HATCH*. *CAPTIVE BORN/HATCH* should be used when it is known that the animal was born in human care, whether or not the parents of the animal are known. Fertilized eggs or gametes which were collected in the wild, but which were born in captivity should be entered as *CAPTIVE BORN/HATCH*, but with *WILD* dam and sire.

UNKNOWN birth type should be used when the birth type is unknown, and although there are some rare exceptions, unknown birth type will usually be associated with unknown parentage, unknown birth date and unknown birth location. There is an important difference between captive-born/hatch animals with unknown parents and animals with both unknown birth type and unknown parents. In the former case it is more likely that the alleles carried by the animal are carried by other animals in the population. In other words, captive-born animals of unknown parentage are not considered possible founders under usual circumstances. On the other hand, animals of unknown birth type and unknown parentage may be considered possible founders, for analysis purposes only, if it is determined that a wild-caught origin is possible or likely given information in other data fields (e.g., date of birth, location of birth).

4.5.5 Birth Date, Birth Date Estimate

You can enter the birth/hatch date by selecting the calendar drop-down or typing directly into the box, and have the option of including a date estimate. In the course of editing or entering an animal's record, dates need to be entered in several fields and the guidelines below should be used in all of those cases.

4.5.6 How to Enter Dates and Date Estimates

PopLink dates follow your computer's regional date settings, with adaptive data-entry labels to clarify the format.

Transaction dates do more than record arrivals and departures. They determine which animals are included in demographic analyses, age classes, and date-based geographic filters. For example, an animal present from its third to fourth birthday is counted in the fourth-year age class and is considered at risk for reproduction (Mx) and death (Qx). Because genetic and demographic filters often use date ranges, accurate transaction dates are essential for population demography.

Date estimates express uncertainty when an exact event date is unknown. They show precision but generally do not affect analyses. **PopLink ignores the estimator and treats the date as exact unless the estimator is "unknown."** Estimate types include:

> ***NONE***
> Use this when the exact event date is known. Enter the date in Transaction Date and *NONE* in Date Estimate.
>
> ***NEAREST UNIT ESTIMATES***
> Use nearest-unit estimates when the date is known only to a day, month, or year. Enter the midpoint of the estimated period in Transaction Date and the appropriate estimator in Date Estimate. For example, if an arrival occurred during a month, enter the 16th for a 31-day month and *Month*. If it occurred during a year, enter 1 July and *Year*. If birth and death are estimated to the same year, enter the birth as 2 May and death as 1 September, both with *Year*.

DATE RANGE ESTIMATES
Use range estimates when an event occurred within several months or years. Enter the midpoint of the range in Transaction Date and the range estimator in Date Estimate. For example, if a transfer occurred in 2021 or 2022, enter 1 January 2022 with *+/- 1 YEAR*. For a decade estimate, enter 1 January 20_5 with *+/- 5 YEARS*. **PopLink uses the Transaction Date value for demographic analysis, so this date should be the range midpoint.**

UNKNOWN DATE
Use *UNKNOWN* when the date cannot be estimated. ***UNKNOWN* tells PopLink to ignore the Transaction Date during analysis, removing those animals from demographic analyses.** These animals should still be entered because they may be needed for genetic pedigrees.

Studbook keepers can often improve date precision and accuracy by using species biology and history. For example, if births occur only in a known season, a year-level estimate may be narrowed to a few months.

Date estimates should be interpreted as "any date within the estimated period." For example, a calendar-year estimate means the event could have occurred on any day of that year. Avoid overlaps between estimated and known events; overlaps may show that the estimate can be refined. If a birth is estimated to a calendar year but a known transfer occurred on 12 August, the birth estimate should be narrowed to the period before that transfer and entered as the midpoint of that uncertain period.

Additional context on birth date estimation includes:

The best estimates use information specific to the animal or species. For example, if a pregnant female is later seen with offspring, the birth likely occurred within the intervening period; offspring condition or behavior may refine the date. Similarly, if nests are checked every few days, hatch dates can often be estimated to the day (*see section 4.4.9*).

For marsupials, bears, cavity-nesting birds, and similar taxa, biology can help estimate birth or hatch dates. Studbook keepers should work with holding institutions to back-calculate from first observation, such as pouch or nest emergence, using species biology or observed parental behavior. Species Notes should explain the method, and Special Data should include the date young were first observed. Other conventions may apply to species with multiple life stages or high fecundity, such as some anurans.

When individual-specific information is limited, especially for wild-caught or privately held adults, birth or hatch dates should still be estimated because they support demographic analyses. Generic conventions may be appropriate (*see section 9.1.2*) and should estimate to the smallest possible time unit. Any standard species convention should be described in the Species Notes.

4.5.7 Rearing

In this field use the pull-down menu to select whether the animal was Hand, Parent, Foster, Colony/Group, Peer, Supplemental, Unknown, or Not Reared; you should not enter free text into this field.

Rearing data are often essential because whether an animal was hand or parent reared may determine population and/or animal management strategies. Rearing history may influence socialization, reproduction, and other parameters. For example, a species manager may want to assess the effect of hand rearing on subsequent reproductive success. Also, in nonseasonal breeders, birth intervals can decrease for dams with hand-reared offspring, so hand rearing information is a potentially important part of any evaluation of reproductive rate.

Although PopLink does not have default rearing types, usually wild-caught animals are *parent reared*; captive-born or unknown origin animals may be any of the rearing types. Rearing type for stillbirths and premature births should be listed as *not reared*. Many studbook keepers will want to develop species specific conventions for rearing types.

There are no established standards for categories for parent reared, hand-reared, foster-reared, partial parent rearing, etc. Categories will vary from species to species, and may be based on length of time, type of individual doing the rearing, etc. Conventions should be based on the biology of the species with an eye toward how rearing might affect management practices.

The Rearing field can be used to set Filters (see Chapter 5). If additional rearing categories are needed, creating a rearing UDF is the best tactic (*see section 4.10* on how to create and use UDFs). A UDF will also allow the species manager to set a Filter to select a specific rearing type for analysis and reports. For example, one studbook keeper created a UDF category "Partial" to describe a situation where rearing was a combination of parent and hand rearing. Conventions for rearing types should be described in Species Notes (*see section 4.16* on species notes).

Rearing data may be difficult to collect. Also, rearing categories are often open to interpretation; a studbook keeper may want to solicit exact dates of rearing and categorize the information to fit the husbandry and management plan. For some species, or even particular situations, it may be advisable to record rearing dates and information as text in Specimen Notes.

4.5.8 Notes

The master data table has a Notes button at the bottom left of the data entry screen. Clicking on this will open a text box which you can use to document any necessary facts about the fields you have just edited or entered. When you enter notes (closing the box saves the notes), the notes are transferred to the Specimen Notes table for the animal you're entering with a description of "Master Table Notes" and the date of entry.

4.5.9 More Guidance on Entering New Animals

Wild Born Animals

When recording the vital statistics of a new wild-born/hatched animal, the animal's parents should be entered as WILD. For birth/hatch date, many animals are captured when young and their likely year or month of birth can only be estimated based on the animal's size at the time of arrival to the first location. Dates of birth/hatch estimated to the nearest calendar year should be entered as 1 July 19__ and *YEAR* to indicate an estimated year of birth. For species that breed seasonally, a more precise date, e.g., May or June, would be more accurate. In situations such as this, an approximate birth/hatch date in the middle of the breeding season should be used (*see section 4.4.4* for more details). Sometimes, birth/hatch dates cannot be reliably estimated to the nearest calendar year. In such cases, the date of birth/hatch should be entered as unknown. Estimated birth/hatch dates must precede all known event dates.

Eggs collected in the wild that hatch in captivity should be entered with the hatch type *CAPTIVE HATCH*.

Captive Born/Hatched Animals

Captive-born/hatched animals are identified by several coordinated data entry procedures. Usually, the exact date of birth/hatch is known and can be entered without an estimate. If only the month or year of birth/hatch is known, it should be entered with a *MONTH* or *YEAR* in the Date Estimate field (*see section 4.4.4* on estimating dates).

Usually, one or both parents are known and their studbook numbers can be entered as the dam and sire (*see section 4.4.2* on how to enter dam and sire). However, for some animals, one or both parent identities will be unknown. Every effort should be made to identify the parents: unknown parentage has profound effects on genetic analyses. If parentage cannot be established, either one or both parent studbook numbers should be entered as *UNK*.

The first event for a captive-born/hatched animal should be a *Birth/hatch* at the birth location. The Birth Type of the animal should be entered as *CAPTIVE BORN/HATCH.* Eggs collected from the wild should have "Captive Hatch" as the first event, with both parents entered as *WILD* (or *WILD#*, when parents or siblings have been individually identified.

Animals Of Unknown Origin
Many studbooks include animals with unknown origins. Every effort must be made to ascertain the true origin of every animal in the studbook. For some of these animals, thorough investigation will eventually identify origin as either wild-caught or captive-born/hatch. For other animals, assumptions or conventions may be invoked to resolve uncertain origins (*see section 9.1.2* on assumptions and conventions). Despite a studbook keeper's best efforts, a few animals will probably have origins that are truly unknowable. Such animals are a problem for genetic analyses because they will eventually require a decision to treat them as wild-caught or to exclude them from analyses.

The first event for animals of unknown origin should be entered as a birth/hatch at an unknown location (UNKNOWN) with unknown birth/hatch type (UNKNOWN). If only the month or year of birth/hatch is known, that should be entered with a Date Estimate of Month or Year; this indicates that only the month or year of birth/hatch is known (*see section 4.4.6* on estimating dates).

Every effort should be made to identify the parents: unknown parentage has profound effects on genetic analyses. If parentage cannot be established, either one or both parent studbook numbers should be entered as (UNK).

4.6 ENTERING/EDITING SEX DATA

Remember that sex data are tracked as a data stream, and an individual may be a single sex for its entire life or switch sexes (e.g. from unknown sex at birth to male or female). To edit existing sex event(s), highlight the desired event and edit the data in the fields; to enter a new sex event, use the Add button. To delete an existing sex event, highlight the desired event and use the Delete button.

For an individual with known sex at birth, use the Sex pull-down menu to designate whether the individual was *male, female, hermaphrodite,* or *abnormal* sex. When entering a new individual, PopLink will autofill the Event Date and Event Date Estimate using the birth date and birth date estimate; you still need to fill in the sex for your new individual. For animals where the sex is known at birth, these fields should be identical,

For an individual that is unsexed at birth, designate the individual as *unknown* sex. Again, the Event Date and Event Date Estimate are autofilled with the birth date and birth date estimate when entering a new individual. If the sex is identified later in the animal's life (e.g. at sexual maturity or through genetic testing), add an additional sex event for the animal, with the appropriate Sex and the date which the individual was officially sexed in the Event Date/Event Date Estimate fields.

If an individual is initially misidentified as one sex and then determined to be the opposite sex, it is important to enter two separate sex events. For example, if an individual is misidentified as a female at birth it will have a first sex event (female, on its birthdate); if it is later found to be male, the studbook keeper should enter a second sex event with an event date of the date the new sex was determined. Tracking changes with multiple events in this way will show population managers that this animal may have originally been managed as a female and may help with interpretation of reproductive success (e.g. if the individual did not reproduce because it was paired for breeding with a male).

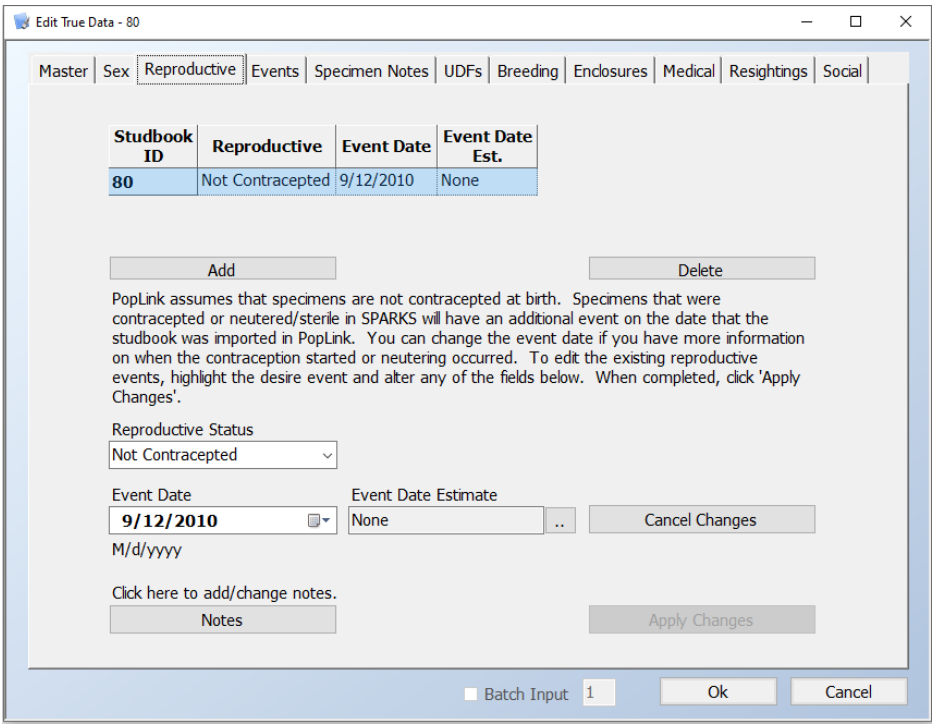
An existing sex event should only be edited in the event of a data entry error. In all other cases, sex should be recorded as a data stream (i.e. changing the sex by adding a new sex event rather than editing the current sex).

Use the Notes button to document any necessary facts about the fields you have just edited or entered (such as sources, discrepancies with institutional records, type of test used for sexing or lab at which sexing took place, etc.). When you enter notes (closing the box saves the notes), the notes are transferred to the Specimen Notes table for the animal you're entering with a description of "Sex Table Notes" and the date of entry.

Note that for demographic analyses, animals whose sex is entered as UNKNOWN, ABNORMAL, or HERMAPHRODITE are considered 50% male and 50% female. Thus, for life table analyses, an abnormal or unknown sex animal is assigned as one-half male and one-half female.

4.7 ENTERING/EDITING REPRODUCTIVE DATA

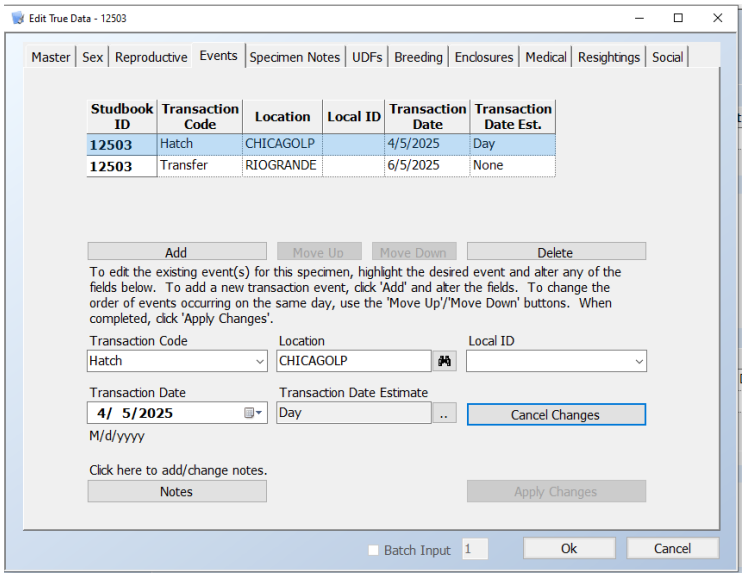
The screen for entering/editing reproductive data for an animal is similar to that for sex data. Remember that reproductive data are tracked as a data stream, and an individual will start out its life as not contracepted and can then be switched to contracepted or neutered/sterile (sometimes multiple times). Not contracepted should be used when an individual's reproductive status is not known, and neutered/sterile should be used when an individual is neutered or reproductively sterile for some other reason.



To edit existing reproductive status event(s), highlight the desired event and edit the data in the fields; to enter a new reproductive status event, use the Add button. When entering a new individual in PopLink, a reproductive event of "Not Contracepted" on the individual's birthdate entered in the Master table will be autofilled.

Remember that for individuals already existing in your studbook, PopLink assumes that individuals are not contracepted at birth. If you get information that an animal has been contracepted or neutered, enter an additional event with the relevant information, and use the Notes box to enter supporting information about the event.
Use the Notes button to document any necessary facts about the fields you have just edited or entered (such as source of information about contraceptive, discrepancies with institutional records, etc.). When you enter notes (closing the box saves the notes), the notes are transferred to the Specimen Notes table for the animal you're entering with a description of "Reproductive Table Notes" and the date of entry.

4.8 ENTERING/EDITING EVENT DATA



Under the Events tab you may edit or delete pre-existing events, add new events, and reorder events that occur on the same day in an animal's record.

4.8.1 Transaction Code

PopLink recognizes eight different Event types: *Captive Birth/Hatch, Wild Capture, Transfer* (to another institution or location), *Release* (into the wild), *Recapture* (from the wild), *Death, Go LTF* (Lost-to-Follow-Up), and *Return From LTF*. Events, or transactions, should provide a continuous record of an animal's history in time and space. The terms "transaction" and "event" are often used interchangeably.

The first event for each animal should be a birth or hatch. In the past, some studbooks have used a wild capture or transfer as the first event (usually for animals that were either wild-caught or of unknown origin). Transfers should not be used as the first event for any animal. When the first event is Transfer, the animal's origin is unclear and must be inferred from data in other fields. A transfer as the first event is ambiguous and implies that the information for that animal is incomplete (e.g., where was the transfer from? Did the studbook keeper intentionally make the first event a transfer, or was capture or birth/hatch mistakenly omitted?). PopLink's Data Validation (Chapter 6) will check whether your studbook has transfers as first events.

The data for each animal should include all known (and unknown) locations and events. When necessary, PopLink and other analytical programs can exclude specific events and locations from reports and analyses using Filters. Thus, a studbook keeper should not exclude any data on location in order to create a geographic subset of their population. The benefit of including all locations could be great. Analyses and reports could be run only on animals that had passed through a specific, albeit obscure location: this might be required to assess a common factor such as disease or behavioral problems. Moreover, most Filters (see Chapter 5) include a geographic criterion (e.g., North America) and a date criterion, so it is important that the studbook record where each animal was located at every point in its history.

For Death events, death dates should typically only be entered if the time and location of death are known. Animals that have disappeared from an institution should be listed as lost-to-follow-up. Under no circumstances should an animal be assumed dead or assigned a death date just to remove it from reports or analyses! If some evidence exists to support an animal's death but the exact death date is not known, death dates should be estimated to the midpoint of the estimated unit (e.g., 1 July for an estimate to calendar year). When the birth date and death date for an animal are estimated to the same calendar year, the dates should be entered as splitting the year into thirds: 2 May as the birth date and 1 September as the death date.

4.8.2 Lost-to-Follow-Up Events

Lost-to-follow-up indicates that an animal's whereabouts are unknown from the date of the *Go LTF* event. An animal is considered lost-to-follow-up (LTF) when its disposition is unknown. Lost-to-follow-up should be used to designate animals whose status is uncertain. This includes animals transferred to institutions that don't report to the studbook keeper, animals that may have (or probably have) died, and animals that have just disappeared.

Animals that have gone to a non-reporting institution or a location where they are not being closely monitored should typically not be "killed off" in the studbook even if they may have (or probably have) died. They should be considered lost-to-follow-up unless evidence of death can be provided. For wild populations that are closely monitored, we typically still advise studbook keepers to only enter death events when they have direct (carcass) or indirect evidence ("death" signal on a radio collar). Presumptions of deaths that are entered into the studbook may severely bias demographic analyses, while lost-to-follow-up removes the animal from the life table without the presumption of death.

There are multiple situations in which an animal can become lost-to-follow-up:

1. Transfer from a known location to a location where the animal will not be tracked: i.e. transfer of an animal to a location that does not (or historically did not) keep records. Therefore, although it is known when and where the animal was sent, there is no information about how long the animal lived there or where the animal was transferred subsequently. In this situation the animal should be recorded as lost-to-follow-up the day it was sent to the new location. This event stream might look like this:

Studbook ID	Transaction Code	Location	Local ID	Transaction Date	Transaction Date Est.
111412	Hatch	RIOGRANDE		5/23/2011	None
111412	Transfer	CHICAGOLP	23760	10/23/2016	None
111412	Go LTF	CHICAGOLP	23760	10/23/2016	None

2. Going LTF at some point after it was transferred to a known location: in some wild populations where individuals are regularly monitored, a convention may be created to identify an animal as LTF if it's last sighted date was more than X months (or years) ago; adding a go LTF event in such instances helps the studbook keeper more easily see the animals in the population that are currently considered alive. This event stream might look like this:

Studbook ID	Transaction Code	Location	Local ID	Transaction Date	Transaction Date Est.
113844	Hatch	ARECIBO		3/24/2013	None
113844	Transfer	RA WILD		1/21/2016	None
113844	Go LTF	RA WILD		6/1/2018	None

3. Disappearance (due to transfer, escape, release, or unknown reason) from a known location on an unknown date, i.e. when an animal is lost within an institution's record system. For example, an animal remains on the institution's inventory for an extended period after the animal had actually been transferred or died. Here, the animal should be recorded as lost-to-follow-up around the last time the animal was known to have been at the institution. Thefts and escapes should be entered as lost-to-follow-up, with an explanatory note entered in the Animal Notes. It is not appropriate to enter thefts or escapes as transfers to unknown or fictional locations. In particular, animals should not be transferred to "creative" locations such as *STOLEN*, *THEFT*, or *ESCAPED*.

Note that PopLink also includes the event option of "Return from LTF". You can use this option if animals are transferred to institutions that don't report to a studbook keeper (Go LTF) and later transfer back to an institution that does report (Return from LTF) or if the studbook keeper receives information about an event (e.g. an animal death) after a long period of non-reporting.

4.8.3 Location

Locations in PopLink should be entered as the location mnemonic (e.g. CHICAGOLP for Lincoln Park Zoo). Use the "Find" button to lookup a mnemonic when necessary (you can also use the LocationList.xls file in My Documents\PopLink to quickly look up mnemonics and locations). These locations and location mnemonics are created and assigned by Species360. If you have a location that does not have a mnemonic in the PopLink location file, you can create your own via User Defined Locations. If you attempt to enter an unrecognized mnemonic (one that is not in the Location List or the User Defined Locations List) in your Event data entry, a pop-up window will be displayed allowing you to add information about that location. After you click OK, the new location is added to the User Defined Location list.

You can view and edit all your user-defined institutions through selecting Edit→"User-Defined Locations":

User Defined Locations

Mnemonic	Edit	Name	Address	City	State	Country	Mail Co
MSF WILD	...	Maricao State Forest	Vivero de Peces de Maricao	Maricao	Puerto Rico	United States of America	3224063
NORTHFORK	...	Northfork	Northfork	El Yunque	Puerto Rico	USA	
PAIR BOND	...	Luquillo Aviary Pair Bonding Cage	Rio Grande Field Office	Rio Grande	Puerto Rico	USA	
PALOHUECO	...	Palo Hueco	Palo Hueco	El Yunque	Puerto Rico	USA	
QG	...	QG	QG	El Yunque	Puerto Rico	USA	
RA WILD	...	Rio Abajo Forest		Rio Abajo	Puerto Rico	USA	

Add

User Defined Synonyms

Synonym	Edit	Real Location Mnemonic
LUQUILLO	...	RIOGRANDE

You can add new user-defined locations or edit existing ones using this screen. In PopLink, these user-defined locations travel with the studbook database, so once you have defined them for your database other PopLink users will always be able to recognize them. Locations are most frequently physical locations, i.e. a specific zoo or breeding center, or geographically distinct and separate areas that animals in a population spend most of their time in but might occasionally transfer between, or even different subpopulations. User Defined Synonyms can be entered and are useful when a mnemonic changes over time for a facility (i.e. when Species360 assigns a new mnemonic).

4.8.4 Local ID

For zoo and aquarium populations, the institutional accession number, entered into the Local ID field, is a unique number used to identify the animal within its location. If the accession number is unknown enter *UNK*. You may also enter other identifiers (house names, etc.) if desired.

4.8.5 Transaction Date/Transaction Date Estimate

To express uncertainty about the transaction dates, date estimates can be entered by using the edit button next to any Date Estimate data entry field. For more information about entering dates and date estimates *see section 4.4.6*.

The sequence of transactions (events) shown in the table is sorted by the Transaction Date field. This seems logical for a transaction with some known transaction date. For transactions with unknown dates but a known sequence (e.g. a transfer occurred between a known birth date and death date, but the date of the transfer is unknown), a date that is between the transaction date of the previous transaction and the transaction date of the next transaction

should be used to place the transaction appropriately in sequence, and an Unknown date estimate should be entered. This date will be ignored by any analysis performed by PopLink, but will be used to correctly sort events. If events have the same transaction date (e.g. a transfer and a death), you can use the "Move Up/Down" buttons to reorder them.

4.8.6 Notes

The Event data table has a Notes button at the bottom left of the data entry screen. Clicking on this will open a text box which you can use to document any necessary facts about the fields you have just edited or entered (such as sources, discrepancies with institutional records, etc.). When you enter notes (closing the box saves the notes), the notes are transferred to the Animal Notes table for the animal you're entering with a description of "Event Table Notes" and the date of entry.

4.9 IMPORTING CORE ANIMAL DATA FROM CSV FILES INTO POPLINK

Because the next steps of data entry for an animal are not mandatory (sections 4.9 and beyond), we will pause here to focus on the second method of getting data into a studbook beyond direct data entry – importing from a CSV file.

Imagine you have maintained an Excel database of individuals in a closely monitored population for years. You have always wanted to work with your database in PopLink, but you could not find the time to manually enter records for all the individuals one-by-one. Or imagine that, each breeding season, the population you monitor has a big pulse of hatches or births, and you always dread the thought of manually entering each and every new individual into your existing PopLink studbook. With the **Import Core Animal Data** function, you have the option of quickly and easily importing large amounts of data stored as a comma-separated values (.csv) file into a new or existing PopLink database, creating initial core records for each individual that you can edit and update with additional data over time.

4.9.1 Formatting the CSV import file

The first row of the CSV file should contain column headers for the database. Those headers must include **ID, Sire, Dam, Sex, Birth/Hatch Type, Birth/Hatch Date, Birth/Hatch Location**, and **Rearing Type**. Each subsequent row represents the data for a single individual, corresponding to each of the column headers above.

PopLink will automatically validate the data as you attempt an import. For more information on the rules governing the data in these columns, *see sections 4.1-4.7*. **Note that a .csv file that contains blank fields in any of the starred (*) columns will not import.** For more details on each column:

- **ID*** – Each studbook ID must be unique within the .csv file and cannot match the ID of any individual already in the studbook. We recommend that you primarily use numeric, sequential studbook IDs and that you don't include leading zeroes, as different software can struggle to interpret the difference between 01, 001, and 1, for example.
- **Sire and Dam*** – Sire and Dam studbook IDs must match the ID of an individual in the .csv file, or in the existing studbook. If the parents of an individual are wild, unknown, or there are multiple potential parents, *WILD*, *UNK*, *MULT*, or *WILD#*, *UNK#*, or *MULT#* can be used. Additionally, the IDs listed for an individual's Sire or Dam must correspond to the correct sex (*Female* for Dam and *Male* for Sire).
- **Birth/Hatch Location*** – Locations in the Birth/Hatch Location field must be mnemonics (i.e., CHICAGOLP) from PopLink's Locations List or locations created by the user with the User Defined Locations function (*see section 4.7.3*).
- **Sex*** – The sex of an individual must be listed as *Male*, *Female*, *Unknown*, *Hermaphrodite* or *Abnormal*.
- **Rearing Type*** - The Rearing Type of an individual must be listed as *Hand*, *Parent*, *Foster*, *Colony/Group*, *Peer*, *Supplemental*, *Unknown*, or *Not Reared*.
- **Birth/Hatch Type*** – The birth or hatch type of an individual must be listed as CAPTIVE, WILD, or UNKNOWN.

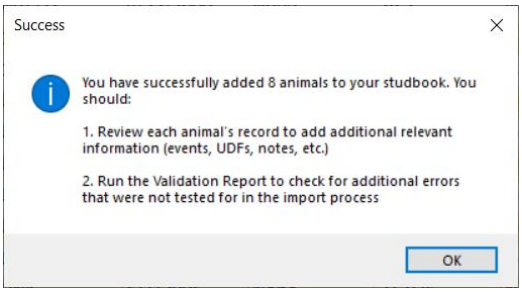
- **Birth/Hatch Date* –** Birth and hatch date formats should be consistent across the .csv import file and match the Current Date Format in the PopLink database, which matches the Date and Time Settings on your computer (M/d/yyyy, dd/MM/yyyy, etc.).
- **Birth/Hatch Date Est**.- These data are optional. PopLink allows some flexibility with the data in this column. For instance, you can specify the estimate interval (e.g., day, month, or year) or the span of the estimate (2 days or 5 years, etc,). PopLink will modify these values on import. For example, if the user listed "2 days" on the .csv file, the estimate will appear as "+/- 2 Days" in PopLink after a successful import. You can also leave this field blank. If there is no Birth/Hatch Date Est. column in a .csv import, or no value for a particular individual, "None" will be listed in PopLink.
- **Note** – These data are optional. If you add a Note column to the .csv import file, you can add a single note for each animal's record which will be uploaded with the label "Note" into the animal's Specimen Notes table. You can also leave this field blank for any animals who have no notes.

Any additional text outside of the text in the above columns will not be imported.

See section 4.1 for more details on how to save an excel file as a .csv.

4.9.2 Importing data

You must import data into an existing database: into a studbook that already has individuals, or into a new, empty database (see Chapter 2: Getting Started in PopLink). Once the CSV has been correctly formatted, you can import the data by opening the desired studbook and selecting File→Import Core Animal Data. In the file selection box navigate to the .csv file and select Open. The import process may take a minute or more depending on the size of the file being imported. Once an import is complete, a pop-up window will open which outlines how many individuals were imported into the database and reminds you to review and validate the new animals' records.



Your imported .csv file is archived in your "Imported Data" folder within your studbook folder.

Each individual record created through an import will also have a Data Import Note automatically added with the date of import, the name of the .csv file where the import data originated, and the login name of the user who created the record.

Creating an individual record through a .csv file import only allows users to import the data above – the core of an animal's record. **Most users will also need to edit each individual to add additional relevant information after this import process**, such as additional Specimen Notes or additional events (transfer, Go LTF, death, etc.,), or UDF data.

This means all individuals created through an import will have a Current Status of "Living" and their current location will be the Birth/Hatch Location listed in the .csv file; edits to their records within PopLink may be needed to enter additional information beyond the core data.

4.9.3 Import error messages

If there are errors in your import file– blanks in required data fields, missing columns, or invalid data entries —the data within the .csv file will not import and PopLink will open and display the original import file with the addition of an errors column. The import file will be renamed with "CoreDataERRORS" added as a suffix to the original file name (i.e. if your file was "TestImport", the new file will be named "TestImport_CoreDataERRORS"). This file contains all of the original data, but for each row with an error, the Errors column will display a code specific to that error. At the bottom of the .csv, PopLink adds a column titled Validation Error Key that shows all potential error codes and corresponding descriptions. You can edit the open file to fix the identified errors, then save and reattempt upload.

In cases where a user did not include a column for studbook IDs in the .csv file, PopLink will display a pop-up notifying the user that "Input file contains no records".

4.10 ENTERING/EDITING SPECIMEN NOTES

The Specimen Notes tab can be used to add notes to a specific animal's record. You may either choose a Note Type from the drop-down menu (Table 1) or enter your own Note Type and enter your note into the Comment box. You may also enter a date the note was edited. If you wish to delete a comment, highlight that comment and click the "Delete" button.

Table 1. Note Types Included In The Drop Down Menu

- Acquisition note
- Adult/adult behavior
- Adult/infant behavior
- Age estimate
- Aggression
- Animal management note
- Antlers/horns
- Artificial insemination
- Behavior note
- Birth note
- Breeder Number
- Breeding encounter
- Breeding management note
- Breeding separation
- Broker
- Carcass note
- Carcass recipient
- Collection data
- Color phase
- Contraception
- Copulatory behavior
- Dam taxon
- Dam/Sire Id's elsewhere
- Death note
- Death number
- Diet
- Disposition note
- Donor's name
- Egg information
- Egg lay date
- Electro ejaculation
- Environment
- Event Table Notes
- Fecal check/worming
- Feeding
- Fledge date
- Foot management
- Fostering note
- Freezebnd
- General activity
- Genetic information
- Gestation behavior
- Grooming
- Group behavior
- Growth stage
- Handrearing note
- House name
- Human interaction
- Identification
- Identity description
- Immobilization
- Incubation note
- Individual behavior
- Litter / Clutch
- Master Table Notes
- Medical diagnosis
- Medical note
- Medical observation
- Medical procedure
- Medical treatment
- Missing / escaped
- Multiple clutching
- Museum number
- Necropsy results
- Neonatal behavior
- Neutering
- Notching mark
- Note
- Old Accession Number
- Old Studbook Number
- Parent ID Assumptions
- Parturition behavior
- Permit
- Physical condition
- Physical / legal arrival
- Possible parents
- Pre-copulatory behavior
- Regional Studbook Number
- Reproductive behavior
- Reproductive Table Notes
- Research observation
- Sex Table Notes
- Sexing note
- Shed/molt

- Sire Taxon
- Stereotypic behavior
- Tag / Band
- Tattoo
- Territoriality
- Transponder ID
- Vendor Taxon
- Vocalization
- Weight / Length

4.10.1 Death Codes

To track more specific information about a death in the Specimen Notes, you can add the following types of notes: Death Notes, Carcass Note, Carcass Recipient, Death Number, Disposition Note, and Necropsy Results.

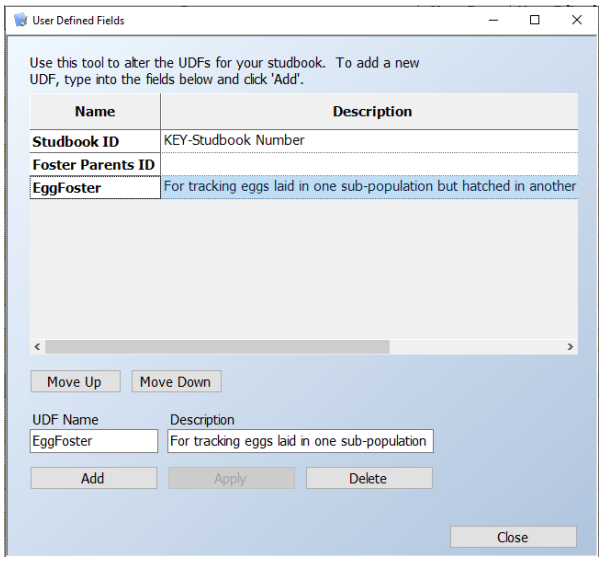
Death Codes imported from SPARKS datasets are stored in the PopLink data in the Local ID associated with the death event (Table 2). If you wish to continue entering death notes in this manner, you can manually enter the letter codes pertaining to specific death information into the Local ID field for any new death event. If you need to translate SPARKS codes into usable notes in the Specimen Notes fields, you can also use these codes. Codes should consist of 4 letters, one letter from each of the four tables below in the following order: 1) Circumstance of death, 2) Carcass Disposition, 3) Necropsy Code-Topographic; 4) Necropsy Code-Etiological. For example, an animal who died from injury from exhibit mate, has an unknown carcass disposition, and no necropsy planned would have a death event Local ID code CHN. An animal who died from a trauma to their musculoskeletal system (identified via necropsy) that was euthanized and buried would have a code of ABCK.

Table 2. SPARKS Death Codes

SPARKS Code	Circumstance of Death	SPARKS Code	Carcass Disposition	SPARKS Code	Necropsy Code - Topographic	SPARKS Code	Necropsy Code - Etiological
A	Euthanasia	A	Incinerated	A	Generalized	A	Genetic & Prenatal
B	Self-Inflicted Injuries	B	Buried	B	Integumentary	B	Bacterial
C	Injury from Exhibit Mate	C	Given to an Institution	C	Musculoskeletal	C	Fungal
D	Malicious Destruction	D	Sold to an Institution	D	Respiratory	D	Metazoan
E	Old Age	E	Mounted or Preserved	E	Cardiovascular	E	PPLO
F	Infection Associated	H	Unknown	F	Hemic and Lymph	F	Protothecal
G	Injury from Predator	I	Rendered	G	Digestive	G	Protozoan
H	Env. or Beh. Conditions			H	Urinary	H	Rickettsial
I	Stillbirth			I	Endocrine	I	Viral
J	Premature Birth			J	Nervous	J	Toxicity
K	Anesth./Restraint Assoc.			K	Reproductive	K	Trauma
L	Died in Transit			L	Sense Organs	L	Circulatory, secondary
M	Stranded/Beached			N	No Necropsy Planned	M	Enervation, secondary
N	Other/Unknown			Y	Necropsy Planned Later	N	Mechanical Abnormality
				X	Unknown (after Necropsy)	O	Metabolism
						P	Nutrition
						R	New Growths
						X	Unknown (after necropsy)

4.11 ENTERING/IMPORTING/EDITING UDF DATA

Before you can enter User Defined Field (UDF) data, you must develop a list of User Defined Fields for your studbook by going to Edit→ User Defined Fields. If you would like to create a new UDF to be used for animals throughout your studbook, go to the Edit drop-down menu and select "User Defined Fields" which will pop-up the dialogue box to the right.



This table will display the existing UDFs in your studbook. To create a new UDF, name the field in the UDF Name field, enter a description (more details on the field, or a listing of the acceptable cases or abbreviations), and click "Add". This new UDF column will then be added to all animals in your studbook, and you will need to edit each animal to give it a UDF value. *See section 3.8* for more details on the types of UDFs that may be useful.

4.11.1 Editing or Entering UDFs for an animal

If User Defined Fields (UDFs) already exist in your database, you can edit an existing animal's values for the defined UDFs or enter values for a new animal under the UDF tab in the animal editor. Select the desired UDF from the drop-down menu on the left, and the desired value for the UDF from the drop-down menu on the right. You can also type into the Value box if desired. **Each animal should only have one UDF row in your database.**

4.11.2 Importing UDF data from a CSV

You can add UDF values to an existing PopLink database by importing records stored in a comma-separated values (.csv) file. See section 4.1 for more details on how to save an excel file as a .csv.

The first row of the file should contain column headers. The only headers that are required for an import to be successful are **Studbook ID**, and the name of at least one existing UDF in your studbook. You can import values for multiple UDFs in the same .csv by adding a column header for each UDF you want to edit. After the headers, each subsequent row represents a single individual and their UDF values.

PopLink will automatically validate for these rules as you attempt an import:

- **Studbook ID**- The studbook ID must be for an existing individual. Each animal should only have one UDF row within your file.
- **UDF values** –Not every individual needs a value for a specific UDF, you can leave blanks fields in your import file. Note that imported UDF values will overwrite any existing values for an individual for a specified UDF, so be sure to carefully check studbook IDs and UDF values in your .csv before you begin.

Once data has been correctly formatted and stored in a .csv file, you can import the data into a PopLink database by selecting File→ Import UDF Data. In the pop-up, navigate to the .csv file and select Open. If the file is error free, a pop-up window will open which outlines how many records were imported into the database and reminds you to review and validate the new records. The imported CSV will be archived in the "Imported Data" folder within your studbook folder (i.e., PopLink Databases\YourStudbookName\Imported Data).

If there are errors in your import file– blanks in required data fields, missing columns, or invalid data entries--the data within the .csv file will not import and PopLink will open and display the original import file with the addition of a column listing the errors for each row. The import file will be renamed with "UDFERRORS" added as a suffix to the original file name name (i.e. if your file was "TestImport", the new file will be named "TestImport_ UDFERRORS"). You can edit the open file to fix the identified errors, then save and reattempt upload.

4.12 ENTERING/EDITING SOCIAL DATA

Under the Social tab you may edit or delete pre-existing Social events, add new events, and reorder events that occur on the same day in an animal's record.

4.12.1 Event Type

There are six options to choose from as Social Event Types. What constitutes each event type is likely species- or even institution-specific, so the studbook keeper should carefully define what types of events fit into each category and document them in Species Notes. Specifics could also be detailed in the Comment field associated with the note:

Introduction (visual) – Often the first step in an introduction process is to give individuals only visual access to one another with complete physical barriers still in place.

Introduction (physical/restricted) – Also known as a protected contact introduction, this step involves partially protected exposure to a new individual, and can vary greatly from species to species. Generally, this involves giving the individuals being introduced access to the same space, but with limited physical access to each other. In aquatic species, this can involve sharing the same water system but still separated by a physical barrier. In terrestrial species, this often involves introduction across a barrier that allows for some tactile, auditory, and/or olfactory exposure.

Introduction (full) – This final step to introduction removes all barriers between individuals and allows full physical and sensory contact.

Altercation – This event type can occur during the introduction process or in an established pair or group of individuals. This category is intended to capture major agonistic events – this includes one individual being aggressive towards group mates, or 2-sided altercations. On a species by species basis, the severity or frequency of the events may be considered when deciding what to record as an Altercation. Use the Comment field to provide details on the severity of the event.

Prosocial – Intended to capture any important positive interaction indicating social compatibility.

Breeding Interaction – This event type is intended to capture information pertaining to an individual's reproductive development and behavior. As with the Altercation or Prosocial category, this event can be one sided (i.e. one individual showing interest or attempting with an uninterested participant) or can involve two or more individuals. These events can be very helpful to reference when planning breeding recommendations.

Other – Intended to capture any species-specific social events missed by the other five categories.

Although each species may have slightly different social dynamics and introduction protocols, ideally you should use these Social Events consistently over time and across institutions in ways relevant to your species. If you encounter an event atypical to your set conventions, give more details in the event Comments field. You should document any standard definitions in the Species Notes section of the Studbook Overview table.

4.12.2 Event Date & Event Date Estimate

Enter the date that the social interaction took place; if it was a multiday event, you can use the start date for the interaction and note in the comments the length of the interaction.

4.12.3 Outcome

The outcome of each social interaction can be scored as positive (+), negative (-), or neutral (0). The outcome of a social interaction can be very subjective and species-dependent. The +/-/0 symbols could be used to represent different words or ideas such as successful/unsuccessful/outcome unclear, or good/bad/neutral, or prosocial/antisocial/no response. Because of this, it is important to develop standard definitions for your species or studbook. The level and type of interaction required to determine +/-/0 will vary by species. Some examples might be:

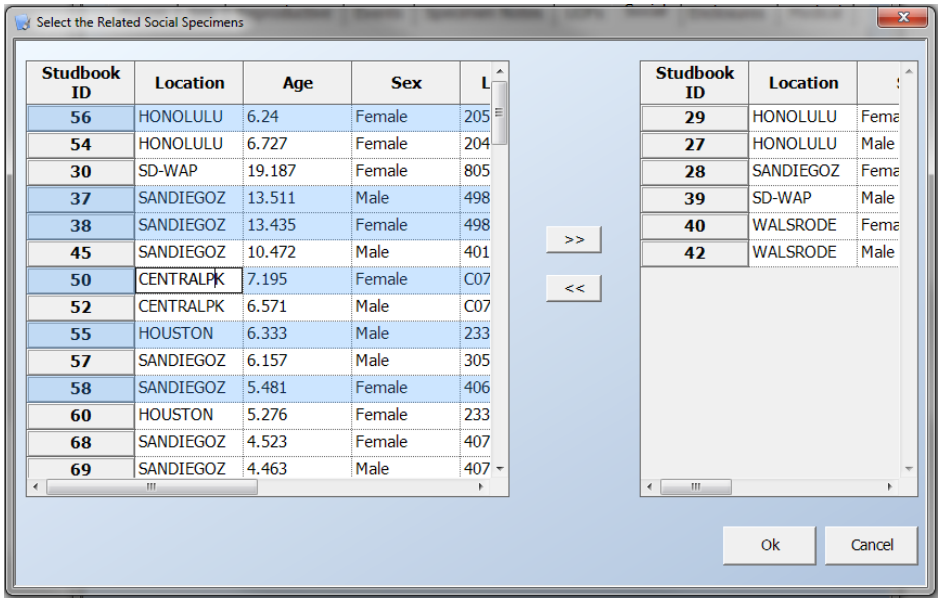
- chimpanzees spending time exhibiting grooming or breeding behavior could be considered positive (+)
- tigers displaying aggressive behavior which is ultimately a part of their normal breeding behavior, could be considered positive(+) or negative(-), depending on your data conventions and the ultimate outcome of the attempted pairing
- wolves presenting play bows as a prosocial invitation to play could be considered a positive (+) social interaction

Species-specific conventions should be recorded in the Species Notes Section of the Studbook Overview.

4.12.4 Related Specimen

Related Specimen refers to the individuals involved with the focal individual in the Social Event. This term does not have any reference to genetic or familial relations. Adding a record to one individual's record adds an identical record to the Social Events Table of any other Related Specimens in the event.

You can type studbook IDs into the Related Animal field separated by commas, but the easier way to enter the associated individuals is to click on the FIND button to pop-up the Animal Selector:

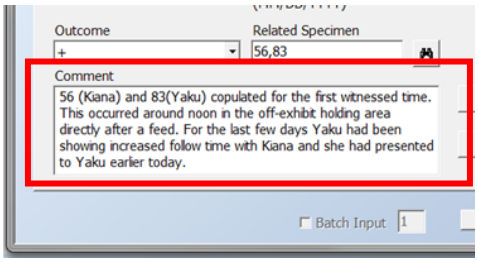


The left-hand table lists all animals in the studbook (living and dead). Clicking on their studbook ID will bring up their animal report; the right-hand table lists all of the Related Specimen(s) that will be involved in the social event. Move individuals back and forth between the tables by selecting them and using the Right and Left arrow buttons. All of the columns in both tables are sortable by clicking on the column headers. You can choose multiple individuals at once by holding the Shift key to select consecutively listed individuals or the Ctrl key to select non-consecutively listed individuals. Once all of the desired individuals are listed on the right, press Ok and the Related Specimen field will be filled in with the Studbook ID Numbers selected.

NOTE: All individuals entered in the studbook – living or deceased – are eligible for entry into a social event at any point in time. There is no check to determine whether an individual was alive during an event, or whether the Related Specimens are in the same Location as the focal individual. Be careful with which individuals you select to make sure that these data are entered accurately.

4.12.5 Comment

The Comment field is important to documenting and understanding the details of a Social Event. This field allows free text of unlimited length, and can be used to document details like the enclosure(s) the event took place in, possible precursors or warning signs leading up to an event, details of the interaction, and justification for the assigned outcome. The Comment section is completely optional – no information is required. As a studbook keeper, it is your responsibility to determine the type and level of information recorded, and to enter that information consistently.



4.12.6 Deleting Individuals From Events And Deleting Entire Events.

When a social event is created in an animal's record, the event is anchored to the individual it was first created in (that individual will be listed first in the Related Specimens field). If you want to delete one of the non-anchor animals from the Related Specimens field, you can simply make a new selection without that individual. If you need to delete the original "anchored animal", open up the edit window for one of the other Related Specimens, and make a new selection of Related Specimens through their record. If you delete an entire Social event its connections to all the individuals involved will be deleted.

4.12.7 More Ideas on How to Use the Social Data Table

If you can't or don't want to track social interactions in detail, you can still use this table to record useful social data for your population. Listed below are four suggested alternate uses of the social data table:

	(+)	0	(-)
1) Confirmed Compatibility	Can live together	---	Cannot Live Together
2) Introduction Outcomes	Last Intro went well	Last intro was neutral	Last intro went poorly
3) Introduction Steps	Progress to next step	Keep trying at this step	Regress introduction steps
4) Free-form social notes	Last event was positive	Last event was neutral	Last event was negative

1) Confirmed Compatibility
   - Record one generic event to signify an individual's ability to successfully live with another animal. This can be a very helpful resource for planning social groups and breeding recommendations.

2) Introduction Outcomes
   - Only record the outcomes of introduction attempts. In other words, this allows you to see the results of each introduction attempt and whether or not it went well.

3) Introductions Steps

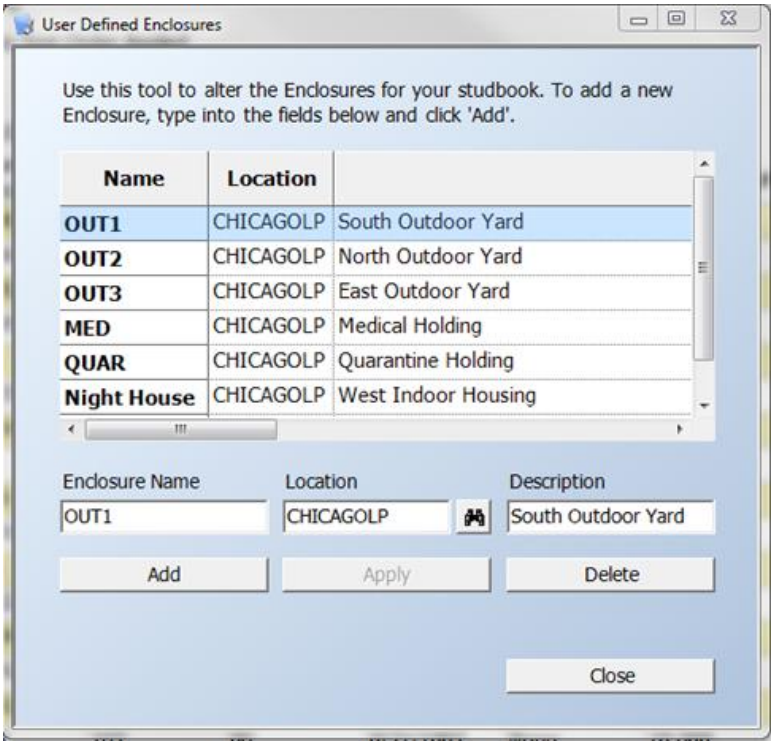
- Similar to #2, use this module to indicate and track the progress of introduction steps. This social module then becomes a useful resource for managers and care staff for communicating the progression of introductions. In other words, this table becomes a reference to see if you should progress to next step (i.e. from visual to protected contact), maintain at current step, or regress introduction steps.

4) Free-form social notes
   - Record any social events, as deemed important by the studbook keeper. However, when referencing the social compatibility report, be aware that the outcomes reflect a wide range of social event types, and consequently need to be interpreted carefully by referencing the social event notes in the social table or in an individual's social records.

4.13 ENTERING/EDITING ENCLOSURES DATA

Before you can create enclosure events in the Enclosures Data Table, you must develop a list of User Defined Enclosures for your studbook by going to Edit→ User Defined Enclosures.

4.13.1 User Defined Enclosures



The User Defined Enclosures pop-up has a table listing all entered enclosures across all institutions. Below that table is an area to edit, add new, or delete enclosures. You can define enclosures from many different institutions or several enclosures at the same institution. To track that, the User Defined Enclosures table lists the **Enclosure Name** (required), **Location** (required), **Description** (optional), and **Date Edited** (auto-filled) for each enclosure. Since **Enclosure Name** and **Location** uniquely define each Enclosure, you can have the same name for Enclosures existing in multiple locations (i.e. there can be an "Exhibit A" at CHICAGOLP, MYSTIC, and CHICAGOBR without any conflict).

4.13.2 Creating New Enclosures

To create a new Enclosure, enter the Enclosure Name (unlimited characters – free text), Location (institutional mnemonic), and Description (free text). Once the required fields are completed, click "Add" and a new line will be added to the User Defined Enclosures table.

4.13.3 Editing Existing Enclosures

To edit an existing enclosure, highlight the desired row and alter any of the three fields in the data entry fields below and click "Apply". When an enclosure is edited in any of the three fields, a dropdown history is visible in the User Defined Enclosures table. Note that editing an existing enclosure's name will change all related data records in the Enclosures data table in individual animal records.

4.13.4 Deleting Enclosures

To delete an existing enclosure, highlight the desired row from the User Defined Enclosures table and click "Delete". Note that once deleted, there is no way to view deleted enclosures. You will be prevented from deleting enclosures that are referenced in an animal's record in the Enclosure Data Table, even if there isn't anyone in the enclosure currently. If an enclosure is extinct (e.g., torn down or no longer used), make note of it in the enclosure description instead of deleting the enclosure. It may be helpful to rename the enclosure in a manner that signifies that it is extinct (i.e., start it with a capital "X" in front of the name to easily see that enclosure doesn't exist anymore (i.e., XexhibitA)).

NOTE: Tracking Changing Enclosure Names

Enclosures' names may change over time. Edit the original enclosure name to reflect the newer name, and make a note about the name in the Description field in the User Defined Enclosures table.

NOTE: Merging And Splitting Enclosures

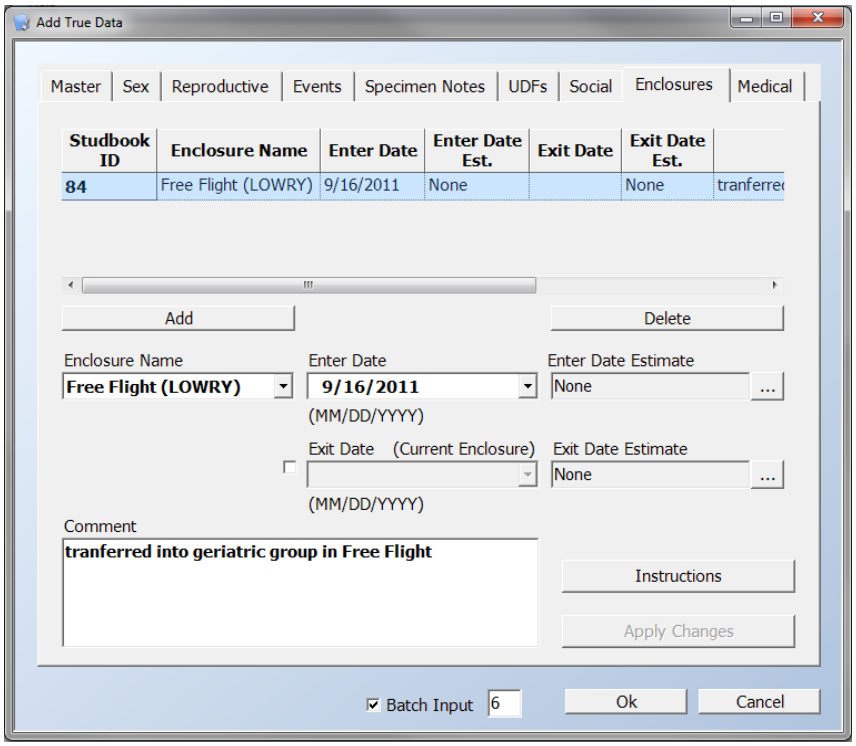
Enclosures may be combined or split to accommodate changing collection and institutional needs over time. Since PopLink only allows an animal to be in one enclosure at a time, it is easiest to create a new User Defined Enclosure to represent each different combination or parts of a split enclosure. For example, if enclosure A, B, and C are combined, it is best to create a new User Defined Enclosure representing all three of those enclosures (i.e. a User Defined Enclosure of ABC, with a description explaining the combination). Following this same logic, when a single enclosure is split, it is easiest to create a new User Defined Enclosure for each "sub-enclosure" created. The Enclosures data table only allows entry into one enclosure at a time, which may be complicated when an individual is given access to more than one enclosure at once. If an individual is given access to more than one enclosure at a time, it is best to create new enclosures to encompass each combination in one entry (e.g., if exhibits A, B, and C exist and can be managed in any combination to form a single or multiple exhibits, also have AB, AC, BC, and ABC as options). Use the Description section to explain what each represents. Only create combinations of Enclosures that are concurrently possible.

Name	Location	Description	Dated Edited
OUT2	CHICAGOLP	North Outdoor Yard	9/28/2011
OUT3	CHICAGOLP	East Outdoor Yard	9/28/2011
MED	CHICAGOLP	Medical Holding	9/28/2011
QUAR	CHICAGOLP	Quarantine Holding	9/28/2011
INDOOR1	CHICAGOLP	West Indoor Housing	9/28/2011
OUT2/3	CHICAGOLP	OUT2 + OUT3	10/19/2011

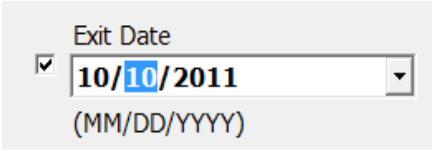
4.13.5 Creating Enclosure Table Records

Once you've created User Defined Enclosures, you can add data into the Enclosures data table. To edit existing Enclosure event(s), highlight the desired event and edit the data in the fields; to enter a new Enclosure event, use the Add button. To delete an existing Enclosure event, highlight the desired event and use the Delete button.

If creating an event for an individual that is currently in an enclosure, specify the Enclosure Name, Enter Date, Enter Date Estimate, and a Comment (optional), and select "Apply Changes". Leave the Exit Date blank to indicate that the individual is currently in the enclosure.



To enter historic enclosure events (e.g. track where an individual has been over its lifetime, use the Exit Date and Exit Date Estimate fields to reflect the timeframe the individual was in an enclosure. To activate these fields so that data can be entered, select the checkbox next to the Exit Date:



PopLink enters today's date as a default when you select the checkbox, but you can edit the Date and the Date Estimate as appropriate.

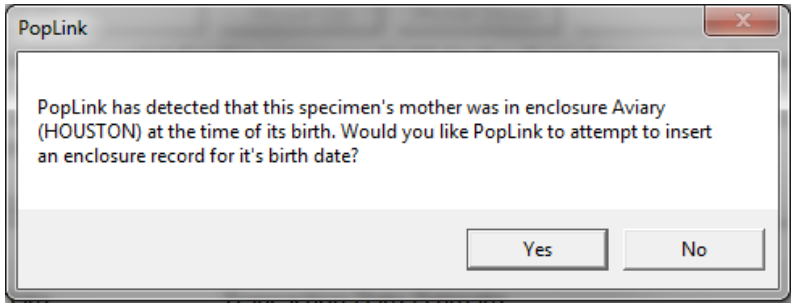
When a new Enclosure event is added that would occur after another event, based on the Enter Date, PopLink attempts to fill in an appropriate Exit Date based on the new record's Enter Date. You should check the Enter and auto-filled Exit dates carefully to assure accuracy and edit the Exit dates if PopLink's auto-entered assumption is incorrect. Note that individuals are not required to have a continuous Enclosures history – there are no data checks for gaps in time during data entry.

NOTE: PopLink doesn't crosscheck location and enclosure location validity (i.e. if the rest of the record says this animal is in CHICAGOLP but the enclosure location is in CHICAGOBR). Be sure to select the correct enclosure for your individual. Also, there are no move up/down buttons for this table - be cognizant to enter events in the same day in chronological order.

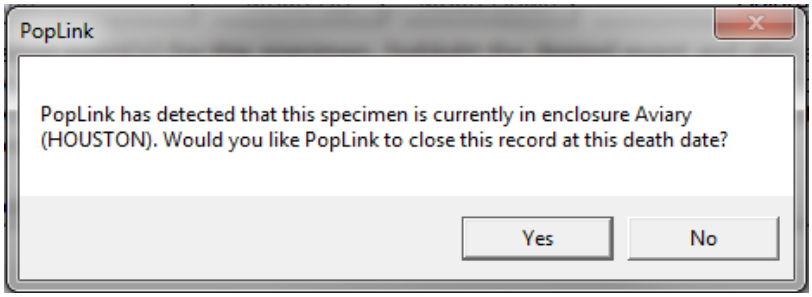
4.13.6 Auto-Adding Birth and Death Information from Events Record

If you are tracking Enclosures in your database, PopLink may offer to assist you in adding enclosures records as you are entering birth and death event data for an animal:

1. **Births -** When a new animal is created, if the Dam of an animal has a current enclosure record, PopLink will ask if you want to add an enclosure event into the same enclosure for the birth of the offspring (the newly created individual) with a pop-up. If "No" is selected, no further action is taken. If "Yes" is selected, an Enclosure event will be added to the new animal's Enclosures record with its birth date as the Start Date and a comment auto-added saying "Born/Hatched in enclosure". Even if an individual is entered into an enclosure on their birth date, there needs to be a comment auto-added by PopLink through this pop-up to count as a birth/hatch in an enclosure in the Enclosure Reports.



2. **Deaths -** When a death event is added to an individual's Events record and the individual is currently in an enclosure, PopLink will prompt you with a pop-up offering to create a death event in their current enclosure. If "No" is selected, no further action is taken. If "Yes" is selected, adds the Death Event Date as an End Date to the individual's current Enclosure record and adds a comment "Died in enclosure". There needs to be a comment auto-added by PopLink through this pop-up to count as a death in an enclosure in the Enclosure Reports.



Examples of auto-added events:

Master | Sex | Reproductive | Events | Specimen Notes | UDFs | Social | Enclosures | Medical | Studbook Overview

Studbook ID	Edit	Enclosure Name	Enter Date	Enter Date Est.	Exit Date	Exit Date Est.	Comment
18	...	Aviary (HOUSTON)	9/6/2011	None		None	
27	...	Aviary (HOUSTON)	9/6/2011	None		None	
28	...	Aviary (HOUSTON)	9/5/2011	None	9/6/2011	None	Died in enclosure.
83	...	Aviary (HOUSTON)	9/6/2011	None		None	Born/Hatched in enclosure.

4.14 ENTERING/EDITING MEDICAL DATA

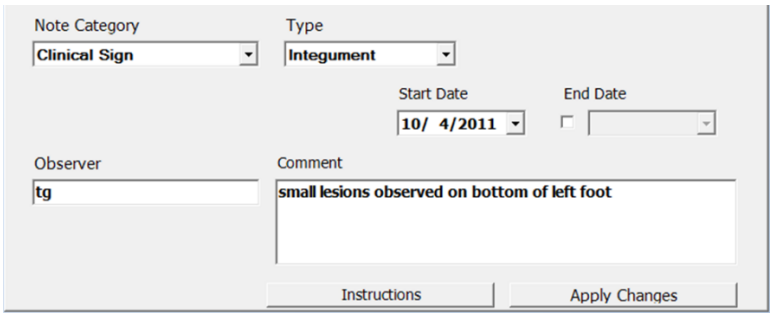
The medical module was designed to keep track of important medical information essential to daily care or population management. Eight different categories of medical notes can be recorded here. Each **Note Category** displays a different data entry configuration with required and optional fields. All the notes types are specialized for

a specific type of medical data, except for the General Medical Note category which can be used for any type of medical information that does not fit in the other seven categories. With all note categories, you can record the **Observer** (optional), which will typically be the person observing the issue and not necessarily the studbook keeper recording the issue in the studbook, and a **Comment** field.

NOTE: Once a medical event is created, everything in the event is editable *EXCEPT* the Category. If the wrong category is selected and "Apply Changes" is pressed, the event will need to be deleted and re-entered with the correct Note Category selected. If the mistake is caught before "Apply Changes" is selected, the Note Category can still be changed.

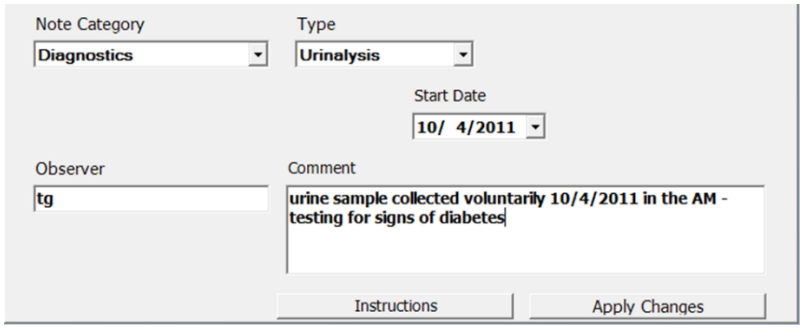
The following figures systematically list and explain the purpose of each Note Category:

4.14.1 Clinical Sign



The **Clinical Sign** category allows you to track any unusual signs/symptoms being displayed by an individual. The **Type** field describes the body system (Cardiopulmonary, Endocrine, Gastrointestinal, Integument, Lymphatic, Musculoskeletal, Nervous, Reproductive, Urinary, or Other). This functionality is somewhat equivalent to a red flag for an individual's health. This type of information can be helpful to query when looking for symptomatic trends in an individual or across a population of individuals. In this category, the **Type** and **Start Date** are the only required fields. The End Date field can be used to reflect the duration of a Clinical Sign; select the check box to be able to edit the End Date field.

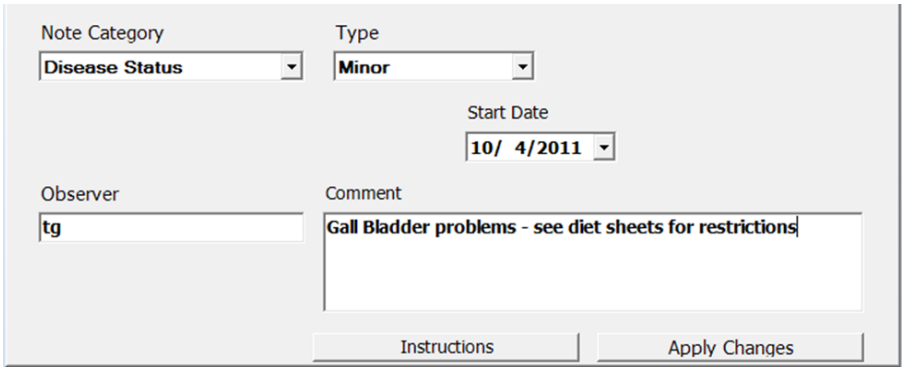
4.14.2 Diagnostics



The **Diagnostics** category is intended to allow users to track any medical tests for an individual. The Diagnostics can be specified by **Type** (Chemistry Panel, Culture, Hemogram, Imaging, Serology, TB Test, Urinalysis, Pathology/Biopsy, or Other). For any Diagnostics type, the **Start Date** should be the date the diagnostics were sampled or taken; the note should be updated later in the Comment section to report the test results. In this category, the **Type** and **Start Date** are the only required fields.

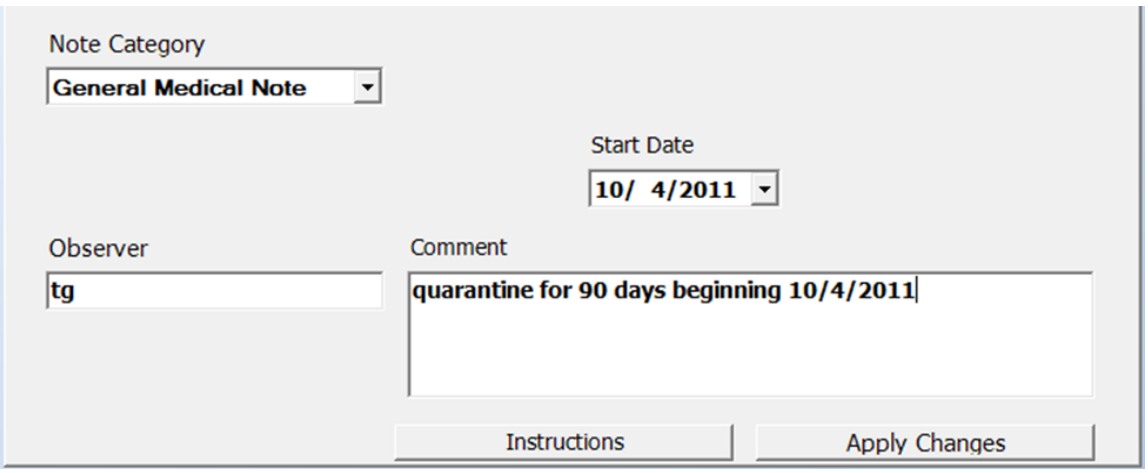
NOTE: The Diagnostics note type can be a useful tool in documenting medical tests and their results. Be sure to use complete and standard accepted veterinary language and avoid using shorthand - think about how others would interpret the note and maintain standards over time. Follow up on all tests and results in the comment section, even if the results are inconclusive.

4.14.3 Disease Status



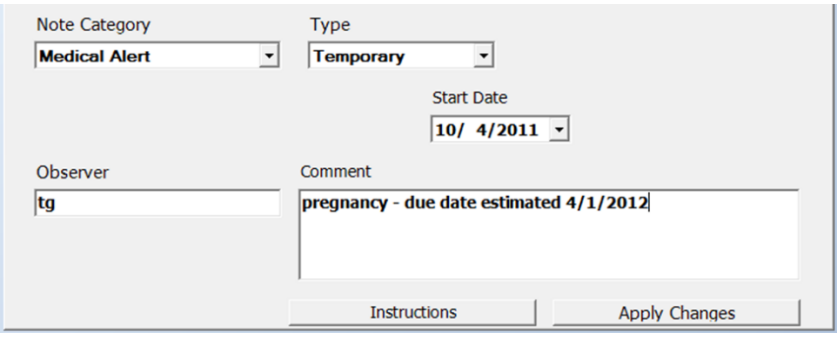
The **Disease Status** category is intended to keep record of significant changes in the condition of an individual (**Type**: Healthy, Minor, Moderate, Severe, Grave, or Other). When a **Disease Status** note is entered, you should include a **Comment** explaining the specifics of the status. In this category, the **Type** and **Start Date** are the only required fields. You could enter a single **Disease Status** note for an individual and edit that note over time to always reflect their current status, or enter multiple **Disease Status** notes to track changes in status over time.

4.14.4 General Medical Note



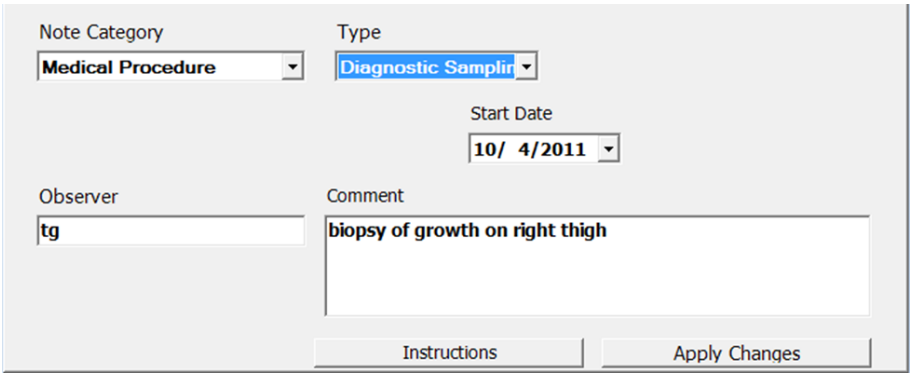
The **General Medical Note** category is intended to allow flexibility in the type of medical information kept. Here, the only required field is the **Start Date**. The **Observer** and **Comment** fields are optional. Use the Comment field to describe more details about what you are noting. If you have common Medical Note types that are frequent across multiple individuals, use a standard description for these in at least part of the comment box (e.g. "LETHARGY NOTED" at the beginning of the note); this will allow you to easily search for individuals with that note using the Filter options (see chapter 5) or sort the Medical Notes table to quickly see affected individuals. Record these conventions in the Studbook Overview's Notes Section.

4.14.5 Medical Alert



The **Medical Alert** category is intended to alert staff to a health condition, allergy, or disease that is important in providing appropriate care for an individual. In this category, the **Type** and **Start Date** are the only required fields, but the details on the alert should be provided in a Comment. The Type field provides three options (Permanent, Temporary, or Other). The **Type** assigned to a Medical Alert describes how long it is applicable (e.g., arthritis would be considered a Permanent condition, pregnancy would be considered Temporary, and Other would be defined as an unknown period of time or as an intermittent condition). Use the **Comment** text box to detail the type of condition and if or when it ends.

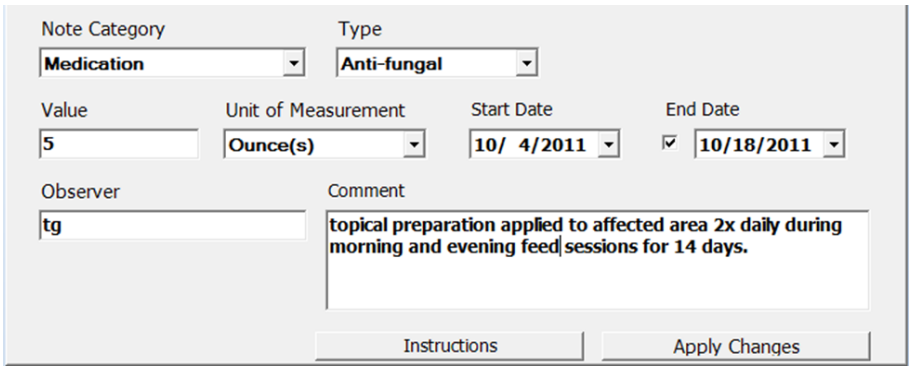
4.14.6 Medical Procedure



The **Medical Procedure** category is intended to track any physical procedure or medically related event with **Types** (Diagnostic Sampling, Medical Exam, Sedation, Surgical Procedure, Visual Assessment, Prescription, or Other). Use the optional Comment text box to detail the **Type** of **Medical Procedure** and any accompanying follow-up. In this category, the **Type** and **Start Date** are the only required fields.

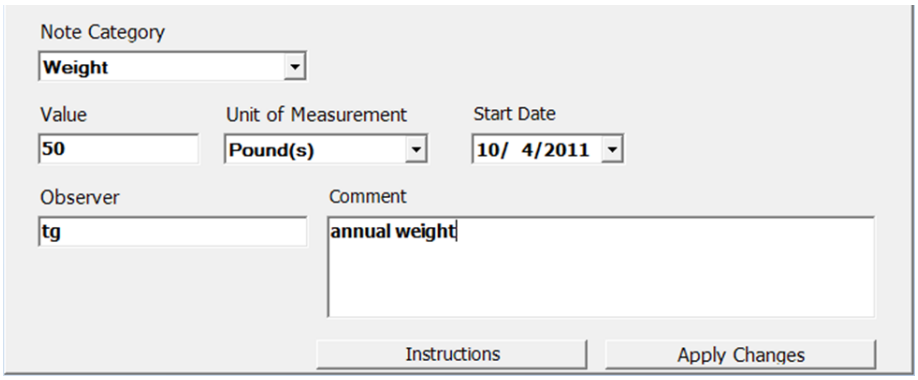
4.14.7 Medication

The **Medication Note** category is intended to document the **Type** of medication (Analgesic, Antibiotic, Anti-fungal, Anti-Inflammatory, AntiParasitic, Behavioral Modifier, Cardiac Modulator, Contraceptive, Gastric Motility, Gastroprotectant, Hormone, Nutraceutical, Respiratory Product, Topical Preparation, Vaccine, or Other), **Value** (numerical amount administered in one dose), **Unit of Measurement** (Microgram(s), Milligram(s), Gram(s), Kilogram(s), Pound(s), or Ounce(s)), and the **Start/End Dates** for a medication. In this category, the **Type, Value, Unit of Measurement**, and **Start Date** are the only required fields. Unless a medication is permanent, there will usually be an End Date as well.



NOTE: To make the Medication Note category effective, use the Comment field to record the dosage frequency of a medication (e.g., 2x daily for 1 week), special dosage instructions (mix powder with 2 oz. of apple juice and administer as the first item for a feed), or any other important information (e.g., do not mix with any citrus fruit – reaction potential). Also, use this space to provide a complete medication prescription description.

4.14.8 Weight



The **Weight** category allows easy tracking of body weight over time. In this category, the **Value**, **Unit of Measurement**, and **Start Date** are the only required fields. In the **Value**, enter the numerical weight (free text), and in the **Unit of Measurement** field, use the dropdown menu to choose from the selection (Microgram(s), Milligram(s), Gram(s), Kilogram(s), Pound(s), or Ounce(s)). The **Comment** section can be useful for tracing possible causes of weight gain/loss, etc.

4.15 ENTERING/IMPORTING BREEDING EFFORT DATA

Historically, it has been difficult to get a complete picture of breeding activity using studbook data alone. Looking back at historical records, it is straightforward to see whether a pair produced offspring as long as those offspring were assigned a studbook ID. However, that is just one piece of the broader breeding story, and many important details are not fully captured in studbook data.

Consider the kinds of questions that often go unanswered: What proportion of a population's reproductive-aged animals were attempting to breed? How long was a pair given physical access to each other during the breeding season? If a pair did not produce living offspring, did they produce eggs, and were any of those eggs fertile? Do pairs produce more offspring when using a specific nest box or breeding enclosure? Using PopLink's **Breeding Effort** module helps fill in these gaps, allowing users to build a more complete understanding of breeding outcomes.

4.15.1 Defining a breeding effort

Before you begin to collect and enter data into the Breeding Effort module, you should first define what a "breeding effort" is for your population. The definition of a breeding effort will depend on species biology, management practices, and monitoring methods.

For example, if you want to quantify the breeding success rate of a population, you need to know not only how many pairs successfully produced offspring, but also how many failed to do so. Even for populations maintained in zoos and aquariums, this can be difficult to determine. With traditional studbook data, it is possible to establish if a potential breeding pair of animals was held at the same facility during the same time, but you generally can't confirm if those individuals were kept in the same enclosure and therefore had an opportunity to breed (or, even if they were in the same enclosure, if they were provided anything they would be required to start breeding, such as a nest box). For this scenario, a breeding effort could be defined as the amount of time a potential breeding pair were given physical access, or the time they were provided physical access with a nest box and any other physical requirements for reproduction. A breeding effort could also be smaller in scope. For instance, for some populations, artificial insemination is an important tool in achieving reproductive success, and each insemination attempt could constitute a breeding effort.

For wild populations breeding efforts might be more challenging to define because of the limits of observation. For example, when monitoring a wild female tiger fitted with a VHF collar, an observed courtship and copulation event with a resident male may constitute a breeding effort. For an established breeding pair of wolves, a breeding effort might be defined as the period the pack occupies a den site each spring. In bird populations monitored through the resighting of banded individuals, breeding may only be detected when a nest is discovered, in which case the nesting attempt itself could be recorded as the breeding effort.

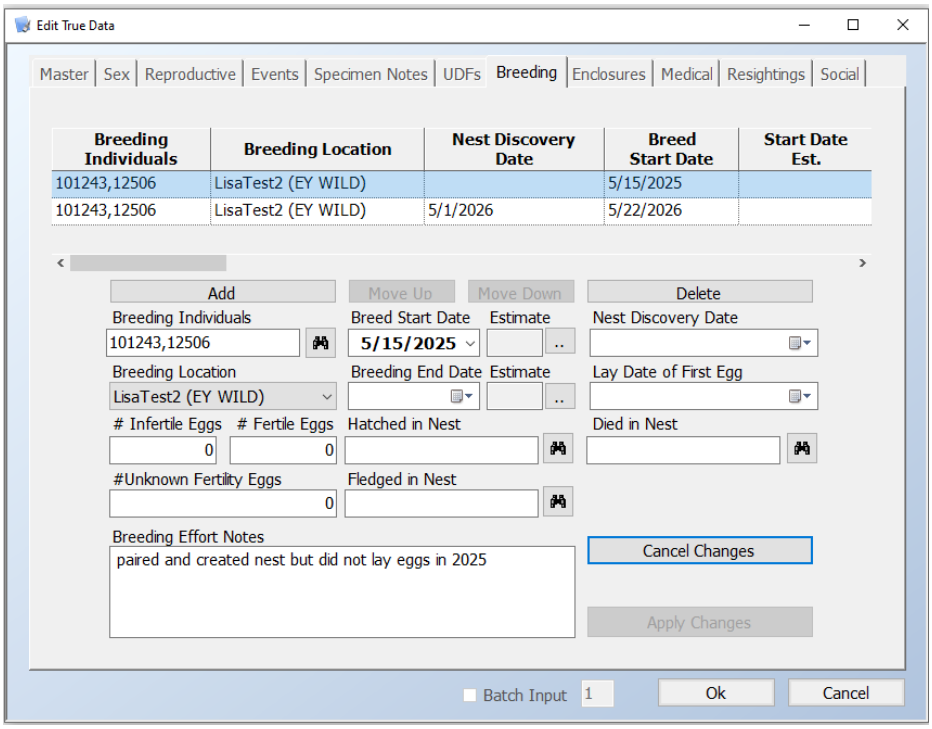
Once a breeding effort has been defined, you should also specify its timeframe by defining when it begins and ends. For seasonal breeders, an entire breeding season may be recorded as a single breeding effort. In closely managed populations, each breeding introduction or insemination attempt may be recorded as a separate breeding effort, even when multiple attempts occur within the same season. For free-ranging species, a breeding effort may span an entire nesting attempt, denning period, or another biologically meaningful reproductive event.

There is no single correct definition of a breeding effort. The key is to have a clear idea of how you plan to use breeding effort data before you begin inputting it, and to consistently maintain that definition throughout the time that you're monitoring the population (or, at least, keeping clear records about when your definition changes, so that you can analyze data with that context). Once you know your intended methods, we recommend documenting your definition of a breeding effort in the Studbook Overview Species Notes section to ensure that future users can interpret the data you have collected.

4.15.2 Entering breeding effort data

You must have the Breeding Effort module clicked on in Edit→"Settings" to view or enter any data.

To manually add breeding effort data for an individual select the "Edit" button located to the right of an animal's Studbook ID or the "Edit Animal" option in the Edit pull-down menu. An animal editor pop-up window will then appear, and selecting the "Breeding" tab will open the breeding effort screen. Select "Add" to create a new blank breeding effort record. Each animal could have multiple breeding efforts added (i.e. multiple rows in this table) over their lifetime.



The field names for the breeding effort data entry pop-up will differ depending on if the species is live bearing or egg laying (entered in Edit→Studbook Overview).

In the breeding effort pop-up window there are a number of fields shared by both live bearing and egg laying species. **Note that the only mandatory fields required to create a breeding effort entry are "Breeding Individuals" and "Breed Start Date":**

Breeding Individuals
In this field, identify which potential breeders are involved in a breeding effort. You can either type the individuals into the field, or you can search by selecting the binocular icon to the right of the field. It is possible to add individuals of unknown sex to a breeding group or create breeding groups comprise entirely of one sex.

If you type the studbook IDs into the field, make sure that each individual ID is separated by a com ma with no space (e.g., 200,201,202). If a breeding effort involved unknown or wild individuals, you can add UNK, MULT or WILD in the Breeding Individuals field.

Selecting the binocular icon will open a pop-up that is pre-filtered to show all living individuals in the population. You can edit the filters by clicking the "Filter" button within the pop-up. Highlight one or more individuals (using control click) or use the right and left arrows to add or remove individuals.

NOTE: You can create breeding effort records for breeding groups made up of only WILD or UNK breeding individuals. To do so, first select the "Edit" button located to the right of any animal's Studbook ID or the "Edit Animal" option in the Edit pull-down menu. Once in the Breeding tab, select "Add" and then delete that individual's studbook ID from the breeding individuals field. You can then type in UNK, WILD or any other combination of breeding individuals you would like. The finished record will be visible in the master Breeding tab, and not tied to the original studbook individual's record.

Breed Start Date and Breeding End Date
Here you can add the start and end date for a breeding effort by either typing the date or selecting from the drop-down menu, as well as any estimate around those dates. **Only the start date is mandatory**, and you could use a known date (i.e. date you opened the breeding cages) or an assumption (a standard date across all potential pairs that is the typical start of a breeding season) or calculate the date based on other data (i.e. a date back-calculated from a nest discovery date based on the age of the oldest egg in a nest). Again, identifying and documenting a consistent data convention across your studbook will be important (document it in the Studbook Overview Species Notes).

Breeding Location
You have the option of adding a breeding location to each breeding effort record. For a zoo or aquarium, a breeding location might be a specific tank, habitat or room. For a free-ranging population, a breeding location might be a specific nest box, colony, lek or den. Before adding a breeding location to a breeding effort record, you first need to create a location using the User Defined Enclosures module (*see section 4.13*). Within the breeding effort pop-up, all User Defined Enclosures will be available for selection in the Breeding Location field drop-down menu.

4.15.3 Entering breeding effort data for Egg Laying species

When entering breeding effort data there are a number of optional fields available only for egg laying species: Nest Discovery Date, Lay Date of First Egg, #Infertile Eggs, #Fertile Eggs, #Unknown Fertility Eggs, Hatched in Nest, Died in Nest, Fledged in Nest.:

#Infertile Eggs, #Fertile Eggs, #Unknown Fertility Eggs
These fields allow you to enter the number of eggs of each type into the breeding effort table.

Hatched in Nest, Fledged in Nest, Died in Nest
In these fields you enter the studbook ID for the individuals in each category. You can either type the studbook IDs (comma separated with no spaces), or search for and select the individuals by clicking on the binoculars icon to the right of the field. PopLink will not check if the potential parents listed in the "breeding individuals" field match the parents listed for an offspring in its individual studbook record (because in some programs, individuals are purposely cross-fostered between nests or dens), so carefully review all studbook IDs associated with each breeding effort record. If no individuals hatched, fledged, or died in the nest, leave the field blank. **Every individual that hatches should be listed in the "hatched" field even if they later fledge or die in the nest**, this ensures that the number of total hatches are tallied correctly when you run one of the Breeding Effort Reports.

NOTE: Nest survival rates can be an important metric in assessing the health of a population, but accurately estimating those rates can be a challenge for free-ranging populations. A key difficulty is that in order to assess the survival rate of a nest, a nest must first be discovered. Unfortunately, researchers rarely find nests immediately after a nesting attempt is initiated. As a result, nests that fail early in an attempt are less likely to be detected. Since these early failures are underrepresented, estimates of nest survival can be biased. A solution, pioneered by Mayfield (1961) and maintained in newer methods, is to incorporate the number of days a nest was under observation into estimates of nest success. What does this have to do with PopLink? The **Nest Discovery Date** and **Breeding End Date** fields allow you to track the number of days a nest was under observation, supporting more accurate and less biased estimates of nest survival.

4.15.4 Entering breeding effort data for Live Bearing species

When entering breeding effort data there are a number of **optional fields** available only for live bearing species:

# of Deaths before Birth
This field allows you to enter the number of offspring that died before birth in a breeding attempt (i.e. prenatal mortality – stillbirths or other prenatal signs that you want to enter). These would likely be individuals that would not receive a studbook ID, but your program may still want to track them as important metrics of pair fertility or breeding success

Pregnancy Confirmed
Here you can add the date at which a pregnancy was confirmed by either typing the date or selecting from the drop-down menu.

Offspring, Died before Independence
In these fields you enter the studbook IDs for the individuals in each category. You can either type the studbook IDs (comma separated with no spaces), or search for and select the individuals by clicking on the binoculars icon. PopLink will not check if the potential parents listed in the "breeding individuals" field match the parents listed for an offspring in its individual studbook record (because in some programs, individuals are purposely cross-fostered between nests or dens), so carefully review all studbook IDs associated with each breeding effort record. **Every individual that is born should be listed in the "offspring" field even if they later die before achieving independence**, this ensures that the number of total offspring are tallied correctly when you run one of the Breeding Effort Reports. You can assess what "independence" is for the purposes of your studbook – you may want to use this as the point until emergence from the den, weaning, or some other point. If no individuals were born or died before independence, leave the field blank.

If you are adding or editing a breeding effort and want to remove the information added to a record before it is saved, you can select "Cancel Changes". Once you have added all of the desired information to a breeding effort record, select "Apply Changes" to formally add the record to the breeding effort table.

Note that when multiple individuals are involved with a breeding effort, entering the data into one of their records will mean it is automatically included in all of them (i.e. visible in their Individual Animal Report, etc.)

NOTE: The "Died in Nest" or "Died Before Independence" fields may be unnecessary – you can always evaluate age at death for any offspring entered into your studbook and assess whether it was before or after a typical fledge date or independence date that might be standard for a species. However, some programs want to tie particular success of a breeding pair or particular nest location to the success of getting offspring to that important milestone. For example, if a particular pair is very successful at hatching chicks but never at getting offspring to fledging, it may be beneficial to analyze that in the context of the overarching breeding analysis that this module will enable. Once again, designing how you'd like to use the data in this table carefully before you begin entering it for your population will mean that you have the best chance at having the data to understand your population!

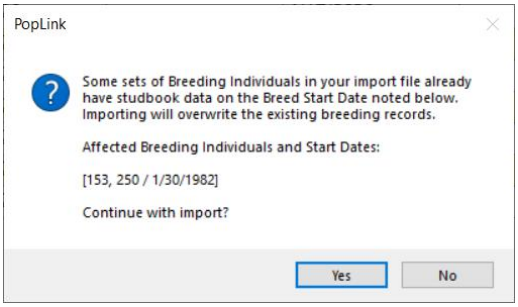
4.15.5 Importing breeding effort data from a CSV File

You can also add breeding effort records to a PopLink database by importing records stored in a comma-separated values (.csv) file. The first row of the file should contain column headers for the breeding effort records. The only headers that are required for an import to be successful are **Breeding Individuals** and **Breed Start Date**. You also have the option of adding headers for any of the fields listed above, but **remember that the fields available for egg laying or living bearing species are different, and the headers for your import must match those available for the species you are working with**. **For <u>egg laying</u> species the potential headers are:** Breeding Individuals, Breeding Location, Nest Discovery Date, Breed Start Date, Start Date Est. Breed End Date, End Date Est., Lay Date First Egg,

Infertile Eggs, Fertile Eggs, Unknown Fertility Eggs, Hatched In Nest, Fledged in Nest, Deaths in Nest, and Breeding Effort Notes. **For <u>live bearing</u> species the potential headers are**: Breeding Individuals, Breeding Location, Breeding Location Discovery Date, Breed Start Date, Start Date Est. Breed End Date, End Date Est. Pregnancy Confirmed, Died Before Birth, Live Offspring, Deaths Before Independence, and Breeding Effort Notes.

After the headers, each subsequent row represents a single breeding effort record for a group of individuals in the studbook.

NOTE: When you import a breeding effort record with the same breeding individuals and breeding start date as an existing record, PopLink **<u>overwrites</u>** the existing record with the information provided in the import file. This allows you to import breeding effort records at the beginning of a breeding season and then update those records by importing outcome data later in the season. Before overwriting any existing records, PopLink displays a pop-up listing the breeding efforts that will be affected and asks whether you want to continue with the import.



There are a few important rules for the data entered into these columns, and PopLink will automatically validate for these rules as you attempt an import.:

- **Breeding Individuals** – IDs can be comma or semi-colon delimited; having a space between IDs is OK. If a breeding effort involved unknown or wild individuals, you can add UNK, MULT or WILD (or UNK#, WILD#, etc.) in the Breeding Individuals field.
- **Breed Start Date** – The breed start date format should be consistent across the .csv import file and match the Current Date Format in the PopLink database, which matches the Date and Time Settings on your computer (M/d/yyyy, d/M/yyyy, etc.).
- **Breeding Location** – If you include breeding locations in your import, note that this field is case sensitive, and any imported breeding location must match those already created within Poplink.

Once data has been correctly formatted and stored in a .csv file, you can import the data into a PopLink database by selecting File→ Import Breeding Efforts Data. In the pop-up, navigate to the .csv file and select Open. If the file is error free, a pop-up window will open which outlines how many records were imported into the database and reminding you to review and validate the new records. Selecting OK on this window will give you access to the newly added data. The imported CSV will also be archived in the "Imported Data" folder within your studbook folder (i.e., PopLink Databases\YourStudbookName\Imported Data).

If there are errors in your import file– blanks in required data fields, missing columns, or invalid data entries--the data within the .csv file will not import and PopLink will open and display the original import file with the addition of a column listing the errors for each breeding effort row. At the bottom of the .csv, PopLink also adds a column titled Validation Error Key that shows all potential error codes and describes the corresponding errors. The import file will be renamed with "BreedingEffortsERRORS" added as a suffix to the original file name (i.e. if your file was "TestImport", the new file will be named "TestImport_BreedingEffortERRORS"). You can edit the open file to fix the identified errors, then save and reattempt upload.

4.16 ENTERING/IMPORTING/EDITING RESIGHTINGS DATA

Regular monitoring of free-ranging animals is essential for assessing a population's demographic status. The ability to identify individual animals based on unique features (e.g., tiger stripe patterns) or human-applied markers (ear tags, bands, VHF collar, etc.), enables the tracking of resightings in the field. The **Resightings** module in PopLink allows users to efficiently enter, store, view and export sightings data for individual studbook animals.

4.16.1 Structuring your Resightings Table

PopLink's basic Resightings table includes only two fields: Resighting Date (mandatory) and Resighting Notes (Optional). However, PopLink allows users to add custom columns (i.e., Resighting Fields) to the resighting table, facilitating the collection and storage of additional data with each resighting record.

NOTE: Data on resightings of marked individuals is a key foundation of analyses that allow researchers to estimate a population's abundance, growth rates, survival rates, and more. The types of questions researchers can ask and the quality of estimates made using resightings data depend on the data collected, and how standardized those data are.

This is where **Resighting Fields** come in. Creating your own resighting fields gives you the opportunity to store any data that may be useful for analysis. For instance, you likely want to record where an individual was encountered, so you could create multiple resighting fields for GPS coordinates or camera trap location. It is important to know how an individual was observed (e.g., seen during a formal transect survey versus opportunistically observed crossing a road), so a resighting field for observation method could be valuable. To facilitate analysis of resighting data it is critical to collect data on factors that might impact the probability of detecting an individual, so that might mean creating resighting fields for weather, time of day, and distance from observer. Finally, if you are interested in assessing habitat use or behavior of marked individuals, you may want to create resighting fields for factors such as habitat type, number of individuals observed with the focal individual, reproductive state, or body condition. **The key is to have a clear idea of how you plan to analyze your resighting data before you begin collecting it.** Once you know your intended methods, you can set up the structure in your Resightings table by creating your custom resighting fields and get out there!

NOTE: If you want to store georeferenced data in resightings fields, you can use any coordinate system you prefer. PopLink does not validate or check these data, and will upload and store them as provided given the diversity of potential coordinate systems. We strongly recommend that if you store georeferenced data in resighting fields, you document the coordinate system (e.g., the datum and projection) in the Studbook Overview Species Notes section. This ensures that the relevant metadata are available to interpret the coordinates you've entered.

4.16.2 Adding and editing resighting fields

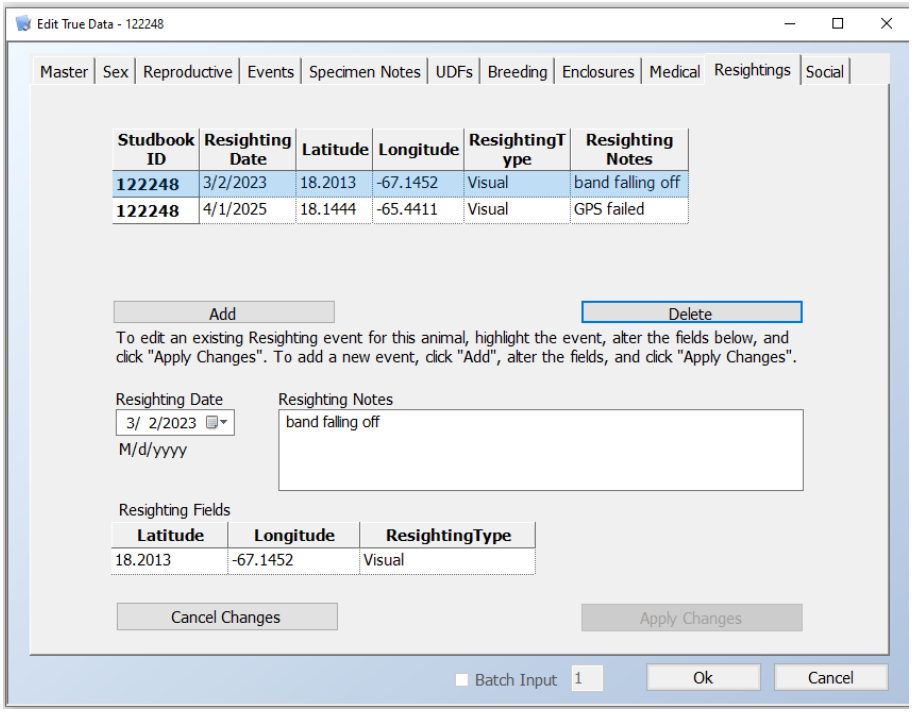
Users can add a resighting field by selecting Edit→ Resighting Fields and a window will display the existing Resighting Fields. In this pop-up, you can:

- Add New: Enter a name and description in the *Resighting Field Name* field and select "Add", and these will be added to the Resighting Fields table.
- Edit Existing: Above, select the row you'd like to edit in the table, and then click below on the field you'd like to edit (Name, Description), and select "Apply".
- Reorder: In this window, selecting a Resighting Field and clicking "Move Up" or "Move Down" will change the order in which each Resightings Field appears in the Resighting table.
- Delete: Above, select a row in the resighting field table and click "Delete". Delete resighting fields with caution, as removing a field from this table will permanently delete all data stored in this column from the database. Note that you cannot delete the Studbook ID or Resighting Notes fields.

Once you've set up the structure of your Resightings table, you can begin entering or importing your data.

4.16.3 Entering resightings data

To manually add resightings data for an individual select the "Edit" button located to the right of a specimen's Studbook ID or the "Edit Specimen" option in the Edit pull-down menu. A specimen editor pop-up window will then appear, and selecting the "Resightings" tab will open the resightings screen.



On this tab, you can:

- Add a new record: Selecting "Add" will create a new blank resightings event visible in the table view in the editor. Enter the date, resightings notes, and values for any Resighting Fields you created. In order for the event to be officially created you need to choose a resighting date and select "Apply Changes".
- Edit an existing resighting record: highlight the row in the table, and edit the fields below. To save, select "Apply Changes"
- Delete: remove a resighting record by highlight the row and clicking "Delete"

If you are adding or editing a resightings event, and want to remove the information added to a record before it is saved, you can select "Cancel Changes". Note that you can create multiple resightings records for an individual for the same date (i.e. if an animal was seen on a camera trap multiple times within a day).

4.16.4 Importing resightings data from a CSV File

You can also add resightings records to a PopLink database by importing records stored in a comma-separated values (.csv) file. In order for an import to be successful, the data stored within the .csv file must be formatted correctly. The first row of the file should contain column headers for the resightings records. Those headers must include **Studbook ID, Resighting Date** and **Resighting Notes**. If you created resightings fields, you have the option of including a column header matching the name of each field created. The order of the Resighting Fields columns in the .csv will not impact the ability of the file to import. After the headers, each subsequent row represents a single resighting record for an individual in the studbook.

There are a few important rules for the data entered into these columns, and PopLink will automatically validate for these rules as you attempt an import.:

- Studbook ID – Studbook IDs for each resighting record in the .csv file must match an existing studbook ID in the PopLink database.

- Resighting Date – Resighting date formats should be consistent across the .csv import file and match the Current Date Format in the PopLink database, which matches the user's Date and Time Settings on their computer (M/d/yyyy, d/M/yyyy, etc.).
- Resighting Notes – A resighting notes column must be included in your .csv, but this field can be left blank for a given record.

Once data has been correctly formatted and stored in a .csv file, you can import the data into a PopLink database by selecting File→ Import Resightings Data. In the pop-up, in the file selection box, navigate to the .csv file and select Open. If the file is error free, a pop-up window will open which outlines how many resightings records were imported into the database and reminding you to review and validate the new records. Selecting OK on this window will give you access to the newly added data. The imported CSV will also be archived in the "Imported Data" folder within your studbook folder (i.e., PopLink Databases\YourStudbookName\Imported Data).

If there are errors in your import file– blanks in required data fields, missing columns, or invalid data entries--the data within the .csv file will not import and PopLink will open and display the original import file with the addition of a column listing the errors for each resighting row. The import file will be renamed with "ResightingsERRORS" added as a suffix to the original file name (i.e. if your file was "TestImport", the new file will be named "TestImport_ResightingsERRORS"). You can edit the open file to fix the identified errors, then save and reattempt upload.

NOTE: Newly imported resighting records are always added to PopLink as new resightings, they never over-write existing records. This allows users to add multiple resightings for the same date, which may be important for some studies. However, if you accidentally import a resightings file with records that were already uploaded to PopLink, you could create true duplicate records. To prevent duplicates, you could make sure to carefully check your resightings table or the Resighting Analysis report to either delete duplicates directly from the database or deal with them post hoc in your data processing before analysis. You could also add a "Sighting ID" field to your resighting fields and assign each new record a unique ID as it is created. You can then quickly scan for repeated IDs and remove any duplicate records as needed

4.16.5 Viewing resightings data

After a resightings record is created, you can view all of the resighting records for the database by navigating to the "Resightings" tab in the main data viewer. To view the resightings record for a single individual, open an "Individual Animal Report" for the individual in question, and click on the "Secondary" tab.

4.17 OTHER GENERAL COMMENTS ON EDITING ANIMALS

4.17.1 Deleted Data

If for some reason you want to delete an entire animal from your database, you can do so using the menu option in the Edit drop-down menu. Within the animal editor you can also delete portions of an individual's record, such as specific rows of data in the Sex, Reproductive, Event, UDF, and Species Notes tables. Be careful, as there is no "undo" option when you are deleting data.

To view data that you have deleted, use the View Deleted Translated Data option in the View drop-down menu. It will display a table with data from specific tables that have been deleted:

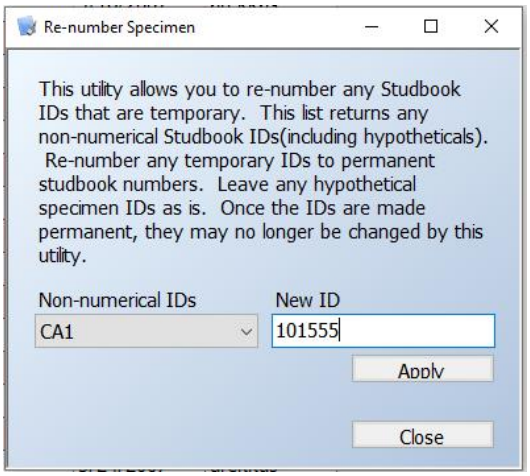
Master | Sex | Reproductive | Events | Specimen Notes | Social | Enclosures | Medical

Studbook ID	Sire	Dam	Hatch Type	Hatch Date	Hatch Date Est.	Rearing	Owner	Date Deleted	User Deleted
1018	WILD	WILD	Wild Hatch	7/1/1977	Unknown	Parent	Not Reported	2/13/2007	cschloss
82	193011	191183	Captive Hatc	7/2/2003	Year	Foster		3/2/2007	arekkas
145	186077	029	Captive Hatc	7/2/1992	Year	Foster		3/12/2007	arekkas
1027	188140	189140	Captive Hatc	7/2/1995	Year	Not Reared		3/14/2007	arekkas
1048	186095	184050	Captive Hatc	7/2/1997	Year	Not Reared		3/20/2007	arekkas
105298	193011	191183	Captive Hatc	4/11/2005	None	Foster		4/2/2007	arekkas

You cannot click on a button to "undelete" these data, but you can reenter them by hand if the deletion was a mistake.

4.17.2 Renumbering Animals

Generally you should not change a permanent studbook number once you have assigned it. If you have assigned a temporary number to an animal, there is a function within PopLink to reassign that individual a permanent studbook number. If you select Re-number Specimen from the Edit pull-down menu, a tool will pop-up which lists all non-numerical IDs in the studbook:



You can select any given non-numerical ID and type in a permanent studbook number to change the animal's ID permanently. Unlike SPARKS, PopLink will not prompt you with the next available numerical studbook ID. You should look up the next available numerical ID before using the Re-number Specimen tool.

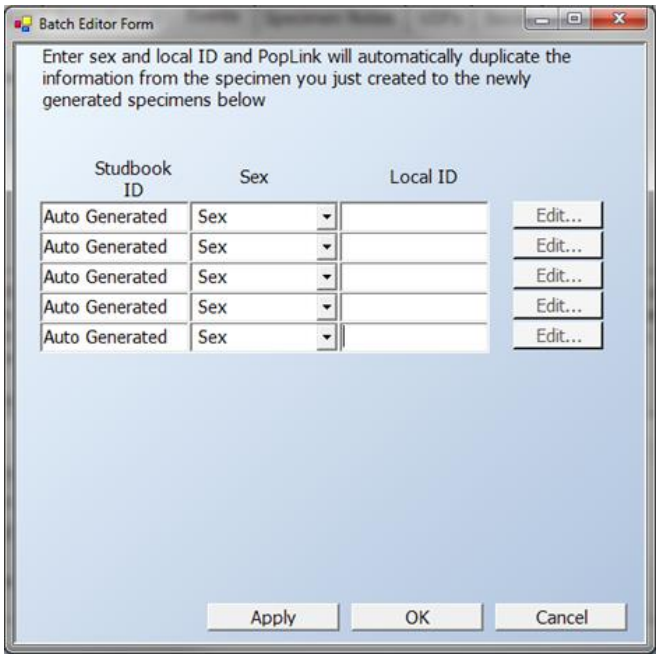
4.17.3 Batch Entering Data

Users have the option to enter a "batch" of similar individuals, which is especially useful when entering large litters or clutches. This function can only be used when Entering a New Specimen (e.g. selecting the "New Specimen" option from the Edit pull-down menu). To duplicate a new animal:

1. Click on the box next to Batch Input in the bottom of the animal editor pop-up window. Enter the total number of duplicate individuals you want to create from the batch editor, including the individual you are currently editing.

2. Enter all relevant information (sex, reproductive, events, social, enclosures, medical, etc.) for the main animal you'll be duplicating, and select OK.

3. The Batch Editor Form pop-up window will be displayed. Use the form to specify the Studbook ID Number (can be a numerical or alphanumerical), sex, and local ID for your duplicated individuals simultaneously, and when done hit "Apply". If Studbook ID is left unchanged, PopLink will then generate sequential studbook IDs for each duplicated animal. In addition, by clicking on the "Edit", you have the option of opening the animal editor window where you can add additional information for each individual. After selecting "OK", the individuals created using the Batch Editor Form will be displayed in your viewer. If "Cancel" is selected any time before "Apply Changes" is pressed, the additional animals will be lost and only the original animal will be created and added to the studbook.



Note that newer options to upload core data from CSV (released in PopLink 3.0) is likely a more efficient way to speed up data entry than this older batch entry tool.

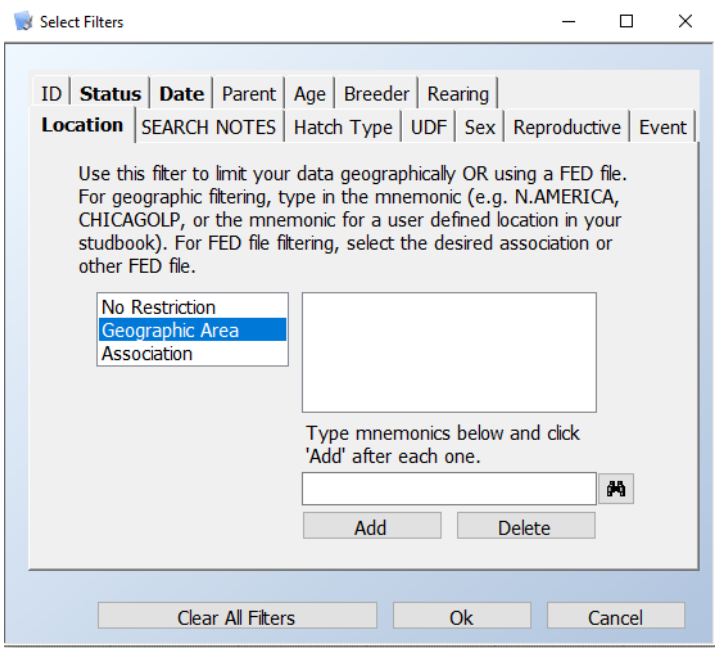
Chapter 5: FILTERING DATA IN POPLINK

5.1 INTRODUCTION/OVERVIEW

Filters can be used to search through studbook databases that are too large to search manually or to ask specific questions that may be helpful in data cleanup, data entry and analysis. For example, you can set filters to limit the data to all the living individuals in North America who have produced offspring, or all the males at a particular location born since 1980. Filtering is also an important way of restricting your data to an appropriate subset for demographic and genetic analysis.

PopLink has two methods for applying filters. If you are looking at the studbook viewer or a report and would like to filter the data, you can set filters for that **individual screen/report** by clicking on the "Select Filters" button located directly above the data. You can also set filters that will apply to **all reports** you run by going to the Reports drop-down menu and selecting **Default filters** from the **Options** area. Note that these Default filters will not apply to the studbook viewer, only to any reports run subsequently. It might be appropriate to set default filters if you have a subset that you consistently want to see; or, filters can be set for an individual screen/report if you frequently change the data subset you'd like to see.

Choosing either filter option will open a pop-up screen in which to select the desired filters. Each filter field has its own tab which can be selected to add filters within that field. A tab name in bold font indicates that filters within that field are currently selected. Once any desired filters have been selected, click the "OK" button at the bottom of the pop-up screen to apply the filters. All selected filters will be displayed at the top of the screen below the "Select Filters" button.



Most filters can be used alone or in combination. When filters in multiple fields are applied, the filters will be compounded. To qualify for a selected filter combination, an individual will need to qualify for *both/all filters together*. For example, if "Captive Born" is selected for "Birth Type" and "Hand" is selected for "Rearing", PopLink will return only captive born animals who were also hand-reared. If "Captive Birth" is selected for "Event" and "Both Parents Wild" for "Parent", PopLink will return only captive born animals whose sire and dam are both wild, such as when an egg is collected from the wild and hatched in captivity.

Some fields have the option of selecting multiple filters within that field; for example, in the "Parent" filter, you could select "Either Parent Wild" AND "Either Parent Unknown". If multiple filters are selected within the same field, PopLink will return animals that meet *at least one of the criteria* (e.g. if both "Either Parent Wild" AND "Either Parent Unknown" are selected in the "Parent" field, PopLink will return animals that have at least one parent Wild or at least one parent Unknown; animals do not necessarily have to have both a Wild and Unknown parent to qualify). These multi-option filters have a check box to the left of each filter option, whereas fields in which only a single option can be selected are chosen by highlighting.

Every filter field has a "No Restriction" option. Each filter is set to this when PopLink is first opened (except for the "Status" filter which is set as "Living" and the "Date" filter which is set as "As of End Date" with today's date). Once filters have been set, the "No Restriction" option can be used to clear existing filters within that field. To clear all filters in all fields, select the "Clear All" button on the filter pop-up window.

PopLink will always display whether filters are set for a given report or the studbook viewer in the information bar at the top of the report.

Some filters can be combined in non-sensical or non-intuitive ways, so with complex filter combinations it is good to always verify that you are getting the dataset you believe you should be. Removing all filters, right-clicking to export to excel, and verifying your filters with the underlying data can sometimes be a helpful data validation for crucial analyses.

NOTE: When you open your dataset for the first time, PopLink automatically filters the data in the main viewer to include only the *LIVING* individuals. This was done because it is a very common view, and it significantly reduces the loading time of large studbooks with many dead individuals. This filter can easily be changed or removed by clicking the "Clear" button in the top left.

5.2 DESCRIPTIONS OF SPECIFIC FILTERS

5.2.1 Location

The Location tab allows you to filter in two ways: 1) by geographic area, which allows you to enter one or more individual institutional mnemonics (e.g. CHICAGOLP, SD-WAP) and/or geographic mnemonics (e.g. ASIA, FLORIDA); or 2) by using a .FED file. These filters will limit your selected report or dataset to individuals who have ever been at a location that falls into the filter; using the filter in combination with other filters can further limit the dataset (e.g., setting Status = Living would limit it to individuals who are currently living at a location within the filter.)

FED files are simply a list of location mnemonics. The FED files pre-loaded in PopLink are based on the most recent versions of each regional zoo association's FED file as of the release. These FED files can be altered by opening them in text editing software and adding or deleting mnemonics. New FED files can be created by saving a list of mnemonics. FED files are stored in your My Documents\PopLink\Federation Files. Note that FED files are not stored within your studbook database; if you would like to use customized FED files on a different computer you will need to manually move them.

When filtering by geographic area, you can enter multiple mnemonics by hitting ADD after each mnemonic; use the FIND button to lookup mnemonics if you are uncertain about spelling. When you have selected all the desired mnemonics, use the "OK" button to set your filters.

5.2.2 Date

The "Date" filter can be used in conjunction with any other filter to confine the dataset to a certain time period – either during a date span, or as of an end date. To add a date filter, highlight one of the options, and windows will appear that allow entry of the appropriate dates. When "as of" or "during" date filters are set without any other filters, PopLink assumes that the desired status of individuals is "Living" and automatically applies this filter condition.

5.2.3 Age

The "Age" filter allows filtering of studbook data to a selected age range. To select an age filter, highlight "Between Ages" and use the start age/stop age entry boxes to set the desired range. When calculating age, PopLink filters everything down to and including the start age, and up to and including the stop age. For example, if the age range was 3.0 to 5.0, individuals that were exactly 3.0, between 3 and 5, and exactly 5.0 would be included in the filter. PopLink calculates an individual's age based on that individual's entered birth date ignoring any birth date estimate; if an individual has an unknown birthdate estimate (i.e. birthdate is unknown), that individual's age cannot be calculated, and that individual is excluded from the filtered data.

5.2.4 Sex

The "Sex" filter allows filtering of studbook data by five different sex types: Female, Male, Abnormal, Hermaphrodite, and Unknown Sex. To select Sex filters, check the box next to one or more of the options. PopLink will return all animals that fit at least one of the criteria. In PopLink, an animal's sex can change throughout its lifetime (e.g. it can go from Unknown sex to Male). In the Sex filter, PopLink filters for animals that had ever had that sex (regardless of whether a date filter has been set or not).

Filtering by SEX: Example	
Record: Studbook ID: 441 Birth Date: 1/13/2004 Sex: Unknown on 1/13/2004 Sex: Female on 4/13/2004	Filter By: Sex = Female Date = As Of 1/13/2004 (Living is automatically turned on and shown in the User Interface)
Results: Animal 441 is included in the filter result set because, although the animal was not designated as female **on** 1/13/2004, it was female at some point in its lifespan **and** it was living as of 1/13/2004.	

5.2.6 Reproductive

The "Reproductive" filter allows filtering of studbook data by three different reproductive types: Not Contracepted, Contracepted, and Neutered/Sterile; select one or more of these types to set Reproductive filters. PopLink will return all animals that fit at least one of the criteria. Like Sex data, an individual can have multiple reproductive statuses throughout its lifetime; this filter returns any individuals that have ***ever*** been a specific reproductive status.

5.2.7 Event

The "Event" filter allows filtering of studbook data by eight different event types: Birth, Wild Capture, Transfer, Release, Recapture, Death, Go LTF, and Return from LTF. To select Event filters, check the box next to the desired option(s); PopLink will return all animals that fit one or more of the criteria. When combined with an As Of date filter, PopLink will return all animals with the event **on** the as of date; when combined with a During date filter, PopLink will return all animals with the event occurring during the date span. When combined with the Location filter, PopLink will return all animals that have a given event occurring at a given location. For example, you may filter for all individuals born at a given institution.

5.2.8 Birth Type

The "Birth Type" filter allows filtering of studbook data by three different birth types: Captive Born, Wild Born, and Unknown; these are based on the birth type field in the Master data table. To select Birth Type filters, check the box next to one or two options. If two options are checked, PopLink will return all animals that fit either criterion.

5.2.9 Parent

The "Parent" filter allows filtering of studbook data by ten different parent types: individuals for which Either or Both parent(s) are Wild, Unknown, MULT, Hypothetical, or Blank. To select Parent filters, check the box next to at least one and no more than nine options. PopLink will return all animals that fit at least one of the criteria.

5.2.10 Rearing

The "Rearing" filter allows filtering of studbook data by six different rearing types: Hand, Parent, Foster, Colony/Group, Unknown, and Not Reared. To select Rearing filters, check the box next to at least one and no more than five options. PopLink will return all animals that fit one of the criteria.

5.2.11 Breeder

The "Breeder" filter allows filtering of studbook data by two breeding histories: Has Bred and Has Not Bred. The breeder/non-breeder designation is based on whether an individual is indicated as a parent in another individual's sire or dam column. Individuals that are possible parents as indicated with MULT are not considered breeders. To select a Breeder filter, highlight one of the options.

5.2.12 Status

The "Status" filter allows filtering of studbook data by four different Status options: Living, Dead, Lost-To-Follow-Up (LTF) and Released. To select a Status filter, highlight one of the options. Only one Status filter may be selected at a time. The Status filter is commonly used with a date filter; setting the Status filter with an "as of" date filters the data to the individuals that may have been Living, Dead, LTF, or Released as of a certain date, regardless of their current status. Setting this filter with a "during" date filters the data to the individuals that were ever Living, Dead, LTF, or Released during a particular date window. Setting this filter without specifying a date filter is the same as setting the "no restriction" date filter.

5.2.13 ID

The "ID" filter allows filtering of studbook data by two different ID types: Numerical and Not Numerical. This filter is useful to indicate the presence of temporary IDs (usually T###), as well as hypothetical individuals in a studbook. To select an ID filter, highlight one of the options. Because this filter allows only two mutually exclusive options, only one may be selected at a time.

5.2.14 UDF

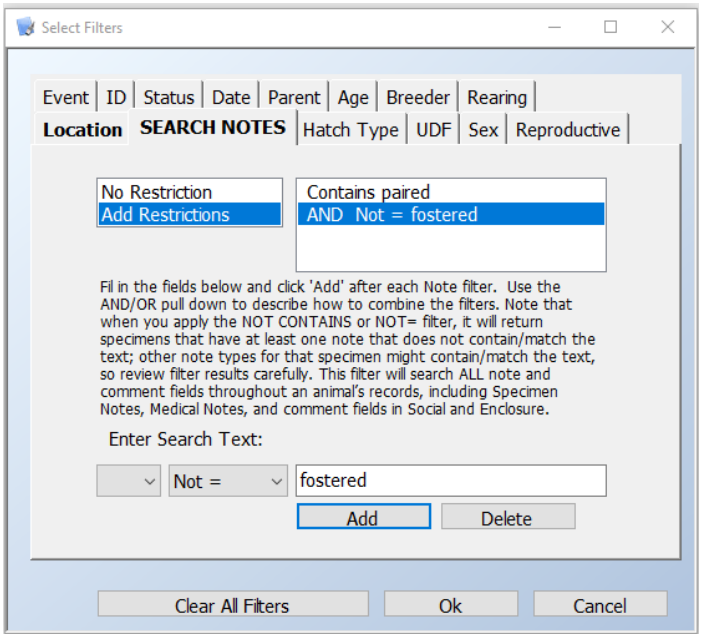
If the studbook you are using has user defined fields, you may filter based on those fields. Under the UDF tab is a drop-down menu with the user defined fields specific to that studbook. Choose the desired field, and enter the value you wish to filter by in the space next to it.

5.3 SEARCH NOTES

The **Search Notes** function allows searching of any note or comment field anywhere in an animal's record, including Specimen Notes, Social, Enclosure, and Medical Data Tables. The search function allows filtering of individuals in the following ways:

- '=' / "Not =": restrict to individuals that have a note that does/does not contain the full, exact text in the search box (the entire note must match)
- "Contains"/"Not Contain": restrict to individuals that contain a specific word or phrase somewhere within a note.

Search terms are not case sensitive. You can add multiple filter conditions at once (using AND or OR). Note that when using Not = or Not Contains, it will return any animals that have at least one note that does not contain or match the text; other note types MAY contain or match the text, so review filter results carefully. Also note that the Search Notes function will return all the **Animals** with a particular note, not restrict down any of the relevant notes tables to only those notes.



NOTE: The **Search Notes** function filters the comments slightly differently in the Social table in comparison to other tables because its table records are connected to multiple individuals. When a phrase is entered in Search Notes, records are limited to **only** those Social events with that search text in the comment field, rather than showing **all** the Social events related to an animal that has that note. This way you can clearly see which animals (listed in the Related Specimens field) have a given social note. For any animals that meet the criteria you set up in the Search Notes tab, PopLink will show all of their records in the rest of the tables (Master, Sex, Reproductive, Events, Specimen Notes, UDFs, Enclosures, and Medical).

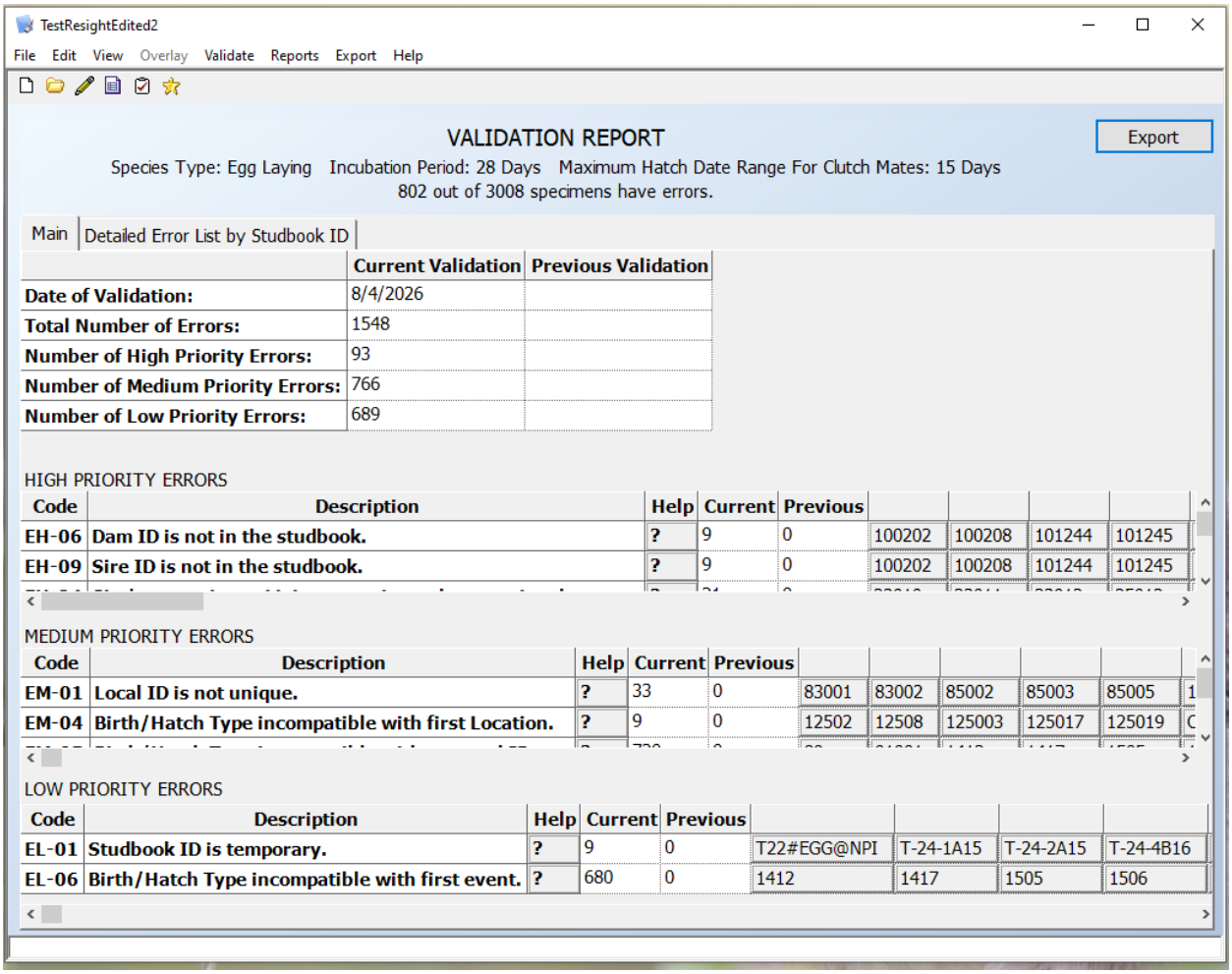
Chapter 6: DATA VALIDATION AND CLEAN-UP IN POPLINK

There are several routines and tools within PopLink that can be used to assist in data clean-up and validation. This chapter describes how you can use these tools to improve the data quality of your studbook database. The tools it covers are:

1. Data Validation Report
2. Database Comparison Tool
3. Reports useful in data clean-up
4. Clean-up Mnemonics Tool
5. UDF Casing Clean-Up Tool
6. Delete Empty UDFs Tool

6.1 DATA VALIDATION REPORT

Under the Validation pull-down menu, you can select "Run Data Validation" to produce a prioritized list of potential errors within your studbook.



In the Main tab, summary information about the studbook, previous validation runs, and the current run are displayed at the top of the report. PopLink prioritizes errors based on their effect on demographic and genetic analyses:

- High Priority errors indicate that the record has major logical inconsistencies or is missing necessary data. These errors may also have a large impact on genetic or demographic analyses.
- Medium Priority errors indicate possible logical inconsistencies or missing data, but the data will likely have a less dramatic effect on genetic or demographic analyses.
- Low Priority errors indicate areas of records that should be reviewed or clarified, but will be unlikely to have a large effect on analyses.

In the "Detailed Error List by Studbook ID" tab, the report lists all studbook errors sorted by ascending Studbook ID number.

PopLink checks your studbook for 58 common errors (Table 3), but the on-screen validation report table will only display errors that occur in your studbook, ranked by priority or by studbook ID. The Help button next to each error gives details on how to resolve the error. The Previous column displays the number of errors of each type you had on your last validation, and the Current column displays the number of errors of each type you have in this run. Note that if you found an error on a previous validation and fixed it, it will not be displayed in the list. PopLink does not run any validation tests for the Breeding, Resightings, Social, Enclosures, or Medical Data Tables (except those that are run when data are entered or imported).

The columns to the right of the "Current" column display the animals which have a given error, and clicking on them links to that animal's Animal Report.

Table 3. Errors Checked for in PopLink Data Validation

ERROR CODE	ERROR DESCRIPTION	HELP ASSISTANCE FOR ERROR
EH-01	Currentness date is more than one year old.	Double-check your currentness date in the Studbook Overview Table. If the currentness date is out-of-date, please update it. The currentness date is the last date you did a complete update of your studbook.
EH-02	Studbook ID is blank.	Assign a studbook ID.
EH-03	Studbook ID is not unique.	Determine if these are two different animals. If they are different animals, assign a new Studbook ID to one. If they are the same animal, consolidate the information into one record. Include a note in the animal's record explaining the Studbook ID change. Verify that the parental ID is correct for the animal's offspring.
EH-04	Dam ID is blank.	Research parentage and enter a Dam ID. If the dam is unknown, enter UNK.
EH-05	Dam ID is not a female.	Check that the correct dam is recorded. Verify the recorded dam's sex.
EH-06	Dam ID is not in the studbook.	Research the parentage of the animal. If the dam is already in the studbook, use the dam's correct Studbook ID as the Dam ID. If the dam is not in the studbook, create a new animal record for the dam and use that Studbook ID as the Dam ID.
EH-07	Sire ID is blank.	Research parentage and enter a Sire ID. If the sire is unknown, enter UNK.
EH-08	Sire ID is not a male.	Check that the correct sire is recorded. Verify the recorded sire's sex.
EH-09	Sire ID is not in the studbook.	Research the parentage of the animal. If the sire is already in the studbook, use the sire's correct Studbook ID as the Sire ID. If the sire is not in the studbook, create a new animal record for the sire and use that Studbook ID as the Sire ID.
EH-10	Birth Date is blank.	Research this animal's history and enter the Birth Date and Estimate.
EH-11	Birth Date is invalid.	Research this animal's history and correct the Birth Date and Estimate.
EH-12	Sex record is missing.	Enter sex information for this animal.
EH-13	Sex is blank.	Research and enter the animal's Sex.
EH-14	Sex is invalid.	Research and correct the animal's Sex.
EH-15	Sex Date is blank.	Research and enter the animal's Sex Date and Estimate. The Sex Date is the date the animal was identified as a given sex (e.g. its birth date if it was sexed at birth).

ERROR CODE	ERROR DESCRIPTION	HELP ASSISTANCE FOR ERROR
EH-16	Sex Date is invalid.	Research this animal's history and correct the Sex Date and Estimate. The Sex Date is the date the animal was identified as a given sex (e.g. its birth date if it was sexed at birth).
EH-17	Event record is missing.	This animal has no Event records. Research the animal's history and enter a first event for this animal. First event must be either birth/hatch or wild capture.
EH-18	Transaction Code is blank.	Enter the event's Transaction Code.
EH-19	Transaction Code is invalid.	Correct the event's Transaction Code.
EH-20	Transaction Date is blank.	Research this animal's history and enter the Transaction Date and Estimate.
EH-21	Transaction Date is invalid.	Research this animal's history and correct the Transaction Date and Estimate.
EH-22	Birth location conflicts with dam's location	This check is only performed for live bearing species. The dam's location does not match the offspring's location on the offspring's birth date. Verify that the offspring's dam, birth date, and birth location are all entered correctly. Check the dam's transfer records and locations. Note that this validation check is only run for captive-born origin individuals.
EH-23	Dam's status is not Living on birth date for live bearing species only.	Verify that the correct dam has been identified. Make sure that event dates are entered correctly for the dam and offspring. Note that this validation check is only run for captive-born origin individuals.
EH-24	Sire's status is not Living on estimated conception date.	Verify that the correct sire has been identified. Make sure that event dates are entered correctly for the sire and offspring. Note that this error will be displayed if offspring were produced via artificial insemination using sperm from a dead sire. Note that this validation check is only run for captive-born/hatch origin individuals.
EH-25	Sire and Dam locations differ on estimated conception date.	Make sure that the correct sire and dam are recorded. Check locations and event dates for sire and dam. Verify that the offspring's birth date is entered correctly. Note that this error will be displayed if offspring were produced via artificial insemination using sperm from sire at another location. Note that this validation check is only run for captive-born origin individuals.
EH-26	Dam's status is not Living on estimated conception date for egg laying species only	Verify that the correct dam has been identified. Make sure that event dates are entered correctly for the dam and offspring. Note that this validation check is only run for captive-born origin individuals.
EH-27	Unrecognized mnemonic	This mnemonic is used in your studbook but is not in the Location List or defined as a User Defined Location. If it is a misspelling of an existing facility in the Locations List, you can correct the spelling; unless it is corrected or added as a user defined location, data on this animal will be excluded from most analyses. Use the Clean Up Mnemonics tool (accessible via the pop-up or through the Validate menu) to fix your mnemonic; *see section 6.3* for more details.
EM-01	Local ID is not unique.	Determine if any of these animals are duplicate records. If they are different animals, verify the Local IDs. If they are the same animal, consolidate the information into one record. Include a note in the animal's record explaining the Studbook ID change. Verify the parental ID for the animal's offspring.
EM-02	Hatch/Birth Type is blank.	Research and enter the animal's Hatch/Birth Type.
EM-03	Hatch/Birth Type is invalid.	Research and correct the animal's Hatch/Birth Type.
EM-04	Hatch/Birth Type incompatible with first Location.	If the first Location is known, the Hatch/Birth Type should not be unknown.
EM-05	Hatch/Birth Type incompatible with parental ID.	Refer to 4.4.3 for more help.
EM-06	Rearing is blank.	Research and enter the animal's Rearing type.
EM-07	Rearing is invalid.	Research and correct the animal's Rearing type.
EM-08	Birth Dates differ in Master and Events table.	Review the dates and estimates and make sure they are exactly the same.
EM-09	First event is before birth date.	Verify that these dates are entered correctly, making sure no event occurs prior to the birth date.
EM-10	Reproductive record is missing.	Enter reproductive status information for this animal.

ERROR CODE	ERROR DESCRIPTION	HELP ASSISTANCE FOR ERROR
EM-11	Reproductive Status is blank.	Research and enter the animal's Reproductive Status.
EM-12	Reproductive Status is invalid.	Research and correct the animal's Reproductive Status.
EM-13	Reproductive Date is blank.	Research this animal's history and enter the Reproductive Date and Estimate.
EM-14	Reproductive Date is invalid.	Research this animal's history and correct the Reproductive Date and Estimate.
EM-15	Location is blank.	Enter the mnemonic for this event's location. If the location is unknown, enter UNKNOWN.
EM-16	First event is not birth, hatch, or wild capture.	An animal's first event must be either Birth/Hatch or Wild Capture. If the animal is of unknown origin, enter the first event as Birth/Hatch at an unknown location, using the best estimate possible for the Birth/Hatch date. The next event in the animal's record should be a transfer to a known location.
EM-17	Invalid event after Go LTF or Release event.	An animal that has Go LTF or Release must have Return From LTF or Recapture prior to any subsequent event. Return from LTF and Recapture are new events added to PopLink that are not in SPARKS. Note that they are not automatically entered by PopLink, and must be entered manually.
EM-18	Events after death.	No events should occur after death. Make sure all events and dates are entered correctly.
EM-19	Interbirth interval is less than gestation period.	This check is only performed for live-bearing species. Review this animal's offspring and verify that the dam is correct. Check that each offspring's birth date is correct.
EL-01	Studbook ID is temporary.	Assign a permanent Studbook ID before studbook publication or population planning.
EL-02	Dam ID is MULT.	These Dam IDs should be entered as MULT# e.g. MULT1. If two animals have the same possible dams, they should have the same MULT# for the Dam ID.
EL-03	No parental ID assumptions recorded.	Animals with MULT# dam should have a Parent ID Assumptions note stating the Studbook IDs of the possible dams. Animals with WILD# dam should have a Parent ID Assumptions note stating the Studbook IDs of the siblings.
EL-04	Sire ID is MULT.	These Sire IDs should be entered as MULT# e.g. MULT1. If two animals have the same possible sires, they should have the same MULT# for the Sire ID.
EL-05	No parental ID assumptions recorded.	Animals with MULT# sire should have a Parent ID Assumptions note stating the Studbook IDs of the possible sires. Animals with WILD# sire should have a Parent ID Assumptions note stating the Studbook IDs of the siblings.
EL-06	Hatch/Birth Type incompatible with first event.	Refer to 4.4.3 for more help.
EL-07	Birth Date in the future.	Research this animal's history and correct the Birth Date and Estimate.
EL-08	Birth Date Estimate is invalid.	Research this animal's history and correct the Birth Date and Estimate.
EL-09	Sex Date in the future.	Research this animal's history and correct the Sex Date and Estimate.
EL-10	Sex Date Estimate is invalid.	Research this animal's history and correct the Sex Date and Estimate.
EL-11	Reproductive Date in the future.	Research this animal's history and correct the Reproductive Date and Estimate.
EL-12	Reproductive Date is invalid.	Research this animal's history and correct the Reproductive Date and Estimate.
EL-13	Transaction Date in the future.	Research this animal's history and correct the Transaction Date and Estimate.
EL-14	Transaction Date is invalid.	Research this animal's history and correct the Transaction Date and Estimate.

After running data validation you should use this report to clean-up any errors that can be resolved. Errors that cannot be resolved or are not true errors should be noted in your Specimen Notes so that next time you run Data Validation and start to "clean up" that animal you know that you already attempted to resolve their data error.

6.2 DATABASE COMPARISON TOOL

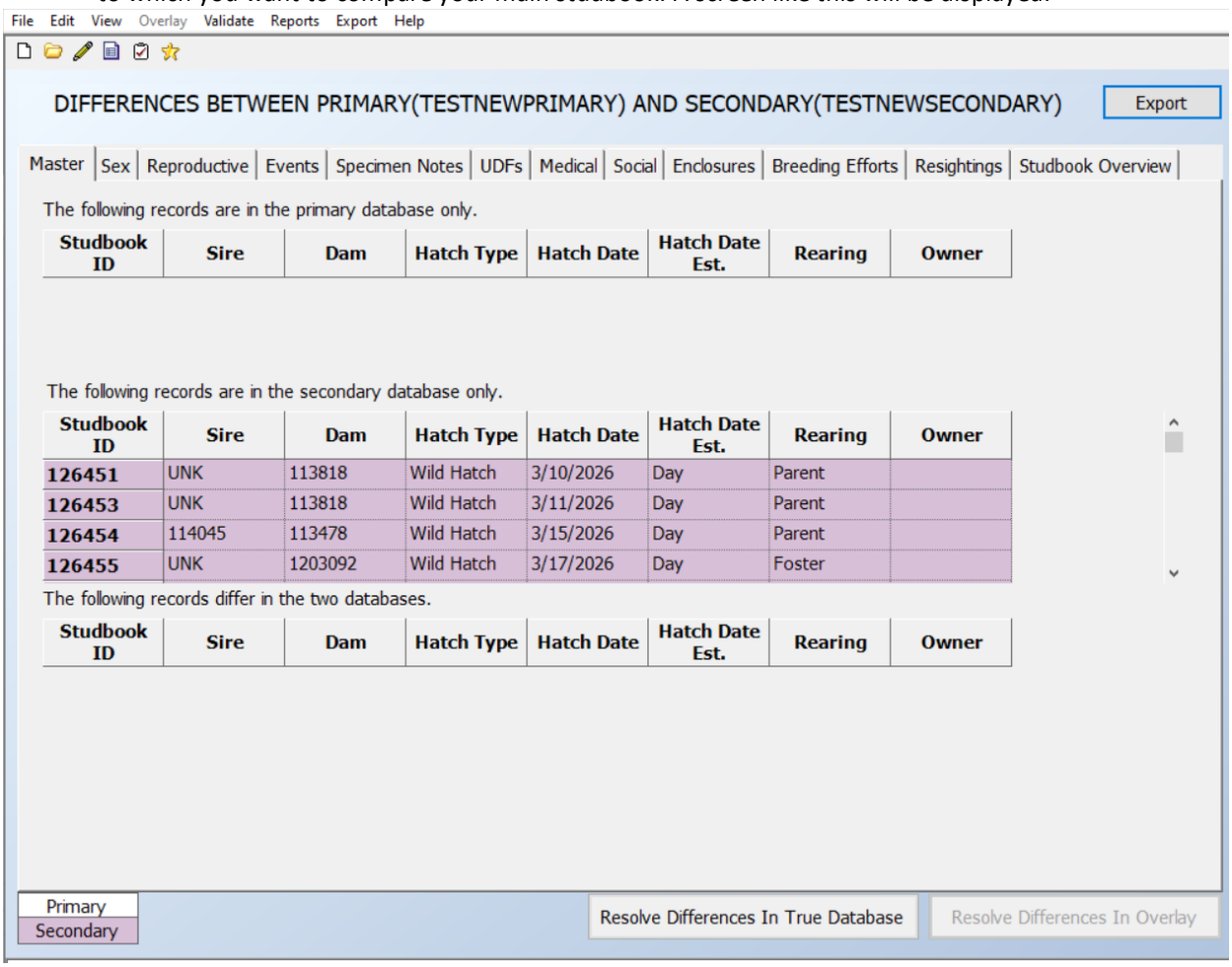
This tool highlights all differences between two studbook databases. You can use the Database Comparison Tool for:

1. Comparing two versions of the same studbook and resolve differences between the two.
2. Importing analytical assumptions into PopLink from an existing analytical studbook (for more information on analytical assumptions, see Chapter 9).

Note that clicking "Export" will produce a report listing all of the identified differences; this report will automatically be displayed in HTML format and also saved in your Primary studbook database folder. When you double-click on the report, it will open in your default web browser, such as Chrome. You can then save the reports as Word documents (File>Save As or by clicking on the "Edit in Word" shortcut button) and edit as desired.

6.2.1 Comparing two versions of the same studbook (*option 1 above*):

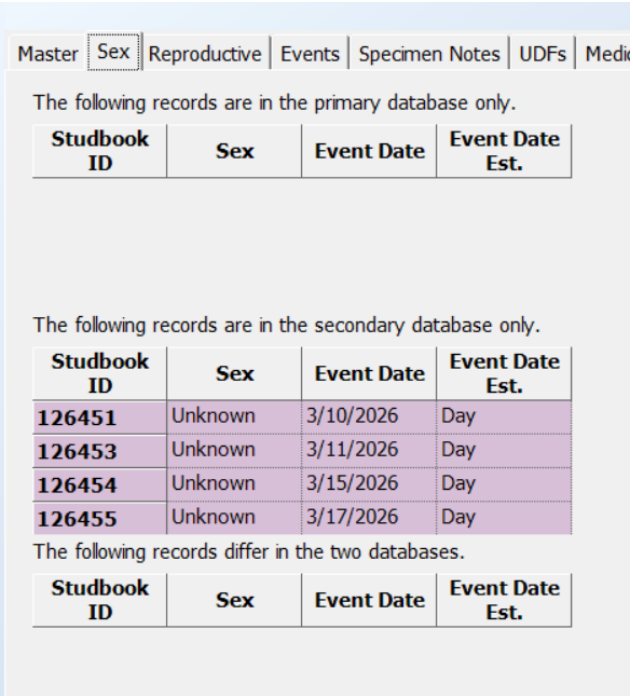
1. Create PopLink databases for both studbooks you want to compare (via the Open/Create New dialogue box when the program is launched, or the File drop-down menu).
2. Open your main studbook database – this will be referred to as your **primary** database, the database you want to add any changes to.
3. Under the File pull-down menu, select "Compare Databases", and select the secondary PopLink studbook to which you want to compare your main studbook. A screen like this will be displayed:



4. Each tab shows animal-by-animal differences between your two studbooks for each PopLink data table. The top two tables on each tab will show animals that are either unique to the primary database or unique to

the secondary database; the final table will display animals that are in both databases, but have differences in particular fields. A few key points:

a. On the Master tab, the top two tables will display entire **individuals** unique to either database. The other tabs (Sex, Reproductive, etc.) will display individual events (sex events, reproductive status events, transaction events) that are different between the two datasets. For example, animal 126451 above is in the secondary database and not the primary—it appears that the secondary dataset may be more up-to-date than the primary one. When you look at the Sex table, you see that in the animal's Sex events as well, as they would also not be found in the primary database:



b. For the bottom table on each tab, you will be able to see the specific data field that is different between the two datasets.

c. Note that for certain data tables (Events, Specimen Notes, Breeding Efforts, Enclosures, and Resightings), it is more difficult for PopLink to tell whether the records being compared between two databases are edited versions of the same row or additional rows added. This means that differences between the two databases in these tables are not always shown in the "records differing in the two databases" section, but each event or note that is unique is shown as "only in the primary" or "only in the secondary". You may need to double check the individual animal's entire record in both databases to make certain you're adding/deleting appropriately, or if you just need to update a record, do it by directly editing the animal in the Primary database.

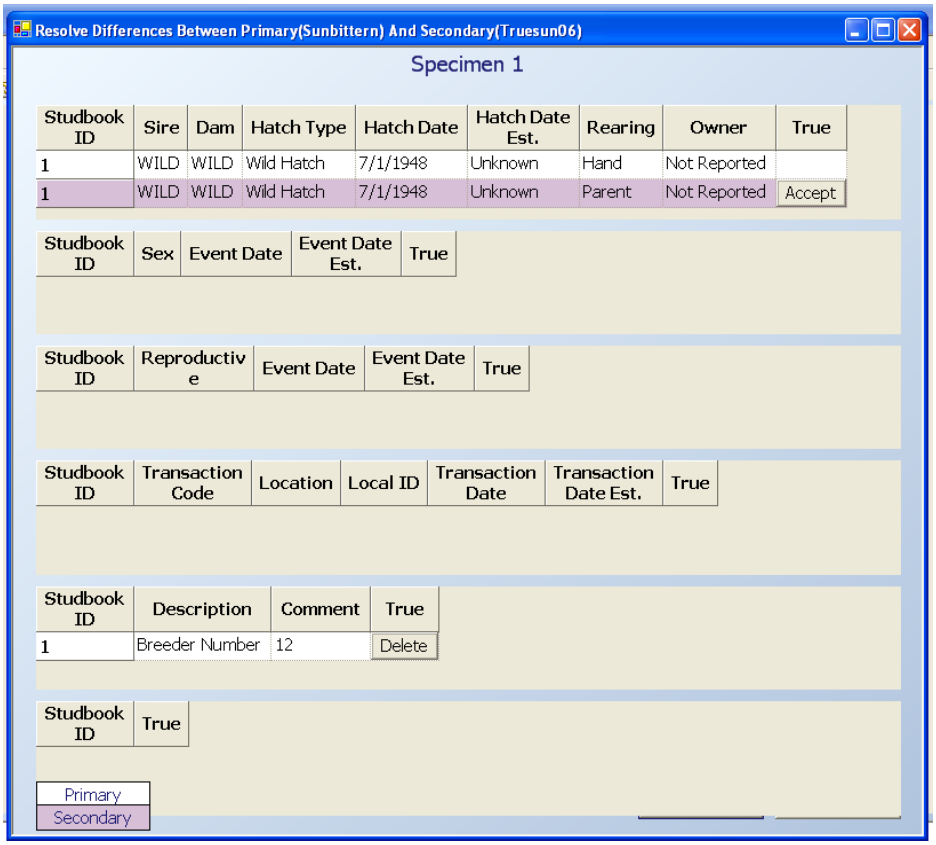
5. To resolve differences between the two datasets, click on the "Resolve Differences" button at the bottom of the screen. A pop-up editor will take you, animal-by-animal, through potential edits. The pop-up has each of the data tables (in order from top to bottom). If discrepancies exist between the records in the two studbooks you are comparing, those discrepancies will be shown, and you have three options:

   a. Use the "Add/Accept" or "Add/Accept All" buttons to apply what is in the **SECONDARY** database to the **PRIMARY** database (e.g. moving data from the SECONDARY to the PRIMARY).

   b. Use the "Delete" or "Delete All" button to delete a row of data that is in your PRIMARY database and **not** in the SECONDARY database.

   c. Leave the data in the primary studbook as is by clicking "Next" to move onto the next animal.

d. Navigate between animals using Back/Next or the dropdown to select/enter an animal ID, which you navigate to by pressing "go".



NOTE: Be **extremely** careful as you are deleting or adding data to your Primary dataset – there is no "UNDO" option in PopLink. Make sure you consider which data are valid before clicking "accept". You can compare specimen reports from each studbook by clicking on the Studbook IDs for each type of data (e.g. clicking on one of the white 1s and the purple 1s in the screen above). You can see a complete set of differences between datasets by exporting a report. Be careful!!

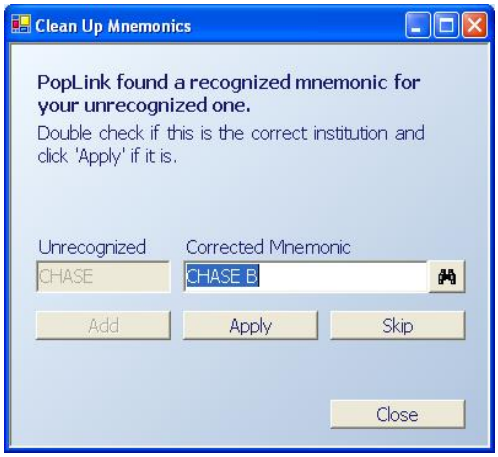
Note that you can also simply use the database comparison tool to generate a list of potential changes and then edit existing animals/enter new animals by hand.

6. Although the Database Comparison Tool will show you differences between the Studbook Overview data in your primary and secondary databases, it will not automatically update any fields in the Studbook Overview table using the "Resolve Differences" editing tool. If there are changes you need to make, edit the studbook overview for your primary database by hand through the studbook viewer.
7. After you've made any edits or changes you'd like, you can re-run the Database Comparison Tool to double-check that you have resolved everything you wish to change.

6.2.2 Importing analytical assumptions into PopLink from an existing analytical studbook (*option 2 above*): While this functionality still exists in PopLink, a newer and easier way to Import Analytical Assumptions into a database is to use the File→Import Overlay option to move overlays between two studbooks. We recommend that option rather than this functionality; *see section 9.2.3* for more details.

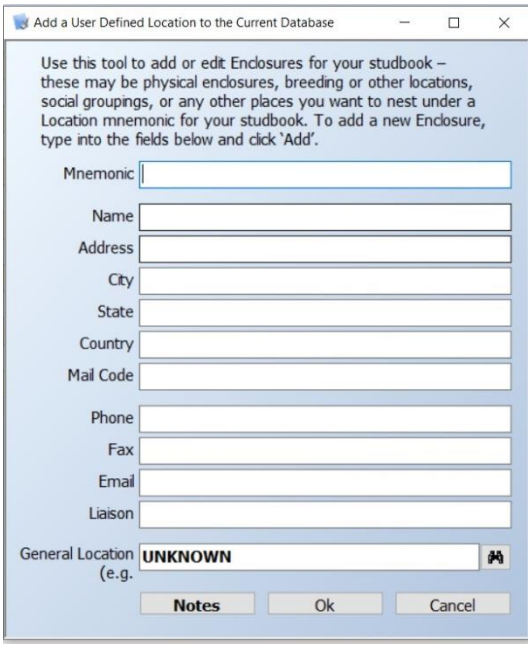
6.3 CLEAN-UP MNEMONICS TOOL

There may be some mnemonics in your dataset that are unrecognized. Selecting Validate→ Clean Up Mnemonics will open a pop-up with two cases of unrecognized mnemonics:



In the left-hand case, PopLink has matched your unrecognized mnemonic to an existing mnemonic (synonyms are used to link different versions of the same institution, such as CHICAGOLP (the true mnemonic) with LINCOLN, LINCOLNPK, LPZS). The "Corrected Mnemonic" will be the institution's true mnemonic. You can use the "find" button to open the Location List (or open the excel version in your Documents\PopLink folder) and double check whether the "Corrected Mnemonic" is what you meant with the unrecognized mnemonic and click Apply to correct your unrecognized mnemonic.

In the right-hand case, there was no recognized mnemonic (real or synonym) in the Location list. This may be because 1) you have created a new spelling for an existing institution, but that spelling is not yet a synonym, or 2) the institution is not in the Location list at all. Double check the Location list: if you have simply created a new spelling you should enter the Correct Mnemonic in the box; if the institution is truly a unique institution, you should add it to your studbook as a User Defined Location. To do so, leave the Unrecognized Mnemonic in the box and click "Add", which will pop-up this box:



Enter as much as you know about this location in these fields, including any notes. For the General Location field, you can enter a regional designation so that the institution will show up in a given Filter view, such as N.AMERICA or EUROPE (add these using the accepted mnemonic for that region, which you can look up using the "find" button).

6.4 UDF CASING CLEAN-UP TOOL

Due to variations in how you've entered data there may be some UDFs with mixed casing (i.e. some of the animals may have "YES" and some may have "yes"). Although not critical to data quality, you can use the Clean Up UDF Casing option in the Validate pull-down menu to assign a consistent casing scheme.

6.5 DELETE EMPTY UDF ROW TOOL

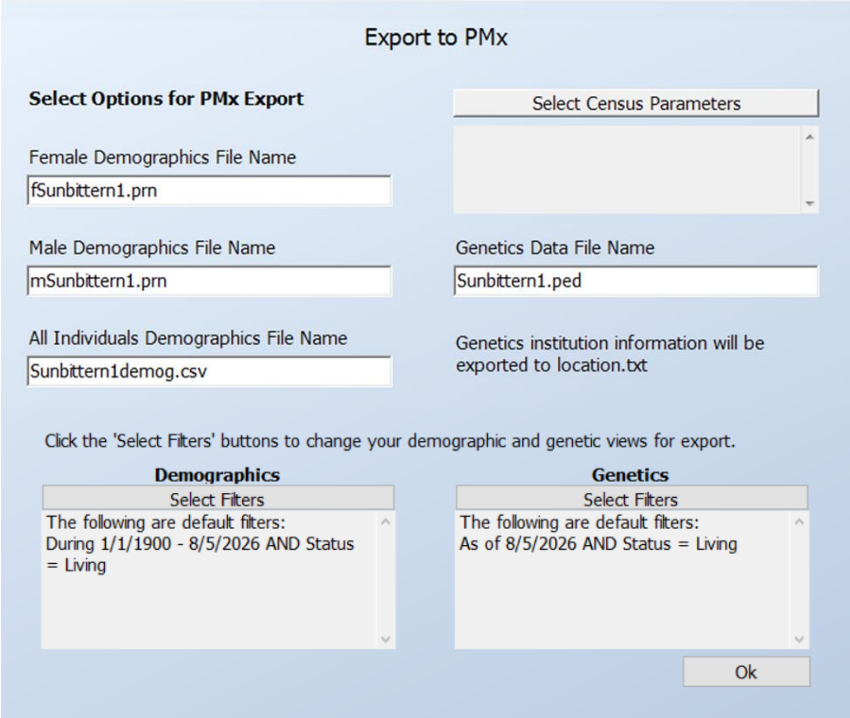
There may be some animals with extra, blank rows in the UDF table (e.g., an animal may have a row with filled data fields and a second row with blank data fields). Although not critical to data quality, you can use the Delete Empty UDF Rows option in the Validate pull-down menu to delete out all of these blank rows, which cleans up the UDF data table.

Chapter 7: EXPORTING DATA FROM POPLINK

7.1 PMx EXPORT

PopLink will create standard PMx export files from your studbook database. You can export from your true studbook (e.g. Sunbittern) or from your studbook with an analytical overlay applied (e.g. Sunbittern + Faust1). The database displayed at the top of the screen will indicate which database is being exported.

When you select the PMx export from the Export drop-down menu, this screen will be displayed:



The file names are defaults that are chosen based on your database name; you can change the file names if you desire, but you should not change the extensions (.prn and .csv for demography files, .ped for genetics files).

For demography, PMx can import either .prn files or a more detailed file (All Individuals Demographics File, a .csv file). For both, the Demography filters chosen will limit your studbook database to a specific population that will be used to calculate life table parameters (M_x, Q_x, L_x, etc.) for the .prn files or which individuals are included in the .csv file. The chosen filters will be displayed in the filter box; you should change the default filters to your desired demographic window, which is generally the period of modern management for your species. You can also set other filters in addition to date and geographic windows.

The Genetic filters are used to create the list of individuals that will be considered living individuals in your current population; PopLink exports this list of animals and their pedigree information to PMx. If desired, you can change the default filters using the "Select Filters" button. PopLink can also export census data for graphing in PMx. Use the Select Census Parameters button to determine the desired filters.

PMx export files are placed in a Folder titled "PMx Exports" within the specific studbook database folder from which the export was created (e.g. My Documents\PopLink\PopLink Databases\Studbook name\PMx Export). When you open PMx, you can navigate to this folder to import the data.

7.1.1 Adding MULT Parentage to PMx Exports

In a standard PMx export, MULT parents are treated as unknown and are therefore excluded from pedigree analysis. To include the potential parents represented by a MULT, edit the exported .ped file before importing it into PMx. Before you edit the .ped file, you first need to know all of the potential parents associated with each MULT (e.g., MULT1 = potential sires studbook (SB) ID 1 and SB ID 2; MULT2 = potential dams SB ID 3 and SB ID 4). Information on MULTs and their potential parents may be stored in different locations. Some studbook keepers maintain a list in the Studbook Overview tab, while others record this information in the Specimen Notes table, in a UDF, or in a separate file outside of PopLink.

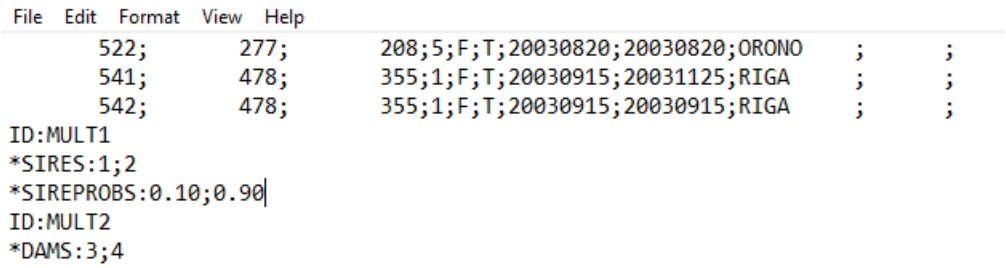
Next, this information must be formatted correctly for PMx to recognize the parents for each MULT. Using the examples of MULT1 and MULT2 above, the correct formatting would be:

```
ID:MULT1
*SIRES:1;2
ID:MULT2
*DAMS:3;4
```

Note that for MULTs containing potential sires, the second line begins with "*SIRES", while for dams, the second line begins with "*DAMS". All potential studbook IDs should be then listed in a semicolon-separated list with no spaces. If you do not specify otherwise, the probability of an individual being the true parent (or the proportional contribution) is divided evenly among all listed parents. For MULT1 above, as written, SB ID 1 and SB ID 2 each have a 50% chance of being the true sire. However, sometimes a studbook keeper may assign a different probability to each potential parent. To ensure these probabilities are included in PMx, you need to add an additional line for each MULT that includes each parent's probability of being the true parent. Make sure to list the probabilities in the same order as the parents. In the example below, SB ID 1 was assigned a probability of 0.1 and SB ID 2 was assigned a probability of 0.9:

```
ID:MULT1
*SIRES:1;2
*SIREPROBS:0.10;0.90
```

Once you have a list of correctly formatted MULT parents, navigate to the PMx export file for the studbook and open the .ped file in a text editor. Next, copy your list of MULTs, scroll to the bottom of the file, and paste your list directly below the last row of data in the .ped file.



Lastly, be sure to save your updated .ped file by navigating to Save As→Save as type: All Files, and give your file a new name followed by .ped (e.g., TEST_MULTS.ped). When you are ready to create a new PMx project, make sure to select your edited .ped file so that the MULT parentage is included. For more information on how PMx handles MULTs, including how the software handles parental probabilities, consult the PMx manual (Traylor-Holzer, 2011).

7.2 TECHNICAL NOTES ON EXPORTS TO PMx

7.2.1 Life Table Calculations

PopLink exports two different files for demographic calculations in PMx, the .prn files and the demog.CSV file. In the .prn files, PopLink has already calculated the life tables with methods that replicate SPARKS' MxQx table calculations. **If you use the demog.CSV file to import into PMx (the more modern method to get demographic data into PMx), all life table calculations are done by PMx rather than PopLink, so the following methods description only refers to calculations for the .prn files.**

The Demographic Window is used to define the population of individuals "at risk" for events. So, if a demographic window of N. America, 1/1/1980-1/1/2006 is selected, the data in the life table would include:

- For individuals born in North America after 1/1/1980 and before 1/1/2006, all data on their life from birth to the point when they leave the risk window (e.g. die or are transferred out of N. America) or it closes (e.g. they are living in North America on 1/1/2006).
- For individuals living in North America on 1/1/1980, all data on their life from 1/1/1980 until they leave the risk window or it closes.
- For individuals living outside of North America on 1/1/1980 but transferred into North America after that date, all data on their life from their date of transfer until they leave the risk window or it closes.

Data on individuals with unknown birthdate estimates are excluded from life table calculations because their age cannot be calculated.

The Life Table tabulates age and sex specific probabilities of death and birth based on the historical data derived from the studbook. Separate life tables are constructed for males and females. The life table PopLink exports to PMx has the following variables:

- **Age Class (x)**
- **Number Alive per Age Class**
- **Age-Specific Mortality Rate (Qx) =** the probability of dying during a specific age class (e.g., between the ages of 0 1 or 5 6 years of age). Calculated, for each sex, as (the number of deaths per age class)/(number of individuals at risk for Qx).
- **Age-Specific Fecundity Rate (Mx) =** the number of same sex offspring an individual is expected to produce (= produced on average) during an age class.
- **Number At Risk for Qx** = Sample size that Qx rate was based on for a given age class.
- **Number At Risk for Mx** = Sample size that Mx rate was based on for a given age class.

7.2.2 Mortality Rate Calculation

No individuals with unknown birthdates are used in mortality rate calculations. Birth date estimates (except for Unk) are ignored—the entered birth date is used in all calculations.

1) Tally the number of deaths in each age class that occurred in the demographic window
    a. Male deaths are attributed to male age classes, female deaths to female age classes
    b. Deaths of unknown sex are tallied as 0.5 to the male and 0.5 to the female age class
2) Tally the number of individuals at risk for death in each age class
    a. An individual that has lived through an entire age class gets tallied as 1.0 for that age class
    b. An individual that has lived through a portion of an age class (e.g. was born midway through a year, or was transferred out midway through a year, or the date window started or ended midway through an age class) is tallied as whatever portion of that age class, *except in case c below*. For example, if an individual was transferred out of the demographic window when 6 years and 3 months old, then for the 6-7 age class that individual would be tallied as 3/12 = 0.25
    c. An individual that dies in a given age class is tallied as 1 for that age class regardless of how long it lived in the age class
    d. Males are attributed to male risk tallies, females to female risk tallies. Unknown sex individuals are tallied 0.5 to male age class tallies and 0.5 to females.

3) Calculate each age-specific mortality rate as (the number of deaths per age class)/(number of individuals at risk for Q_x)

7.2.3 Fecundity Rate Calculation

No individuals with unknown birthdates are used in fecundity rate calculations. Birth date estimates (except for Unk) are ignored—the entered birth date is used in all calculations.

1) Tally the number of births that occurred to parents in each age class during the demographic window
    a. For births of known sex individuals with known-age parents, the birth is split between parents and assigned to the parent's age class, e.g. 0.5 of the birth is assigned to the dam's age class and 0.5 of the birth is assigned to the sire's age class.
    b. For births of unknown sex individuals with known-age parents, the birth is split between parents and assigned to the parent's age class, e.g. 0.5 of the birth is assigned to the dam's age class and 0.5 of the birth is assigned to the sire's age class.
    c. For births of known or unknown sex individuals with unknown parent(s) or parents with unknown age, the birth is split between sire and dam (0.5 to each), and tallied as an unknown sire birth or an unknown dam birth (e.g. a generic bin for all animals with unknown parents).
        i. If one parent is known and one is unknown, 0.5 is assigned to the age class of the known parent and 0.5 is added to the unknown parent tally.
        ii. After initial M_x calculations are made, PopLink allows users to select if they want to proportionally distribute data from unknown parents; see 3a for more details.
2) Tally the number of individuals at risk for reproduction in each age class
    a. An individual that has lived through an entire age class gets tallied as 1.0 for that age class
    b. An individual that has lived through a portion of an age class (e.g. was born midway through a year, or was transferred out midway through a year, or the date window started or ended midway through an age class) is tallied as whatever portion of that age class. For example, if an individual was transferred out of the demographic window when 6 years and 3 months old, then for the 6-7 age class that individual would be tallied as 3/12 = 0.25
    c. Males are attributed to male risk tallies, females to female risk tallies. Unknown sex individuals are tallied 0.5 to male age class tallies and 0.5 to females.
3) Calculate each age-specific fecundity rate as (number of births attributed to a particular age class)/(number of individuals at risk for that age class)
    a. If user selects option to include offspring attributed to unknown parents, these births are proportionally assigned in proportion to the M_x values that have already been observed.

Note that in the PMx export files, the more detailed demographic export file (All Individuals Demographics File, a .csv file) contains the raw data on individual animals, and PMx calculates life table statistics rather than using PopLink-calculated life table statistics. See the PMx manual for more details on how those calculations are made using the raw data in the .csv file.

7.2.4 Genetic Export

PopLink does not perform genetic calculations during the export to PMx. PopLink compiles information on pedigree, status, location, and identification to export to PMx in .ped files which are then used by PMx for genetic calculations. See the PMx manual for more information on genetic calculations (Traylor-Holzer, 2011).

7.3 EXPORT to Excel/CSV

To ensure that all input studbook data can be simply exported in the case that you want to stop using PopLink to maintain your studbook, the Export→Export to Excel/CSV function exports all studbook data into both an excel workbook with each table shown in a different tab, and in individual CSV files for each table. Upon export, you can find the files in your studbook's folder (typically in Documents\PopLink\PopLink Databases\Your Studbook Name\Studbook Export).

Chapter 8: POPLINK REPORTS

There are a variety of PopLink reports that help you clean up and analyze your data. **We recommend that before you rely on reports and filtering within PopLink, you run Data Validation and prioritize clean-up of at least high-priority errors, as errors will impact report calculations and interpretation.**

In the Reports pull-down menu, you have the option to run a wide variety of reports:

1. Age Outliers Report
2. Age Pyramid Report
3. Breeding Efforts Reports (only visible if module is selected in Settings)
    a. Breeding Efforts Detailed
    b. Breeding Efforts Summary
4. Census Details Report
5. Census Report
6. Current Animals by Location Report
7. Enclosure Report (Only visible if module is selected in Settings)
8. Focal Individual Enclosure Report (Only visible if module is selected in Settings)
9. Historic/Current Institution List
10. Individual Animal Report
11. Life Table Report
12. Lost to Follow Up Report
13. Medical Notes Report (Only visible if module is selected in Settings)
14. Pedigree Reports
    a. Animals With UNK/MULT Parentage and Descendants Report
    b. Living Animals With UNK/MULT in Pedigree Diagram
    c. Antecedent List
    d. Antecedent Diagram
    e. Descendent List
    f. Descendent Diagram
    g. Living Descendant List
15. Proportion of Population Reproducing
16. Reproductive Report
17. Resighting Reports (only visible if module is selected in Settings)
    a. Resightings Analysis
    b. Most Recent Resightings
18. Social Compatibility Report (Only visible if selected in Settings)
19. AnimalStudbook Report
20. Summary Counts Report
21. Survival Tool Report
22. Unknown Age Report

We will describe each of these reports in detail. Note that in the Options section of the Report pull-down menu, you have two options: 1) "Run Reports In New Window", which will pop-up a new window with each report you subsequently run (rather than running them all in the main viewer window), and 2) Select Default Filters, which will set filters that will apply to all the Reports run through this menu (see Chapter 5 for more details).

Many reports contain an "EXPORT" button in the upper-right corner. By clicking on this button, a formatted report is automatically displayed on the screen and saved in your studbook folder. The default format for these reports is HTML (e.g. they will pop-up in your default web browser). If you want the reports to regularly be displayed in another format by default, you navigate to your studbook folder, find a report, right-click on the HTML report, select "Open With", and "Choose Program" to select another program to use (typically Word or Excel). You can select the "Always use this program" option, which will change the default file format reports are displayed in. You

can also keep your default format as HTML and save the reports from within your browser with alternate formats (File → Save As).

In addition, you are able to export the tables in most reports directly to Excel by right clicking within the table and selecting "Export to Excel". Note that if you would like to save multiple versions of the same report within your studbook folder, you will need to re-name each report.

Finally, in many of the reports, you're able to double-click on an animal's ID and pop-up the Individual Animal Report, which can be useful in interpreting the report's results.

8.1 AGE OUTLIERS REPORT

AGE OUTLIERS REPORT

Export

10 Oldest Dead Other Sex | 10 Oldest Living Females | 10 Oldest Living Males | 10 Oldest Living Other Sex | 10 Oldest Dead Females | 10 Oldest Dead Males

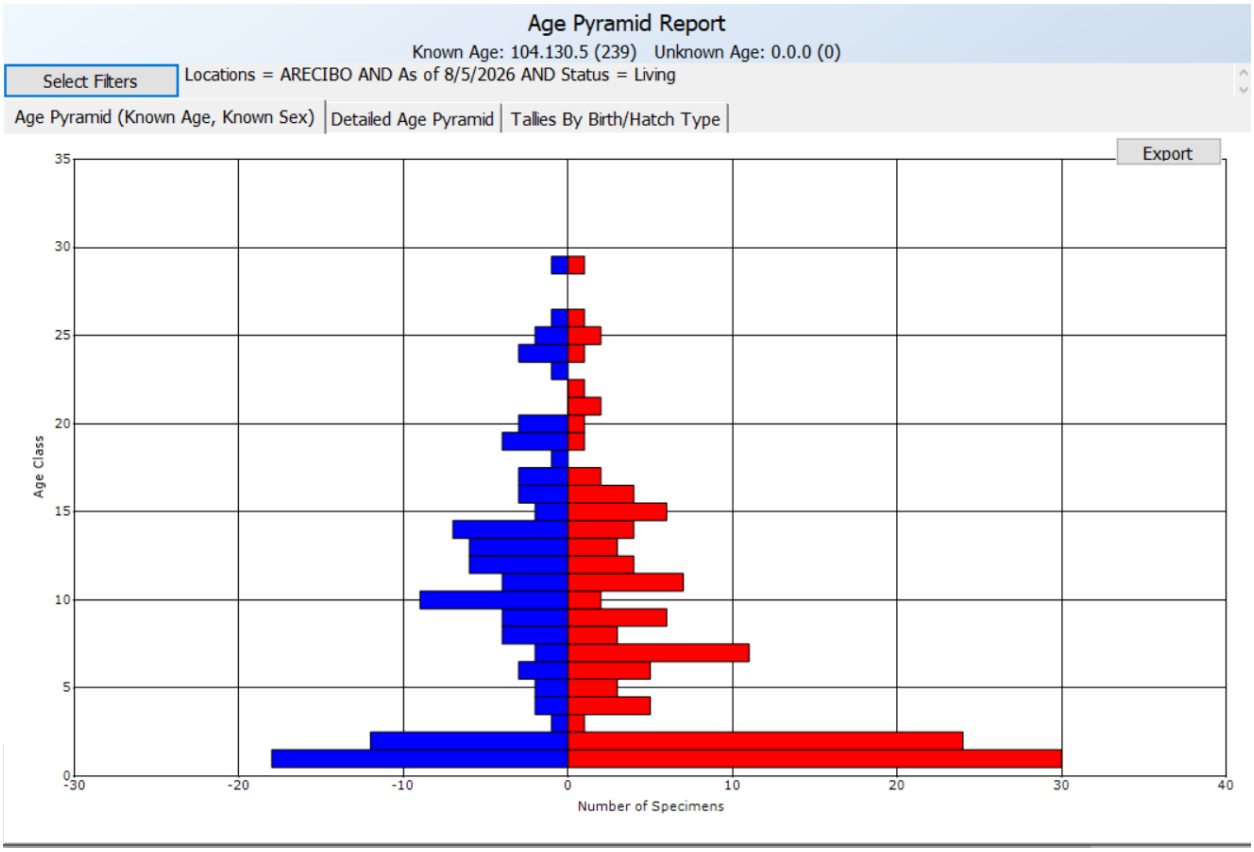
Studbook ID	Current Sex	Hatch Type	Current Age	Current Age Est.	First Location	Current Location
173113	Female	Captive Hatch	31.072	Day	RIOGRANDE	RIOGRANDE
173567	Female	Captive Hatch	30.141	Day	RIOGRANDE	ARECIBO
189549	Female	Captive Hatch	29.648	None	RIOGRANDE	ARECIBO
191183	Female	Captive Hatch	29.101	None	RIOGRANDE	RIOGRANDE
188503	Female	Captive Hatch	27.806	None	RIOGRANDE	ARECIBO
188502	Female	Captive Hatch	26.919	None	RIOGRANDE	RIOGRANDE
173103	Female	Captive Hatch	26.056	None	RIOGRANDE	RIOGRANDE
195074	Female	Captive Hatch	25.933	None	RIOGRANDE	RIOGRANDE
174116	Female	Captive Hatch	25.467	Day	RIOGRANDE	RIOGRANDE
156000	Female	Wild Hatch	23.417	Month	EY WILD	RIOGRANDE

This report lists separate tables with the 10 oldest living and dead individuals of each sex. This report can be useful to look for age outliers – individuals that are exceptionally old and may affect your mortality and life table analyses. Current ages or ages at death may be accurate for these individuals, but if an individual has an exceptionally old age and is at an institution you haven't received a studbook update from recently, or the individual is historic and data might not be accurate, you should consider whether the individual is really still living or should be made lost to follow-up in your studbook or analytical overlay. Individuals with unknown age estimates will not be displayed in this report.

8.2 AGE PYRAMID REPORT

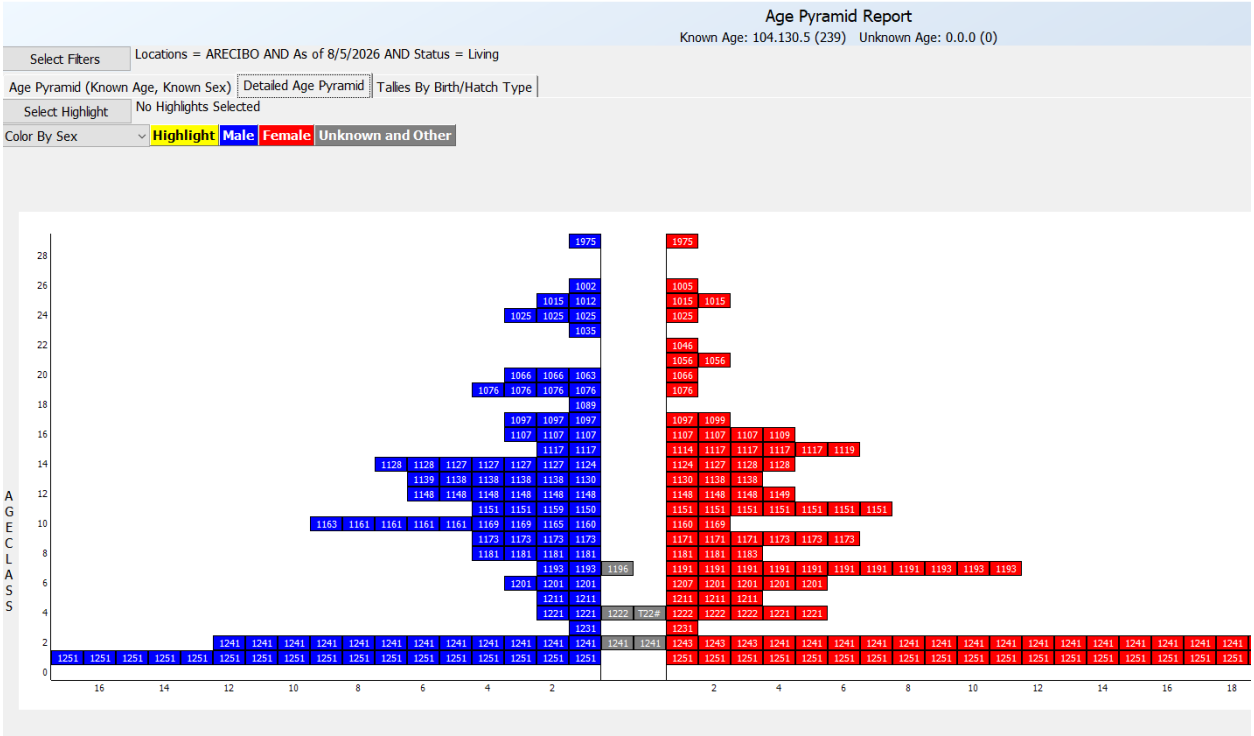
The Age Pyramid Report includes three separate tabs with detailed information about animals in the studbook; this report can be limited using the "Select Filters" button. The default filters that are applied are *STATUS = living* and *DATE = as of today's date.* These default filters for STATUS and DATE cannot be changed for the age report, however, additional filters for other fields may be selected. The three tabs display:

8.2.1 Age Pyramid for Known Age, Known Sex Animals



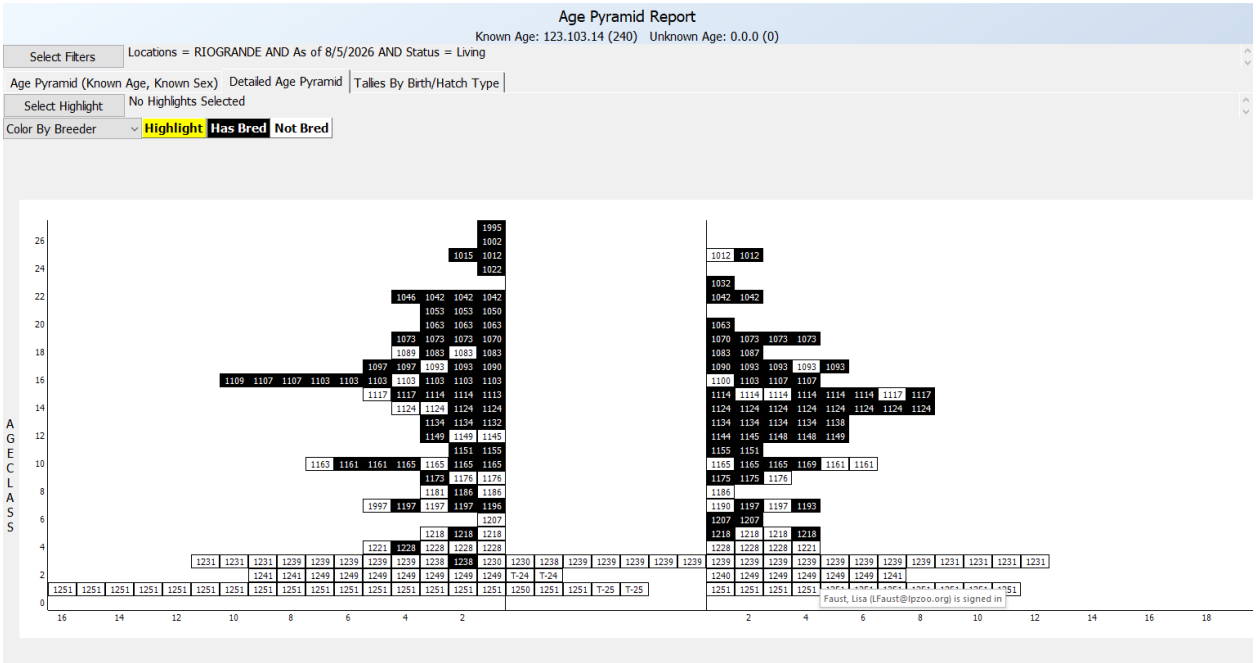
This figure will give a general picture of the population's age structure. Note that any unknown sex and unknown age individuals are not included in this pyramid; you can see how many individuals are excluded by looking at the Known Age and Unknown Age totals directly below the report title.

8.2.2 Detailed Age Pyramid



The detailed age pyramid lists specific animal numbers for individuals in each age class; clicking on the animal numbers will pop-up an Individual Animal Report. Within this report, you have several ways of looking at subsets of your animals:

a. Select Highlights: You can highlight based on any of the standard filter criteria; highlighted individuals will be displayed in yellow on your pyramid. For example, you could highlight based on a UDF field or a location mnemonic
b. Color by (using the pull-down menu):
    i. Sex: This is the default highlighting, with males on the left in blue, females on the right in red, and unknown sex individuals in the middle section of the pyramid in gray.
    ii. Parent: Selecting this option will code your individuals as:
        1. Individuals with WILD/WILD parents (green)
        2. Mixed (orange): individuals with one parent with a studbook ID and the other parent with *WILD*
        3. Individuals UNK, MULT, or some combination (e.g. dam UNK, sire MULT, or dam UNK, sire 23) (pink).
    iii. Breeder: selecting this option will code individuals as:
        1. Has Bred (black)
        2. Has Not Bred (white)



iv. Parent and Breeder: this option combines the two above options, showing Founder/Has Bred, Founder/ has not bred, etc.

Note that individuals in the Detailed Age Pyramid are only known age individuals; if you would like to see the unknown age animals in your population, you can do that via the Unknown Age Report.

8.2.3 Tallies by Birth/Hatch Type

Age Pyramid Report

Known Age: 123.103.14 (240) Unknown Age: 0.0.0 (0)

Select Filters | Locations = RIOGRANDE AND As of 8/5/2026 AND Status = Living

Age Pyramid (Known Age, Known Sex) | Detailed Age Pyramid | Tallies By Birth/Hatch Type

	Total				Wild Hatch				Captive Hatch				Unknown			
Age Class	**M**	**F**	**U**	**O**	**M**	**F**	**U**	**O**	**M**	**F**	**U**	**O**	**M**	**F**	**U**	**O**
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1	21	11	5	0	0	1	2	0	21	10	3	0	0	0	0	0
2	9	7	2	0	1	1	0	0	8	6	2	0	0	0	0	0
3	11	12	7	0	1	2	1	0	10	10	6	0	0	0	0	0
4	5	4	0	0	0	0	0	0	5	4	0	0	0	0	0	0
5	3	4	0	0	0	0	0	0	3	4	0	0	0	0	0	0
6	1	2	0	0	0	0	0	0	1	2	0	0	0	0	0	0
7	5	4	0	0	0	0	0	0	5	4	0	0	0	0	0	0
8	3	1	0	0	0	0	0	0	3	1	0	0	0	0	0	0

This tab displays counts of the number of individuals in each age class in your population; the table is organized by birth type (total, wild born, captive born, and unknown birth type) and separated by sex (Male, Female, Unknown, Abnormal/Other).

8.3 BREEDING EFFORT REPORTS

These reports are only shown if the Breeding Efforts module is turned on in Edit → Settings.

8.3.1. Breeding Efforts Detailed

The Breeding Efforts Detailed report produces a table with every individual breeding effort recorded in chronological order (oldest to newest) and provides details on the potential parents involved in and the offspring produced from each breeding effort.

Breeding Effort Detailed Report

Breeding Event ID	Breeding Individuals	Breeding Location	Location	Breeding Location Disco	Breed Start Date	Start Date Est.	Breed End Date	End Date Est.	Pregnancy Confirmed
2024-1	190,191	Room 1	CHICAGOLP	7/5/2024	7/1/2024		7/30/2024		7/15/2024
2025-1	143,149	Room 2	CHICAGOLP	7/3/2025	7/1/2025		7/30/2025		7/15/2025
2026-1	185,186	Room 1	CHICAGOLP	7/8/2026	7/1/2026		7/30/2026		7/25/2026

When you select this report, a pop-up opens giving you the option to filter the report to see "All" individuals or "Focal Individuals", which gives you the option of typing in the studbook IDs (comma separated) of all individuals you would like to view the breeding efforts for.

This report shows the data you entered for each breeding effort record (potential parents, location, start and end dates, etc.,), but also adds several new columns of data for all parents and offspring listed in a breeding effort. Since breeding effort data requirements differ for live-bearing and egg-laying species, the Breeding Effort Detailed report also varies depending on the species type. New data fields created in this report are:

1. **Location:** the mnemonic location tied to the Breeding Location you entered in the table
2. **Offspring/Hatched/Fledged/Deaths** by sex: These fields list the numbers of individuals of each sex (Male, Female, or Other) for all individuals listed in the Offspring, Hatched in Nest, Fledged in Nest, or Deaths in Nest fields. "Other" includes all PopLink's sexes that are not Male or Female.
3. **Deaths Before Independence:** This field lists the studbook numbers for all individuals listed in the "Died before Independence" field for live-bearing species.
4. **Different Parents**: This field looks at all the individuals listed across the fields where individual offspring studbook IDs are listed (i.e. Hatched in Nest, Offspring, Fledged in Nest, Died in Nest, or Died before Independence) and checks whether the parents of any of these offspring do not match the potential parents listed in a breeding effort record. If any do not match, their studbook ID will be listed in the "Different Parents" column of the report.

NOTE: The Different Parents column can be used as a validation check (e.g., did you enter the right breeding individuals for these offspring?), but it can also be used to track breeding efforts that involve the cross-fostering of eggs or offspring. For example, U.S. endangered species recovery efforts like the Puerto Rican Parrot or Mexican Wolf have been successful in taking *ex situ*-born offspring and placing them in the nest or den of wild pairs to support population growth and increase genetic diversity. For these programs, a "breeding effort" might include both wild-born offspring and a cross-fostering attempt, and the "breeding individuals" listed could be the foster parents. The Different Parents column would flag the cross-fostered individuals, allowing you to quickly filter your report to focus on the outcomes of cross-fostering events.

5. **UNK/MULT Parents**: If an individual listed as an offspring in any of the fields in a breeding effort record has UNK or MULT parents in its studbook record, their studbook ID will be listed in the "UNK/MULT Parents" column of the report. You might use these data to help you flag and assign multiple potential parents to an offspring (i.e. changing an UNK to a MULT based on the potential parents of one sex).
6. **Breeder 1, Breeder 2, etc.**: For each of the potential parents listed in a breeding effort record, this report creates columns with information specific to that parent. For example, the first individual listed

in the breeding effort record is designated as "Breeder 1". For that individual the report creates columns for their birth date (Breeder 1 Bdate) and birth date estimate (Breeder 1 Bdate Est), sex (Breeder 1 Sex), origin (Breeder 1 Origin), age at which they produced their first offspring (Breeder 1 Age at 1st Offspring), and whether they had produced an offspring before the start date of the breeding effort record (Breeder 1 Previous Offspring?).

8.3.2. Breeding Effort Summary

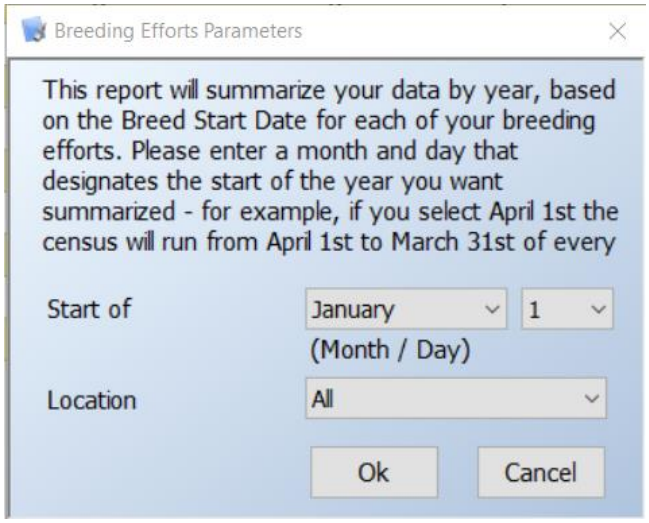
Breeding Effort Summary Report

Select Date / Location Census year starts: January 1 (all years) Location: All

Census Start Date	Census End Date	# of Breeding Pairs/Groups	# of Pairs/Groups with Eggs	# Pairs/Groups with Fertile Eggs	# Pairs/Groups with Offspring	# Pairs/Groups with Fledged Offspring	% Pairs Producing Fertile Eggs	% Pai Live
1/1/2021	12/31/2021	1	1	1	0	0	100.00	0.00
1/1/2022	12/31/2022	2	1	1	2	1	50.00	100.00
1/1/2023	12/31/2023	1	1	1	1	1	100.00	100.00
1/1/2024	12/31/2024	2	2	2	2	2	100.00	100.00
1/1/2025	12/31/2025	7	7	7	7	6	100.00	100.00
1/1/2026	12/31/2026	2	0	0	1	0	0.00	50.00

The Breeding Effort Summary report calculates a set of summary statistics for all breeding effort records in a year (365 days). When you select this report, a pop-up opens giving you the option to filter the report based on a specified starting date (i.e. the start of your breeding season) or the location of a breeding effort record.

The default is to run the report summarizing the breeding efforts that occur beginning on January 1st to December 31st of a year, but for some species (e.g., seasonal breeders) it may be more informative to select an alternate date on which to census the population.



For reference, the starting and ending dates are listed within the **Census Start Date** and **Census End Date** columns of the report. It is important to note that the Breeding Effort Summary assigns breeding effort records to a reporting year based on their ***Breed Start Date*** field. For instance, if a breeding effort began on December 15, 2025, and continued through February 15, 2026, that effort would be included in the 2025 column of the table when using the default January 1 to December 31 reporting period.

For locations, the filter is based on the mnemonic for a User Defined Location or a location on PopLink's "Location List"(e.g., CHICAGOLP), not for a specific "Breeding Location" that may have been created as a User Defined Enclosure (e.g., Breeding Room 1). Once you open the report, you can adjust these filters by selecting the "Select Date/ Location" button at the top of the screen.

This report calculates statistics based on your breeding efforts data that include the total number of eggs or offspring produced, the total number of offspring deaths, and the total number of pairs or groups producing offspring or eggs across breeding efforts in a year. The report only reflects the data entered in your breeding efforts records – if you only record breeding efforts for pairs that successfully produce offspring, then the "% pairs" calculations might only be based on a subset of your population (assuming there are additional breeding events that *did not* result in live offspring).

You can use this report to look at general trends in productivity and breeding success over time for your population. Once again, be aware that since breeding effort data requirements differ for live-bearing and egg-laying species, this report also varies depending on the species type.

The fields for live-bearing species are:

1. **# of Breeding Pairs/Groups**: The total number of pairs/breeding groups involved in a breeding effort in a year. If the same pair/group has multiple breeding efforts in a year, each of those is counted separately.
2. **# Pairs/Groups with Prenatal Mortality**: The total number of pairs/groups involved in a breeding effort in a year that had an offspring listed in the "# Deaths before Birth" field.
3. **% Pairs Producing Live Offspring**: The percentage of all pairs/groups involved in a breeding effort in a year that produced at least one individual listed in the "Offspring" field.
4. **Total Offspring**: The sum of the number of offspring listed in the "Offspring" field across all breeding effort records in a year.
5. **Offspring Male/Female/Other**: The sum of the number of offspring listed in the "Offspring" field broken down by sex across all breeding effort records in a year. The sex for each offspring is taken from each individual's studbook record. "Other" includes all PopLink's sexes that are not Male or Female.
6. **Total Deaths**: The sum of the number of offspring listed in the "Died before Independence" field across all breeding effort records in a year.

Additional fields for egg-laying species are:

7. **# of Pairs/Groups with Eggs**: The total number of pairs/groups involved in a breeding effort in a year that had eggs listed in the "Infertile Eggs", "Fertile Eggs", or "Unknown Fertility Eggs" fields.
8. **# of Pairs/Groups with Fertile Eggs**: The total number of pairs/groups involved in a breeding effort in a year that had eggs listed in the "Fertile Eggs" field.
9. **# of Pairs/Groups with Offspring**: The total number of pairs/groups involved in a breeding effort in a year that had offspring listed in the "Hatched in Nest" field.
10. **# of Pairs/Groups with Fledged Offspring**: The total number of pairs/groups involved in a breeding effort in a year that had offspring listed in the "Fledged in Nest" field.
11. **% Pairs Producing Fertile Eggs/Live Offspring/Fledged Offspring**: For each category, the percentage of all pairs/groups involved in a breeding effort in a year that produced at least one individual/egg listed in the "# Fertile Eggs", "Hatched in Nest, or "Fledged in Nest" fields.
12. **Total Eggs**: The sum of the number of eggs listed in the "Infertile Eggs", "Fertile Eggs", or "Unknown Fertility Eggs" fields for the breeding efforts in a year.
13. **Fertile/Infertile/Unknown Fertility Eggs**: For each category, the total number of eggs listed in the corresponding "Infertile Eggs," "Fertile Eggs," or "Unknown Fertility Eggs" field across all breeding efforts in a year.
14. **Hatched in Nest**: The sum of the number of offspring listed in the "Hatched in Nest" field for all breeding effort records in a year.
15. **Hatched Male/Female/Other**: The sum of the number of offspring listed in the "Hatched in Nest" field broken down by sex for all breeding effort records in a year. The sex for each offspring is taken from each individual's studbook record. "Other" includes all PopLink's sexes that are not Male or Female.

16. **Fledged in Nest**: The sum of the number of offspring listed in the "Fledged in Nest" field for all breeding effort records in a year.

8.4 CENSUS DETAILS REPORT

The Census Details report tallies the number of various events that occur during each year for your population.

When you select the Report, a pop-up will ask you to enter a month and day that each annual census will be taken on. You will be asked to enter a month and day each annual census will be started on. The default is to run the report starting on January 1st (e.g. PopLink will count all events that occur between January 1st and December 31st in a year) but for some species (e.g. seasonal breeders, populations where individuals are reintroduced at a certain time of year, etc.) it may be more informative to select an alternate date on which to start the census. Generally you should leave the year at the default (last year), but you can enter an earlier year if you don't want certain years' data displayed.

You will then be given the option of limiting your data geographically (either to a region or set of mnemonics, or by using a FED file), and/or by User Defined Field.

If there are any individuals with improperly entered first events (i.e. the first event record is not a birth or capture), PopLink will display a warning. These animals affect the Census Details report, and errors in the records should be fixed; more details on individuals with this error can be found in the Validation Report.

Census Details
Census taken from January 01 to December 31
No restrictions on location AND No restrictions on UDFs

	Hatch					Death					Enter					Exit					Transfer			
Year	M	F	U	O	T	M	F	U	O	T	M	F	U	O	T	M	F	U	O	T	M	F	U	O
2025	67	109	55	0	231	8	11	33	0	52	---	---	---	---	---	---	---	---	---	---	42	70	13	0
2024	63	75	56	0	194	28	15	32	0	75	---	---	---	---	---	---	---	---	---	---	87	100	23	0
2023	68	76	61	0	205	24	16	35	0	75	---	---	---	---	---	---	---	---	---	---	62	67	11	0
2022	34	47	107	0	188	31	24	37	0	92	---	---	---	---	---	---	---	---	---	---	62	50	26	0
2021	63	68	46	0	177	17	17	35	0	69	---	---	---	---	---	---	---	---	---	---	85	62	6	0
2020	36	40	90	0	166	31	24	49	0	104	---	---	---	---	---	---	---	---	---	---	41	45	22	0
2019	66	56	40	0	162	7	15	28	0	50	---	---	---	---	---	---	---	---	---	---	26	21	12	0
2018	50	39	34	0	123	22	12	32	0	66	---	---	---	---	---	---	---	---	---	---	17	12	2	0
2017	62	46	37	0	145	34	17	37	0	88	---	---	---	---	---	---	---	---	---	---	79	45	14	0
2016	47	35	32	0	114	23	25	26	0	74	---	---	---	---	---	---	---	---	---	---	56	51	4	0
2015	48	45	23	0	116	28	17	21	0	66	---	---	---	---	---	---	---	---	---	---	50	48	4	0
2014	48	37	42	0	127	7	12	37	0	56	---	---	---	---	---	---	---	---	---	---	22	15	2	0
2013	56	45	2	0	104	19	16	2	0	28	---	---	---	---	---	---	---	---	---	---	20	19	0	0

The Census Details report tallies annual numbers of various events based on data in the Event Data Table: births/hatches; deaths; entrances into the geographic window you selected; exits from the geographic window; transfers; captures from the wild; releases; recaptures; go LTFs; and return from LTF (the last six tallies are not pictured in the screen capture above). The Enter/Exit columns are only tallied if you select a geographic window; if there are values, they can be interpreted as the number of times transfers occurred from <u>outside</u> the location(s) in the geographic filter to <u>inside</u> the filter.

8.5 CENSUS REPORT

When you select the Census Report, a pop-up will ask you to enter a month and day that each annual census will be taken on. The default is to run the report as of December 31st, but for some species (e.g. seasonal breeders, populations where individuals are reintroduced at a certain time of year, etc.) it may be more informative to select an alternate date on which to census the population. Generally you should leave the year at the default (last year), but you can enter an earlier year if you don't want certain years' data displayed.

You will then be given the option of limiting your data geographically, either to a region or set of mnemonics, or by using a FED file. You may also filter for animals that have a specific User Defined Field.

Census Report
Census taken on December 31 of every year.
No restrictions on location AND No restrictions on UDFs

Year	Male	Female	Unknown	Other	Total	Annual Lambda (N)	Geometric Mean		Wild Hatch	Unknown	Captive Hatch	Annual Lambda (Captive)	Geometric Mean	
2025	549	606	214	0	1369	1.151			405	6	958	1.108		
2024	490	507	192	0	1189	1.082	1.116	last 2 years	323	1	865	1.030	1.068	last 2 years
2023	472	457	170	0	1099	1.109	1.114	last 3 years	259	0	840	1.063	1.067	last 3 years
2022	439	406	146	0	991	1.088	1.107	last 4 years	201	0	790	1.045	1.061	last 4 years
2021	443	390	78	0	911	1.123	1.110	last 5 years	155	0	756	1.092	1.067	last 5 years
2020	397	342	72	0	811	1.053	1.101	last 6 years	119	0	692	1.022	1.060	last 6 years
2019	400	336	34	0	770	1.151	1.108	last 7 years	93	0	677	1.132	1.070	last 7 years
2018	344	302	23	0	669	1.050	1.100	last 8 years	71	0	598	1.066	1.069	last 8 years
2017	332	283	22	0	637	0.977	1.086	last 9 years	76	0	561	0.986	1.060	last 9 years
2016	339	286	27	0	652	1.057	1.083	last 10 years	82	1	569	1.040	1.058	last 10 years
2015	317	278	22	0	617	1.058	1.081	last 11 years	69	1	547	1.042	1.056	last 11 years
2014	301	260	22	0	583	1.113	1.083	last 12 years	57	1	525	1.105	1.060	last 12 years
2013	265	240	19	0	524	1.127	1.087	last 13 years	48	1	475	1.110	1.064	last 13 years
2012	230	216	19	0	465	1.134	1.090	last 14 years	36	1	428	1.123	1.068	last 14 years

The Census Report lists the number of living individuals in your selected geographic region (or the entire studbook) by sex and birth type. The annual growth rate (lambda, or λ) is calculated for the total population as

Annual lambda = (Population size this year)/(Population size last year)

Lambda > 1.0 indicates a growing population, Lambda < 1.0 indicates a declining population, and Lambda = 1.0 indicates a stable population. Lambdas can fluctuate widely from year to year, so a more appropriate "average" growth rate is the geometric mean lambda, which is also displayed in the table for different time frames. For example, in this population over the past 5 years the total population has been growing, on average, at 1.014, or 1.4% per year. Note that the left-hand lambdas are growth rates for the Total population size and the right-hand lambdas are growth rates for the captive-born portion of the population. These statistics are calculated for the captive-born portion of the population because population managers are frequently interested in the population's rate of growth from captive reproduction.

Note that for the results on origin, the numbers of individuals should not be interpreted as the numbers of individuals that were wild born, captive born, etc. during the census year. These tallies are based on the specified origin of the individuals who are living on the census date in the selected set of institutions. In the example above, 1369 individuals are living as of 31st December 2025; of those, 958 were captive-hatched and 405 were wild-hatched.

8.6 CURRENT ANIMALS BY LOCATION REPORT

Sunbittern - Current Animals by Location

Current Animals by Location

Export

Select Filters

As of 7/9/2026 AND Status = Living

24.32.25(81) at 8 Locations

Location	Male	Female	Unknown	Other	Total	Location Name
ASHEBORO	13	15	10	0	38	North Carolina Zoo
CHICAGOLP	0	2	0	0	2	Lincoln Park Zoological Gardens
EL PASO	0	1	0	0	1	El Paso Zoo
FORTWORTH	5	6	9	0	20	Fort Worth Zoological Park
GREEN NSC	0	1	0	0	1	Greensboro Science Center
PUEBLO	0	1	0	0	1	Pueblo Zoo
ST LOUIS	5	5	6	0	16	Saint Louis Zoological Park
TOLEDO	1	1	0	0	2	Toledo Zoological Gardens

This report gives a quick summary of the number of living individuals at each location.

8.7 ENCLOSURE REPORT

This report is only shown if the Enclosures module is turned on in Edit → Settings

superbbirdofparadise - Enclosure Report

Enclosure Report

With a "During" date span, this report shows the group composition in an enclosure at each change in composition - each time one or more animals enter or leave an enclosure. With an "As of" date, the report shows group composition in an enclosure as of that date.

All Enclosures as of 9/15/2011

Enclosure Name	Location	Start Date	End Date	Male	Female	Unknc
Outdoor1	HOUSTON	9/15/2011	9/15/2011	0	0	0
Outdoor2	HOUSTON	9/15/2011	9/15/2011	1	0	0
Indoor1	HOUSTON	9/15/2011	9/15/2011	1	1	0
Indoor2	HOUSTON	9/15/2011	9/15/2011	0	0	0
Aviary	HOUSTON	9/15/2011	9/15/2011	3	0	1
Free Flight	LOWRY	9/15/2011	9/15/2011	0	0	0

When the Enclosure Report is selected from the Report menu, a pop-up gives you the option to view the history of an enclosure during a span of time or as of a certain date. It also allows you to specify which enclosure you are interested in (either Show All or select a particular enclosure from the drop-down). Once the appropriate information is entered, the Enclosure Report is generated.

In the report, each row is a record of each social group within an enclosure. Each new row indicates that an animal has moved in/out of that enclosure, thus changing the group composition in the enclosure.
The report's columns are:

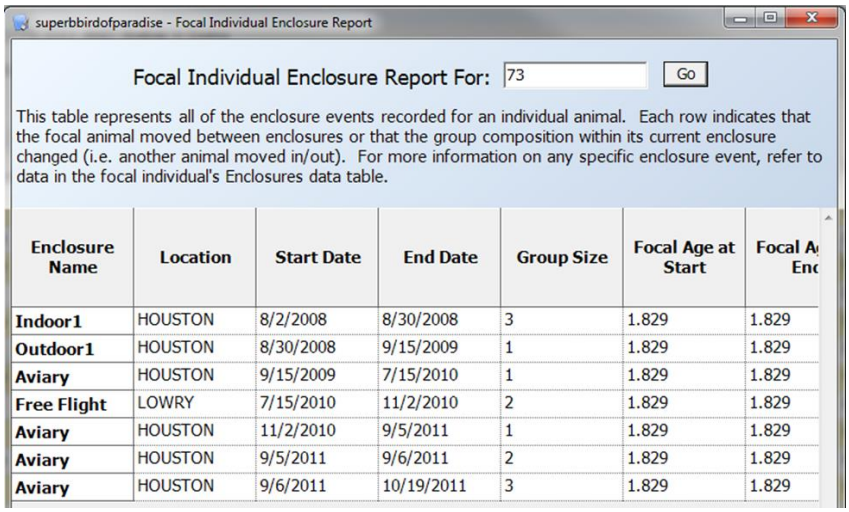
Enclosure Name – Name of the Enclosure, as defined in the User Defined Enclosures list
Location – The institutional mnemonic describing the site of an Enclosure, as defined in the User Defined Enclosures list
Start/End Date – The date an individual entered the focal enclosure or that the group situation changed (start date) until the day before the next social group change (end date)
Male/Female/Unknown – The number of individuals of each sex residing in each enclosure during the date span.
Enclosure Size – The number of individuals in the enclosure
Enclosure Male/Female Age Range at Start/End – The sex-specific age ranges of all animals in the social group at the start and end dates.
Born/Hatched, Died, In, Out – These fields list the Studbook IDs of animals that enter/exit an enclosure or social group via being born/hatched into the enclosure, being transferred in or out of the enclosure, or dying. Even if an individual is entered into/exited from an enclosure on their birth/death date, there must be a comment added by PopLink to count as a born/died in an enclosure.

Enclosure Members – The Studbook IDs & House Names of all the individuals in the enclosure

NOTE: If you select a During date span that starts before or ends after there are any individuals in the enclosure you're showing, there will still be a row in the report but there will be 0 individuals listed in the row. If the "As Of" filter is applied, the born/hatched, died, in, and out columns will be empty as this reflects the enclosure group composition on a single day. When "Show All" Enclosures filters are applied, note that if there's an enclosure listed in the User Defined Enclosures tab that has never had any animals in it, it will still show up in this table (with population sizes of 0).

8.8 FOCAL INDIVIDUAL ENCLOSURE REPORT

This report is only shown if the Enclosures module is turned on in Edit → Settings



superbbirdofparadise - Focal Individual Enclosure Report

Focal Individual Enclosure Report For: 73 Go

This table represents all of the enclosure events recorded for an individual animal. Each row indicates that the focal animal moved between enclosures or that the group composition within its current enclosure changed (i.e. another animal moved in/out). For more information on any specific enclosure event, refer to data in the focal individual's Enclosures data table.

Enclosure Name	Location	Start Date	End Date	Group Size	Focal Age at Start	Focal A Enc
Indoor1	HOUSTON	8/2/2008	8/30/2008	3	1.829	1.829
Outdoor1	HOUSTON	8/30/2008	9/15/2009	1	1.829	1.829
Aviary	HOUSTON	9/15/2009	7/15/2010	1	1.829	1.829
Free Flight	LOWRY	7/15/2010	11/2/2010	2	1.829	1.829
Aviary	HOUSTON	11/2/2010	9/5/2011	1	1.829	1.829
Aviary	HOUSTON	9/5/2011	9/6/2011	2	1.829	1.829
Aviary	HOUSTON	9/6/2011	10/19/2011	3	1.829	1.829

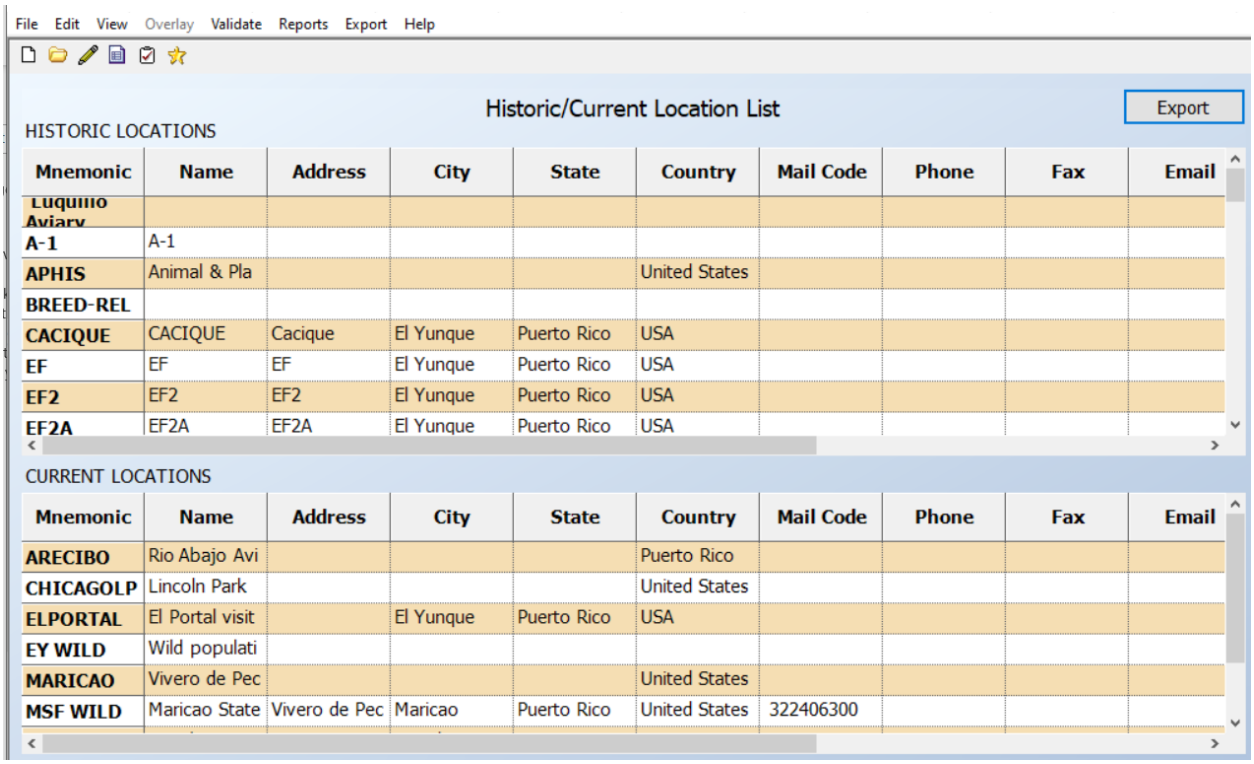
To generate a Focal Individual Enclosure Report, enter the Studbook ID for the desired animal and select "Go".

In this report, each row indicates that the focal individual has either 1) moved enclosures or 2) that the group composition within its current enclosure has changed (i.e. another individual has moved in/out). The report's columns are:

Enclosure Name – Name of the Enclosure, as defined in the User Defined Enclosures list
Location – The institutional mnemonic describing the site of an Enclosure, as defined in the User Defined Enclosures list
Start/End Date – The date the individual entered a new enclosure or that the group situation changed (start date) until the day of the next social group change (end date)
Group Size – The number of individuals in the enclosure (this includes the focal individual)
Focal Age at Start/End – The focal individual's age at the start and end date of an enclosure event.
Group Male/Female Age Range at Start/End – The sex-specific age ranges of other animals in the social group at the start and end dates, excluding the focal individual.
Born/Hatched, Died, In, Out – These fields list the Studbook IDs of animals that enter/exit an enclosure or social group via being born/hatched into the enclosure, being transferred in or out of the enclosure, or dying. Even if an individual is entered into/exited out of an enclosure on their birth/death date, there must be a comment added by PopLink to count as a born/died in an enclosure.
Group Members – The Studbook IDs and House Names of all the individuals in the enclosure, including the focal individual.

You can use this report to look at which enclosures an individual has been in over its lifetime, which other animals it has been with, and which life history stages the animal has been with (e.g. has the focal individual ever been housed with adult males?).

8.9 HISTORIC/CURRENT LOCATIONS LIST



Mnemonic	Name	Address	City	State	Country	Mail Code	Phone	Fax	Email
Luquillo Aviary									
A-1	A-1								
APHIS	Animal & Pla				United States				
BREED-REL									
CACIQUE	CACIQUE	Cacique	El Yunque	Puerto Rico	USA				
EF	EF	EF	El Yunque	Puerto Rico	USA				
EF2	EF2	EF2	El Yunque	Puerto Rico	USA				
EF2A	EF2A	EF2A	El Yunque	Puerto Rico	USA				

Mnemonic	Name	Address	City	State	Country	Mail Code	Phone	Fax	Email
ARECIBO	Rio Abajo Avi				Puerto Rico				
CHICAGOLP	Lincoln Park				United States				
ELPORTAL	El Portal visit		El Yunque	Puerto Rico	USA				
EY WILD	Wild populati								
MARICAO	Vivero de Pec				United States				
MSF WILD	Maricao State	Vivero de Pec	Maricao	Puerto Rico	United States	322406300			

This report lists the historic and current locations that any individuals in the studbook have been held at. Current locations include institutions that are currently housing living individuals. Historical locations include any locations that are not currently holding any individuals in the studbook, but have done so in the past. Both recognized mnemonics and user defined mnemonics are included in this report.

8.10 LIFE TABLE REPORT

Life Table Report

Export

Select Filters

During 8/5/2000 - 8/5/2026 AND Status = Living

Please note that the following numbers are calculated slightly differently than SPARKS.
For each offspring, each parent gets 0.5 of the birth attributed to him/her.
There are 2676 total births in the demographic window.
2557.5 births are attributed to known parents with a known age.
0 births are attributed to known parents with an unknown age.
118.5 births are attributed to unknown parents.
This means that 4% of the total births are attributed to unknown parents or parents with unknown ages.
For this report, the births were proportionally factored into the fecundity.

	Fecundity (Mx)				Mortality (Qx)			
Age Class	Male Mx	N at Risk	Female Mx	N at Risk	Male Qx	N at Risk	Female Qx	N at Risk
0- 1	0.000	1057.7	0.000	1058.1	0.239	1348.4	0.227	1337.1
1- 2	0.000	914.9	0.004	904.8	0.099	977.7	0.061	945.0
2- 3	0.021	739.7	0.040	735.3	0.071	776.0	0.056	766.0
3- 4	0.092	599.8	0.143	602.1	0.054	624.1	0.033	615.3
4- 5	0.162	506.1	0.209	495.9	0.027	514.2	0.028	505.1
5- 6	0.228	438.6	0.296	423.0	0.032	447.6	0.043	434.6
6- 7	0.328	383.2	0.399	362.0	0.028	389.3	0.038	369.1
7- 8	0.422	332.8	0.396	307.2	0.035	338.6	0.035	313.4
8- 9	0.415	297.0	0.485	271.0	0.023	300.6	0.026	273.8
9-10	0.486	272.1	0.467	245.7	0.018	274.8	0.036	249.7
10-11	0.436	248.0	0.446	223.6	0.016	249.8	0.018	225.9
11-12	0.374	228.6	0.387	207.4	0.017	230.5	0.024	210.3
12-13	0.441	210.4	0.438	189.5	0.009	211.0	0.031	192.0
13-14	0.354	192.4	0.351	160.6	0.015	193.9	0.042	165.2

This report generates fecundity (Mx) and mortality (Qx) values at each age class for males and females in the studbook. Note: for each offspring, each parent gets 0.5 of the birth attributed to him/her. If a birth is attributed to unknown parents or parents of unknown ages, you have the option of proportionally factoring these births into the fecundity. *See section 7.2* for more details on how these values are calculated.

8.11 LOST TO FOLLOW UP REPORT

Lost To Follow Up Report

Select Filters

No Filters Applied

Studbook ID	Current Status	Current Location	Transaction Date	Transaction Date Est.	LTF Age
111856	LTF	ARECIBO	3/20/2013	None	0.003
109714	LTF	ARECIBO	6/15/2013	Month	4.235
EF5	LTF	EF	1/1/1985	None	---
EF2M	LTF	EF2	9/15/1975	Year	---
EF3F	LTF	EF2A	1/1/1986	Year	---
EF3M	LTF	EF2A	1/1/1986	Year	---
EF41	LTF	EF3	1/1/1995	Year	---

This report lists all the animals whose current/final status is lost to follow up (i.e. their last event is Go LTF), as well as the location, date, and age when they went LTF. You can use this report as a quick reference list for individuals whose final status you may want to research further.

8.12 MEDICAL NOTES REPORT

This report is only shown if the Medical module is turned on in Edit → Settings

superbbirdofparadise - Medical Note Report

Medical Notes Report For: 55 Go

Enter a specific studbook ID or "ALL" to generate this report for all individuals in the studbook. The displayed animal's sex, age, and enclosure are as of the Medical Note's Start Date

Studbook ID	Sex	Age	Enclosure Name	Category	Type	Value	M
55	Male	0	Indoor2 (HOU	Medical Proce	Visual Assess	.	.
55	Male	0	Indoor2 (HOU	Weight	.	50	G
55	Male	0.019	Indoor2 (HOU	Clinical Sign	Cardiopulmon	.	.
55	Male	0.019	Indoor2 (HOU	Diagnostics	Culture	.	.
55	Male	0.022	Indoor2 (HOU	Medication	Antibiotic	25	M
55	Male	0.06	Indoor2 (HOU	General Medi	.	.	.
55	Male	0.999	Indoor2 (HOU	Weight	.	75	G
55	Male	4.112	Free Flight (LO	Medication	Vaccine	25	M

To generate a Medical Notes Report, enter the Studbook ID for the desired animal and press "Go".

The Medical Notes Report includes all the medical notes recorded for the focal individual, as well as the individual's **Sex, Age,** and **Enclosure Name** as of the medical note date, if enclosure data is recorded in the Enclosure data table.

As not every medical note type has data in all the fields, some fields in this report will display "." to reflect unnecessary fields.

8.13 ANIMALS WITH UNK/MULT PARENTAGE AND DESCENDANTS REPORT

SPECIMENS WITH UNK/MULT PARENTAGE AND DESCENDANTS

Export

Select Filters No Filters Applied

SPECIMENS WITH UNKNOWN PARENTAGE

Studbook ID	Current Status	Sire	Dam	Birth Date	Birth Date Est.	First Location	Second Location	Current Location	# Total Living Desc	% Total Living Popul	
119	Dead	UNK	UNK	1/1/1965	Year	SANDIEGOZ	FORTWORTH	FORTWORTH	54	23.8%	892
542	LTF	UNK	UNK	1/1/1988	Year	LAKEBUENA	MCMORRIS	KENNY R	0	0.0%	
481	LTF	UNK	UNK	1/1/1986	Year	LAKEBUENA	MCMORRIS	GARCIA G	0	0.0%	
427	Dead	UNK	UNK	1/1/1984	Year	CHATFIELD	BUFFALO	BUFFALO	0	0.0%	
426	Dead	UNK	UNK	1/1/1984	Year	CHATFIELD	BUFFALO	HATTIESBG	0	0.0%	
255	Dead	UNK	UNK	1/1/1976	Year	LOSANGELE	FORTWORTH	FORTWORTH	0	0.0%	
212	Dead	UNK	UNK	1/1/1974	Year	ADELAIDE	BROWNSVIL	BROWNSVIL	0	0.0%	
211	LTF	UNK	UNK	1/1/1974	Year	ADELAIDE	WINNIPEG	CHISHOLM	0	0.0%	
540	Living	UNK	UNK	1/1/1988	Year	LAKEBUENA	GULF BREZ	GULF BREZ	1	0.4%	540

SPECIMENS WITH MULT PARENTAGE

Studbook ID	Current Status	Sire	Dam	Birth Date	Birth Date Est.	First Location	Second Location	Current Location	# Total Living Desc	% Total Living Popul
885	LTF	MULT	MULT	1/21/1995	None	HORSE CAV	HORSE CAV	HORSE CAV	0	0.0%

This report lists all individuals (living and dead) that have an UNK or MULT sire or dam, or have one or both parents that are not in the studbook. The table displays the number of living descendants the individual has. On the right-hand side of the table, the individual animal numbers of the living descendants are listed and can be used to open up animal reports for the descendant. This report can be used to help investigate which individual descendant needs further research on pedigree or analytical assumptions; clean-up can be prioritized based on the number of living descendants (e.g. individuals who may currently be eligible for breeding). For more details, see Chapter 9 on making analytical assumptions for unknown pedigree animals.

8.14 LIVING ANIMALS WITH UNK/MULT IN PEDIGREE REPORT

Living Specimens With UNK/MULT In Pedigree

Select Filters No Filters Applied

Studbook ID	Sire	Dam	Current Age	Current Sex	Current Location	First Location	% Pedigree Unknown
12502	UNK	UNK	1.04	Unknown	MSF WILD	MSF WILD	100.0%
12503	UNK	UNK	1.333	Unknown	RIOGRANDE	MSF WILD	100.0%
12504	UNK	UNK	1.333	Unknown	MSF WILD	MSF WILD	100.0%
12505	UNK	UNK	1.333	Unknown	MSF WILD	MSF WILD	100.0%
12506	UNK	UNK	1.314	Unknown	MSF WILD	MSF WILD	100.0%
12507	UNK	UNK	1.314	Unknown	MSF WILD	MSF WILD	100.0%
12508	UNK	UNK	1.314	Unknown	MSF WILD	MSF WILD	100.0%

This report lists all the living individuals with an UNK or MULT ancestors anywhere in their pedigree (e.g., sire, dam, grandparent, great-grandparent, etc.) Typically these individuals might not be used to make breeding pairs because of the unknownness in their pedigree, and this report can be used to start to investigate which individuals may need further research on pedigree or analytical assumptions. For more details, see Chapter 9 on making analytical assumptions for unknown pedigree animals.

8.15 ANTECEDENT LIST REPORT and DIAGRAM

The Antecedent report gives a list of all the ancestors for a given focal animal:

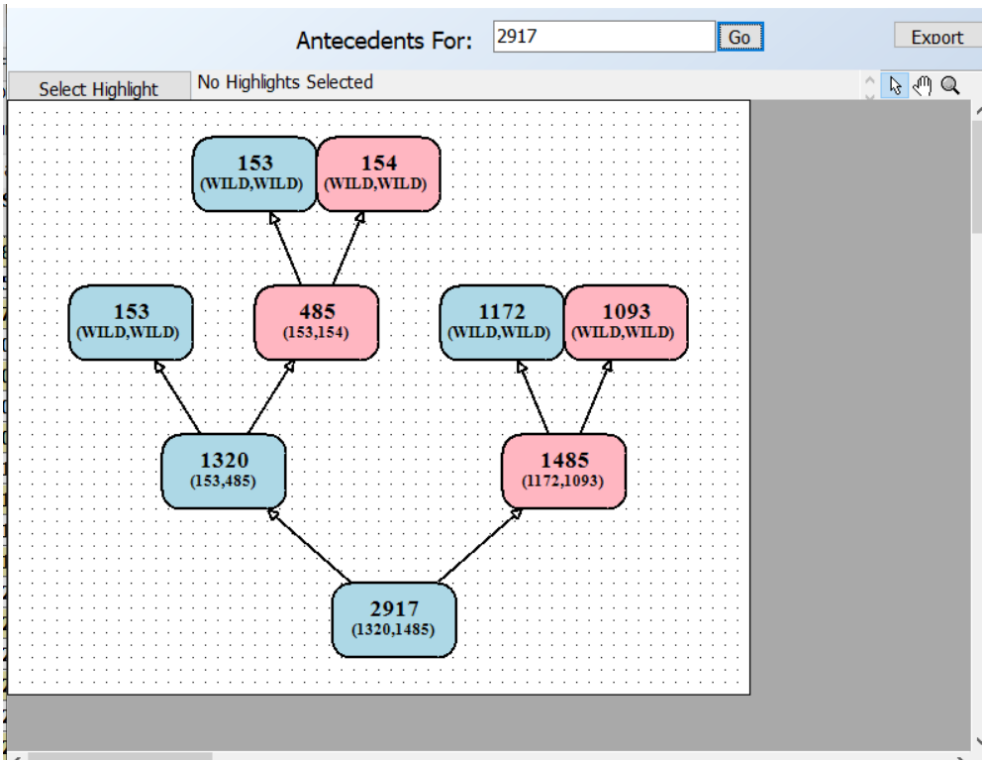
Antecedents For: 12510 Go Antecedants Diagram

Select Filters No Filters Applied

Studbook ID	Sire	Dam	Generations Removed	Birth Date	Birth Date Est.	Current Status	Current Age	Current Sex	Current Location	First Location
100227	188140	189540	4	7/26/2000	None	Dead	14.234	Male	RIOGRANDE	RIOGRANDE
101244	SF2B	SF2B	4	3/16/2001	Day	Living	25.388	Female	RIOGRANDE	RIOGRANDE
101246	SF2B	SF2B	3	3/20/2001	Day	Living	25.377	Male	MARICAO	RIOGRANDE
101251	194082	195118	3	7/2/2001	Year	Dead	18.114	Female	RIOGRANDE	RIOGRANDE
104296	WILD SF1T 2004	WILD SF1T 2004	3	4/15/2004	None	Dead	16.287	Female	RIOGRANDE	SF1A
106321	100227	101244	3	5/21/2006	None	Living	20.208	Male	RIOGRANDE	RIOGRANDE
107683	188506	189549	3	4/15/2007	None	Living	19.307	Male	ARECIBO	ARECIBO
108342	101246	101251	2	4/22/2008	None	Living	18.286	Male	RIOGRANDE	RIOGRANDE
109354	197225	197224	2	5/1/2009	None	Living	17.262	Female	RIOGRANDE	RIOGRANDE
109068	198532	198536	3	4/9/2009	None	Living	17.322	Female	ARECIBO	ARECIBO

In this case, animal 225 has 12 antecedents in the studbook. The Generations Removed column lists how many generations a given animal is *from the focal individual.* Thus individuals with generations removed of 1 would be the animal's parents, 2 would be grandparents, etc.

If you click on the Antecedents Diagram button next to the report, or select the Antecedents Diagram report from the Pedigree Reports section, you can get a quick visual diagram of the relationships of the individuals in the Antecedents table:



In this diagram, males are blue, females are pink, and unknown/abnormal sexes are grey. Each individual's parents are listed below their ID in parentheses (sire, dam).

Double-clicking on a box will open up that individual's animal report. Using the hand tool in the upper right-hand corner of the report allows you to "grab" and move the diagram. Selecting the magnifying glass tool in the upper right-hand corner allows you to zoom in on an area of the diagram by left-clicking your mouse and zoom out on an area by right-clicking your mouse.

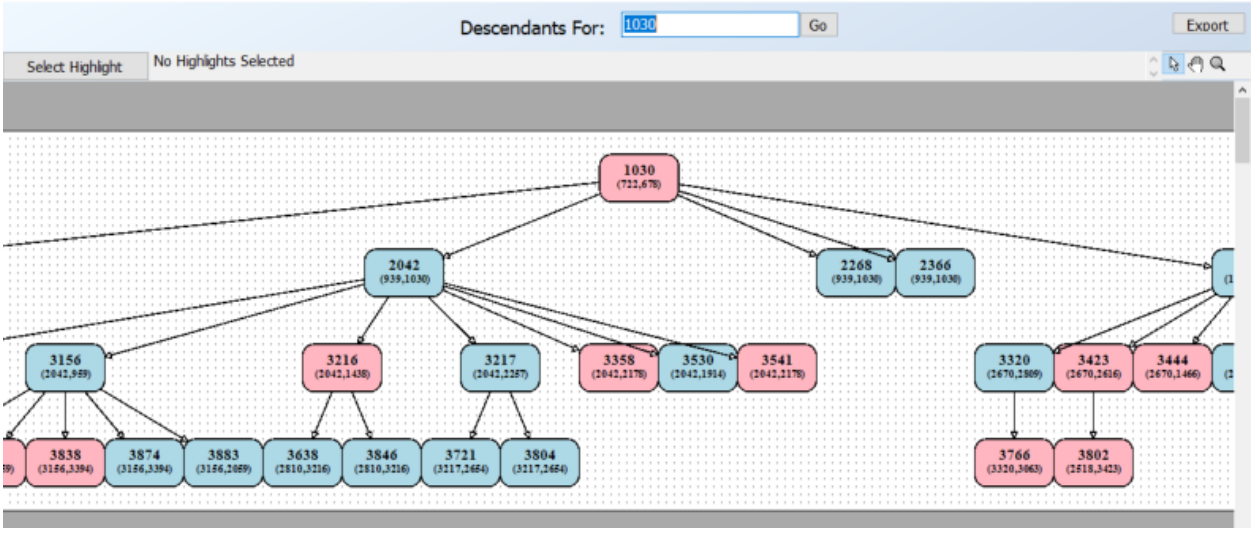
8.16 DESCENDANT LIST REPORT and DIAGRAM

This report is identical to the Antecedents List report except that it focuses on all the **Descendants** for a focal individual:

Descendants For: 1030 Go Descendants Diagram

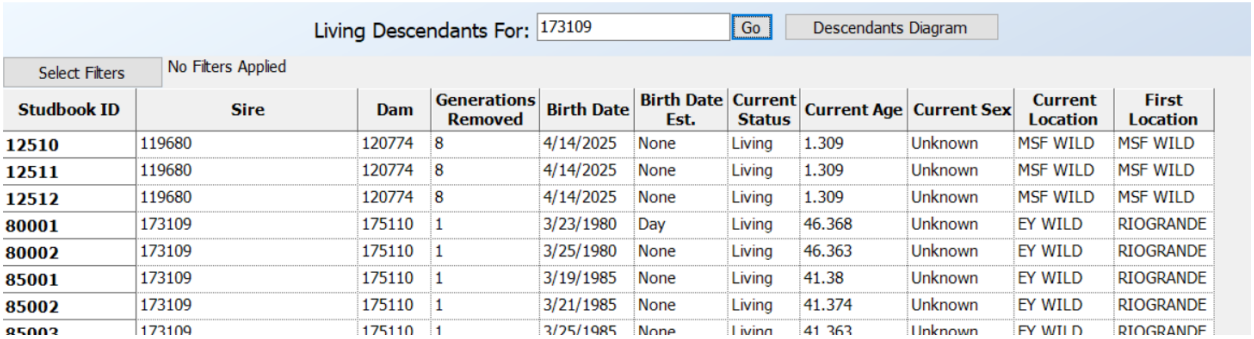
Select Filters No Filters Applied

Studbook ID	Sire	Dam	Generations Removed	Birth Date	Birth Date Est.	Current Status	Current Age	Current Sex	Current Location	First Location
1739	939	1030	1	11/11/1979	None	Dead	17.262	Male	SAIGON	DRESDEN Z
2042	939	1030	1	4/19/1985	None	Living	41.295	Male	JERSEY	DRESDEN Z
2268	939	1030	1	6/7/1989	None	Dead	0	Male	DRESDEN Z	DRESDEN Z
2366	939	1030	1	6/16/1990	None	Dead	12.359	Male	ZURICH	DRESDEN Z
2670	1248	1030	1	11/7/1994	None	Dead	29.235	Male	ZURICH	DRESDEN Z
2907	2042	2257	2	10/17/1999	None	Living	26.801	Male	JERSEY	JERSEY
3156	2042	959	2	5/13/2004	None	Living	22.229	Male	BOISSIERE	JERSEY



8.17 LIVING DESCENDANT LIST REPORT

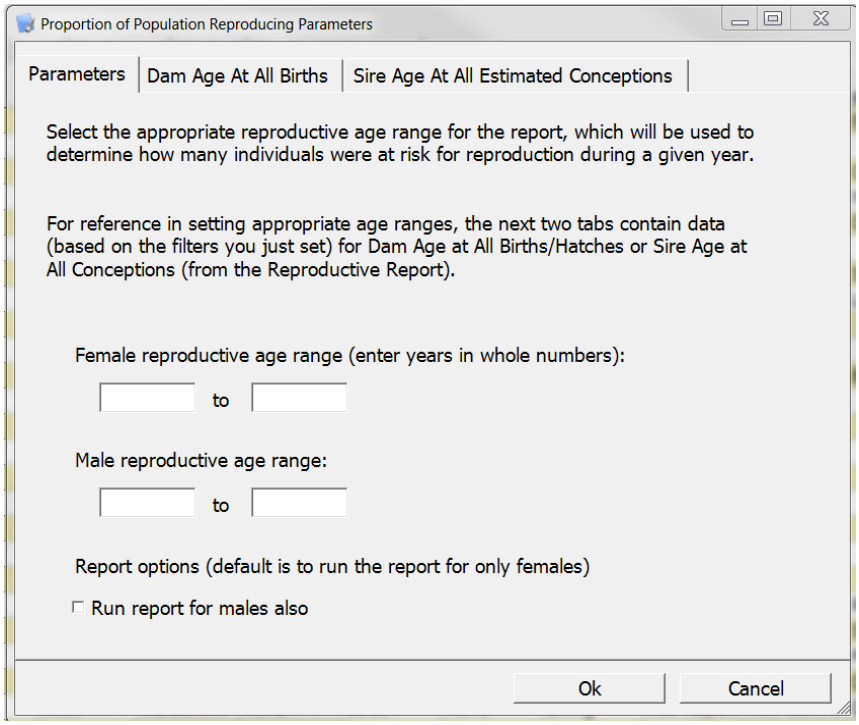
This Living Descendant List report gives a subset of only the living descendants for any animal:



Studbook ID	Sire	Dam	Generations Removed	Birth Date	Birth Date Est.	Current Status	Current Age	Current Sex	Current Location	First Location
12510	119680	120774	8	4/14/2025	None	Living	1.309	Unknown	MSF WILD	MSF WILD
12511	119680	120774	8	4/14/2025	None	Living	1.309	Unknown	MSF WILD	MSF WILD
12512	119680	120774	8	4/14/2025	None	Living	1.309	Unknown	MSF WILD	MSF WILD
80001	173109	175110	1	3/23/1980	Day	Living	46.368	Unknown	EY WILD	RIOGRANDE
80002	173109	175110	1	3/25/1980	None	Living	46.363	Unknown	EY WILD	RIOGRANDE
85001	173109	175110	1	3/19/1985	None	Living	41.38	Unknown	EY WILD	RIOGRANDE
85002	173109	175110	1	3/21/1985	None	Living	41.374	Unknown	EY WILD	RIOGRANDE
85003	173109	175110	1	3/25/1985	None	Living	41.363	Unknown	EY WILD	RIOGRANDE

8.18 PROPORTION OF POPULATION REPRODUCING REPORT

This report calculates the proportion of the adult population that produced offspring, doing so on an annual basis so you can look at your population's productivity over time. When you select the report, a pop-up will ask you to select a date window, as well as add institutional/geographic filters or UDF filters. A second pop-up then asks for additional report parameters:



The female and male age classes should be set to define either the entire reproductive window or a subset of the reproductive window you're interested in looking at (e.g. if you're interested in the proportion of older vs. younger dams reproducing – you could run two reports with different female reproductive age ranges). You can use the data in the next two tabs of this pop-up (Dam Age At All Births/Hatches, Sire Age At All Estimated Conceptions) to inform your choices on the age ranges to use. Note that if your oldest female produced offspring at 9.8 years, you should put 10 in the box so all of the nine-year-old age class is included.

You can use the check box to run the report for both males and females (females are most typically the sex of interest in this report).

AfricanWildDog2011b - Proportion of Population Reproducing

Litters

PROPORTION OF POPULATION REPRODUCING

Species Type: Live Bearing Gestation Period: 70 Days Maximum Birth Date Range For Litter Mates: 3 Days

This report summarizes the proportion of each sex producing offspring in any given calendar year. Note that the denominator (# of females/males at risk) includes all animals living within your filter conditions, some of which may never have had access to a reproductive partner. If your population has a large number of offspring with unknown dams, each of those offspring is considered its own litter/clutch; if these individuals are likely litter/clutch-mates, then the proportion of your population reproducing is likely lower than the report calculations. To see more details on the tallied litters/clutches, use the button to the right to pop-up a litters report.

Filters applied to parents: During 1/1/1980 - 8/30/2012 AND Female Age = 1 to 12 AND Male Age = 1 to 14

Year	Total Births	# Litters to Identified Dams	# Litters to Unknown Dams	Total # Litters	# Females @ Risk	Proportion of Females Reproducing		Total # Litters	# Males @ Risk	Proportion of Males Reproducing
2011	9	1	0	1	73	0.014		1	94	0.011
2010	27	4	0	4	71	0.056		4	91	0.044
2009	50	8	0	8	72	0.111		8	90	0.089
2008	5	2	0	2	78	0.026		2	99	0.02
2007	39	6	0	6	73	0.082		6	103	0.058
2006	67	13	0	13	71	0.183		13	92	0.141
2005	59	11	0	11	62	0.177		11	83	0.133

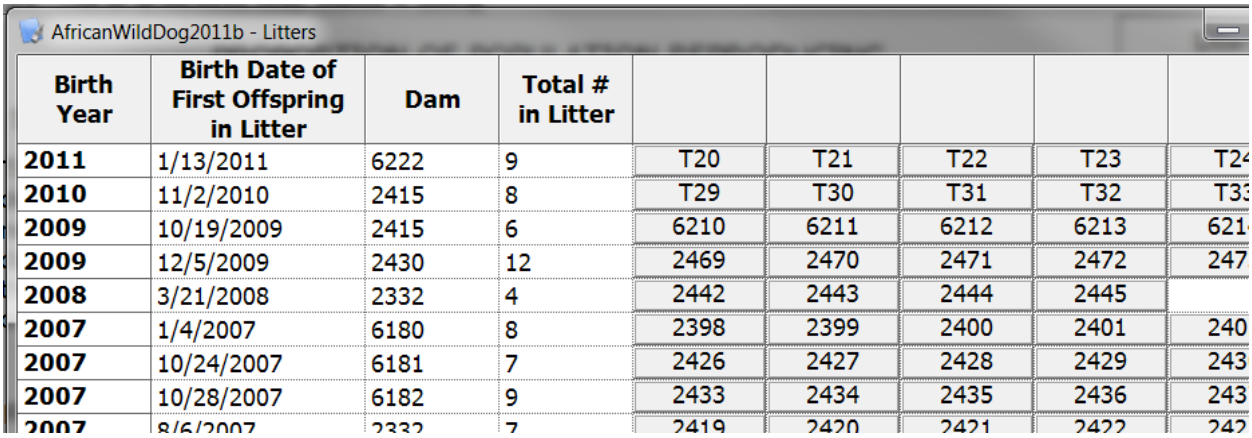
Once you've set your report parameters, the report is generated. At the top, it includes basic background about your species (e.g., Species Type, Gestation Period, and the birth date range used to delineate litters – see the Studbook Overview help section for more details about this parameter).

The report tallies data for each calendar year. The fields, and some details on their calculations, are:

- **Total births/hatches:** a tally of the number of births/hatches in that calendar year. This is based on captive-born individuals with birth events within any geographic/UDF filter conditions you've set; the tally excludes any births/hatches to unknown-age parents (because they can't be included in the # Females @ Risk column, as without a known age they can't be fit into the filter conditions) and excludes a birth/hatch if its birthdate is unknown (i.e., has an Unknown date estimate). The tally is restricted based on the female reproductive age range you set – if that age range is 1-5 rather than the entire reproductive age range, only offspring born to dams between the ages of 1-5 are tallied. Note that the tally in this report might be slightly different than that in the Census Details report because it excludes births that are not captive-born and/or to unknown-aged parents.
- **# Litters/Clutches to Identified Dams:** a tally of the number of litters/clutches born to identified dams in that calendar year. Identified dams have known, real studbook IDs (e.g. 1, 215) or have specific, standardized IDs based on parental assumptions, such as UNK6 or MULT3, which are used to identify litters/clutches of individuals as coming from the same dam. Litters/Clutches are defined based on the Maximum Birth/Hatch Date Range defined in the Studbook Overview table. If a litter/clutch's birthdates overlap a year (e.g. the first in the litter is born on December 31st and the next offspring are born on January 1st and after), the litter is assigned to the year of the first offspring's birthdate.
- **# Litters/Clutches to Unknown Dams:** a tally of the number of litters/clutches born to dams with generic UNK, MULT or other un-identifiable IDs. Note that even if the offspring to these dams might be littermates (e.g. born at the same institution on the same date), PopLink does not make any assumptions based on that. Instead, every individual born to an unknown dam is counted as its own litter/clutch. If your studbook has many offspring with UNK or MULT dams that in reality might be part of litters, then the proportion of females (or males) reproducing will be inaccurate (i.e., higher than it should be).
- **Total # Litters/Clutches =** # Litters/Clutches to Identified Dams + # Litters to Unknown Dams

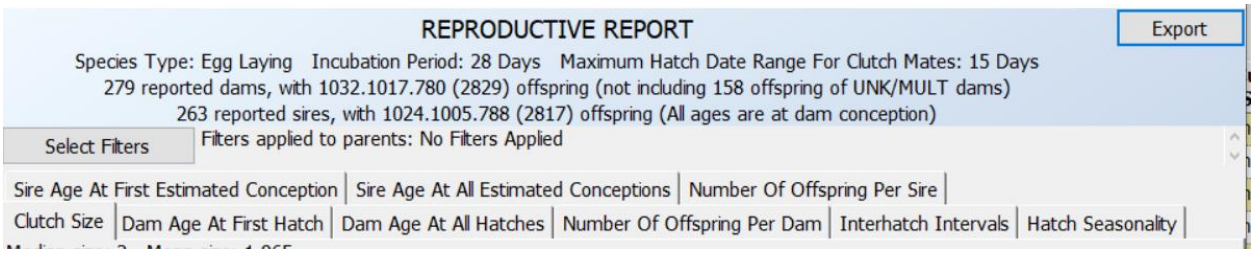
- **# Females @ Risk:** the number of females who were living in your filter conditions (e.g., geographic, UDF, and reproductive age range) in a given calendar year. Note that this does not necessarily mean these females were in a potential breeding situation (i.e. housed with a mate).
- **Proportion of Females Reproducing =** Total # Litters / # Females @ Risk. This is the proportion of the females in your population that had at least one reproductive episode (i.e.,. produced a litter/clutch) in a given year. If your species is able to have multiple reproductive events in a given year and that practice is wide-spread, it is possible for the proportion of females reproducing to be greater than one.
- **Total # of Litters/Clutches (optional)**: same as above
- **# Males @ Risk (optional)**: same as above
- **Proportion of Males Reproducing (optional)**: same as above

In the upper right-hand corner of the report, the "Litters" button will pop-up a secondary report that gives details on all the litters/clutches included in the report. This pop-up is useful as a data validation tool, as it helps you find particular litter/clutch sizes that might be suspicious (e.g., large litters/clutches that are listed in your Reproductive Report but you can't find them in your studbook). You can pop-up the offspring's animal reports by clicking on the button with their ID.


AfricanWildDog2011b - Litters

Birth Year	Birth Date of First Offspring in Litter	Dam	Total # in Litter					
2011	1/13/2011	6222	9	T20	T21	T22	T23	T24
2010	11/2/2010	2415	8	T29	T30	T31	T32	T33
2009	10/19/2009	2415	6	6210	6211	6212	6213	621
2009	12/5/2009	2430	12	2469	2470	2471	2472	247
2008	3/21/2008	2332	4	2442	2443	2444	2445	
2007	1/4/2007	6180	8	2398	2399	2400	2401	240
2007	10/24/2007	6181	7	2426	2427	2428	2429	243
2007	10/28/2007	6182	9	2433	2434	2435	2436	243
2007	8/6/2007	2332	7	2419	2420	2421	2422	242

8.19 REPRODUCTIVE REPORT



The Reproductive Report displays general reproductive information pertaining to your population and includes nine separate tabs with detailed reproductive information. The general information at the top of the report includes the reproductive information that you entered when you first created your studbook (e.g. species type and incubation period). The reproductive report can be limited using the "Select Filters" button. In the reproductive report, **all filters are applied to the parents, NOT the offspring.** So, for example, if you filter to "living during 1/1/1980 and 1/1/2000", the litter/clutch size tab will reflect all offspring born to PARENTS who lived during that date window; the offspring in question may or may not have been born during the date window. There are no default filters for this report (i.e. default is No Restriction). All reported ages of sires are ages when the dam conceived the offspring in question (*see*

section 3.3.1 for calculation of estimated conception date). All tables can be exported to Excel by right clicking on the table and selecting "Export to Excel".

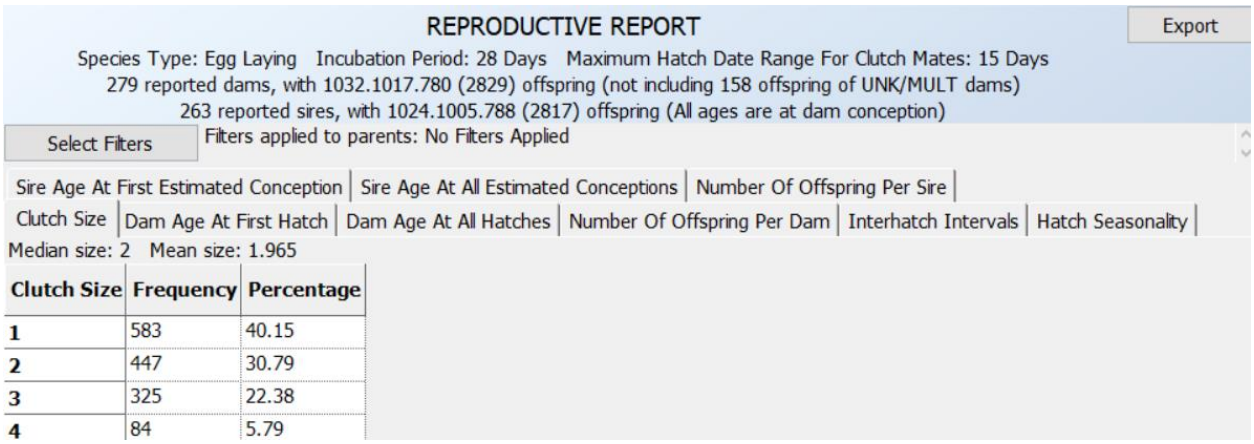
Note that, for informational purposes, dams and sires with Unknown birth date estimates are displayed in the nine tables in the Reproductive Report in PopLink. Ages at birth for these individuals are not used to calculate any of the mean/median statistics displayed at the top of some tables.

The report tallies reproduction information from known/individually identified dams and sires, meaning dams/sires that have known studbook IDs (e.g. 1, 215). In addition, in relevant tabs (Litter/Clutch Size, Birth Seasonality) where it is counting individual clutches, it includes data from dams or sires that use standard studbook conventions to indicate specific individuals (e.g. UNK5, MULT3). The report does not include any data from offspring born to generic dams or sires (e.g. UNK, MULT).

In addition to the nine tabs, the reproductive report displays the number of reported dams with offspring, the number of offspring (Male.Female.Unknown/Abnormal (Total)) born to those dams, the total number of offspring born to UNK/MULT dams, the number of reported sires, and the number of offspring (Male.Female.Unknown/Abnormal (Total)) born to those sires. The nine tabs display Litter/Clutch Size, Interbirth/Interhatch Intervals, Birth/Hatch Seasonality, Dam Age at First Birth/Hatch, Dam Age at All Births/Hatches, Number of Offspring Per Dam, Sire Age At First Estimated Conception, Sire Age at All Estimated Conceptions, and Number of Offspring Per Sire.

8.19.1 Litter/Clutch Size

The litter or clutch size tab lists all observed litter sizes and the frequency and percentage of each litter size within your studbook and filter restrictions. Note that litters are defined based on the Maximum Birth/Hatch Date Range defined in the Studbook Overview tab.



Clutch Size	Frequency	Percentage
1	583	40.15
2	447	30.79
3	325	22.38
4	84	5.79

Note that if you wish to see more details on individual litters/clutches, you can use the Litter/Clutch pop-up in the Proportion of Population Reproducing Report – *see section 8.18* for more details.

8.19.2 Interbirth/Interhatch Intervals

The Interbirth Interval tab lists all interbirth intervals in days for each dam's consecutive offspring. Intervals are calculated from the date of birth/hatch of the last offspring of one litter/clutch to the date of birth of the first offspring of the next consecutive litter/clutch. The report is ordered by increasing interbirth interval and both dams and offspring may be listed more than once.

REPRODUCTIVE REPORT

Export

Species Type: Egg Laying Incubation Period: 28 Days Maximum Hatch Date Range For Clutch Mates: 15 Days
279 reported dams, with 1032.1017.780 (2829) offspring (not including 158 offspring of UNK/MULT dams)
263 reported sires, with 1024.1005.788 (2817) offspring (All ages are at dam conception)

Select Filters | Filters applied to parents: No Filters Applied

Sire Age At First Estimated Conception | Sire Age At All Estimated Conceptions | Number Of Offspring Per Sire
Clutch Size | Dam Age At First Hatch | Dam Age At All Hatches | Number Of Offspring Per Dam | Interhatch Intervals | Hatch Seasonality

Intervals are calculated from the last of a clutch to the first of the next clutch.

Studbook ID	Interval (Days)	Offspring1	Hatch Date	Hatch Date Est.	Offspring2	Hatch Date	Hatch Date Est.
100552	14	1181119	4/9/2018	None	1181120	4/23/2018	None
178112	15	183020	4/9/1983	Day	183327	4/24/1983	None
104614	15	17007	4/21/2017	None	17010	5/6/2017	None

8.19.3 Birth/Hatch Seasonality

The Birth Seasonality tab lists both the number and percentage of litters/clutches that occur in each month. Only litters/clutches with birth/hatch date estimates of None, Day, or Month are included in this analysis.

REPRODUCTIVE REPORT

Export

Species Type: Egg Laying Incubation Period: 28 Days Maximum Hatch Date Range For Clutch Mates: 15 Days
279 reported dams, with 1032.1017.780 (2829) offspring (not including 158 offspring of UNK/MULT dams)
263 reported sires, with 1024.1005.788 (2817) offspring (All ages are at dam conception)

Select Filters | Filters applied to parents: No Filters Applied

Sire Age At First Estimated Conception | Sire Age At All Estimated Conceptions | Number Of Offspring Per Sire
Clutch Size | Dam Age At First Hatch | Dam Age At All Hatches | Number Of Offspring Per Dam | Interhatch Intervals | Hatch Seasonality

First of clutch must have a hatch date estimate of None, Day, or Month to be counted.

Month	Number of Clutches	Percentage
January	18	1.25
February	65	4.50
March	543	37.63

8.19.4 Dam Age at First Birth/Hatch

This tab lists all dams with offspring, their age at the time of their first offspring's birth/hatch, their birth/hatch date and estimate, the ID of their first offspring, and their first offspring's birth/hatch date and birth/hatch date estimate. The table is ordered in ascending order of dam's age at first birth/hatch. You can view the Animal Report of any dam by double clicking on the Studbook ID or of any offspring by clicking on the Offspring's ID.

REPRODUCTIVE REPORT

Export

Species Type: Live Bearing Gestation Period: 70 Days Maximum Birth Date Range For Litter Mates: 3 Days
104 reported dams, with 368.323.329 (1020) offspring (not including 102 offspring of UNK/MULT dams)
97 reported sires, with 355.307.292 (954) offspring (All ages are at dam conception)

Select Filters | Filters applied to parents: No Filters Applied

Sire Age At First Estimated Conception | Sire Age At All Estimated Conceptions | Number Of Offspring Per Sire
Litter Size | Dam Age At First Birth | Dam Age At All Births | Number Of Offspring Per Dam | Interbirth Intervals | Birth Seasonality

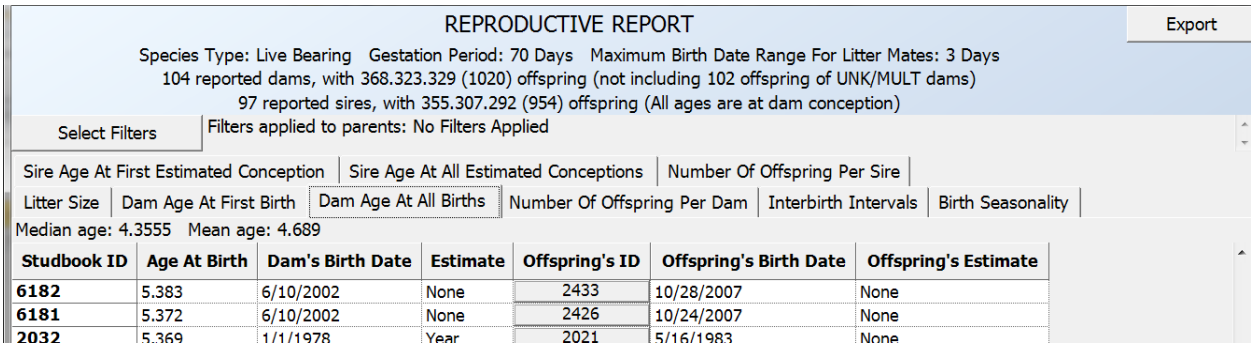
Median age: 3.389 Mean age: 3.69

Studbook ID	Age At Birth	Dam's Birth Date	Estimate	First Offspring's ID	First Offspring's Birth Date	First Offspring's Estimate
6222	1.218	10/25/2009	None	T20	1/13/2011	None
3014	1.454	12/14/1994	None	3741	5/28/1996	None
2332	1.632	5/7/2005	None	2418	12/24/2006	None
1879	1.717	2/29/1992	None	1929	11/17/1993	None
950	1.736	6/1/1982	None	1060	2/25/1984	None

8.19.5 Dam Age at All Births/Hatches

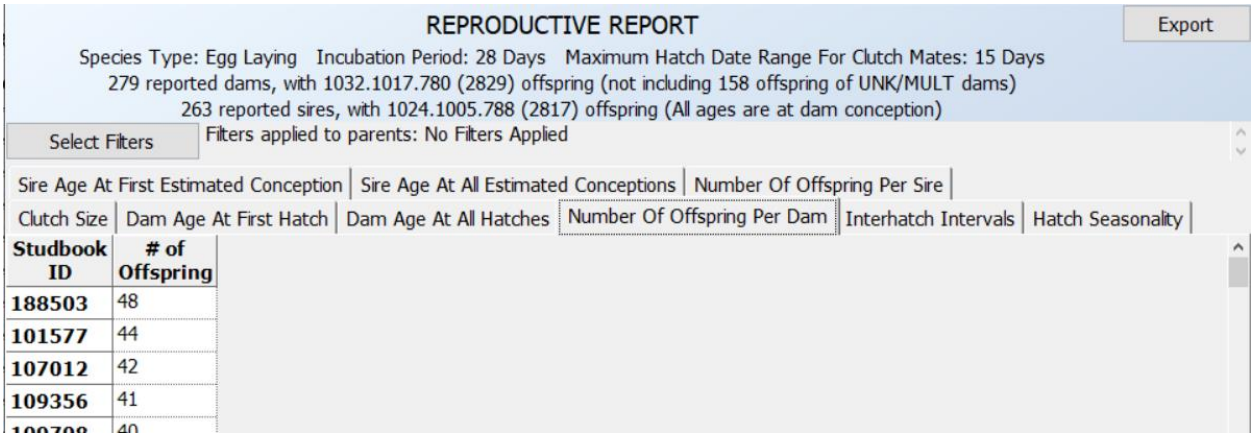
This tab lists all dams with offspring, their age at the time of each offspring's birth/hatch, their birth/hatch date and estimate, and the ID, birth/hatch date, and birth/hatch date estimate of each of their offspring. A dam with more

than one offspring will be listed more than once. The table is sorted in ascending order by dam's Age at Birth/Hatch. You can view the Animal Report of any dam by double clicking on the Studbook ID or any offspring by clicking on the Offspring's ID.



8.19.6 Number of Offspring Per Dam

The Number of Offspring Per Dam tab lists the number of offspring born to each dam throughout the dam's life. This list is ordered in descending number of offspring.



8.19.7 Sire Age At First Estimated Conception

Identical to 8.19.4, but with sires and based on conception date rather than birth/hatch date.

8.19.8 Sire Age at All Estimated Conceptions

Identical to 8.19.5, but with sires and based on conception date rather than birth/hatch date.

8.19.9 Number of Offspring Per Sire

Identical to 8.19.6, but with sires.

8.19.10 Exporting the Reproductive Report

The Reproductive Report can be exported using the "Export" button in the upper-right corner; each table can be exported using the right-click "export to excel" functionality. When the Reproductive Report is exported, the PopLink HTML export differs from the PopLink Reproductive Report displayed on the screen in the following ways:

- Dam Age at First Birth/hatch is simplified into two tables that list 1) the 10 youngest dams at first reproduction by ascending age, and 2) the 10 oldest dams at first reproduction by descending age. Dams with UNK birthdate estimates are excluded from these tables.
- Dam Age for All Births/Hatches is simplified into one table that lists the 10 reproductive events (single births or litters of offspring) of the oldest females listed in descending order of age at reproduction. Note that a female may be listed more than once in this report if she has had multiple reproduction events at ages older than those of other females.

- Sire Age at First Birth/Hatch is simplified into two tables that list 1) the 10 youngest sires at first reproduction by ascending age, and 2) the 10 oldest sires at first reproduction by descending age. Sires with UNK birthdate estimates are excluded from these tables.
- Sire Age for All Births/Hatches is simplified into one table that lists the 10 reproductive events (single births or litters of offspring) of the oldest males listed in descending order of age at reproduction. Note that a male may be listed more than once in this report if he has had multiple reproduction events at ages older than those of other males.
- The Number of Offspring Per Dam and The Number of Offspring Per Sire are each simplified to list only the 10 dams and 10 sires with the greatest number of offspring.
- The Interbirth/Interhatch Interval is modified to include only the 10 shortest intervals between single births or litters. Interbirth intervals of births within the same litter are ignored in this list.

8.20 RESIGHTINGS REPORTS

These reports are only shown if the Resightings module is turned on in Edit → Settings

8.20.1 Resightings Analysis

The Resightings Analysis Report displays all animals with resighting records within a specified date range. When you select this report, a pop-up opens where you can define the date range to include. You can modify this date range at any time by selecting "Select Dates" at the top of the screen within the report.

Resighting Analysis Report

Select Dates | Resighting and Event Date Range: 1/1/1753 - 8/5/2026

Studbook ID	Event	Location	Transaction Date	Transaction Date Est.	Sex	Birth Type	Rearing	Age at Event	Latitude	Longitude	ResightingType	Resighting Note
111772	Hatch	ARECIBO	4/11/2011	Day	Male	Captive Hatch	Parent	0.00				
111772	Transfer	RA WILD	12/18/2012	None	Male	Captive Hatch	Parent	1.69				
111772	Resighting		12/31/2012	None	Male	Captive Hatch	Parent	1.73	18.2388	-66.0352	Visual	
111772	Resighting		12/31/2012	None	Male	Captive Hatch	Parent	1.73				
111772	Resighting		12/15/2015	None	Male	Captive Hatch	Parent	4.68	18.4022	-65.9719	Transmitter	
111772	Resighting		12/15/2015	None	Male	Captive Hatch	Parent	4.68				
111772	Go LTF	RA WILD	6/1/2017	None	Male	Captive Hatch	Parent	6.15				
1171069	Hatch	ARECIBO	4/16/2017	None	Female	Captive Hatch	Foster	0.00				
1171069	Transfer	RA WILD	5/21/2019	None	Female	Captive Hatch	Foster	2.10				
1171069	Resighting		5/30/2019	None	Female	Captive Hatch	Foster	2.12	18.4512	-66.062	Visual	
1171069	Resighting		5/30/2019	None	Female	Captive Hatch	Foster	2.12				
1171069	Death	RA WILD	3/11/2021	None	Female	Captive Hatch	Foster	3.90				

This report shows all the animal's resighting records (i.e. one or more rows) along with all the information you entered for each resighting. If an animal was sighted at least once within the date range of the filter, the report also includes all relevant event records on that animal, even if the resightings listed occur before or after the date range.

The report's columns are:

- **Event** - In the "Event" column, the data from the animal's Events table is combined with the data from its Resightings table to make a composite list of events that may include all the physical events (Birth/Hatch, Transfer, Death, Release, Go LTF, Return from LTF) as well as Resightings. Each event is given an individual row.
- **Location** – Lists the location where an "event" or resighting took place, if specified.
- **Transaction Date** – For a "Resighting" this is the resighting date, for an event this is the event date.
- **Transaction Date Est**.—Lists any date estimates specified for an event date.
- Individual Attributes—For each record, the report includes the individual's **sex**, **birth type, rearing type**, and **age at each event date**.

- **Resighting Note** and **Resighting Fields** - Each row includes any custom Resighting Fields or Resighting Notes you may have created or entered.

Records are sorted first by studbook ID and then by transaction date in ascending order. As a result, all records for an individual are grouped together, with the oldest sightings appearing first.

NOTE: This report includes information on when an individual enters or leaves a population, which can be critical context for mark–recapture analyses. Birth records might indicate when an individual entered the population, while death records indicate when it permanently left the population, and transfer, release, or go LTF events may be important context for analysis. Incorporating these events can improve estimates of survival and other demographic parameters, so this table attempts to be inclusive of all the information that your studbook might hold that might be relevant for designing a mark-recapture analysis.

You can also use the data in this report to provide some context to your monitoring – it may help you assess whether you're more frequently seeing certain ages, sexes, or other types of individuals (i.e. perhaps you have a release program, and you are frequently seeing the captive-hatched animals but not the wild-hatched). If you're including spatial Resightings Fields in your monitoring data and have individuals at multiple sites, mapping those coordinates and looking at the events within this report may help you assess whether an individual has moved between sites (and if you need to enter a "Transfer" event).

8.20.2 Most Recent Resighting

Most Recent Resighting Report

Select Date | Date Used to Calculate Time Since Resighting: 8/5/2026

Studbook ID	Sex	Status	Last Resighted	Location at Sighting Date	Time Since Last Sighting (Yrs)	Resighting Notes
111772	Male	LTF	12/15/2015	RA WILD	10.65	
119148	Male	Living	1/1/2023	RA WILD	3.59	band not very visible
122248	Unknown	Living	4/1/2025	RA WILD	1.35	GPS failed
124362	Male	Living	4/1/2025	RA WILD	1.35	
1171069	Female	Dead	5/30/2019	RA WILD	7.19	

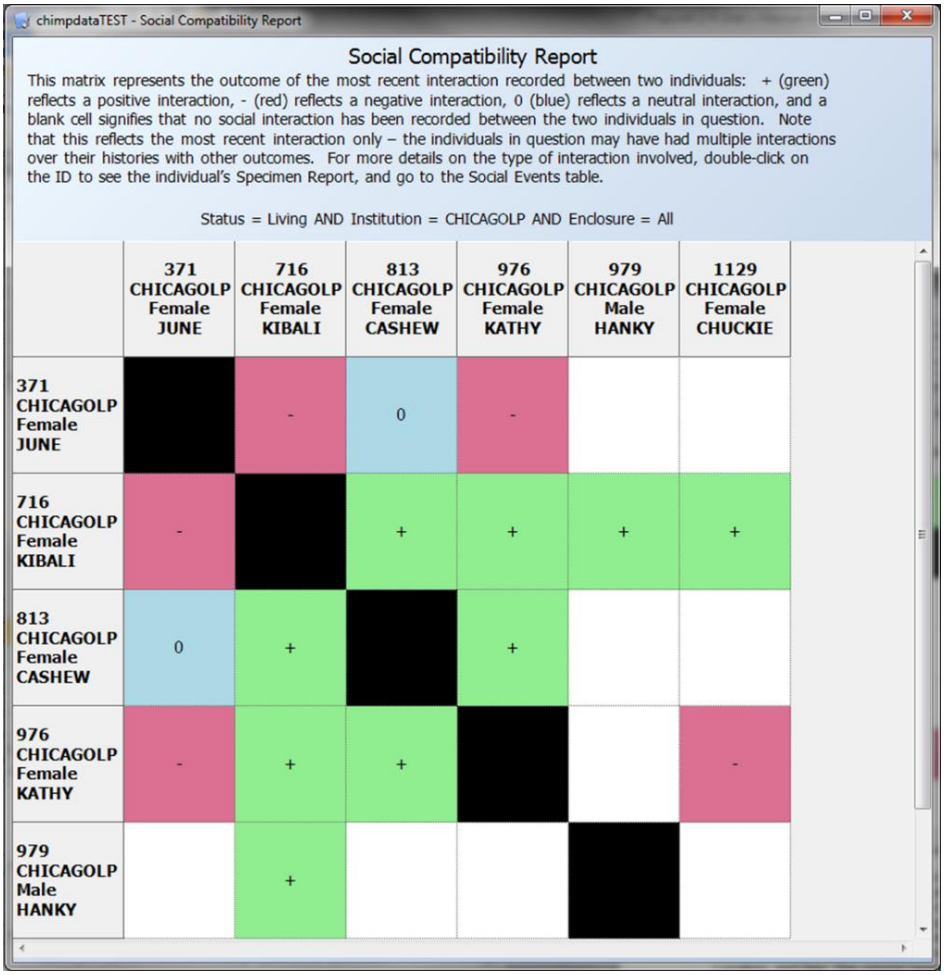
The Most Recent Resighting report helps you answer that important question, "*When was the last time I saw them*?". If you are managing a free-ranging population, the answer may help inform an individual's status in your studbook. For example, your database may follow a convention that any individual not observed for more than one year is considered deceased or classified as lost to follow-up. This report can help you quickly identify such individuals and keep your database up to date.

When you select this report, a pop-up opens prompting you to specify a reference date. PopLink uses this date to calculate the amount of time that has elapsed since each individual's last resighting. Once you select this date, click "Ok" and a table appears showing a row for the most recent sighting for each individual with at least one resighting.

- **Time Since Last Sighting (Yrs)** - This column displays the number of years between an individual's most recent resighting and the selected reference date. For example, if an individual was last resighted on July 1, 2025, and you select July 1, 2026 as the reference date, the value in this column will be 1. If you choose a reference date that is before the last reported resighting occurred, the Time Since Last Sighting (Yrs) value will be negative.

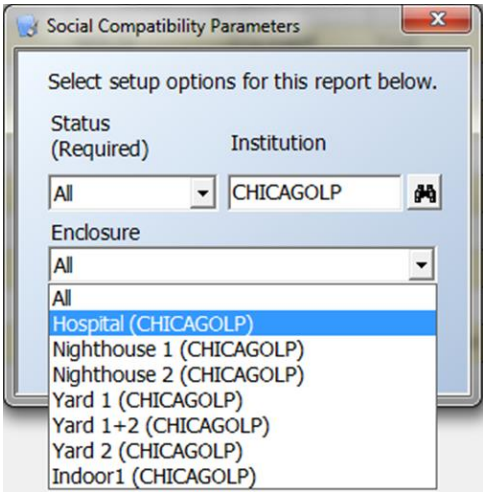
- Individual Attributes – The report also lists the **sex**, **status**, studbook **location** at resighting (either a location from PopLink's Location List or a User Defined Location, not any locations you've specified in resightings fields), and any **resighting notes**.

8.21 SOCIAL COMPATIBILITY REPORT



	371 CHICAGOLP Female JUNE	716 CHICAGOLP Female KIBALI	813 CHICAGOLP Female CASHEW	976 CHICAGOLP Female KATHY	979 CHICAGOLP Male HANKY	1129 CHICAGOLP Female CHUCKIE
371 CHICAGOLP Female JUNE		-	0	-		
716 CHICAGOLP Female KIBALI	-		+	+	+	+
813 CHICAGOLP Female CASHEW	0	+		+		
976 CHICAGOLP Female KATHY	-	+	+			-
979 CHICAGOLP Male HANKY		+				

The Social Compatibility Report is a pairwise matrix of all individuals which have a social interaction recorded in the Social data table. At each matrix intersection, compatibility based on the outcome of the most recent social event between the two individuals recorded in the Social data table. The outcome of a social event can be positive, negative, neutral, or none (meaning there hasn't ever been a social event between those two individuals) – represented as green with a "+", red with a "-", blue with a "0", or a blank box, respectively. The column and row headers automatically display the Studbook ID Number, current Location, Sex, and House Name. The column headers display the *current* location of an animal, but not necessarily the same location that individual was in when a Social Event took place. Double-clicking on the column or row header will pop-up an animal report where you can see the in-depth data this report is based on in the Social data table.

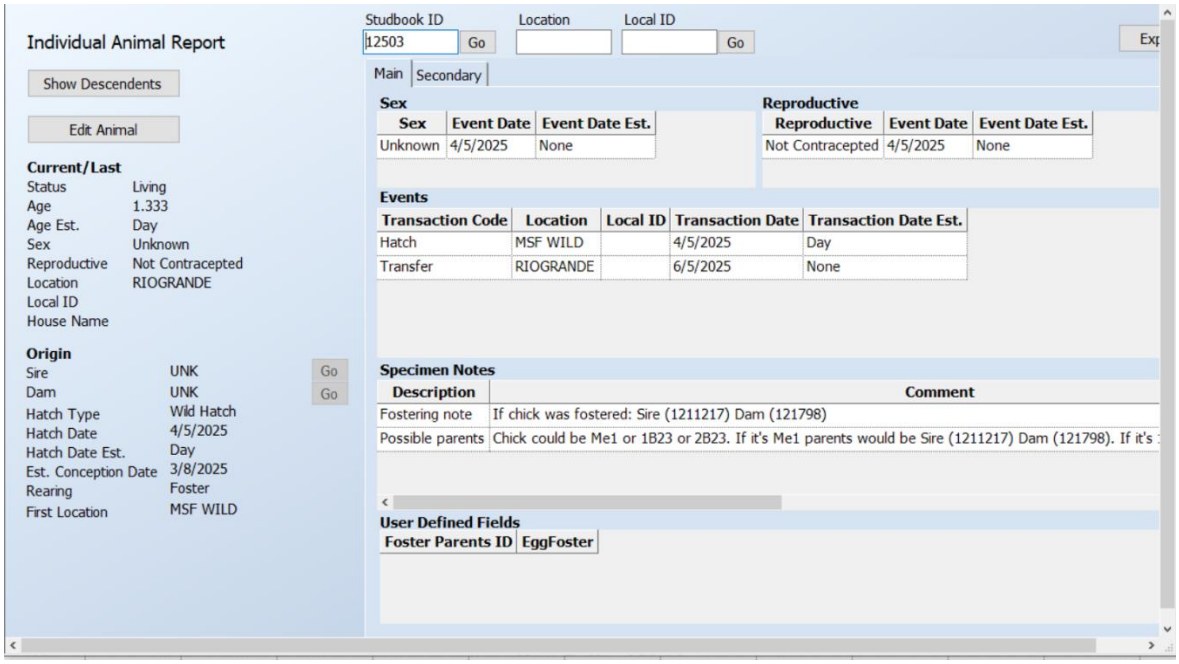


PopLink allows you to filter this report using an initial pop-up, the Social Compatibility Parameters box. Here, you can specify a **Status** (Living, Dead, or All), **Location** (mnemonic), and **Enclosure** (User Defined Enclosures). If **Location** is left blank, the Social Compatibility Report will default to display all locations, or you can specify a specific location by entering that location's mnemonic (see above). When Location is specified, the **Enclosure** dropdown filters down to display only that location's enclosures. Once the report is generated, the filters are indicated directly above the table.

NOTE: The Social Compatibility Report is only as complete as the data in the Social data table. You should recognize that there are many social interactions between individuals that are either not observed or have not been recorded in that table. In addition, the social events table may include multiple interactions over a lifetime for two individuals, while this report boils all of those interactions down to the single, most recent event.

8.22 INDIVIDUAL ANIMAL REPORT

The Individual Animal Report is a one-page version of **all** the studbook data for a particular animal. Clicking on the "Go" buttons next to Sire and Dam will pop-up their individual reports. Clicking on the "Show Descendants" button will display a list of all descendants for the selected individual. Clicking on "Edit Animal" will pop open the editor. If the individual is dead, the information displayed in the top left reflects that animal's last data (e.g. last institution, age at death, last sex). If still living, these data reflect the individual's current status.



The Main tab in the Individual Animal Report displays the Sex, Reproductive, Events, Animal Notes, and User Defined Fields tables for an individual.

Main | Secondary

Sex

Sex	Event Date	Event Date Est.
Unknown	4/5/2025	None

Reproductive

Reproductive	Event Date	Event Date Est.
Not Contracepted	4/5/2025	None

Events

Transaction Code	Location	Local ID	Transaction Date	Transaction Date Est.
Hatch	MSF WILD		4/5/2025	Day
Transfer	RIOGRANDE		6/5/2025	None

Specimen Notes

Description	Comment
Fostering note	If chick was fostered: Sire (1211217) Dam (121798)
Possible parents	Chick could be Me1 or 1B23 or 2B23. If it's Me1 parents would be Sire (1211217) Dam (121798). If it's

User Defined Fields

Foster Parents ID	EggFoster

The Secondary tab displays the data recorded in the optional Social, Enclosures, Medical, Breeding and Resightings modules. This tab is only shown when at least one of the modules is shown in the Settings options.

Main | Secondary

Social Events

Event	Event Date	Date Est.	Outcome	Comment	Related Specimen
Breeding Interaction	6/10/2026	None	+		12502,1251086,12514
Introduction - full	6/10/2026	None	-		12502,1251086

Enclosures

Enclosure Name	Enter Date	Enter Date Est.	Exit Date	Exit Date Est.	Comment
Bonding B (RA WILD)	6/10/2026	None		None	test

Medical Notes

Category	Type	Value	Unit of Measurement	Start Date	End Date	Observer	Comment
General Medical Note				6/10/2026		Lisa	test thing one
Disease Status	Minor			6/10/2026		e	s
Medication	Anti-fungal	3	Gram(s)	6/10/2026		3	3

Breeding

Breeding Individuals	Breeding Location	Nest Discovery Date	Breed Start Date	Start Date Est.	Breed End Da
12502	Bonding B (RA WILD)		8/5/2026		

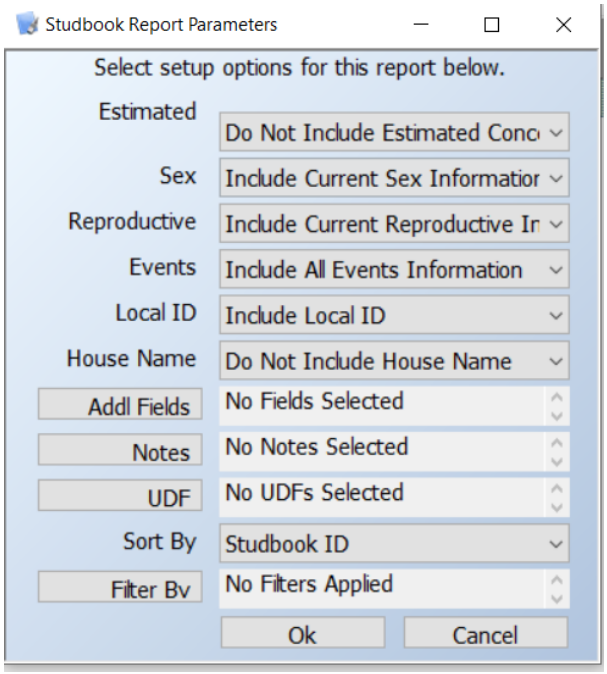
Resightings

Resighting Date	Latitude	Longitude	ResightingType	Resighting Notes

Long comment fields in Specimen Notes, Social Events, Enclosures, Medical, Breeding, and Resightings Notes may be difficult to view within the Individual Animal Report. To view the entire animal note description, double-click on the Note number and a text box will pop-up that displays the animal note in its entirety.

8.23 STUDBOOK REPORT

The Studbook Report produces a formatted table of animals. After choosing the Studbook Report option, you will be prompted to set specific options for the report:



For the Sex, Reproductive, Events, Local ID, and House Name fields you have the option of including **all** events/information or the **current** (or last, if the animal is dead, released, LTF) value for each of the fields. In the "Add Fields/Notes/UDF" boxes, you can select specific animal notes, UDF fields, and fields like rearing, ownership, and birth/hatch type for display on the report. You also have the option of sorting the report by Studbook ID, birth date, or current location. You can select filters for the report by clicking on the "Filter By" button.

Selecting **current** for all the fields will produce a table with a single line per animal. Selecting **all** will display a table with all events listed, all Sex Events listed, etc.:

STUDBOOK REPORT

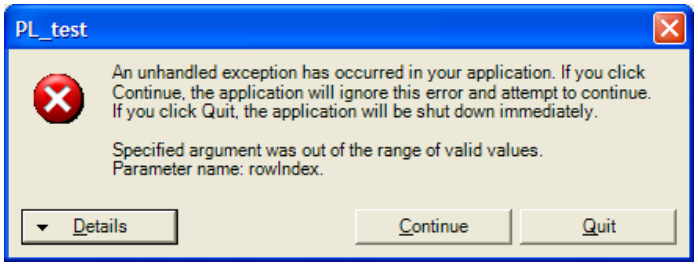
1093.1081.834 (3008) at 33 Locations

Export

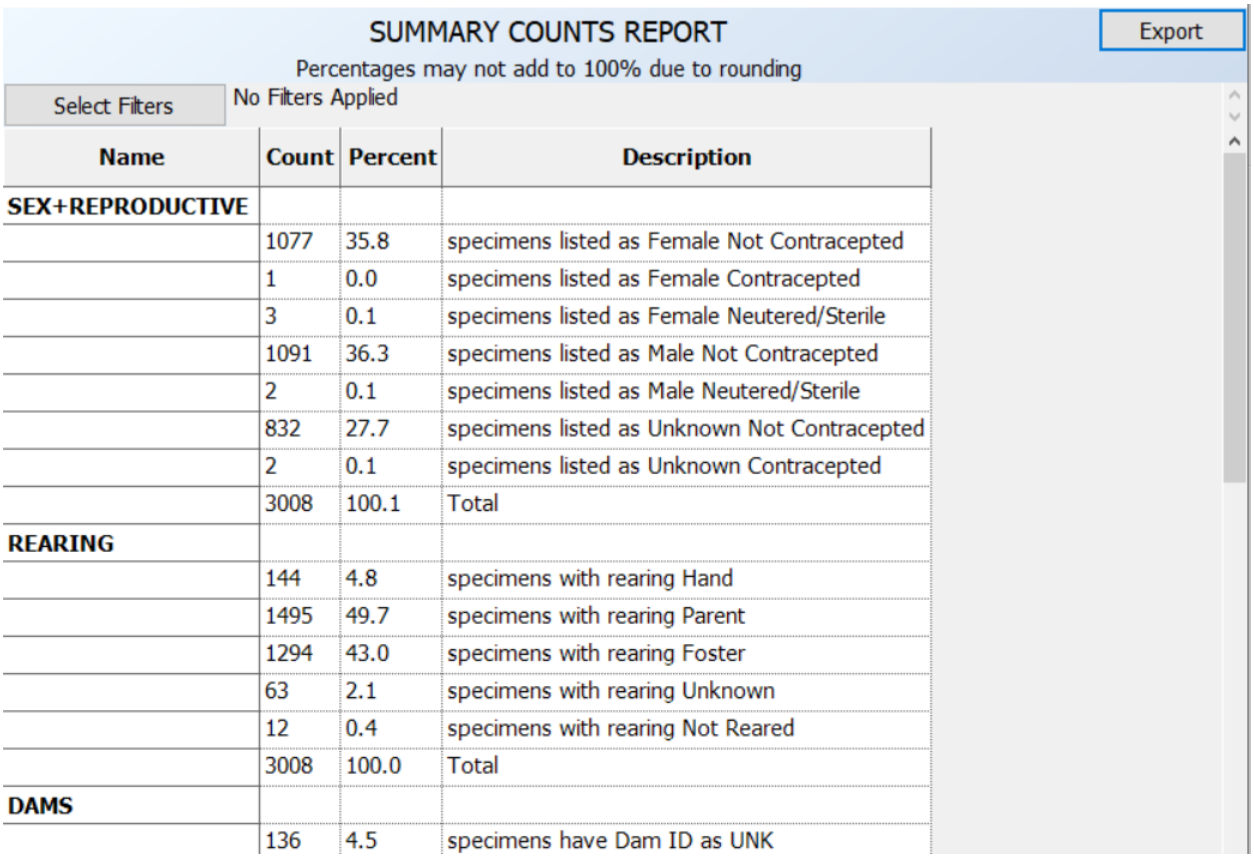
Select Filters | No Filters Applied

Studbook ID	Hatch Date	Hatch Date Est.	Sire	Dam	Sex	Reproductive	Event	Location	Local ID	Date	Date Est.
1410	3/28/2014	None	100556	104612	Unknown	Not Contrace	Hatch	ARECIBO		3/28/2014	None
							Death	ARECIBO		4/7/2014	None
1411	3/30/2014	None	101257	109708	Unknown	Not Contrace	Hatch	ARECIBO		3/30/2014	None
							Death	ARECIBO		4/7/2014	None
1412	4/17/2014	None	102592	100552	Unknown	Not Contrace	Hatch	RA WILD		4/17/2014	None
							Death	RA WILD		4/17/2014	None
1413	4/6/2014	None	101571	100553	Unknown	Not Contrace	Hatch	ARECIBO		4/6/2014	None
							Death	ARECIBO		4/22/2014	None
1414	4/10/2014	None	101571	100553	Unknown	Not Contrace	Hatch	ARECIBO		4/10/2014	None

Note that if you select to include UDFs in your studbook report and you have animals that have multiple UDF rows, you will receive this error when running the report:



8.24 SUMMARY COUNTS REPORT



SUMMARY COUNTS REPORT

Export

Percentages may not add to 100% due to rounding

Select Filters

No Filters Applied

Name	Count	Percent	Description
SEX+REPRODUCTIVE			
	1077	35.8	specimens listed as Female Not Contracepted
	1	0.0	specimens listed as Female Contracepted
	3	0.1	specimens listed as Female Neutered/Sterile
	1091	36.3	specimens listed as Male Not Contracepted
	2	0.1	specimens listed as Male Neutered/Sterile
	832	27.7	specimens listed as Unknown Not Contracepted
	2	0.1	specimens listed as Unknown Contracepted
	3008	100.1	Total
REARING			
	144	4.8	specimens with rearing Hand
	1495	49.7	specimens with rearing Parent
	1294	43.0	specimens with rearing Foster
	63	2.1	specimens with rearing Unknown
	12	0.4	specimens with rearing Not Reared
	3008	100.0	Total
DAMS			
	136	4.5	specimens have Dam ID as UNK

The Summary Counts Report gives basic details on the types of animals within your dataset. You can set filters for the report using the "Select Filters" button and export using the "Export" button. Note that the report tallies all relevant states for a category but does not report any states that have no individuals. For example, in the screen above, this studbook had no individuals with *Colony/Group* rearing type, so the line for that rearing type is not shown in the report.

8.23 SURVIVAL TOOL REPORT

For full details on this report, please see Appendix 1.

8.24 UNKNOWN AGE REPORT

Unknown Age Report

21.17.0 (38) unknown age specimens out of 1093.1081.834 (3008) total specimens

Select Filters

No Filters Applied

Studbook ID	Minimum Age	Current Sex	Current Location	First Location	Current Status	Hatch Date	Hatch Date Est.
168083	34.401	Male	ARECIBO	EY WILD	Dead	7/2/1968	Unknown
CA1	0	Male	SF1A	UNKNOWN	Dead	7/2/1985	Unknown
CA2	LTF	Female	UNKNOWN	EY WILD	LTF	7/2/1985	Unknown
EF1A1	LTF	Male	EM2	EF3	LTF	7/2/1992	Unknown
EF1F	LTF	Female	EY WILD	EY WILD	LTF	7/2/1971	Unknown
EF1M	LTF	Male	EY WILD	EY WILD	LTF	7/2/1971	Unknown
EF2F	0.701	Female	EF2	UNKNOWN	Dead	7/2/1972	Unknown
EF2M	LTF	Male	EF2	UNKNOWN	LTF	7/2/1973	Unknown
EF3F	LTF	Female	EF2A	UNKNOWN	LTF	7/2/1976	Unknown
EF3M	LTF	Male	EF2A	UNKNOWN	LTF	7/2/1976	Unknown
EF5	LTF	Male	EF	UNKNOWN	LTF	7/2/1981	Unknown

This report lists all individuals in your population with birth date estimates of *UNKNOWN.* Because their birth date is unknown, these individuals cannot be assigned to an age class and cannot be used in any of your demographic analyses (mortality and fecundity rate calculations).

The **minimum age** in this report is the time from the animal's first known transaction date to the present or the animal's death. Because it is based on the first known transaction date, you know that the animal in question is *at least* that old; you can use this information to make an analytical assumption about the animal's age if you would like the animal included in your demographic analyses. See Chapter 9 for more details on making analytical assumptions.

Chapter 9: ANALYTICAL DATA AND OVERLAYS IN POPLINK

9.1 BACKGROUND CONCEPTS

Although a studbook is intended to be a true and accurate record of a population's history, we often need to use assumptions, half-truths, and necessary fictions for the purpose of population management. PopLink has the ability to hold both TRUE studbook data and ANALYTICAL or hypothetical data on each individual. Your main studbook database should always contain your true data. In PopLink, you can also create an **overlay** that you can use to enter and store any analytical changes to your dataset. Before explaining the technical details of creating and maintaining analytical data in PopLink, we'll provide some background on the differences between true and analytical data, and why creating analytical data is necessary.

9.1.1 True Data vs. Analytical Data

A studbook is the best possible representation of the truth as it is currently known. Each studbook must contain an unambiguous representation of what is known and what is not known about every animal in the population. Although studbooks may contain minor assumptions or estimates, such as birth dates estimated to the month or year, information that is truly unknown should be entered as such. This is important because what is known and factual should never be confused with what has been assumed, in case new information emerges in the future.

Analytical studbooks, in contrast, are constructed to facilitate population management by including assumptions, half-truths, and necessary fictions. They may contain significant assumptions about variables such as dates of birth, transfer, death, parentage, and origin (e.g., captive-born or wild-caught). In some cases, analytical studbooks contain hypothetical animals (ancestors) created to complete the pedigree and facilitate genetic analyses. In effect, an analytical studbook "fills in" what the studbook keeper doesn't know and can't find out.

9.1.2 Assumptions and Conventions

Assumptions in an analytical studbook must be clearly documented to avoid any confusion between fact and "fiction." The assumptions in analytical studbooks should be updated as often as necessary to incorporate new information or new hypotheses about unknown data. Before an analytical studbook with assumptions is created, the true studbook on which an analytical studbook is based must be as complete, consistent, and correct as possible. First, the true studbook should be updated to contain all available information. Unknown information should be indicated as unknown rather than left blank to avoid ambiguity. Data Validation routines should be run and errors or inconsistencies should be resolved or documented. Once a studbook dataset reflects the truth as it is currently known, analytical assumptions can be created.

Although a studbook should be the best representation of the true history of the population, most studbooks will contain a few minor assumptions and/or conventions.

Conventions are rules developed by the studbook keeper for consistent application of assumptions. Conventions are usually based on the biology or husbandry of the studbook species; they are usually applied to the population at large. Most conventions combine common sense, logic, and biology into a simple rule to be used when data are unknown or unclear. One common example is a species that breeds once per year and can only be imported from the wild as juveniles (e.g., older than 6 months, younger than 18 months). A convention might be developed to set the birth date for all wild-caught animals, with unknown birth dates, as January (estimated to month) of the previous year. Another example might deal with animals of unknown origin (wild-caught or captive-born) that enter the population before the first reported captive birth. A convention could be established that all animals entering the population before the first reported captive birth are wild-caught. Conventions should be outlined in the Species Notes (in the Studbook Overview Table), and noted in the Animal Notes whenever they are applied to a given animal.

One of the most common types of conventions is the method for back dating births from the date young are first observed or heard. Marsupials, bears, cavity nesting birds, and other species whose young are not likely to be noticed

until sometime after birth, will have conventions for estimating date of birth. These should be carefully documented in the Species Notes and Animal Notes.

Most minor assumptions are guided by information provided by reliable sources; they fill the gap between partial information, hints, and suspicions on the part of individuals and institutions reporting to the studbook keeper. Assumptions are usually specific to a single animal, or to a group of animals held at the same institution. For example, estimates of age to particular calendar years (e.g., 2023 or 2024) would usually be considered minor assumptions. It is difficult to generalize about what might be considered a minor assumption. In most cases, inclusion of minor assumptions in the studbook is dependent on the studbook keeper's good judgment. Any assumption should be documented in the Animal Notes for that animal.

It is essential that all assumptions and conventions be documented in the database in the Studbook Overview; you may benefit from consulting with a population biologist before you create conventions and apply them to the studbook or analytical database, as they may have insights on how or whether assumptions might impact data analysis and data exports to other analytical software.

9.1.3 Why Do We Need Analytical Data?

One of the main goals in creating analytical data is to fill in unknown data in a pedigree, allowing us to more accurately estimate inbreeding and genetic variation within the population. For a captive population, the amount of genetic variation (or more specifically, gene diversity) is typically estimated from the number of founding animals and the relationships among the founders' living descendants. Inbreeding is determined from the degree of relatedness between an individual's parents. A complete and accurate pedigree is necessary to accurately assess both gene diversity and inbreeding and is therefore important in maintaining the genetic health of a captive population.

In addition to the benefits to population-wide genetic analysis, creating analytical assumptions to resolve an individual animal's pedigree can ensure that that individual and/or its offspring are included in a breeding plan. Population managers don't typically make breeding recommendations for individuals with unknownness in their pedigree unless it is demographically necessary; creating analytical assumptions for these animals can allow them to be added to the breeding population. Although there are costs to consider when making assumptions in an analytical studbook, the genetic costs of leaving data true and accurate, but unknown are generally greater than the cost of mistaken or incorrect assumptions (Willis 1993).

Analytical assumptions can also be important to demographic analyses. For example, if a large proportion of a population is wild caught with unknown birth dates, those animals cannot be used in calculations of mortality or fecundity rates. Although the animals' true birthdates can never be known, it may be possible to make an analytical assumption based on the import history (e.g., assume that all wild-caught animals were captured as infants) and import date (e.g., all individuals are estimated to be two years old at import, and birth date is estimated as two years before recorded import date). Creating an analytical assumption in such cases allows the animals with unknown birth dates to be utilized in demographic analyses.

9.2 GENERAL FEATURES of OVERLAYS

To create analytical assumptions for animals in your studbook, you first need to create the overlay in which they will be stored. In the View drop-down menu, selecting the Overlays option will display this screen:

Overlays

Overlays are used to store analytical data about your studbook specimens. Any data that is known and verified should be stored in your main (true) studbook. Use the overlay to store your hypotheses or best guesses about unknown data. You can then use your overlay in your genetic and demographic analyses.

Name	Edit	Description	Date Created	User Created	Note Date	User
Overlay 2	...	ID, Wild Nest, Parentage Assumptions	4/19/2007	cschloss	11/27/2007	cschlo
Overlay 2 and WN	...	ID, Wild Nest, Parentage Assumptions	6/3/2008	cschloss	6/10/2008	Sarah
LTF RA WILD to DEAD v2	...	v1 + 2017 deaths are made LTF and 2018 LTFs are made dead	4/30/2019	lfaust	4/30/2019	lfaust
MolecularSamplingOverlay	...	removing suspect relationships from founding and early generation birds	1/30/2019	lfaust	6/26/2019	lfaust
v5: RAW hurricane deaths only	...	Deaths occuring Sept - Dec 2017 from Maria in RAW made LTF	1/9/2022	LFaust	1/9/2022	LFaust
2026OverlayforExportwithEKinships+resolvingUnk	...	making UNK potential founders wild/wild+previous MolecSampl	2/12/2026	LFaust	2/12/2026	LFaust

New | Open | Copy | Delete

Selecting "New" will display a dialogue box that will allow you to name and describe a new overlay. Your studbook database can have multiple overlays which would be displayed in this table once created. Multiple overlays may be useful if 1) you have different levels of confidence in your analytical data that you want to differentiate between (e.g. having an overlay for data you are reasonably certain about and another with assumptions that you are less confident about); 2) you want to test different hypotheses related to the population (i.e. what would be the impact of making two founders related or full siblings. The "Copy" option allows you to take an already created overlay, copy and rename it, and add additional changes to it.

Highlighting an overlay (e.g., Overlay 2) and selecting "Open" will apply that overlay to your studbook data; when you do this, the top display bar reflects that the overlay is applied:

PRP_2026_16Jan + Overlay 2

File Edit View Overlay Validate Reports Export Help

Without your overlay applied (e.g. PRP_2026_16Jan), your studbook viewer displays all the TRUE data for your studbook. With the overlay applied (e.g. PRP_2026_16Jan+ Overlay 2), the studbook viewer displays *analytical* data in any fields that have analytical changes and *true* data for all other fields. This is clearly displayed in the viewer with analytical data displayed in red and true data is displayed in black (e.g. see 104296 and 104291 below).

Filter | Clear | No Filters Applied

Totals: 1093.1081.835 (3009) at 33 Locations | No Sort Order Applied

Currentness Date: 1/16/2026 | Current Date Format: M/d/yyyy

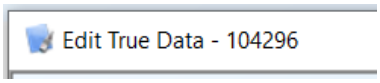
Master | Sex | Reproductive | Events | Specimen Notes | UDFs | Studbook Overview | Breeding | Enclosures | Medical | Resightings | Social

Studbook ID	Edit	Current Sex	Current Location	Current Local ID	Sire	Dam	Hatch Date	Hatch Date Est.	Current Age	Current Age Est.
104290	...	Male	RIOGRANDE	Cordaniz Atre	193011	191183	3/21/2004	None	0.214	None
104291	...	Male	RIOGRANDE		UNK	UNK	3/29/2004	Day	8.542	Day
104292	...	Female	RIOGRANDE		UNK	UNK	4/11/2004	Day	8.405	Day
104296	...	Female	RIOGRANDE		WILD	WILD	4/15/2004	None	16.287	None
104607	...	Female	RA WILD		196514	196521	2/14/2004	None	2.768	None

When opened and applied to a studbook, overlay data will be used in all reports and analyses (e.g. data exports, all reports in the report menu, data validation, etc.). To close an overlay, use the Remove Overlay menu option in the Overlay drop-down menu.

9.2.1 Editing Analytical Data and Creating Hypothetical Specimens

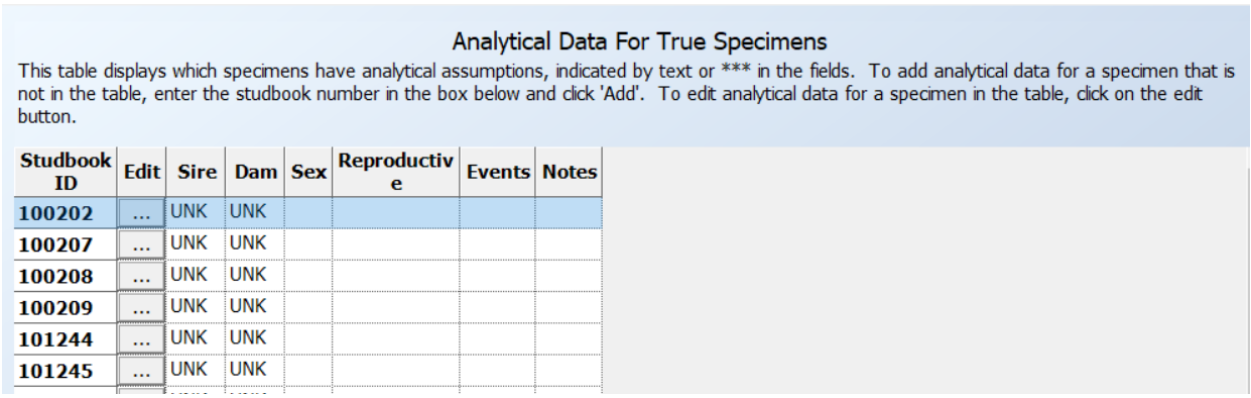
Once an overlay has been created, you can start to add analytical assumptions about parentage, sex, birth or death dates, or other unknown data (for more information on how to make assumptions, see the second half of this chapter). **All editing of analytical data will occur through the overlay drop-down menu.** Note that if you click on the "edit" button in the main studbook viewer, the pop-up animal editor always indicates that you are editing *true* data:



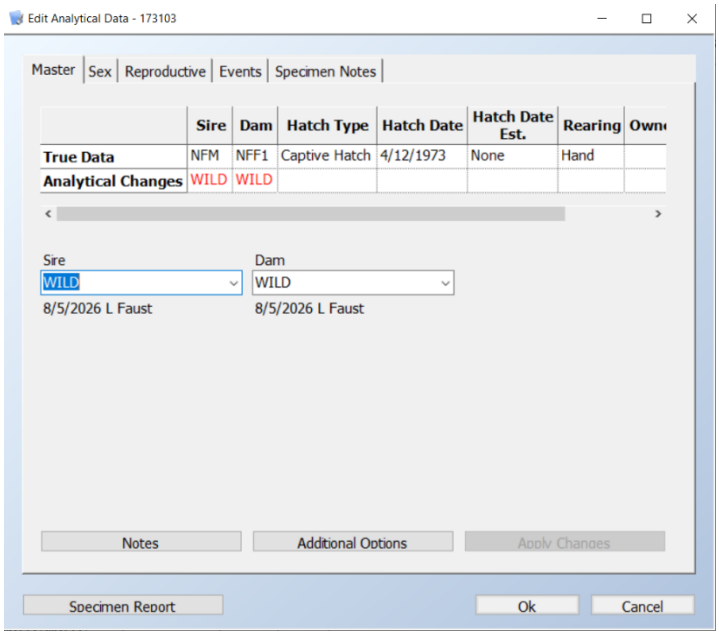
There are two types of analytical edits you can make within PopLink:

1. **Making analytical assumptions for already-existing animals**

   This is accessed via the Overlay drop-down menu and the Analytical Data for True Specimens option, which displays a table of all the existing analytical data in your overlay.



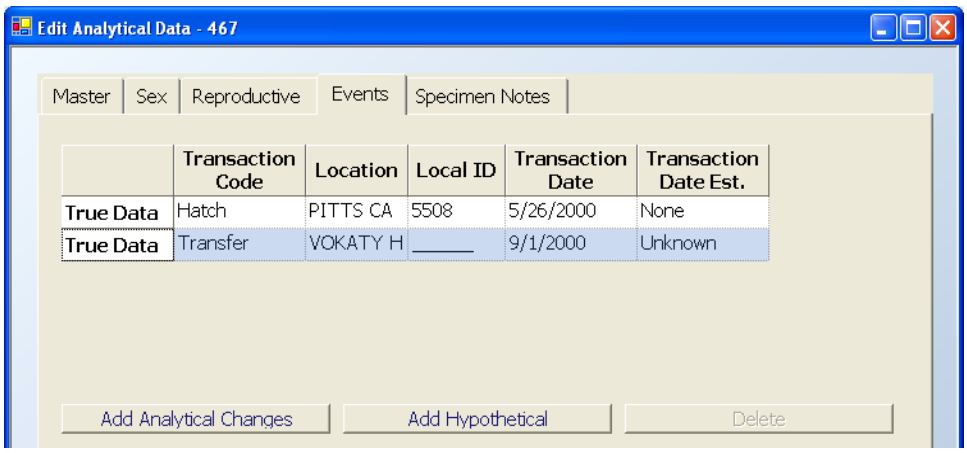
   You can edit analytical data for an already existing animal in this table by clicking on the "Edit" button. Typing an animal number into the box in the lower-left of the screen and clicking "Add" will allow you to add analytical data for an animal not already in the table; an Analytical Data animal editor will pop-up:

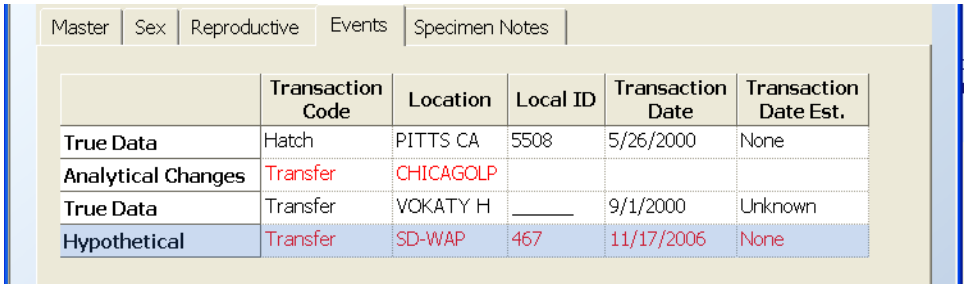


This editor displays the True data for the animal and any Analytical Changes that may have been made for the animal; rows of Analytical data will always apply to the True data row directly above them (e.g. in the Events table, where there may be multiple True data rows). The five tabs allow analytical edits on specific fields most relevant to analytical assumptions (parentage, sex, reproductive status, and types and locations of transactions). Where relevant, PopLink "fills in" other fields with data that will not affect analyses or that does not require analytical assumptions; clicking the "Additional Options" button shows those fields.

You can use the Specimen Notes tab (or the Notes buttons on individual editing screens) to enter comments about the assumptions you're making. Any notes will be stored in the overlay only, not in the True data, and will be stored with mention of each table, e.g. "Master Analytical Notes"

For Sex, Reproductive, and Event data, you can 1) modify an existing event by creating analytical assumptions or 2) add a new, completely hypothetical event. For example, on the Events tab, if the final transfer for animal 467 was actually to CHICAGOLP, you would highlight the True Data row and click "Add Analytical Changes", and then add the data by filling in the appropriate fields. If you needed to create a third transfer for this animal, you would click "Add Hypothetical", and could then transfer the animal to SD-WAP:





2. Making hypothetical animals to create pedigree relationships for already-existing animals

If you have an existing animal with UNK pedigree and need to create hypothetical pedigree relationships for that animal (see the second half of this chapter for more details on how to do that), you could create an entirely hypothetical animal in your analytical overlay. In the Overlay drop-down menu select "Hypothetical Specimen", which will display a table of all existing hypothetical animals; you can use the Add box in the left-hand corner to add individuals to this table, just as in the Analytical Data table above.

Hypothetical Specimens

This table displays specimens that are entirely hypothetical. To add an entirely hypothetical specimen that is not in the table, enter a new hypothetical studbook number (HYP#) in the box below and click 'Add'. To edit the hypothetical specimen in the table, click on the edit button.

Studbook ID	Edit	Sire	Dam	Sex	Reproductive	Events	Notes
EF21986F	...	UNK	UNK	***	***	***	***
EF21986M	...	UNK	UNK	***	***	***	***

By convention, hypothetical animals have unknown birth and other event dates (so they are not used for demographic analyses) and go LTF so they are not counted as living individuals within the studbook.

9.2.2 Generating Overlay Reports

You can see a quick summary of all analytical changes in your overlay by running an Overlay Report in the Overlay drop-down menu. The Overlay report is split into two tables: 1) Hypothetical Specimens, and 2) Analytical Data for True Specimens. For each animal with analytical data, this report summarizes what data table and data field the change was made in, what the True data are, and what the Overlay data are.

OVERLAY REPORT

Export

HYPOTHETICAL SPECIMENS

Studbook ID	Sire	Dam	Sex	First Location	
EF21986F	UNK	UNK		UNKNOWN	Identification: it is unknown which birds were in EF2 in 1986
EF21986M	UNK	UNK		UNKNOWN	Identification: ID of the birds in EF 2 in 1986 is unknown
HYP4	UNK	UNK		UNKNOWN	Identification: This male has a scar on the right eye and a stainless steel band on the right
HYP44	UNK	UNK		UNKNOWN	Identification: Male in breeding pair in nest SF1T in 2001. Part of a new pair in this nest th
HYP45	UNK	UNK		UNKNOWN	Identification: Female in breeding pair in nest SF1T in 2001. Part of new breeding pair in tl
HYPSF1T1997-1999	SF1T3	SF1T4		SF1T	Identification: This is either Y277-245 or Y276-233 or Y8-2 or Y9-5. It has banding (Green

ANALYTICAL DATA FOR TRUE SPECIMENS

Studbook ID	Table	Field	True	Overlay	Notes
100208	Master	Dam	SF1T UNK	SF1T4	Identification: Chick 91
		Sire	SF1T UNK	SF1T3	
		Hatch Date Est.	None	Year	
	Sex	Event Date Est.	None	Year	
	Events	Transaction Date Est.		Year	
101254	Master	Dam	SF1T	HYP45	
		Sire	SF1T	HYP44	
101255		Dam	UNK	HYP45	
		Sire	UNK	HYP44	

9.2.3 Importing Overlay Data

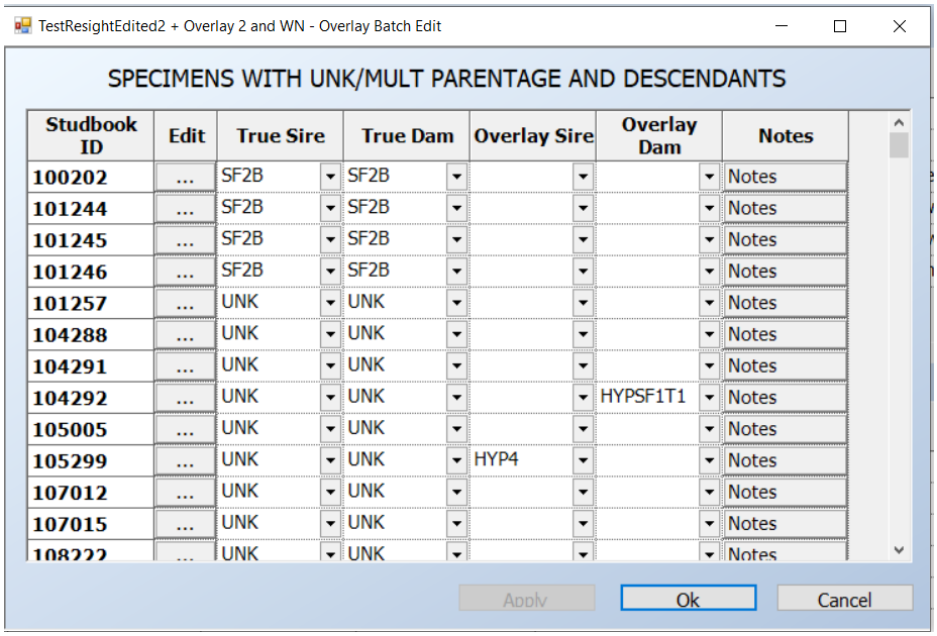
Users have the option to import overlay data from a different version of the same studbook. To use this option, open the studbook without the overlay (the one which you'd like to import the overlay into). Select File → Import Overlay Data, and a window is displayed listing the existing studbooks; the Overlay column indicates whether those existing studbooks have one or more overlays attached. By double clicking on the studbook with the desired overlay, the overlay is imported into the studbook and can be opened by selecting View → Overlays. If you are trying to import an overlay that has the same title as an overlay currently in your studbook, a window will pop-up asking you to re-name the imported overlay.

You should use caution when using this option; PopLink does not check whether the studbooks are the same species, or if any changes have been made to individuals that overlay data are being applied for in the newer version of the studbook. As long as a studbook ID matches between the two studbooks, PopLink will apply overlay data even if it is nonsensical. PopLink will drop analytical data for true animals not tied to a studbook ID in the current studbook.

9.2.4 Batch editing in an Overlay

By selecting the Overlay→ Batch Edits menu item, PopLink allows you to rapidly assign analytical parentage to animals with unknown or MULT parentage. Use the Overlay Sire and Overlay Dam columns to easily assign alternate parents. Use the Notes box to document background on your assumptions.

Caution: You should not use this window to edit true sire or dam information; that should be done following the procedures in Chapter 4!



Studbook ID	Edit	True Sire	True Dam	Overlay Sire	Overlay Dam	Notes
100202	...	SF2B	SF2B			Notes
101244	...	SF2B	SF2B			Notes
101245	...	SF2B	SF2B			Notes
101246	...	SF2B	SF2B			Notes
101257	...	UNK	UNK			Notes
104288	...	UNK	UNK			Notes
104291	...	UNK	UNK			Notes
104292	...	UNK	UNK		HYPSF1T1	Notes
105005	...	UNK	UNK			Notes
105299	...	UNK	UNK	HYP4		Notes
107012	...	UNK	UNK			Notes
107015	...	UNK	UNK			Notes
108222	...	UNK	UNK			Notes

9.2.5 Where to Document

Assumptions should always be carefully documented so that any future studbook keeper or data analyst who uses your studbook will understand what information is true and what information is assumed/fiction. Notes on assumptions (why and how the assumptions were made) should also be placed in:

3. the Species Notes section of a studbook (for general assumptions and conventions that may affect many animals in a population)
4. the Specimen Notes section (*see section 4.9*) of an individual animal record (for changes or assumptions affecting a specific individual).

9.2.6 How to Identify When Analytical Assumptions are Necessary

To construct a useful analytical studbook, you must first learn exactly what information is unknown or missing in the true studbook. Data may fall into several categories of unknownness:

1) truly unknowable (e.g., origins of animals obtained in the early 1900s, when records were not kept as consistently);
2) missing or not yet available (e.g., sex of newborns or origin of animals obtained by institutions known to have good records); and
3) not yet investigated (i.e., pertinent institutions and sources haven't been asked yet).

With enough work on the part of the studbook keeper, all unknown or missing studbook data should eventually fall into the first two categories (unknowable or missing), although this may be an ongoing process.

PopLink includes several features to identify the unknown or missing data in your studbook that are relevant to population management. These are briefly mentioned here, and are discussed in detail in the reports chapter (the relevant section numbers are included after each report name):

1. *Living animals with UNK/MULT in pedigree Report (see section 8.14)*
   This report includes individuals with unknownness anywhere in their pedigree (e.g. for some animals, the parents may be known but there may be an ancestor with unknown parentage further back in the pedigree). This report can quickly help you identify individuals in the current population that have any amount of unknownness in their pedigree.

2. *Animals with UNK/MULT parentage and descendants Report (see section 8.13)*
   This report includes all (living and dead) individuals with UNK or MULT for one or both of their parents. This report includes columns for each individual that indicate the number of descendants they have in the living population, helping you to prioritize individuals for pedigree research (i.e., those individuals with the greatest number of descendants in the managed population should be prioritized first).

3. *Unknown Age Report (see section 8.26)*
   This report returns all living and dead individuals with a birth date estimate of UNK in your studbook database. If these individuals make up a large proportion of your population (you can check by looking in your Summary Counts Report, *section 8.24*), or if many of these individuals are still alive, it may be important to create birth date assumptions for the individuals in the table. The table includes each individual's minimum age, calculated as the minimum amount of time the individual has been living in a recognized institution.

4. *Unknown Sex*
   Although there is no automatic report to generate a list of unknown sex individuals, these can be easily identified by filtering your dataset to *Status = Living*, using the appropriate geographic or FED file filters, and sorting the Master Data Table by the "Current Sex" column. These individuals can also be seen in the Age Pyramid report (*see section 8.2*).

In addition, running Data Validation can indicate data errors that may cause data to be interpreted as UNKNOWN, such as blank sire or dam fields or sire or dam fields filled with studbook IDs that are not found in the dataset.

9.2.7 How to Determine if UNKNOWN Parentage is Really Unknowable

1. Focus on animals with living descendants in the managed population. Unknowns that are dead/LTF/released with no living descendants in the population are not important for genetic management, though they may be relevant to other analyses.
2. Begin by investigating the animals with the most impact on the population (i.e., those with the most living descendants in the managed population). The Animals with UNK/MULT Parentage and Descendants report is sorted by this criterion, so start at the top of the list and work down.
3. Research the unknown parents of animals by contacting each institution that reported having the specific animal in question. The first holding institution may be the best source of information about the origin of an animal, although subsequent holding institutions may have better historic records. Also, it may be helpful to request records on all other animals of the same species present at the institution within several years of the birth of the animal in question (i.e., a historic taxon report) to help identify possible parents.
4. If you have extra time and energy, internet searches, government quarantine records, and talking with people who have been in the zoo community for a long time may help uncover useful information about institutions or facilities related to the animal in question.
5. If you cannot resolve unknownness, leave the unknowns in the true studbook and develop assumptions to incorporate into an analytical overlay.

9.2.8 What to Do With MULT Parentage

While careful documentation of MULT parentage (where more than one known individual could be the possible parent) is appropriate and important for record keeping within the true studbook database, without further analytical assumptions, this type of parental notation is not useful for genetic analyses with the current software. Under current software, MULT parentage does not assign relationships between individual animals, so that in the genetic analyses, MULT parents provide the same amount of pedigree information as UNK parents (i.e., no information). Information from MULT notes and other research should be used to develop parentage assumption in the analytical overlay.

9.3 CONCEPTS BEHIND MAKING SOUND ANALYTICAL ASSUMPTIONS[2]

9.3.1 Assumptions for animals with unknown origin and/or unknown parentage

Although creating assumptions to replace unknown data is best done on a case-by-case basis, there are some general principles that may apply to many populations. The most common types of unknowns that affect genetic analyses are unknown parentage and unknown origin, so assumptions for these will be addressed here.

There are two possible options for an animal of unknown origin and unknown parentage: it is either related to individuals in the living population or it is unrelated and represents a unique genetic lineage. To determine the likelihood of each option, one must consider the details about the animal's record (birthdate, location of first event) and weigh the completeness and accuracy of this data for each decision. Use the outline below as a key to help you think through important evidence that may influence your decisions when trying to create assumptions for animals with unknown ancestry. See Table 4 below to determine possible changes to make in the analytical studbook and the consequences of such changes.

9.3.2 Evidence to consider when making birth origin or parentage assumptions

A. Birth date

1. The animal was born before the first recorded captive birth for the species.
   Assume wild born.
2. The animal was born when captive births were frequent and widespread.
   Assume captive born (unless other evidence suggests otherwise).
3. Birth date unknown or born when imports and captive births were equally common.
   Make no assumptions and move on to review other evidence.

B. Birth location or first source of entry into the population

1. The animal was obtained from a known dealer.
   a. The dealer was known to be an importer of wild caught animals.
      Assume wild born.
   b. The dealer was known to buy and sell captive born animals.
      Assume captive born.
   c. The dealer handled both imports of wild born animals and transfers of captive born animals.
      Make no assumptions and move on to review other evidence.
2. The animal's birth location or source is not known.
   a. The animal is most likely not related to other animals in the population, based on its probable source or other evidence.
      Give the animal wild parents.
   b. The animal is most likely related to other animals in the population.
      Make no assumptions unless other evidence allows you to connect the animal to an existing family line.
3. The animal first appeared at a known institution. First, investigate potential parentage by determining if there were potential parents of reproductive age at the individual's institution during the time frame of interest, and excluding any that might have already been pregnant.

[2] This section is based on the approaches used by the AZA Population Management Center to create analytical assumptions.

a. There were no potential parents recorded at the institution.
   Give the animal (and all similar animals originating from the institution) hypothetical wild-caught parents unless other evidence suggests a relationship to another family line or institution.
b. There were potential parents (males and females of reproductive age) at the institution at the time of the unknown's conception and birth.
   i. There was only one set of potential parents at the institution.
      Assume these animals were the parents unless evidence suggests otherwise.
   ii. There was more than one possible sire or dam at the institution.
      1. The potential sires/dams are closely related.
         Arbitrarily choose one of the relatives as the sire/dam or else choose the most likely one based on information such as breeding age, number of living descendants, social dominance, genetic connections, etc. Consider the relative that incorporates the most lineages, to cover all genetic bases (e.g., if the potential parents are animals A and B where A is the parent of B, choosing the offspring B as the assumed parent is more genetically conservative because it incorporates another lineage—animal B's other parent).
      2. The potential sires/dams are not related or their relationships are not known.
         a. One potential sire/dam produced far more living descendants
            Assume most prolific male/female is the sire/dam.
         b. Two potential sires/dams produced an equivalent number of living descendants.
            Make no assumptions or construct a hypothetical parent that is a genetic combination of the two potential parents.
         c. Many potential sires/dams produced (or are assumed to have produced) many living descendants. Number of founders at institution not known.
            Make no assumptions or construct hypotheticals to make everyone at the institution related to some degree (to avoid inbreeding).
         d. Many potential sires/dams produced many living descendants and number of founders at institution is known.
            Construct hypothetical parents to make everyone at the institution equivalently related to some degree. Determine hypotheticals and relationships using Equation 9 in Willis, 2001 (see Black Hole section below).

Table 4. Basic assumptions about animals with UNK or MULT parentage and the consequences of those assumptions.

	Animal most likely is…	Studbook Data	Assumption	Consequence	Genetic consequence (for the individual and the population)
1.	**captive born** and probably **related** to others in population	Sire = UNK Dam = UNK or Sire = MULT# Dam = MULT#	Choose the most probable parents at the time and institution of animal's origin to be the sire and dam. Example: Choose potential sire or dam with the most living descendants.	Unknown animal becomes a relative in an existing family.	Animal has an estimated genetic value now. Estimates of GD may increase or decrease depending on whether family was previously under- or overrepresented. Choosing the most probable parents may help avoid potential inbreeding.
2.	**captive born** and probably **unrelated** to rest of population	Sire = UNK Dam = UNK	Sire = HYP# Dam = HYP# -------- OR --------- Sire = WILD Dam = WILD (not really wild in this case, just unrelated)	Unknown animal becomes the offspring of hypothetical founders. ---------- Unknown animal becomes a new founder.	Animal becomes valuable genetically. Estimates of GD increase. ---------- Animal becomes very valuable genetically. Estimates of GD increase.
3.	**wild born** and **unrelated** to others in the population	Sire = UNK Dam = UNK	Sire = WILD Dam = WILD	Unknown animal becomes a new founder.	Animal becomes very valuable genetically. Estimates of GD increase.
4.	**wild born** and **related** to others in the population (sibs or clutch mates)	Sire = UNK Dam = UNK	Sire = WILD# Dam = WILD#	Unknown animal becomes the offspring of wild founders.	Animals become valuable genetically. Estimates of GD increase.

9.3.3 Hypothetical ancestors

Hypothetical ancestors can be created to deal with unknown or uncertain portions of an animal's pedigree. These hypothetical animals are often created to be the ancestors of living animals that originated at the same institution, but whose parents cannot be identified. Create records for each hypothetical parent as needed and give these hypothetical parents WILD/WILD parents of their own. Capture locations and dates for the hypothetical animals can be based on assumptions or conventions (e.g., average age at which animals of this species are caught, or logical age of hypothetical animal at the time of the real animal's birth date) and are not relevant if the analytical studbook is only used for genetic, and not demographic, analyses. (The true studbook should be used for demographic analyses).

9.3.4 Groups and black hole assumptions

Pedigree assumptions for group-living animals are more complicated than the cases previously mentioned. A simple and resolvable case of group unknownness is a group of presumably interrelated animals at a single institution where parentage was not recorded—a "black hole" in the pedigree of the population. If the number of animals starting the "black hole" can be estimated and the number of animals produced is known, one can calculate the likely relatedness of the unpedigreed offspring coming out of the group using Equation 9 and Table 2 from Willis 2001. Equation 9 estimates the effective number of alleles in the group:

$$\hat{A}_2 = \frac{Max - Min}{\ln(Max) - \ln(Min)}$$

where *Max* is the maximum number of effective alleles contributed by the founders of the black hole and *Min* is the minimum number of effective alleles that could have possibly been contributed (usually four--two alleles from a single male and two alleles from a single female):

Max = [# founding males + # founding females] x 2 alleles each
Min = [1 male + 1 female] x 2 alleles each = 4

For example, if a black hole group were started from 2 males and 4 females, the maximum number of effective alleles contributed if all reproduced would be twelve: 2 males + 4 females = 6 founders x 2 alleles for each founder = 12. The minimum number of effective alleles would be four: 1 male + 1 female = 2 x 2 alleles for each = 4. Completing the equation gives a value of 7.28 = $\hat{A}_2$.

Using the number of effective alleles ($\hat{A}_2$) and knowing the number of unpedigreed individuals coming out of the black hole group, one can use Table 2 of Willis 2001 to estimate the likely relatedness of the unpedigreed individuals. For example, if $\hat{A}_2$ = 7.28 and there are 10 unpedigreed animals coming out of the black hole, the estimated relatedness would be closest to first cousins. Once a relationship among the unpedigreed animals has been estimated, then a hypothetical pedigree can be constructed to create that relationship in the analytical studbook.

Adapted from Table 2 Willis 2001 (corrected)		No. of animals from unpedigreed population				
Kinship	Relationship	5	10	15	20	Infinite
	full of full	2.353	2.5	2.553	2.581	2.667
0.25	Full sibs	3.333	3.636	3.75	3.81	4
0.1875	1P, 1GP	4	4.571	4.8	4.923	5.333
0.125	Half sibs	5	6.154	6.667	6.957	8
0.0625	2 GP	6.667	9.412	10.091	11.852	16
0.03125	1 GP	8	12.8	16	18.286	32
0	None	10	20	30	40	n/a

P = parent, GP = grandparent

Some group-living populations are too complicated for the black hole solution presented here. If a population has always lived in groups and parentage has never been tracked and will continue to not be tracked in the future, then a non-pedigree-based genetic management strategy will be required. A pure group management strategy does not require parentage assumptions and is beyond the scope and purpose of this monograph.

9.3.5 Genetic consequences of assumptions

The dangers of unknown or missing data in a pedigree lie in the risk of either underestimating or overestimating gene diversity. Estimations of gene diversity will differ based on whether unknown ancestry animals are included or excluded from the breeding population (Table 5).

Table 5. Genetic consequences of two potential errors that can occur when animals with unknown ancestry are included or excluded in a breeding program (modified from Willis 1993).

		"Truth"	
		Unrelated (wild)	**Related**
Decision	**Breed as unrelated (wild)**	**CORRECT**	**INCORRECT INCLUSION** Risk inbreeding Underestimate F Overestimate GD
	Do not breed at all	**INCORRECT EXCLUSION** Lose alleles Underestimate GD	**CORRECT**

Animals with unknown pedigrees could be potential new founders or descendants of lineages not yet represented in the population. If we completely exclude such unknown pedigree animals from genetic analysis, we may be underestimating gene diversity of the captive population and throwing out rare or unique alleles. On the other hand, if we include unknown animals in the breeding population based on the assumption that they are completely unrelated to all others in the population, then we may be overestimating gene diversity in the population. Furthermore, we risk inadvertently inbreeding animals because the relationship between an unknown pedigree animal and any other animal in the population is completely unknown—a potential mate could be a close relative or entirely unrelated.

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APPENDIX 1: POPLINK SURVIVAL TOOL

A1.1 INTRODUCTION

Correct and accurate interpretation of mortality data of captive populations is essential to the continued success of the cooperative management programs, day-to-day management of animals at zoos and aquariums, and the reputation of zoos and aquariums in the eyes of the public, the media, and animal advocacy groups. The PopLink Survival Tool was created through the support of an Association of Zoo and Aquariums Conservation Endowment Fund grant. The goal of the project was to develop a new, scientifically rigorous, standardized approach to the analysis, interpretation, and presentation of mortality data from zoos and aquariums. Through this software tool, we apply new advances and alternative approaches to the analysis of mortality data. The tool gives users the ability to generate a clear, well-documented report describing mortality data that should assist in communication both internally (within a zoo) and externally to members of the press and public. It also uses new methods to evaluate data quality and to calculate estimates of mortality for use in population management.

The Survival Tool allows the user to conduct three types of analyses:

1. **Descriptive Survival Statistics:** this produces a concise description of survival information for communication, public relations, and general audience purposes
2. **Analytical Survival Statistics:** this produces detailed survival analysis results, data tables and figures for use in population management
3. **Expert Survival Statistics:** this allows expert users to adjust the analysis starting age

Note that the decisions made in the design (methodology, statistical testing) of the Survival Tool were focused on making a useful tool for population management and communication. Those interested in using the Survival Tool for research should make sure they understand the implications of those decisions and assess alternate methodologies using more complete statistical analysis software.

A1.2 TERMINOLOGY

Median life expectancy: the age to which half the individuals in the analysis survive. This can also be thought of as the "typical" life expectancy for a population, or how long the "typical" individual in a population can be expected to live. Median life expectancy is a standard measure used by human and animal demographers to compare life expectancies within and between populations or species.

For humans, for example, median life expectancy for individuals in the United States that survive to their first birthday is approximately 77.5 years. The correct interpretation of these statistics is that, if he/she survives the first year of life, the "typical" American will live to be around 77; that half of all Americans can be expected to die before they reach 77 and half will live longer than 77.

Maximum longevity: the age of the oldest observed individual for a population, whether censored (still living at the analysis end date, transferred out of the window, or lost to follow up (LTF)) or dead. It is not necessarily the biologically possible maximum age, but only reflects the individuals included in the analysis. For humans, for example, the maximum longevity (documented) is 122 years.

Lifespan: the time from birth or hatching until death for an individual animal. Species do not have lifespans.

Survivorship (L_x): the probability that a newborn individual will be alive at age x. Survivorship is a cumulative measure (i.e. the survivorship of age class 10 is influenced by all of the survival rates in all the age classes from birth until 10). Survivorship is represented as L_x in life tables, and can also be called the Kaplan Meier estimate or the Product Limit Estimator

Mortality rate (Q_x)**:** the probability that an animal alive at age x will die during that age class

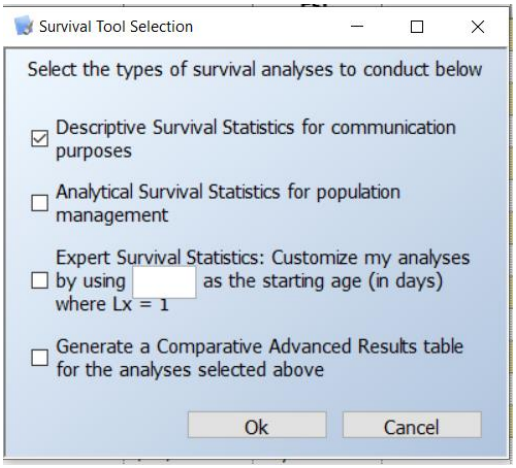
Survival rate (P_x)**:** the probability that an animal alive at age x will survive to age x+1; Note that survival rate is not cumulative but is over a single age class, and that Qx + Px = 1

A1.3 HOW TO RUN AN ANALYSIS IN THE SURVIVAL TOOL

Before you run your analyses in the Survival Tool, it's a good idea to get a sense of your data quality. You can do this by running

1. **The Data Validation routine:** certain data validation errors will affect your survival statistics, either by excluding an individual animal with errors from the analysis or including only part of its data. Errors to especially look out for and correct, if possible, are:
    a. EH-01: Currentness date is more than one year old – if your database is not reasonably current (a year or more out of date), you probably want to use the currentness date for your end date for the analysis window (see below). Using the currentness date ensures that you are only including individuals in the analysis for as long as you have tracked them.
    b. EM-17: Invalid Event after Go LTF or Release Event – if your database has death events directly after Go LTF events, the individual's age at death is not usable in the Survival Analyses. Removing the Go LTF event or having the individual Return from LTF before death will ensure that the data are included. See the Validation section of the manual for more details.
    c. EM-18: Events after Death: this error, like EM-17, signals some uncertainty around the terminal events for an individual – the death events which the Survival Tool is trying to analyze.
2. **The PopLink Age Outliers report:** check for data errors and impossibly old individuals; if there are "undead" individuals in your studbook that are no longer tracked but have likely died, these individuals may skew your survival statistics.

Once you've evaluated data quality issues in your studbook, select the Survival Tool option in the Reports menu. You are prompted to select which type(s) of analysis you'd like to run:



You can run single or multiple reports at once. For the Expert Survival Statistics report, you need to enter the age in days at which you'd like your analyses to start (see the Expert report description below on how to choose this age). The bottom check-box can be selected to generate a separate pop-up window with advanced results for any of the analyses you've run (see below for further details).

After making this selection, you'll be prompted to make filter decisions about the **analysis window.**

The Survival Tool analyses are based on survival records which trace an individual's life from its entry into "the population" to its exit out of "the population". The population in question is defined by the analysis window entered

when you begin running the Survival Tool and can be based on a time window using a start date and end date and, if desired, a geographic or institutional window such as North America, AZA institutions, or Germany (these are entered using mnemonics*, see Location List in section 3.17*). You can also further filter the data by UDF, origin, etc. with the Additional Filters option. Individuals are excluded and included in this window as described in the Detailed Methodology section (*A1.9.1*).

PopLink will then generate results for the report you selected to run; this can take a few minutes depending on the size and complexity of your dataset. The next sections give details on the general methodological approaches and on each report; specific calculations are included in the Detailed Methodology section at the end.

A1.4 GENERAL METHODOLOGY USED IN THE SURVIVAL TOOL

Survival probabilities are calculated using the non-parametric Kaplan Meier approach, also called the Product-Limit estimator (Klein and Moeschberger 1997; Skalski et al. 2005). This approach is useful because it is applicable regardless of right censoring (e.g. individuals that are alive at the end of the analysis window) or left truncation (also called staggered entry; e.g. individuals that enter the dataset after their birthdate). As many captive datasets have both right censored and left-truncated data, Kaplan-Meier estimates were deemed to be generally more appropriate than other analytical methods that can be affected by these types of data. Further details on equations used to calculate survival probabilities can be found in the section later in this appendix entitled "Calculations of Kaplan Meier Survival Probabilities" (*A1.9.2*).

Data quality has an important effect on whether estimates are reliable and can be used for communication and management. The PopLink Survival Tool uses five data quality tests to determine whether sufficient high quality data exist to make reliable estimates of key survival parameters:

1. Can the median life expectancy be calculated? The median life expectancy cannot be calculated if there are not enough deaths relative to the size of the living population in your subset of data.
2. Is sample size (number of individuals at risk) greater than 20 individuals at the median?
3. Is the 95% Confidence Interval (CI) bounded? That is, are both limits to the 95% Confidence Interval defined?
4. Is the sample size in the first age class of analysis (e.g. the first day of analysis) greater than 30 individuals?
5. Is the length of the 95% CI < 33% of the maximum longevity?

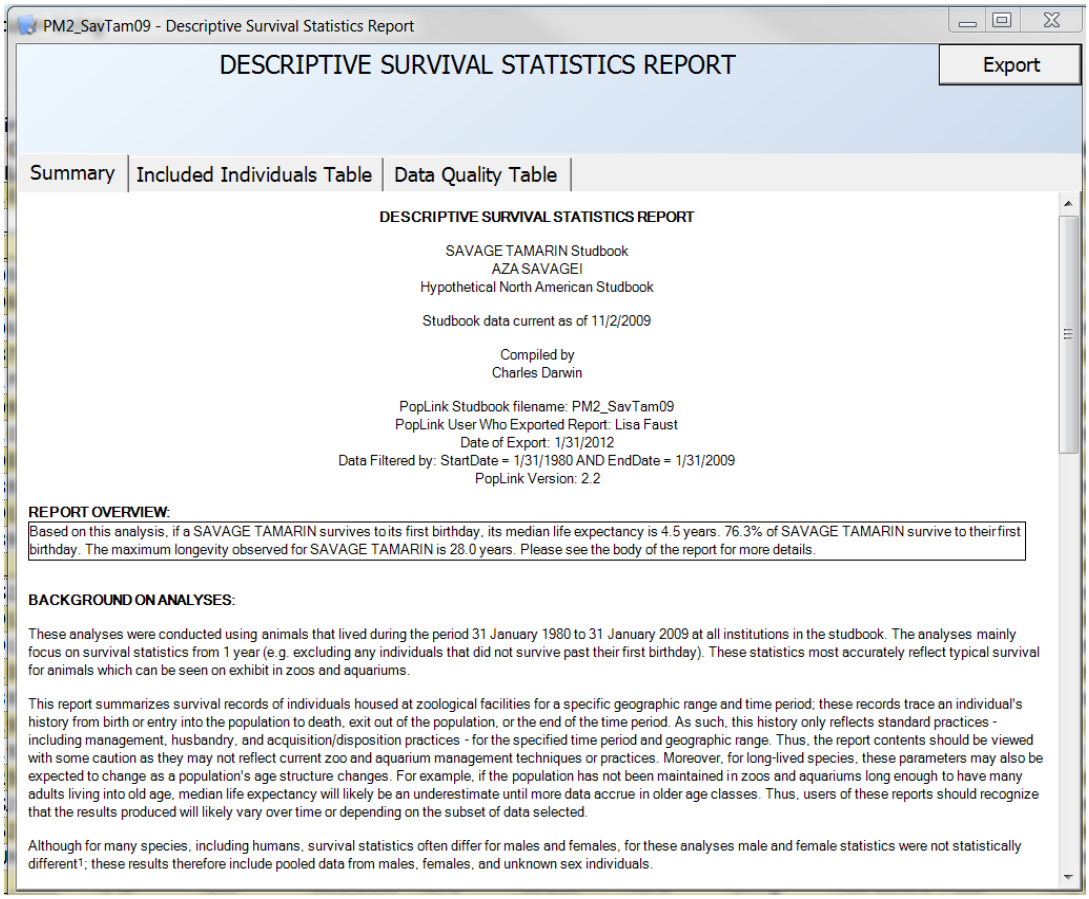
If a data subset (pooled, male, or female) fail any of these tests, results for that data subset are viewed as unreliable and are not reported.

Statistical comparisons of male and female survival statistics are used to determine whether data can be pooled together or need to be separated by sex. If male and female survival patterns are not found to be statistically significantly different, PopLink reports results for a pooled dataset in which sex is ignored; this has the benefits of increasing sample size, and therefore reliability of estimates, if there are no true differences in survival between males and females. If significant differences are found, PopLink reports information for males and females separately; in this case, unknown sex individuals in the sample are proportionally included in the analysis as described in the Detailed Methodology section.

A1.5 DESCRIPTIVE SURVIVAL STATISTICS REPORT

The majority of the statistics calculated in the Descriptive Survival Statistics Report are based on a **starting age of 365 days** – the median life expectancy, confidence intervals, and the age to which 25% of individuals survive exclude any individuals who did not survive to their first birthday. These individuals are excluded because this Report is focused on providing median survival estimates for the typical individual that survives the vulnerable infant stage. In other words, this report answers the question, 'how long is this species expected to live once it has reached its first birthday?'

After selecting the Descriptive Survival Statistics Report option and setting your demographic window, PopLink produces a report with three tabs: **Summary, Included Individuals Table,** and **Data Quality Table.**



1. The **Summary tab** displays the Descriptive Survival Statistics Report, designed to produce a concise description of survival information for communication, public relations, and general audience purposes. To produce the results included in the report, PopLink:
    a. **Calculates Kaplan Meier survival probabilities, median life expectancies, confidence intervals around the median life expectancy, the age to which 25% of individuals survive, and 1st year survival rates** for the Pooled, Male and Female data subsets as described in the Detailed Methodology section.
    b. **Determines whether Pooled, Male, and Female subsets pass the five data quality tests**. Data subsets that fail data quality tests that affect how results are displayed.
    c. If male and female data are of sufficient quality, **compares the confidence intervals around median life expectancies** to determine whether male and female median life expectancies are statistically different (*see A1.9.5*). If the medians are not statistically different (i.e. CIs overlap) pooled results are displayed; if the medians are statistically different (i.e. CIs do not overlap), medians are reported for males and females separately.
2. The **Included Individuals Table** shows the partial or full lifespans of each individual included in the survival analyses; see the Detailed Methodology section (*see A1.9.1*) for more on how this table is constructed. In addition to excluding individuals with unknownness in their record as described in the Detailed Methodology Section, the Descriptive Survival Statistics Report excludes **any individual which has died before their first birthday** from the analysis. These individuals are excluded because the report is focused on providing an estimate of median life expectancy of individuals **which survive the vulnerable 1st year of**

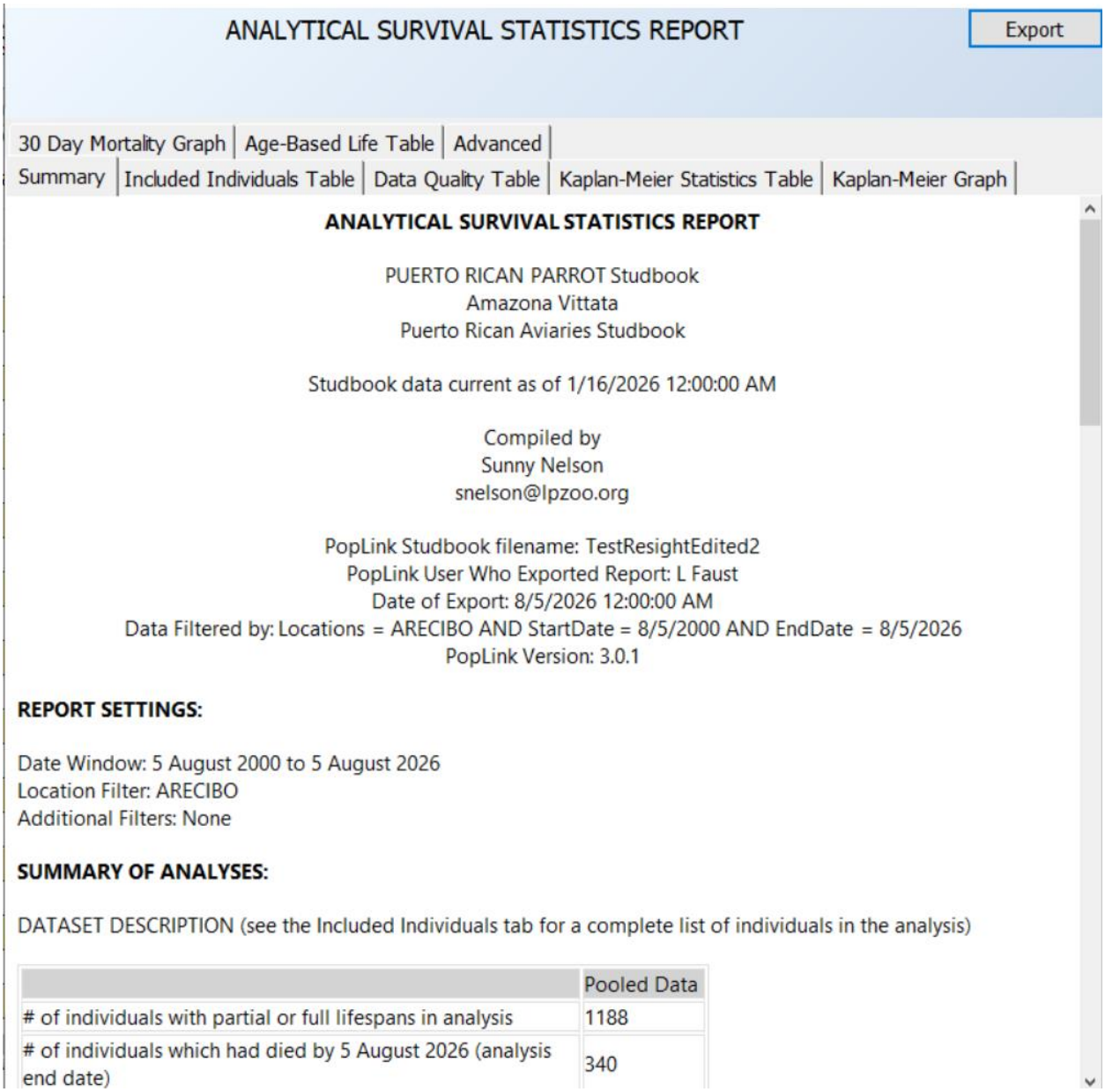
life. If desired, users can run the Analytical Survival Statistics Report, which does not exclude these individuals, for comparison.

3. The **Data Quality Table** displays results of the five data quality tests for males, females, and the overall pooled sample.

If a subset of data fails any of the 5 tests, no results for either that subset or pooled data will be displayed. You can see why the subset failed by looking at the results of the five data quality tests in the Data Quality Table.

You can use the **EXPORT** button to send the Report and the Included Individuals table to files in your studbook databases folder. The Report is exported as DESCRIPTIVE SURVIVAL STATISTICS REPORT.htm and can be opened in your default web-browser by double-clicking on the file or in Word by right-clicking on the file and choosing "Open With" Microsoft Word. The Included Individuals table is exported to DESCRIPTIVE SURVIVAL STATISTICS INCLUDED INDIVIDUALS TABLE.csv and double-clicking will open the table in Excel.

A1.6 ANALYTICAL SURVIVAL STATISTICS REPORT



The Analytical Survival Statistics Report calculates its statistics based on a **starting age of 0 days** - all animals in the window are included in the analysis.

After selecting the Analytical Survival Statistics Report option and setting your demographic window, PopLink produces a report with multiple tabs: **Summary, Included Individuals Table, Data Quality Table, Kaplan-Meier Statistics Table, Kaplan-Meier Graph, 30 Day Mortality Graph, Age-Based Life Table,** and **Advanced.**

1. The **Summary tab** displays the Analytical Survival Statistics Report including statistical results, data quality results, and summary details of the most important survival parameters. To produce the results included in these tabs, PopLink:
    a. **Calculates Kaplan Meier survival probabilities and median life expectancies** for the Pooled data and the Male and Female subsets as described in the Detailed Methodology section.
    b. **Determines whether Pooled, Male, and Female subsets pass the five data quality tests** and produces the Data Quality Table.
    c. **Compares the survival curves** of males and females using the log-rank test (see Detailed Methodology). If the curves are not significantly different, the data are pooled for further analyses. If the curves are significantly different, results are reported for males and females separately.
    d. **Determines which results to display** based on whether data quality filters have been passed and whether male and female curves are statistically different.
2. The **Included Individuals table** shows the partial or full lifespans of each individual included in the survival analyses; see the Detailed Methodology section (*see A1.9.1*) for more on how this table is constructed. Unlike in the Descriptive report, the Analytical Survival Statistics Report does not exclude individuals whose birth date and death date are identical. However, since Kaplan-Meier probabilities must start at 1.0 at the starting age (day 0), one day is added to the death date for any individuals with identical birth and death dates. This does not substantially change results.
3. The **Data Quality table** which reports data quality test results for the Pooled, Male, and Female datasets
4. The **Kaplan Meier Survival Statistics Table** and the **Kaplan Meier Graph** reports and displays the survival rates by age at death (in days). If this table is blank, it means that data quality tests were failed.
5. The **30 Day Mortality Graph** shows the distribution of male, female, and unknown sex deaths in the first 30 days; this graph can be useful when looking for patterns in early mortality.
6. The **Age-Based Life Table**, which is created as described in the Detailed Methodology section (*see A1.9.3*). If this table is blank, it means that data quality tests were failed. The estimates in this life table can be used in population management software such as PMx or Vortex. Note that Life Table estimates calculated by the Survival Tool may be different than those calculated by the main life table report in PopLink, but they should be more precise estimates because they are based on finer time units (days vs. tenths of years in the regular life table report). If this table is blank, it means that data quality tests were failed.
7. The **Advanced** tab lists all Analytical Survival Statistics results in an easy-to-extract (via copy and paste into Excel) format. See the Comparative Advanced Results section (*see section A1.8*) for more details on results included in this tab.

You can use the **EXPORT** button to send the Report and the Included Individuals table to files in your studbook databases folder. The Report is exported as ANALYTICAL SURVIVAL STATISTICS REPORT.htm and can be opened in your default web-browser by double-clicking on the file or in Word by right-clicking on the file and choosing "Open With" Microsoft Word. The Included Individuals table is exported to ANALYTICAL SURVIVAL STATISTICS INCLUDED INDIVIDUALS TABLE.csv and double-clicking will open the table in Excel.

A1.7 EXPERT SURVIVAL STATISTICS REPORT

The Expert Survival Statistics Report allows the user to define the starting age for survival analyses. This might be appropriate if you are interested in determining survival parameters from a specific point in a species' life history. For example, for bird populations it might be appropriate to look at survival from fledging rather than from starting at 365 days (the first birthday, the methodology used in the Descriptive report). For bear populations it might be

appropriate to look at survival from emergence from the den, as the quality of studbook data may be questionable (e.g. institutions may inconsistently report how many individuals were born, be unable to estimate how many were born and died before emergence, etc.). For species in which most individuals are wild-caught and few births are recorded, sample sizes may not be appropriate in the early ages. The decision on the starting age for analysis should be made by those who understand how to interpret the patterns in mortality.

After selecting the Expert Survival Statistics Report option and setting your demographic window, PopLink produces a report with multiple tabs: **Advanced, Included Individuals Table, Data Quality Table, Kaplan-Meier Statistics Table, Kaplan-Meier Graph.**

EXPERT SURVIVAL STATISTICS REPORT

Export

Advanced | Included Individuals Table | Data Quality Table | Kaplan-Meier Statistics Table | Kaplan-Meier Graph

Description	
ANALYSIS WINDOW BACKGROUND	
Type of analysis	Expert
Analysis start age (days)	30
Analysis window start date	8/5/2000
Analysis window end date	8/5/2026
Location window	ARECIBO
Additional filters	No Filters Applied
# of years in window	25.999
Total population size on end date	239
# of specimens with birth date = death date	166
DATASET INFORMATION	
Total number of specimens	939
# of males	446
# of females	438
# of other sex specimens	55
# of wild origin specimens	33
# of captive origin specimens	906
# of unknown origin specimens	0
# of left truncated specimens	171
# of specimens that entered after window start date	99

1. The **Advanced** tab lists all Expert Survival Statistics results in an easy-to-extract (via copy and paste into Excel) format. See the Comparative Advanced Results section for more details on results included in this tab.
2. The **Included Individuals table** shows the partial or full lifespans of each individual included in the survival analyses; see the Detailed Methodology section (*A1.9.1*) for more on how this table is constructed. The Expert Survival Statistics Report excludes any individuals whose age at death is less than the start age entered at the beginning of the analysis.
3. The **Data Quality table** which reports data quality test results for the Pooled, Male, and Female datasets
4. The **Kaplan Meier Survival Statistics Table** and the **Kaplan Meier Graph** reports and displays the survival rates by age at death; note that the start age entered at the beginning of the analysis is the day in which the Kaplan Meier Survival Probability is 1.0. If this table is blank, it means that data quality tests were failed.

A1.8 COMPARATIVE ADVANCED RESULTS

COMPARATIVE ADVANCED RESULTS

Note that all results are displayed in this table regardless of whether data quality criteria are failed. Please see the PopLink manual for mor

Analytical | Expert

Description	
ANALYSIS WINDOW BACKGROUND	
Type of analysis	Analytical
Analysis start age (days)	0
Analysis window start date	8/5/2000
Analysis window end date	8/5/2026
Location window	ARECIBO
Additional filters	No Filters Applied
# of years in window	25.999
Total population size on end date	239
# of specimens with birth date = death date	166
DATASET INFORMATION	
Total number of specimens	1188
# of males	480
# of females	488
# of other sex specimens	220
# of wild origin specimens	57
# of captive origin specimens	1131

A Comparative Advanced Results table is created if you selected the option at the beginning of your analysis. It will produce a concise set of results for pooled, male, and female data subsets for all reports that you selected, including the descriptive report. This table was designed so that results can be easily extracted (right-click to export to Excel) and used in further analyses. There are several categories of results included:

1. **Analysis Window Background:** gives details on the setup parameters for the specific analysis
2. **Dataset Information:** gives counts of the number and types of individuals included in your analysis. These counts can give you a sense of your sample size and further structure within your Included Individuals (e.g. the number of wild-caught vs. captive-born individuals). Note that the *# of left-truncated specimens* includes individuals that entered the geographic window after their birth or were alive at the start of the window, and the *# of right-censored specimens* includes those that were still alive at the end of the date window and that exited the geographic window. Note that the *# of individuals with birth date = death date* is presented for reference, as these individuals are handled differently depending on the report. In the Descriptive report, they are excluded from the analysis (and are not included in any of the rest of the counts in Dataset Information); in the Analytical report they are included in the analysis, and thus and are included in the counts in this section.
3. **Maximum Longevity:** gives ages and studbook numbers for the oldest censored, dead, and overall (oldest of censored or dead) individuals. Note that the user-entered maximum longevity may be slightly higher than entered (e.g. 70 is entered but 70.00014 is displayed); this is rounding error in translating between years and days, and the impact is minimal.
4. **Survival Statistics Summary:** gives median life expectancy, 84% and 95% CI (95% CI are displayed in all reports, 84% are used for statistical analysis of comparison of medians), as well as results (observed and expected deaths, χ^2 test statistic) of log-rank test comparing male and female curves

5. **General Dataset Quality:** gives counts of the number of records with estimated birth or death dates, and information on when sample size becomes "small" (below 30 individuals at risk)
6. **Data Quality Tests**: gives results for the 5 data quality tests

A.1.9 DETAILED METHODOLOGY USED IN THE SURVIVAL ANALYSES

A1.9.1 Inclusion/Exclusion of Individuals

Individuals included in a specific analysis can be viewed in the Included Individuals Table. The Survival Tool determines which portions of an individual's lifespan is included/excluded by extracting the subset of individuals from your studbook that lived for any period of time during your extraction window (the date and institutional filters you set at the beginning of the report).

Individual animals "enter" the analysis by 1) being born into the population (defined by the analysis window), 2) being transferred into the geographic window after the start date, or 3) being alive in the geographic window on the start date; the last two types of entry are referred to as ***left truncated*** data. Individuals "exit" the analysis by 1) dying within the analysis window, 2) being transferred out of the geographic window before the end date, or 3) being alive in the geographic window on the end date; the last two types of exit are referred to as ***right censored*** data.

If an individual enters, exits, and reenters the analysis window (e.g. if the window is North America and an animal is transferred to Europe and then back to North America), the individual will have multiple survival records in the Included Individuals table. The number of animals affected by this is reported in the Advanced tab of each report; if this number is very high (or a substantial proportion of your animals), this violates one of the assumptions of survival analysis and you may want to read further on how it impacts your analytical results [Klein and Moeschberger 1997].

Inclusion of an individual is straightforward if all of its event dates are known and the institutions at which it was housed are recognized and fall within the geographic window. If an individual has estimated event dates (e.g. date estimator = D, M, Y, etc.), date estimators are ignored and the actual event date is used in analyses. When individuals have unknown event dates (date estimator = U) and/or have an event at an unrecognized location, all or a portion of their life may be excluded from the analyses:

1. **All individuals with unknown birthdates (birthdate estimator = U) are excluded from the Survival Tool analyses**, because age at death or censoring cannot be calculated for such individuals. If your population has a large number of animals with unknown birthdates (and/or if there are few animals with known birth dates to base your survival analyses on), you may consider making analytical assumptions for these animals so they can be used in analyses. The Unknown Age Report will be a good starting point for finding and making assumptions about these individuals.
2. For individuals with other unknown event dates (death, transfers, etc.) that make it difficult to determine whether they are in the analytical window or not, the Tool attempts to include as much of their lifespan as possible in the analyses. **In cases where there is too much uncertainty in whether or when an individual entered or exited the analytical window, the individual is excluded from all Survival Tool analyses.** These cases are complex; to summarize them we use the following notation: U = unknown event date, K = known event date, A = window start date, B = window close date. Event streams go from left to right in time, so a sequence KUAKKB can be interpreted as an event with a known date, then an event with an unknown date, then the window start date, known date, known date, window close date. The summarized rules for exclusion of part or all of an individual's lifespan from the analyses are:
    a. If all unknown event dates are before or after the date window and the date window is bracketed by known dates, the individual is included (e.g. KUKABKK or KABKU)
    b. If all unknown event dates are bracketed between two known event dates and within the date window, the individual is included (e.g. AKUKB)
    c. If the individual has an known event date that falls within the window and has no unknown event dates after that point, the individual is included from that known event date until the window closes (e.g. KAUKB – individual's lifespan is only included from the last K to B)

   d. If there is an unknown date within the window but there is a known date that falls within the window before the unknown date, the individual will be censored at the last known date (e.g. KAKUB – individuals' lifespan is only included from A to K)
   e. In all other cases of unknown/known event combinations, the entire individual is excluded from the analysis.
3. When individuals have events at unknown/unrecognized institutions (for which the event date is not UNK), it will be treated as a transfer out of the geographic window (e.g. the individual will be censored on that date). If they have an event at an institution within the geographic window after that and before the window close date, an additional survival record will be created for them in the table (e.g. in this rare case, an individual will have two separate survival records, one from entry date to censor date, and a second from re-entry date to close date). This creation of a double record also occurs if an individual is transferred out of and back into the region and all institutions are known.

In addition, individuals are excluded for specific analyses based on the starting age used in the analysis:

1. In the Descriptive Survival Statistics Report, the starting age = day 365; individuals that die before their first birthday are excluded from the analysis.
2. In the Analytical Survival Statistics Report, the starting age = day 0; all individuals are included in the analyses
3. In the Expert Survival Statistics Report, the starting age is user-defined, and individuals that died at an age less than the starting age are excluded from the analyses.

A1.9.2 Calculations of Kaplan Meier survival probabilities

Using the individual records in the Included Individuals table, survival statistics are calculated following methodology described in Klein and Moeschberger (1997). PopLink constructs the Kaplan Meier Statistics table with a survival probability (*L*) at every time *t* that an individual in the sample dies or is censored. The resulting table has a row for each survival time, and columns for age, number of deaths observed, the number at risk (e.g. the number surviving to that age), the mortality rate (Qx) for that age class (# of deaths divided by # at risk), and the Kaplan Meier estimate *L:*

$$L_t = \prod_{t_i \le t} \left[1 - \frac{d_i}{N_i} \right]$$ (Klein & Moeschberger equation. 4.6.1, modified for clarity, p116)

where *d* is the number of deaths and *N* is the number at risk, and each age's survival probability is multiplied together. By definition, at the starting age for the analysis survivorship is 1.0 (note that in the Descriptive report, start age = day 365; for the Analytical report, start age = day 0; for the Export report, start age = user defined). Estimates in the table are made until the maximum longevity of the dataset; if this is estimated (based on user entry), values are extrapolated from the oldest age at death in the sample to the estimated maximum longevity using an exponential decay function (Klein and Moeschberger 1997).

To calculate the exact median life expectancy (where L_t = 0.5), PopLink uses linear interpolation (unless one of the Kaplan Meier estimates falls exactly on 0.5). If (x_0, L_0) is the smallest (survival time in days, survival probability) pair > 0.5, (x_1,L_1) is the largest pair < 0.5, and (x, 0.5) is the pair of interest,

$$x = x_0 + \left(\frac{(L_0 - 0.5)(x_1 - x_0)}{L_0 - L_1} \right)$$ (K & M equation. 5.4.8, modified for clarity, p116)

PopLink makes these calculations for pooled, male, and female data subsets. For analyses that require separation by sex, individuals with other sex codes, including unknown sex, abnormal sex, hermaphrodite, etc., are distributed proportionally by sex ratio and infant mortality between males and females:

D_x = deaths, N_x = number of individuals, *M* = males, *F* = females, *U* = unknown/other sex; Q_x = mortality rate at a given age

If $D_M + D_F > 0$ at age *x*, distribute proportionally by sex ratio and infant mortality:

$$MaleQx = \frac{D_M + D_U \frac{D_M}{D_M + D_F}}{N_M + N_U \frac{N_M}{N_M + N_F}} \quad FemaleQx = \frac{D_F + D_U \frac{D_F}{D_M + D_F}}{N_F + N_U \frac{N_F}{N_M + N_F}}$$

If $D_M + D_F = 0$ at age x, distribute proportionally according to sex ratio:

$$MaleQx = \frac{D_U \frac{N_M}{N_M + N_F}}{N_M + N_U \frac{N_M}{N_M + N_F}} \quad FemaleQx = \frac{D_U \frac{N_F}{N_M + N_F}}{N_F + N_U \frac{N_F}{N_M + N_F}}$$

These adjusted mortality rates are used in the Kaplan Meier Statistics Table to calculate adjusted Kaplan Meier survival probabilities.

A1.9.3 Calculations of Age-based Life Table

Using the Kaplan Meier survival probabilities, PopLink also generates an age-based life table with 1 year age cohorts for use in population management software such as PM2000 and ZooRisk; this life table is only created for the Analytical report. PopLink generates a table with values for Pooled, Male, and Female subsets (with unknowns incorporated into males and females as described above). This table displays the age class, number of individuals at risk, survival rate (Lx), and mortality rate (Qx). The survival rates from the Kaplan Meier Statistics table, which in that table are given for every age at death in the sample, are collapsed into annual estimates. If a Kaplan-Meier estimate does not fall exactly on the start of an age class, the estimate of the last Kaplan-Meier entry before that age is used. At risk values are the value of the last Kaplan-Meier entry before the age of interest—for example, if a survival time of 1.8 years had an at risk of 210 individuals and the next survival time was 2.3 years with an at risk of 200, the at risk value for the 2 year old age class in the life table would be 210 individuals. Mortality rates are then back-calculated from survival rates:

$$L_x = L_{x-1} * (1 - Q_{x-1})$$

A1.9.4 Calculations of Confidence Intervals around Median Life Expectancy

Confidence intervals are calculated based on a log-transformed confidence interval (Klein and Moeschberger 1997) where the interval is defined by calculating Z for each survival time *t*

$$Z = \frac{\{\ln[-\ln(\hat{L})] - \ln[-\ln(0.5)]\}[\hat{L}\ln(\hat{L})]}{\sqrt{\hat{V}}}$$ (K&M equation 4.5.5, modified for clarity, p112)

where *L* is the Kaplan Meier survival estimate and the standard error of *L* is

$$\sqrt{\hat{V}} = \hat{L}^2 \sum_{t_i \le t} \frac{d_i}{N_i(N_i - d_i)}$$ (K&M equation 4.2.2, modified for clarity, p84)

where *d* = deaths and *N* = number at risk at a given time. The reported confidence intervals are the 95% Confidence intervals (Z is $\pm$ 1.96); these CIs are the values of *L* where Z $\le$ 1.96 and Z $\ge$ 1.96.

A1.9.5 Statistical Comparisons of Male and Female Survival Statistics

Comparisons of median life expectancies using confidence intervals

In the Descriptive Report, the statistical test used to determine whether male and female data subsets are reported separately or pooled together is a comparison of the median life expectancies of each sex. Significance is determined by comparing whether the 84% confidence intervals (Z = $\pm$ 1.386) around each

median overlap. 84% CIs are used rather than 95% CIs because comparisons of overlapping CIs using 95% are extremely conservative (Schenker and Gentleman, 2001). Payton, Greenstone, and Schenker (2003) determined that 83-84% confidence intervals produce the appropriate type I error rate of $\alpha = 0.05$. Note that these comparisons using the simplifying assumption that the standard errors of the two medians are approximately equal (Payton et al., 2003); this should be true for the majority of populations but results should be interpreted carefully if the standard errors of the medians have large differences. If the 84% CIs overlapped and the null hypothesis that male and female median life expectancies are not different is supported, the data are pooled for further analyses. If the CIs do not overlap and the null hypothesis is rejected, medians are reported for males and females separately.

Comparison of survival curves using the log rank test

For the Analytical and Expert reports the log rank test is used to compare survival curves between data subsets. In the Analytical tool, male and female survival probabilities (incorporating unknown sex individuals as described above) are compared. The log-rank test is based on the number of observed and expected deaths at each survival interval (Klein and Moeschberger 1997, Skalski et al 2005). To conduct the test, PopLink calculates

O_{male} = the sum of male deaths (observed)
O_{female}= the sum of female deaths (observed)
E_{male}= the sum of male deaths (expected)
E_{female}= the sum of female deaths (expected)

Where expected deaths are calculated using the number of individuals (male or female) at risk at a survival interval multiplied by the pooled mortality rate (i.e. the mortality rate expected if there was no difference between male and female mortality rates). These calculations exclude any extrapolated values that are used because the oldest individual in a data subset is censored (e.g. values that are displayed in red at the end of the Kaplan Meier table). Then, ZooRisk calculates the log-rank test statistic as

$$\chi^2 = \frac{(O_{male} - E_{male})^2}{E_{male}} + \frac{(O_{female} - E_{female})^2}{E_{female}}$$

This is compared to the chi-square distribution with 1 degree of freedom to test for significance.

A.1.9.6 REFERENCES

Klein JP, Moeschberger ML. 1997. Survival Analysis: Techniques for Censored and Truncated Data. Springer: New York.

Payton ME, Greenstone MH, Schenker N. 2003. Overlapping confidence intervals or standard error intervals: What do they mean in terms of statistical significance? Journal of Insect Science, 3(34): 1-6.

Schenker N, Gentleman, JF. 2001. On judging the significance of differences by examining the overlap between confidence intervals. The American Statistician 55(3): 182-186.

Skalski, JR, Ryding, KE, Millspaugh, JJ. 2005. Wildlife Demography: Analysis of Sex, Age, and Count Data. Elsevier, Inc: Massachusetts.

APPENDIX 2: ACCESSING POPLINK DATA IN MICROSOFT SQL SERVER MANAGEMENT STUDIO

The underlying studbook database storage system for PopLink 2.5 has been changed from the binary file (data.bin) used in version 1.3 and before to a SQL database. You won't see this difference when you're looking at your database in PopLink, but the under-the-hood change means that your studbook data are stored in a way that is more permanent, secure, and accessible. With a SQL database, "power" users can use a different program, SQL Server Management Studio (SSMS), to view and export data and write custom queries for more detailed analyses.

To utilize these features, there is one additional installation procedure; complete this step after PopLink has been installed. To install:

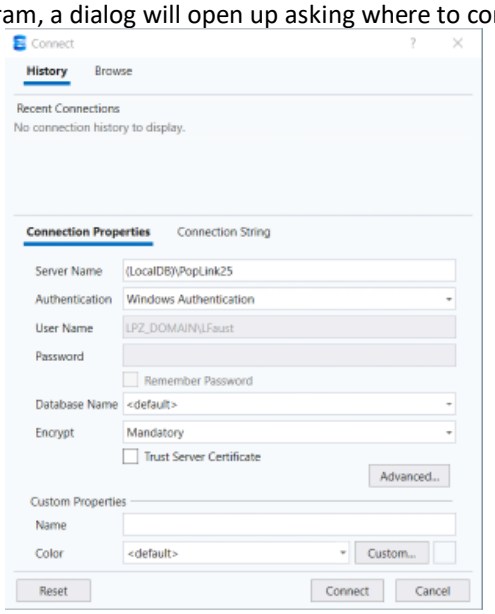
1. Go to https://learn.microsoft.com/en-us/ssms/install/install
2. Download the most current version of SQL Server Management Studio (version 22 at the time of PopLink 3.0 release).
3. Run your downloaded SSMS file. In the dialogue boxes,
    a. Accept licensing terms of installation,
    b. Enter your name and company,
    c. Use the default selection on feature selection. Click "Finish" and installation is complete.

If you have trouble downloading questions about how to install, please email us at software@lpzoo.org.

We recommend reviewing SQL Server Management Studio's Tutorial (under the Help menu in the program) and other Help features as needed. However, we're including assistance with some of the basic features of SSMS to assist you in exploring your studbook data.

A2.1 Starting and Connecting to SQL Server

1.) Run SQL Server Management Studio
2.) When you open the program, a dialog will open up asking where to connect:



3.) For 'Server name', type: "(LocalDB)\PopLink25". Leave all other values at their default, click "Connect".

A2.2 Displaying Data In A Table

1.) Once the program connects to your local SQL service you should see an 'Object Explorer' window on the left side. Expand the 'Databases' folder in order to view the databases created by PopLink.

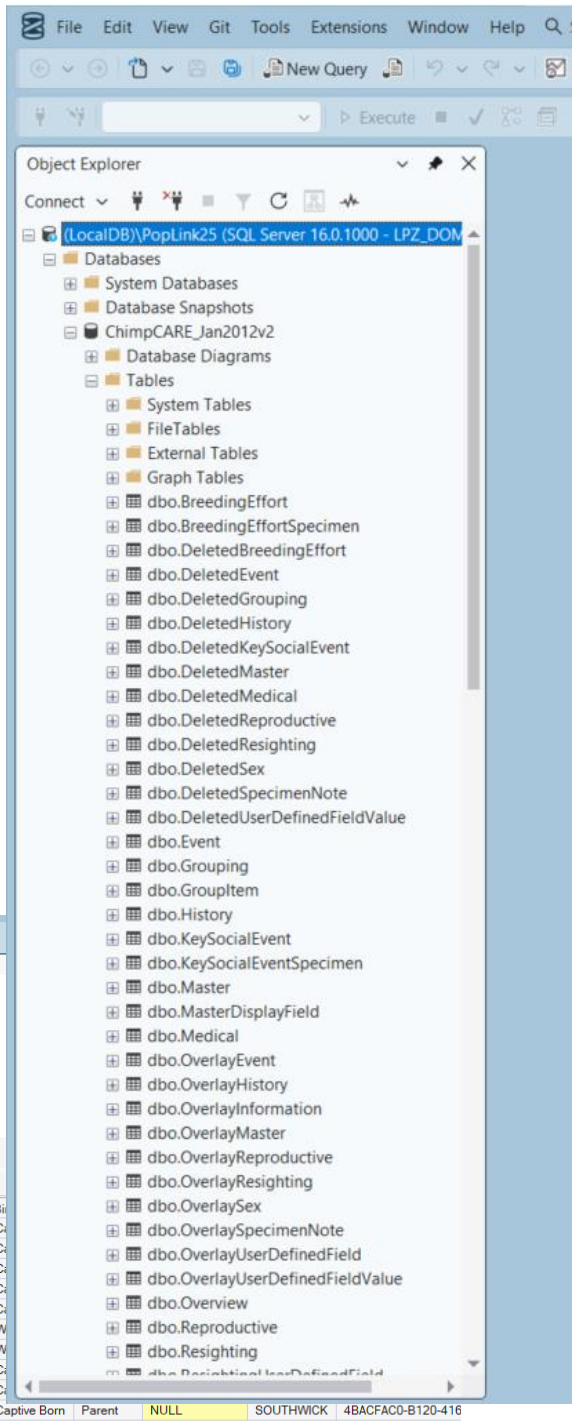
2.) Expand a particular database folder to display its database objects.

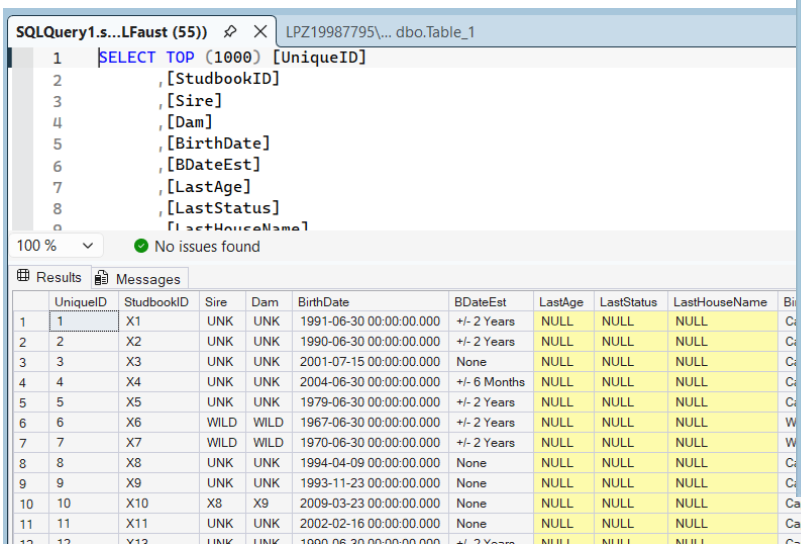
3.) To display the list of tables in the database expand the tables folder, as shown in the figure to the right. The studbook's main data are stored in dbo.Master, dbo.Event, dbo.Reproductive, dbo.Sex, dbo.AnimalNote, and dbo.Overview. There are many additional tables stored that are related to optional data modules in the software.

4.) In order to display the data contained in a table, right-click on the table to display and select 'Select Top 1000 Rows'.

5.) The window on the right of the Object Explorer will display all the data in the table in a grid-like view, as in the example below.

6.) **IMPORTANT NOTE: Unless absolutely necessary, do not manipulate the data displayed in the grid. This will change the data in your database (viewed through SQL Server or through PopLink) without any of the data validation checks that occur when you enter data within PopLink.**





A2.3 Custom Database Queries

Custom database queries can be run to pull only database information that you're interested in. This could also include "joining" multiple tables with a single query in order to pull data from multiple tables into one grid of information. To run a custom query:

1.) Select a database from the expanded database list in 'Object Explorer'.
2.) Click the 'New Query' button, usually above the 'Object Explorer' window:
3.) A 'New Query Editor' window will open in the right pane.
4.) In the editor pane, write a query and then click the "Execute" button; if the query does not contain any error, it will display the result set in a window below the query. If it does contain any errors then it will display the errors in a new window below the query:
5.) For more information on query syntax please go here: http://www.w3schools.com/sql/default.asp. This resource contains very useful information regarding properly querying a database. The information ranges from basic to advanced.

A2.4 Exporting Data

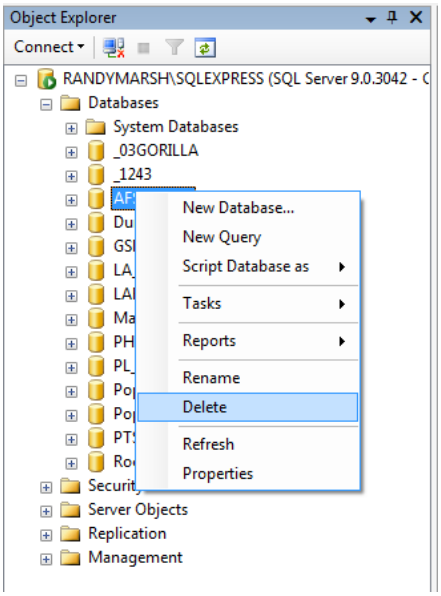
Data can be exported from SQL to a number of different formats. Any table (either a database table or a table created by a query) can be copied and pasted into Excel.

1. Once the table you wish to export is in the right-hand viewer, highlight the rows you wish to export
2. Right-click on the highlighted area and select Copy
3. Open Excel and hit Control-V or select Edit → Paste
4. Note that the data will be pasted in without column headers, which you will have to enter by hand.

A2.5 Deleting a Database

In previous versions of PopLink you could delete databases in two ways:

1. through the program in the Open Database dialogue box (File→Open Database, highlighting the database you want to delete, and selecting Delete Database) or
2. via windows explorer by deleting the studbook folder in My Documents\PopLink\PopLink Databases.

In PopLink 3.0, if you delete the studbook folder using windows explorer, you must also delete the database through SQL Server. Deleting a studbook through PopLink (option 1 above) is best because it avoids this step. To delete the database within SQL Server:

1.) In the Object Explorer window, expand the Databases folder to include all your studbook databases opened with PopLink.
2.) Right-click on the database you want to delete and click "Delete".
3.) The "Delete Object" dialog box will open. Click "Ok" and it will delete the database.