

VERSION 1.0

# USER MANUAL FOR GROUP MANAGEMENT IN PM<sub>x</sub>



## USER MANUAL FOR GROUP MANAGEMENT IN PMx

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### **About this Manual:**

The User Manual for Group Management in PMx was developed as a complement of the User Manual for the software PMx. This version (1.0) is written to describe the characteristics of the Group Management Package (with the group pedigree template and the converter, *group2PMx*) and functionalities of group pedigree analysis in PMx version 1.3.20150612. Periodic changes and revisions will be performed to this User Manual as the functionalities of the Group Management Package and group pedigree analysis in PMx continue to be expanded and updated. This Manual and the Group Management Package are distributed free of charge and are available on: [www.vortex10.org/PMx.aspx](http://www.vortex10.org/PMx.aspx) or [https://github.com/BelenJM/Group\\_Management](https://github.com/BelenJM/Group_Management)

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Many thanks to the following Manual contributors for useful suggestions:

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### **Citations.**

The Group-Management Package and *group2PMx* should be cited as:

Jiménez-Mena, B.; Schad, K.; Hanna, N. & Lacy, R.C. (2015) Pedigree analysis for the genetic management of group-living species. *Methods in Ecology and Evolution* (submitted).

Jiménez-Mena, B.; Schad, K. & Lacy, R.C. (2015) User Manual for group management in PMx. Available from <http://www.vortex10.org/PMx.aspx> or [https://github.com/BelenJM/Group\\_Management](https://github.com/BelenJM/Group_Management)

The PMx software should be cited as:

Ballou, J.D., Lacy, R.C., & Pollak, J.P. (2014) PMx: Software for demographic and genetic analysis and management of pedigreed populations (Version 1.3.20150713). Chicago Zoological Society, Brookfield, Illinois, USA. Available from <http://www.vortex10.org/PMx.aspx>

Lacy, R.C.; Ballou, J.D. & Pollak, J.P. (2012) PMx: Software package for demographic and genetic analysis and management of pedigreed populations. *Methods in Ecology & Evolution* 3:433-437.

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## SECTION 1: Introduction

One of the main aims of zoos and aquariums is to contribute to the conservation of biodiversity by retaining as much genetic diversity of the species as possible, as well as maintaining the sustainability of their *ex situ* collections. This is generally done by registering the information about each individual in the population, their parentage and breeding pairs. Using this pedigree information to design the breeding programs, it is possible to manage the population. However, there are numerous species/taxa that i) cannot be individually identified and ii) are typically managed in tanks/groups and thus the control of matings is complicated (Wang, 2004). Many groups of amphibians, reptiles, fishes, birds and also mammals, such as primates and ungulates (Wang, 2004; Smith, 2010), are group-living organisms. In order to optimally manage these kinds of organisms and address their challenges, zoos and aquariums have worked on extending the use of pedigree analysis for managing groups, in so called *group management* (Leus *et al.*, 2011).

The software PMx (Ballou *et al.*, 2014; Lacy *et al.*, 2012) allows the conservation community to perform demographic and genetic analysis of populations from which pedigree data are available. This program was created to analyze pedigree data from individual records as registered and stored in SPARKS (ISIS, 2012) and PopLink (Faust *et al.*, 2012), but also allows for the analysis of data from group-living organisms. The package described in this manual helps storing and importing group data into PMx. This package consists of:

- (i) a **data entry sheet in Excel** that allows registration of group data, and
- (ii) **group2PMx**, a converter that transforms the Excel file into a .csv file readable by PMx.

Note that the data entry sheet in Excel can also be used for individual records in addition to groups. This will allow conservation managers outside the zoo and aquarium community (without access to SPARKS or PopLink) to have a user-friendly template in Excel in which to register the individuals of the population and still perform an analysis in PMx.

Given a complete and accurate pedigree, individual management is the best strategy to manage a population. In general, one should be aware that group management will not be as accurate as individual management, but it is better than not managing the population at all and thus becomes the recommended strategy for managers of these types of organisms.

## Getting started

### System requirements

*group2PMx.exe* is written in Python 2.7 . It has been tested on Windows XP and 7. *group2PMx* can run on 32-bit or 64-bit processors. For Linux users, the Python script is provided. See the PMx Manual for information about the system requirements of PMx (Traylor-Holzer, 2011).

### Installation

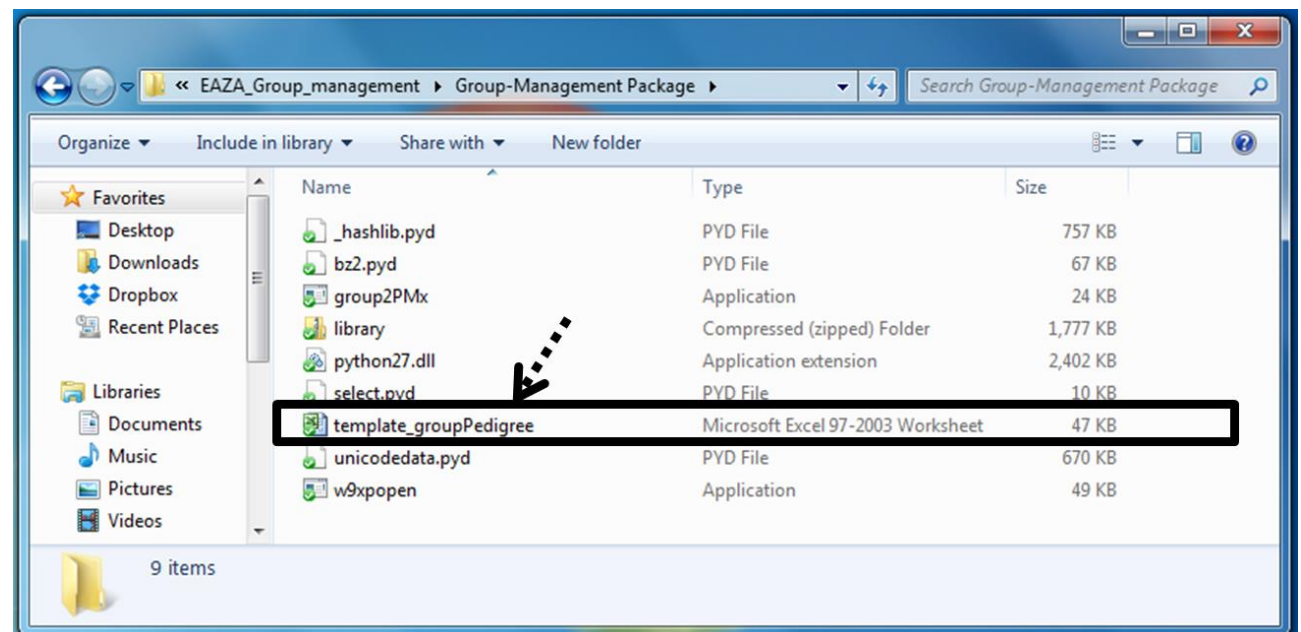
The package is freely available from the website: [www.vortex10.org/PMx.aspx](http://www.vortex10.org/PMx.aspx), or [https://github.com/BelenJM/Group\\_Management](https://github.com/BelenJM/Group_Management) . Click “Save File” and choose the folder where to store it in your computer. Unzip the .zip file.

## SECTION 2: the group data entry sheet template

The group data can be stored in the group data entry sheet template provided in the Group Management Package. In this section, we describe the structure of the data entry sheet and how to fill it in with the group data collected from the population to be managed.

### Location

The Excel spreadsheet *template\_groupPedigree* is found in the main folder of the Group-Management Package.





## Structure of the data entry sheet

Note that the format for some data fields in PMx is more flexible than what is described below. However, to avoid confusion it is better to use the rules given here. For a more complete description of the various formats that can be used with PMx, refer to the PMx manual (Traylor-Holzer, 2011).

### *Header section (blue background)*

The first lines of the spreadsheet correspond to the header where information about the dataset and analysis can be filled in (i.e., species, dates, authorships, etc.). Each line begins with '\*'. The structure must not be modified. As stated in the spreadsheet, the user can add other header lines, if useful, and these should always start with '#'. These header lines are ignored by PMx but can be useful for the manager for clarification. For example, the header line starting with *\*Dates* indicates to PMx the start and end dates for the genetic and demographic analysis, with the following format. For example,

\*Dates: 01/01/1970 <= 28/02/2011

### *Lines required for PMx (purple background)*

The row below *#Name of the fields* (indicated below) should not be erased or modified as it makes reference to the entered data of the group/individual and is needed for the correct function of PMx. Note that this line specifies the sequence of data fields in all individual records, so it is critical that it be included and correct. Each semicolon separates a different column ("," indicates an entry in a new cell in the Excel spreadsheet); we will use this notation throughout the document.

\*FIELDS: ID; Entity; Size; Sire; Dam; Sex; ReproStat; Selected; Living;  
BirthType; DOB; DOBest; DOD; DODest; Location; Rearing; BirthLoc;  
BProgram; BCountry; Necr1; LocalID; Program; Country; Transponder; Tag;  
Tattoo; Color; AsstRep

Several header rows (with first cell as \*MULT, \*MULTPROBS and \*MOVE) describe the format of lines that specify the structure of the parentage data and move records sections. These lines begin with '\*' and are ignored by PMx.

### *Group/Individual entries*

Each group/individual record must be registered in one line/row. The data fields' names from above that are filled in red are required by PMx and thus should be filled for each group/individual. The field columns in blue are not essential and PMx can work without this information. The fields must remain in the given order (see above *Lines required for PMx*). There cannot be any blank rows in this section; a commented line (a row starting with #) can be used instead.

The required entries (in Red) are:

- **ID:** The identifier used for a group/individual throughout the project, typically the studbook number. To avoid errors in computations in PMx, it is required that a group name must start with the letter “G”; the rest is flexible to the User. For instance, a group can be named using the word “GROUP” (lowercase or uppercase) followed by letters (“A”, “B”, etc.). A space can be added between GROUP and the letter, (e.g., “GROUP G”). Whichever option is chosen (“GROUPG”, “GROUP G”, “GroupG”, “Group\_G”), it must be consistent throughout the pedigree because PMx would recognize “GROUPG” and “GROUP G” as different groups.
- **Entity:** This field should be filled with “GROUP” when group-managing a population. If the Entity field is left blank, PMx assumes that the row is an individual.
- **Size:** The number of individuals forming the group. If the Size field is left blank, PMx assumes this to be 1.
- **Sire:** For individuals, this entry corresponds to the unique ID of the sire (male parent), or “WILD” or “UNK” if the individual is wild caught or has an unknown origin. For groups, this entry has a different meaning and corresponds to the breeding type that has generated the creation of the group. The options are “GROUP”, “MERGE”, “SPLIT” (see Section 5 for an explanation of each of these terms). For these, an extra line indicating the parental group name is required to be inserted in the Parentage data section (see below). As for individuals, this entry can also be “WILD” if the group is wild caught.
- **Dam:** For individuals, this corresponds to the unique ID of the dam (female parent), or “WILD” or “UNK” if the dam is wild caught or unknown, respectively. For groups, this entry must always be filled by “GROUP” (see below the explanation for this term) and an extra line indicating the parental group name is required to be inserted in the Parentage data section (see below). Other options are: “WILD” if the group/individual is wild caught.
- **Sex:** The gender of a group/individual. The options are “Female”, “Male”, “Hermaphrodite”, “Abnormal”, “Asexual”, “Unknown” (or “U”) or “Both”. When a group is formed by all females or all males, the sex should be indicated as “Female” or “Male”. Whenever the sex is not known or individuals of both sexes are mixed together, the sex should be indicated as “Unknown” or “Both”.
- **ReproStat:** The reproductive status of a group/individual. The options are: “Fertile” (living individuals that are presumed capable of breeding), “Contracepted” (living individuals contracepted), and “Sterilized” (individuals permanently sterilized). If group/individuals are not listed as “Contracepted” or “Sterilized” in the studbook, they will appear as Fertile in PMx by default, which may or may not be accurate.
- **Selected:** This entry indicates if this group/individual is selected to be part of the breeding program. The options are “True” or “False”. “True” means that it can be used for breeding; “False” means that it should be excluded from genetic calculations on the managed breeding population.
- **Living:** This indicates whether or not the group/individual is currently living

or, alternately, no longer exists in the population. The options are: "True" or "False".

- **BirthType**: The birth origin of the group/individual. The options are: "Wild Born", "Captive Born", "Other", or "Unknown".
- **DOB**: The date of birth or hatch of the group/individual, formatted as `yyyymmdd` (e.g., 15 March 2011 should be entered as 20110315).
- **DOBest**: The date of birth estimate indicates the resolution to which the birth date can be estimated, if it is not a known date. Fields are coded as "Exact" (a blank or "None" is also treated as exact), "U" (for an unknown date), "Y" or "Year" (known only to year), "M" or "Month" (known only to month), or "D" or "Day", with each of Y, M, and D optionally followed by an integer to indicate the number of years, months, or days to which a date is known (e.g., +/- 2 months would be entered as "M2").
- **DOD**: The date of death is the date of the group/individual's actual death even if this occurred outside of the project date span. Date fields in text files must be formatted as `yyyymmdd` (e.g., "20110315").
- **DODest**: The date of death estimate is the resolution to which the death date can be estimated, if it is not a known date. Same format as DOBest (see above).
- **Location**: The current (or last in the case of not living group/ individual) location of the group/individual. The location is usually indicated by the institution's ISIS mnemonic (i.e the mnemonic is "MADRID Z" for Zoo Aquarium de Madrid). If a group/individual left the scope of the project (e.g., was transferred outside the region or association), then Location may not reflect the current living place. It can be left blank.

The optional entries (in Blue) can be deleted by the user if they are not going to be used (and updating the row below *#Name of the fields*, see above *Lines required for PMx*). They are not used for any calculations within PMx, but they can be used for filtering and sorting which animals are displayed in tables in PMx. These optional entries are:

- **Rearing**: The rearing type of the group/individual. The options are: "Parent", "Hand", "Foster", "Peer", "Supplemental", "Unknown", "None", "Colony"/"Group".
- **BirthLoc**: The location of birth or hatch of the group/individual. This can be the institution's ISIS mnemonic (e.g., "MADRID Z" for Zoo Aquarium de Madrid).
- **Bprogram**: The breeding program that the group/individual belongs to at the time of birth.
- **Bcountry**: The country of birth or hatch of the group/individual.
- **Necr1**: This necropsy note indicates any comment related to the necropsy.
- **LocalID**: The local ID of the group/individual used by the institution indicated in the Location field.
- **Program**: The breeding program that the group/individual is currently part of.
- **Country**: The current country where the group/individual is located.
- **Transponder**: The transponder number of the group/individual used by the



- institution indicated in the Location field.
- **Tag**: The tag description of the group/individual used by the institution indicated in the Location field.
- **Tattoo**: The tattoo description of the group/individual used by the institution indicated in the Location field.
- **Color**: The color phase or pattern observed and recorded for the group/individual.
- **AsstRep**: This indicates if any type of assisted reproduction was used to breed the group/individual. The options are: “NotAsstRep” or “AsstRep”.

### *Parentage data section*

Depending on the information given in Sire/Dam, some extra information is needed. If a group is formed by a GROUP, MERGE, or SPLIT (and therefore, Sire = GROUP, MERGE, or SPLIT and Dam=GROUP; see Section 5), information about the parental groups/individuals' ID and the number of individuals contributed by each group must be inserted in this section (note that there are several currently acceptable formats). Instead of the actual count number, it is possible to use a proportion to show how much of the parental group is included here (e.g., 0.3).

The format should be:

```
*IDAM: name of the group/individual; dam1ID; prob1
*IDAM: name of the group/individual; dam2ID; prob2
```

where the *dam IDs* are the IDs of the parental groups and *prob* is the number of individuals or probability (proportional contribution) of each parental group. For example, if GroupM has been formed with 5 and 6 individuals from GroupAAR and GroupCPH, respectively, the parentage line is as follows:

```
*IDAM: GroupM; GroupAAR; 5
*IDAM: GroupM; GroupCPH; 6
```

Instead of listing all parental groups and their contributions on separate lines, we can write the same information in a more condensed format using \*IDAMS (with an 'S') and \*IDAMPROBS:

```
*IDAMS: name of the group/individual; dam1ID; dam2ID
*IDAMPROBS: name of the group/individual; prob2; prob2
```

And the example,

```
*IDAMS: GroupM; GroupAAR; GroupCPH
*IDAMPROBS: GroupM; 5; 6
```

Note that “IDAM” does not explicitly refer to the sex of the individuals; it just indicates the parental group from which the group/individual was generated. In the

case of a SEXUAL MERGE (see Breeding Systems for groups in Section 5) we use both \*IDAM (and \*IDAMS) and \*ISIRE (or \*ISIRES). In this case we actually know that a specific group has only males and another specific group has only females, and we are using both groups to create the new offspring group. Then the user can indicate the extra lines for the parents as follows:

\*IDAM: name of the group/individual; damID; prob

\*ISIRE: name of the group/individual; sireID; prob

Or equivalently:

\*IDAMS: name of the group/individual; dam1ID; dam2ID

\*IDAMPROBS: name of the group/individual; prob2; prob2

\*ISIRES: name of the group/individual; sire1ID; sire2ID

\*ISIREPROBS: name of the group/individual; prob2; prob2

If the number of individuals that form the group or probabilities are not specified (in either style above), they are assumed to be equal across all possible group sires or dams.

### *Move records section*

The record of individuals moved in and out of populations can be inserted in this section with the format indicated below:

\*MOVE: ID;DateIn; DateInEst; InType; DateOut; DateOutEst; OutType; Location; Notes

**ID:** The group/individual identifier.

**DateIn:** The date of the “move/transfer” event. The date fields coded as specified above for DOB and DOD.

**DateInEst:** The resolution to which the DateIn date can be estimated, as detailed before for DOBest and DODest.

**InType:** This indicates how the individual or group entered the population. The options are: “birth”, “capture”, “found” (individual/group that appeared in the exhibit and no one knows how it got there, e.g., an unobserved birth, a wild animal that got into the exhibit, etc.), “import” (individual/group obtained from another institution outside from the scope of the studbook), “leftentry” or “entry” (individual/group that entered the population sometime after its birth, but it is not recorded previously in the studbook. Differs from “Import” in which there is no specification about where it came from).

**DateOut:** The date when the group/individual left the population. The date fields coded as specified above for DOB and DOD.

**DateOutEst:** The resolution to which the DateOut date can be estimated, as detailed before for DOBest and DODest.

**OutType:** This indicates how the group/individual left the population. The options are: “death”, “release” (individual/group released into the wild),

“lost” (there is any information about the individual/group), “export” (sent out of the population to some location that is not included in the studbook), “rightexit” or “exit” (removed from the population by an unspecified means), or “alive”. In the case of groups, whenever an individual is being merged with a group or other individuals, it should be specified as “exit”.

**Location:** The new location of the group/individual, indicated by the institution’s ISIS mnemonic.

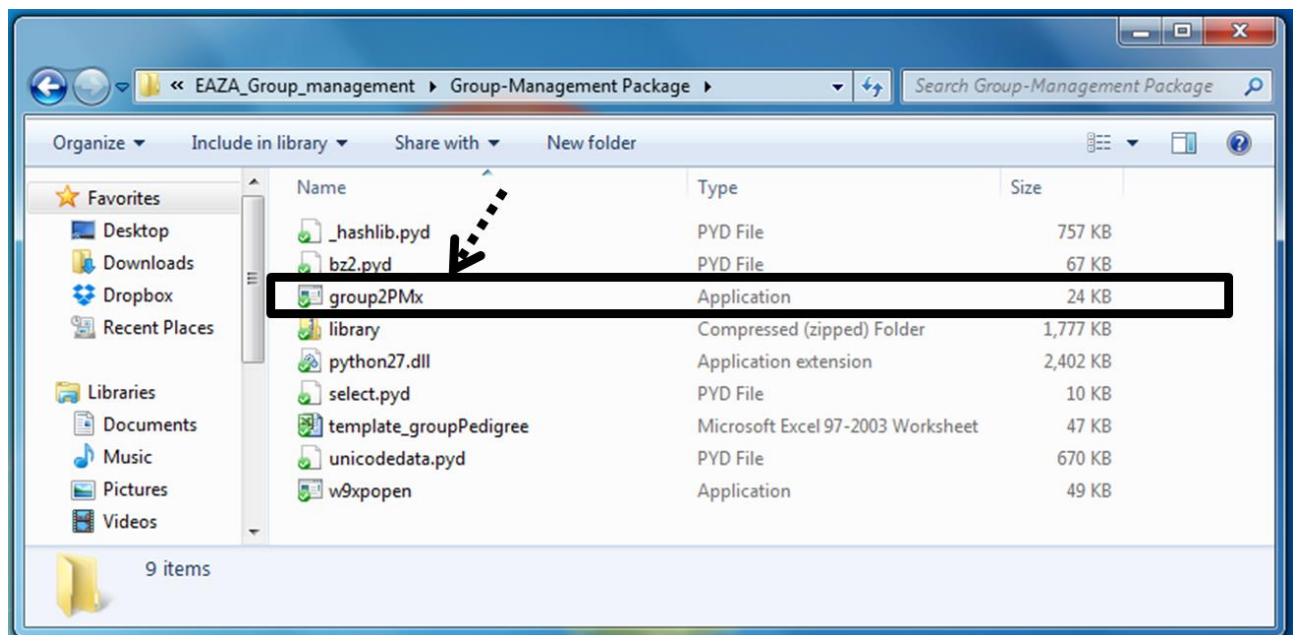
**Notes:** The notes can be any additional text about this group/individual.

## SECTION 3: Importing the group pedigree data into PMx (group2PMx)

In this section, we describe how to convert the Excel data entry sheet filled with the pedigree data into a file readable by PMx. The user needs to run *group2PMx*, which with just one click will easily convert the data.

### Location

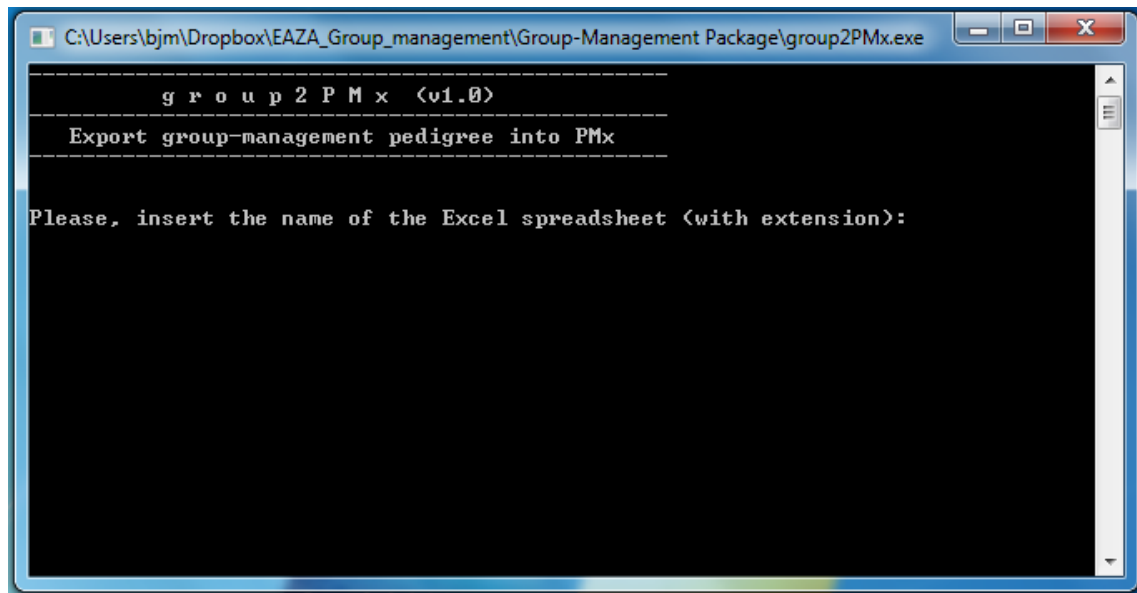
The executable *group2PMx* is located in the Group Management Package.



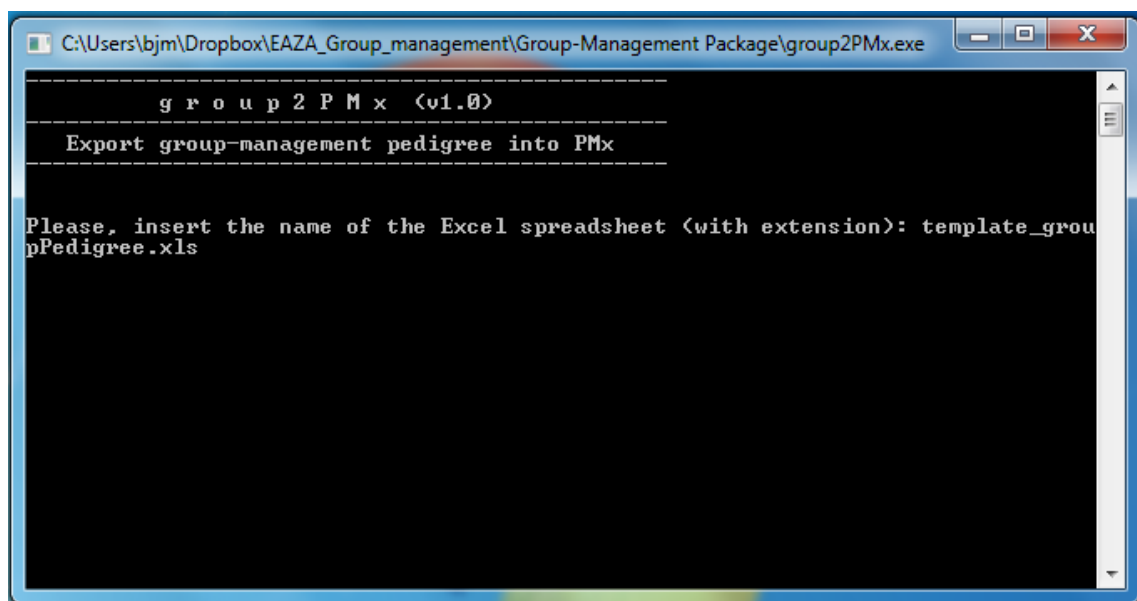
The folder contains other files apart from the *template\_groupPedigree* Excel template and the *group2PMx* executable; these files are required by the converter and should not be deleted or moved.

### Steps to convert the pedigree file

Double-click on *group2PMx*. A black screen will appear where you need to specify the name of the spreadsheet file (do not forget the extension: .xls, .xlsx, etc).

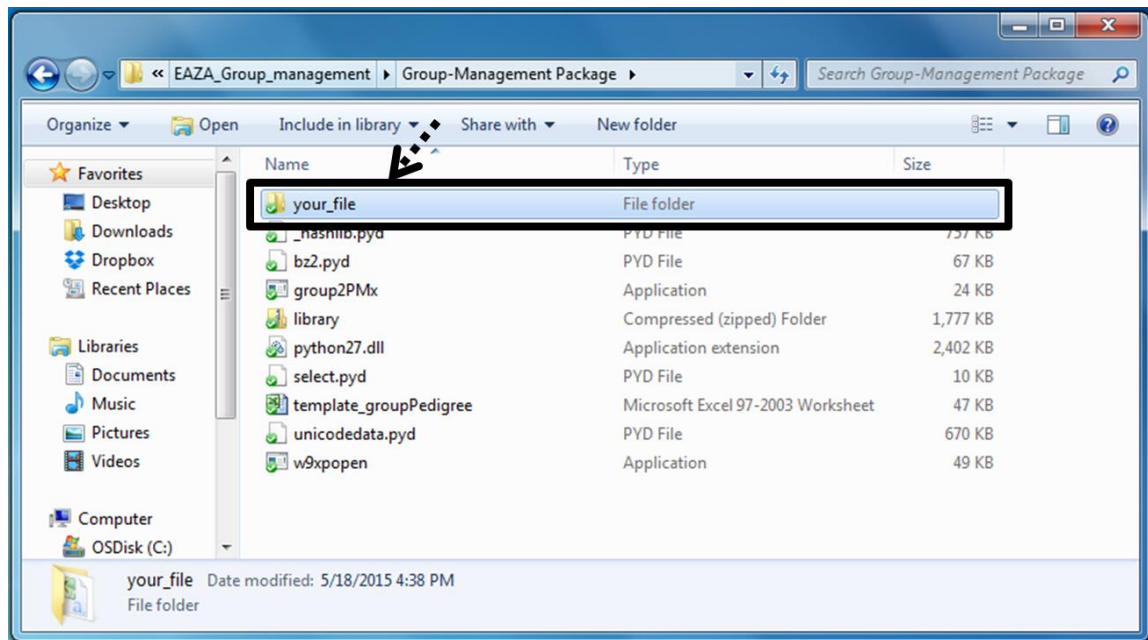


If the spreadsheet is in the same folder as the executable, the user can just provide the name of the file and the extension (for example: "template\_groupPedigree.xls"). If the spreadsheet is in another folder than the executable, the relative path should be provided (for example: C:\Documents\ ... \template\_groupPedigree.xls).

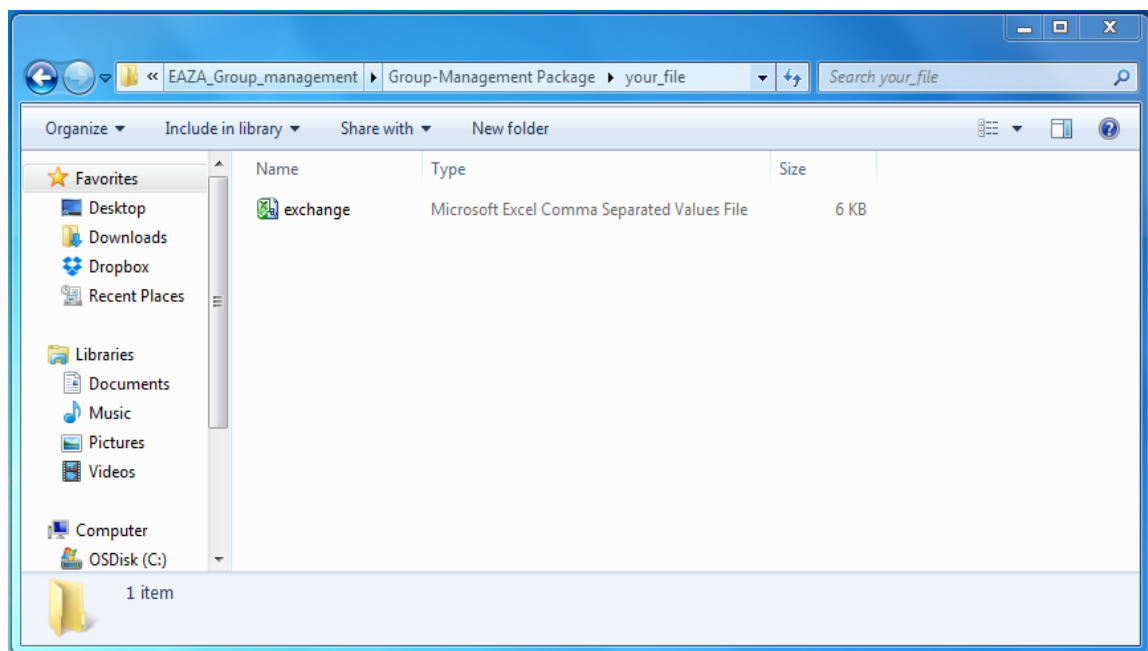


## Output file

After specifying the correct path and name of the file, a subfolder, "your\_file", should have been created. If the subfolder does not appear, try to reload the main folder.



The exchange file generated by *group2PMx* should be inside the subfolder “your\_file”.





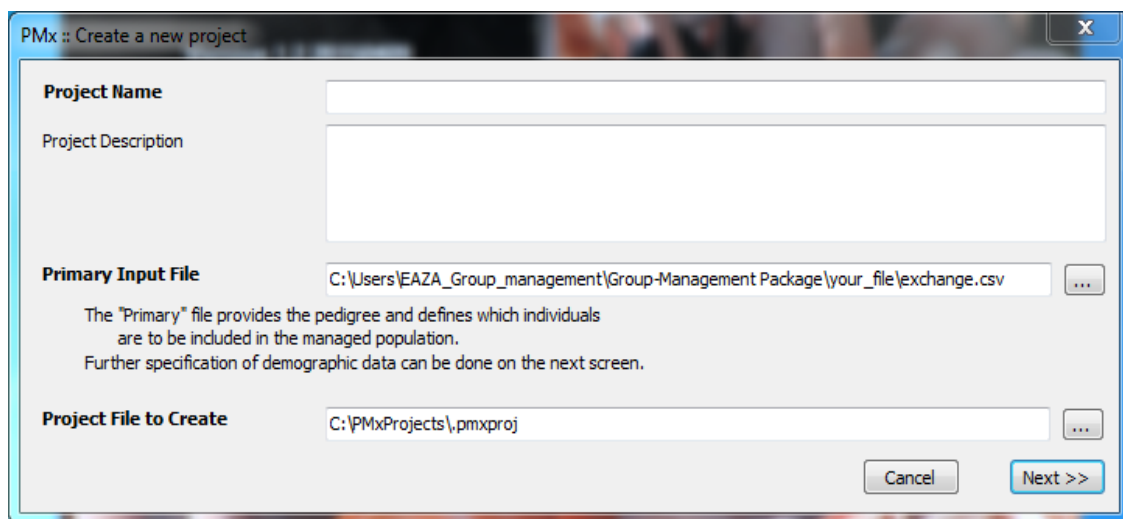
## SECTION 4: Creating a project in PMx from the converted file

Here we summarize the steps to start using PMx with our data and how to create a project. The information found below has been obtained and adapted from the PMx manual (Traylor-Holzer, 2011).

1. The software PMx and the Manual, if not installed yet, can be downloaded from: <http://www.vortex10.org/PMx.aspx>
2. Once PMx is installed on your computer, open it.



3. Select *New Project* and create a project name.
4. The exchange.csv file can now be used directly in PMx as the "Primary input file". Then click on *Next*.

The image shows a screenshot of the "PMx :: Create a new project" dialog box. The dialog has a title bar with the text "PMx :: Create a new project" and a close button (X). Inside the dialog, there are several fields and buttons. At the top, there is a "Project Name" field with a text input box. Below it is a "Project Description" field with a larger text input box. Further down is the "Primary Input File" section, which includes a text input box containing the path "C:\Users\EAZA\_Group\_management\Group-Management Package\your\_file\exchange.csv" and a button with three dots (ellipsis) to the right. Below this input box is a paragraph of text: "The 'Primary' file provides the pedigree and defines which individuals are to be included in the managed population. Further specification of demographic data can be done on the next screen." At the bottom of the dialog is the "Project File to Create" section, which includes a text input box containing the path "C:\PMxProjects\pmxproj" and a button with three dots (ellipsis) to the right. In the bottom right corner of the dialog, there are two buttons: "Cancel" and "Next >>".

5. No *Demography* or *Additional Optional Input File* needs to be specified because enough information is already contained in the spreadsheet (the *Primary Input File - exchange.csv*). See Traylor-Holzer (2011) to read more about other Input files.
6. Click on *Create*. Once PMx opens to the initial **Project Notes** screen, select *File > Save Project*.

PMx :: Create a new project

Demography Input Files (Optional -- specify files if the population view for demography is to be different than for genetics)

☒ Life tables in .PRN format

Female  ...

Male  ...

☐ Move records in .CSV format

for Demography  ...

for Genetics  ...

☐ Move records in .MOV format  ...

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

**Additional Optional Input Files**

Census  ...

Associations  ...

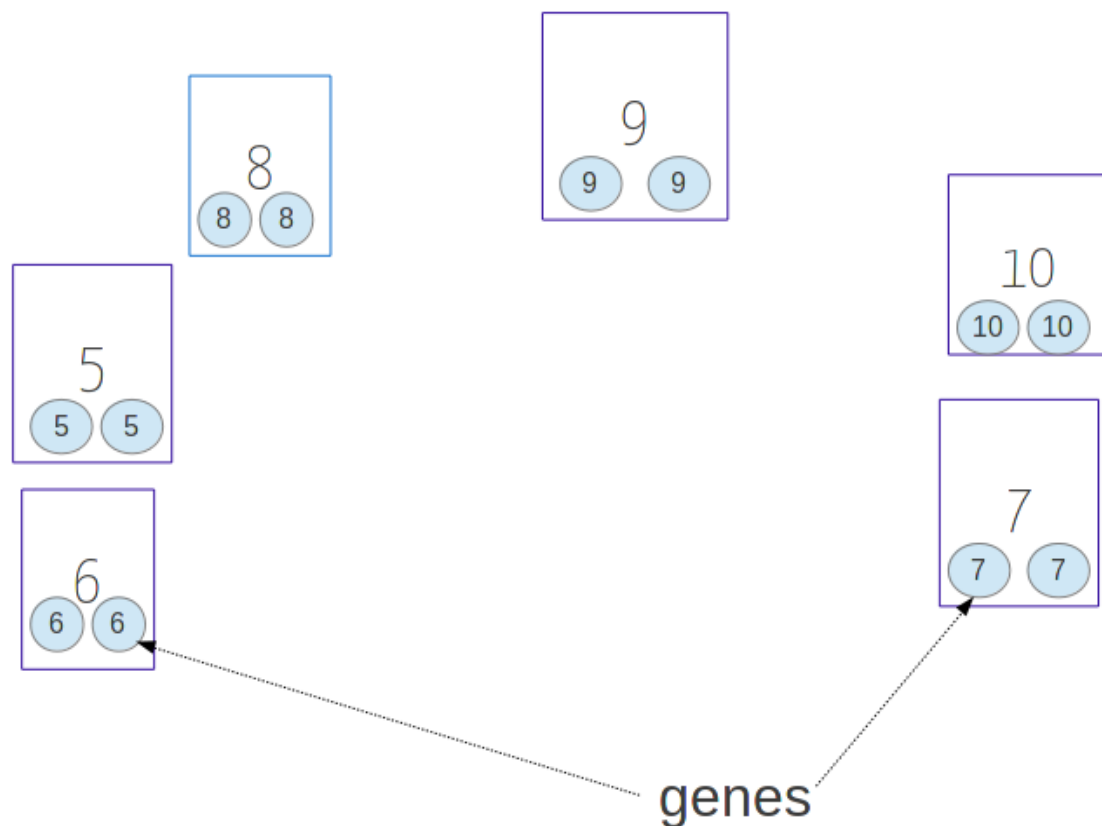
<< Back Cancel Create

## SECTION 5: Navigating into pedigree analysis of group management

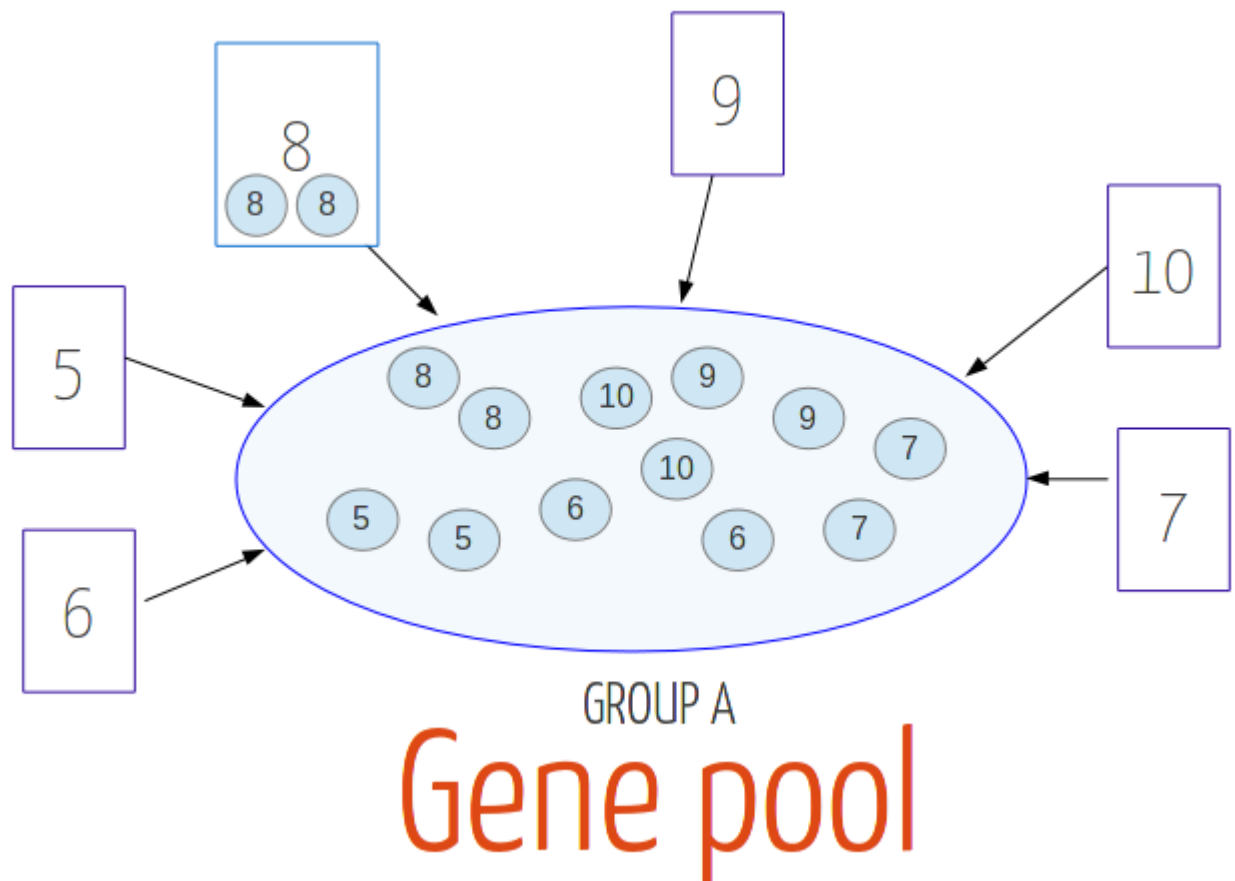
### Understanding group management

Like individual management, group management is based on the theory of population genetics. It is important to note that once we define a group containing some individuals, we no longer speak about individuals, but instead about a virtual set of genes coming from those individuals. That is exactly the definition of a 'group' in group management: a gene pool of the genes from the individuals. The information about which genes belong to which individual is not used. Any entity can form a group, i.e. with any ploidy (e.g. haploid, diploid, tetraploid). For convenience, here we describe all of the concepts in terms of groups that consist of diploid individuals.

When we include several individuals/groups in the same enclosure to form a new group (for example, 'GROUPA', formed by individuals with studbook IDs 5, 6, 7, 8, 9 and 10), assuming all the individuals are different from one another and are diploid, the individuals contribute their genes to the gene pool as in Figures 2 and 3.



**Figure 2:** basic scheme representing the genes of the individuals 5, 6, 7, 8, 9, 10



**Figure 3:** representation of the individuals contributing to form the gene pool that corresponds to groupA. The six individuals are diploid and contribute with two genes to the gene pool. Just for representation, we indicate individual 8 with the two genes on it.

## Breeding systems of groups

Computations of genetic parameters for groups in PMx are different depending on the breeding system used to form the offspring group.

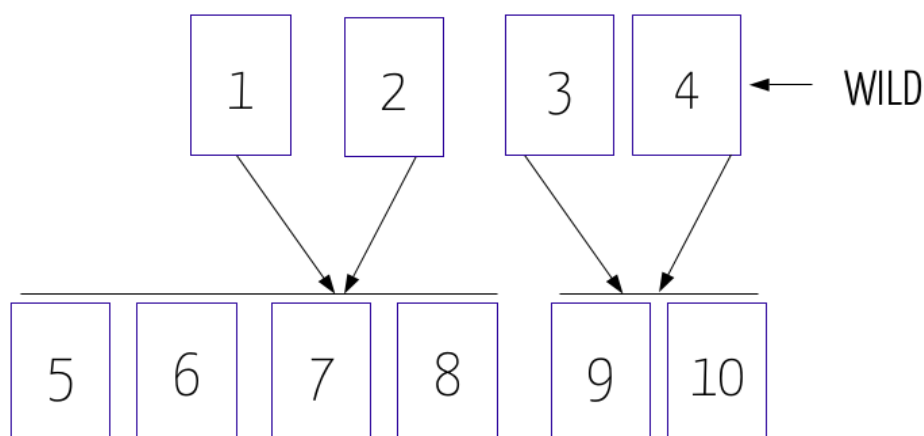
The different breeding systems are MERGE, SPLIT and EXTRACT, detailed below.

### *Merge*

In general, this term refers to the union of individuals or existing groups to form a single group.

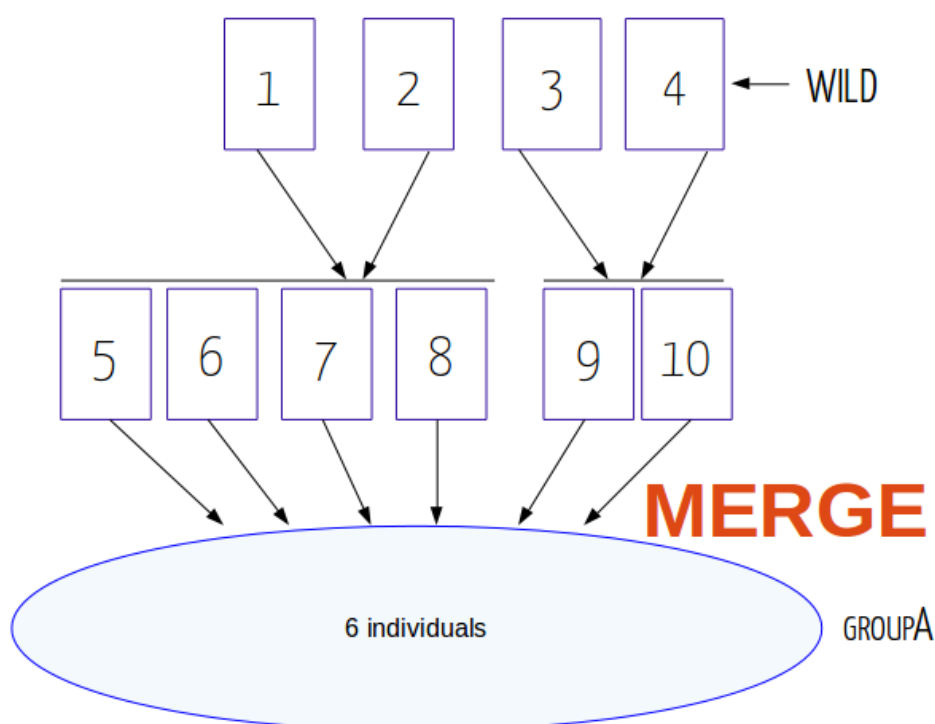
We present five management situations where the field 'Sire' should be filled in with MERGE:

- Merge of individuals: let's study the pedigree example represented in Figure 4.



**Figure 4:** example of a pedigree describing the relationship between ten individuals with ID 1-10. Individuals are represented by square symbols. Generations are connected by a vertical line.

Wild-origin individuals 1, 2, 3, and 4 have given birth to offspring 5, 6, 7, 8, 9, and 10 (Figure 4). Let's imagine we want to form a group with all the offspring and name it 'GROUPA' (Figure 5).



**Figure 5:** pedigree example in which the individuals 5, 6, 7, 8, 9, 10 are merged to form 'GROUPA'

The data from Figure 5 would be entered in the condensed form as follows:

GROUPA; GROUP; 6; MERGE; GROUP; ...

\*IDAMS: GROUPA; 1; 2; 3; 4

\*IDAMPROBS: GROUPA; 2; 2; 1; 1

Or

GROUPA; GROUP; 6; MERGE; GROUP; ...

\*IDAM: GROUPA; 1; 2

\*IDAM: GROUPA; 2; 2

\*IDAM: GROUPA; 3; 1

\*IDAM: GROUPA; 4; 1

Note that it would also work to first create individuals 5, 6, 7, 8, 9, and 10 from their parents, and then create GROUPA by merging those 6 individuals (each described as a “Dam” of GROUPA).

The above entries use number of individuals, but they can be transformed to probabilities by dividing by 6, the total size of 'GROUPA'.

GROUPA; GROUP; 6; MERGE; GROUP; ...

\*IDAMS: GROUPA; 1; 2; 3; 4

\*IDAMPROBS: GROUPA; 0.33; 0.33; 0.16; 0.16

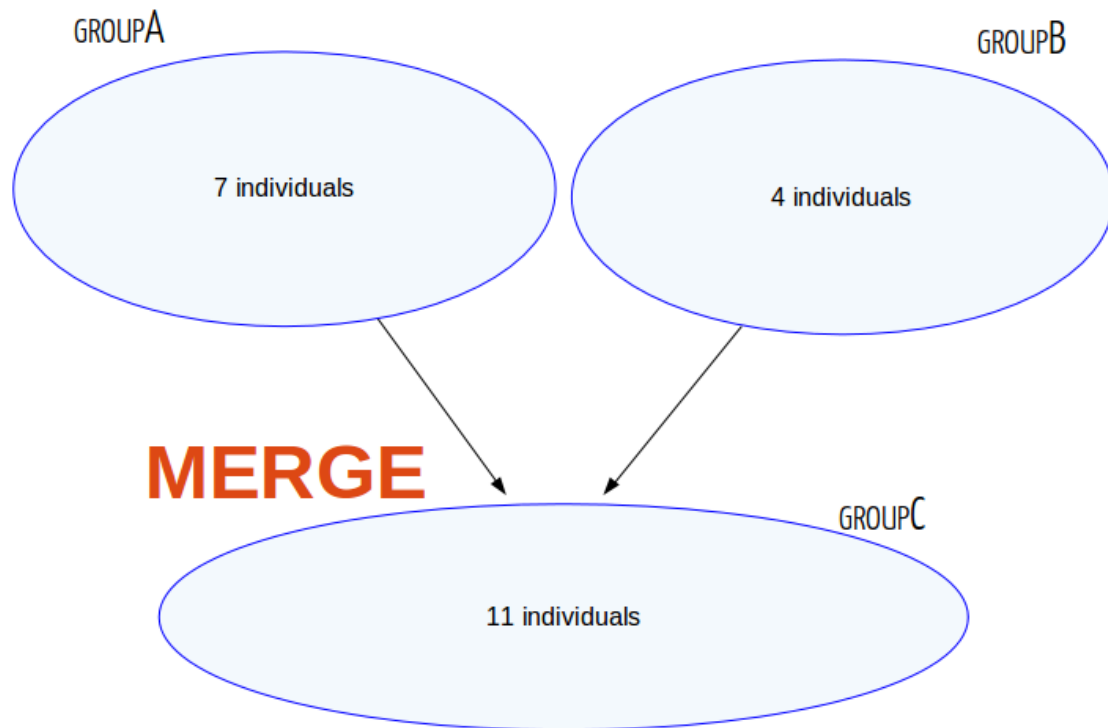
## EXIT

As a consequence of the merge, the individuals of Figure 5 included in 'GROUPA' (5, 6, 7, 8, 9, 10) are no longer identifiable. Therefore, we need to include 'MOVE' rows indicating that the individuals have “Exited” the population. Below is an example of one of the MOVE rows (one row per individual for more information about the information to add in the “MOVE” row, see *Section 2 -extra lines “MOVE” row*). The date corresponds to the date in which 'GROUPA' was formed.

IMOVE: 3; ; ; 20060302; ; Exit;

- Merge of two or more groups: in Figure 6, 'GROUPC' is formed as a merge of two groups ('GROUPA' and 'GROUPB'). The sum of the individuals from 'GROUPA' and 'GROUPB' will form the total of 'GROUPC'.



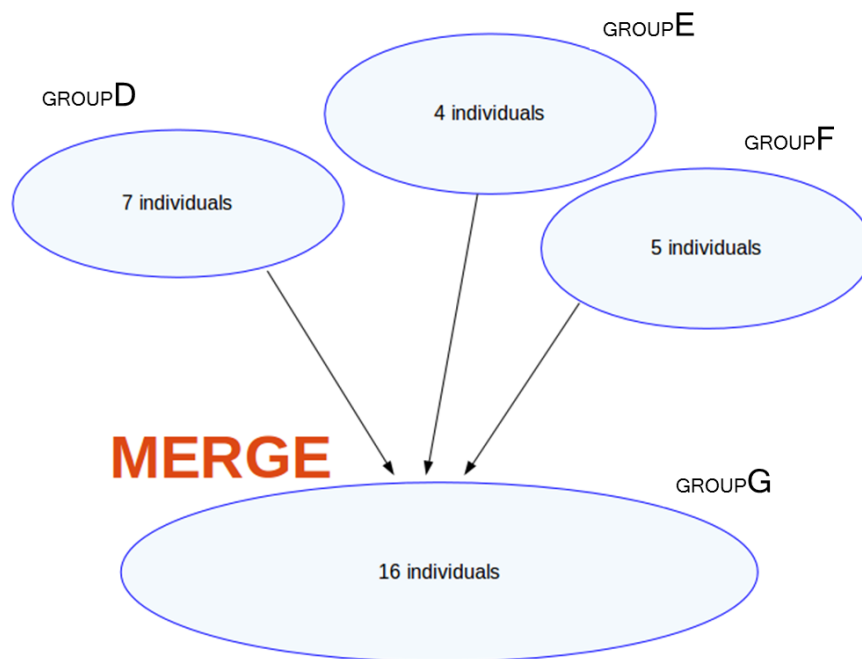


**Figure 6:** pedigree example in which two groups are merged to form 'GROUPC'

We will indicate this in our Excel sheet (using the condensed form) as:

```
GROUPC; GROUP; 11; MERGE; GROUP; ...  
*IDAMS: GROUPC; GROUPA; GROUPB  
*IDAMPROBS: GROUPC; 7; 4
```

In another example (Figure 7), 'GROUPG' is formed as a merge of three groups ('GROUPD', 'GROUPE' and 'GROUPF'). As before, the sum of the individuals from 'GROUPD', 'GROUPE' and 'GROUPF' will form the total of 'GROUPG'.



**Figure 7:** pedigree example in which three groups are merged to form 'GROUPG'

We will indicate this in our Excel sheet as:

```

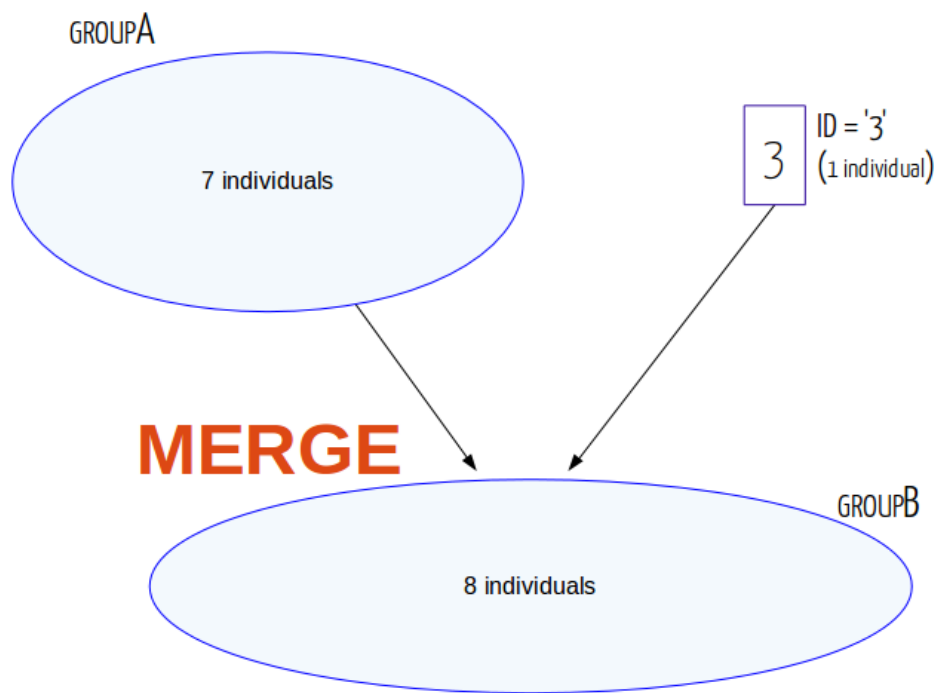
GROUPG; GROUP; 16; MERGE; GROUP; ...
*DAMS: GROUPG; GROUPD; GROUPE; GROUPF
*IDAMPROBS: GROUPG; 7; 4; 5
  
```

- Merge of an all-male group with an all-female group: this is a particular case of merging two groups, where we know with certainty that one of the groups is formed by all males, and the other group is all females. This is called a *sexual merge*. For example, if in Figure 6, GROUPA contains only males and GROUPB contains only females, we have

```

GROUPC; GROUP; 11; MERGE; GROUP; ...
*IDAM: GROUPA; 7
*ISIRE: GROUPB; 4
  
```

- Merge of an individual with an already existing group: As we can see in the pedigree example from Figure 8, an individual (with ID=3) is introduced into 'GROUPA', creating 'GROUPB'.



**Figure 8:** pedigree example in which one group and a single individual are merged to form 'GROUPB'

In the Excel data entry sheet, we can indicate this by:

```
GROUPB; GROUP; 8; MERGE; GROUP; ...
*IDAMS: GROUPB; GROUPA; 3
*IDAMSPROB: GROUPB; 7; 1
```

### *Split*

This term refers to the situation in which a group reproduces and gives birth to a new generation of individuals, or when part of a group is separated from a parental group to form another group or an independent individual.

- The group is formed by reproduction of a parental group. The offspring can either stay in the same enclosure as the parental group (and then the original group will increase in size) or be separated to form a new independent group.

If the offspring stay in the same parental group, the size of the new group (formed by the parents and offspring) has increased. Let's imagine GROUPA, formed by 5 individuals, is the parental group. GROUPA reproduces and gives birth to 4 offspring that stay in the same enclosure as the parents. Now we have GROUPA\_OFFS with a total size of 9 individuals. This is indicated in the Excel sheet as:

```
GROUPA_OFFS; GROUP; 9; SPLIT; GROUP; ...
*IDAM: GROUPA_OFFS; GROUPA; 9
```

GROUPA is eliminated as it does no longer exist:

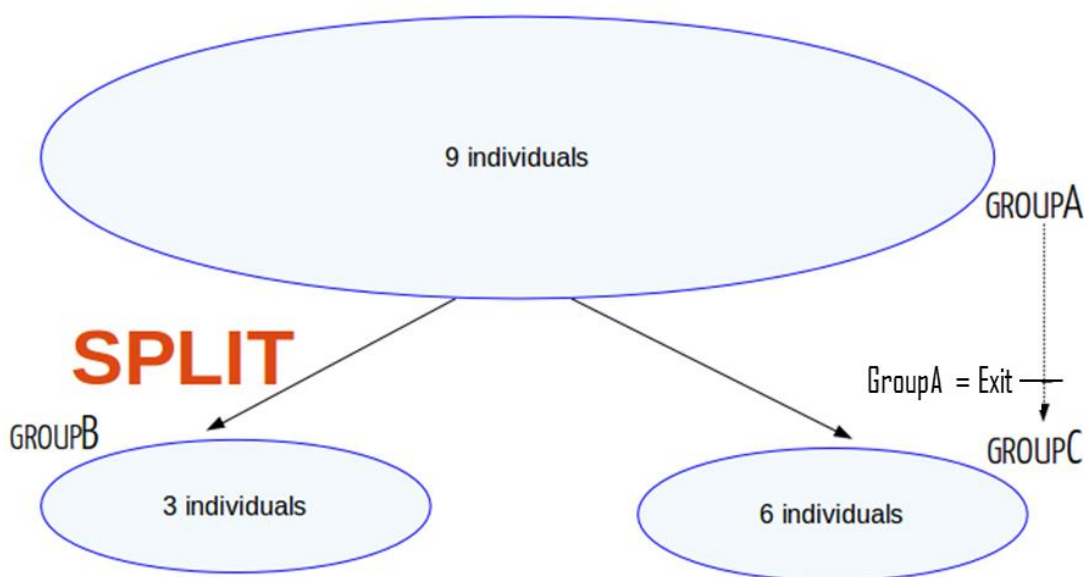
\*IMOVE: GROUPA; ; ; 20070302; ; Exit;

If the offspring are separated from the parents into a new group, we indicate it as creating a new group (GROUPB):

GROUPB; GROUP; 4; SPLIT; GROUP; ...

\*IDAM: GROUPB; GROUPA; 4

- Split a group to form two separated groups: Let's assume that from 'GROUPA', we want to extract 3 individuals and form 'GROUPB'. 'GROUPA' is no longer the same group with the same genetic material, so we denote this new “stage” of 'GROUPA' as a new group 'GROUPC' containing the remaining individuals from 'GROUPA' and eliminate 'GROUPA'.



**Figure 9:** pedigree example in which a group ('GROUPB') is formed by a split from 3 individuals from 'GROUPA'.

In our Excel sheet, we indicate the split of 'GROUPA' in 'GROUPB' and 'GROUPC' as:

GROUPB; GROUP; 3; SPLIT; GROUP; ...

GROUPC; GROUP; 6; SPLIT; GROUP; ...

\*IDAM: GROUPB; GROUPA; 3

\*IDAM: GROUPC; GROUPA; 6

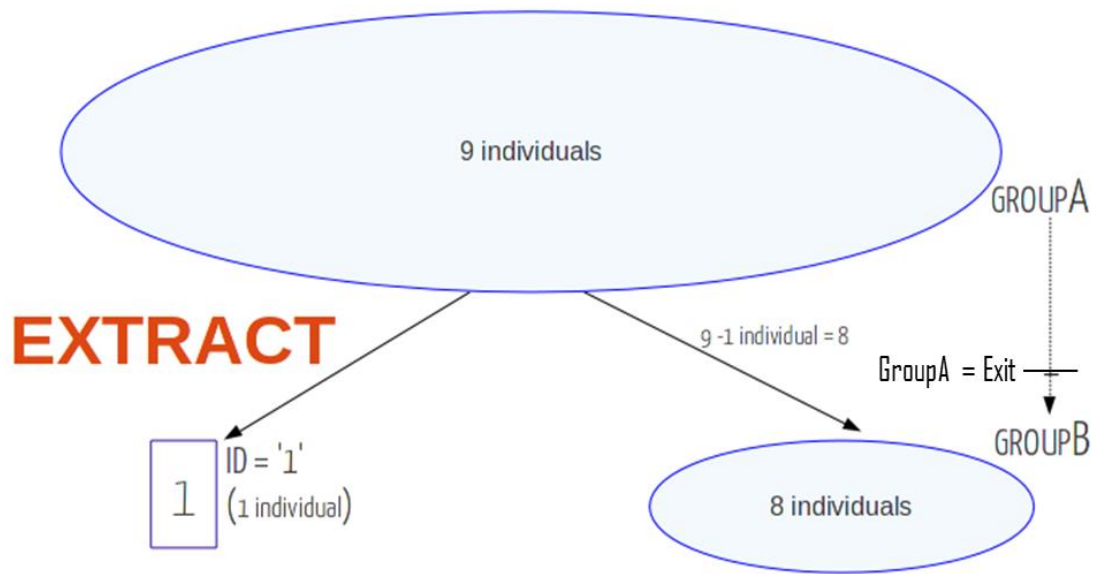
IMOVE: GROUPA; ; ; 20070302; ; Exit

- Split a single individual from a group: we will indicate this by the term EXTRACT (see EXTRACT section below).

### *Extract*

This term refers to an individual that has been separated or extracted from the group it belonged to. This new entity will be assumed to be an individual by PMx.

Let's study this case with the example represented in Figure 10.



**Figure 10:** pedigree example in which an individual is created by an extraction from 'GROUPA'

The individual "1" is extracted from 'GROUPA'. 'GROUPA' no longer has the same genetic information, thus, we create another group ('GROUPB') which is smaller than 'GROUPA' by 1 individual, and eliminate 'GROUPA':

```
1; INDIVIDUAL; 1; EXTRACT; GROUPA; ...
GROUPB; GROUP; 8; SPLIT; GROUP; ...
*IDAM: GROUPB; GROUPA; 8
IMOVE: GROUPA; ; ; 20080305; ; Exit;
```

Note that if GROUPA is left to exist in the data set (i.e., not recorded as EXIT), and GROUPB is never formed, then the remaining GROUPA after the removal of the individual will be assumed to have not changed genetically and to still be of size = 9 diploid individuals.

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## USER MANUAL FOR GROUP MANAGEMENT IN PMx

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### **About this Manual:**

The User Manual for Group Management in PMx was developed as a complement of the User Manual for the software PMx. This version (1.0) is written to describe the characteristics of the Group Management Package (with the group pedigree template and the converter, *group2PMx*) and functionalities of group pedigree analysis in PMx version 1.3.20150612. Periodic changes and revisions will be performed to this User Manual as the functionalities of the Group Management Package and group pedigree analysis in PMx continue to be expanded and updated. This Manual and the Group Management Package are distributed free of charge and are available on: [www.vortex10.org/PMx.aspx](http://www.vortex10.org/PMx.aspx) or <https://sourceforge.net/projects/groupmanagement/>

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Many thanks to the following Manual contributors for useful suggestions:

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**Susan Bailey**

### **Citations.**

The Group-Management Package and *group2PMx* should be cited as:

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Jiménez-Mena, B.; Schad, K. & Lacy, R.C. (2015) User Manual for group management in PMx. Available from <http://www.vortex10.org/PMx.aspx> or <https://sourceforge.net/projects/groupmanagement/>

The PMx software should be cited as:

Ballou, J.D., Lacy, R.C., & Pollak, J.P. (2014) PMx: Software for demographic and genetic analysis and management of pedigreed populations (Version 1.3.20150713). Chicago Zoological Society, Brookfield, Illinois, USA. Available from <http://www.vortex10.org/PMx.aspx>

Lacy, R.C.; Ballou, J.D. & Pollak, J.P. (2012) PMx: Software package for demographic and genetic analysis and management of pedigreed populations. *Methods in Ecology & Evolution* 3:433-437.

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## SECTION 1: Introduction

One of the main aims of zoos and aquariums is to contribute to the conservation of biodiversity by retaining as much genetic diversity of the species as possible, as well as maintaining the sustainability of their *ex situ* collections. This is generally done by registering the information about each individual in the population, their parentage and breeding pairs. Using this pedigree information to design the breeding programs, it is possible to manage the population. However, there are numerous species/taxa that i) cannot be individually identified and ii) are typically managed in tanks/groups and thus the control of matings is complicated (Wang, 2004). Many groups of amphibians, reptiles, fishes, birds and also mammals, such as primates and ungulates (Wang, 2004; Smith, 2010), are group-living organisms. In order to optimally manage these kinds of organisms and address their challenges, zoos and aquariums have worked on extending the use of pedigree analysis for managing groups, in so called *group management* (Leus *et al.*, 2011).

The software PMx (Ballou *et al.*, 2014; Lacy *et al.*, 2012) allows the conservation community to perform demographic and genetic analysis of populations from which pedigree data are available. This program was created to analyze pedigree data from individual records as registered and stored in SPARKS (ISIS, 2012) and PopLink (Faust *et al.*, 2012), but also allows for the analysis of data from group-living organisms. The package described in this manual helps storing and importing group data into PMx. This package consists of:

- (i) a **data entry sheet in Excel** that allows registration of group data, and
- (ii) **group2PMx**, a converter that transforms the Excel file into a .csv file readable by PMx.

Note that the data entry sheet in Excel can also be used for individual records in addition to groups. This will allow conservation managers outside the zoo and aquarium community (without access to SPARKS or PopLink) to have a user-friendly template in Excel in which to register the individuals of the population and still perform an analysis in PMx.

Given a complete and accurate pedigree, individual management is the best strategy to manage a population. In general, one should be aware that group management will not be as accurate as individual management, but it is better than not managing the population at all and thus becomes the recommended strategy for managers of these types of organisms.

## Getting started

### System requirements

*group2PMx.exe* is written in Python 2.7 . It has been tested on Windows XP and 7. *group2PMx* can run on 32-bit or 64-bit processors. For Linux users, the Python script is provided. See the PMx Manual for information about the system requirements of PMx (Traylor-Holzer, 2011).

### Installation

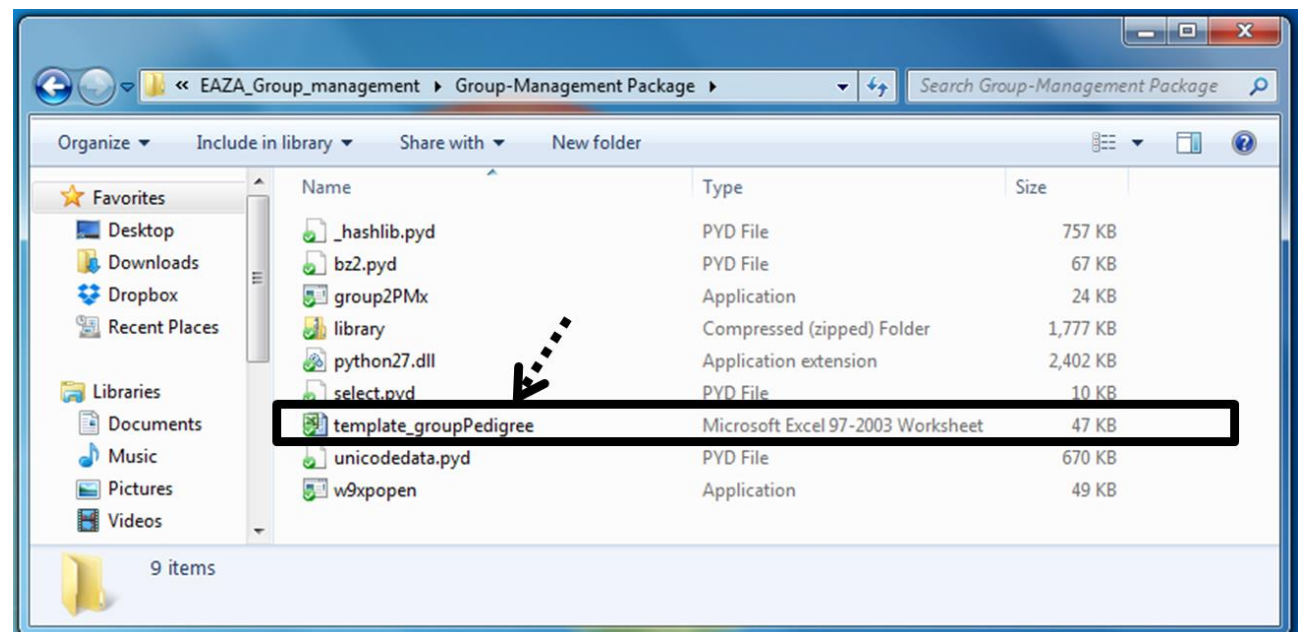
The package is freely available from the website: [www.vortex10.org/PMx.aspx](http://www.vortex10.org/PMx.aspx), or <https://sourceforge.net/projects/groupmanagement/> Click “Save File” and choose the folder where to store it in your computer. Unzip the .zip file.

## SECTION 2: the group data entry sheet template

The group data can be stored in the group data entry sheet template provided in the Group Management Package. In this section, we describe the structure of the data entry sheet and how to fill it in with the group data collected from the population to be managed.

### Location

The Excel spreadsheet *template\_groupPedigree* is found in the main folder of the Group-Management Package.



## Structure of the data entry sheet

Note that the format for some data fields in PMx is more flexible than what is described below. However, to avoid confusion it is better to use the rules given here. For a more complete description of the various formats that can be used with PMx, refer to the PMx manual (Traylor-Holzer, 2011).

### *Header section (blue background)*

The first lines of the spreadsheet correspond to the header where information about the dataset and analysis can be filled in (i.e., species, dates, authorships, etc.). Each line begins with '\*'. The structure must not be modified. As stated in the spreadsheet, the user can add other header lines, if useful, and these should always start with '#'. These header lines are ignored by PMx but can be useful for the manager for clarification. For example, the header line starting with *\*Dates* indicates to PMx the start and end dates for the genetic and demographic analysis, with the following format. For example,

\*Dates: 01/01/1970 <= 28/02/2011

### *Lines required for PMx (purple background)*

The row below *#Name of the fields* (indicated below) should not be erased or modified as it makes reference to the entered data of the group/individual and is needed for the correct function of PMx. Note that this line specifies the sequence of data fields in all individual records, so it is critical that it be included and correct. Each semicolon separates a different column ("," indicates an entry in a new cell in the Excel spreadsheet); we will use this notation throughout the document.

\*FIELDS: ID; Entity; Size; Sire; Dam; Sex; ReproStat; Selected; Living;  
BirthType; DOB; DOBest; DOD; DODest; Location; Rearing; BirthLoc;  
BProgram; BCountry; Necr1; LocalID; Program; Country; Transponder; Tag;  
Tattoo; Color; AsstRep

Several header rows (with first cell as \*MULT, \*MULTPROBS and \*MOVE) describe the format of lines that specify the structure of the parentage data and move records sections. These lines begin with '\*' and are ignored by PMx.

### *Group/Individual entries*

Each group/individual record must be registered in one line/row. The data fields' names from above that are filled in red are required by PMx and thus should be filled for each group/individual. The field columns in blue are not essential and PMx can work without this information. The fields must remain in the given order (see above *Lines required for PMx*). There cannot be any blank rows in this section; a commented line (a row starting with #) can be used instead.

The required entries (in Red) are:

- **ID:** The identifier used for a group/individual throughout the project, typically the studbook number. To avoid errors in computations in PMx, it is required that a group name must start with the letter “G”; the rest is flexible to the User. For instance, a group can be named using the word “GROUP” (lowercase or uppercase) followed by letters (“A”, “B”, etc.). A space can be added between GROUP and the letter, (e.g., “GROUP G”). Whichever option is chosen (“GROUPG”, “GROUP G”, “GroupG”, “Group\_G”), it must be consistent throughout the pedigree because PMx would recognize “GROUPG” and “GROUP G” as different groups.
- **Entity:** This field should be filled with “GROUP” when group-managing a population. If the Entity field is left blank, PMx assumes that the row is an individual.
- **Size:** The number of individuals forming the group. If the Size field is left blank, PMx assumes this to be 1.
- **Sire:** For individuals, this entry corresponds to the unique ID of the sire (male parent), or “WILD” or “UNK” if the individual is wild caught or has an unknown origin. For groups, this entry has a different meaning and corresponds to the breeding type that has generated the creation of the group. The options are “GROUP”, “MERGE”, “SPLIT” (see Section 5 for an explanation of each of these terms). For these, an extra line indicating the parental group name is required to be inserted in the Parentage data section (see below). As for individuals, this entry can also be “WILD” if the group is wild caught.
- **Dam:** For individuals, this corresponds to the unique ID of the dam (female parent), or “WILD” or “UNK” if the dam is wild caught or unknown, respectively. For groups, this entry must always be filled by “GROUP” (see below the explanation for this term) and an extra line indicating the parental group name is required to be inserted in the Parentage data section (see below). Other options are: “WILD” if the group/individual is wild caught.
- **Sex:** The gender of a group/individual. The options are “Female”, “Male”, “Hermaphrodite”, “Abnormal”, “Asexual”, “Unknown” (or “U”) or “Both”. When a group is formed by all females or all males, the sex should be indicated as “Female” or “Male”. Whenever the sex is not known or individuals of both sexes are mixed together, the sex should be indicated as “Unknown” or “Both”.
- **ReproStat:** The reproductive status of a group/individual. The options are: “Fertile” (living individuals that are presumed capable of breeding), “Contracepted” (living individuals contracepted), and “Sterilized” (individuals permanently sterilized). If group/individuals are not listed as “Contracepted” or “Sterilized” in the studbook, they will appear as Fertile in PMx by default, which may or may not be accurate.
- **Selected:** This entry indicates if this group/individual is selected to be part of the breeding program. The options are “True” or “False”. “True” means that it can be used for breeding; “False” means that it should be excluded from genetic calculations on the managed breeding population.
- **Living:** This indicates whether or not the group/individual is currently living



or, alternately, no longer exists in the population. The options are: "True" or "False".

- **BirthType**: The birth origin of the group/individual. The options are: "Wild Born", "Captive Born", "Other", or "Unknown".
- **DOB**: The date of birth or hatch of the group/individual, formatted as `yyyymmdd` (e.g., 15 March 2011 should be entered as 20110315).
- **DOBest**: The date of birth estimate indicates the resolution to which the birth date can be estimated, if it is not a known date. Fields are coded as "Exact" (a blank or "None" is also treated as exact), "U" (for an unknown date), "Y" or "Year" (known only to year), "M" or "Month" (known only to month), or "D" or "Day", with each of Y, M, and D optionally followed by an integer to indicate the number of years, months, or days to which a date is known (e.g., +/- 2 months would be entered as "M2").
- **DOD**: The date of death is the date of the group/individual's actual death even if this occurred outside of the project date span. Date fields in text files must be formatted as `yyyymmdd` (e.g., "20110315").
- **DODest**: The date of death estimate is the resolution to which the death date can be estimated, if it is not a known date. Same format as DOBest (see above).
- **Location**: The current (or last in the case of not living group/ individual) location of the group/individual. The location is usually indicated by the institution's ISIS mnemonic (i.e the mnemonic is "MADRID Z" for Zoo Aquarium de Madrid). If a group/individual left the scope of the project (e.g., was transferred outside the region or association), then Location may not reflect the current living place. It can be left blank.

The optional entries (in Blue) can be deleted by the user if they are not going to be used (and updating the row below *#Name of the fields*, see above *Lines required for PMx*). They are not used for any calculations within PMx, but they can be used for filtering and sorting which animals are displayed in tables in PMx. These optional entries are:

- **Rearing**: The rearing type of the group/individual. The options are: "Parent", "Hand", "Foster", "Peer", "Supplemental", "Unknown", "None", "Colony"/"Group".
- **BirthLoc**: The location of birth or hatch of the group/individual. This can be the institution's ISIS mnemonic (e.g., "MADRID Z" for Zoo Aquarium de Madrid).
- **Bprogram**: The breeding program that the group/individual belongs to at the time of birth.
- **Bcountry**: The country of birth or hatch of the group/individual.
- **Necr1**: This necropsy note indicates any comment related to the necropsy.
- **LocalID**: The local ID of the group/individual used by the institution indicated in the Location field.
- **Program**: The breeding program that the group/individual is currently part of.
- **Country**: The current country where the group/individual is located.
- **Transponder**: The transponder number of the group/individual used by the

- institution indicated in the Location field.
- **Tag**: The tag description of the group/individual used by the institution indicated in the Location field.
- **Tattoo**: The tattoo description of the group/individual used by the institution indicated in the Location field.
- **Color**: The color phase or pattern observed and recorded for the group/individual.
- **AsstRep**: This indicates if any type of assisted reproduction was used to breed the group/individual. The options are: “NotAsstRep” or “AsstRep”.

### *Parentage data section*

Depending on the information given in Sire/Dam, some extra information is needed. If a group is formed by a GROUP, MERGE, or SPLIT (and therefore, Sire = GROUP, MERGE, or SPLIT and Dam=GROUP; see Section 5), information about the parental groups/individuals' ID and the number of individuals contributed by each group must be inserted in this section (note that there are several currently acceptable formats). Instead of the actual count number, it is possible to use a proportion to show how much of the parental group is included here (e.g., 0.3).

The format should be:

```
*IDAM: name of the group/individual; dam1ID; prob1
*IDAM: name of the group/individual; dam2ID; prob2
```

where the *dam IDs* are the IDs of the parental groups and *prob* is the number of individuals or probability (proportional contribution) of each parental group. For example, if GroupM has been formed with 5 and 6 individuals from GroupAAR and GroupCPH, respectively, the parentage line is as follows:

```
*IDAM: GroupM; GroupAAR; 5
*IDAM: GroupM; GroupCPH; 6
```

Instead of listing all parental groups and their contributions on separate lines, we can write the same information in a more condensed format using \*IDAMS (with an 'S') and \*IDAMPROBS:

```
*IDAMS: name of the group/individual; dam1ID; dam2ID
*IDAMPROBS: name of the group/individual; prob2; prob2
```

And the example,

```
*IDAMS: GroupM; GroupAAR; GroupCPH
*IDAMPROBS: GroupM; 5; 6
```

Note that “IDAM” does not explicitly refer to the sex of the individuals; it just indicates the parental group from which the group/individual was generated. In the

case of a SEXUAL MERGE (see Breeding Systems for groups in Section 5) we use both \*IDAM (and \*IDAMS) and \*ISIRE (or \*ISIRES). In this case we actually know that a specific group has only males and another specific group has only females, and we are using both groups to create the new offspring group. Then the user can indicate the extra lines for the parents as follows:

\*IDAM: name of the group/individual; damID; prob

\*ISIRE: name of the group/individual; sireID; prob

Or equivalently:

\*IDAMS: name of the group/individual; dam1ID; dam2ID

\*IDAMPROBS: name of the group/individual; prob2; prob2

\*ISIRES: name of the group/individual; sire1ID; sire2ID

\*ISIREPROBS: name of the group/individual; prob2; prob2

If the number of individuals that form the group or probabilities are not specified (in either style above), they are assumed to be equal across all possible group sires or dams.

### *Move records section*

The record of individuals moved in and out of populations can be inserted in this section with the format indicated below:

\*MOVE: ID;DateIn; DateInEst; InType; DateOut; DateOutEst; OutType; Location; Notes

**ID:** The group/individual identifier.

**DateIn:** The date of the “move/transfer” event. The date fields coded as specified above for DOB and DOD.

**DateInEst:** The resolution to which the DateIn date can be estimated, as detailed before for DOBest and DODest.

**InType:** This indicates how the individual or group entered the population. The options are: “birth”, “capture”, “found” (individual/group that appeared in the exhibit and no one knows how it got there, e.g., an unobserved birth, a wild animal that got into the exhibit, etc.), “import” (individual/group obtained from another institution), “leftentry” or “entry” (individual/group that entered the population sometime after its birth, but it is not recorded previously in the studbook. Differs from “Import” in which there is no specification about where it came from).

**DateOut:** The date when the group/individual left the population. The date fields coded as specified above for DOB and DOD.

**DateOutEst:** The resolution to which the DateOut date can be estimated, as detailed before for DOBest and DODest.

**OutType:** This indicates how the group/individual left the population. The options are: “death”, “release” (individual/group released into the wild), “lost” (there is any information about the individual/group), “export” (sent out of the population to some location that is not included in the

studbook), “rightexit” or “exit” (removed from the population by an unspecified means), or “alive”. In the case of groups, whenever an individual is being merged with a group or other individuals, it should be specified as “exit”.

**Location:** The new location of the group/individual, indicated by the institution’s ISIS mnemonic.

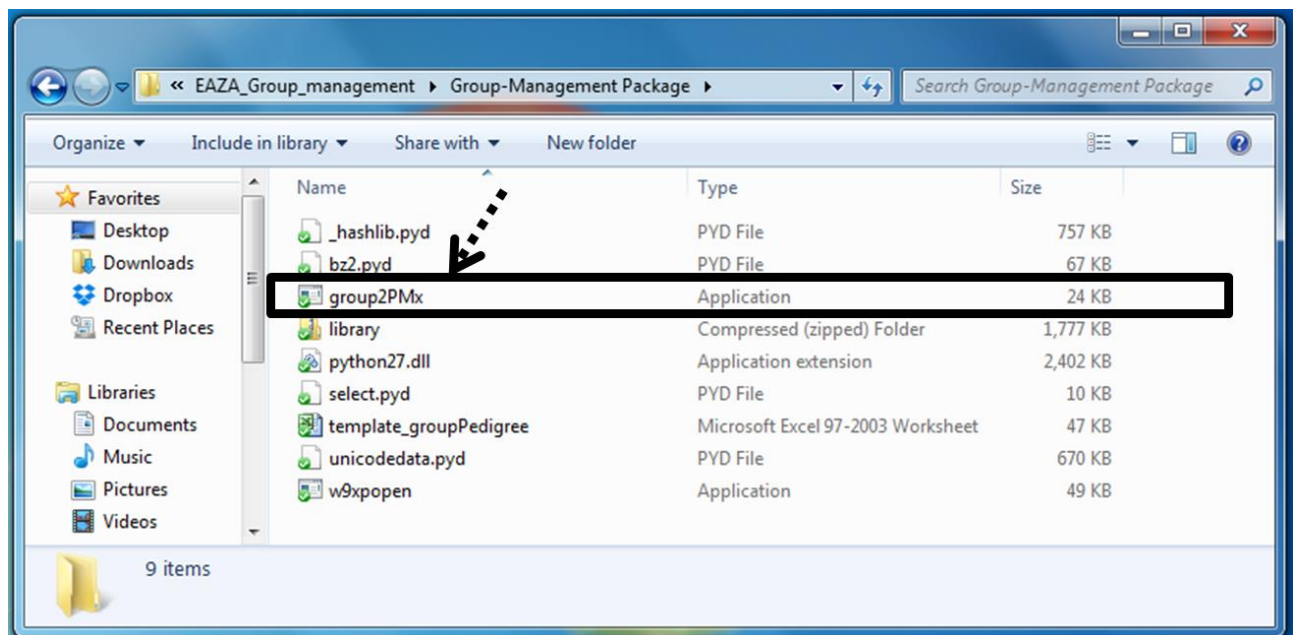
**Notes:** The notes can be any additional text about this group/individual.

## SECTION 3: Importing the group pedigree data into PMx (group2PMx)

In this section, we describe how to convert the Excel data entry sheet filled with the pedigree data into a file readable by PMx. The user needs to run *group2PMx*, which with just one click will easily convert the data.

### Location

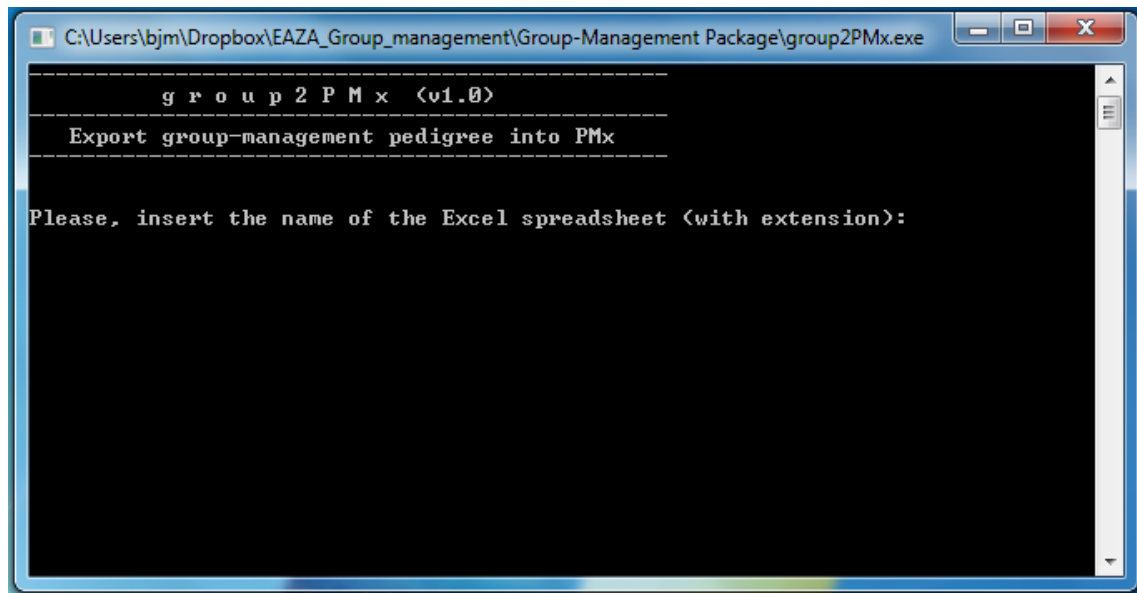
The executable *group2PMx* is located in the Group Management Package.



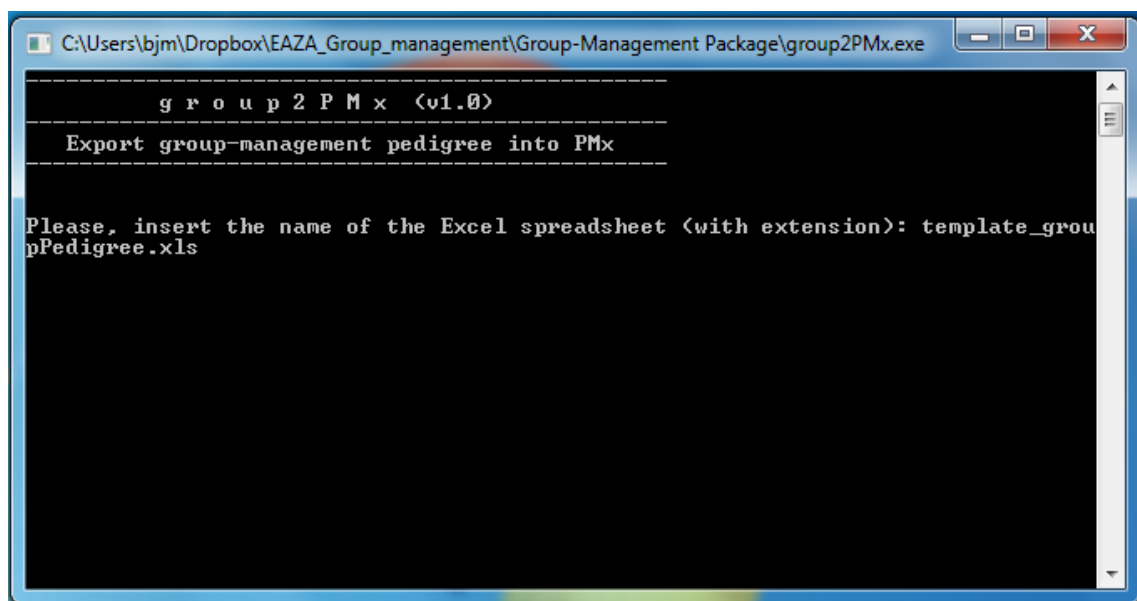
The folder contains other files apart from the *template\_groupPedigree* Excel template and the *group2PMx* executable; these files are required by the converter and should not be deleted or moved.

### Steps to convert the pedigree file

Double-click on *group2PMx*. A black screen will appear where you need to specify the name of the spreadsheet file (do not forget the extension: .xls, .xlsx, etc).

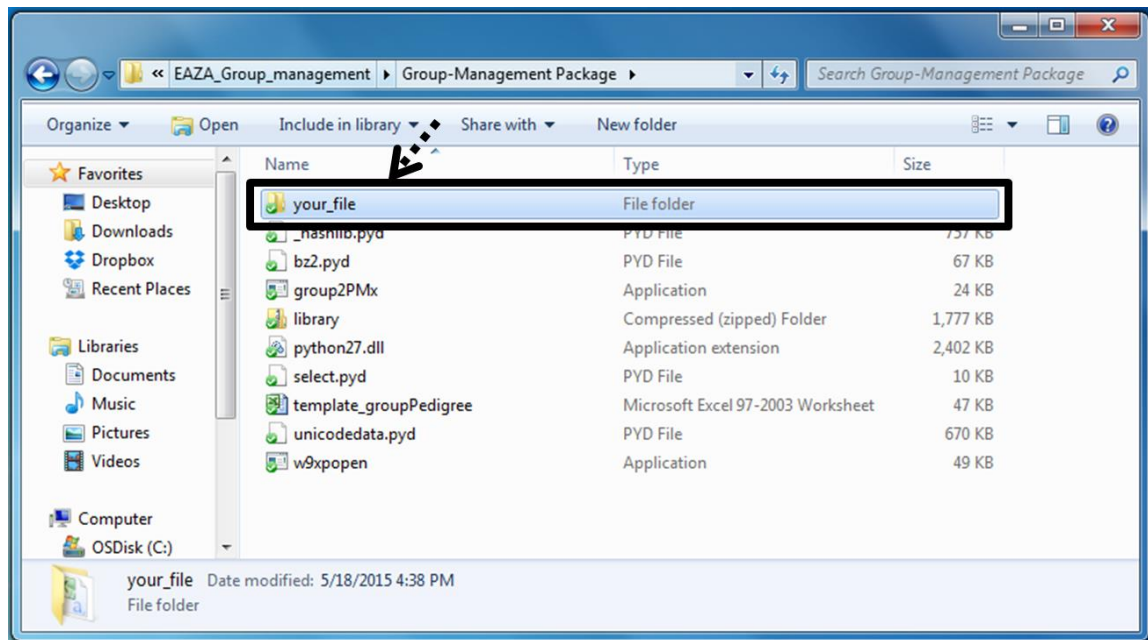


If the spreadsheet is in the same folder as the executable, the user can just provide the name of the file and the extension (for example: "template\_groupPedigree.xls"). If the spreadsheet is in another folder than the executable, the relative path should be provided (for example: C:\Documents\ ... \template\_groupPedigree.xls).

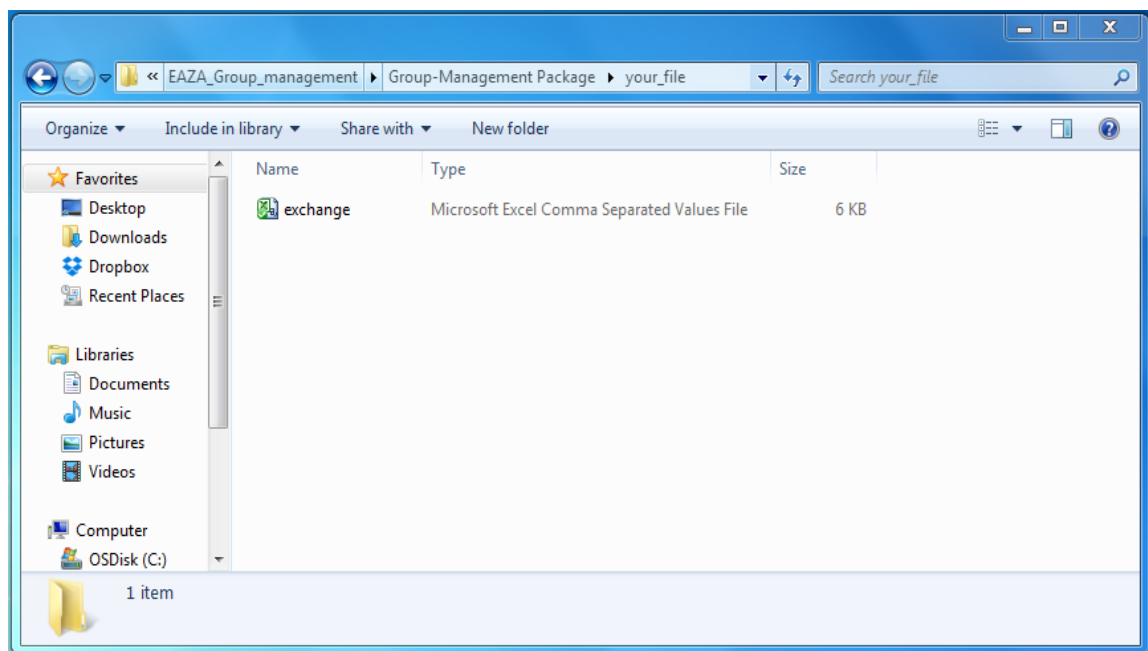


## Output file

After specifying the correct path and name of the file, a subfolder, "your\_file", should have been created. If the subfolder does not appear, try to reload the main folder.



The exchange file generated by *group2PMx* should be inside the subfolder “your\_file”.



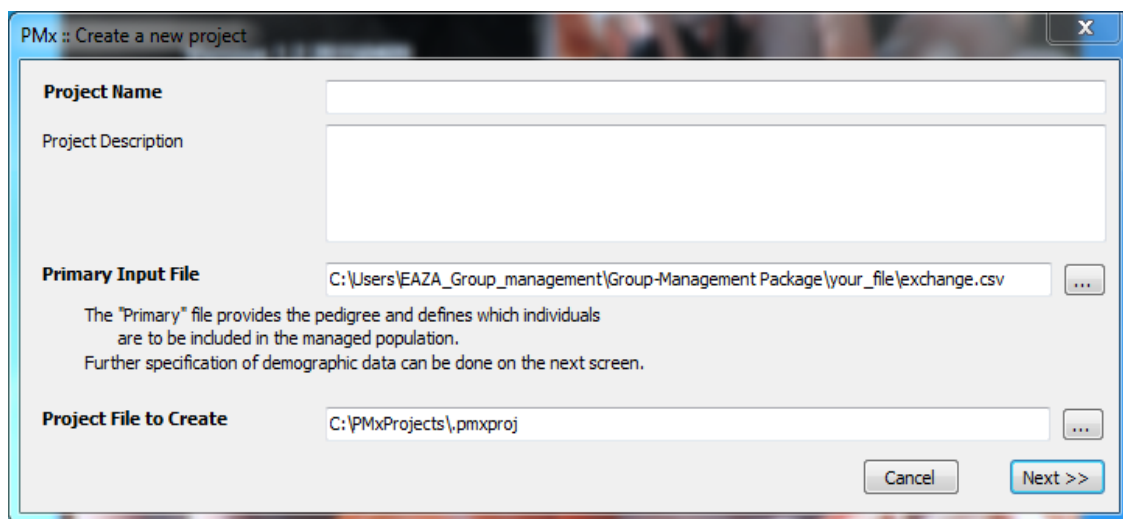
## SECTION 4: Creating a project in PMx from the converted file

Here we summarize the steps to start using PMx with our data and how to create a project. The information found below has been obtained and adapted from the PMx manual (Traylor-Holzer, 2011).

1. The software PMx and the Manual, if not installed yet, can be downloaded from: <http://www.vortex10.org/PMx.aspx>
2. Once PMx is installed on your computer, open it.



3. Select *New Project* and create a project name.
4. The exchange.csv file can now be used directly in PMx as the “Primary input file”. Then click on *Next*.

The image shows a screenshot of the "PMx :: Create a new project" dialog box. It has a title bar with a close button (X). The dialog contains several fields and buttons. At the top, there is a "Project Name" field and a "Project Description" field. Below these, there is a "Primary Input File" field with the path "C:\Users\EAZA\_Group\_management\Group-Management Package\your\_file\exchange.csv" and a browse button (...). A note below this field states: "The 'Primary' file provides the pedigree and defines which individuals are to be included in the managed population. Further specification of demographic data can be done on the next screen." At the bottom, there is a "Project File to Create" field with the path "C:\PMxProjects\pmxproj" and a browse button (...). There are two buttons at the bottom right: "Cancel" and "Next >>".



5. No *Demography* or *Additional Optional Input File* needs to be specified because enough information is already contained in the spreadsheet (the *Primary Input File - exchange.csv*). See Traylor-Holzer (2011) to read more about other Input files.
6. Click on *Create*. Once PMx opens to the initial **Project Notes** screen, select *File > Save Project*.

PMx :: Create a new project

Demography Input Files (Optional -- specify files if the population view for demography is to be different than for genetics)

☒ Life tables in .PRN format

Female

Male

☐ Move records in .CSV format

for Demography

for Genetics

☐ Move records in .MOV format

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

**Additional Optional Input Files**

Census

Associations

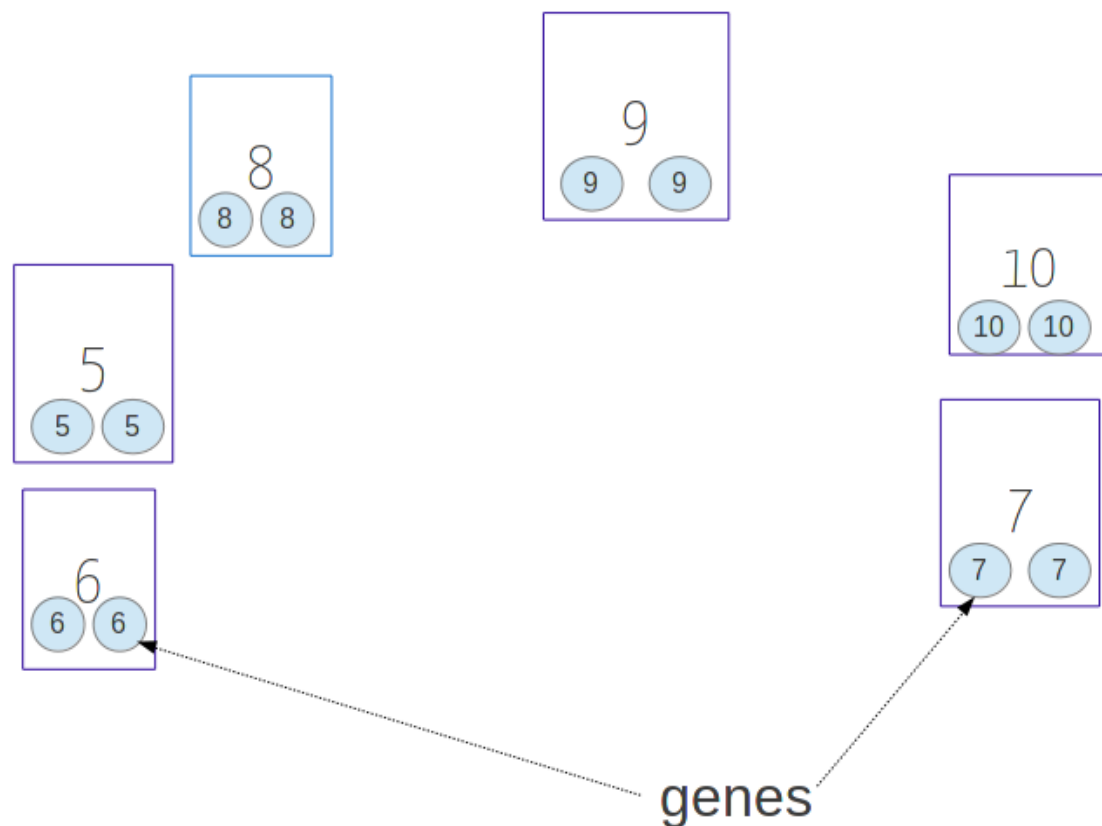
<< Back Cancel Create

## SECTION 5: Navigating into pedigree analysis of group management

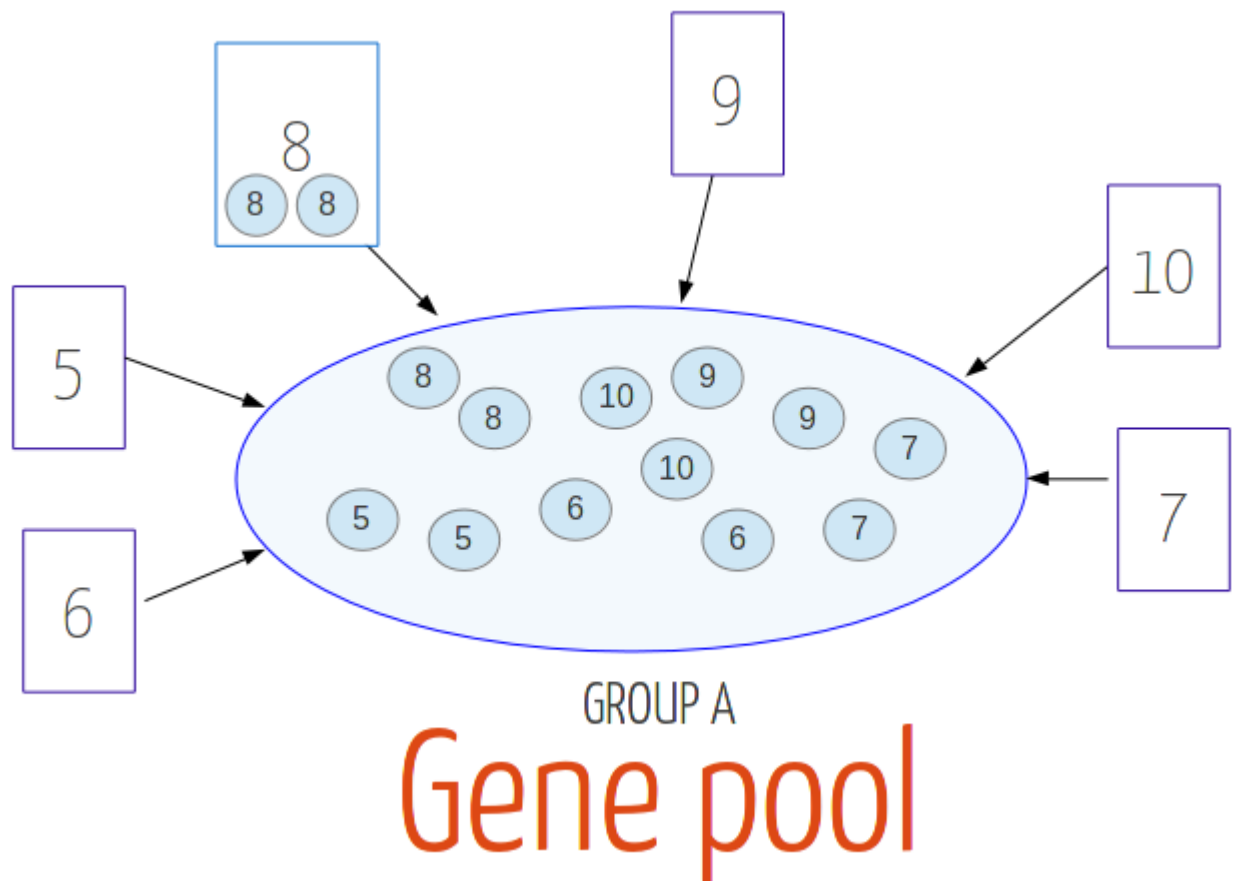
### Understanding group management

Like individual management, group management is based on the theory of population genetics. It is important to note that once we define a group containing some individuals, we no longer speak about individuals, but instead about a virtual set of genes coming from those individuals. That is exactly the definition of a 'group' in group management: a gene pool of the genes from the individuals. The information about which genes belong to which individual is not used. Any entity can form a group, i.e. with any ploidy (e.g. haploid, diploid, tetraploid). For convenience, here we describe all of the concepts in terms of groups that consist of diploid individuals.

When we include several individuals/groups in the same enclosure to form a new group (for example, 'GROUPA', formed by individuals with studbook IDs 5, 6, 7, 8, 9 and 10), assuming all the individuals are different from one another and are diploid, the individuals contribute their genes to the gene pool as in Figures 2 and 3.



**Figure 2:** basic scheme representing the genes of the individuals 5, 6, 7, 8, 9, 10



**Figure 3:** representation of the individuals contributing to form the gene pool that corresponds to groupA. The six individuals are diploid and contribute with two genes to the gene pool. Just for representation, we indicate individual 8 with the two genes on it.

## Breeding systems of groups

Computations of genetic parameters for groups in PMx are different depending on the breeding system used to form the offspring group.

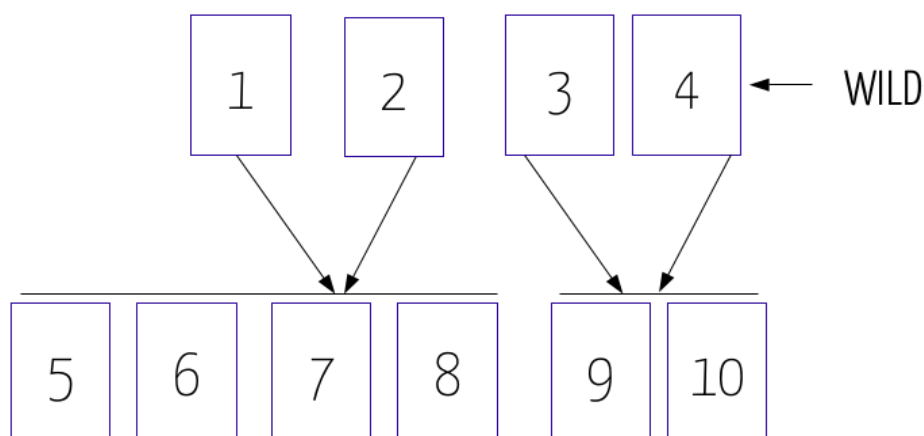
The different breeding systems are MERGE, SPLIT and EXTRACT, detailed below.

### *Merge*

In general, this term refers to the union of individuals or existing groups to form a single group.

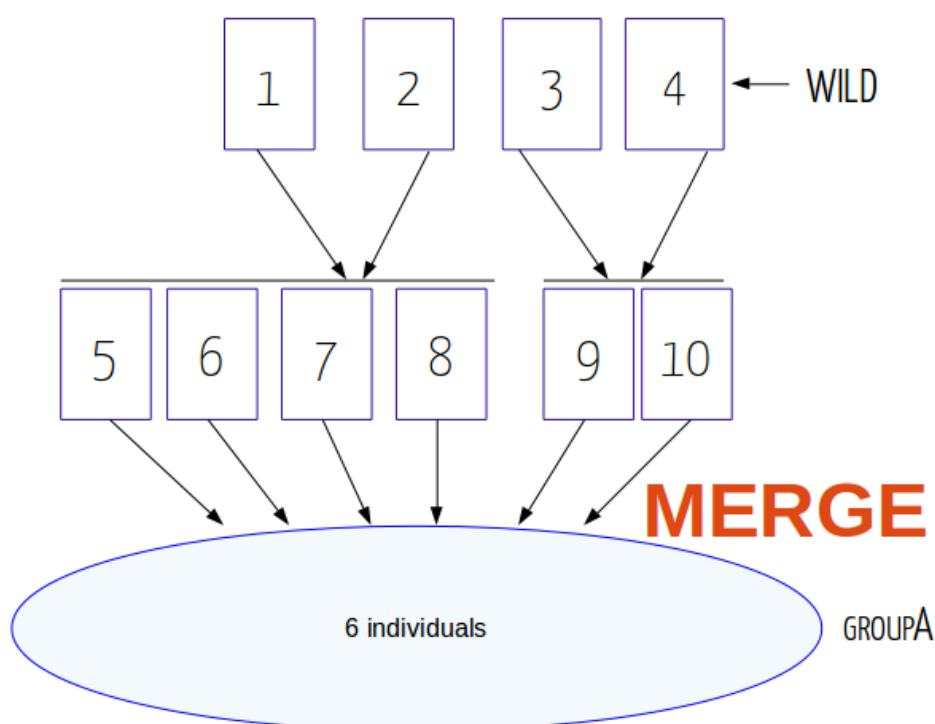
We present five management situations where the field 'Sire' should be filled in with MERGE:

- Merge of individuals: let's study the pedigree example represented in Figure 4.



**Figure 4:** example of a pedigree describing the relationship between ten individuals with ID 1-10. Individuals are represented by square symbols. Generations are connected by a vertical line.

Wild-origin individuals 1, 2, 3, and 4 have given birth to offspring 5, 6, 7, 8, 9, and 10 (Figure 4). Let's imagine we want to form a group with all the offspring and name it 'GROUPA' (Figure 5).



**Figure 5:** pedigree example in which the individuals 5, 6, 7, 8, 9, 10 are merged to form 'GROUPA'

The data from Figure 5 would be entered in the condensed form as follows:

GROUPA; GROUP; 6; MERGE; GROUP; ...

\*IDAMS: GROUPA; 1; 2; 3; 4

\*IDAMPROBS: GROUPA; 2; 2; 1; 1

Or

GROUPA; GROUP; 6; MERGE; GROUP; ...

\*IDAM: GROUPA; 1; 2

\*IDAM: GROUPA; 2; 2

\*IDAM: GROUPA; 3; 1

\*IDAM: GROUPA; 4; 1

Note that it would also work to first create individuals 5, 6, 7, 8, 9, and 10 from their parents, and then create GROUPA by merging those 6 individuals (each described as a “Dam” of GROUPA).

The above entries use number of individuals, but they can be transformed to probabilities by dividing by 6, the total size of 'GROUPA'.

GROUPA; GROUP; 6; MERGE; GROUP; ...

\*IDAMS: GROUPA; 1; 2; 3; 4

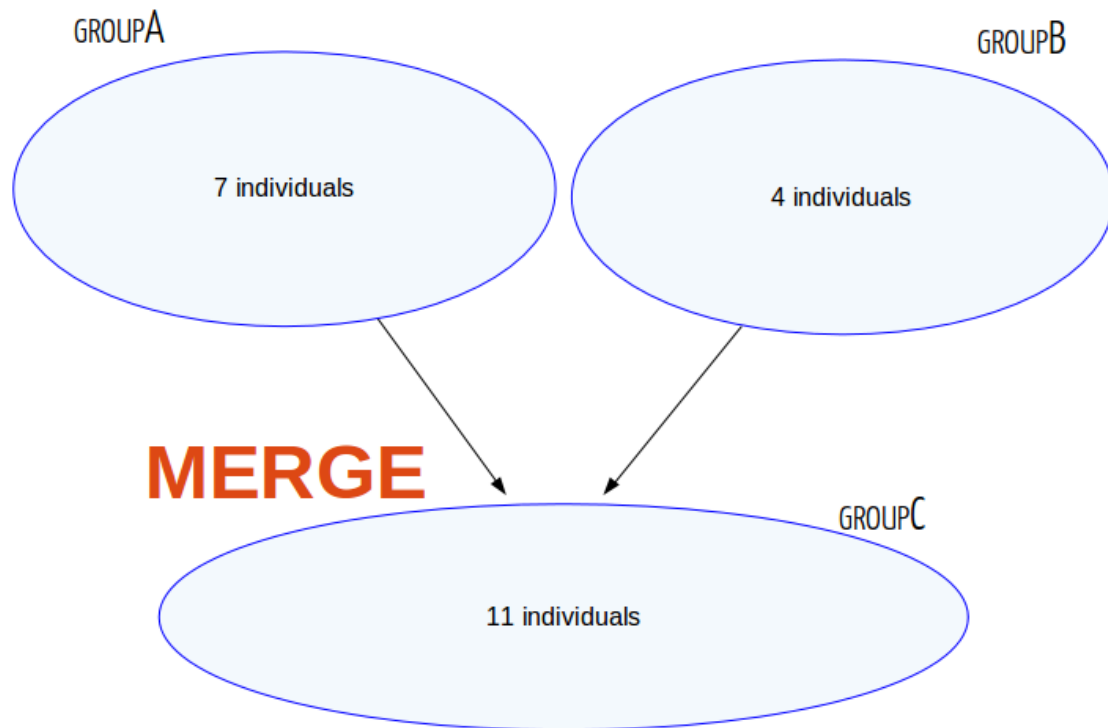
\*IDAMPROBS: GROUPA; 0.33; 0.33; 0.16; 0.16

## EXIT

As a consequence of the merge, the individuals of Figure 5 included in 'GROUPA' (5, 6, 7, 8, 9, 10) are no longer identifiable. Therefore, we need to include 'MOVE' rows indicating that the individuals have “Exited” the population. Below is an example of one of the MOVE rows (one row per individual for more information about the information to add in the “MOVE” row, see *Section 2 -extra lines “MOVE” row*). The date corresponds to the date in which 'GROUPA' was formed.

IMOVE: 3; ; ; 20060302; ; Exit;

- Merge of two or more groups: in Figure 6, 'GROUPC' is formed as a merge of two groups ('GROUPA' and 'GROUPB'). The sum of the individuals from 'GROUPA' and 'GROUPB' will form the total of 'GROUPC'.

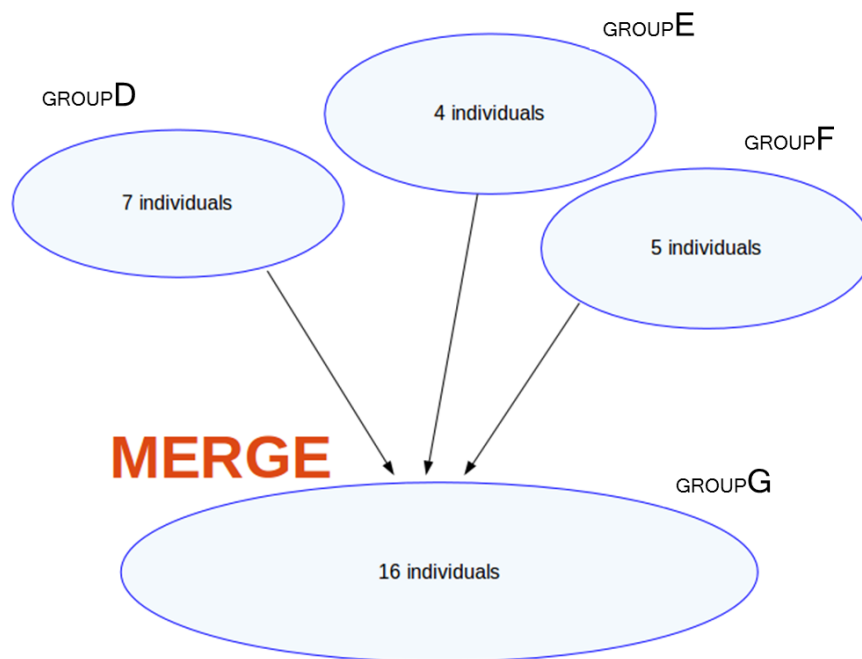


**Figure 6:** pedigree example in which two groups are merged to form 'GROUPC'

We will indicate this in our Excel sheet (using the condensed form) as:

```
GROUPC; GROUP; 11; MERGE; GROUP; ...  
*IDAMS: GROUPC; GROUPA; GROUPB  
*IDAMPROBS: GROUPC; 7; 4
```

In another example (Figure 7), 'GROUPG' is formed as a merge of three groups ('GROUPD', 'GROUPE' and 'GROUPF'). As before, the sum of the individuals from 'GROUPD', 'GROUPE' and 'GROUPF' will form the total of 'GROUPG'.



**Figure 7:** pedigree example in which three groups are merged to form 'GROUPG'

We will indicate this in our Excel sheet as:

```

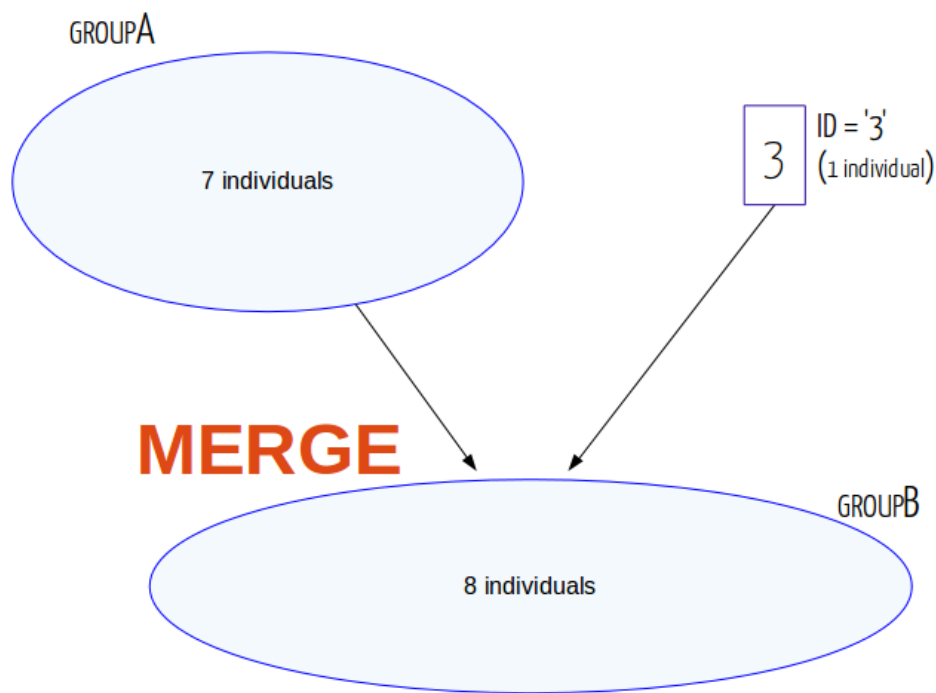
GROUPG; GROUP; 16; MERGE; GROUP; ...
*DAMS: GROUPG; GROUPD; GROUPE; GROUPF
*IDAMPROBS: GROUPG; 7; 4; 5
  
```

- Merge of an all-male group with an all-female group: this is a particular case of merging two groups, where we know with certainty that one of the groups is formed by all males, and the other group is all females. This is called a *sexual merge*. For example, if in Figure 6, GROUPA contains only males and GROUPB contains only females, we have

```

GROUPC; GROUP; 11; MERGE; GROUP; ...
*IDAM: GROUPA; 7
*ISIRE: GROUPB; 4
  
```

- Merge of an individual with an already existing group: As we can see in the pedigree example from Figure 8, an individual (with ID=3) is introduced into 'GROUPA', creating 'GROUPB'.



**Figure 8:** pedigree example in which one group and a single individual are merged to form 'GROUPB'

In the Excel data entry sheet, we can indicate this by:

```
GROUPB; GROUP; 8; MERGE; GROUP; ...
*IDAMS: GROUPB; GROUPA; 3
*IDAMSPROB: GROUPB; 7; 1
```

### *Split*

This term refers to the situation in which a group reproduces and gives birth to a new generation of individuals, or when part of a group is separated from a parental group to form another group or an independent individual.

- The group is formed by reproduction of a parental group. The offspring can either stay in the same enclosure as the parental group (and then the original group will increase in size) or be separated to form a new independent group.

If the offspring stay in the same parental group, the size of the new group (formed by the parents and offspring) has increased. Let's imagine GROUPA, formed by 5 individuals, is the parental group. GROUPA reproduces and gives birth to 4 offspring that stay in the same enclosure as the parents. Now we have GROUPA\_OFFS with a total size of 9 individuals. This is indicated in the Excel sheet as:

```
GROUPA_OFFS; GROUP; 9; SPLIT; GROUP; ...
*IDAM: GROUPA_OFFS; GROUPA; 9
```

GROUPA is eliminated as it does no longer exist:



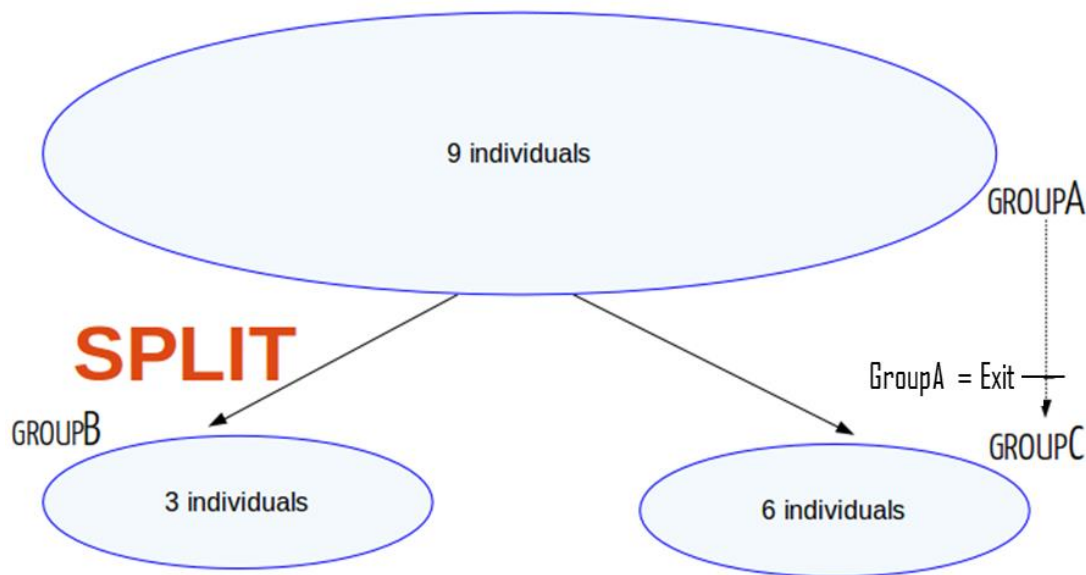
\*IMOVE: GROUPA; ; ; 20070302; ; Exit;

If the offspring are separated from the parents into a new group, we indicate it as creating a new group (GROUPB):

GROUPB; GROUP; 4; SPLIT; GROUP; ...

\*IDAM: GROUPB; GROUPA; 4

- Split a group to form two separated groups: Let's assume that from 'GROUPA', we want to extract 3 individuals and form 'GROUPB'. 'GROUPA' is no longer the same group with the same genetic material, so we denote this new “stage” of 'GROUPA' as a new group 'GROUPC' containing the remaining individuals from 'GROUPA' and eliminate 'GROUPA'.



**Figure 9:** pedigree example in which a group ('GROUPB') is formed by a split from 3 individuals from 'GROUPA'.

In our Excel sheet, we indicate the split of 'GROUPA' in 'GROUPB' and 'GROUPC' as:

GROUPB; GROUP; 3; SPLIT; GROUP; ...

GROUPC; GROUP; 6; SPLIT; GROUP; ...

\*IDAM: GROUPB; GROUPA; 3

\*IDAM: GROUPC; GROUPA; 6

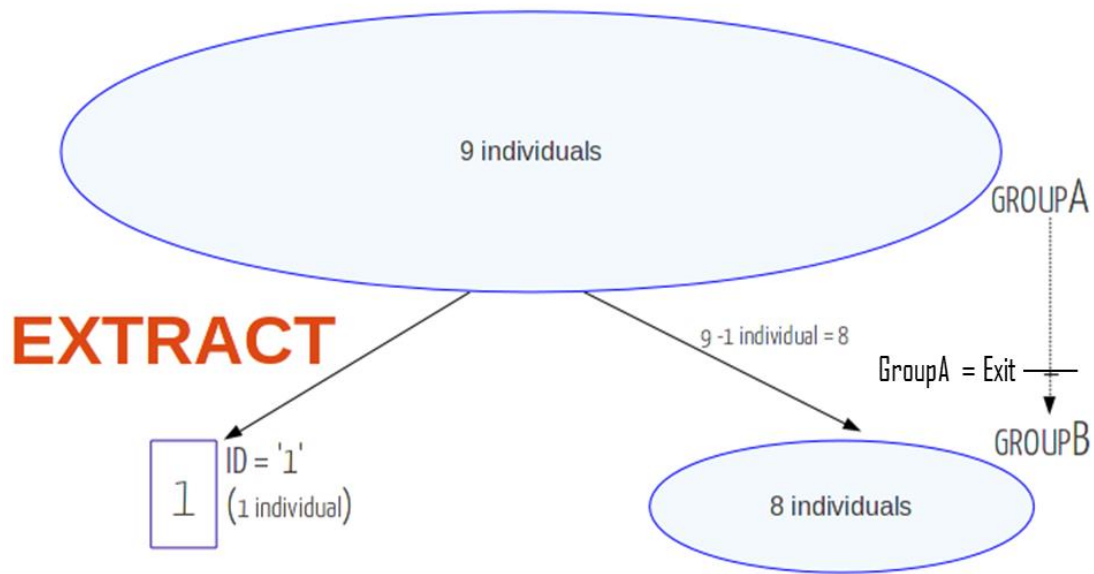
IMOVE: GROUPA; ; ; 20070302; ; Exit

- Split a single individual from a group: we will indicate this by the term EXTRACT (see EXTRACT section below).

### *Extract*

This term refers to an individual that has been separated or extracted from the group it belonged to. This new entity will be assumed to be an individual by PMx.

Let's study this case with the example represented in Figure 10.



**Figure 10:** pedigree example in which an individual is created by an extraction from 'GROUPA'

The individual "1" is extracted from 'GROUPA'. 'GROUPA' no longer has the same genetic information, thus, we create another group ('GROUPB') which is smaller than 'GROUPA' by 1 individual, and eliminate 'GROUPA':

```
1; INDIVIDUAL; 1; EXTRACT; GROUPA; ...
GROUPB; GROUP; 8; SPLIT; GROUP; ...
*IDAM: GROUPB; GROUPA; 8
IMOVE: GROUPA; ; ; 20080305; ; Exit;
```

Note that if GROUPA is left to exist in the data set (i.e., not recorded as EXIT), and GROUPB is never formed, then the remaining GROUPA after the removal of the individual will be assumed to have not changed genetically and to still be of size = 9 diploid individuals.

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