

Select how you are submitting data.

## File Type

- ☒ Excel  
☐ Text

## File Content

- ☒ Pedigree(s) file only; genotypes not provided  
☐ Pedigree(s) and genotypes in one file  
☐ Pedigree(s) and genotypes in separate files  
☐ Breeders only; pedigree obtained from database

## Select Pedigree File

Browse...

No file selected

## Minimum Parent Age (years)

4.0

Read and Check Pedigree

☐ Debug on

## Input File Handling:

- This software requires an input file for each breeding colony to be analyzed. Multiple separate pedigrees within the same breeding colony can be accommodated within the same input file.
- If an animal is missing information on one parent, that cell should be blank. For animals with no information on either parent, both cells under "Sire ID" and "Dam ID" should be blank. For animals with information on one parent a unique "placeholder" ID (designated as UnkownID and UnkID in Pedigree Brower tab) will be assigned by the software to represent the unknown parent. *Please be aware that animals with no parents will be treated as founders in these calculations, i.e., sources of new genetic variation in the colony.*
- Genotypic information for a single locus can be included in the genetic analyses. See Pedigree File Format and Genotype File Format below for file descriptions. Observed genotypic information can be supplied for any members of the pedigree. Designation of two alleles is required as currently there is no accommodation for partial genetic information for an individual. Please contact R. Mark Sharp (mailto:rmsharp@me.com?)

Subject=nprcmanager:%20Need%20to%20allow%20partial%20genetic%20information) if you need to be able to enter partial genetic information.

## Pedigree File Format Details:

The following columns names are reserved and will be recognized:

*Ego ID*, *Sire ID*, *Dam ID*, and *Sex* are required columns.

Either *Age* or *Birth* must also be provided.

- Use the Allowable Names listed in the table below. Allowable Name case and order are not significant. The first Allowable Name listed for each column is the name used internally and is the name used in examples and output.
- If the *Age* column is provided, the program will use the user-specified age.
- Otherwise, the program will calculate age based on the *Birth* column and the current date, or the *Death*, *Departure*, or *Exit* columns, if provided.
- *Exit* dates, if provided, will supercede *Death* and *Departure* dates. If *Exit* is not provided, *Death* and *Departure* will be combined based on which date is chronologically first. (This functions primarily to catch clerical errors or historical changes in record-keeping practices).
- Dates should be in the format YYYY-MM-DD (this date option can be found under the "English-U.K." locale option under the "Format Cells -> Number -> Date" menu in Excel 2010).
- Genotype data may be supplied within the pedigree file or in a separate genotype file. Only two additional columns (*first* and *second*) are required when the genotypes are provided within the pedigree file. The columns are described below.

Allowable Name	Description of Information	Data Format
id, egoid, ego_id	Ego ID: Unique animal identifier	Alphanumeric characters (no symbols)
sire, sireid, sire_id	Sire ID: Unique identifier of the ego's father	Alphanumeric characters (no symbols)
dam, damid, dam_id	Dam ID: Unique identifier of the ego's mother	Alphanumeric characters (no symbols)
sex	Sex: Ego's sex	Sex can be indicated by any of the following: Male: ("male", "m", "1"), Female: ("female", "f", "2"), Unknown: ("unknown", "u", "3"), Hermaphrodite: ("hermaphrodite", "h", "4")
age	Age: Age at exit, or current age of the ego.	Age in decimal years
birth, birthdate, birth_date	Birth: Ego's date of birth	YYYY-MM-DD Format
death	Death: Ego's date of death	YYYY-MM-DD Format

departure	Departure: Ego's date of sale	YYYY-MM-DD Format
exit	Exit: Ego's date of exit from the colony. (Supercedes Death or Departure information)	YYYY-MM-DD Format
allele_1	Allele 1: Alphanumeric representation of first allele	Currently limited to alphanumeric values, underscores, spaces and dashes. Other characters have not been tested.
allele_2	Allele 2: Alphanumeric representation of second allele	Currently limited to alphanumeric values, underscores, spaces and dashes. Other characters have not been tested.

- You will need to save your input file as a plain text file (either .txt or .csv), in order to upload it correctly. To do this, you may use the "Save As" function in Excel to save a spreadsheet in a "tab-delimited" or "comma-delimited" file format.
- Select the correct file type, and then click on "Select Input File" to upload the file.
- *The pedigree information displayed in the Pedigree Browser will not appear exactly the same as the input file.* The pedigree shown in the Pedigree Browser has been built using input file contents that may be used to produce other columns of information displayed. Input file processing will include:
  - A check for the 4 required fields: Ego ID, Sire ID, Dam ID, and Sex.
  - A check for either Age or Birth information.
  - A new row entry will be added for any Sire or Dam that do not already have their own row as an Ego.
  - Animals will be checked to ensure that their sex is consistent throughout the file.
  - Duplicate rows will be removed.
  - If Death or Departure date columns have been included, an "Exit" column will be built. Otherwise, Exit date assignment will be skipped if an Exit date column was provided in the input file.
  - If Birth dates have been included, age will be calculated as  $(\text{Birth Date} - \text{Exit Date}) / 365.25$ . If no Death, Departure, or Exit dates are provided, it is assumed that the ego is still alive, and Age will be calculated as  $(\text{Birth Date} - \text{Today's Date}) / 365.25$ . Age calculation will be skipped if an Age information column is included in the input file.
  - Generation numbers will be added to each ego.
  - Families (Pedigrees) will be numbered and this information will be added to each ego.

## Genotype File Format Details:

The following columns names are reserved and will be recognized:

Columns *id*, *first\_name*, and *second\_name* are required columns.

Columns *first* and *second* will be automatically generated and cannot be present.

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- Use the Allowable Names listed in the table below. Allowable Name case and order are not significant. The Allowable Name listed for each column is the name used internally and is the name used in examples and output.
- Genotype data can be supplied within the pedigree file or in this genotype file. Only two additional columns (*first* and *second* are required when the genotypes are provided within the pedigree file. See table above for a description. The genotype file columns are described below.

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Allowable Name	Description of Information	Data Format
id	ID: Unique animal identifier	Alphanumeric characters (no symbols)
allele_1	Allele 1: Alphanumeric representation of first allele	Currently limited to alphanumeric values, underscores, spaces and dashes.
allele_2	Allele 2: Alphanumeric representation of second allele	Currently limited to alphanumeric values, underscores, spaces and dashes. Other characters have not been tested.

- You will need to save your genotype file as a plain text file (either .txt or .csv), in order to upload it correctly. To do this, you may use the "Save As" function in Excel to save a spreadsheet in a "tab-delimited" or "comma-delimited" file format.
- Select the correct file type, and then click on "Select Genotype File" to upload the file.