

A short tutorial for Familias

Introduction

Familias is a program for computing probabilities for pedigrees. We assume one has measured the alleles of two or more persons at some loci, and that the frequencies and other properties of these alleles in the general population are known. The likelihoods of different pedigrees can then be computed, and likelihood ratios (the “Paternity Index”) can be output. If a prior distribution on the possible pedigrees is given, the posterior is output. The program can even generate lists of possible pedigrees, based on user input.

The data can be input into the program interactively, or via specific file formats. The data may be saved to file or read from file at any time. For example, data like allele frequencies and mutation rates may be input once and saved to files, and then later be input from these files. At the end, several types of reports giving overviews of the computation may be generated.

Overview of use

A standard use of the program may consist of following these steps:

1. Add data about the allele system frequencies and properties by clicking on the icon depicting a document. Data can be read in using the “Add” button, or the “Read from file” button (see the [manual](#) for file formats). It is smart to save this data to a file (using the diskette icon) before continuing, for later re-use.
2. Add the relevant persons, that is, the persons for whom you have DNA data, and possibly additional persons that are needed to define specific relationships between these. This is done with the person form, obtained by clicking on the yellow face on the tool bar. For a standard paternity case, the mother, putative father, and child should be defined here.
3. Add the fixed, known relationships between the persons added in the previous step. This is done with the fixed relations form, obtained by clicking on the red and yellow icon on the tool bar. For a standard paternity case, the parent-child relationship between the mother and the child is added.
4. Add the DNA information for the persons in this particular case, by clicking on the next icon (the lab tray).
5. At this point, it is again smart to save your data, possibly to a differently named file.
6. You are now ready to consider the alternative pedigrees, using the last icon on the tool bar. The simplest approach is to use the “Add” button to construct each of the pedigrees you want to compare: Usually, there are two alternative pedigrees. In a standard paternity case, you would generate one pedigree with no

added relationships (containing only the mother-child relationship added as fixed above) and one pedigree with the added parent-child relationship between the putative father and the child. To make the computations, hit the “Probability” button on the “Pedigrees” box. The value 1 will be listed after the first pedigree, while the second (and following) pedigree will be followed by its likelihood ratio compared to the first pedigree. Various buttons may be used to investigate the results further, and various reports may be output: See the [manual](#) for details.

An example

The easiest use for the program is for standard paternity cases. However, here we present a more complex example. A woman M has 3 sons S1, S2, and S3, and the question is if a putative father PF is the father of all, some, or none of these sons. DNA data is available for S1, S2, S3, and PF. Data from 8 loci is given. In all loci, all alleles have frequency 0.05. The alleles observed in the data are numbered 1,2,3,4. With this notation, S1, S2, S3 and PF have observations given in the table below:

Locus	S1	S2	S3	PF
sys1	1,2	3,4	3,4	1,3
sys2	1,2	3	1,2	2,3
sys3	1,2	3,4	1,2	1,4
sys4	1,2	3,4	3,4	1,4
sys5	1,2	3,4	3	1,3
sys6	1	1,2	3	1,3
sys7	1,2	1,2	3,4	2,3
sys8	1,2	2,3	3,4	2,3

Let us start with entering the general allele information. Click on the icon looking like a rolled-up document, and the “General DNA Data” form appears. This form gives an overview of the allele systems entered. To enter a new system, click on “Add”. The “Allele system” form appears. Each of the alleles in the system must be entered by entering a name and a frequency in the lowest fields, followed by clicking “Add”. Only alleles that appear in the case-related data need to be explicitly entered, so that the frequencies need not sum to 1. Note that the tab button may be useful. When the four alleles 1,2,3,4 have been entered, click on OK, and the system appears in the “General DNA Data” form. Continue with the other 7 systems. At this point, it may be a good idea to save the current information entered to a file. This is done by clicking on the floppy disc icon. If you are lazy, you can also download the finished file [here](#), and read it into the

program using the “opening folder” icon. Note that data may also be read in using a standardized file format; see the [manual](#).

We continue with entering the relevant persons. Start by clicking on the yellow and green face icon. The “Persons” form appears. Write in “S1” in the “Person” field, check “Male”, and “Is Child”. Checking the “Is Child” box guarantees that when pedigrees are later generated, none are generated where this person has children. The “Year of Birth” box may be left open; if a year is given, it is only used to influence the set of possible pedigrees later generated. Click “Add”, and go on to enter S2, S3, M, and PF in a similar fashion. The finished file may be downloaded [here](#).

To enter the known relations between M and her three sons, use the “Known Relations” form, which appears by clicking the icon with the red circle and square. The result can be seen [here](#). We then go on to the stage where the DNA data is entered. Click on the blue lab dish icon. The “Case-Related DNA Data” form appears. To enter data for a person, double-click on that person. Each observation must be entered by writing in, or choosing, the system name, and the two allele names, followed by clicking “Add”. If only one allele has been observed for a person in a system, that allele must be entered twice. Click “OK” when all information for this person has been entered. You can always go back and add or remove data later. After you have added your data, it is again smart to save the work you have done to some file, using the “Save as” choice from the “File” menu. The finished file may be downloaded [here](#). Note that DNA data may also be read in on a special file format, see the [manual](#).

We are now ready to generate the relevant pedigrees for which we would like likelihoods computed. We start by clicking on the icon with the multicolored rings, and the “Pedigrees” form appears. One way to generate the pedigrees is to do it manually, using the “Add” button on the “Pedigrees” form. It produces a form called “Pedigree”, where the relationships can be entered. For example the pedigree where PF is the father of S1 and S3 but not S2 is generated by adding the two father-son relationships PF-S1 and PF-S3. (Note that, in other examples than ours, one may need to add “extra” persons in order to define certain relationships. For example, to specify that two persons are full siblings, their parents must be added. This can be done in the “Pedigree” form with the “Persons” button). A total of 8 pedigrees, for all possibilities for fatherhood of PF of S1, S2, and S3, should be constructed. The result may be downloaded [here](#).

Note that Familias contains functions for automatic generation of sets of pedigrees. This may be useful in situations when a large number of pedigrees should be considered possible. In the example above, clicking the button “Generate” (and keeping the default settings) will generate a

total of 24 pedigrees. Inspecting these (by double-clicking on corresponding lines in the “Pedigrees” form), one can see a number of incestuous pedigrees, where for example PF may be both the father of M and the father of her children. To avoid this, one can go back to the “Persons” form and give both M and PF the same birth year. The known relations between the mother and her sons must be re-entered. Removing all previous pedigrees and generating new ones with the “Generate” button results in the 8 pedigrees we are interested in.

To compute likelihood ratios and probabilities for our set of pedigrees, click on the “Probability” button on the “Pedigrees” form. The first pedigree (the one where PF is not the father of any of M’s sons, if you have followed the instructions above) will receive the result 1, while all following pedigrees will be followed by their likelihood ratio compared to the first pedigree. A number of possibilities exist for displaying the results differently: Using the “Scale” button, one may find likelihood ratios relative to other pedigrees than the first, or see the likelihood for each pedigree directly. The “Syst” button is used to restrict results to be based on only a subset of the loci; that way, one can study the sensitivity of results to various observations. Using the “Prob” button, one may compute posterior probabilities for the pedigrees, instead of just likelihood ratios. The posterior probability is then based on prior probabilities for the various pedigrees. These are by default equal for all pedigrees, but can be changed using the “Probability options” button, see the [manual](#). The “Sort” button may be used to sort pedigrees according to their likelihoods.

Several ways exist to report and export the results. The “Report” button generates a long report containing all information which has been used in the computations. The “Report CSV” button will create a shorter overview of computed likelihood ratios, in a comma separated values format, suitable for reading by for example Excel or OpenOffice Calc. The “Report only LR” generates a file with the single result value (when only two pedigrees are considered).