

GeneShare Instructions

What the program does

This program will help you to understand two fundamental concepts:

- (1) The sharing of genes between related individuals
- (2) The nature of inbreeding

The simplest version of the program allows you to study a first-cousin mating pedigree. and to look at the following close relationships:

- (a) Parent-offspring
- (b) Siblings
- (c) Grandparent-grandchild
- (d) First cousins
- (e) Uncle-nephew (or aunt-niece etc)

If you want to go into greater depth, you can look at two different ways of measuring relationships, and then see how these relate to the inbreeding coefficient.

'Simulation' or 'Calculation'

When the program starts, you will need to nominate one of two starting conditions. The first is 'Simulation'. In this mode, the program will display a pedigree containing various genotypes on the screen. You can see the genotypes, and see directly how much gene sharing there is between related individuals, or how much inbreeding. Look in the 'Information' menu for more details about this mode.

The second mode is 'Calculation'. Only the basic pedigree is shown in this case. The aim is to draw descent pathways, and to calculate the expected relationships and inbreeding. In this mode you can also edit the pedigree or make up a new one yourself.

You can switch freely between the two modes from the File menu. However there is a limit to the size of a pedigree that can fit on the screen in Simulation mode, a maximum of four individuals per generation and six generations.

Multiple chromosomes or single chromosome

The default mode for simulations in this program is multiple chromosomes. The program then assumes a chromosome number of 23, as in humans, including a sex chromosome constitution of XX in females and XY in males. For brevity of notation, the non-sex chromosomes are labelled A, B, C . . . V rather than 1, 2, 3 . . . 22. Each chromosome acts as an independent unit.

The alternative is a single chromosome. This has 32 units, including the centromere region.

Stored pedigrees and saved pedigrees

The program contains four stored pedigrees:

- (1) First cousin mating pedigree (4 generations)
- (2) Sib mating (6 generations)
- (3) Multiple mating (2 generations)
- (4) Self-fertilisation (6 generations)

The program also allows you to save pedigrees which you have designed or edited, and to retrieve them later.

Editing a pedigree or starting a new pedigree

The program allows you to design new pedigrees or edit old ones. However you need to be in 'Calculation' mode to do this. In this mode, females and males are shown with conventional small circles and squares.

A template is provided for the four possible actions:

- (i) Add female
- (ii) Add male
- (iii) Add descent line
- (iv) Adjust individual

Each of the 'Add' operations can be undone. In addition, if none of the four templates is highlighted, then clicking on an individual will select it and allow it to be deleted. Decent lines can be deleted by selecting the individuals connected by the line. Double-clicking an individual also selects it for editing.

Haplo-diploid inheritance

This mode of inheritance, with diploid females and haploid males, occurs in social insects. It is a specialised form of inheritance which need not concern you if you are just interested in relationships under normal Mendelian inheritance. Calculation mode cannot be used while haplo-diploid inheritance is in effect.

Another specialised form of inheritance, of interest in plants, is self-fertilisation. A single pedigree of this type is included amongst the stored pedigrees. Calculation mode is not available for this pedigree.

Structure of the program

GeneShare is a flexible program which allows you to run through the simulations and exercises in any order. Simulations are simpler to understand than calculations. However simulations are followed by screens which ask you to enter the expected value. For the more complex pedigrees, this may require the use of Calculation mode. So you may choose to return to Simulation mode after expected values have been calculated.