

Teacher's guide to GeneShare

The GeneShare program contains a mixture of simple and advanced components. At its simplest level, the program can be used by students to see genetic relationships in close relatives. At its more complex level, students can calculate inbreeding and genetic relationship coefficients in complex pedigrees.

'Simulation' or 'Calculation'

The program has two basic modes. The first is **Simulation**. In this mode, the program displays genotypes directly on the screen. It allows the student to examine the consequences of different mating schemes. The simulation can be either of 23 independent chromosomes, including a sex chromosome, or a single chromosome with a limited amount of crossingover.

The first, and simplest, pedigree, is of first cousin mating. The simulation requires the student to fill in all genotypes in the pedigree. Once the pedigree is complete, the program suggests, but does not require, that the student studies a number of the simpler family relationships:

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

In each case, the program requires the student to select a pair of individuals of the correct type, and then to count up the observed degree of relationship. The answers are checked by the program. Because chance is built into the simulations, the observed coefficients will not exactly equal their expected value. Student can also input the expected value, which is checked by the program.

The student can also examine the degree of inbreeding of any individual in the pedigree. In this pedigree, the only individual expected to show any inbreeding is the offspring of the first cousin mating.

Calculation mode does not involve the direct display of genotypes. This mode focuses on calculating the inbreeding coefficient or the degree of relationship.

The main use for this mode is in complex pedigrees. Calculating the inbreeding coefficient requires that all pathways to common ancestors be recognised. The student clicks on an individual, and the program asks for closed pathways to be outlined. The program can assist by finding pathways that the student has missed. The student is then asked to calculate the inbreeding coefficient by summing the contributions from all pathways. The program provides the basic formula, but particularly for the more complicated cases this can be a difficult exercise.

Types of coefficient

Inbreeding is measured using the simple and conventional coefficient of inbreeding. However measuring the degree of relationship between different individuals is more complicated, and two

coefficients are used by the program to measure this. The first measure is the **coefficient of relationship**, which simply counts up the fraction of genes or chromosomes shared between the two individuals. This measure has the desirable property of being one for identical individuals, one-half for parent-offspring, and zero for unrelated individuals. However it is not properly defined if one or the other individual is inbred. In this case, the **coefficient of coancestry**, as defined by Malécot, is preferable, since it copes readily with all cases of inbreeding. The disadvantage of this coefficient is that it is one-half for identical non-inbred individuals, and one-quarter for parent-offspring.

The program starts off by using the coefficient of relationship. Students who only deal with non-inbred individuals, may not come into contact with the coefficient of coancestry.

Different types of inheritance

The program contains the facility for haplo-diploid inheritance, as in social insects, rather than normal Mendelian inheritance. It can be used for any pedigree, although one of the standard pedigrees, multiple mating, is included specifically for this type of inheritance. Calculation mode is not available when haplo-diploid inheritance is selected. However students can still check observed and expected relationship coefficients following a simulation.

A multiple-generation self-fertilisation pedigree is also included. Calculation mode is again not available for this pedigree.

Constructing and saving pedigrees

The program allows students to either edit a pedigree or to construct a new one. Instructions for doing this are given within the program. New pedigrees may either be used immediately, or more conveniently, saved to disk for later retrieval and study.

Student instructions

This set of instructions is intended for teachers. A separate set of text instructions is provided for students, duplicating the information given in the program. The student instructions contain some information not provided in the present set. Most concepts are also treated pictorially and in more detail in the Information menu of the program.