

## Instructions for the Hardy-Weinberg program

This program simulates the sampling of a population, and the test for agreement with Hardy-Weinberg, or random-mating, expectations. There is a single variable locus, with two alleles. There is no dominance, so the three possible genotypes can be scored directly.

There are two tasks which have to be carried out in this exercise. The first is to sample the required number of individuals in the population. The second is to calculate gene frequencies, and to test whether the population is in agreement with Hardy-Weinberg frequencies, using a chi-square test.

These two tasks can be carried out at separate times. The first task is necessarily done at the computer screen. The second is best done away from it. Therefore the program contains the facility to allow you to leave the program, and to come back later to put in your results. The computer generates a population based on the name, or number, that you put in. If you come back and put in the same number, the computer will assume that you have the same population as previously. You do not have to re-sample the individuals.

### Controlling the simulation

When you start the program, there will be a blank screen with two buttons at the bottom labelled **Start sampling** and **Stop sampling**. The latter will be inactivated. As soon as you start sampling, the situation is reversed, so that only the Stop button will be active.

It is important not to allow the initial sampling to become too large. After 5 - 10 individuals have appeared, you should turn off sampling, and make sure that you can score the variable character.

If cages are available, you will find it easier to group genotypes by putting them into cages. Otherwise you will need to score individuals by hand. You can move individuals around on the screen. Be careful if individuals are lying very close to each other, since it becomes difficult to control which individual you are picking up.

Once you have scored them and written down the numbers, you may find it convenient to get individuals out of the way. The **Clear screen** command from the **File** menu is provided to do this. Notice that the use of this command has no effect on the sampling process.

There is a minimum sample size which is accepted by the program. You can read this number when the program starts up and displays a screen which gives some information about the simulation.

## **Putting in Answers**

Go to the **Answers** item in the **Questions and Answers** menu. You will be shown a dialog box with fields to enter the observed numbers, gene frequencies and chi-square value. If you have just generated a sample, the program will prompt you by putting the appropriate total number in place. However you can edit this number if you wish to do the calculations for some other population size. If you have re-started the program to put in answers, the program will not know what size sample you have generated, and you will have to enter it yourself. Make sure that you enter the correct sample size, otherwise the program will mark your genotype numbers as wrong.

You should carry out the calculations to a level of accuracy which enables you to put in answers which are correct to 3 significant figures.