## The Fisher-Wright program - Instructor's guide

This is a simple demonstration of the Fisher-Wright model of population structure (sometimes called the Wright-Fisher model). The program contains no analytical function in its present form. However it is useful as a visual demonstration of the way in which populations are generated, and as a means of viewing gene relationships in a finite population.

The Fisher-Wright model is the basis for the Popsim program. It may be worth emphasising to students that the two programs provide different views of the same process. Since only the numbers are printed out in the Popsim program, and many populations are simulated at the same time, the overall amount of information is much greater in that program. However the Fisher-Wright program gives a much better visual demonstration of the processes underlying the fluctuation in gene frequencies.

Two basic messages can be emphasised, related to loss of alleles and to levels of heterozygosity/homozygosity. The first is that the fluctuation in gene frequencies is due to the loss of some alleles and the rise in numbers of others.

The first point can be seen from a simulation with two alleles. Typically the simulation will lead to near or complete loss of one allele in the number of generations which fit on the screen. The relationships can then be investigated in more detail.

This is a reasonably typical run in which the frequency of one allele decreases overall:

| Gen. | - - |
| :---: | :---: |
|  | 1010 |
|  | 128 |
|  | 119 |
| $3 \Leftrightarrow \rightarrow 0$ | 146 |
| 4 ( 4 - | 146 |
| 5 ¢ | 1010 |
|  | 146 |
|  | 1010 |
|  | 911 |
|  | 911 |
|  | 119 |
| 11 四 | 146 |
|  | 164 |

Sorting and showing lines of descent reveals that all of the genes by generation 12 trace to two original genes, which happen to be of different types:


Single generation analyses show how many alleles remain after one round of sampling:

## Gen.

0


## 1010

128

Multiple alleles may show the patterns without tracing lines of descent. However it should be noted that a maximum of 20 alleles can be distinguished, and possibly less depending on the video card.

The main use of diploid sampling is to show the increase in homozygosity, and to illustrate plainly how this relates to inbreeding:

## Gen.













