**Name:** Olabiyi Aderemi Obayomi **Student I.D:** 850210428

**Genetic Drift**

**PROBLEM**

Genetic drift is a term borrowed from population genetics where it is used to explain changes in gene frequency through random sampling of the population, affecting the gene pool of a small population particularly. Large populations are not immune to genetic drift it is just that it is highly unlikely and if it does, will take a long time. Genetic drift can lead to large changes in populations over a short period of time. It is one of the mechanisms by which the population converges to a single dominant member. In the population, one dominant allele becomes fixed i.e. all members of the population have that allele. There are basically two events that may lead to genetic drift:

1. When a population is dramatically reduced due to an environmental catastrophe and the individuals left over start a new population this is called the **bottleneck effect**
2. When a small population from an originally large population arrives at a new habitat such as an Island and then start a new population, this is called the **founders effect.**

**SOLUTION**

In order to simulate this genetic phenomenon as a result of a totally random process, the following assumptions were made:

There is no selection, no mutation, no sex, no crossing over, all individuals in the population have equal fitness, generations do not overlap, and population size is constant after bottle neck or founders effect.

My program requires a desired population size, number of alleles, and the number of generations as input parameters for the simulation.

**How it works**

* Get parameter values using a graphical user interface (GUI)
* Where N equals the number of alleles, generate an initial population vector whose length is the population size of 1 to N alleles chosen at random
* Randomly generate the proportion of the initial population lost due to bottle neck or founders effect and then generate the left over population from it
* Randomly select individuals from the left over population into a new population for the number of generations specified
* At each generation calculate the frequency (proportion) of each allele by getting the sum of the allele divided by the population size
* Plot allele frequency against number of generations.