

Genetic Drift

Advanced article

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Genetic drift consists of changes in allele frequencies due to sampling error. Even if all individuals in a population have the same opportunities to mate, their reproductive contributions to the next generation will vary due to random chance alone. In any population of finite size, this sampling error will cause gene frequencies to fluctuate from generation to generation. Genetic changes due to drift are neither directional nor predictable in any deterministic way. Nonetheless, genetic drift leads to evolutionary change even in the absence of mutation, natural selection or gene flow.

All populations of finite size experience genetic drift to some extent, with effects that are inversely proportional to the 'effective population size', N_e . Effective population size is a mathematical abstraction used to correct for factors such as variance among individuals in reproductive output or temporal fluctuations in population size. More precisely, the effective population size is the number of individuals that would be found in an ideal population that undergoes the same amount of drift as the real population. (*See Effective Population Size.*)

A simple mathematical model of drift can be constructed by assuming that individuals are diploid, so that the gene pool has a size of $2N_e$. The 'homozygosity' of the population, denoted as F , is the probability that two alleles chosen randomly from this pool are identical. By definition, F ranges from 0 to 1. Because the probability of the same gene reproducing twice is $1/(2N_e)$, F increases over time as

$$F_{t+1} = 1/(2N_e) + [1 - 1/(2N_e)]F_t \quad (1)$$

'Heterozygosity', the probability that two random alleles are different, is denoted by H and calculated as $H = 1 - F$. From this, it follows that H will decrease over time:

$$H_{t+1} = [1 - 1/(2N_e)]H_t \quad (2)$$

and

$$H_t = [1 - 1/(2N_e)]^t H_0 \quad (3)$$

The major implication is that all populations of finite size will eventually drift to 'fixation', where $H = 0$ and only a single allele remains, unless diversity is maintained by mutation, gene flow or natural selection. Because genetic drift is a random process, different populations may reach fixation for different alleles.

Empirically, random genetic drift has been studied in natural and experimental populations of innumerable plants, animals and other organisms. Often, the effective size of a population is inferred from its genetic composition. Genetic drift provides a theoretical framework with which to evaluate the effects of habitat fragmentation, population bottlenecks, founder effects and captive breeding programs. Finally, drift provides a simple null model for population genetics. The effects of other microevolutionary forces (mutation, gene flow and natural selection) can be studied by adding them to this model. (*See Darwin and the Idea of Natural Selection; Mutational Change in Evolution.*)

See also

- Effective Population Size
- Fixation Probabilities and Times
- Genetic Variation: Polymorphisms and Mutations
- Heterozygosity
- Polymorphisms: Origins and Maintenance
- Population Genetics
- Population Genetics: Historical Aspects