Here, we discuss information and results presented in the following article:

Tajima, F. (1989). The effect of change in population size on DNA polymorphism. *Genetics*, *123*(3), 597-601.

The author studies the effect of change in population size on the number of segregating sites (singletons) and the average number of nucleotide differences (shared diversity).

In Table 1 the population starts out with no genetic diversity and a very small population size. Over time the population size increases until . In Table 2 the population is in equilibrium and at time zero the population is reduced to one 100th the initial population size. The population then grows until .

In Table 1 and 2 the column outlined in red represents the average number of pairwise differences between DNA sequences. The remaining columns represent the number of segregating sites in the sample.

There are two important things to note from these two tables. First, when the population starts out very small the average number of pairwise differences (sample size of 2) increases very slowly compared to the number of segregating sites in larger sample sizes. This is shown in Table 1. Second, when the population is recovering from a crash the number of segregating sites, in larger sample sizes, decreases quicker compared to the average number of pairwise differences (sample size of 2). This is demonstrated in Table 2.



These results have implications for neutrality tests of molecular markers. Namely, demographic events can exhibit signals that look like selection even under neutral conditions. For example, during a bottleneck, rare mutations are lost more readily than are common mutations and transient positive Tajima’s *D* values are expected. As a population starts to recover from a bottleneck, there is a temporary excess of new mutations at rare frequencies, and negative Tajima’s *D* values are expected (Figure 1). Eventually, the population starts to stabilize because nucleotide diversity increases as rare haplotypes either increase in the population or are lost, which overtime increases the average number of segregating sites between haplotypes.

**Figure 1.**

A close up of a map

Description generated with very high confidence