

**Name of Populus model:** Inbreeding

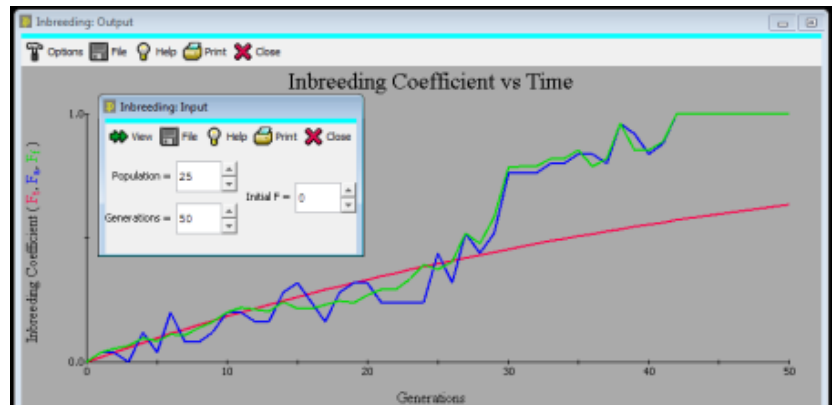
**Mathematical basis for model:**

$$F_t = 1 - \left(1 - \frac{1}{2N}\right)^t$$

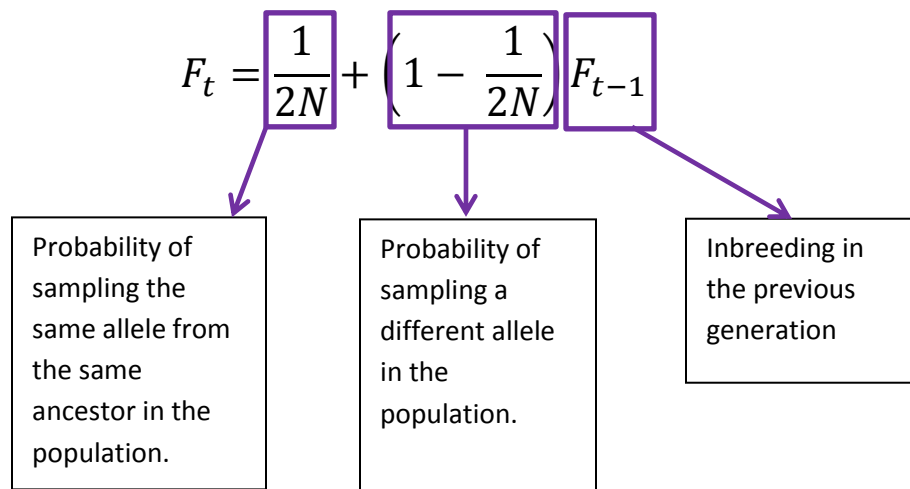
$F_t$  = inbreeding coefficient at time  $t$

$N$  = population size

$T$  = time



**Recursion equation from which the model equation is derived**



**What does this model tell us?**

Over time, drift causes some alleles to be lost and other alleles to increase in frequency in the population. In the absence of mutation and migration, drift leads to inbreeding. In these cases, no new variation is being introduced, and additional variation is being lost by drift. Thus, individuals are more and more likely to carry the same ancestral allele.

This model tells us that inbreeding at time  $t$  is a result of two factors: 1) sampling the same allele from the same ancestor in the current generation and 2) inbreeding in previous generations.

**Interpreting Populus simulation**

Populus plots the **average inbreeding coefficient ( $F_t$ ) in red.**

Populus uses Monte Carlo to simulate realistic values for  $F_i$  and  $F_p$ .

- $F_i$  = autozygosity of individuals (plotted in blue?)
- $F_p$  = autozygosity of entire population (plotted in green?)
- “measures differ when individuals are autozygous but do not carry the same allele.”
  - **WHAT DOES THIS MEAN?**