

Effective population size

Peter Beerli

August 27, 2009

In the population models an important parameter was the number of individuals in the population. This number determines how fast the system loses alleles, if there is no mutation. The Wright-Fisher model has 3 properties that are noteworthy (from Ewens [2004]):

- the largest nonunit eigenvalue $\lambda_2 = 1 - \frac{1}{2N}$
- the probability that two genes taken at random are descendants of the same parent gene is $1/(2N)$.
- the variance of moving from generation t to $t + 1$ is $var(x(t+1)|x(t)) = x(t)(1-x(t))/(2N)$ where $x(t)$ is the fraction of A_1 genes in generation t .

We can use these properties to define the effective population size of natural populations that are more complicated than our model population by:

- $N_e^{(e)}$ is the eigenvalue effective population size = $1/(2(1-\lambda_2))$
- $N_e^{(i)}$ is the inbreeding effective population size = $1/(2\pi_2)$
- $N_e^{(v)}$ is the variance effective population size: the variance = $\frac{x(t)(1-x(t))}{2var(x(t+1)|x(t))}$

For the Canning model we get in reference to the Wright-Fisher model

$$N_e^{(e)} = (N - 0.5)/\sigma^2 \tag{1}$$

$$N_e^{(i)} = (N - 0.5)/\sigma^2 \quad (\text{taking into account } \sigma^2 \text{ in the calculations of descendents}) \tag{2}$$

$$N_e^{(v)} = (N - 0.5)/\sigma^2 \tag{3}$$

We see that all different N_e are the same for the Canning model. Since the Wright-Fisher model is a special case of the Canning model and the constants (the 0.5) involved are small, we may assume that when taking mutation into account (see later chapters) that a mutation scaled variant of the population size

$$\theta = 4N\mu/\sigma^2 \quad (4)$$

approximates the effective population size in cases where the generations do not overlap. For such populations a potential adjustment is

$$N_e^* = N_e k / 2N \quad (5)$$

where k is the number of individuals dying each time unit, this leaves the Wright-Fisher model calculations unchanged because $k = 2N$ but changes the values for the Moran model with $k = 1$ to

$$N_e^{(e)} = N_e^{(i)} = N_e^{(v)} = \frac{1}{2}N \quad (6)$$

Compare this result to the time of fixation of alleles, there the Moran model fixes about in half of the time of the other models.

[Discussion of extension of the simple concept to a diploid Canning model, differences among sexes, and other complications are still missing in this chapter]