

5.1.5 Mutating Population

The previous example of a binary sequence of length N can be recast and interpreted in terms of the evolution of a (haploid) population of fixed size as follows. Let us assume that A_1 and A_2 denote two forms of a particular allele. In each generation any individual is replaced by an offspring that mostly retains its progenitor's allele, but may mutate to the other form at some rate. In this model the total population size is fixed to N , while the sub-populations N_1 and N_2 may vary. A particular state of the population is thus described by $N_1 = n$ and $N_2 = N - n$, and since $n = 0, 1, \dots, N$ there are $N + 1$ possible states. At a particular time, the system may be in any one of these states with probability $p(n, t)$, and we would like to follow the evolution of these probabilities.

After an individual replication event (A_1 to A_1 at rate $-\mu_2$, A_1 to A_2 at rate μ_2 , A_2 to A_1 at rate μ_1 , or A_2 to A_2 at rate $-\mu_1$), the number N either stays the same, or changes by unity. Thus the transition rate matrix only has non-zero terms along or adjoining to the diagonal. For example

$$R_{n,n+1} = \mu_2(n + 1), \quad \text{and} \quad R_{n,n-1} = \mu_1(N - n + 1), \quad (5.1.15)$$

where the former indicates that a population of $n + 1$ A_1 s can decrease by unity if any one of them mutates to A_2 , while a population with $n - 1$ A_1 s increases by unity if any of A_2 s mutates to A_1 . The diagonal terms are obtained from the normalization condition in Eq. (5.1.13) resulting in the Master equation

$$\frac{dp(n, t)}{dt} = \mu_2(n + 1)p(n + 1) + \mu_1(N - n + 1)p(n - 1) - \mu_2np(n) - \mu_1(N - n)p(n), \quad (5.1.16)$$

for $0 < n < N$, and with boundary terms

$$\frac{dp(0, t)}{dt} = \mu_2p(1) - \mu_1Np(0), \quad \text{and} \quad \frac{dp(N, t)}{dt} = \mu_1p(N - 1) - \mu_2Np(N). \quad (5.1.17)$$

The above equation looks complicated, but in fact admits a simple solution as justified in the different context described next.