

F_{ST} calculations

Consider a neutral locus z . First calculate the average genotypic value at z ,

$$\bar{z} = \frac{1}{2 \sum_{j=1}^{N_d} N_j} \sum_{j=1}^{N_d} \sum_{i=1}^{N_j} (z_{ij,1} + z_{ij,2}), \quad (1)$$

where N_d is the number of patches in the population, N_j is the number of individuals in patch j , and $z_{ij,1}$ and $z_{ij,2}$ are respectively the genotypic value at the paternal and maternal locus of individual indexed $i \in \{1, \dots, N_j\}$ in group indexed $j \in \{1, \dots, N_d\}$. And the total variance in the population is

$$\sigma^2 = \frac{1}{2 \sum_{j=1}^{N_d} N_j} \sum_{j=1}^{N_d} \sum_{i=1}^{N_j} (z_{ij,1} - \bar{z})^2 + (z_{ij,2} - \bar{z})^2, \quad (2)$$

The genetic variance among patches is

$$\sigma_{\text{among patches}}^2 = \frac{1}{N_d} \sum_{j=1}^{N_d} (\bar{z}_j - \bar{z})^2, \quad (3)$$

where

$$\bar{z}_j = \frac{1}{2N_j} \sum_{i=1}^{N_j} (z_{ij,1} + z_{ij,2}) \quad (4)$$

is the average z genotypic value in patch j . The genetic variance within patches is

$$\sigma_{\text{within patches}}^2 = \frac{1}{N_d} \sum_{j=1}^{N_d} \frac{1}{2N_j} \sum_{i=1}^{N_j} (z_{ij,1} - \bar{z}_j)^2 + (z_{ij,2} - \bar{z}_j)^2. \quad (5)$$

The genetic differentiation among patches is then given by

$$F_{ST, \text{among patches}} = \frac{\sigma_{\text{among patches}}^2}{\sigma_{\text{among patches}}^2 + \sigma_{\text{within patches}}^2} = \frac{\sigma_{\text{among patches}}^2}{\sigma^2}. \quad (6)$$