

Appendix 2 to:

Measures of Genetic Diversity

Analysis of molecular variance: Example 1

This model, also called AMOVA, measures gene diversity among populations with specific reference to areas of a region in a continent (situation 3, slide 26).

We have: i = individuals, j = alleles, k = populations

$$Y_{ki(j)} = Y + a_k + b_{k(i)} + w_{ki(j)}$$

Where,

- $Y_{ki(j)}$ = a value between 0 and 1 for the j^{th} allele of individual i^{th} of the k^{th} population
- a_k = the effect of the k^{th} population, with variance σ^2a
- $b_{k(i)}$ = the effect of the i^{th} individual within the k^{th} population, with variance σ^2b
- $w_{ki(j)}$ = the effect of the j^{th} locus of individual i^{th} of the k^{th} population, with variance σ^2w
- n = the product of i, j and k, that is, the total number of observations

Source of variation	df	SS	MS	EMS
Among populations	$(k - 1)$	$\Sigma X_{...k^2/ij} - X_{...}^2/ijk$	MS_a	$\sigma^2w + 2\sigma^2b + 2n\sigma^2a$
Among individuals/pop.	$k(i - 1)$	$\Sigma \Sigma X_{i...k^2/j} - \Sigma ...k^2/ij$	MS_b	$\sigma^2w + 2\sigma^2b$
Within individuals	$ki(j - 1)$	$\Sigma \Sigma \Sigma X_{ijk^2} - \Sigma \Sigma X_{i...k^2/j}$	MS_w	σ^2w
Total	$kij - 1$	$\Sigma \Sigma \Sigma X_{ijk^2} - X_{...}^2/ijk$		

Variances and F statistics estimates	
$\sigma^2a = F_{ST}\sigma^2$	$F_{IT} = (\sigma^2a + \sigma^2b)/\sigma^2$
$\sigma^2b = (F_{IT} - F_{ST})\sigma^2$	$F_{ST} = \sigma^2a/\sigma^2$
$\sigma^2w = (1 - F_{IT})\sigma^2$	$F_{IS} = \sigma^2b/(\sigma^2b + \sigma^2w)$
$\sigma^2 = \sigma^2w + \sigma^2b + \sigma^2a$	

Where,

- σ^2a = the parametric value of the variance between populations that carry identical alleles. It is estimated by $(MS_a - MS_b)/2n$
- σ^2b = the parametric value of the variance between individuals within each population. It is estimated by $(MS_b - MS_w)/2$
- σ^2w = the parametric value of the variance within individuals or the measure of the probability that alleles within loci be different. It is estimated by the mean square within individuals (CMW)