

Optimum selection and OU processes

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Biology 550D

Analyzing various kinds of data with morphometrics

A casual outline. Participation compulsory. Issues for discussion:

- Within individuals. Growth: What about allometry?

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- Multiple species on a phylogeny

What causes change in quantitative characters?

For neutral mutation and genetic drift, can show that for a quantitative character with additive genetic variance V_A and population size N the genetic (additive) value of the population mean is:

$$\text{Var}(\Delta \bar{g}) = V_A/N$$

If mutation and drift are at equilibrium:

$$E[V_A^{(t+1)}] = V_A^{(t)} \left(1 - \frac{1}{2N}\right) + V_M$$

In neutral traits additive genetic variance rules

so that

$$E[V_A] = 2NV_M$$

whereby

$$\text{Var}[\Delta \bar{g}] = (2NV_M) / N = 2V_M$$

an analog of Kimura's result for neutral mutation.

Thus to transform characters to independent Brownian motions of equal evolutionary variance, we could use the additive genetic variance V_A .

With multiple characters ...

There is a precise analogue of this for multiple characters:

$$E[\mathbf{A}^{(t+1)}] = \mathbf{A}^{(t)} \left(1 - \frac{1}{2N}\right) + \mathbf{M}$$

where \mathbf{A} is the additive genetic covariances, and \mathbf{M} is the covariance matrix of pleiotropic effects of mutation.

$$E[\mathbf{A}] = 2N\mathbf{M}$$

and

$$\text{Var}[\Delta\bar{\mathbf{g}}] = (2NM)/N = 2\mathbf{M}$$

so as long as mutations cause expected change zero (i.e. they are not near some biological limit), the effect of genetic drift is that the mean phenotype wanders according to the mutational covariances. The constant additive genetic variance assumption was used by Russ Lande.

References for multivariate Brownian motion

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