Quantitative evolution of morphology
Properties of Brownian motion evolution of a single quantitative trait

Most likely outcome = starting value

Variance of the outcomes = number of step × (rate parameter)^2

Outcomes are normally distributed (reason is Central Limit Theorem: each step adds a random variable, sum of many random variables forms a normal distribution)
Brownian motion function for 2 traits

randomwalk <- function(n,r=1) {
  scores <- matrix(ncol=3, nrow=n)
  scores[1,] <- c(1,0,0)
  for (i in 2:n) {
    scores[i,1]=i
    scores[i,2]=scores[i-1,2]+rnorm(1, mean=0, sd=sqrt(r))
    scores[i,3]=scores[i-1,3]+rnorm(1, mean=0, sd=sqrt(r))
  }
  return(as.data.frame(scores))
}

# This function generates a Brownian-motion random walk
# in two traits for n number of generations. The default step
# variance is 1. Written by David Polly, 2008.
#
Quantitative evolutionary theory

\[ \Delta \bar{z} = \beta G \]

Selection coefficients can be:
- Random
- Directional
- Stabilizing
- Etc.

Additive genetic variance – covariance matrix

To properly model evolution

Additive genetic covariance matrix of traits for a single species

- Normally this is estimated from parent-offspring data
- Phenotypic covariance matrix (for a single species) can arguably be substituted
- Don’t use covariance matrix based on multiple species because this confounds phenotypic covariances and phylogenetic covariances

Use this covariance matrix to construct shape space

Estimate step rates from phylogeny (e.g., Martins and Hansen, 1997; Gingerich, 1993, etc.)
Figure 1. Change in human stature as a model for evolution from one generation (A) to the next (B) in response to a gradient of selection (represented by the diagonal line superimposed in A). Population samples are normal on a logarithmic scale, with means of 5.140 and 5.145 ln units (corresponding to statures of 170.7 and 171.6 cm, respectively) and a common standard deviation of 0.05 ln units. Vertical lines within normal curves are standard deviation [s.d.] units. Heritability $h^2$ is assumed to be 0.5, which means that a selection differential $S$ of 0.01 ln units, equivalent to a selection intensity $i$ of 0.2 standard deviation units (dashed normal curve in B), is required to achieve a response of 0.005 ln units ($R$) – equivalent to the response of 0.1 s.d. units shown here ($R'$; solid normal curve in B). Selection gradient in A indicates how sizes are favored in relation to an arbitrarily small positive non-zero constant $a$ at $\bar{x} - 4$ s.d. The gradient $g$ shown here is that required to achieve a change in means of 0.1 s.d. units for $h^2 = 0.5$ (compare to the corresponding gradient for $h^2 = 1.0$). This change is independent of population size and equally efficient for populations of small or large effective size. The expected response $R'$ has a limit of approximately 0.124 standard deviation units in this example (inset box at right in lower panel shows how $S'$ is related to $g$). Documentation of higher rates indicates that such a linear gradient is probably not representative and truncation selection may be more common in nature than is generally recognized. The selection and response notation here follows Falconer (1981; with $a$ added to scale gradient slope to unit area under normal curve).
Adaptive landscape

Wright, 1932 (original concept for allele frequency and reproductive fitness)
Simpson 1944 (phenotypic concept for macro evolution)
Lande, 1976 (quantitative theory for phenotypes)

Brownian motion
analogous to evolution on a flat adaptive landscape where random bumps appear and disappear

Directional selection
analogous to a flat adaptive landscape that is tilted up in one direction

Shape model in landmark space
PC scores in shape space
Procrustes distance from ancestral (consensus) shape

Stabilizing selection
analogous to classic adaptive peak

Drift
Perfectly flat landscape where change occurs by chance sampling from one generation to the next. Change is small and a function of population size (where population size is average number of breeding individuals in the species through the period of interest)

Shape model in landmark space
PC scores in shape space
Procrustes distance from ancestral (consensus) shape

The curvature and slope of a divergence graph depend on the type of selection and the rate of evolution.

Mode of selection

Rate
Applied to hominin tooth shape

Possible issues with this kind of modeling:

- Does not model the gain or loss of features
- Presumes that trait covariances don’t change
- Presumes that evolutionary transitions in phenotypes are continuous
Phenotypic Space

Dynamic developmental interactions

Developmental Genetic Parameter Space
New Frontiers: Alternative approaches

“Homology free” geometric methods that can accommodate gain and loss of features

Non-linear shape spaces that can be used to model interactions of genetic, developmental, and environmental effect

Homologous landmarks  “Homology free” outline semilandmarks  “Homology free” surface semilandmarks

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Estimated trajectory of pinniped calcaneum evolution

Further reading


Polly, P. D. 2004. On the simulation of the evolution of morphological shape: multivariate shape under selection and drift. Palaeontologia Electronica, 7.2.7A: 28pp, 2.3MB.  