

Keynote: Insight into old and new methods: geometric morphometrics and phylogenetic inference from a linear maximum likelihood point of view

Speaker: Joe Felsenstein and Fred Bookstein, University of Washington

Abstract:

When change of landmark configurations of forms along a phylogeny occurs by covarying ("colored") Brownian Motion, and present-day rotations of individual specimens may possibly covary with the forms, a linear model can be analysed in a likelihood framework when changes of forms along the phylogeny and rotations of the specimens are small. Several methodological caveats follow:

Superpositions? After superposing forms at their centroids one can treat rotation either linearly or nonlinearly, or by incorporating it into the model without correcting for it before the statistical analysis. Do not ever divide by size, as that discards a genuine biological property. If rotation is to be removed prior to analysis do not use a Procrustes superposition, but instead a Boas superposition that does not discard size.

Phylogenetic inference should analyze forms, not shapes. Morphospace? Don't go there, as it makes no difference and serves only to mystify people. Principal components? A desperate resort when we don't have any model of selective or developmental factors. When stochastic effects are larger, a Markov Chain Monte Carlo (MCMC) method may take them into account nonlinearly in a suitable way. We're working on it, because today's GMM is obviously unsuited for phylogenetic and functional work. We want a truly evo-devo orphometrics to replace it as soon as possible.