Using molecular and morphological data to connect fossils to a phylogeny

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Abstract: This talk describes a method for using measurable morphological characters to connect a fossil species (or multiple species) to a phylogeny of present-day forms, presumable inferred using their molecular sequences. If there is uncertainty about the phylogeny of the present-day forms this may be represented by using multiple phylogenies for them, which are either inferred from bootstrap samples or are samples from a posterior distribution in Bayesian inference. The method assumes that we can model changes of the quantiatively measurable characters as covarying Brownian Motion along the phylogeny (the branch lengths on the phylogeny should either reflect a molecular clock, or should reflect rates of change of the molecules that can be assumed to be proportional to the rates of morphological change). The basic strategy is to infer the covariance matrix of the morphological changes by using the neontological data, and then use those find the optimal connections for the fossils. Interestingly, this turns out to involve minimization of one relatively simple quantity. Usually the time scale of change of the molecules will not be available. In that case, the scaling constant can be inferred in this analysis. This provides a general framework for using fossils to calibrate molecular clocks. Extensions of this approach to more general models such as the covarying Ornstein-Uhlenbeck model, to use of within-species variation, and to stratigraphic sampling models will be described if time is deep enough.