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Stochastic models in phylogenetic comparative methods: analytical properties and parameter estimation

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Abstract

Phylogenetic comparative methods are well established tools for using inter–species variation to analyse phenotypic evolution and adaptation. They are generally hampered, however, by predominantly univariate approaches and failure to include uncertainty and measurement error in the phylogeny as well as the measured traits. This thesis addresses all these three issues.

First, by investigating the effects of correlated measurement errors on a phylogenetic regression. Second, by developing a multivariate Ornstein–Uhlenbeck model combined with a maximum–likelihood estimation package in R. This model allows, uniquely, a direct way of testing adaptive coevolution.

Third, accounting for the often substantial phylogenetic uncertainty in comparative studies requires an explicit model for the tree. Based on recently developed conditioned branching processes, with Brownian and Ornstein–Uhlenbeck evolution on top, expected species similarities are derived, together with phylogenetic confidence intervals for the optimal trait value. Finally, inspired by these developments, the phylogenetic framework is illustrated by an exploration of questions concerning "time since hybridization", the distribution of which proves to be asymptotically exponential.