**Jointly Modeling Discrete and Continuous Traits**

**as a Means of Discovering Hidden Rate Heterogeneity**

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**Abstract**

Rates of evolution have changed throughout the history of life and produced the rich diversity of morphology, behaviour, and ecology that characterizes the biodiversity we see today. As such, models favoring variation in rates and states has fast become the rule, as opposed to the rare exception in empirical applications of comparative methods. The challenge then becomes how to model this heterogeneous process with the limitation that, for most comparative biologists, our data comes exclusively from extant species. Our model, which we call hOUwie, uses hidden Markov models as a statistically rigorous way to learn about variation in the evolutionary process. hOUwie is composed of two processes: one describes the evolution of a discrete character (such as whether a mammal is a carnivore, herbivore, or omnivore) and the other the evolution of a continuous character (such as mammalian body size). To model the evolution of our continuous character we have chosen to use an Ornstein-Uhlenbeck (OU) model. In evolutionary biology, we use it to model the change in traits through time, which is the product of two antagonistic forces continuously pulling trait values towards some optimal value and randomly moving away from the optimum. The dynamics of these forces can also vary by so-called “regimes”. Under a typical OU model, these underlying regimes are taken as a given and are defined a priori leaving no room for inference about the evolution of the regimes themselves. To resolve this problem, we will model the evolution of these regimes as a discrete character via the aforementioned hidden Markov model. One of the most important properties we will utilize is the inclusion of hidden states. Hidden states give us a way to learn about the variation in the evolutionary process without the necessity of it being linked to one of our explanatory variables.

**Introduction**