

Bayesian Ancestral Reconstruction for Bat Echolocation

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Abstract

Ancestral reconstruction can be understood as an interpolation between measured characteristics of existing populations to those of their common ancestors. Doing so provides an insight into the characteristics of organisms that lived millions of years ago. Such reconstructions are inherently uncertain, making this an ideal application area for Bayesian statistics. As such, Gaussian processes serve as a basis for many probabilistic models for trait evolution, which assume that measured characteristics, or some transformation of those characteristics, are jointly Gaussian distributed. While these models do provide a theoretical basis for uncertainty quantification in ancestral reconstruction, practical approaches to their implementation have proven challenging. Here, I present a flexible Bayesian approach to ancestral reconstruction, applied to bat echolocation calls. This represents a fully Bayesian approach to inference within the Phylogenetic Gaussian Process Regression framework for Function-Valued Traits, producing an ancestral reconstruction for which any uncertainty in this model may be quantified. The framework is generalised to collections of discrete and continuous traits, based on an efficient approximate Bayesian inference scheme. This efficient approach is then applied to the reconstruction of bat echolocation calls, providing new insights into the developmental pathways of this remarkable characteristic. It is the complexity of bat echolocation that motivates the proposed approach to evolutionary inference, however, the resulting statistical methods are broadly applicable within the field of Evolutionary Biology.