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Page 1 (Records 1 -- 1)

◀ [1] ▶

Record 1 of 1
Title: Bayesian Analysis of Biogeography when the Number of Areas is Large
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Abstract: Historical biogeography is increasingly studied from an explicitly statistical perspective, using stochastic models to describe the evolution of species range as a continuous-time Markov process of dispersal between and extinction within a set of discrete geographic areas. The main constraint of these methods is the computational limit on the number of areas that can be specified. We propose a Bayesian approach for inferring biogeographic history that extends the application of biogeographic models to the analysis of more realistic problems that involve a large number of areas. Our solution is based on a "data-augmentation" approach, in which we first populate the tree with a history of biogeographic events that is consistent with the observed species ranges at the tips of the tree. We then calculate the likelihood of a given history by adopting a mechanistic interpretation of the instantaneous-rate matrix, which specifies both the exponential waiting times between biogeographic events and the relative probabilities of each biogeographic change. We develop this approach in a Bayesian framework, marginalizing over all possible biogeographic histories using Markov chain Monte Carlo (MCMC). Besides dramatically increasing the number of areas that can be accommodated in a biogeographic analysis, our method allows the parameters of a given biogeographic model to be estimated and different biogeographic models to be objectively compared. Our approach is implemented in the program, BayArea. [ancestral area analysis; Bayesian biogeographic inference; data augmentation; historical biogeography; Markov chain Monte Carlo.].

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