

Understanding the tripartite approach to Bayesian divergence time estimation

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Abstract: Placing evolutionary events in the context of geological time is a fundamental goal in paleobiology and macroevolution. In this article we describe the tripartite model used for Bayesian estimation of time calibrated phylogenetic trees. The model can be readily separated into its component models: the substitution model, the clock model and the tree model. We provide an overview of the most widely used models for each component and highlight the advantages of implementing the tripartite model within a Bayesian framework.

Keywords: Bayesian phylogenetics, paleobiology, species divergence times, morphological clock, fossil calibration

JEL classifications: A12, B34, C56, D78, E90

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1 Introduction

2 A brief introduction to Bayesian inference in phylogenetics

2.1 The model likelihood

2.2 The prior

2.3 The posterior

3 A tripartite model for divergence time estimation

4 Substitution models

5 Clock models

5.0.1 Strict Clock

5.0.2 Uncorrelated Clock

5.0.3 Autocorrelated Clock

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5.0.4 Local Clocks

5.0.5 Other Models of Evolutionary Rate Variation

6 Tree models for time-calibrated tree inference

6.0.1 Models of speciation, extinction and sampling

$$\lambda\lambda = 1/\lambda\lambda\lambda nnn + 1n\lambda\mu nn - 1n\mu$$

$$t = 0\rho\psi/n\psi$$

6.0.2 The uniform tree model

6.0.3 Coalescent tree models

6.0.4 Biogeographic dating

7 Expanding the potential of the tripartite model within the Bayesian framework

$dr\lambda\mu$

$$d = \lambda - \mu, r = \frac{\mu}{\lambda}$$

$$\lambda = \frac{d}{(1-r)}, \mu = \frac{rd}{(1-r)}.$$

8 Conclusions

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The likelihood the prior and the posterior

Hierarchical Models

Maximum Likelihood and Bayesian Estimation

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