

Introducing a general class of species diversification models for phylogenetic trees

Francisco Richter

September 7, 2020

Abstract

Phylogenetic trees are types of networks that describe the temporal relationship between individuals, species, or other units that are subject to evolutionary diversification. Many phylogenetic trees are constructed from molecular data that is often only available for extant species, and hence they lack all or some of the branches that did not make it into the present. This feature makes inference on the diversification process challenging. For relatively simple diversification models, analytical or numerical methods to compute the likelihood exist, but these do not work for more realistic models in which the likelihood depends on properties of the missing lineages. In this article, we study a general class of species diversification models, and we provide an expectation-maximization framework in combination with a uniform sampling scheme to perform maximum likelihood estimation of the parameters of the diversification process.