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*Distance-based summaries and modeling of evolutionary trees*

Ranked tree shapes are used to model evolutionary relationships for evolutionary biology and phylodynamics. Bayesian methods explore the posterior distribution of trees, however assessing uncertainty and summarizing distributions remains challenging. Similarly, in many instances, one seeks to summarize samples of trees obtained from different samples and environments, and wishes to assess stability and generalizability of these summaries. Here, we exploit recently proposed distance of unlabeled evolutionary trees and provide a combinatorial optimization algorithm for estimating Fréchet means and variances. We show the applicability of our summary statistics for studying popular tree distributions and for studying the evolution of viruses.