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Species tree inference by the STAR method, and generalizations

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(Submitted on 19 Apr 2012)

The multispecies coalescent model describes the generation of gene trees from a rooted metric species tree, and thus provides a framework for the inference of species trees from sampled gene trees. We prove that the STAR method of Liu et al., and generalizations of it, are statistically consistent methods of topological species tree inference under this model. We discuss the impact of gene tree sampling schemes for species tree inference using generalized STAR methods, and reinterpret the original STAR as a consensus method based on clades.

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