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(j.rhodes@alaska.edu). *Gene Trees from Species Trees: Testing Multispecies Coalescent Model Fit*. Preliminary report.

The evolutionary histories of gene samples can differ from their species history for a variety of biological reasons, such as incomplete lineage sorting or lateral gene transfer. Given a collection of gene trees, how can we test whether ILS alone, as modeled by the multispecies coalescent on a tree, can explain them, or whether a more complex model, such as on a species network, is needed? One approach is through summarizing the gene trees by quartet concordance factors (frequencies of quartet topologies they display), and using log-likelihood ratio statistics in a standard hypothesis testing framework to judge model fit.

However, the coalescent predicts that concordance factors lie on a set with a singularity, and using a standard χ^2 distribution for measuring fit is problematic in its vicinity. Moreover, the data sets of the most interest, with significant amounts of incomplete lineage sorting, always lie near the singularity. To address this, we derive a new asymptotic approximation to the distribution of the log-likelihood ratio test statistic, and show its improved behavior throughout the model space. We briefly describe work underway to extend testing from 4-taxon trees to large ones. (Received January 19, 2018)