Does gene tree discordance explain the mismatch between macroevolutionary models and empirical patterns of tree shape and branching times?

Supplementary Figures

Tanja Stadler\textsuperscript{1,2,*}, James H. Degnan\textsuperscript{3}, Noah A. Rosenberg\textsuperscript{4}

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\textsuperscript{1} ETH Zürich, Department of Biosystems Science and Engineering, Mattenstrasse 26, 4058 Basel, Switzerland
\textsuperscript{2} Swiss Institute of Bioinformatics (SIB), Switzerland
\textsuperscript{3} Department of Mathematics and Statistics, University of New Mexico, 311 Terrace NE, Albuquerque, NM, 87131, USA
\textsuperscript{4} Department of Biology, Stanford University, 371 Serra Mall, Stanford, CA 94305, USA
* Corresponding author: tanja.stadler@bsse.ethz.ch
Figure 1: (Supplementary Figure). Mean Sackin statistic of gene trees divided by mean Sackin statistic of species trees ($\bar{S}_g / \bar{S}_s$). Solid lines correspond to complete species sampling $\rho = 1$, dashed lines to sampling probability $\rho = 0.75$, and dot-dashed lines to sampling probability $\rho = 0.5$. Plots are obtained based on 100,000 simulated species tree–gene tree pairs at each choice of parameter values, taking means separately for the gene trees and the species trees.
Figure 2: (Supplementary Figure). Mean number of cherries in gene trees divided by mean number of cherries in species trees ($H_g/H_s$). Solid lines correspond to complete species sampling $\rho = 1$, dashed lines to sampling probability $\rho = 0.75$, and dot-dashed lines to sampling probability $\rho = 0.5$. Plots are obtained based on 100,000 simulated species tree–gene tree pairs at each choice of parameter values, taking means separately for the gene trees and the species trees.
Figure 3: (Supplementary Figure). The $\gamma$ statistic for empirical trees from TreeBASE. Each black dot represents a tree. The figure also shows simulated species tree $\gamma_s$ values. The species tree $\gamma_s$ value depends on turnover and species sampling; line colors indicate turnover, and line type indicates species sampling, as in Figure 2. Note that in the simulations, we subtracted mean species tree $\gamma_s$ values from mean gene tree $\gamma_g$ values to produce $\bar{\gamma}_g - \bar{\gamma}_s$. As the number of points is too low here to obtain mean $\gamma$ values for empirical trees at each tree size, we only plot each empirically observed $\gamma$ statistic.