



Comparison of four different parameter sets for gymnosperm-wide BEAST analysis. Analyses are based on the same data sets, and differ only in tree model (yule vs. birth-death) and tree topology (no constraints vs. constraints to resemble the ML output, i.e. setting Ginkgo as sister to Pinaceae, Gnetophytes and Cupressophytes). Each tree is the result of four independent MCMC runs with 5×10^8 generations each. 95% HPD intervals are given.