

Using minimum estimated coalescence times to infer species trees.

Short-term visit to NIMBioS for Michael DeGiorgio on March 28-30, 2012.

Through a simulation and empirical study, we explored the performance of GLASS, and related methods such as STEM, for inferring species trees. For the simulation study, we explored the accuracy of estimating species trees based on the species-tree inference method (STEM1 or STEM2), the gene-tree inference method (maximum likelihood or Bayesian), the alignment length, the mutation rate, and the number of alleles sampled per species. For the empirical study, we used a multilocus great ape dataset to investigate the properties of estimating species trees based on the species-tree inference method (STEM1 or STEM2), the gene-tree inference method (maximum likelihood or Bayesian), and the alignment length. The next step is to prove a couple of theoretical results about inferring species trees based on GLASS and related methods. This work should be completed by summer 2012 and will be submitted to the journal *Systematic Biology*.

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