Fast Algorithms for Computing Phylogenetic Divergence Time

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Abstract—The inference of species divergence time is a key step in most phylogenetic studies. Methods have been available for the last ten years to perform the inference, but the performance of the methods does not yet scale well to studies with hundreds of taxa and thousands of DNA base pairs. For example, a study of 349 primate taxa was estimated to require over 9 months of processing time. In this work, we present a new algorithm, AncestralAge, that significantly improves the performance of the divergence time process. We demonstrate a new method for the computation of phylogenetic likelihood and experimentally illustrate a 90% improvement in computation time on the dataset of 349 taxa with over 60,000 DNA base pairs. Additionally, we show a new method for the computation of the Bayesian prior on node ages that is experimentally shown to reduce the time for this computation on the 349 taxa dataset by 99%.