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Letter to the Editor

The relative utility of sequence divergence and phylogenetic informativeness profiling in phylogenetic study design

Recently, Moeller and Townsend (2011) reanalyzed data from our paper (Makowsky et al., 2010) and compared the application of phylogentic informativeness profiling (Townsend, 2007) to simple sequence divergence for assessment of phylogenetic performance of different genes in a Bayesian framework. Briefly, Moeller and Townsend (2011) used site-specific rates of evolution to produce phylogenetic informativeness profiles for each of 12 genes from 28 taxa given a well-established ("known") phylogeny, and the results of their reanalysis generally agreed with ours. Notably, they demonstrated that phylogenetic informativeness profiling can be employed even in the absence of divergence time estimates, and that the shape of the phylogenetic informativeness profile can explain patterns of posterior probability support for correct nodes. Moeller and Townsend (2011) concluded their response by suggesting that workers refrain from employing sequence divergence to predict the ability of a nucleotide fragment to reconstruct evolutionary relationships. Herein, we will explain the potential utility and practicality of considering sequence divergence when designing a phylogenetic study.

The phylogenetic informativeness profile requires robust sampling to obtain reliable estimates of site-specific rates of evolution (Moeller and Townsend (2011) used 28 vertebrate taxa for 12 genes, and Townsend (2007) used 22 muroid rodent taxa for four genes, the latter based on the data set of Steppan et al. (2004)). However, in the initial stages of a phylogenetic study, researchers may not be able to invest the time, effort and money to produce the data for such analyses. We (Makowsky et al., 2010) showed that the genes preferable for pursuit of more complete taxon sampling can be determined by simply calculating overall sequence divergence for a few samples that represent the greatest potential divergence. Additionally, Moeller and Townsend (2011) succinctly detailed the numerous assumptions and parameter estimates that informativness profiling requires, compared to our approach, which requires relatively few parameters and assumptions. The power of considering sequence divergence is in the early stages of study design, when a few sequences can lend insight into the potential phylogenetic utility of a gene (or other sequence region). In contrast, the strength of phylogenetic informativeness profiling may often lie in later stages of study design, and provides more detailed information about how a gene will function within a phylogenetic study. Most molecular systematists already consider sequence divergence for initial study design. Makowsky et al. (2010) confirm that this a valid approach with considerable power, and provide theoretically and empirically-determined guidelines for choice of genes based on divergence levels. This may be especially useful for understudied taxonomic groups for which little data are available. Use of phylogenetic informativeness profiles (Townsend, 2007; Moeller and Townsend, 2011) based on analyses of closely related organisms with the availability of considerable data *a priori* may provide highly valuable information for later analysis stages, but need not be the first step.

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