

PhyloSTemS: a new graphical tool to investigate temporal signal of heterochronous sequences at various evolutionary scales

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Abstract

Molecular tip-dating of phylogenetic trees is a growing discipline that uses DNA sequences sampled at different points in time to co-estimate the timing of evolutionary events with rates of molecular evolution. Such inferences should only be performed when there is sufficient temporal signal within the analysed dataset. Hence, it is important for researchers to be able to test their dataset for the amount and consistency of temporal signal prior to any tip-dating inference. For this purpose, the most popular method considered to-date has been the “root-to-tip regression” which consist in fitting a linear regression of the number of substitutions accumulated from the root to the tips of a phylogenetic tree as a function of sampling times. The main limitation of the regression method, in its current implementation, relies in the fact that the temporal signal can only be tested at the whole tree evolutionary scale. To fill this methodological gap, we introduce PhyloSTemS, a new graphical and user-friendly tool developed to investigate temporal signal at every evolutionary scale of a phylogenetic tree. PhyloSTemS allows detecting without a priori whether any subset of a tree would contain sufficient temporal signal for tip-based inference to be performed. We provide a “how to” guide by running PhyloSTemS on empirical datasets and supply guidance for results interpretation. PhyloSTemS is freely available at <https://pvbmt-apps.cirad.fr/apps/phylostems>.

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