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Anderson, Cajsa Lisa

cajsa.anderson@ebc.uu.se

#### TITLE

All we need now is fossils; a new phylogenetic dating method (PATHd8) allowing thousands of taxa and multiple fossil constraints.

#### ABSTRACT

Estimation of divergence times in phylogenetic trees using sequence data becomes increasingly popular, but so far dating studies have given widely different results, and especially datings of the lower nodes within the angiosperms and metazoans, have given much older ages than those obtained from the fossil record. It has been concluded in different studies that more taxa, and more fossils are needed for more reliable age estimates. For this reason, a dating method that can handle very large data sets with multiple fossil constraints is necessary.

Chronograms obtained by e.g. penalized likelihood and Bayesian methods, often adds a large "ghost range" to the fossil record, and produces chronograms with a more or less smooth appearance, even if the corresponding phylograms have apparently very heterogeneous rates. Compared to the other methods, our recently developed method, PATHd8, gives the results with the best agreement with the fossil record, which coincides with the least smooth appearance of the chronograms. When other programs often run into computational problems when analysing trees with hundreds of leaves, PATHd8 has no problems analysing thousands of taxa instantaneously. An arbitrary number of fossil age constraints can be specified, either as fixed-, minimum or maximum age.

With our new method, the biggest problem in dating studies is that we need more fossils, and these fossils must be well dated and assigned to the correct branches of the phylogeny. Therefore, to accomplish divergence time estimates, which hopefully approximate the real ages, biologists now need to cooperate with palaeontologists.