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# Combining relaxed clocks with gene transfers to date species trees

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## Abstract

The molecular clock hypothesis and its relaxed offspring have provided powerful ways to date clades in the tree of life. Combined with dated fossils of ancient organisms, they give insight into the diversification of life on Earth. Yet, in clades where dated fossils are scarce, their predictions are highly uncertain and imprecise. This is particularly the case during the first few billion years in the history of life when all life was unicellular and left little fossilized remains. In this talk I present a new method to improve dating estimates provided by molecular clocks when dated fossils are rare. This method is based on the analysis of Lateral Gene Transfers (LGTs).

LGTs provide a way to order in time two nodes of a species tree with respect to each other, because transfers necessarily occur between contemporaneous species. Recently new methods have been developed to identify LGTs at the genomic scale (Szollosi et al. 2013), but these LGTs are just starting to be used to date phylogenies. Here I present a method that combines LGT-based information with molecular clock models to date phylogenies. I show results obtained on simulations as well as on empirical alignments. This new method is implemented in RevBayes.

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