



Quantitative Biology > Quantitative Methods

Low-parameter phylogenetic estimation under the general Markov model

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In their 2008 and 2009 papers, Sumner and colleagues introduced the "squangles" - a small set of Markov invariants for phylogenetic quartets. The squangles are consistent with the general Markov model (GM) and can be used to infer quartets without the need to explicitly estimate all parameters. As GM is inhomogeneous and hence non-stationary, the squangles are expected to perform well compared to standard approaches when there are changes in base-composition amongst species. However, GM includes the IID assumption, so the squangles should be confounded by data generated with invariant sites or with rate-variation across sites. Here we implement the squangles in a least-squares setting that returns quartets weighted by either confidence or internal edge lengths; and use these as input into a variety of quartet-based supertree methods. For the first time, we quantitatively investigate the robustness of the squangles to the breaking of IID assumptions on both simulated and real data sets; and we suggest a modification that improves the performance of the squangles in the presence of invariant sites. Our conclusion is that the squangles provide a novel tool for phylogenetic estimation that is complementary to methods that explicitly account for rate-variation across sites, but rely on homogeneous - and hence stationary - models.

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