

Algorithmic Decomposition of Most Parsimonious Sets

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Abstract

Parsimony search typically finds several most parsimonious trees. Our goal is take a set of most parsimonious trees as input and algorithmically identify strongly supported evolutionary hypotheses across the set. We do not require that algorithms produce a single tree, thereby overcoming some of the limitations of consensus methods. Additionally, in contrast to most consensus methods, our method is sensitive as to how edge weights differ across the input set. Our approach has thus far yielded an interesting tree decomposition that in turn gives rise to a functional mapping between trees. We expect that the functional mapping will prove useful as a bounding technique during parsimony search itself. We also consider generalizations of the technique in which parsimony scores across the input set are not necessarily homogeneous, but are within a constant bound from most parsimonious.

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