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# Cases In Which Ancestral Maximum Likelihood Will Be Confusingly Misleading

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## Abstract

Ancestral maximum likelihood (AML) is a phylogenetic tree reconstruction criteria that “lies between” maximum parsimony (MP) and maximum likelihood (ML). ML has long been known to be statistically consistent. On the other hand, Felsenstein (1978) showed that MP is statistically inconsistent, and even positively misleading: There are cases where the parsimony criteria, applied to data generated according to one tree topology, will be optimized on a different tree topology. The question of whether AML is statistically consistent or not has been open for a long time. Mosel, Roch, and Steel (2009) have shown that AML can “shrink” short tree edges, resulting in a star tree with no internal resolution, which yields a better AML score than the original (resolved) model. This result implies that AML is statistically inconsistent, but not that it is positively misleading, because the star tree is compatible with any other topology. We show that AML is confusingly misleading: For some simple, four taxa (resolved) tree, the ancestral likelihood optimization criteria is maximized on an incorrect (resolved) tree topology, as well as on a star tree (both with specific edge lengths), while the tree with the original, correct topology, has strictly lower ancestral likelihood. Interestingly, the two short edges in the incorrect, resolved tree topology are of length zero, and are not adjacent, so this resolved tree is in fact a simple path. While for MP, the underlying phenomenon can be described as long edge *attraction*, it turns out that here we have long edge *repulsion*.

**Keywords:** Phylogenetic reconstruction, Ancestral maximum likelihood, Maximum parsimony, Statistical consistency.

## 1 Introduction

The ancestral maximum likelihood (AML) problem, also called *most parsimonious likelihood* [3, 19], is a maximum likelihood variant of phylogenetic tree reconstruction. Given a set of  $m$  input sequences,

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