

Author's Accepted Manuscript

The optimal rate for resolving a near-polytomy in a phylogeny

Mike Steel, Christoph Leuenberger



PII: S0022-5193(17)30112-1
DOI: <http://dx.doi.org/10.1016/j.jtbi.2017.02.037>
Reference: YJTBI8993

To appear in: *Journal of Theoretical Biology*

Received date: 30 November 2016
Revised date: 25 February 2017
Accepted date: 28 February 2017

Cite this article as: Mike Steel and Christoph Leuenberger, The optimal rate for resolving a near-polytomy in a phylogeny, *Journal of Theoretical Biology*, <http://dx.doi.org/10.1016/j.jtbi.2017.02.037>

This is a PDF file of an unedited manuscript that has been accepted for publication. As a service to our customers we are providing this early version of the manuscript. The manuscript will undergo copyediting, typesetting, and a review of the resulting galley proof before it is published in its final citable form. Please note that during the production process errors may be discovered which could affect the content, and all legal disclaimers that apply to the journal pertain.

THE OPTIMAL RATE FOR RESOLVING A NEAR-POLYTOMY IN A PHYLOGENY

MIKE STEEL¹ AND CHRISTOPH LEUENBERGER²

Affiliations: ¹Biomathematics Research Centre, University of Canterbury, 8041, Christchurch, New Zealand; ²Département de mathématiques, Université de Fribourg, Chemin du Musée 3, 1705 Fribourg, Switzerland.

Email: mike.steel@canterbury.ac.nz, christoph.leuenberger@unifr.ch

Corresponding author: Mike Steel

March 1, 2017

ABSTRACT. The reconstruction of phylogenetic trees from discrete character data typically relies on models that assume the characters evolve under a continuous-time Markov process operating at some overall rate λ . When λ is too high or too low, it becomes difficult to distinguish a short interior edge from a polytomy (the tree that results from collapsing the edge). In this note, we investigate the rate that maximizes the expected log-likelihood ratio (i.e. the Kullback–Leibler separation) between the four-leaf unresolved (star) tree and a four-leaf binary tree with interior edge length ϵ . For a simple two-state model, we show that as ϵ converges to 0 the optimal rate also converges to zero when the four pendant edges have equal length. However, when the four pendant branches have unequal length, two local optima can arise, and it is possible for the globally optimal rate to converge to a non-zero constant as $\epsilon \rightarrow 0$. Moreover, in the setting where the four pendant branches have equal lengths and either (i) we replace the two-state model by an infinite-state model or (ii) we retain the two-state model and replace the Kullback–Leibler separation by Euclidean distance as the maximization goal, then the optimal rate also converges to a non-zero constant.

Keywords: Phylogenetic tree, Markov process, Optimal rate, Kullback–Leibler separation, Fisher information

Download English Version:

<https://daneshyari.com/en/article/5760054>

Download Persian Version:

<https://daneshyari.com/article/5760054>

[Daneshyari.com](https://daneshyari.com)