

Origins and losses of parasitism

an analysis of the phylogenetic tree of life with a parsimony-like algorithm

Abstract

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1 Introduction

This paper is about the further development of parsimony algorithms for non-binary trees, applied to the currently largest phylogeny synthesis tree of Open Tree Of Life, with the application to the ancestral state reconstruction of parasitism.

Researchers of the phylogenies have been dealt with the ancestral state reconstruction in the 60s. The first methods were only brute force **TODO: Quelle, siehe Fitch: Camin and Sokal 1965**. Next came a set of parsimony algorithms such as: Fitch-parsimony, Wagner-parsimony ... **TODO: Quellen!, Jahreszahlen?**. With more and more data, we got new options for calculating probabilities and using next to ancestral states, given branch lengths. The likelihood based algorithms came more in interest. Our focus came with another 'data extension'. We wanted to work with the biggest phylogenetic tree which exists at this moment, which goes over all observed species. For most species there is no phylogeny, but only a taxonomic classification. So the biggest 'phylogenetic tree' is a synthesis of phylogenetic trees filled with a taxonomic tree. **TODO: hier Quelle/Hinweis zur datenbank: Open tree of life...** This tree is not binary and therefore the developed algorithms are not directly applicable. We have looked at the algorithms that are generally suited to our data, to develop them further for the binary case, and finally to compare their usability with our sythesis trees.

We have only decided on parsimony algorithms since we have no information on branch lengths and no other additional information like different transition probabilities of our states.

Bibliography