

DETECTION OF ADAPTIVE SHIFTS ON PHYLOGENIES USING SHIFTED STOCHASTIC PROCESSES ON A TREE

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Comparative and evolutive ecologists are interested in the distribution of quantitative traits among related species. The classical framework for these distributions consists of a random process running along the branches of a phylogenetic tree relating the species. We consider shifts in the process parameters, which reveal fast adaptation to changes of ecological niches. We show that models with shifts are not identifiable in general. Constraining the models to be parsimonious in the number of shifts partially alleviates the problem but several evolutionary scenarios can still provide the same joint distribution for the extant species. We provide a recursive algorithm to enumerate all the equivalent scenarios and to count the number of effectively different scenarios. We introduce an incomplete-data framework and develop a maximum likelihood estimation procedure based on the EM algorithm. We also propose a model selection procedure, based on the cardinal of effective scenarios, to estimate the number of shifts and for which we prove an oracle inequality. Eventually, we will discuss the generalization of this approach to multivariate traits as well as the case where the phylogenetic tree is not actually a tree.

Keywords: Random process on tree, Ornstein-Uhlenbeck process, Change-point detection, Adaptive shifts, Phylogeny, Model selection.

References:

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