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Some statistical methods for phylogenetic trees with application to HIV disease. (English)

[Zbl 0970.62074]


Summary: Phylogenetic trees are commonly used to describe the evolutionary history of a group of species, but may also be used to study an evolving virus such as HIV. These trees are high-dimensional, non-real-valued data objects, with a specific pattern of built-in dependencies that violate the assumptions of many traditional statistical methodologies. We have found that these problems can often be overcome by defining:

(i) an appropriate measure of correlation applicable to phylogenetic trees, (ii) an appropriate distance metric on trees, and (iii) an appropriate way to describe the probability distribution of phylogenetic trees.

This paper describes these statistical tools and applies them to a variety of HIV-related examples of phylogenetic tree data.

MSC:

62P10 Applications of statistics to biology and medical sciences; meta analysis

92D15 Problems related to evolution

Keywords:
molecular evolution; generalized correlation; tree comparison metrics; Markov chain Monte Carlo

Software:

fastDNAml

Full Text: DOI

References:


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