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Statistical approach to tests involving phylogenies. (English) [Zbl 1090.62123](#)

Gascuel, Olivier (ed.), Mathematics of evolution and phylogeny. Oxford: Oxford University Press (ISBN 0-19-856610-7/hbk). 91-120 (2005).

Summary: This chapter reviews statistical testing involving phylogenies. We present both the classical framework with the use of sampling distributions involving the bootstrap and permutation tests and the Bayesian approach using posterior distributions. We give some examples of direct tests for deciding whether the data support a given tree or trees that share a particular property, comparative analyses using tests that condition on the phylogeny being known are also discussed.

We introduce a continuous parameter space that enables one to avoid the delicate problem of comparing exponentially many possible models with a finite amount of data. This chapter contains a review of the literature on parametric tests in phylogenetics and some suggestions of nonparametric tests. We also present some open questions that have to be solved by mathematical statisticians to provide the theoretical justification of both current testing strategies and as yet underdeveloped areas of statistical testing in non-standard frameworks.

For the entire collection see [[Zbl 1104.92332](#)].

MSC:

[62P10](#) Applications of statistics to biology and medical sciences; meta analysis

Cited in **9** Documents

[92D15](#) Problems related to evolution

[62G10](#) Nonparametric hypothesis testing

[62F03](#) Parametric hypothesis testing

Keywords:

[topology of tree spaces](#); [bootstrap](#)