

Method, maximum likelihood

The maximum likelihood method is a general principle in statistics wherein the statistical hypothesis that assigns the highest probability to the observed data is preferred. A statistical hypothesis assigns a probability value (in the case of discrete data, a probability between 0 and 1, or in the case of continuous data, a non-negative probability density) to all conceivable data. The probability value assigned to the observed data is called the likelihood of the hypothesis. The hypothesis can consist of structural components such as a [tree](#) topology or parameters such as [edge](#) lengths, or both. Maximum likelihood is generally considered superior to many other approaches due to its theoretically and empirically observed favourable properties.

Phylogenetic trees that are based on a specific sequence evolution model such as the [Jukes–Cantor model](#) can be estimated using maximum likelihood (Felsenstein 1981). This may require some approximations to make the inference computationally tractable.

Reference

– Felsenstein, Joseph. 1981. “Evolutionary trees from DNA sequences: A maximum likelihood approach.” *Journal of Molecular Evolution* 17: 368–376.

In other languages

GE: maximale Wahrscheinlichkeit

FR: maximum de vraisemblance

IT: massima verosimiglianza

[TR](#)