

Methods, distance-based

The data used as a basis for phylogenetic inference commonly arises from gene sequencing procedures or by performing a number of phenotypic measurements. However, the way the data is used varies from method to method. In distance-based methods, the data is first transformed into a [distance matrix](#) that gives, for each pair of [taxa](#), a pairwise distance. The distance can be, for instance, the number of characters that differ between the two taxa divided by the length of the sequences. (Note that in case a specific sequence evolution model, such as the common Jukes-Cantor model is used, it may be beneficial to carry out a correction based on the model.)

Once a distance matrix is computed, a distance-based method ignores the original data and bases its operation only on the distance matrix. A popular distance-based method is the [neighbour joining](#) method. An example of a method that is *not* distance-based is the [maximum parsimony](#) method.

Reference

– Lemey, Philippe, Marco Salemi, and Anne-Mieke Vandamme, eds. 2009. *The Phylogenetic Handbook: A Practical Approach to Phylogenetic Analysis and Hypothesis Testing*. 2nd ed. Cambridge: Cambridge University Press.

In other languages

DE: distanzbasierte Methoden
FR: méthodes basées sur les distances
IT: metodi basati sulla distanza

[TR](#)