

## The comparison between Distance and character based methods in Phylogentic study

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**Abstract:** Phylogeny is one of the most powerful tools which can provide the most meaningful insights for numerous applications in science such as medicine, biology, ecology and consevation. There are many methods that can be used for reconstructing phylogentic trees from molecular data. Generally, the methods are classified in to two major groups based on kind of data used and algorithm approach or method: 1. Distance-based method (phonetic) includes Unweighted pair group method with arithmetic mean (UPGMA) and neiebor-joining (NJ) and 2. Characters-based method (cladistics) includes maximum parsimony (MP), maximum likelihood (ML) and bayesian inference (IB). In the distance method, a distance matrix of pairwise differences is estimated between all paires aligned sequences. This distance matrix will then be used in reconstructing the phylogenetic tree. However, they tend to rely on the rate of evolution being approximately equal among lineages. The distance-matrix method started by calculating some measure of dissimilarity of each pair of operational taxonomic units (OUTs) to produce a pairwise distance matrix, and then infer the phylogenetic relationships of the OUTs from the matrix [1, 2, 3]. In contrast, the character state method can use any set of discrete characters, such as morphological characters and sequence data. This method maintains the original character statues of taxa, and, hence, can be used to reconstruct the character state of ancestral nodes. The character state method makes an effort to find the phylogenetic tree, which has an optimal value of an attribute that is thought to be significant. Although distance-based methods are more rapid and less computationally severe than character-based methods, the actual characters are discarded once the distance matrix is derived. The character-based methods construct use of all known evolutionary information, such as the individual substitutions among the sequences, to find out the most possible ancestral relationships [4, 5]. In addition, character-based methods operate on the sequences, or on functions derived from the sequences directly, rather than pairwise distances. Therefore, these methods try to avoid the loss of information that occurs when sequences are converted into distances [4].

**Keywords:** Distance-based method; Characters-based method; Phylogenetic; Pairwise differences; Sequence data.

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