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| **Discrete Methods** |
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| Maximum Parsimony |
| Maximum Likelihood |
| Bayesian Inference |

According to Homology of characters in data matrices

**Distance Methods**

Neighbor Joining

UPGMA

* All nucleotide sites change independently
* When evolutionary rates vary from site to site, than data set needs to be corrected
* The substitution rate is constant over time and in different lineages
* The base composition is at equilibrium
* The conditional probabilities of nucleotide substitutions are the same for all sites and not change over time

Evalution trees

Confidence Level:

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Comparisons---------------------

-Partition Distance

-Kishini-Hasegawa test

-Distance test

-Likelihood ratio test

Bootstrap/jackknife (internal support)

Bremer Support (parsimony)

Consistency index and retention index

UPGMA

Script que permita realizar a criação

Conjunto de sequências de DNA – formato FASTA

Clustering Hierárquico