TABLE 27.4. Molecular phylogenetic methods

Method	Description
Parsimony	Possible trees are compared and each is given a score that is a reflection of the minimum number of character state changes (e.g., amino acid substitutions) that would be required over evolutionary time to fit the sequences into that tree. The optimal tree is considered to be the one requiring the fewest changes (the most parsimonious tree).
Distance	The optimal tree is generated by first calculating the estimated evolutionary distance between all pairs of sequences. These distances are then used to generate a tree in which the branch patterns and lengths best represent the distance matrix.
Maximum likelihood	This method is similar to parsimony methods in that possible trees are compared and given a score. The score is based on how likely the given sequences are to have evolved in a particular tree given a model of amino acid or nucleotide substitution probabilities. The optimal tree is considered to be the one that has the highest probability.
Bayesian	A variant of maximum likelihood in which the likelihood of a tree itself is calculated.