

PHYLOGENETIC ANALYSIS

INTRODUCTION

- Phylogenetic analysis is the study of the evolutionary development of a species or a group of organisms or a particular characteristic of an organism. Phylogenetic analysis using molecular data such as DNA sequence for genes and amino acid sequence for proteins is very common not only in the field of evolutionary biology but also in the wide fields of molecular biology.

IMPORTANCE

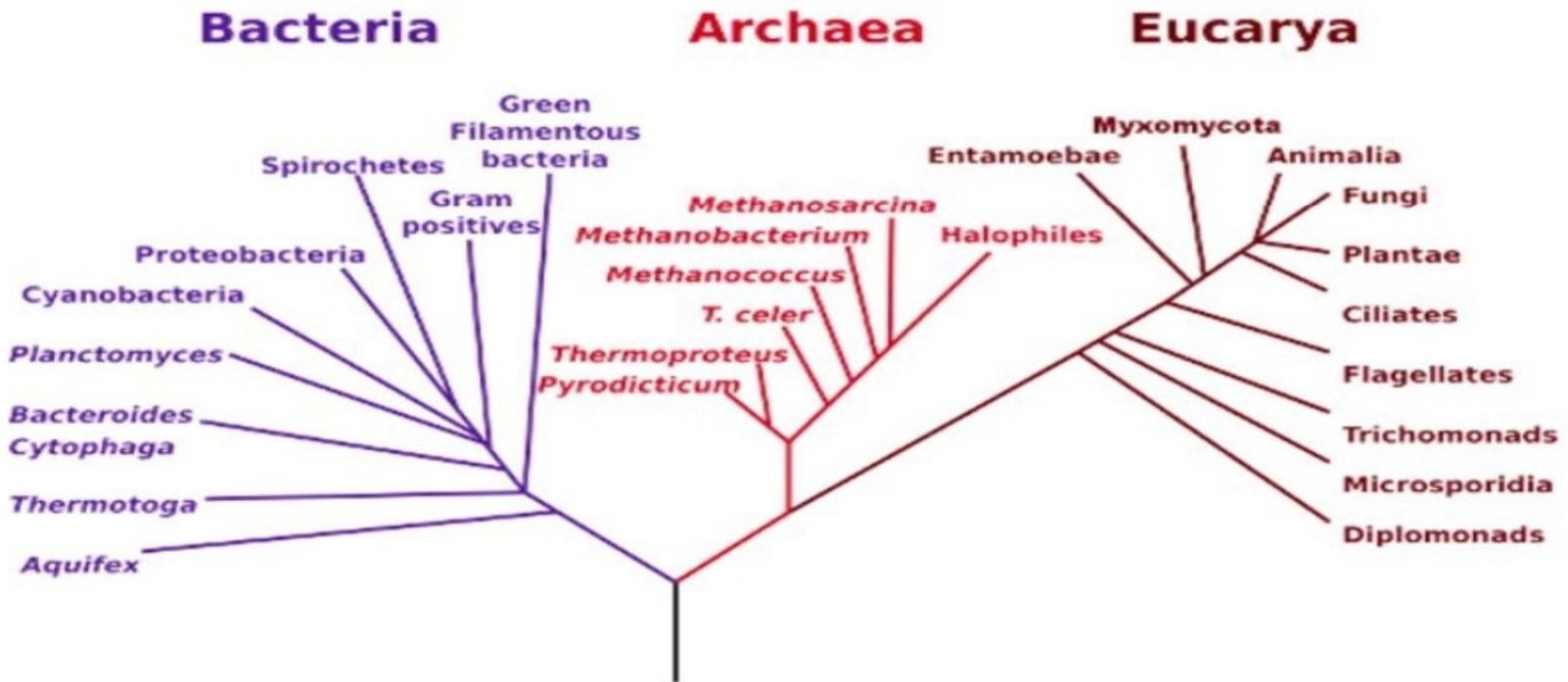
- Phylogenetics is important because it enriches understanding of how genes, genomes, species (and molecular sequences more generally) evolve.

Phylogenetic Trees

- Scientists use a tool called a phylogenetic tree to show the evolutionary pathways and connections among organisms. A phylogenetic tree is a diagram used to reflect evolutionary relationships among organisms or groups of organisms. Scientists consider phylogenetic trees to be a hypothesis of the evolutionary past since one cannot go back to confirm the proposed relationships.

Phylogenetic Trees

Tree of life



PHYLOGENETIC METHODS

- Distance matrix
- Maximum parsimony
- Maximum likelihood

Distance matrix

- A distance matrix is calculated from the sequence dataset
- Algorithms: Fitch-Margoliash, Neighbor-Joining or UPGMA in tree building
- Simple, finds only one tree
- Somewhat old-fashioned (OK if your alignment is good and evolutionary distances are short)

Maximum parsimony

- Maximum Parsimony is a character-based approach that infers a phylogenetic tree by minimizing the total number of evolutionary steps required to explain a given set of data assigned on the leaves.

Maximum likelihood

- Creation all possible trees like maximum parsimony method but instead of retaining trees with shortest evolutionary steps.
- Each tree generated is calculated for the probability that it reflects each position of the sequence data.
- It is more realistic tree estimation because it does not assume equal transition.