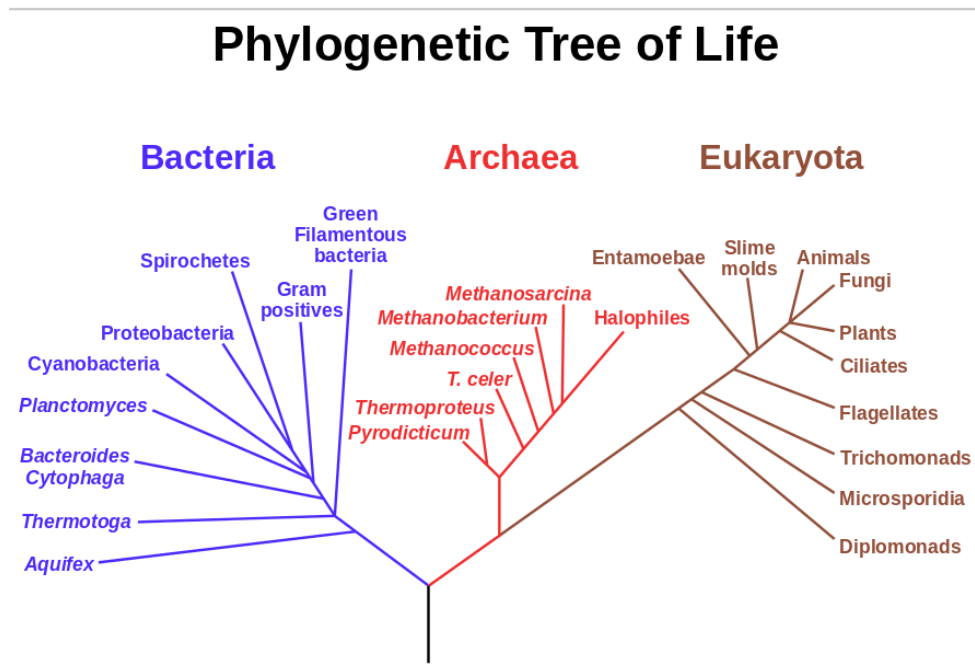


## CONCEPT: PHYLOGENETIC TREES

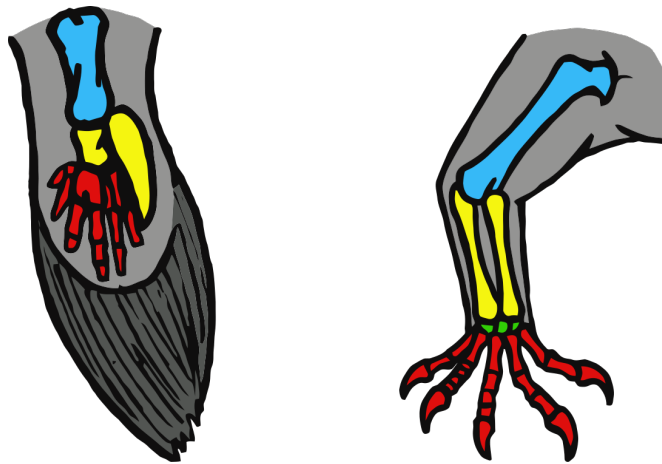
- **Phylogenetic trees** are \_\_\_\_\_ representations of *phylogeny*
  - **Phylogeny** is the evolutionary relationship among a group of organisms
  - A phylogenetic tree consists of multiple structures
    - **Nodes** represent different organisms being compared
      - **Terminal nodes** are organisms for which we have data (usually present-day organisms)
      - **Internal nodes** are common ancestors that existed before divergence
    - **Branches** represent evolutionary connections between organisms
      - Often, the length of the branch represents the amount of time between divergence
  - **Rooted** trees are trees with an internal node that represents a common ancestor to all other nodes on the tree

## EXAMPLE:



- Phylogenetic trees are often constructed using \_\_\_\_\_
  - **Homology** refers to similarities among various species that are due to a common shared ancestor
    - Can have *homologous* DNA sequences and phenotypic traits
  - A **monophyletic group (clade)** is a group of species all descended from the groups most common ancestor
  - The **cladistics approach** reconstructs phylogenetic tree by comparing all possible pathways of evolution
    - **Principle of parsimony** states that the preferred hypothesis (tree) is the simplest one

**EXAMPLE:** Homologous Structures



**PRACTICE:**

1. Which of the following structures on a phylogenetic tree represents the evolutionary connections between organisms?
  - a. Internal node
  - b. Terminal node
  - c. Branches
  - d. Roots
  
2. Which principle is NOT used to construct a phylogenetic tree?
  - a. Principle of parsimony
  - b. Cladistics approach
  - c. Principle of speciation
  - d. Homology