**Constructing Phylogenetic Trees**

**Stepwise Clustering**

* Concept: Iteratively merge the most similar sequences into clusters.
* UPGMA (Unweighted Pair Group Method with Arithmetic Mean).
* Works best with ultrametric data (constant mutation rates).

Example: Align human, chimp, gorilla sequences and cluster stepwise.

**Fitch-Margoliash Method**

* Distance-based method using least-squares fit.
* Minimizes the error between observed and predicted distances.
* More accurate than UPGMA for unequal mutation rates.

**Parsimony & Likelihood Approaches**

1. **Maximum Parsimony**
   * Choose the tree with the **least evolutionary changes**.
   * Simple, but computationally intensive with many sequences.
2. **Maximum Likelihood**
   * Uses probability models of sequence evolution.
   * Finds the most probable tree given the data.
   * Very accurate, but computationally heavy.

**🧪 Lab: Building Trees with MEGA or PhyML**

* Collect mitochondrial COI sequences from 5 animals.
* Construct trees using:
  + UPGMA (stepwise clustering).
  + Maximum Parsimony.
  + Maximum Likelihood.
* Compare differences in tree structure.

Activity: Identify which method gave the most biologically realistic tree.

**Quick Review**

1. Which method assumes equal mutation rates?
2. How does Maximum Parsimony differ from Maximum Likelihood?
3. Why might different methods produce slightly different trees?