**Introduction to Phylogenetics – Drawing Tree Diagrams & Methods**

**What is Phylogenetics?**

Study of evolutionary relationships among organisms using genetic information.

* Uses sequence data (DNA, RNA, proteins).
* Applications:
  + Evolutionary biology.
  + Tracing disease outbreaks (e.g., COVID-19 variants).
  + Comparative genomics.

**Analogy:**

* Family tree = genealogy of people.
* Phylogenetic tree = genealogy of species/genes.

**Types of Phylogenetic Trees**

1. **Rooted Tree**
   * Has a single common ancestor (root).
   * Shows evolutionary direction (who evolved from whom).
2. **Unrooted Tree**
   * Shows relationships but not evolutionary direction.
   * Useful when the common ancestor is unknown.

**Example for board illustration:**

* Rooted tree of humans, chimpanzees, gorillas.
* Unrooted tree showing relationships without root.

**Basic Tree-Building Methods**

1. **Distance-Based Methods**
   * Build trees based on pairwise sequence differences.
   * Examples: UPGMA (Unweighted Pair Group Method), Neighbor-Joining.
2. **Character-Based Methods**
   * Use actual nucleotide/amino acid characters.
   * Examples: Maximum Parsimony, Maximum Likelihood.

**🧪 Lab Session: Drawing a Simple Phylogenetic Tree**

**Objective:** Build and visualize a phylogenetic tree from DNA sequences.

**Steps:**

1. Collect 4–5 cytochrome c protein sequences (e.g., human, mouse, chicken, yeast).
2. Align them using Clustal Omega (from Week 6 lab).
3. Use **Phylogeny.fr** or **MEGA software** to generate tree.
4. Observe output:
   * Identify conserved/variable regions.
   * Discuss branch lengths and clustering.

**Activity:**

* Students draw a simple rooted tree on paper based on alignment data.
* Compare their sketches with the software-generated tree.

**Quick Review Questions**

1. What is the difference between a rooted and unrooted phylogenetic tree?
2. Which methods are distance-based and which are character-based?
3. Give one real-life example where phylogenetics is applied.