**Project1**

**Basic Phylogenetic Tree Construction for Evolutionary Analysis of Influenza Strains**

**Objective:** Build a phylogenetic tree of influenza virus hemagglutinin (HA) gene to study evolutionary relationships.

**Data Source:**

* NCBI Virus Database → search “Influenza A hemagglutinin” → download ~10–15 FASTA sequences from different years/regions.

**Steps:**

1. Download sequences in FASTA format from NCBI Virus.
2. Align sequences using **Clustal Omega (online)** or **MUSCLE (in MEGA software)**.
3. Construct a phylogenetic tree in **MEGA** (Neighbor-Joining or Maximum Likelihood).
4. Annotate the tree with strain names and collection years.
5. Interpret how strains cluster (e.g., by subtype, geography, or year).

**Deliverables:**

* Aligned FASTA file
* Tree image (with labels)
* 2–3 page report: “How do influenza strains evolve and cluster?”