Assignment: Detecting selection pressures in viral genomes using HyPhy

Objective:

To understand how to use Hyphy for detecting selection pressures on viral genomes and to interpret the results in the context of viral evolution and pathogenesis.

Preparation

Ensure you have access to a computer with Hyphy installed.

Review the slides presented today on on the basics of molecular evolution and selection analyses and decide which analysis best fits your hypothesis

Each student or group will choose a specific viral gene dataset (e.g., from HIV, Influenza, SARS-CoV-2) available from databases like GenBank or specific viral genome repositories. I recommend - https://www.bv-brc.org/