

Preparation

Ensure you have access to a computer with Hyphy installed.

Review the slides presented today 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/>

Data retrieval

Download the nucleotide sequences of their assigned viral gene.

Align the sequences using tools like MACSE or codon-msa

It is important to generate codon-aware alignments, otherwise the selection analyses will fail.