

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.

Hyphy Analysis

- Students will go through the following steps in Hyphy
 - **Input Preparation:** Import the aligned sequences into Hyphy.
 - **Model Selection:** Select an appropriate substitution model.
 - **Selection Analysis:** Run selection analysis using methods such as SLAC (Single Likelihood Ancestor Counting), FEL (Fixed Effects Likelihood), and MEME (Mixed Effects Model of Evolution).