

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).

Results Interpretation

Students will interpret the results of their analysis, focusing on:

- Identifying sites under positive or negative selection.
- Understanding the biological significance of these sites in the context of viral evolution.
- Comparing the results from different methods (SLAC, FEL, MEME) and discussing any discrepancies.