

# Hands-on workshop component

- Choose a dataset (one of your own, or one of the examples we provide)
  - Use examples and code provided throughout the slides
  - <https://github.com/veg/selection-tutorial/tree/main/data>
- Run several different selection analyses on this file ([datamonkey.org](https://datamonkey.org))
- Use HyPhy Vision to compile results and visualizations
- Think about your results, do they make sense?

# **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.