

Preliminaries

- Please confirm access to **HyPhy**: <http://hyphy.org/download/>
 - <https://youtu.be/fgNrPbOTpxE>
 - You can do a datamonkey.org based tutorial, but if you have Linux or OS X, you can also do a command line tutorial for more features.
- General user questions and feedback: <https://github.com/veg/hyphy/issues>
- **Datamonkey** web-app:
 - <http://www.datamonkey.org>
 - YouTube example videos (channel HyPhy vision)
 - <https://www.youtube.com/channel/UCIgRnbJjbOWhshe5ThhaWGw/videos>
- Test datasets and practical instructions: www.hyphy.org (search for “Detect Selection”)
- Example datasets at <https://github.com/veg/selection-tutorial/>

Outline

- Brief background and examples of natural selection
- **dN/dS** as a tool to measure the action of natural selection, explained using the first counting method for estimating dN/dS (Nei-Gojobori, 1986) and its extensions.
- Codon substitution models — the basis of modern (1998-) dN/dS estimation approaches
- Different types of selection analyses enabled by **dN/dS**, told by examples from West Nile virus and HIV and analogies from image analysis
 - Gene-wide selection (BUSTED)
 - Lineage-specific selection (aBSREL)
 - Site-level **episodic** selection (FEL, MEME)
 - Site-level **pervasive** selection (SLAC, FEL, FUBAR)
 - Relaxed or intensified selection (RELAX)
 - Detecting **differences** in selective pressure (CONTRAST-FEL)
- Confounding processes (synonymous rate variation, recombination, multiple nucleotide substitutions)
- On the suitability of dN/dS for within-species inference