

# Preliminaries

- Please confirm access to **HyPhy**: <http://hyphy.org/download/>
  - <https://youtu.be/fgNrPbOTpxE>
  - You can do a [datamonkey.org](http://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](http://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