Preliminaries

- Please confirm access to **HyPhy**: http://hyphy.org/download/

  - https://youtu.be/fgNrPbOTpxE (How to install HyPhy)

  - You can do a datamonkey.org based tutorial, but if you have Linux or OSX, 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 (Tutorials)

- Example datasets at https://github.com/veg/selection-tutorial/

  - Test datasets and practical instructions: www.hyphy.org (search for "Detect Selection")

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

- Confounding processes (synonymous rate variation, recombination, multiple nucleotide substitutions)

- On the suitability of dN/dS for within-species inference

- 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 (MEME)

  - Site-level **pervasive** selection (SLAC, FEL, FUBAR)

  - Relaxed or intensified selection (RELAX)

  - Detecting **differences** in selective pressure (Contrast-FEL)