





Quantifying Natural Selection in Coding Sequences

Sergei L Kosakovsky Pond
Professor of Biology
Institute for Genomics and Evolutionary Medicine @ Temple University

 spond@temple.edu
 <http://lab.hyphy.org>
 github.com/spond
 [@sergeilkp](https://twitter.com/sergeilkp)

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/>