### **HyPhy - Title TBD**

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#### **Abstract**

Here we announce the latest release of the HyPhy comparative sequence analysis software package. HyPhy is widely used, actively supported, open source and freely available on a multitude of platforms. The codebase is available at http://github.com/veg/hyphy. Documentation, tutorials and downloads are available at http://hyphy.org.

#### Introduction

HyPhy (Hypothesis testing using Phyloginies) is an open source software package for comparative sequence analysis using stochastic evolutionary models. Since it's initial release in 2005 [1] HyPhy has become an integral tool for the bioinformatics community with over 10,000 registered users, over 2,000 peer-reviewed citations and approximately 1,000 HyPhy jobs processed each week on the datamonkey web server [2,3,4]. Extensions and improvements to the HyPhy package have been ongoing since its inception, with active feedback between users and developers producing new features tailored to the specific needs of the research community. Here we announce the release of the newest version of HyPhy (version 2.4.0) and document how the software has been (1) packaged for easy use in a variety of settings (2) optimized for larger datasets (3) redesigned to follow modern bioinformatics best practices and (4) extended to include common methods out of the box.

### **Packaged for Easy Use in a Variety of Settings**

The users of HyPhy vary greatly in their technological proficiency, spanning the spectrum from biologists unfamiliar with the command line to bioinformaticians who want to incorporate HyPhy into their own software. To meet the needs of this divers user set, HyPhy has been packaged and distributed for use in multiple different forms. These include: - Standard command line tool (Download: github.com/veg/hyphy; Tutorial: {to be written}) - Interactive command line prompt (Download: github.com/veg/hyphy; Tutorial: hyphy.org/tutorials/current-release-tutorial/) - Online web-service (datamonkey.hyphy.org) - Desktop GUI application (Download: github.com/veg/hyphygui; Tutorial: hyphy.org/tutorials/current-release-tutorial\_gui/) - Galaxy [5] Tools (Installable from the galaxy tool-shed; available pre-installed at galaxy.hyphy.org) - Integration with the Python Programming Language (Download: github.com/sjspielman/phyphy; Tutorial: sjspielman.org/phyphy/) [6] - MEGA [7] Integration

#### References

#### 1. HyPhy: hypothesis testing using phylogenies

S. L. K. Pond, S. D. W. Frost, S. V. Muse

Bioinformatics (2004-10-27) https://doi.org/bbcz2p

DOI: 10.1093/bioinformatics/bti079 · PMID: 15509596

# 2. Datamonkey: rapid detection of selective pressure on individual sites of codon alignments

S. L. K. Pond, S. D. W. Frost

Bioinformatics (2005-02-15) https://doi.org/c2bz9d

DOI: <u>10.1093/bioinformatics/bti320</u> · PMID: <u>15713735</u>

## 3. Datamonkey 2010: a suite of phylogenetic analysis tools for evolutionary biology

W. Delport, A. F. Y. Poon, S. D. W. Frost, S. L. Kosakovsky Pond

Bioinformatics (2010-07-29) https://doi.org/bz8k5p

DOI: 10.1093/bioinformatics/btq429 · PMID: 20671151 · PMCID: PMC2944195

## 4. Datamonkey 2.0: A Modern Web Application for Characterizing Selective and Other Evolutionary Processes

Steven Weaver, Stephen D Shank, Stephanie J Spielman, Michael Li, Spencer V Muse, Sergei L Kosakovsky Pond

Molecular Biology and Evolution (2018-01-02) https://doi.org/gdbs4n

DOI: 10.1093/molbev/msx335 · PMID: 29301006 · PMCID: PMC5850112

## 5. The Galaxy platform for accessible, reproducible and collaborative biomedical analyses: 2018 update

Enis Afgan, Dannon Baker, Bérénice Batut, Marius van den Beek, Dave Bouvier, Martin Čech, John Chilton, Dave Clements, Nate Coraor, Björn A Grüning, ... Daniel Blankenberg

Nucleic Acids Research (2018-05-22) https://doi.org/gdwxpr

DOI: 10.1093/nar/gky379 · PMID: 29790989 · PMCID: PMC6030816

## 6. phyphy: Python package for facilitating the execution and parsing of HyPhy standard analyses

Stephanie J. Spielman

The Journal of Open Source Software (2018-01-17) <a href="https://doi.org/gfxxzf">https://doi.org/gfxxzf</a>

DOI: 10.21105/joss.00514

#### 7. MEGA X: Molecular Evolutionary Genetics Analysis across Computing Platforms

Sudhir Kumar, Glen Stecher, Michael Li, Christina Knyaz, Koichiro Tamura

Molecular Biology and Evolution (2018-05-02) https://doi.org/gd39d8

DOI: <u>10.1093/molbev/msy096</u> · PMID: <u>29722887</u> · PMCID: <u>PMC5967553</u>