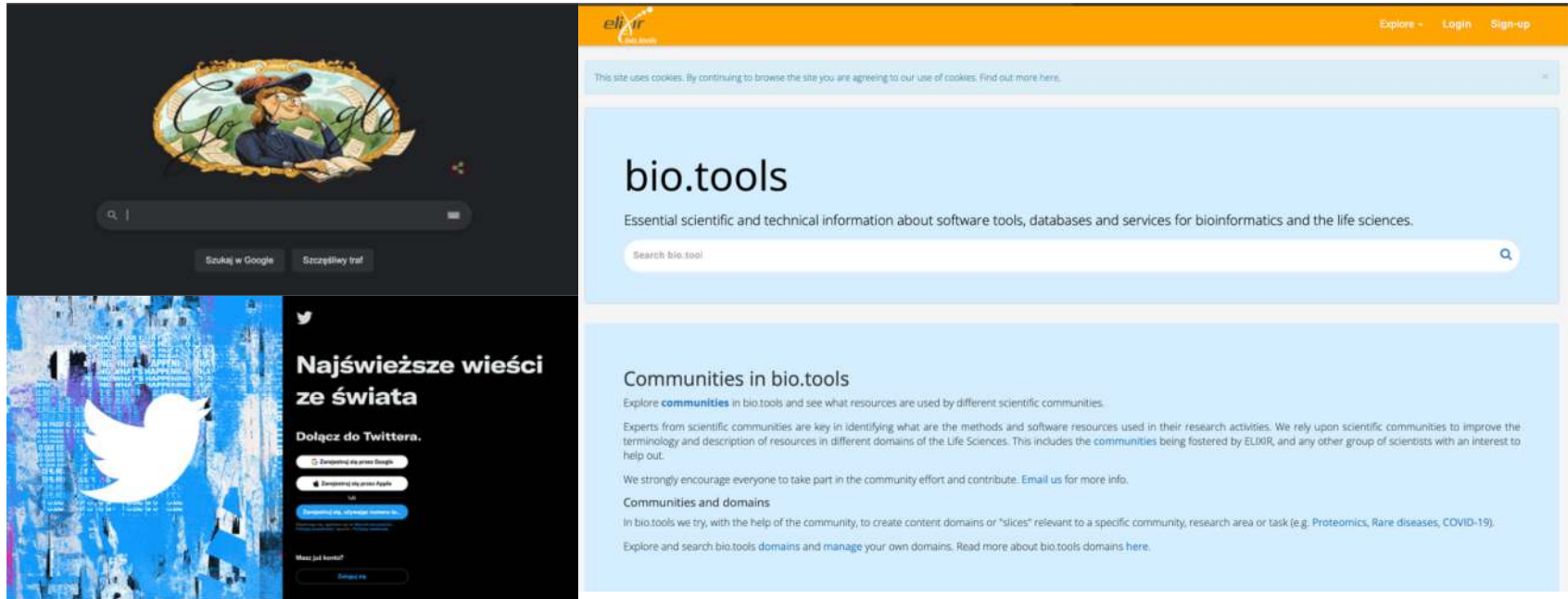


How to get software you need





When you know what to do but you don't know how



GBE

Predicted Input of Uncultured Fungal Symbionts to a Lichen Symbiosis from Metagenome-Assembled Genomes

Workshop on phylogenomics

Biotoools

Nucleic acids

Resources for the processing and analysis of nucleic acid sequences, structural and other data. They provide analytical methods to interpret and explore nucleic acid sequence and structural data in context of gene structure, genetic variation, and the regulation of gene expression.

DNA	▶	RNA	▶
Genetic mapping	▶	Read mapping	▶
Functional, regulatory and non-coding RNA	▶	Methylation analysis	▶
DNA polymorphism	▶	SNP detection	▶
Nucleic acid sequence analysis	▶	Nucleic acid sites, features and motifs	▶
Nucleic acid feature detection	▶	Transcription factor binding site prediction	▶
Transcription factors and regulatory sites	▶	Transcriptional regulatory element prediction	▶
Nucleic acid structure analysis	▶	RNA secondary structure prediction	▶

 Everything: phylogenomics x Search bio.tools 174 tools Explore - Login Sign-up

Sort by Score Updated Added Name Citation Count Publication Date Display as Compact Detailed

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Berkeley Phylogenomics Group

The Berkeley Phylogenomics Group provides a series of web servers for phylogenomic analysis: classification of sequences to pre-computed families and subfamilies using the PhyloFacts Phylogenomic Encyclopedia, FlowerPower clustering of proteins sharing the same domain architecture, MUSCLE multiple sequence alignment, SATCHMO simultaneous alignment and tree construction, and SCI-PHY subfamily identification.

Phylogenomics Sequence sites, features and motifs Phylogenetics Gene and protein families Protein folds and structural domains

Tree-based sequence alignment Multiple sequence alignment Sequence alignment

Web application

Clann

Constructing consensus trees and supertrees from multiple source trees

Phylogenomics

Phylogenetic tree reconciliation

Command-line tool GPL-2.0

MSMC

This software implements MSMC, a method to infer population size and gene flow from multiple genome sequences

When you know what to do but you don't know how (to install)

- apt get install (linux)
- Pip (python) / CRAN Repository (R) / Bioconductor
- Download from a website (java packages)
- **Git clone and follow the instructions (unix)**
- Conda (unix)

When you know what to do but you don't know how (to install)

The screenshot displays the GitHub repository for PhyKIT. The left sidebar lists files: LICENSE.md, Makefile, Pipfile, Pipfile.lock, README.md, change_log.txt, codecov.yml, phykit-runner.py, requirements.txt, and setup.py. The main content area shows the README with the PhyKIT logo and the tagline "a toolkit for examining multiple sequence alignments and trees". The right sidebar contains repository statistics and sections for Releases, Packages, Contributors, and Deployments. A white arrow points to the "v1.12.4 Latest" release in the Releases section.

File	Description	Time
LICENSE.md	added exemplary scripts for creating the initial codebase	4 years ago
Makefile	create commandline interface runners for each function a...	3 years ago
Pipfile	created layout of docs	4 years ago
Pipfile.lock	created layout of docs	4 years ago
README.md	removed patreon badge	last year
change_log.txt	calculations of pairwise identity in alignment now support...	2 months ago
codecov.yml	Add codecov.yml	4 years ago
phykit-runner.py	Clean up entrypoint and runner	4 years ago
requirements.txt	updated versions of biopython, numpy, and scipy	4 months ago
setup.py	updated versions of biopython, numpy, and scipy	4 months ago

Releases 19

✓ **v1.12.4** **Latest**
on Dec 15, 2023

+ 18 releases

Packages

No packages published

Contributors 4

- JLSteenwyk Jacob L. Steenwyk
- TJBIII Thomas Buida
- hyphaltip Jason Stajich
- dependabot[bot]

Deployments 68

✓ github-pages 2 months ago

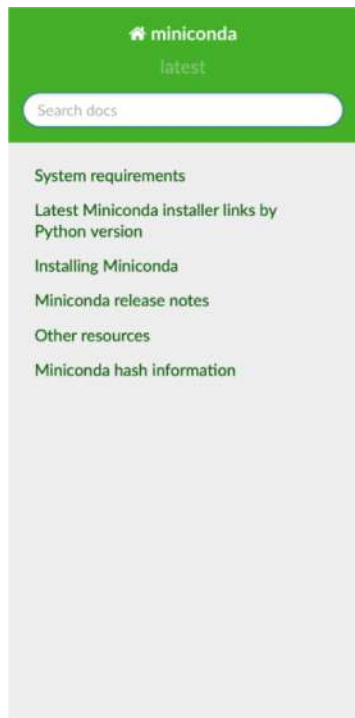
+ 67 deployments

When you know what to do but you don't know how (to install)

- apt get install (linux)
- Pip (python) / CRAN Repository (R) / Bioconductor
- Download from a website (java packages)
- Git clone and follow the instructions
- **Conda!**



A package manager and environment management system



🏠 / Miniconda

Miniconda

Miniconda is a free minimal installer for conda. It is a small bootstrap version of Anaconda that includes only conda, Python, the packages they both depend on, and a small number of other useful packages (like pip, zlib, and a few others). If you need more packages, use the `conda install` command to install from thousands of packages available by default in Anaconda's public repo, or from other channels, like conda-forge or bioconda.

Is Miniconda the right conda install for you? The [Anaconda or Miniconda](#) page lists some reasons why you might want one installation over the other.

- [System requirements](#)
- [Latest Miniconda installer links by Python version](#)
- [Installing Miniconda](#)
- [Miniconda release notes](#)
- [Other resources](#)
- [Miniconda hash information](#)

Latest Miniconda installer links

This list of installers is for the latest release of Python: 3.11.5. For installers for older versions of Python, see [Other installer links](#). For an archive of Miniconda versions, see <https://repo.anaconda.com/miniconda/>.

Installation with conda



Bioconda lets you install thousands of software packages related to biomedical research using the [conda](#) package manager.

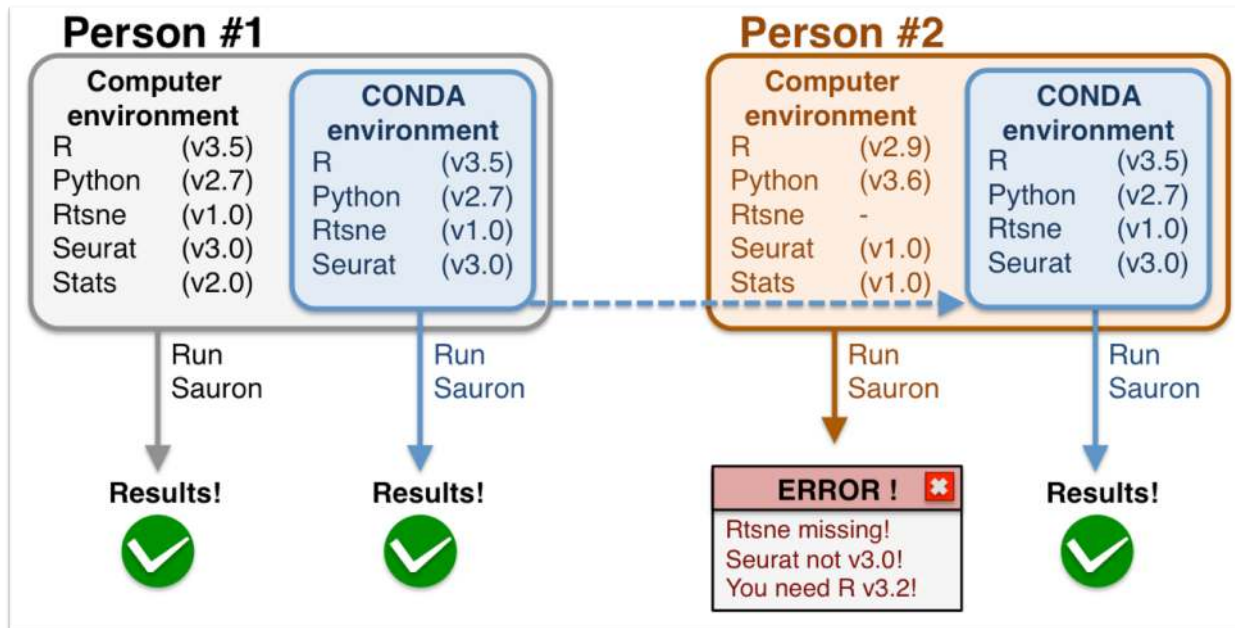


```
phylogenomics@krumlov:[~]$ conda install bioconda::blast
```



A package manager and environment management system

Enables easy installation
Takes care of dependencies
You can create environments



```
phylogenomics@krumlov:[~]$ conda create -n environment
```



The Fast Cross-Platform Package Manager

part of mamba-org

Package Manager [mamba](#)

Package Server [quetz](#)

Package Builder [boa](#)

 **mamba**



CI

passing

 gitter

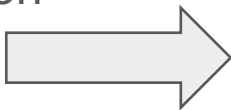
join chat

 docs

passing

When you know what to do, you have a software but you don't know how to start

Always check documentation



PhyKIT

Search docs

About

Usage

- General usage
- Alignment-based functions
- Tree-based functions
- Alignment- and tree-based functions

Tutorials

Change log

Other software

FAQ

[Docs](#) » [Usage](#)

Usage

PhyKIT helps process and analyze multiple sequence alignments and phylogenies.

Generally, all functions are designed to help understand the contents of alignments (e.g., gc content or the number of parsimony informative sites) and the shape of trees (e.g., treeness, degree of violation of a molecular clock).

Some help messages indicate that summary statistics are reported (e.g., bipartition_support_stats). Summary statistics include mean, median, 25th percentile, 75th percentile, minimum, maximum, standard deviation, and variance. These functions typically have a verbose option that allows users to get the underlying data used to calculate summary statistics.

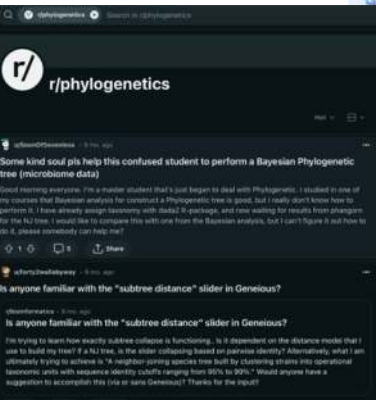
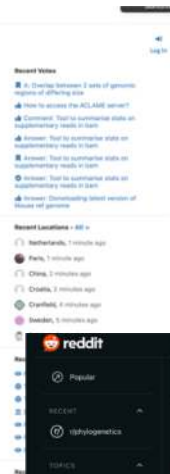
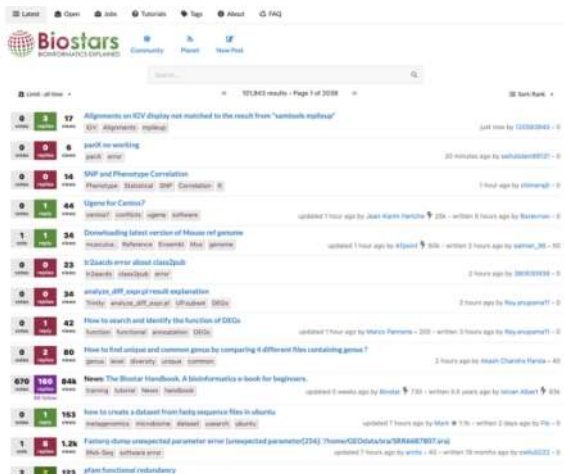
General usage

Calling functions

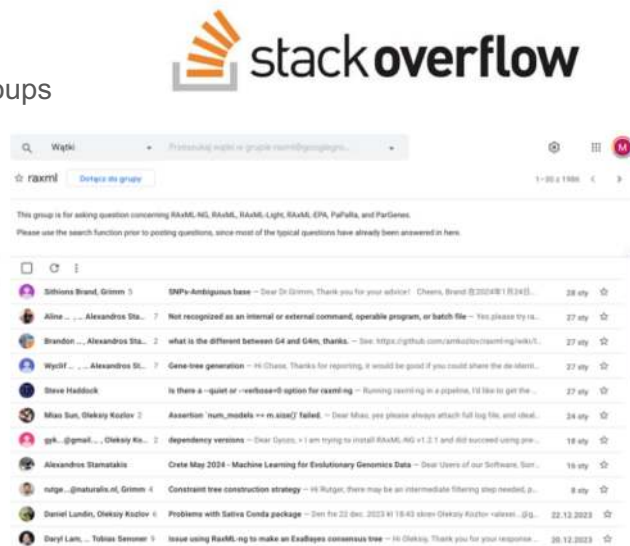
```
phykit <command> [optional command arguments]
```

Command specific help messages can be viewed by adding a `-h/--help` argument after the command. For example, to see the help message for the command 'treeness', execute:

When you know what to do, you have a software, you know how, but something doesn't work



google groups



Questions?