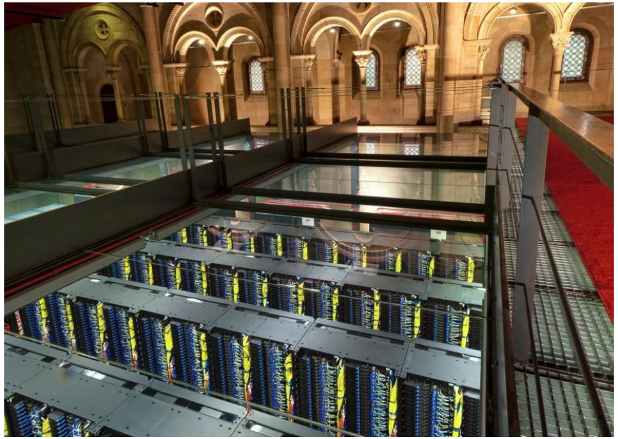
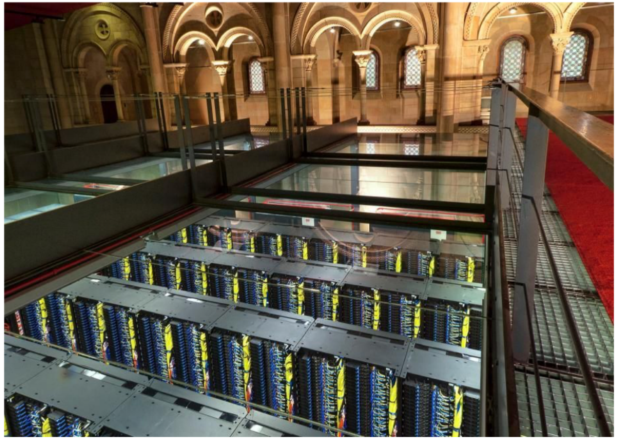
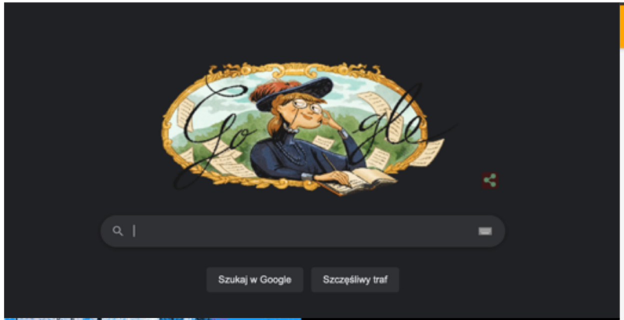
How to get software you need



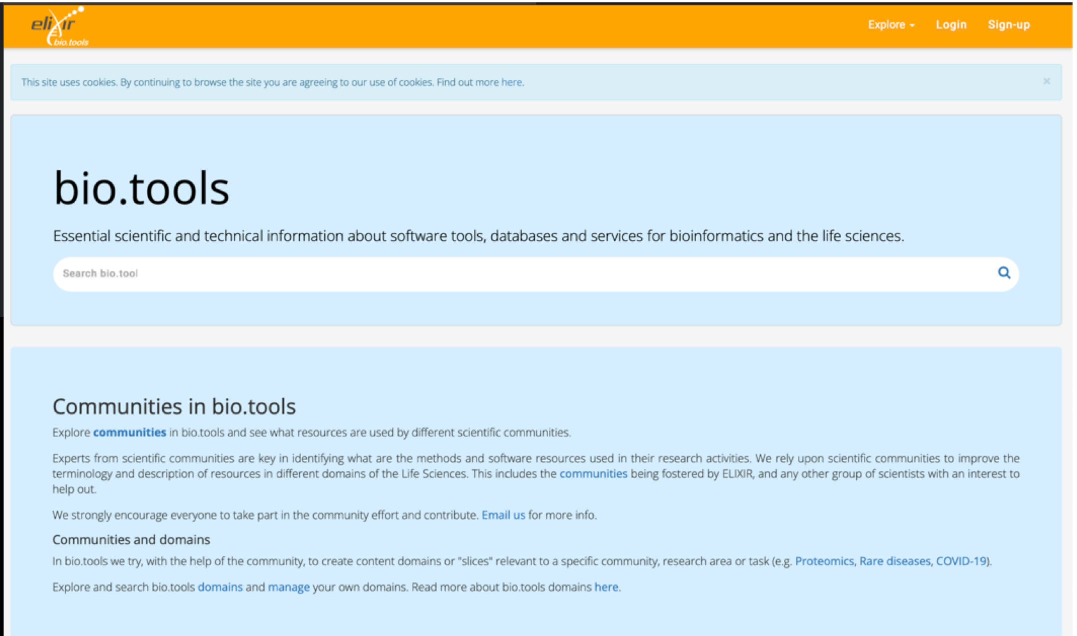


When you know what to do but you don’t know how




Najświeższe wieści ze świata

Dołącz do Twittera.



This site uses cookies. By continuing to browse the site you are agreeing to our use of cookies. Find out more here.

bio.tools

Essential scientific and technical information about software tools, databases and services for bioinformatics and the life sciences.

Communities in bio.tools

Explore **communities** in bio.tools and see what resources are used by different scientific communities.

Experts from scientific communities are key in identifying what are the methods and software resources used in their research activities. We rely upon scientific communities to improve the terminology and description of resources in different domains of the Life Sciences. This includes the communities being fostered by ELIXIR, and any other group of scientists with an interest to help out.

We strongly encourage everyone to take part in the community effort and contribute. Email us for more info.

Communities and domains

In bio.tools we try, with the help of the community, to create content domains or "slices" relevant to a specific community, research area or task (e.g. Proteomics, Rare diseases, COVID-19).

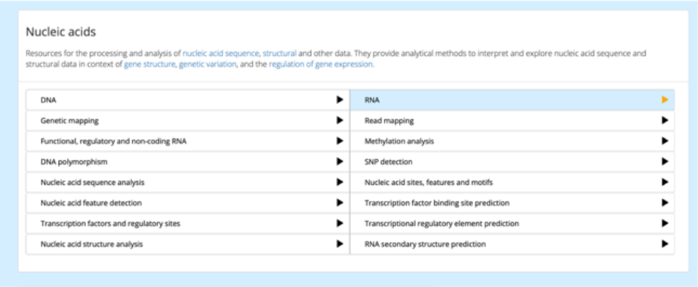
Explore and search bio.tools domains and manage your own domains. Read more about bio.tools domains here.


GBE

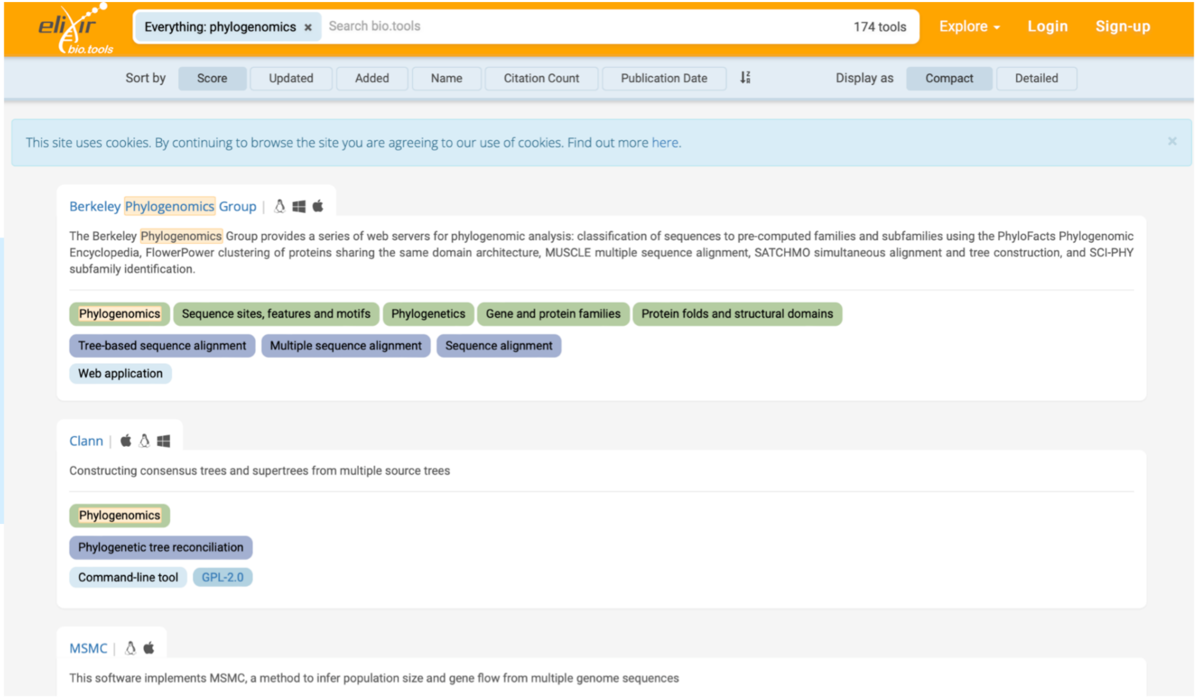
Predicted Input of Uncultured Fungal Symbionts to a Lichen Symbiosis from Metagenome-Assembled Genomes

Workshop on phylogenomics

Biotools



Resources for the processing and analysis of nucleic acid sequence, 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.



This site uses cookies. By continuing to browse the site you are agreeing to our use of cookies. Find out more here.

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

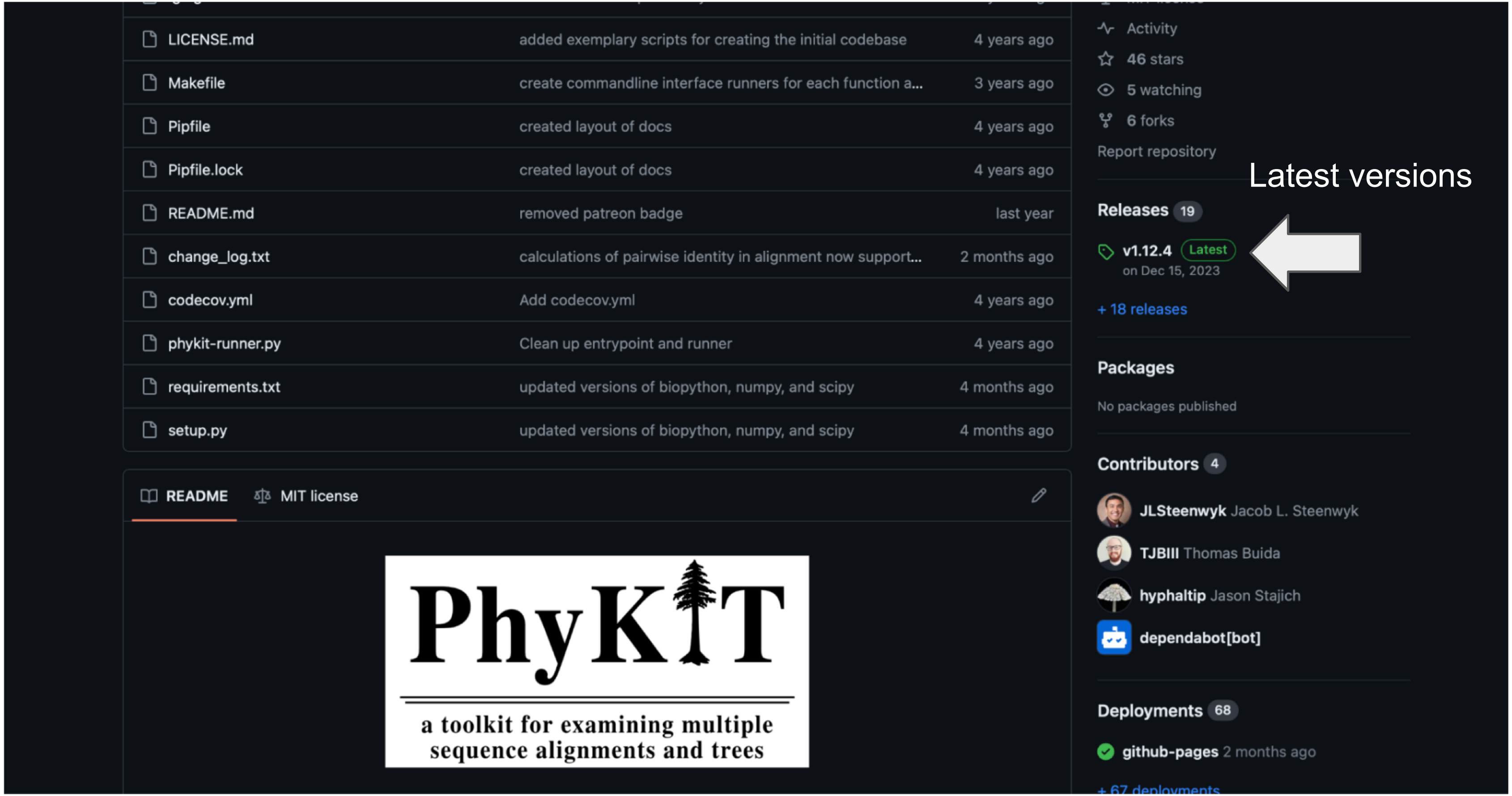
MSMC |

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)



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

README MIT license

PhyKIT

a toolkit for examining multiple sequence alignments and trees

Activity
46 stars
5 watching
6 forks
Report repository

Releases 19

v1.12.4 Latest
on Dec 15, 2023

+ 18 releases

Latest versions

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

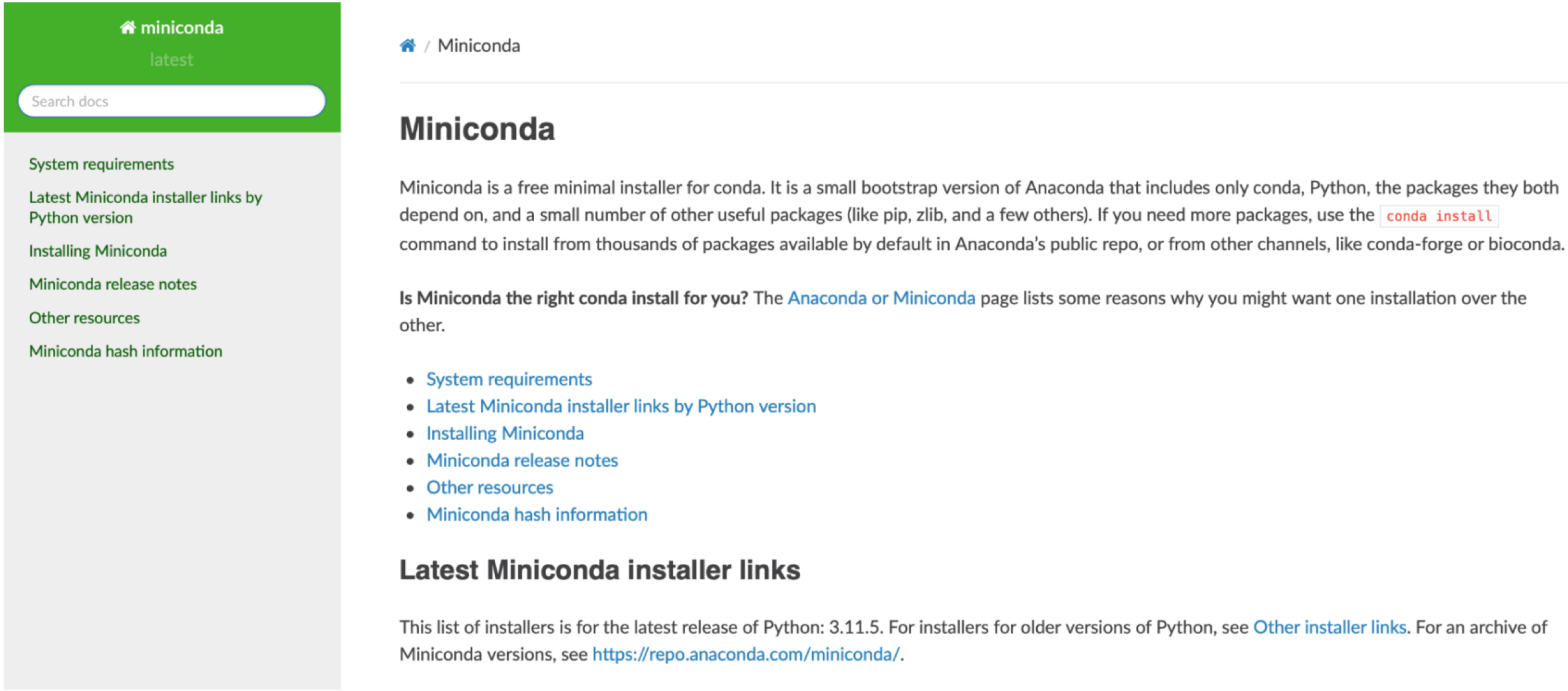
+ 67 deployments

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!**

CONDA

A package manager and environment management system



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

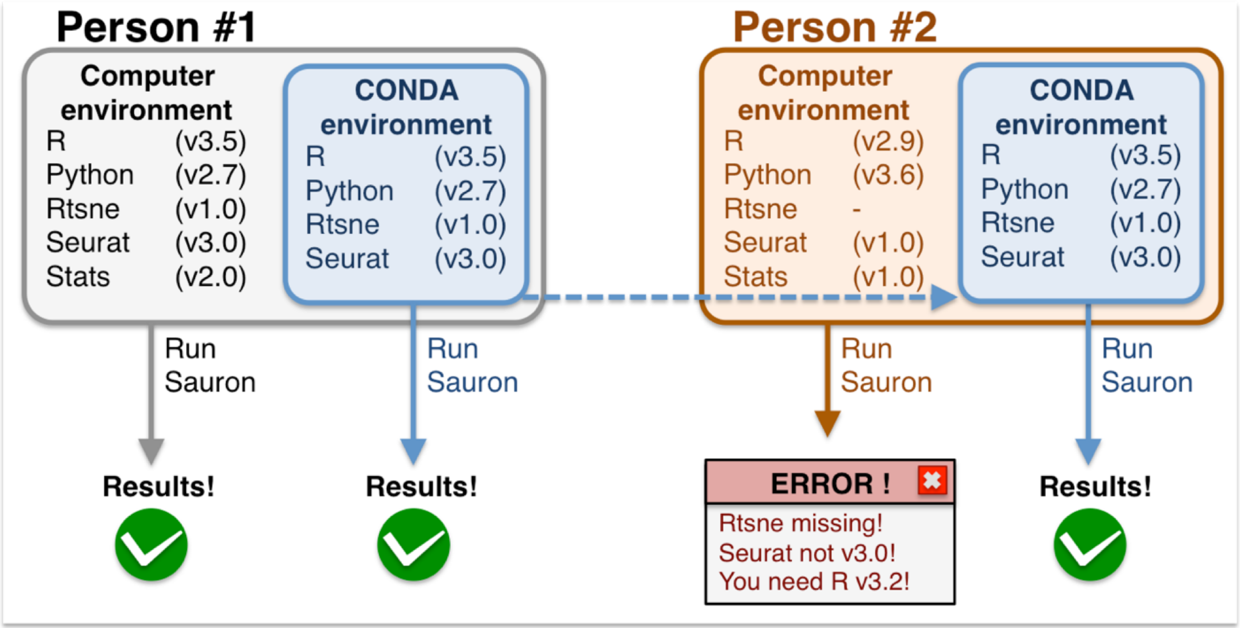
Bioconda lets you install thousands of software packages related to biomedical research using the conda package manager.

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

CONDA

A package manager and environment management system

Enables easy installation
Takes care of dependencies
You can create environments



Person #1

Computer environment
R (v3.5)
Python (v2.7)
Rtsne (v1.0)
Seurat (v3.0)
Stats (v2.0)

CONDA environment
R (v3.5)
Python (v2.7)
Rtsne (v1.0)
Seurat (v3.0)

Run Sauron

Results!

Run Sauron

Results!

Person #2

Computer environment
R (v2.9)
Python (v3.6)
Rtsne -
Seurat (v1.0)
Stats (v1.0)

CONDA environment
R (v3.5)
Python (v2.7)
Rtsne (v1.0)
Seurat (v3.0)

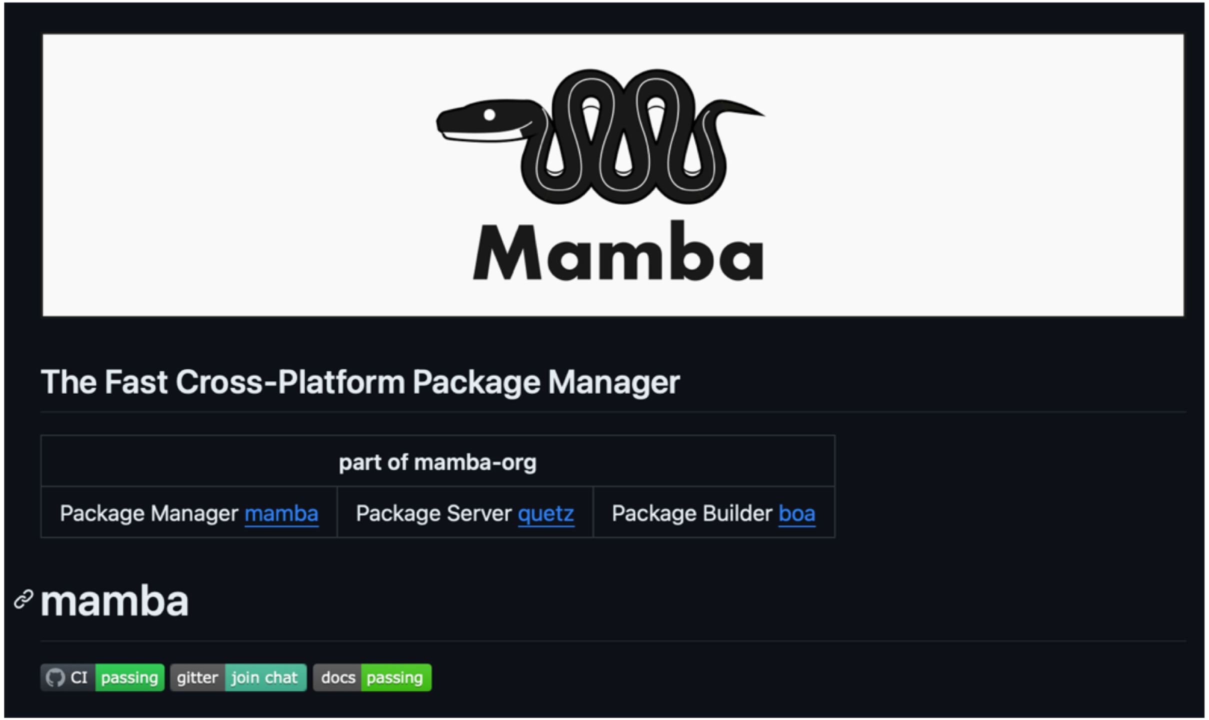
Run Sauron

ERROR !
Rtsne missing!
Seurat not v3.0!
You need R v3.2!

Run Sauron

Results!

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



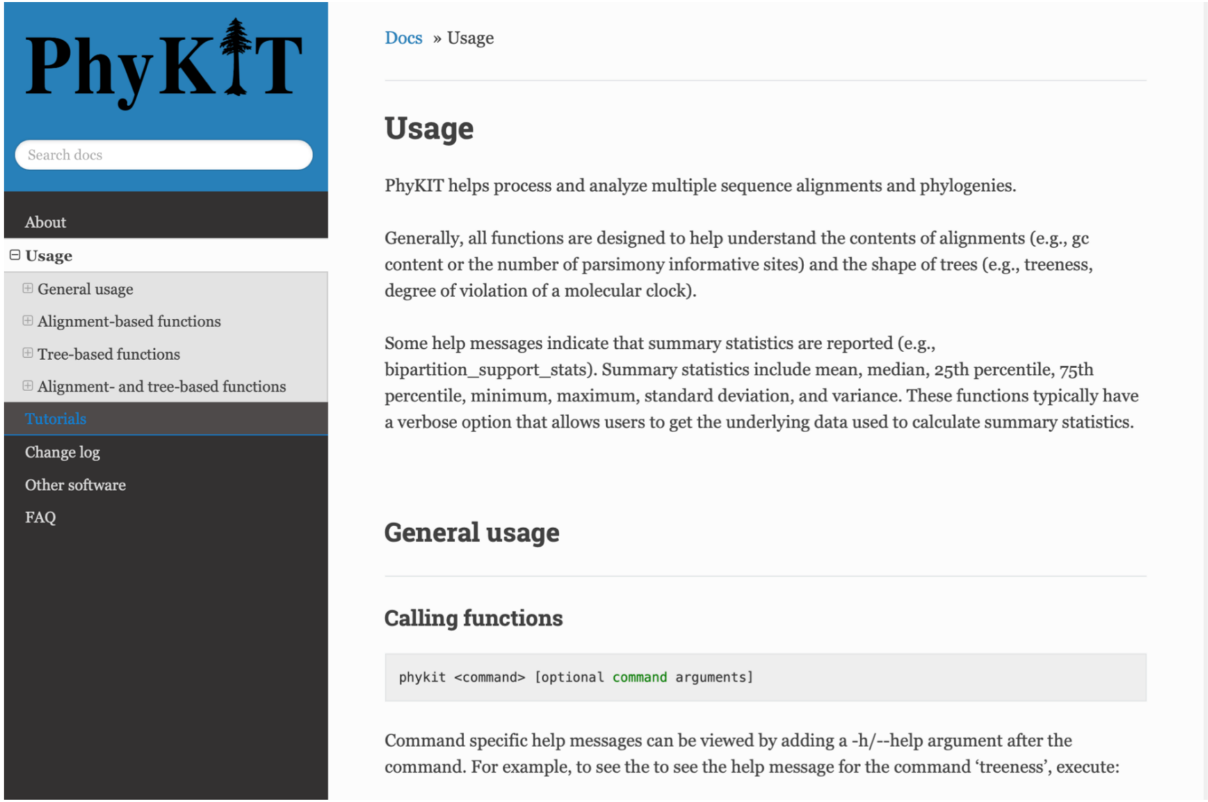
The Fast Cross-Platform Package Manager

part of mamba-org		
Package Manager mamba	Package Server quetz	Package Builder boa

mamba

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

Always check documentation



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.

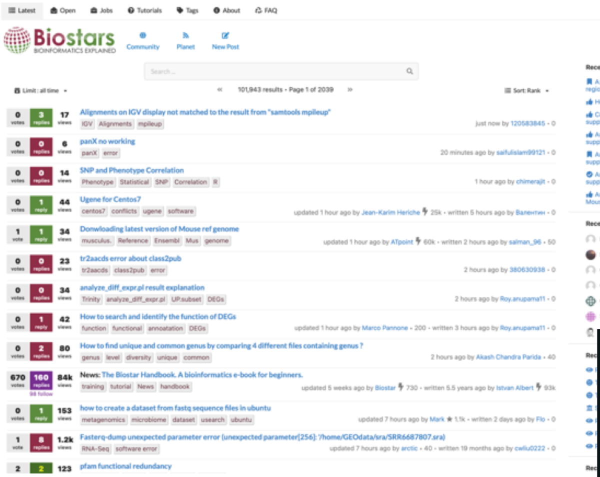
General usage

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 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



101,943 results • Page 1 of 2039

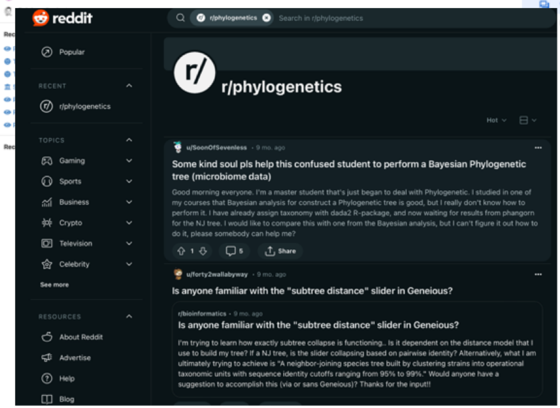
votes	replies	views	title	tags	activity
0	3	17	Alignments on IGV display not matched to the result from "samtools mpileup"	IGV, Alignments, mpileup	just now by 120583845 • 0
0	0	6	panX no working	panX, error	20 minutes ago by saifulislam99121 • 0
0	0	14	SNP and Phenotype Correlation	Phenotype, Statistical, SNP, Correlation, R	1 hour ago by chimerajit • 0
0	1	44	Ugene for Centos7	centos7, conflicts, ugene, software	updated 1 hour ago by Jean-Karim Heriche 25k • written 5 hours ago by Валентин • 0
1	1	34	Donwloading latest version of Mouse ref genome	musculus., Reference, Ensembl, Mus, genome	updated 1 hour ago by ATpoint 60k • written 2 hours ago by salman_96 • 50
0	0	23	tr2aacds error about class2pub	tr2aacds, class2pub, error	2 hours ago by 380630938 • 0
0	0	34	analyze_diff_expr.pl result explanation	Trinity, analyze_diff_expr.pl, UP.subset, DEGs	2 hours ago by Roy.anupama11 • 0
0	1	42	How to search and identify the function of DEGs	function, functional, annoatation, DEGs	updated 1 hour ago by Marco Pannone • 200 • written 3 hours ago by Roy.anupama11 • 0
0	2	80	How to find unique and common genus by comparing 4 different files containing genus ?	genus, level, diversity, unique, common	2 hours ago by Akash Chandra Parida • 40
670	160 98 follow	84k	News: The Biostar Handbook. A bioinformatics e-book for beginners.	training, tutorial, News, handbook	updated 5 weeks ago by Biostar 730 • written 5.5 years ago by Istvan Albert 93k
0	1	153	how to create a dataset from fastq sequence files in ubuntu	metagenomics, microbiome, dataset, usearch, ubuntu	updated 7 hours ago by Mark ★ 1.1k • written 2 days ago by Flo • 0
1	8	1.2k	Fasterq-dump unexpected parameter error (unexpected parameter[256]: '/home/GEOdata/sra/SRR6687807.sra)	RNA-Seq, software error	updated 7 hours ago by arctic • 40 • written 19 months ago by cwliu0222 • 0
2	2	123	pfam functional redundancy		

Recent Votes

- A: Overlap between 2 sets of genomic regions of differing size
- How to access the ACLAME server?
- Comment: Tool to summarise stats on supplementary reads in bam
- Answer: Tool to summarise stats on supplementary reads in bam
- Answer: Tool to summarise stats on supplementary reads in bam
- Answer: Tool to summarise stats on supplementary reads in bam
- Answer: Donwloading latest version of Mouse ref genome

Recent Locations • All »

- Netherlands, 1 minute ago
- Paris, 1 minute ago
- China, 2 minutes ago
- Croatia, 2 minutes ago
- Cranfield, 4 minutes ago
- Sweden, 5 minutes ago



r/phylogenetics

u/SoonOfSevenless • 9 mo. ago

Some kind soul pls help this confused student to perform a Bayesian Phylogenetic tree (microbiome data)

Good morning everyone. I'm a master student that's just began to deal with Phylogenetic. I studied in one of my courses that Bayesian analysis for construct a Phylogenetic tree is good, but I really don't know how to perform it. I have already assign taxonomy with dada2 R-package, and now waiting for results from phangorn for the NJ tree. I would like to compare this with one from the Bayesian analysis, but I can't figure it out how to do it, please somebody can help me?

1 • 5

u/forty2wallabyway • 9 mo. ago

Is anyone familiar with the "subtree distance" slider in Geneious?

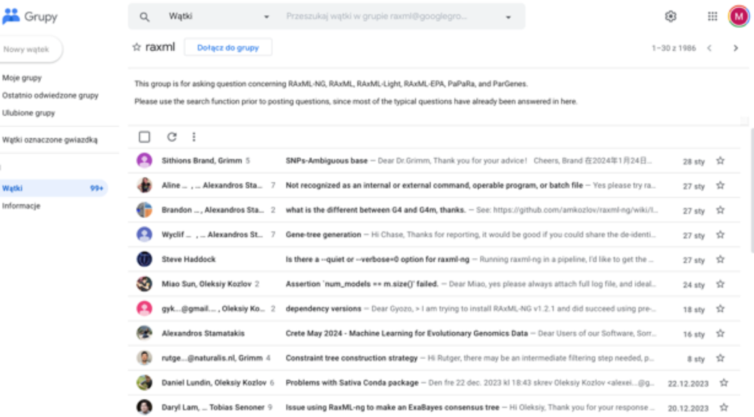
r/bioinformatics • 9 mo. ago

Is anyone familiar with the "subtree distance" slider in Geneious?

I'm trying to learn how exactly subtree collapse is functioning.. Is it dependent on the distance model that I use to build my tree? If a NJ tree, is the slider collapsing based on pairwise identity? Alternatively, what I am ultimately trying to achieve is "A neighbor-joining species tree built by clustering strains into operational taxonomic units with sequence identity cutoffs ranging from 95% to 99%." Would anyone have a suggestion to accomplish this (via or sans Geneious)? Thanks for the input!!

stackoverflow

google groups



☆ raxml

This group is for asking question concerning RAxML-NG, RAxML, RAxML-Light, RAxML-EPA, PaPaRa, and ParGenes.

Please use the search function prior to posting questions, since most of the typical questions have already been answered in here.

Sithions Brand, Grimm 5	**SNPs-Ambiguous base** – Dear Dr.Grimm, Thank you for your advice! Cheers, Brand 在2024年1月24日...	28 sty	☆
Aline ... , ... Alexandros Sta... 7	**Not recognized as an internal or external command, operable program, or batch file** – Yes please try ra...	27 sty	☆
Brandon ... , Alexandros Sta... 2	**what is the different between G4 and G4m, thanks.** – See: https://github.com/amkozlov/raxml-ng/wiki/I...	27 sty	☆
Wyclif ... , ... Alexandros St... 7	**Gene-tree generation** – Hi Chase, Thanks for reporting, it would be good if you could share the de-identi...	27 sty	☆
Steve Haddock	**Is there a --quiet or --verbose=0 option for raxml-ng** – Running raxml-ng in a pipeline, I'd like to get the ...	27 sty	☆
Miao Sun, Oleksiy Kozlov 2	**Assertion `num_models == m.size()' failed.** – Dear Miao, yes please always attach full log file, and ideal...	24 sty	☆
gyk...@gmail... , Oleksiy Ko... 2	**dependency versions** – Dear Gyozo, > I am trying to install RAxML-NG v1.2.1 and did succeed using pre-...	18 sty	☆
Alexandros Stamatakis	**Crete May 2024 - Machine Learning for Evolutionary Genomics Data** – Dear Users of our Software, Sorr...	16 sty	☆
rutge...@naturalis.nl, Grimm 4	**Constraint tree construction strategy** – Hi Rutger, there may be an intermediate filtering step needed, p...	8 sty	☆
Daniel Lundin, Oleksiy Kozlov 6	**Problems with Sativa Conda package** – Den fre 22 dec. 2023 kl 18:43 skrev Oleksiy Kozlov <alexei...@g...	22.12.2023	☆
Daryl Lam, ... Tobias Senoner 9	**Issue using RaxML-ng to make an ExaBayes consensus tree** – Hi Oleksiy, Thank you for your response ...	20.12.2023	☆

Questions?