How to get software you need
When you know what to do but you don’t know how
Biotools

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 so-phy subfamily identification.

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

- **Clann**
  - Constructing consensus trees and supertrees from multiple source trees

- **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)
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- Conda!
A package manager and environment management system
Installation with conda
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
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.
Questions?