

SUMAC: Supermatrix Constructor version 1.0 Manual

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Chapter 1

Introduction

1.1 About SUMAC

SUMAC (Supermatrix Constructor) is a Python package to data-mine GenBank, construct phylogenetic supermatrices, and assess the phylogenetic decisiveness of a matrix given the pattern of missing sequence data. It is designed to be run as a command-line program, though the modules can also be imported and used in other Python scripts. SUMAC will assemble supermatrices for any taxonomic group recognized in GenBank, and is optimized to run on multicore processors and clusters by utilizing multiple parallel processes.

When run from the command-line, SUMAC will perform a number of steps to construct a supermatrix. First, SUMAC creates a local SQLite3 (Hipp and Kennedy, 2007) database of the specified GenBank division (e.g. PLN or MAM), automatically downloading sequences from NCBI if necessary. Using NCBI taxonomy, SUMAC searches the local database for all sequences in the user-specified ingroup and outgroup. Found sequences are then clustered as putative homologs in one of two ways: (1) performing exhaustive all-by-all BLASTn (Camacho et al., 2009) comparisons of each ingroup and outgroup sequence and using a single-linkage hierarchical clustering algorithm, or (2) user-provided guide sequences that typify each cluster are BLASTed against all ingroup and outgroup sequences. For more details about the clustering algorithms used please see Freyman (2015). Once clustering is complete, SUMAC discards clusters that are not phylogenetically informative (< 4 taxa), and aligns each cluster of sequences using MAFFT (Katoh et al., 2002) with the `--adjustdirection` flag to ensure correct sequence polarity. The individual locus alignments are saved to enable gene tree inference, and then the alignments are

concatenated by species binomial (based on the NCBI taxonomy) to create the final supermatrix. Finally, a number of metrics are reported, a graph indicating taxon coverage density is generated, and spreadsheets (in CSV format) are produced with information about each DNA region and GenBank accession used in the supermatrix. There are many options described in detail later in this manual.

1.2 Citing the Program

If you use SUMAC for a published paper please cite the following release note:

Freyman, W.A. In prep. SUMAC: software for constructing phylogenetic supermatrices and assessing partially decisive taxon coverage.

1.3 Installation

1.3.1 Dependencies

The following dependencies must be installed to run SUMAC:

- Python 2.7
- Biopython
- MAFFT v6.9+
- BLAST+

matplotlib should also be installed if you want SUMAC to generate graphs.

1.3.2 Installing Dependencies on Linux

The following commands install the requirements for Debian GNU/Ubuntu Linux systems:

```
sudo pip install numpy
sudo pip install matplotlib
sudo pip install biopython
sudo apt-get install ncbi-blast+
sudo apt-get install mafft
```

1.3.3 Installing Requirements on Mac

The following commands install the requirements of Mac OS X:

```
sudo pip install numpy
sudo pip install matplotlib
sudo pip install biopython
```

Install BLAST by downloading the appropriate executable from:

<ftp://ftp.ncbi.nlm.nih.gov/blast/executables/blast+/LATEST/>

Install MAFFT from here:

<http://mafft.cbrc.jp/alignment/software/>

1.3.4 Installing SUMAC

To install SUMAC use this command:

```
sudo pip install sumac
```

If you prefer to use the development version in the Git repository use these commands:

```
git clone https://github.com/wf8/sumac.git
cd sumac/src
python setup.py install
```

1.4 License and Warranty

SUMAC is free software; you can redistribute it and/or modify it under the terms of the GNU General Public License as published by the Free Software Foundation; either version 3 of the License, or (at your option) any later version.

The program is distributed in the hope that it will be useful, but WITHOUT ANY WARRANTY; without even the implied warranty of MERCHANTABILITY or FITNESS FOR A PARTICULAR PURPOSE. See the GNU General Public License for more details (<http://www.gnu.org/copyleft/gpl.html>).

Chapter 2

Quick Start Tutorial

This chapter provides the quick way to get started using SUMAC. There are many details described in Chapter 3 that would likely be helpful.

2.1 Construct a Supermatrix

The most basic usage of SUMAC is to build a supermatrix with the following command:

```
python -m sumac -d pln -i Onagraceae -o Lythraceae
```

This command is an example of the minimum amount of input required to run SUMAC. The first part of the command `python -m sumac` runs the SUMAC module. The `-d pln` tell SUMAC to download the PLN (Plant) GenBank division. The `-i Onagraceae` and `-o Lythraceae` tells SUMAC to search the PLN division for all sequences within the taxonomic groups Onagraceae (the ingroup) and Lythraceae (the outgroup). SUMAC will then perform all-by-all BLAST comparisons of each sequence, build clusters of putatively homologous sequences, and construct a supermatrix.

Unless you are on a large multi-core system, the clustering will take a long time to be performed since well over 5000 sequences will be found. To speed up the supermatrix construction, you could make a FASTA file of guide sequences to define each cluster. Each guide sequence should be an example of a sequence commonly used for phylogenetic analysis. Then you could then use this command:

```
python -m sumac -d pln -i Onagraceae -o Lythraceae -g guides.fasta
```

Which approach is better for constructing supermatrices? Using guide sequences makes supermatrix construction much faster, however it requires a priori knowledge of which DNA regions will be used in the supermatrix. Performing all-by-all BLAST comparisons is computationally more expensive, but it effectively data-mines GenBank in an exploratory fashion, so that sequence data not necessarily used in previous systematic studies can also be incorporated into the supermatrix. The decision will depend on the size of the taxonomic group being analyzed and the computational resources available.

To calculate the partial decisiveness (PD) and Missing Sequence Decisiveness Scores (MSDS) for the data matrix, run SUMAC with the `--decisiveness` flag. See Freyman (2015) for an explanation of these metrics. Please be aware that the decisiveness computations can be time consuming.

2.2 Explanation of the Output Files

SUMAC will output the following files:

1. `alignments/combined.fasta` The final aligned supermatrix in FASTA format.
2. `alignments/N.fasta` The alignment of gene region N where N is an integer > 0 .
3. `clusters/N.fasta` The unaligned raw sequence cluster of gene region N .
4. `gb_search_results` File used by SUMAC to save the results of the GenBank sequence search in case the search is re-run. This file is not human readable.
5. `genbank_accessions.csv` A table with each GenBank accession used, ordered by gene region and taxon (like the appendices found in most systematics papers).
6. `gene_regions.csv` A table with the number of taxa, the aligned length, the percent missing data, and the taxon coverage density of each gene region used in the supermatrix.
7. `plot.pdf` A figure that shows how much sequence data was available for each taxon for each gene region.
8. `sumac_log` Log of the SUMAC run, and contains a great deal of information about the supermatrix construction, including final metrics such as the partial decisiveness (PD) of the supermatrix.

Chapter 3

SUMAC in Detail

3.1 Downloading GenBank

3.1.1 GenBank Division

The first time you run SUMAC you must specify which GenBank division to download with the `-d div` option, where `div` is the GenBank designated three letter code of the division (PLN, MAM, etc). Once SUMAC has downloaded the GenBank division, future SUMAC runs may leave out the `-d div` option to avoid repeatedly download the same files.

3.1.2 GenBank File Path

By default, each SUMAC run searches for the downloaded GenBank files in `./genbank/`, a subdirectory of the current run's directory. It may be useful to save the GenBank files outside of the current working directory, in which case you can specify the absolute path of the GenBank files with the `-p path` option. For example, if you want to build multiple supermatrices (or different versions of the same one) each in a different working directory it is helpful to use `-p /genbank` so that all SUMAC runs use the same copy of the GenBank files.

3.2 Specifying Ingroup and Outgroup

The `-i` and `-o` options must be used to specify which ingroup and outgroup to search for. The taxonomic names must be those used by GenBank. If a SUMAC run is repeated with the

same ingroup and outgroup, SUMAC will load the previous search results to save time.

3.3 Using Guide Sequences

Guide sequences should be in a single standard FASTA file specified using the `-g` option. The names of the guide sequences will be ignored, and each of the ingroup and outgroup sequences will be BLASTed against the guide sequences.

3.4 Homologous Sequence Thresholds

3.4.1 BLAST E-value

By default, SUMAC uses a threshold default BLASTn e-value $1.0e - 10$. This can be changed with the `-e` option.

3.4.2 Sequence Length Similarity

SUMAC uses a default threshold of sequence length percent similarity of 0.5. This can be changed with the `-l` option.

3.5 Partial Decisiveness

blah blah

3.6 Supermatrix Figure

blah blah

Bibliography

- Camacho, C., Coulouris, G., Avagyan, V., Ma, N., Papadopoulos, J., Bealer, K., and Madden, T. L. (2009). BLAST+: architecture and applications. *BMC Bioinformatics*, 10(1):421.
- Freyman, W. (2015). SUMAC: software for constructing phylogenetic supermatrices and assessing partially decisive taxon coverage. *In prep.*
- Hipp, D. R. and Kennedy, D. (2007). Sqlite. <http://www.sqlite.org>.
- Katoh, K., Misawa, K., Kuma, K.-i., and Miyata, T. (2002). Mafft: a novel method for rapid multiple sequence alignment based on fast fourier transform. *Nucleic acids research*, 30(14):3059–3066.