

Phylogenetics and Molecular Evolution/Filogenética e Evolução Molecular

Octávio S. Paulo

Computational Biology and Population Genomics Group (CoBiG2)



**Ciências
ULisboa**

Faculdade
de Ciências
da Universidade
de Lisboa



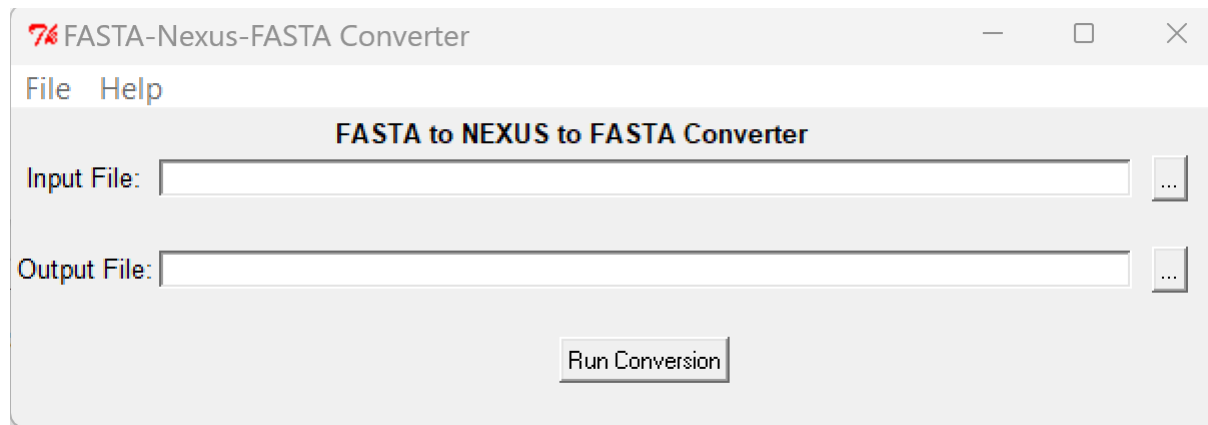
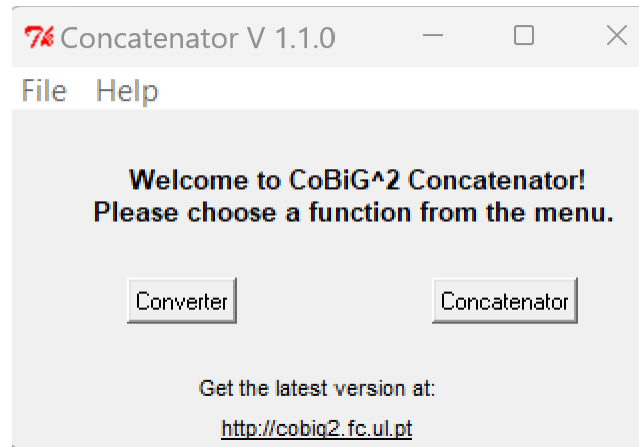
CoBiG2
<http://cobig2.fc.ul.pt>

**Computational
Biology & Population
Genomics Group**

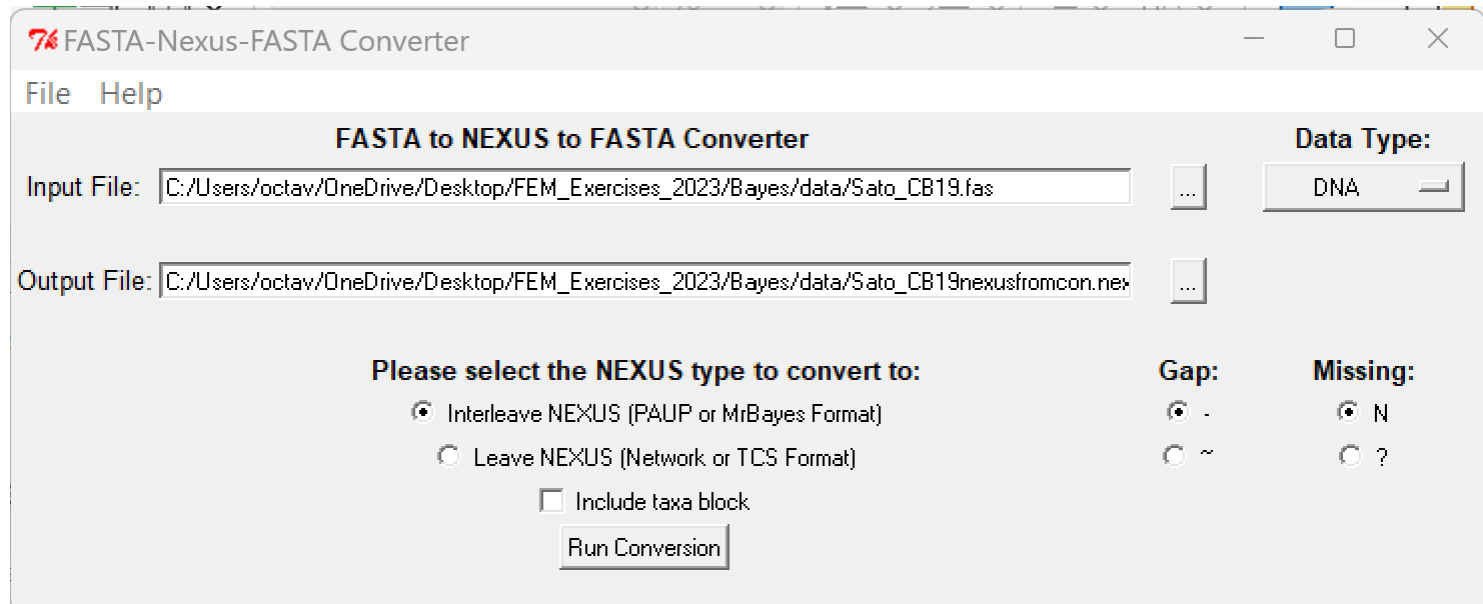


CE3C
centre for ecology, evolution
and environmental changes

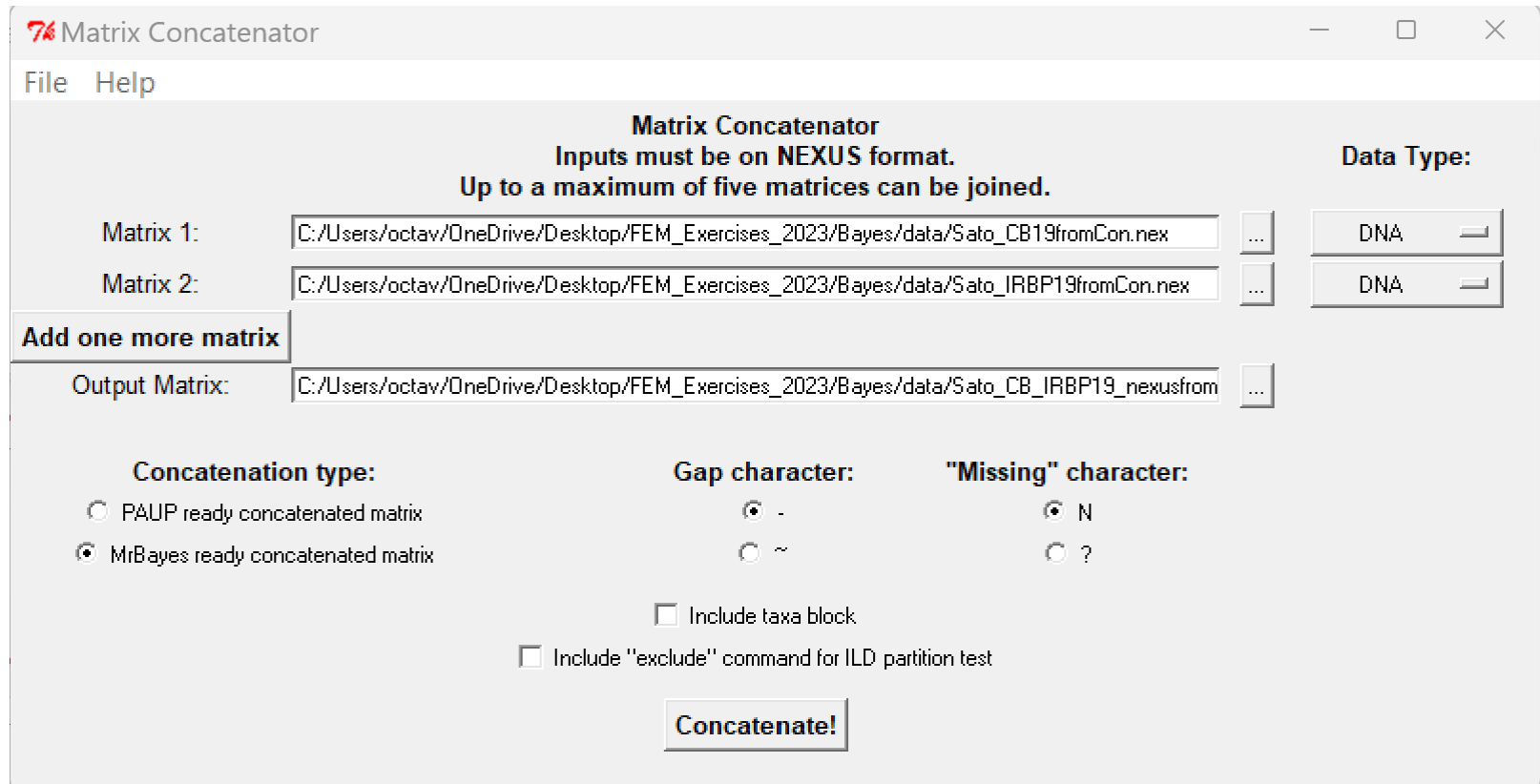
Concatenator

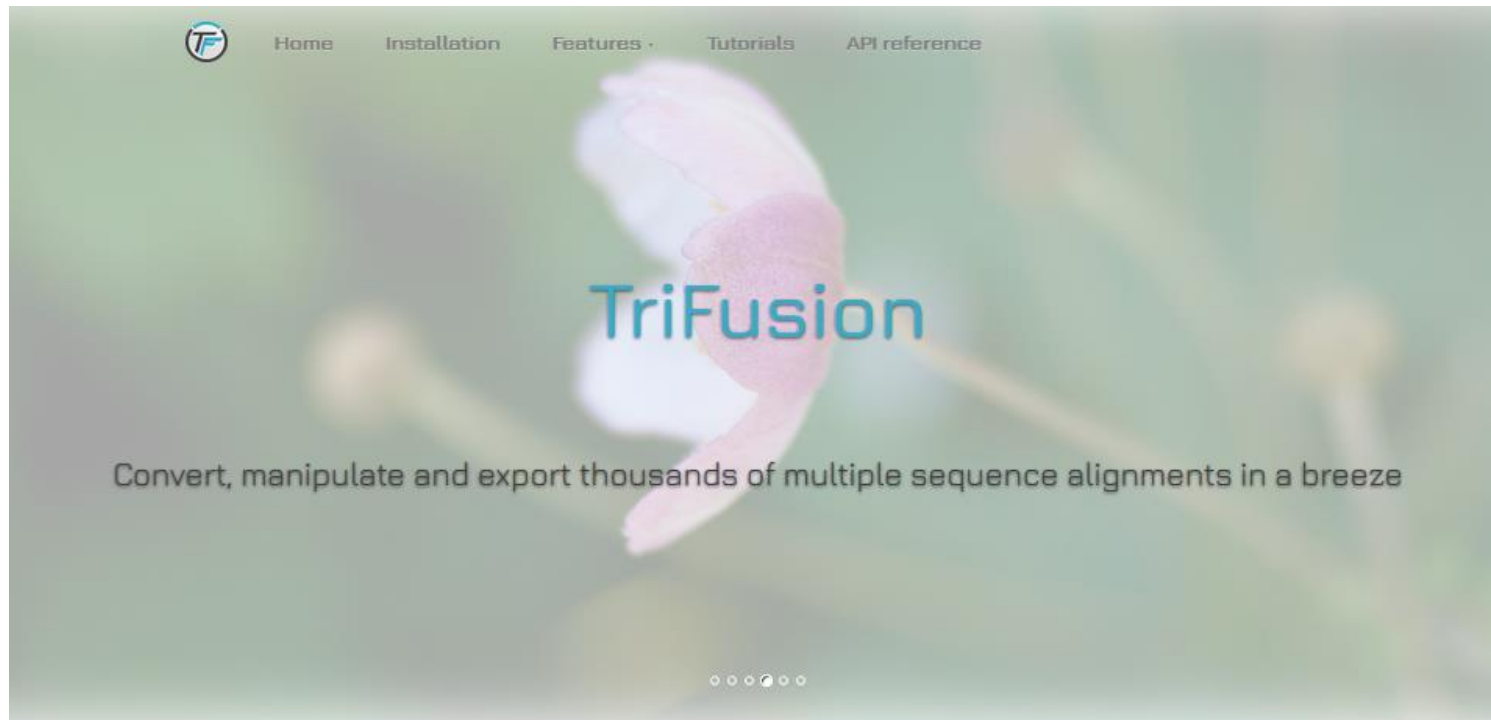


Concatenator/Converter Fasta-Nexus



Concatenator/Concatenate (to 5 genes)





Get Started on TriFusion



Download

Installers are available for Windows, MacOS and several Unix distro's. PPAs are available Debian and Ubuntu and AUR packages for ArchLinux.

[Get TriFusion](#)



User Guide

Get the latest documentation on the full features of TriFusion, how to operate GUI and command line versions of TriFusion, and more!

[Download guide](#)



View on GitHub

TriFusion is and will always be free software (under GPLv3 license). Feel free to view and modify the source code, hosted on GitHub.

[View Source](#)



Welcome to TriFusion

Streamlining phylogenomic data gathering, processing and visualization

Start by clicking 'Menu > Open file(s)', by typing 'Ctrl + O' or simply **drag and drop** your files into TriFusion's window

Quick Open Project

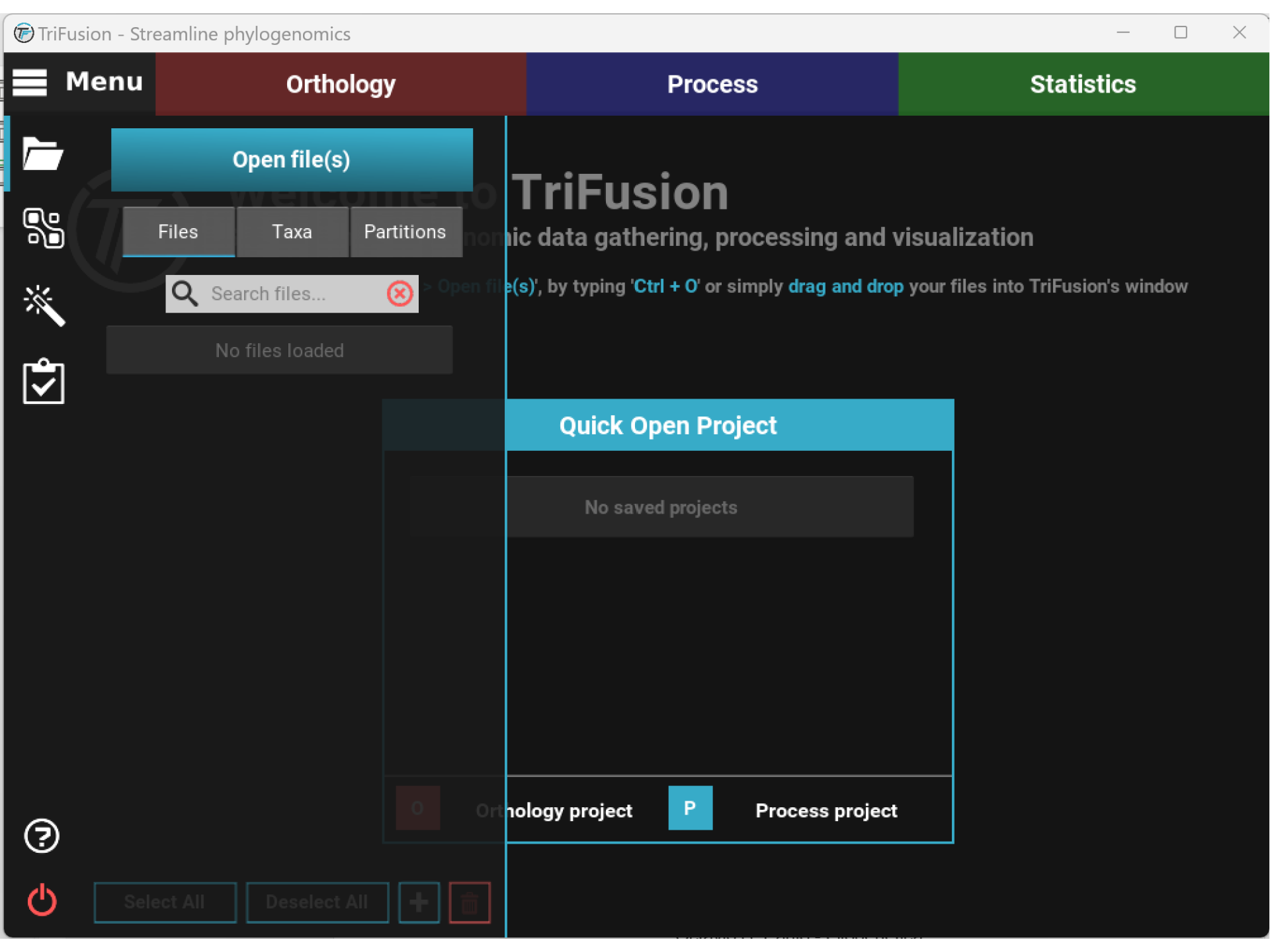
No saved projects

O

Orthology project

P

Process project



Open file(s)

Files Taxa Partitions

Search files... [X]

No files loaded

TriFusion

Phylogenomic data gathering, processing and visualization

> Open file(s), by typing 'Ctrl + O' or simply drag and drop your files into TriFusion's window

Quick Open Project

No saved projects



Orthology project



Process project



Select All

Deselect All



Menu

Orthology

Process

Statistics

My Computer

C:

G:

octav

Bookmarks



Input data type

Alignment/Sequence set

Proteome



C:\\Users\\octav\\Dropbox\\AArea_In_Out\\1_temp



Clear Selection

Name

..\\

Camila_ERGA_Nature_2023.pdf

Forestry_2022_Nature Ecology and Evolution.pdf

Jupiter.pdf

Mike.docx

Mike_orituary_2023.pdf

Nei_Orituary_2023.pdf

Sato_CB19.fas

Sato_IRBP19.FAS

Video_teclado1.mp4

video_teclado2.mp4

Find:

Aa

All

Load selection

Load & go back

Cancel

Choose your destiny

Conversion

Concatenation

Execute

View Queue

Clear Options

 **Menu****Orthology****Process****Statistics**

Choose your destiny

Conversion**Concatenation**

General

Data set

Select the active taxa data set to perform operations

**Active files****Active taxa****Output Format**

Choose the format of the output file(s). Multiple formats may be chosen

Fasta**Output directory**

Save output file(s) to the selected directory.

Select...**Show additional options****Execute****View Queue****Clear Options**

Choose your destiny

Conversion

Concatenation

Revert a concatenated file?



OFF

General

Data set

Select the active taxa data set to perform operations



Active files

Active taxa

Output Format

Choose the format of the output file(s). Multiple formats may be chosen

Fasta

Output file

Save output file to the selected file.

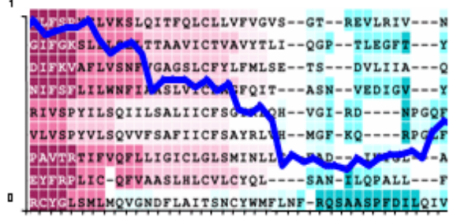
Select...

Show additional options

Execute

View Queue

Clear Options



The GUIDANCE2 Server

Server for alignment confidence score

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Select Algorithm GUIDANCE2 ▾

Type your sequences ([FASTA format only](#)) * large strings should be uploaded as files

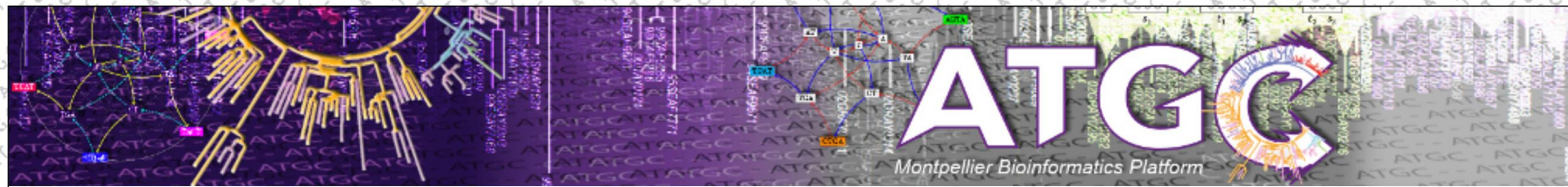
OR

Upload your sequences file ([FASTA format only](#)) Browse... No file selected.

Sequences Type: Amino Acids Nucleotides Codons

Select the MSA algorithm MAFFT (default) ▾

Warning: PRANK is significantly more time consuming. MAFFT is the fastest.



PhyML 3.0: new algorithms, methods and utilities

Please cite:

"New Algorithms and Methods to Estimate Maximum-Likelihood Phylogenies: Assessing the Performance of PhyML 3.0."
Guindon S., Dufayard J.F., Lefort V., Anisimova M., Hordijk W., Gascuel O.
Systematic Biology, 59(3):307-21, 2010.

Get the latest PhyML releases from [GitHub](#).

PhyML online execution

▼ Input Data

Sequence alignment
(PHYLIP format)

Drop alignment file here



or

Browse...

No file selected.

file example (DNA file)
DNA amino-Acids

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Online execution

Source code on GitHub

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PhyML versions

User guide

Binaries

Databases

Datasets

IQTree <http://iqtree.cibiv.univie.ac.at/>

IQ-TREE web server: fast and accurate phylogenetic trees under maximum likelihood

Server load: 103%

Trifinopoulos J, Nguyen LT, von Haeseler A, Minh BQ (2016) *Nucl. Acids Res.* 44 (W1): W232-W235. [doi: 10.1093/nar/gkw256](https://doi.org/10.1093/nar/gkw256)

Tree Inference

Model Selection

Analysis Results

For a quick start, take a look at the [tutorial](#) for the IQ-TREE web server.

Please visit the [IQ-TREE homepage](#) for more information or if you want to download the main software.

Data Privacy Statement: All your personal data are strictly confidential and will not be shared with any third parties. Your data will be automatically deleted after 180 days.

Input Data

Alignment file :

Browse...

Show example >

Use example alignment: Yes

?

Sequence type:

- Auto-detect DNA Protein Codon
 DNA->AA Binary Morphology

?

Partition file:

This field is optional.

Browse...

Show example >

Partition type:

- Edge-linked
 Edge-unlinked

?

Substitution Model Options

Substitution model:

Auto



?

FreeRate heterogeneity: Yes [+R]

Rate heterogeneity:

- Gamma [+G] Invar. sites [+I]

?


#rate categories:

4




State frequency:

- Empirical (from data) AA model (from matrix) ML-optimized



CIPRES Cyberinfrastructure for
Phylogenetic Research



ACCESS | Advancing
Innovation

SIMONS FOUNDATION

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All submissions are
working normally.

Welcome to CIPRES, a public resource for phylogenetics and population biology.

CIPRES provides all researchers with a simple browser interface for access to community codes run efficiently on large computational resources of the NSF ACCESS project. You can also access these same capabilities programatically via the [CIPRES REST API](#). **Geneious Prime USERS! Our [Geneious Plugin](#) allows you to run MrBayes, RAxML, and IQ-Tree on CIPRES.**

High Performance Parallel Codes for Large Tree Inference, Sequence Alignment, and Population Biology: including RAxML, MrBayes, BEAST, BEAST2, IQ-Tree and more.

[Complete parallel code list here.](#)

Serial Codes for Sequence Alignment:

ClustalW; Divvier; MPBOOT; PREQUAL; PROBCONS; and PROBALIGN

[Sign up now](#), and get 1000 hours of compute time for free!