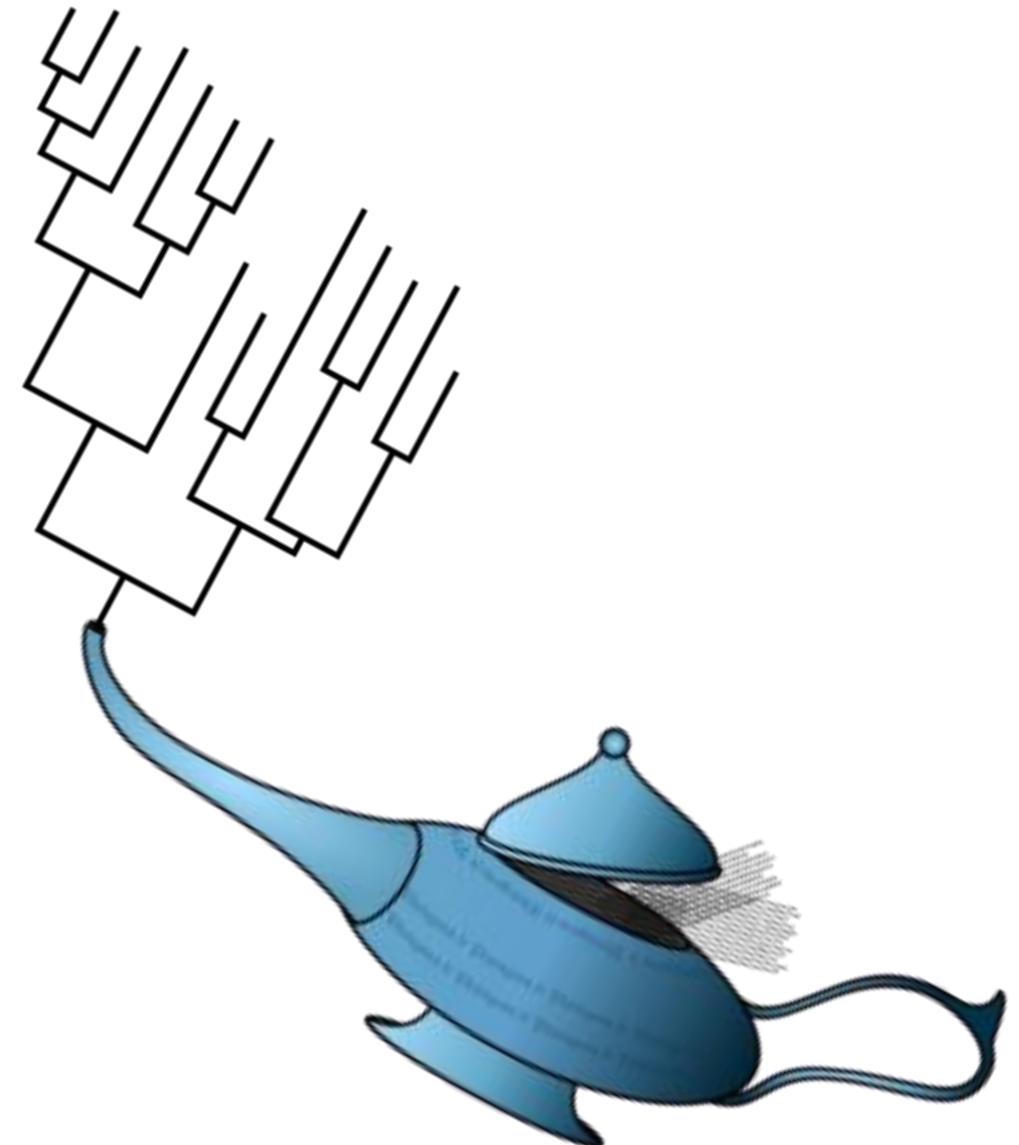


Building phylogenetic tree

Summer School:
„from fungal morphology to genotype”

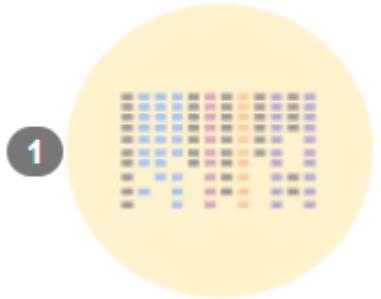


Julia Pawłowska

University of Warsaw

30.08.2024

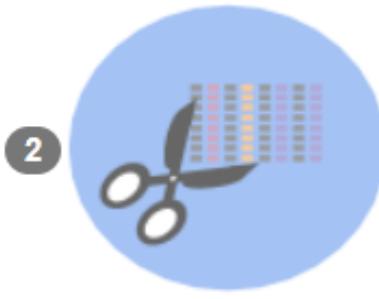
General pipeline



1

Multiple Alignment

- MAFFT
- MUSCLE
- Clustal Omega



2

Alignment Curation

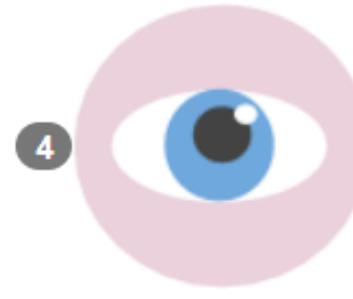
- BMGE
- Gblocks
- Noisy
- trimAl



3

Tree Inference

- FastME
- TNT
- PhyML+SMS
- PhyML
- FastTree
- MrBayes

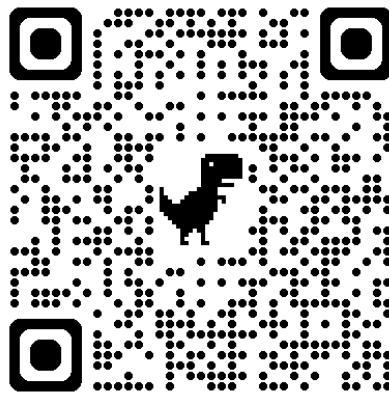


4

Tree Rendering

- Newick Display

Automatic tool: <https://ngphylogeny.fr/>



The screenshot shows the NGPhylogeny.fr homepage. At the top, there is a dark banner with the text "ATAAAAAGAACTCAACATTCTGGGAAGTTCATTAGAATG" and "ATAAAAAGAACACAAGATTGGGAAGTCCATTGAAATG". Below this is the "NGPhylogeny.fr" logo. The main navigation menu includes "Home", "Phylogeny Analysis", "Tools", "Workspace" (with a notification count of 0), "Documentation", and "About". A central call-to-action box contains the text "Robust phylogenetic analysis for everyone." followed by a bullet point: "Free, simple to use web service dedicated to reconstructing and analysing phylogenetic relationships between molecular sequences." Below this is a green button with the text "Let's GO ! with One Click Workflow". To the right of the button is a small illustration of a blue genie lamp with a white sprout of a phylogenetic tree emerging from it.



› One Click

Fully automatic workflow
Default tools + default parameters.



› Advanced

Semi automatic workflow
Default tools + custom parameters



› A la Carte

Custom workflow
Custom tools + Custom parameters.

[Home](#)[Phylogeny Analysis](#)[Tools](#)[Workspace](#) 0[Documentation](#)[About](#)[Login](#)

► One Click Workflows

Select your workflow

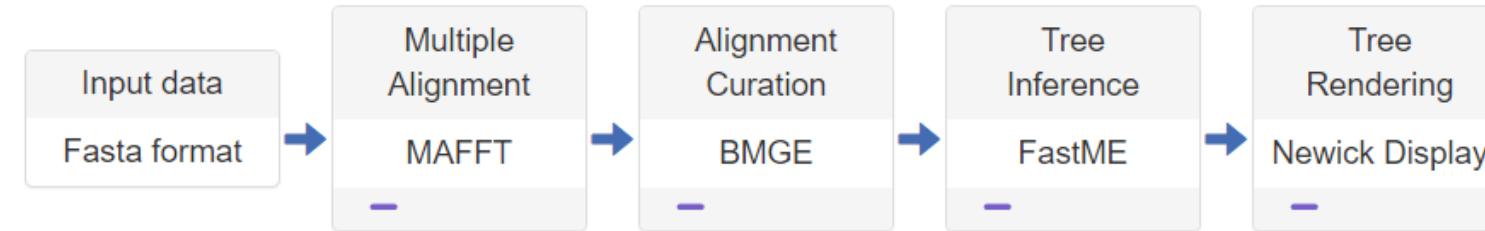
FastME/OneClick

PhyML/OneClick

PhyML+SMS/OneClick

FastTree/OneClick

Workflow skeleton



Choose input data

Input Data (Fasta format with more than 3 sequences)

Input file

Choose file To Upload

Choose File

Pasted text

 FastME/OneClick

 PhyML/OneClick

 PhyML+SMS/OneClick

 FastTree/OneClick

Input data

Fasta format

Multiple
Alignment

MAFFT

Alignment
Curation

BMGE

Tree
Inference

FastME

Choose input data

Input Data (Fasta format with more than 3 sequences)

Input file

1 files were chosen

Choose File



Pluteus_test_tree.txt

size: 6.50 KB type: txt



Pasted text

Blast run*

Galaxyfile*

Submit

Example



History

[Refresh](#)[Reuse](#)

Url	ngphylogeny.fr/workspace/history/3555895aec5a0983	
Name	NGPhylogeny Analyse - FastME/OneClick	
e-mail		

Tool	Step	File Name	Status							
Newick Display	15.	All tree images							.tar	
	14.	Tree image							.svg	
FastME	13.	Mapping between short sequence id and names (useful to interpret some bootstrap log files if any)							.txt	
	12.	Output Tree							.nhx	
	11.	FastME Distance matrix							.txt	
	10.	FastME Information							.txt	
	9.	BMGE Cleaned sequences Html							.html	

PRESTO - Phylogenetic tReE viSualisaTiOn -

Tree Layout

Phylogram

Linear

Dendrogram

Radial

Slanted

Tree ordering



Increasing ladderizing



decreasing ladderizing



Retrieve original order

Tree settings

0.10



Multiple Sequence Alignment Viewer - the MSAViewer - a BioJS component.

Import Sorting Filter Selection Vis.elements Color scheme Extras Export Help

ID	Label	2	4	6	8	10	12	14	16	18	20	22	24	26	28	30	32	34	36	38	40	42	44	46	48	50	52	54	56	58					
1	Pluteus fenzlii	G	G	A	T	C	A	T	T	A	G	T	G	A	A	T	T	G	T	G	A	G	T	T	G	C	T	G	A						
2	MF356557.1	A	C	C	T	G	C	G	G	A	A	G	G	A	T	C	A	T	T	A	G	T	G	A	T	T	G	G	T						
3	MF356558.1	A	C	C	T	G	C	G	G	A	A	G	G	A	T	C	A	T	T	A	G	T	G	A	T	T	G	G	T						
4	MF356566.1	A	C	C	T	G	C	G	G	A	A	G	G	A	T	C	A	T	T	A	G	T	G	A	T	T	G	G	T						
5	MF356563.1	A	C	C	T	G	C	G	G	A	A	G	G	A	T	C	A	T	T	A	G	T	G	A	T	T	G	G	T						
6	HM562120.1	A	A	G	G	T	T	T	C	C	G	T	A	G	G	T	G	A	A	C	T	G	C	G	G	A	T	G	A	T					
7	NR_119874.1	A	A	A	G	T	C	G	T	A	A	C	A	A	G	G	T	T	C	C	G	G	A	A	G	G	A	T	A	A	A	C	T		
8	OP541611.1	A	G	G	T	G	A	C	C	T	G	C	G	G	A	A	G	G	A	T	C	A	T	T	A	G	T	G	T	G	C	A	C	C	
9	PP938231.1	A	A	G	G	T	T	T	C	C	G	T	A	G	G	T	G	A	A	C	T	G	C	G	G	A	T	A	T	G	T	G	A	T	T
10	PP836267.1	T	C	A	T	T	A	G	T	G	A	A	T	A	A	A	C	T	T	G	T	G	A	G	T	T	G	C	A	C	A	C	A	C	
11	OM970924.1	T	G	G	A	A	G	T	A	A	A	G	T	C	G	T	A	G	G	T	T	C	G	G	A	A	G	G	A	T	C	A	T	T	
12	KX216308.1	T	A	G	T	G	A	C	C	T	G	C	G	G	A	G	G	A	T	C	A	T	T	A	G	T	G	T	G	C	A	A	C	T	