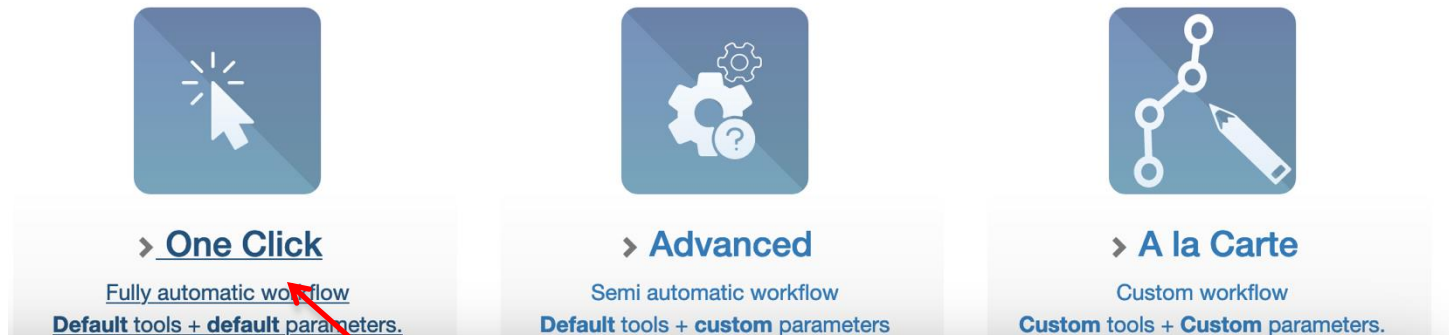


PHYLOGENY: This tutorial explains how to use the online phylogeny website at <https://ngphylogeny.fr/> to perform phylogenetic analyses.



For the PhyML and FastME, choose One Click and use the unaligned sequences

➤ One Click Workflows

Select your workflow

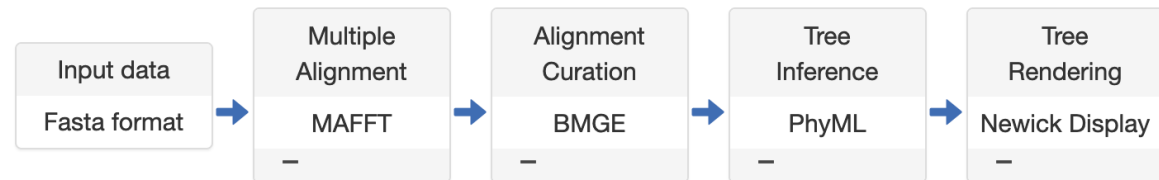
⚙️ PhyML/OneClick

⚙️ PhyML+SMS/OneClick

⚙️ FastTree/OneClick

⚙️ FastME/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

```
>BR110MP90
TAATATCAATAGAAGAATTAGCCAAAATTACGTCCTGTCAAACCCC
CTATGGTAAATAGAAAAATAAATCCGATAGCTCATAGGGATGAAGG
AGTTAAAGTAATTTGGGAGCCATGGTATGTTGCGAGTCATCTAAAA
ATTTTGATTCCAGTAGGAAGTCAATAATTATGTGGCTGATGTGA
AGTAAGCTCGAGTATCAACATCTATCCCTACTGTAAATATATGATG
GGCTCACACTACAAATCCTAGCAGACCAATTGCTATTATAGCATAA
ATTATTCCTAATAAACCGAAAGCTTCCTTTTTGCCACTTTCTTGTC
TAATAATATGAGAAATTATTCCGAAACCAGGTAAAAATTAGAATATA
AACTTCAGGATGTCCGAAAAATCAAAATAAATGCTGATAAAGAATA
```

Paste the unaligned sequences (fasta format) into the box. The program recognizes whether it is DNA or protein.

Then hit submit

Submit

📖 Example



Wait for the results

Info ! This page is will be refreshed in 3 sec.

Url	ngphylogeny.fr/workspace/history/80763b7e3de7b6c3	
Name	NGPhylogeny Analyse - PhyML/OneClick	
e-mail		

View trees with these links

PhyML	12.	PhyML Newick tree	✓	+	⚙	>	↓	👁.nhx	Viewer	iTol
	11.	PhyML Statistics	✓	+	⚙	>	↓	👁.txt		
	10.	PhyML log	✓	+	⚙	>	↓	👁.txt		
BMGE	9.	BMGE Cleaned sequences Html	✓	+	⚙	>	↓	👁.html		
	8.	BMGE Cleaned sequences Nexus	✓	+	⚙	>	↓	👁.nex		
	7.	BMGE Cleaned sequences Fasta	✓	+	⚙	>	↓	👁.fasta	MSAViewer	
	6.	BMGE Cleaned sequences Phylip	✓	+	⚙	>	↓	👁.phylip		
Sequence type detection	5.	Type information file pasted_data	✓	+	⚙	>	↓	👁.txt		
MAFFT	4.	Mafft output logs	✓	+	⚙	>	↓	👁.txt		
	3.	Guide Tree	✓	+	⚙	>	↓	👁.txt		
	2.	Mafft alignment	✓	+	⚙	>	↓	👁.fasta	MSAViewer	
Upload File	1.	pasted_data	✓	+	⚙	>	↓	👁.fasta	MSAViewer	

View alignments here

PRESTO - Phylogenetic tReE viSualisaTiOn -

Tree Layout

☒ Phylogram

☐ Dendrogram

☒ Linear

☐ Radial

☐ Slanted

Tree ordering



Increasing ladderizing



decreasing ladderizing



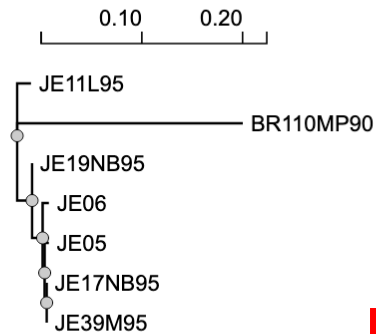
Retrieve original order

Tree settings

☐ Display support values

☐ Display branch length

☐ align text



Use the tools above and the buttons to the left to generate a tree with branch lengths.



› 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.

For the Parsimony (TNT)
option, select A la Carte

› **A La Carte** Using the workflow maker, customize your workflow by selecting the right tools

› Name

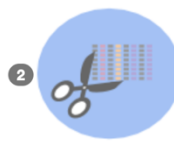
 Workflow name..

› Tools



Multiple Alignment

- ☐ MAFFT
- ☐ MUSCLE
- ☒ Clustal Omega



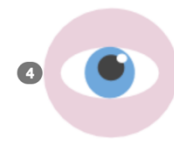
Alignment Curation

- ☒ BMGE
- ☐ Gblocks
- ☐ Noisy
- ☐ trimAl



Tree Inference

- ☐ FastME
- ☒ TNT
- ☐ PhyML+SMS
- ☐ PhyML
- ☐ FastTree



Tree Rendering

- ☒ Newick Display




Here you can select
different alignment
programs and phylogenetic
analysis options including
Maximum Parsimony (TNT)

Robust phylogenetic analysis for everyone.

➤ Free, simple to use web service dedicated to reconstructing and analysing phylogenetic relationships between molecular sequences.

▶ Let's GO ! with One Click Workflow

For Bootstrap test,
choose Advanced

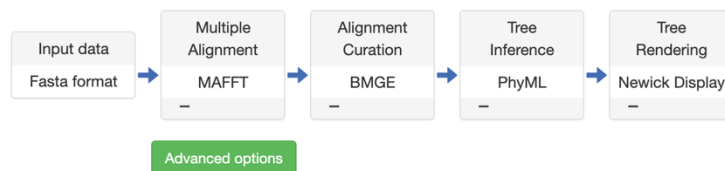
		
➤ One Click	➤ Advanced	➤ A la Carte
Fully automatic workflow Default tools + default parameters.	Semi automatic workflow Default tools + custom parameters	Custom workflow Custom tools + Custom parameters.

Advanced Workflows

Select your workflow

- PhyML/OneClick
- PhyML+SMS/OneClick
- FastTree/OneClick
- FastME/OneClick

Workflow skeleton



PhyML/OneClick

Workflow skeleton



Configure your workflow

MAFFT
BMGE
PhyML
Newick Display

Input data

Choose a file or Paste content
(Fasta format with more than 3 sequences)

Choose File No file chosen

Blast runs

Files in session

Example

Click on Advanced options and paste the unaligned sequences (Fasta format) into the box.

MAFFT

BMGE

PhyML

Newick Display

[Example](#)

MAFFT

+

BMGE

+

PhyML

-

interleaved format (if input is phylip)

☒ Interleaved

Data type

☐ Nucleic acids

☐ Amino acids

☒ Auto detect

Evolutionary model (if DNA data)

GTR

Evolutionary model (if Protein data)

LG

Equilibrium frequencies (if DNA data)

ML/Model

Empirical: frequencies are estimated by counting the occurrences in the alignment.
ML/Model: frequencies are estimated using ML for nucleotides or defined by the

Change Equilibrium frequencies to ML/Model

MAFFT

BMGE

PhyML

Newick Display

Scroll down and click Bootstrap for Statistical test for branch support

1 means no gamma model

Parameter of the gamma model

estimated

'e' if you want PhyML to estimate it

Tree topology search

☐ NNI (Nearest Neighbor Interchange)

☒ SPR (Subtree Pruning and Regraphing)

☐ Best of NNI and SPR

Optimise parameter

Tree topology, Branch length, Model paramete

Statistical test for branch support

Bootstrap

Use aLRT or aBayes to save computing time.

Number of bootstrap replicates

100

Must be a positive integer

Seed value used to initiate the random number generator

123456

0 to random seed

Then hit Submit

Submit

Tool	Step	File Name	Status	
Newick Display	19.	All tree images	✓	+ ⚙ > ⬇️ 📄.tar
	18.	Tree image	✓	+ ⚙ > ⬇️ 📄.svg
PhyML	17.	Mapping between short sequence id and names (useful to interpret some bootstrap log files if any)	✓	+ ⚙ > ⬇️ 📄.txt
	16.	PhyML Newick tree	✓	+ ⚙ > ⬇️ 📄.nhx Viewer ITol
	15.	PhyML Statistics	✓	+ ⚙ > ⬇️ 📄.txt
	14.	PhyML log	✓	+ ⚙ > ⬇️ 📄.txt
	13.	PhyML bootstrap trees: align.phy_phyml_boot_trees.txt	✓	+ ⚙ > ⬇️ 📄.nhx Viewer ITol
	12.	Booster: Tree with [id avg transfer distances depth] as branch labels: tbe_raw_tree.nhx	✓	+ ⚙ > ⬇️ 📄.nhx Viewer ITol
	11.	Booster: Tree with normalized supports: tbe_norm_tree.nhx	✓	+ ⚙ > ⬇️ 📄.nhx Viewer ITol
	10.	Booster: tbe_log.txt	✓	+ ⚙ > ⬇️ 📄.txt
BMGE	9.	BMGE Cleaned sequences Html	✓	+ ⚙ > ⬇️ 📄.html
	8.	BMGE Cleaned sequences Nexus	✓	+ ⚙ > ⬇️ 📄.nex
	7.	BMGE Cleaned sequences Fasta	✓	+ ⚙ > ⬇️ 📄.fasta MSAViewer
	6.	BMGE Cleaned sequences Phylip	✓	+ ⚙ > ⬇️ 📄.phylip
Sequence	-	-	-	-

Click here to view the
PhyML Newick tree

After opening the tree,
click Display support
values to view the
Bootstrap values

[Home](#)
Phylogeny Analysis

Go back

PRESTO - Phylogenetic tReE

Tree Layout

☐ Phylogram
☒ Linear
☐ Radial
☒ Dendrogram
☐ Slanted

Tree ordering

Increasing ladderizing
 decreasing ladderizing
 Retrieve original order

Tree settings

☒ Display support values
☐ Display branch length
☐ align text