

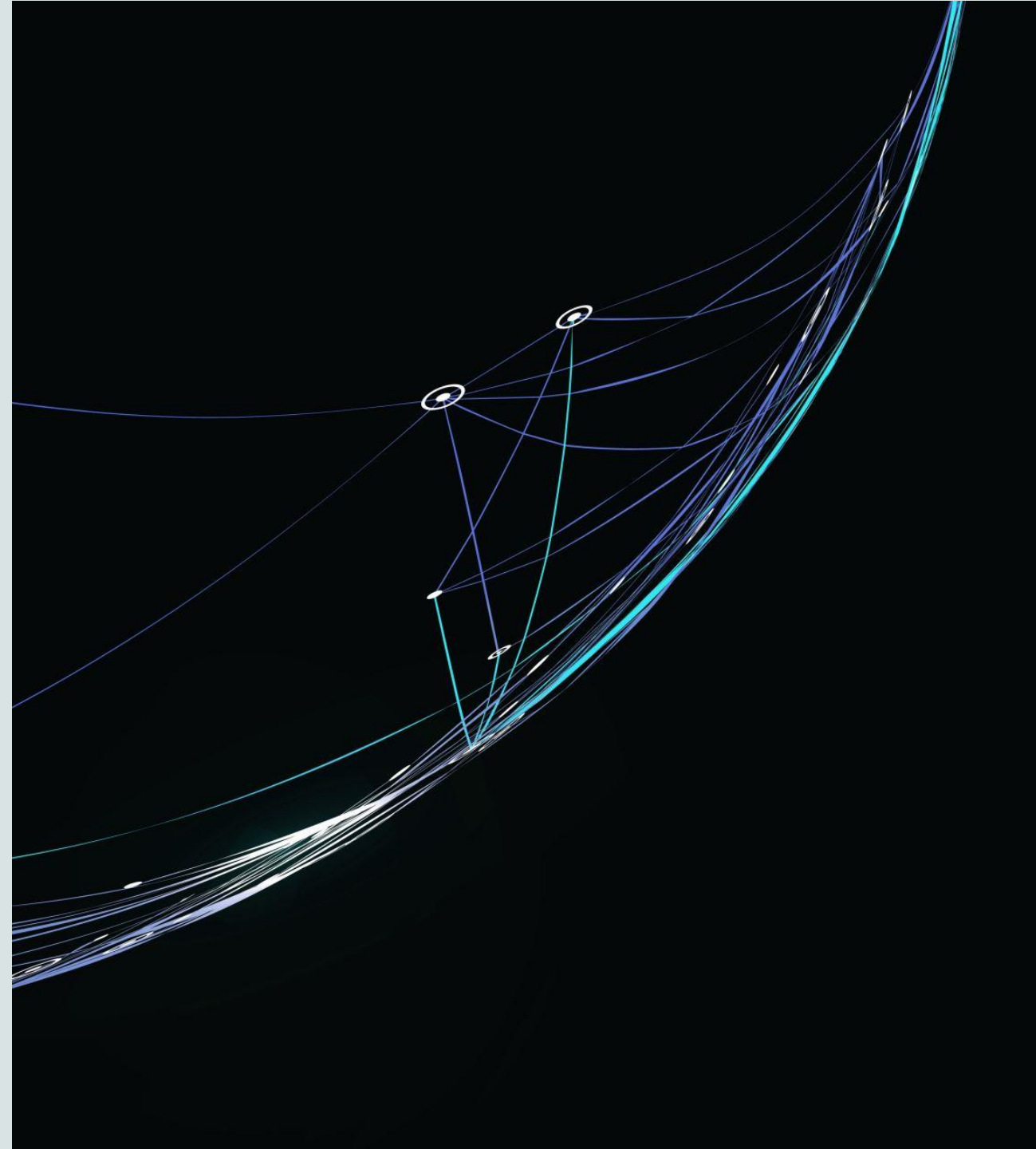
IQ-TREE: Fast and Accurate Phylogenetic Tree Interference



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A Fast and Effective Stochastic Algorithm for Estimating Maximum-Likelihood (ML) Phylogenies

- Open Source software for building phylogenetic trees using Maximum Likelihood
- Designed for speed, accuracy and usability
- Widely used in bioinformatics, especially for analyzing DNA, RNA, or protein sequence alignments to infer evolutionary relationships between species, genes, or proteins
- Works with aligned sequences (alignment needs to be run with e.g. MAFFT)
- Different evolutionary models can be used (DNA-, Protein-, Codon-Models...)
- Output data can be visualized into trees (FIGTree, StudioR)

IQ-Tree vs RAxML/PhyML

- Higher likelihoods between 62.2% and 87.1% of the studied alignments (same CPU time)
- Fast performance on large scale datasets
- Built in ModelFinder and Ultrafast Bootstrap
- User-friendly and widely cited

Core Features

- ModelFinder (automatic model selection)
- Ultrafast Bootstrap (UFBoot)
- Partitioned analysis
- Multiple data types supported
- Highly parallelized (multithreading)

Data formats

- Input: FASTA, NEXUS, PHYLIP, CLUSTAL
- Output: .iqtree (main report file); .treefile (ML in NEWICK format); .log (logfiles of the entire run, reports, bugs)

Applications

- Evolutionary Biology: Investigating the evolutionary relationships amongst species
- Comparative Genomics: comparing genetic material across different organisms to understand evolutionary processes
- Functional Genomics: exploring the function and evolution of genes and proteins

Running IQ-TREE Online: Creating a Phylogenetic Tree

- Visit: <http://iqtree.cibiv.univie.ac.at>
- Click on Tab “Tree Inference”:
 - In the Input Data window, upload Alignment file (FASTA format)
 - For Sequence type, choose Protein
 - (Optional) Add your email to get notified when the job is done
- Click Submit Job

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

Server load: 4% Trifinopoulos J, Nguyen LT, von Haeseler A, Minh BQ (2016) *Nucl. Acids Res.* 44 (W1): W232-W235. doi: 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 ?
☐ Codon F1x4 ☐ Codon F3x4 ?

Ascertainment bias correction: ☐ Yes [+ASC] ?

Branch Support Analysis

Bootstrap analysis: ☐ None ☒ Ultrafast ☐ Standard ?

Number of bootstrap alignments: 1000 ?

Create .ufboot file: ☐ Yes (write bootstrap trees to .ufboot file) ?

Maximum iterations: 1000 ?

Minimum correlation coefficient: 0.99 ?

Single branch tests: ?

SH-aLRT branch test: ☐ No ☒ Yes #replicates: 1000 ?

Approximate Bayes test: ☐ Yes ?

IQ-TREE Search Parameters

Perturbation strength: 0.5 ?

IQ-TREE stopping rule: 100 ?

Email (optional, to retrieve results): SUBMIT JOB

Running IQTREE Online: Where to Find Your Tree?

- Click on Tab “Analysis Results”:
 - Click on “Query Status” until the job status changes to “Success”

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

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Tree Inference Model Selection Analysis Results

User name or Email: trishoculus@gmail.com QUERY STATUS

No.	Submission Time	Status
1	2025-05-26 20:06	Success
2	2025-05-26 19:52	Success

Summary Run Log Full Result

Please bookmark the following link to later monitor/retrieve results:
<http://iqtree.cibiv.univie.ac.at/?user=trishoculus@gmail.com&jobid=250526200657>

An email will be sent to trishoculus@gmail.com once the job is finished. If you want to monitor the progress, click on Run Log above. If you hit QUERY STATUS, the page is reloaded. You can [download IQ-TREE](#) and run it locally with the command-line:
`path_to_iqtree -s MAFFT_aligned_sequences.txt -st AA -n TEST -bb 1000 -alrt 1000`

Note: The CPU time limit is 24 hours and RAM limit is 1GB. Your job will be stopped if it exceeds these limits. (In that case, please download the stopped job and use the above command-line to resume the run from the last checkpoint on your local PC as described [here](#).)

Job has FINISHED! Detailed analysis can be found in the Full Result tab. You can click on DOWNLOAD SELECTED JOBS to retrieve all result files.

The tree below was visualized with [ete-view](#).
Support values written on the branches: SH-aLRT support (%) / ultrafast bootstrap support (%)

DOWNLOAD SELECTED JOBS

Running IQTREE Online: Where to Find Your Tree?

- After the job status changes to “Success”, go to “Full Result” Tab in order to obtain results and see the tree
- To get the output files, click on “Download Selected Jobs”
- From the downloaded folder, use .treefile file for tree visualization in RStudio

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

Server load: 4% Trifinopoulos I, Nguyen LT, von Haeseler A, Minh BQ (2016) *Nucl. Acids Res.* 44 (W1): W232-W235. doi: 10.1093/nar/gkw256

Tree Inference Model Selection Analysis Results

User name or Email: trishoculus@gmail.com QUERY STATUS

Summary Run Log Full Result

IQ-TREE 1.6.12 built Aug 15 2019

Input file name: MAFFT_aligned_sequences.txt
Type of analysis: ModelFinder + tree reconstruction + ultrafast bootstrap (1000 replicates)
Random seed number: 208070

REFERENCES

To cite ModelFinder please use:
Subha Kalyaanamoorthy, Bui Quang Minh, Thomas KF Wong, Arndt von Haeseler, and Lars S Jernlin (2017) ModelFinder: Fast model selection for accurate phylogenetic estimates. *Nature Methods*, 14:587-589. <https://doi.org/10.1038/nmeth.4285>

To cite IQ-TREE please use:
Lam-Tung Nguyen, Heiko A. Schmidt, Arndt von Haeseler, and Bui Quang Minh (2015) IQ-TREE: A fast and effective stochastic algorithm for estimating maximum likelihood phylogenies. *Mol Biol Evol*, 32:268-274. <https://doi.org/10.1093/molbev/msu300>

Since you used ultrafast bootstrap (UFBoot) please also cite:
Diep Thi Hoang, Olga Chernomor, Arndt von Haeseler, Bui Quang Minh, and Le Sy Vinh (2017) UFBoot2: Improving the ultrafast bootstrap approximation. *Mol Biol Evol*, in press. <https://doi.org/10.1093/molbev/msx281>

SEQUENCE ALIGNMENT

Input data: 100 sequences with 265 amino-acid sites
Number of constant sites: 69 (= 26.0377% of all sites)
Number of invariant (constant or ambiguous constant) sites: 69 (= 26.0377% of all sites)
Number of parsimony informative sites: 161
Number of distinct site patterns: 223

ModelFinder

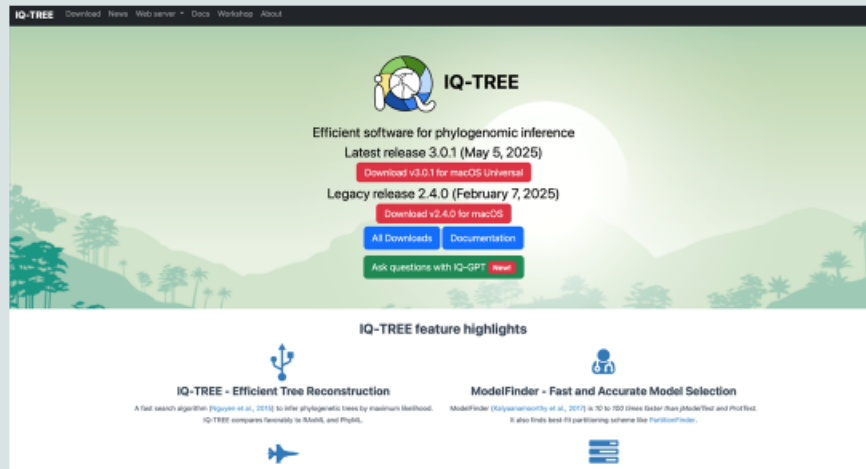
Best-fit model according to BIC: WAG+P+G4

List of models sorted by BIC scores:

Model	LogL	AIC	w-AIC	AICc	w-AICc	BIC	w-BIC
WAG+P+G4	-5949.4823	12332.9646	+ 0.6510	14345.9858	- 0.0000	13109.7659	+ 0.9173
WAG+P+I+G4	-5949.1056	12334.2112	+ 0.3490	14409.9504	- 0.0000	13114.5923	+ 0.0821
WAG+G4	-6010.0295	12416.0590	- 0.0000	13610.0590	+ 1.0000	13124.8455	- 0.0005
WAG+I+G4	-6009.4162	12416.8323	- 0.0000	13641.4477	- 0.0000	13129.1986	- 0.0001
JTT+G4	-6021.5917	12439.1834	- 0.0000	13633.1834	- 0.0000	13147.9699	- 0.0000
LG+P+G4	-5969.1094	12372.2188	- 0.0000	14385.2401	- 0.0000	13149.0202	- 0.0000
JTTDCMut+G4	-6023.2616	12442.5231	- 0.0000	13636.5231	- 0.0000	13151.1096	- 0.0000
JTT+I+G4	-6021.2508	12440.5016	- 0.0000	13665.1170	- 0.0000	13152.8678	- 0.0000
LG+P+I+G4	-5969.1062	12374.2125	- 0.0000	14449.9516	- 0.0000	13154.5936	- 0.0000
JTTDCMut+I+G4	-6022.3520	12442.7041	- 0.0000	13667.3195	- 0.0000	13155.0703	- 0.0000
JTTDCMut+P+G4	-5982.7370	12399.4741	- 0.0000	14412.4954	- 0.0000	13176.2755	- 0.0000
JTT+P+G4	-5983.0332	12400.0664	- 0.0000	14413.0877	- 0.0000	13176.8678	- 0.0000
LG+G4	-6036.1316	12468.2632	- 0.0000	13662.2632	- 0.0000	13177.0497	- 0.0000
JTTDCMut+P+I+G4	-5982.4218	12409.8436	- 0.0000	14476.5827	- 0.0000	13181.2247	- 0.0000

DOWNLOAD SELECTED JOBS

Running IQ-TREE Locally on Your Computer



- Visit iqtree.org in order to download the latest version of IQ-TREE
- Unzip the downloaded folder
- Place your aligned FASTA file in the same folder as the IQ-TREE executable
- Open Terminal (Mac/Linux) or Command (Windows)
- Run following command to start the analysis:

```
(base) trisha@Trivunas-MacBook-Pro iqtree-3.0-2.1-macOS % cd bin
(base) trisha@Trivunas-MacBook-Pro bin % ls

iqtree3
(base) trisha@Trivunas-MacBook-Pro bin % ./iqtree3 -s ../MAFFT_aligned_sequences.txt -st AA -m TEST -bb 1000 -alrt 1000
IQ-TREE version 3.0.1 for MacOS Intel 64-bit built May 5 2025
Developed by Bui Quang Minh, Thomas Wong, Nhan Ly-Trong, Huaiyan Ren
Contributed by Lam-Tung Nguyen, Dominik Schrempf, Chris Bielow,
Olga Chernomor, Michael Woodhams, Diep Thi Hoang, Heiko Schmidt
```

Running IQ-TREE Locally on your Computer - Output

- Four Output files created and saved in same folder where Input file is located:
 - .treefile: the phylogenetic tree
 - .iqtree: summary of results and settings
 - .log: full command-line log
 - .mldist: matrix showing pairwise sequence differences
- If you want to re-run the same file, add -redo at the end of your command to overwrite the old results

```
-----  
| FINALIZING TREE SEARCH |  
-----  
Performs final model parameters optimization  
Estimate model parameters (epsilon = 0.010)  
1. Initial log-likelihood: -5931.587  
Optimal log-likelihood: -5931.586  
Proportion of invariable sites: 0.149  
Gamma shape alpha: 1.242  
Parameters optimization took 1 rounds (0.126 sec)  
BEST SCORE FOUND : -5931.586  
  
Testing tree branches by SH-like aLRT with 1000 replicates...  
0.418 sec.  
Creating bootstrap support values...  
Split supports printed to NEXUS file ../MAFFT_aligned_sequences.txt.splits.nex  
Total tree length: 5.439  
  
Total number of iterations: 150  
CPU time used for tree search: 168.453 sec (0h:2m:48s)  
Wall-clock time used for tree search: 169.442 sec (0h:2m:49s)  
Total CPU time used: 215.835 sec (0h:3m:35s)  
Total wall-clock time used: 217.063 sec (0h:3m:37s)  
  
Computing bootstrap consensus tree...  
Reading input file ../MAFFT_aligned_sequences.txt.splits.nex...  
100 taxa and 694 splits.  
Consensus tree written to ../MAFFT_aligned_sequences.txt.contree  
Reading input trees file ../MAFFT_aligned_sequences.txt.contree  
Log-likelihood of consensus tree: -5931.606  
  
Analysis results written to:  
IQ-TREE report: ../MAFFT_aligned_sequences.txt.iqtree  
Maximum-likelihood tree: ../MAFFT_aligned_sequences.txt.treefile  
Likelihood distances: ../MAFFT_aligned_sequences.txt.mldist  
  
Ultrafast bootstrap approximation results written to:  
Split support values: ../MAFFT_aligned_sequences.txt.splits.nex  
Consensus tree: ../MAFFT_aligned_sequences.txt.contree  
Screen log file: ../MAFFT_aligned_sequences.txt.log  
  
Date and Time: Mon May 26 21:17:57 2025  
(base) trisha@Trivunas-MacBook-Pro bin %
```

Visualization with RStudio

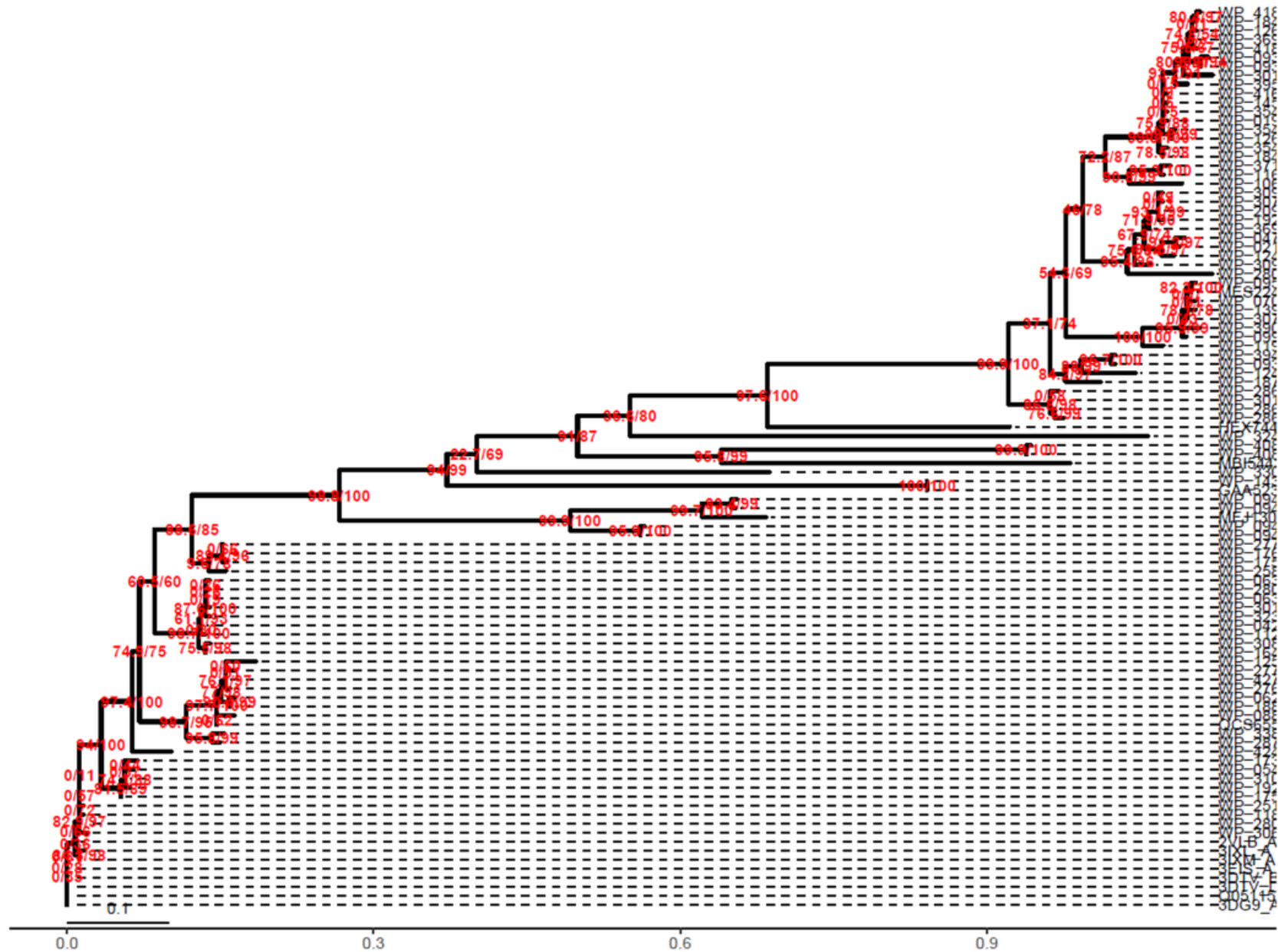
Read is generated through .treefile
into Rstudio

Best-fit model according to BIC:
WAG+F+G4

```
if (!requireNamespace("BiocManager", quietly=TRUE)) install.packages("BiocManager")
if (!requireNamespace("ggtree", quietly=TRUE)) BiocManager::install("ggtree")
if (!requireNamespace("ape", quietly=TRUE)) install.packages("ape")
library(ape)
library(ggtree)
library(ggplot2)
tree <- read.tree("C:/Users/andre/Downloads/MAFFT_aligned_sequences.txt.treefile")
tree <- ladderize(tree)
best_fit_tree_plot <- ggtree(tree, branch.length="branch.length") +
  geom_tree(linewidth=1) +
  geom_tiplab(size=3, align=TRUE, linetype="dashed", linesize=0.5) +
  geom_text2(aes(subset=!isTip, label=label), color="red", size=3, fontface="bold") +
  theme_tree2() +
  ggtitle("Phylogenetic Tree\nBest-Fit Model (BIC): WAG+F+G4") +
  theme(plot.title=element_text(hjust=0.5, size=16, face="bold", color="darkblue"),
        panel.background=element_rect(fill="white"),
        legend.position="none") +
  geom_treescale(x=0, y=-1, offset=1, fontsize=3)
print(best_fit_tree_plot)
ggsave("C:/Users/andre/Downloads/tree_with_WAGF_G4_model.pdf", best_fit_tree_plot,
       width=10, height=8, dpi=300)
```


Phylogenetic Tree

Best-Fit Model (BIC): WAG+F+G4



```
if (!requireNamespace("BiocManager", quietly = TRUE)) install.packages("BiocManager")
if (!requireNamespace("ggtree", quietly = TRUE)) BiocManager::install("ggtree")
if (!requireNamespace("ape", quietly = TRUE)) install.packages("ape")

library(ape)
library(ggtree)
library(ggplot2)

tree <- read.tree("C:/Users/andre/Downloads/MAFFT_aligned_sequences.txt.treefile")

plot(tree, main="Simple Tree")

fancy_plot <- ggtree(tree) +
  geom_tiplab(size=3) +
  geom_tree() +
  theme_tree2() +
  ggtitle("Phylogenetic Tree from IQ-TREE")

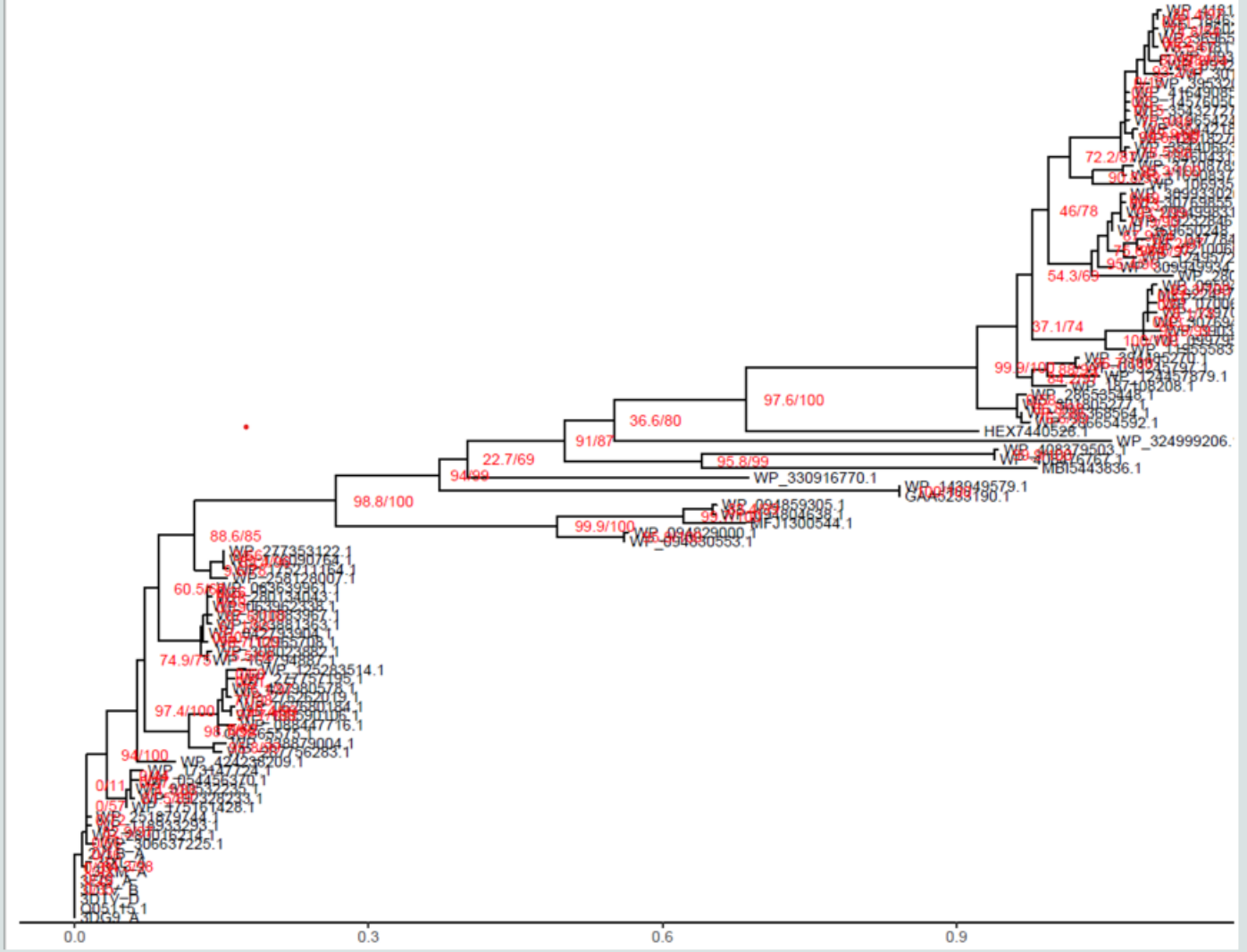
print(fancy_plot)

fancy_plot_with_bootstrap <- fancy_plot +
  geom_text2(aes(subset=!isTip, label=label), hjust=-0.3, size=3, color="red") +
  ggtitle("Tree with Bootstrap Support")

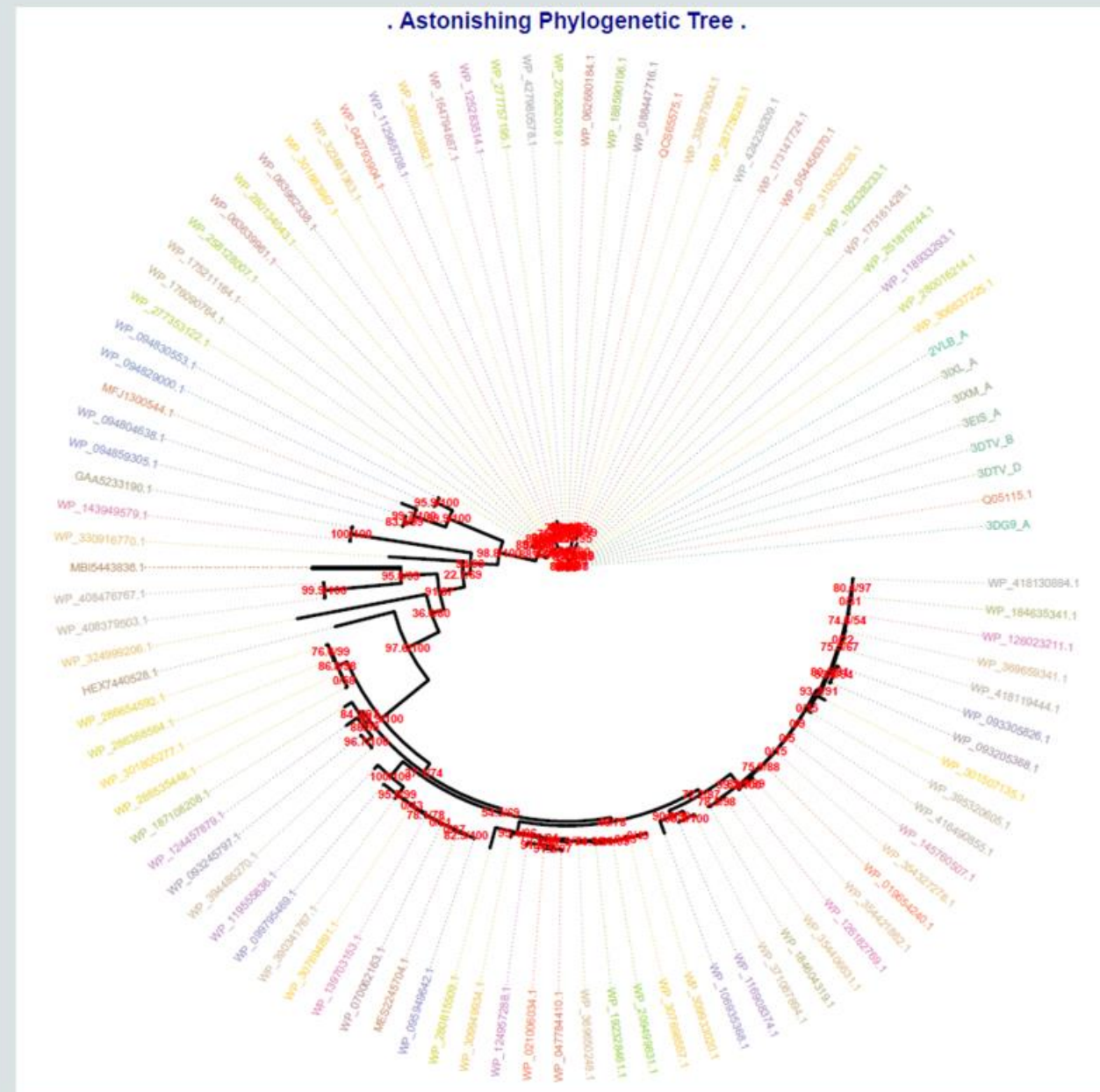
print(fancy_plot_with_bootstrap)

ggsave("my_tree_plot.pdf", fancy_plot_with_bootstrap, width=10, height=8)
```

Tree with Bootstrap Support




```
if (!requireNamespace("BiocManager", quietly=TRUE)) install.packages("BiocManager")
if (!requireNamespace("ggtree", quietly=TRUE)) BiocManager::install("ggtree")
if (!requireNamespace("ape", quietly=TRUE)) install.packages("ape")
if (!requireNamespace("RColorBrewer", quietly=TRUE)) install.packages("RColorBrewer")
library(ape)
library(ggtree)
library(ggplot2)
library(RColorBrewer)
tree <- read.tree("C:/Users/andre/Downloads/MAFFT_aligned_sequences.txt.treefile")
tree <- ladderize(tree)
num_tips <- length(tree$tip.label)
tip_colors <- colorRampPalette(brewer.pal(8, "Set2"))(num_tips)
astonishing_tree <- ggtree(tree, layout="circular", branch.length="branch.length") +
  geom_tree(linewidth=1.2, color="black") +
  geom_tiplab2(aes(color=label), size=3, offset=0.5, align=TRUE, linesize=0.4) +
  scale_color_manual(values=tip_colors) +
  geom_text2(aes(subset=!isTip, label=label), color="red", size=3, fontface="bold") +
  geom_treescale(x=0, y=-2, offset=1, fontsize=3) +
  theme(plot.title=element_text(hjust=0.5, size=18, face="bold", color="darkblue"),
        panel.background=element_rect(fill="white"),
        panel.grid=element_blank(),
        legend.position="none") +
  ggtitle("🌿 Astonishing Phylogenetic Tree 🌿")
print(astonishing_tree)
ggsave("C:/Users/andre/Downloads/astonishing_tree.pdf", astonishing_tree, width=12,
        height=12, dpi=300)
```



*THANK YOU FOR YOUR
ATTENTION!*