

# OneTwoTree

## A step-by-step tutorial

This tutorial guides users in the process of phylogeny reconstruction using OneTwoTree.

OneTwoTree is an online tree reconstruction tool, designed to generate phylogenies in an unsupervised manner, aiming to a wide range of users' expertise.

Mainly, the tutorial will describe how to reconstruct different types of phylogenies using the tool. For a full description of each feature and its underlying pipeline please visit the online [OVERVIEW](#) page and the paper.

The topics covered by this tutorial are:

- 1) How to get a tree in a click.
- 2) How to handle your input.
- 3) How to root your tree
- 4) Phylogeny inference:
  - a. How to add topological constraints.
  - b. How to obtain time-calibrated phylogeny.
  - c. Bootstrapping.
- 5) Navigating through the Results page.
- 6) Follow-up analyses. *Coming soon!*

If you don't have your own data and wish to try out OneTwoTree, click on the [Load example](#) button to obtain sample data.

## 1) How to get a tree in a click

First, make sure that your operational mode is set to *Phylogeny reconstruction* under the *Running options* (this is the default):

Running options:

☒ Phylogeny reconstruction

☐ Obtain orthologous loci

Next, paste your input list or upload it as a file in *txt* or *csv* formats. This file should not contain any headers. To see an example, click on **Load example**.

**Input**

Upload a file with your list of TaxIDs/species names([see explanation on NCBI](#)), or paste the list in the window:

**Choose file**

Paste your list

**Load example** **Clear**

**Filter options**

Include species descendants: ☐ No

☒ Filter intraspecific variants

☒ Filter hybrids

☒ Filter open nomenclature

The input can include both taxa names and TaxIDs, without any further specifications. You can also combine between species names and higher-ranked taxa.

**Note:** Currently, OneTwoTree supports species names separated by a *space* character between the genus and species names, and *not* other characters such as *underscore* or *dot*.

Fill in your Email address and give an informative job title for your own convenience.

**Email address**

Enter email

**Job title (optional)**

Add a descriptive job title to

Clicking the **Submit** button will produce a tree following your input list with all default parameters (namely, an unrooted, Maximum Likelihood phylogeny based on a supermatrix).

## 2) How to handle your input

There are several ways to retrieve sequences. The default parameters of the *Filter options* will fetch sequences only for the specified taxa. The filtering options include:

- 1 Include species descendants:** The basic taxonomic unit of operation in OneTwoTree is the species-level. If you wish to retrieve sequences below the species-level (e.g., subspecies), change this parameter to “Yes”.  
Note: This option is ignored in case the input name is a higher-ranked taxon (e.g., if the input name is a genus, all of its descendants, including intraspecific variants, are retrieved; for these to be omitted users should use the filters in #2).
- 2 Filter intraspecific varieties/ Filter hybrids/ Filter open nomenclature:** Modify these filters to obtain intraspecific variants, hybrids and open nomenclature conventions. For example, in case the *Filter intraspecific variants* is unchecked, then intraspecific variants sequences will be included in the analysis.
- 3 Merge intraspecific varieties:** In case there are intraspecific varieties in the results, as well as their progenitor species (i.e., the binomial species name), their sequences can be unified into a single tip in the phylogeny.  
Note: The progenitor must be included in the original list (or under a higher-taxa) for its sequences to be included in the analysis. For example if the input includes *Iris caucaisca* (TaxID 292549) and *Iris caucasica subsp. turcica* (TaxID 995789), the merge option will retrieve all sequences in the database that belong to both TaxIDs, and will be placed under TaxID 292549. The phylogeny itself will include only *Iris caucaisca* and not *Iris caucasica subsp. turcica*.

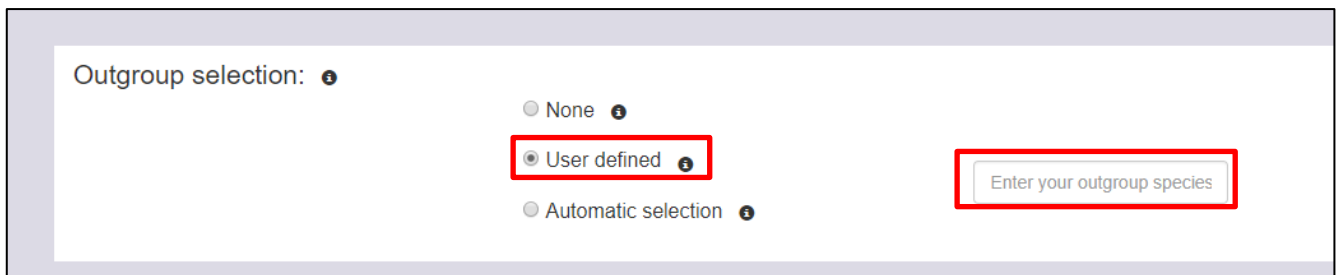
The screenshot shows the OneTwoTree web interface. On the left, there is a 'Choose file' button and a text area labeled 'Paste your list'. To the right of the text area are 'Load example' and 'Clear' buttons. Further right is the 'Filter options' section, which includes a dropdown menu for 'Include species descendants' (set to 'No') and three checkboxes: 'Filter intraspecific varieties', 'Filter hybrids', and 'Filter open nomenclature'. Three red circles with numbers 1, 2, and 3 are overlaid on the interface: circle 1 is around the 'Include species descendants' dropdown, circle 2 is around the 'Filter intraspecific varieties' checkbox, and circle 3 is around the 'Merge intraspecific varieties' checkbox (which is unchecked).

### 3) How to root your tree

Click on Advanced parameters.

The first parameter that can be modified is the *Outgroup selection* section. Once an outgroup is added to a phylogeny users can root the tree and determine the direction of evolution.

There are two ways to add an outgroup to the analysis. First, users can specify a taxon name or a TaxID in the designated input box. The specified name can be one of the names already part of the input list or not.



Outgroup selection: ⓘ

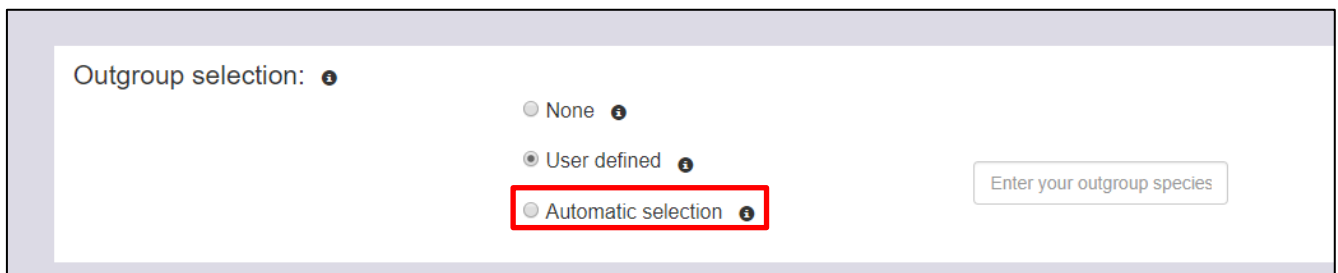
☐ None ⓘ

☒ User defined ⓘ

☐ Automatic selection ⓘ

Enter your outgroup species

Second, users may choose to allow an automatic selection of the outgroup. Choosing this option will substantially increase the running time.



Outgroup selection: ⓘ

☐ None ⓘ

☐ User defined ⓘ

☒ Automatic selection ⓘ

Enter your outgroup species

### 4) Phylogeny inference

Click on Advanced parameters.

Under the *Phylogeny inference* section you can alter the inference tool (Maximum Likelihood or Bayesian approach). Each inference tool has its own supported set of *Nucleotide models*.



Phylogeny inference:

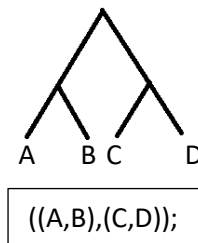
Tool: RAxML ▼

Nucleotide model: GTRCAT ▼

Enable bootstrap: ☐ On ☒ Off

### a) How to add topological constraints

Adding a constraint means that there is a prior hypothesis or knowledge regarding several taxonomic groupings. OneTwoTree enables to take such knowledge under consideration. The constraint itself should be provided in a NEWICK format. For example, here is a tree plot with its NEWICK representation:



In this case taxa A and B are constrained to be more closely related to each other than either one is to C or D. For example: Consider an input list that contains 10 species A-J. The phylogenetic relationship between four of these species (A-D) is known such that A and B form a monophyletic group and C + D form a monophyletic group, while there is no other knowledge regarding any other taxonomic groupings. Then, the constrain phylogeny shown above represents this constraint. In case species A-D are known to form a clade, and E+F are external to this clade but their relationship is unknown, the supplied NEWICK representation should be **(A,B,C,D);**.

Branch lengths supplied in the NEWICK format are ignored. Paste your constraint tree in the designated place or load a file.

Phylogeny inference:

Tool: RAXML

Nucleotide model: GTRCAT

Tree type: Supermatrix tree

Enable bootstrap: On Off

Constraint tree:

Load example

Clear

Load your tree

Note: Adding a constraint tree when working with the ExaML tool for phylogeny inference, all taxa should appear in the user-constraint tree, otherwise an unconstraint tree will be produced.

### b) How to obtain an ultrametric tree

The divergence time estimation option will only be enabled if the tree is about to be rooted (see *Root your tree* section to find out how this can be done).

### Using RAxML or ExaML as an inference tool

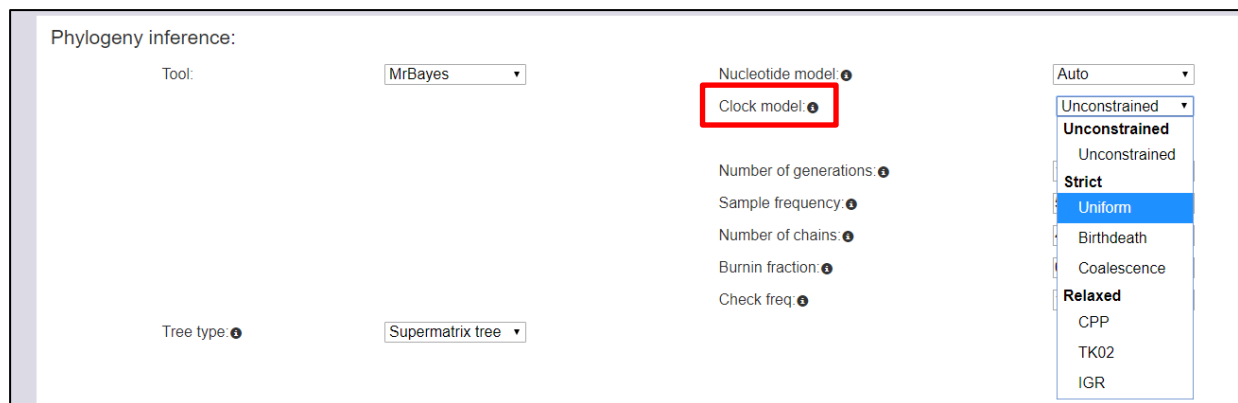
To get an ultrametric tree: First choose to root your tree, then the *Divergence time estimation* option will appear under the *Phylogeny inference* section. Set the *Divergence time estimation* to *Yes* for an ultrametric tree output.



A screenshot of a web interface showing a dropdown menu for "Divergence time estimation:". The menu is open, and the option "Yes" is selected. The entire dropdown menu is highlighted with a red rectangular border.

### Using MrBayes as an inference tool

To obtain an ultrametric tree using MrBayes the clock model should be any of the Strict or Relaxed clock models.



A screenshot of the "Phylogeny inference:" settings panel. The "Tool:" dropdown is set to "MrBayes". The "Tree type:" dropdown is set to "Supermatrix tree". The "Nucleotide model:" dropdown is set to "Auto". The "Clock model:" dropdown is open, showing a list of options: "Unconstrained", "Unconstrained", "Strict", "Uniform", "Birthdeath", "Coalescence", "Relaxed", "CPP", "TK02", and "IGR". The "Clock model:" dropdown is highlighted with a red rectangular border.

### c) How to obtain time-calibrated phylogeny

Users can obtain a time-calibrated tree by adding calibration points. Constraining the divergence time of a certain ancestral node in the phylogeny helps to calibrate the branch lengths according to a time scale defined by the user. Usually, these time estimates are based on fossil data. To use this option, first set the *Divergence time* estimation parameter to Yes.

Divergence time estimation:	<input type="text" value="Yes"/>
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#### Using RAxML or ExaML as an inference tool

Two optimized tools are available: (1) treePL or (2) PLL-DPPDiv.

#### Using MrBayes as an inference tool

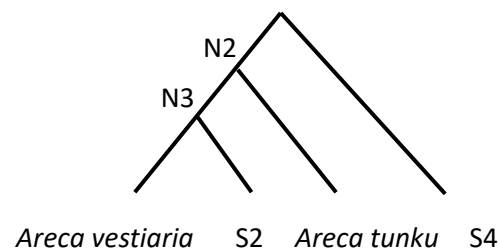
MrBayes has the option to calibrate nodes according to user-supplied data.

Note: When using MrBayes, only clock models that support the uniform branch-length prior can be applied together with user-provided calibration points.

For both phylogeny inference tools, users can add calibration points by defining a split (i.e., two taxa names that the desired calibration point is their most recent common ancestor) together with two time estimations – minimal and maximal ages of the relative split. In case no calibration points are provided, the tree will be calibrated relatively to a root age of 1.

Node dating:	
<div><div>Areca tunku,Areca vestiaria,0.2,0.4</div><div>Areca catechu,Areca triandra,0.5,0.7</div></div>	<div>Load example</div> <div>Clear</div>
<div>Load your splits</div>	

In the example shown above there are two splits that are calibrated, one in each line. The first number in each row represents the minimal age and the second one represents the maximal age. In this case, the first specifies that *Areca tunku* and *Areca vestiaria* diverged before 0.2 and 0.4 million years ago. Note that these two species need not form a monophyletic group. For example, if the inferred topology was:



The constraint will apply to N2.

## d) Bootstrapping

Under the ML approach one can add splits reliability support using a rapid bootstrap estimation. Click the *Enable bootstrap* option and specify the number of replicates.

Note: Choosing this option will substantially increase the running time.

Phylogeny inference:

Tool:

Nucleotide model:

☒ Enable bootstrap

☐ On ☐ Off

Bootstrap iteration number:

## Navigating through the Results page

When the analysis is finished, the resulting phylogeny together with various other files are produced. All outputs are further available for download in a zip format, as well as a single-file download option. Users can also view their resulting phylogeny and a table representing the clusters that comprise the MSA.

Parameters/User input:

Submitted on: 12/10/2017, 10:16:53 AM

Species selection options:  
Include Species Descendants: No

Name resolution: None

Database selection: NCBI

Filter options:  
Filter Hybrids: on  
Filter SubSp: on  
Filter Unresolved: on  
Merge SubSp/Variants: off

Rerun is Off

Outgroup\_flag: None

Genome selection: all

Clustering options:  
Clustering method: Ortho  
seq\_Ratio: 0.5  
Ortho\_inflation: 1.5

Alignment parameters:

Areca catechu  
Areca concinna  
Areca hutchinsoniana  
264298  
Areca macrocalyx  
Areca rheophytica  
Areca triandra  
Areca tunku  
Areca vestiaria

- 1 Users can browse the parameters according to which the analysis was run.
- 2 In this window users will see the input as provided by them. These names will not necessarily represent the names that appear in the final phylogeny.



### Results:

1

2

3

4

5

6

7

8

Final species list: [\[download\]](#)

MSA file: [\[ fasta \]](#) [\[ nexus \]](#)

Partition file: [\[download\]](#)

Tree file: [\[download\]](#)

Species vs. Accession numbers matrix: [\[download\]](#)

Species with data in Genbank: 9

User Selected Outgroup: NULL

Species in final alignment file: 9

[Download all output](#)

- 1

The *Final species list* contains the list of taxa that exist in the phylogeny. The will not necessarily match the set of names provided by the user (in case of name resolution conventions and/or data availability).
- 2

A *Multiple Sequence Alignment* file is available both in FASTA and in NEXUS formats.
- 3

The *Partition file* contains the positions of each marker in the final concatenated MSA.
- 4

Tree file is the resulting phylogeny. Apart from being ready for download, it is presented online (see below) using the WASABI platform (Veidenberg *et al.* 2016).
- 5

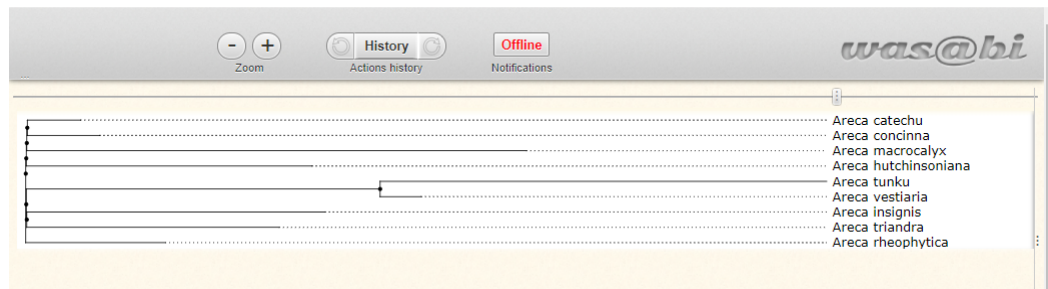
A matrix representing the taxa in the phylogeny, together with the accessions of the respective markers used in the MSA.
- 6

The number of taxa that had sequence data in GenBank, prior to any additional processing.
- 7

If user selected to add an outgroup, the selected (or user-chosen) one will be presented here.
- 8

The number of taxa in the final concatenated MSA (and therefore in the final phylogeny), after passing all filtering processes.

Tree:



Using the WASABI platform (Veidenberg *et al.* 2016) users can view, once the analysis is completed, their resulting phylogeny.

Clusters table:

1	2	3	4	5	6	7
Cluster	Description	Type	Median Length	Num of species	Included	Download
1	PRK	NUC	680	6	yes	Aligned ▼
3	Areca hutchinsoniana gene for ITS1, 5.8S rRNA, ITS2, complete sequence, clone: 2.	NUC	723	6	yes	Aligned ▼
2	RPB2	NUC	913	4	yes	Aligned ▼

This table summarizes all clusters that were found in the data of the taxa in question. From this set of markers the final supermatrix was built:

- 1 Cluster number.
- 2 The name of the cluster.
- 3 Genome type – NUC for nuclear, mtDNA for mitochondrial or cpDNA for chloroplast.
- 4 The median length of all available sequences belonging to that marker, from the taxa in question.
- 5 The number of species that had available data for this marker, from the taxa in question.
- 6 Was this marker included in the final supermatrix – Yes/No.
- 7 Users can choose to download each cluster in an unaligned, aligned, or both, manners.