



< Back

wf.seq_to_tree.seq_to_tree/0.0.13

0.0.13 ▾

About Parameters Graph Executions Development

New to this workflow? Here are some resources to get you started:



Use Test Data

Use Test Data ▾

Import Bulk Data

	🚩	Output directory	Prefix of outputted files.	Input multi-FASTA file	Alignment mode (see About for details)	Trimming mode	Gappyne... threshold	Integer for number of UFBoot replicates to run
⬆	⚠	–	seq_to...	–	auto	smart-gap	0.9	1000

Output directory ⓘ

Select a directory

Select Folder

Empty path

Prefix of outputted files. ⓘ

seq_to_tree

Input multi-FASTA file ⓘ

Select a file

Select File

Empty path

Alignment mode (see About for details) ⓘ

auto ▾

Trimming mode ⓘ

smart-gap ▾

Gappyness threshold ⓘ

0.9

Integer for number of UFBoot replicates to run ⓘ

1000

+ Add Row

Seq to tree

Runtime Statistics

coming soon

coming soon



⚠ Errors in row 1

Launch Workflow