

# Phylogenetics and Molecular Evolution/Filogenética e Evolução Molecular

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de Lisboa



**Computational  
Biology & Population  
Genomics Group**



## Download

Link to BETA version of [SplitsTree5](#) (for testing purposes).

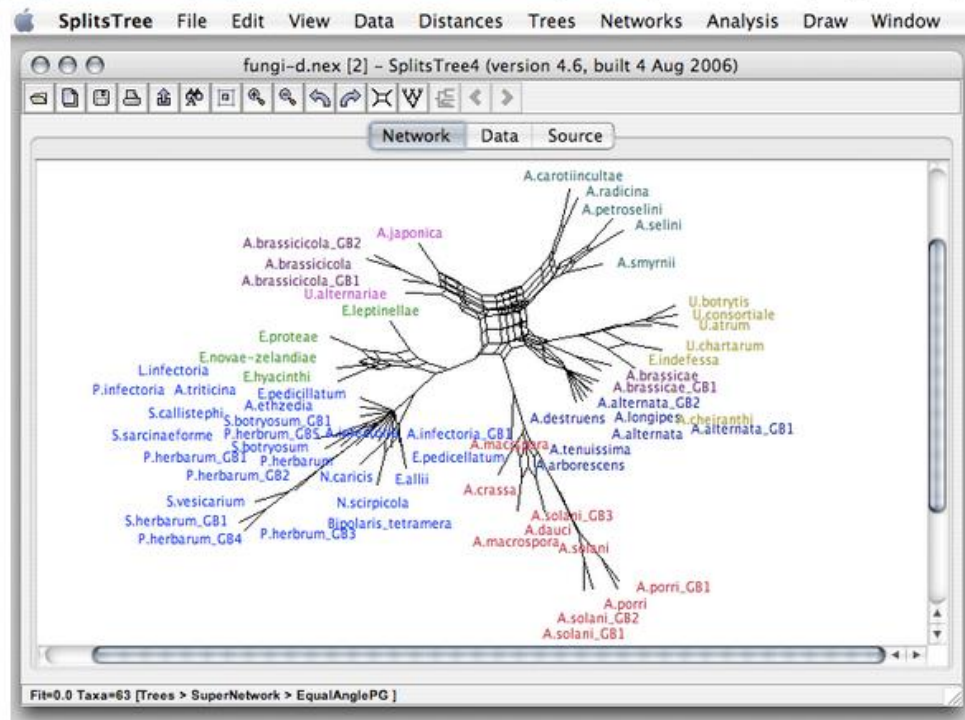
Link to talk given at [ISMB18](#).

## Description

SplitsTree4 is the leading application for computing unrooted phylogenetic networks from molecular sequence data. Given an alignment of sequences, a distance matrix or a set of trees, the program will compute a phylogenetic tree or network using methods such as split decomposition, neighbor-net, consensus network, super networks methods or methods for computing hybridization or simple recombination networks.

SplitsTree4 is an all-new implementation of the [SplitsTree3](#) software written in Java. Superficially, this new program is similar to previous versions of this software. However, there are substantial differences. The new program has many new features, see the [manual](#) for details.

If you use SplitsTree in work in any way, then please cite the following paper: D. H. Huson and D. Bryant, [Application of Phylogenetic Networks in Evolutionary Studies](#), Mol. Biol. Evol., 23(2):254-267, 2006.



Huson and Bryant 2006 MBE

# SplitsTree 4

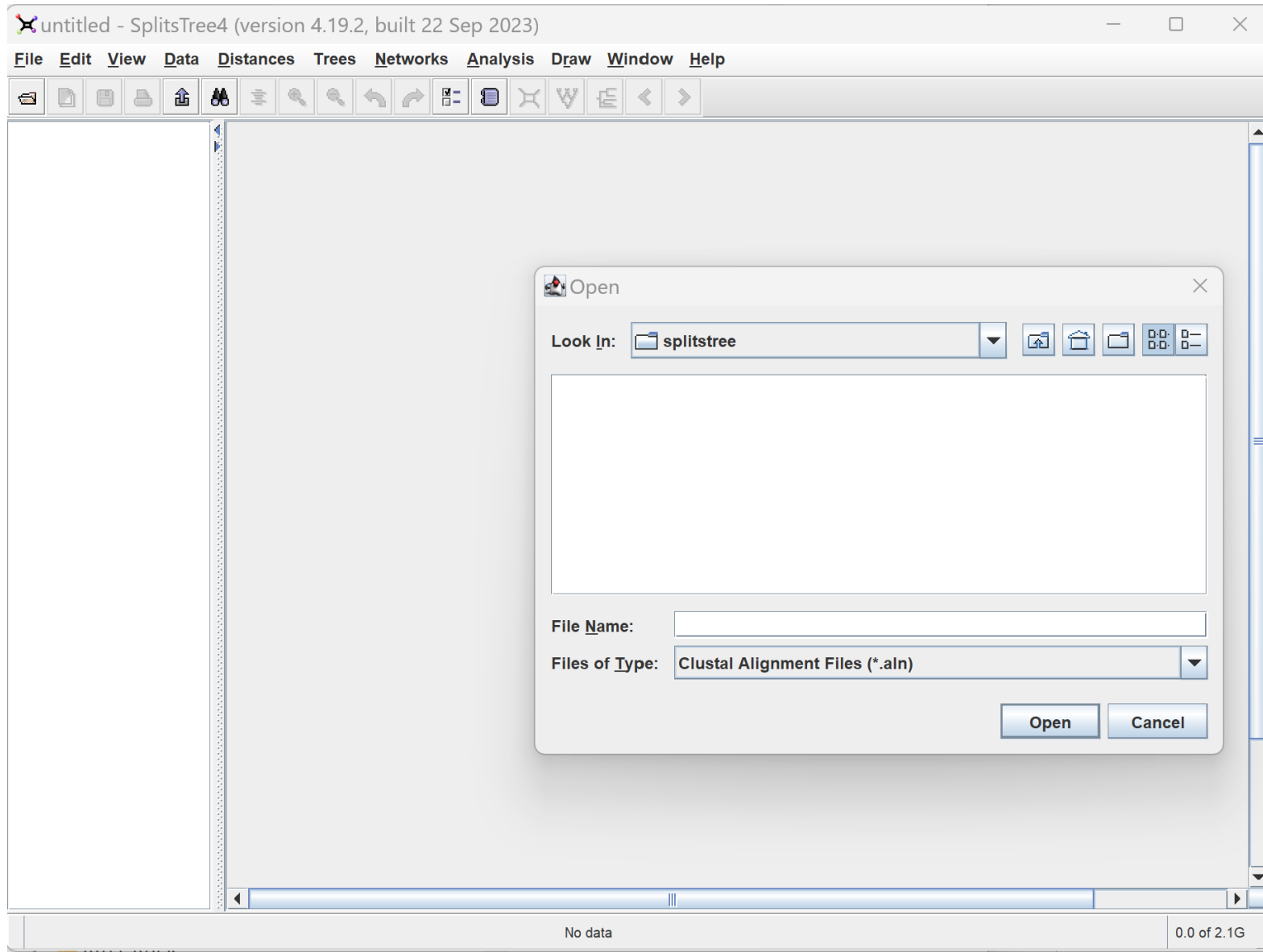
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Daniel H. Huson and David Bryant

September 22, 2023



# SplitsTree 4



# SplitsTree 4

## 9 Building and Drawing Networks

The `Network` menu provides methods for computing phylogenetic networks from character sequences, distances and trees.

Methods that compute a split network directly from character sequences provided in the `Characters` block are `ParsimonySplits`, `MedianNetwork`, `MedianJoining` and `SpectralSplits`. Note that the Median network method requires binary sequences. However, given DNA or RNA, this program will detect all sites that contain precisely two character-states and will build a Median network from these.

The `MedianJoining` method computes an unrooted network from binary sequences, DNA and other multi-state sequences. This is an implementation of the algorithm described in [4]. In the case of non-binary sequences, the resulting network will not be a split network.

Two methods for computing split networks from distances provided in the `Distances` block are `SplitDecomposition` and `NeighborNet`.

If a set of phylogenetic trees in the `Trees` block all contain the full set of taxa listed in the `Taxa` block, then the `ConsensusNetwork` method can be applied to compute a consensus network. If, however, the `Trees` block contains partial trees, that is, trees that do not necessarily all involve identical sets of taxa, then the `SuperNetwork` or `FilteredSuperNetwork` method can be used to compute a super network.

The `Draw` menu determines which algorithm is used to construct the final visualization of the tree or network. Existing methods are `EqualAngle`, `RootedEqualAngle` and `Phylogram`. Additionally, the `Draw→Hide Selected Splits` can be used to remove selected splits from the network and the `Draw→Select Trees` can be used to highlight different trees contained in a split network.

# SplitsTree 4

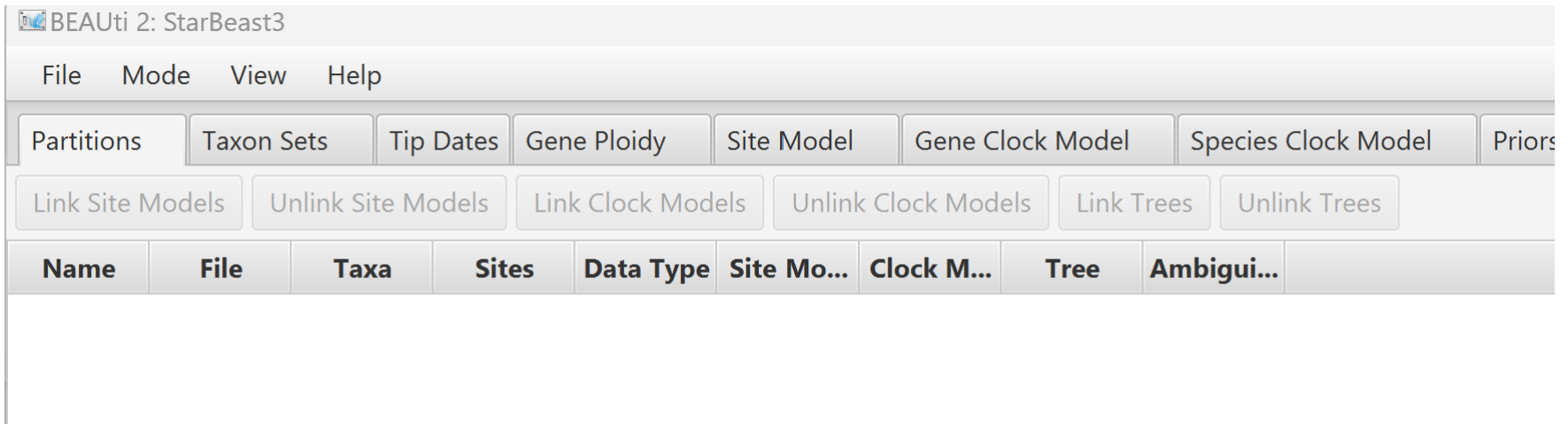
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- [1] Sarah C. Ayling and Terence A. Brown. Novel methodology for construction and pruning of quasi-median networks. *BMC Bioinformatics*, 9:115, 2008.
- [2] H.-J. Bandelt and A. W. M. Dress. A canonical decomposition theory for metrics on a finite set. *Advances in Mathematics*, 92:47–105, 1992.
- [3] H.-J. Bandelt, P. Forster, B. C. Sykes, and M. B. Richards. Mitochondrial portraits of human population using median networks. *Genetics*, 141:743–753, 1995.
- [4] Hans-Jürgen Bandelt, Peter Forster, and Arne Röhl. Median-joining networks for inferring intraspecific phylogenies. *Molecular Biology and Evolution*, 16:37–48, 1999.

# starBeast

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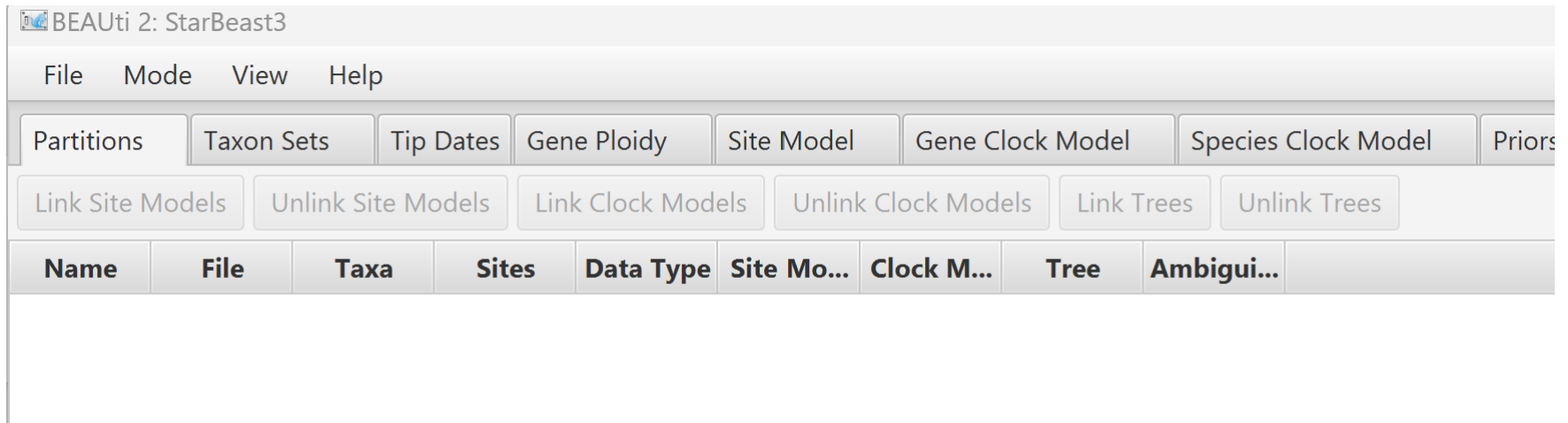
## File template starBeast3



# starBeast

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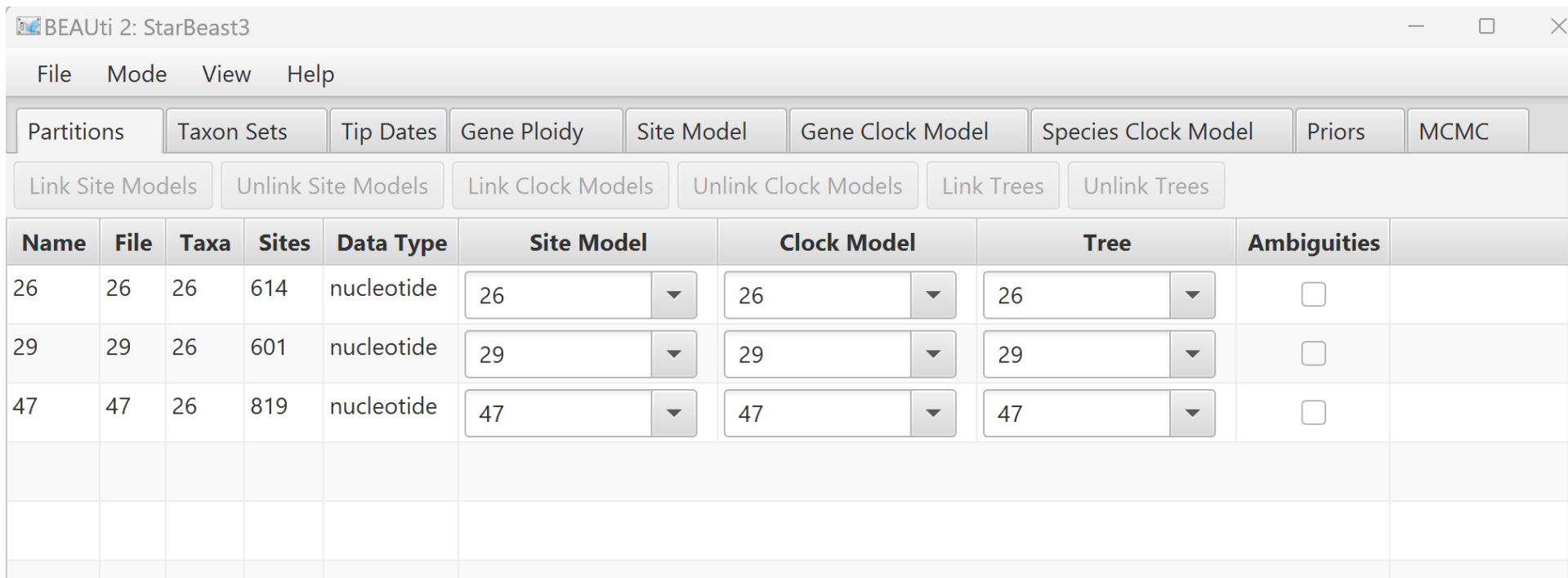
## File template starBeast3





# starBeast

File Import alignments (nexus, um por gene)

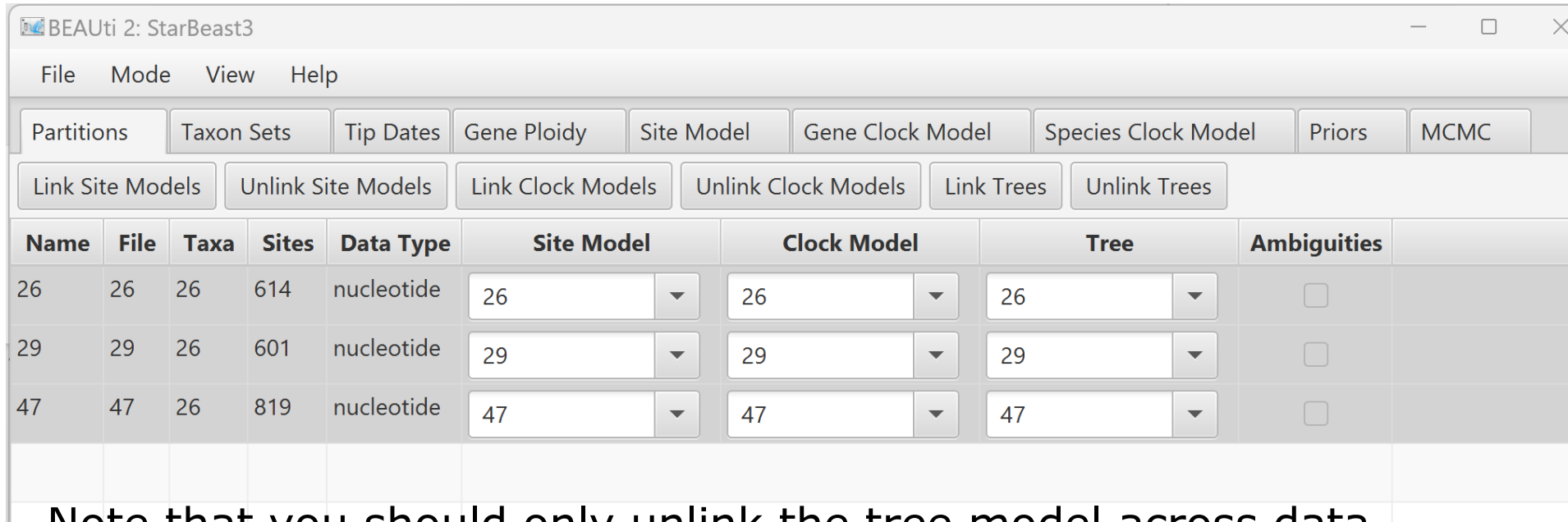


The screenshot shows the BEAUti 2: StarBeast3 interface. At the top, there is a menu bar with 'File', 'Mode', 'View', and 'Help'. Below the menu bar are several tabs: 'Partitions', 'Taxon Sets', 'Tip Dates', 'Gene Ploidy', 'Site Model', 'Gene Clock Model', 'Species Clock Model', 'Priors', and 'MCMC'. Underneath these tabs are buttons for 'Link Site Models', 'Unlink Site Models', 'Link Clock Models', 'Unlink Clock Models', 'Link Trees', and 'Unlink Trees'. The main area contains a table with the following columns: Name, File, Taxa, Sites, Data Type, Site Model, Clock Model, Tree, and Ambiguities. The table has three rows of data.

Name	File	Taxa	Sites	Data Type	Site Model	Clock Model	Tree	Ambiguities
26	26	26	614	nucleotide	26	26	26	<input type="checkbox"/>
29	29	26	601	nucleotide	29	29	29	<input type="checkbox"/>
47	47	26	819	nucleotide	47	47	47	<input type="checkbox"/>

# starBeast

## Default unlink



The screenshot shows the BEAUti 2: StarBeast3 interface. The top menu bar includes 'File', 'Mode', 'View', and 'Help'. Below the menu is a row of tabs: 'Partitions', 'Taxon Sets', 'Tip Dates', 'Gene Ploidy', 'Site Model', 'Gene Clock Model', 'Species Clock Model', 'Priors', and 'MCMC'. A second row of buttons includes 'Link Site Models', 'Unlink Site Models', 'Link Clock Models', 'Unlink Clock Models', 'Link Trees', and 'Unlink Trees'. The main table displays data partitions with columns for Name, File, Taxa, Sites, Data Type, Site Model, Clock Model, Tree, and Ambiguities. The 'Tree' column contains dropdown menus with the partition ID selected. The 'Ambiguities' column contains checkboxes.

Name	File	Taxa	Sites	Data Type	Site Model	Clock Model	Tree	Ambiguities
26	26	26	614	nucleotide	26	26	26	<input type="checkbox"/>
29	29	26	601	nucleotide	29	29	29	<input type="checkbox"/>
47	47	26	819	nucleotide	47	47	47	<input type="checkbox"/>

Note that you should only unlink the tree model across data partitions that are actually genetically unlinked. For example, in most organisms all the mitochondrial genes are effectively linked due to a lack of recombination and they should be set up to use the same tree model in a \*BEAST analysis. It could also be that for this analysis a linked model would perform better.

# Taxon set

BEAUti 2: StarBeast3

File Mode View Help

Partitions Taxon Sets ? Tip Dates Gene Ploidy Site Model Gene Clock Model Species Clock Model Priors MCMC

filter:

Taxon	Species/Population
Thomomys_bottae_xerophilus	T
Thomomys_talpoides_ocius	T
Thomomys_bottae_ruidosae	T
Thomomys_bottae_bottae	T
Thomomys_townsendii_townsendii	T
Thomomys_bottae_cactophilus	T
Thomomys_bottae_laticeps	T
Thomomys_idahoensis_pygmaeus_a	T
Thomomys_talpoides_yakimensis	T
Thomomys_idahoensis_pygmaeus_b	T
Thomomys_bottae_alpinus	T
Thomomys_talpoides_bridgeri	T
Thomomys_bottae_saxatilis	T

Fill down

Guess

# Taxon set

BEAUti 2: StarBeast3

File Mode View Help

Partitions Taxon Sets Tip Dates Gene Ploidy Site Model Gene Clock Model Species Clock Model Priors MCMC

filter:

Taxon
Thomomys_bottae_xerophilus
Thomomys_talpoides_ocius
Thomomys_bottae_ruidosae
Thomomys_bottae_bottae
Thomomys_townsendii_townsendii
Thomomys_bottae_cactophilus
Thomomys_bottae_laticeps
Thomomys_idahoensis_pygmaeus_a
Thomomys_talpoides_yakimensis
Thomomys_idahoensis_pygmaeus_b
Thomomys_bottae_alpinus
Thomomys_talpoides_bridgeri
Thomomys_bottae_saxatilis

Fill down Guess

use everything

split on character  and take group(s):

use regular expressi...

read from file

# Taxon set

BEAUi 2: StarBeast3

File Mode View Help

Partitions Taxon Sets Tip Dates Gene Ploidy Site Model Gene Clock Model Species Clock Model Priors MCMC

filter:

Taxon	Species/Population
Thomomys_talpoides_ocius	talpoides
Thomomys_talpoides_yakimensis	talpoides
Thomomys_talpoides_bridgeri	talpoides
Thomomys_townsendii_townsendii	townsendii
Thomomys_townsendii_relictus	townsendii
Thomomys_idahoensis_pygmaeus_a	idahoensis
Thomomys_idahoensis_pygmaeus_b	idahoensis
Thomomys_umbrinus_chihuahuae	umbrinus
Thomomys_umbrinus_atroavarius	umbrinus
Thomomys_monticola_a	monticola
Thomomys_monticola_b	monticola
Thomomys_bottae_xerophilus	bottae
Thomomys_bottae_ruidosae	bottae

Fill down Guess

# Gene Ploidy

The screenshot shows the BEAUi 2: StarBeast3 software interface. The window title is "BEAUi 2: StarBeast3". The menu bar includes "File", "Mode", "View", and "Help". The main panel has several tabs: "Partitions", "Taxon Sets", "Tip Dates", "Gene Ploidy" (which is selected and has a help icon), "Site Model", "Gene Clock Model", "Species Clock Model", "Priors", and "MCMC". Under the "Gene Ploidy" tab, there are three entries, each with a dropdown menu and a text input field for "Ploidy":

- treePrior.t:26: Ploidy 2.0
- treePrior.t:29: Ploidy 2.0
- treePrior.t:47: Ploidy 2.0

# Site model

The screenshot shows the BEAUti 2: StarBeast3 interface with the Site Model configuration window open. The window title is "BEAUti 2: StarBeast3". The menu bar includes "File", "Mode", "View", and "Help". The main toolbar contains tabs for "Partitions", "Taxon Sets", "Tip Dates", "Gene Ploidy", "Site Model", "Gene Clock Model", "Species Clock Model", "Priors", and "MCMC". The "Site Model" tab is active, showing a dropdown menu for "Gamma Site Model". The configuration options are as follows:

Parameter	Value	Options
Substitution Rate	1.0	estimate (checkbox)
Gamma Category Count	0	
Proportion Invariant	0.0	estimate (checkbox)
Subst Model	HKY	
Kappa	2.0	estimate (checkbox checked)
Frequencies	Empirical	

# Site model

The screenshot shows the BEAUti 2: StarBeast3 interface with the Site Model tab selected. The left sidebar shows a list of partitions with 26, 29, and 47 highlighted. The main panel is configured for the Gamma Site Model. The Substitution Rate is set to 1.0, Gamma Category Count is 0, and Proportion Invariant is 0.0. The Subst Model is set to HKY, with Kappa set to 2.0 and Frequencies set to Empirical. The 'estimate' checkboxes are visible for Substitution Rate, Proportion Invariant, and Kappa.

BEAUti 2: StarBeast3

File Mode View Help

Partitions Taxon Sets Tip Dates Gene Ploidy Site Model Gene Clock Model Species Clock Model Priors MCMC

Partition

- 26
- 29
- 47

Gamma Site Model

Substitution Rate 1.0 estimate

Gamma Category Count 0

Proportion Invariant 0.0 estimate

Subst Model

HKY

Kappa 2.0 estimate

Frequencies Empirical



# Site model

The screenshot shows the BEAUi 2: StarBeast3 software interface. The window title is "BEAUi 2: StarBeast3". The menu bar includes "File", "Mode", "View", and "Help". The main interface has several tabs: "Partitions", "Taxon Sets", "Tip Dates", "Gene Ploidy", "Site Model", "Gene Clock Model", "Species Clock Model", "Priors", and "MCMC". The "Site Model" tab is active, showing a dropdown menu for "Gamma Site Model". Below this, there are several parameters for the selected partition (47):

- Substitution Rate:** A text input field containing "1.0", with a question mark icon and an "estimate" checkbox.
- Gamma Category Count:** A text input field containing "0", with a question mark icon.
- Proportion Invariant:** A text input field containing "0.0", with a question mark icon and an "estimate" checkbox.
- Subst Model:** A dropdown menu showing "HKY", with a question mark icon.
- Kappa:** A text input field containing "2.0", with a question mark icon, an "estimate" checkbox, and a checked checkbox.
- Frequencies:** A dropdown menu showing "Empirical", with a question mark icon and an "estimate" checkbox.

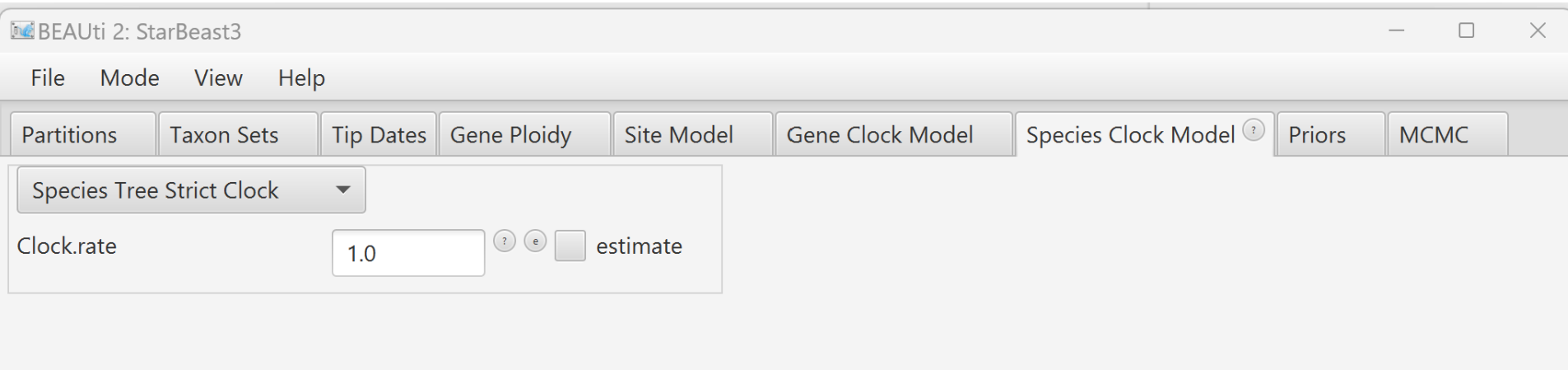
On the left side, a "Partition" list is visible, with partitions 26, 29, and 47 listed. Partition 47 is currently selected and highlighted.

# Gene clock model

The screenshot shows the BEAUi 2: StarBeast3 software interface. The window title is "BEAUi 2: StarBeast3". The menu bar includes "File", "Mode", "View", and "Help". The main panel has several tabs: "Partitions", "Taxon Sets", "Tip Dates", "Gene Ploidy", "Site Model", "Gene Clock Model" (which is active and has a help icon), "Species Clock Model", "Priors", and "MCMC". Below the tabs, there is a text instruction: "Select which partition clock rates to estimate. Unestimated rates default to 1. All rates below are relative to the species tree clock rate." Below this instruction is a table with three columns: "Partition", a checkbox, and an empty column. The table has four rows with the following data:

Partition	<input type="checkbox"/>	
26	<input type="checkbox"/>	
29	<input checked="" type="checkbox"/>	
47	<input checked="" type="checkbox"/>	

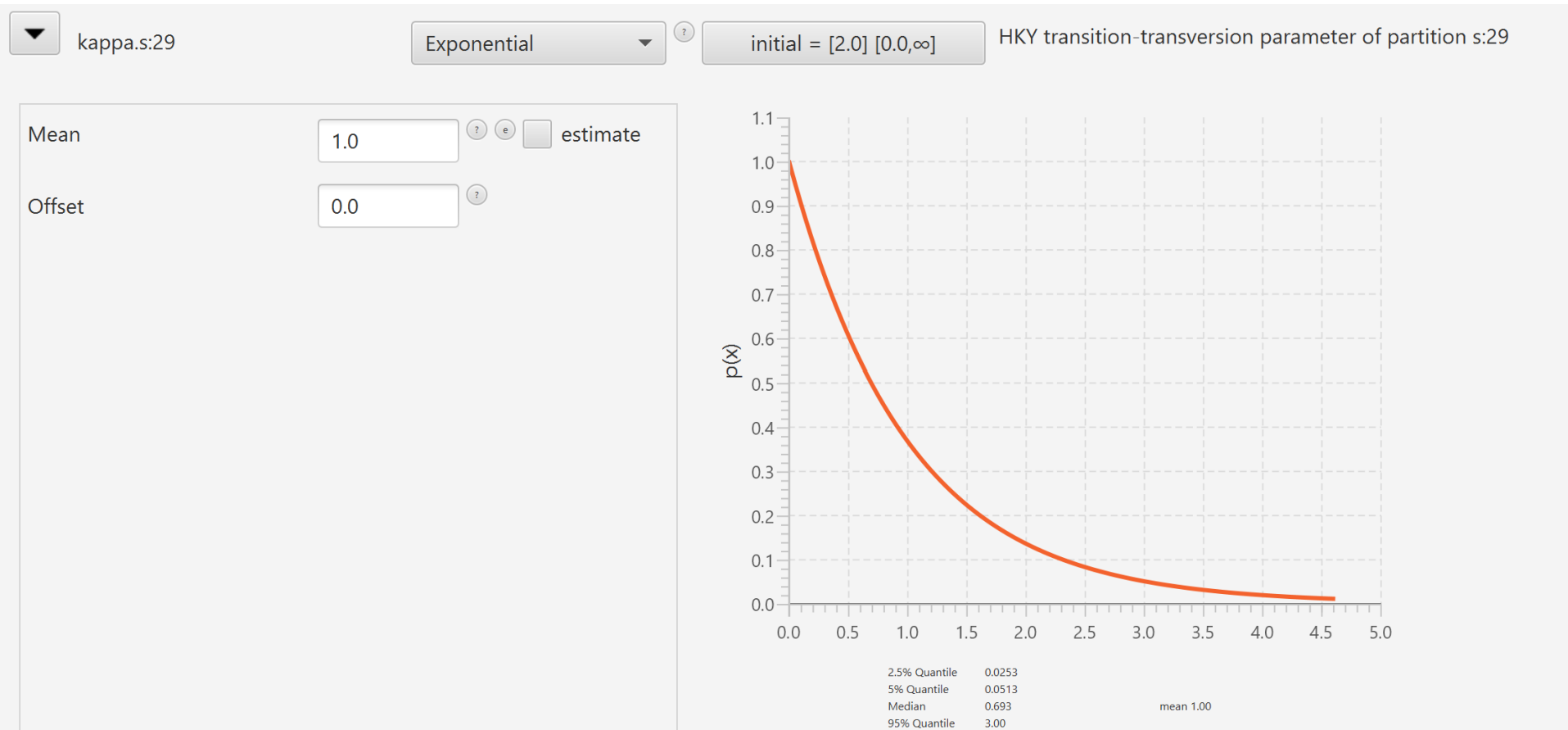
# Species clock model



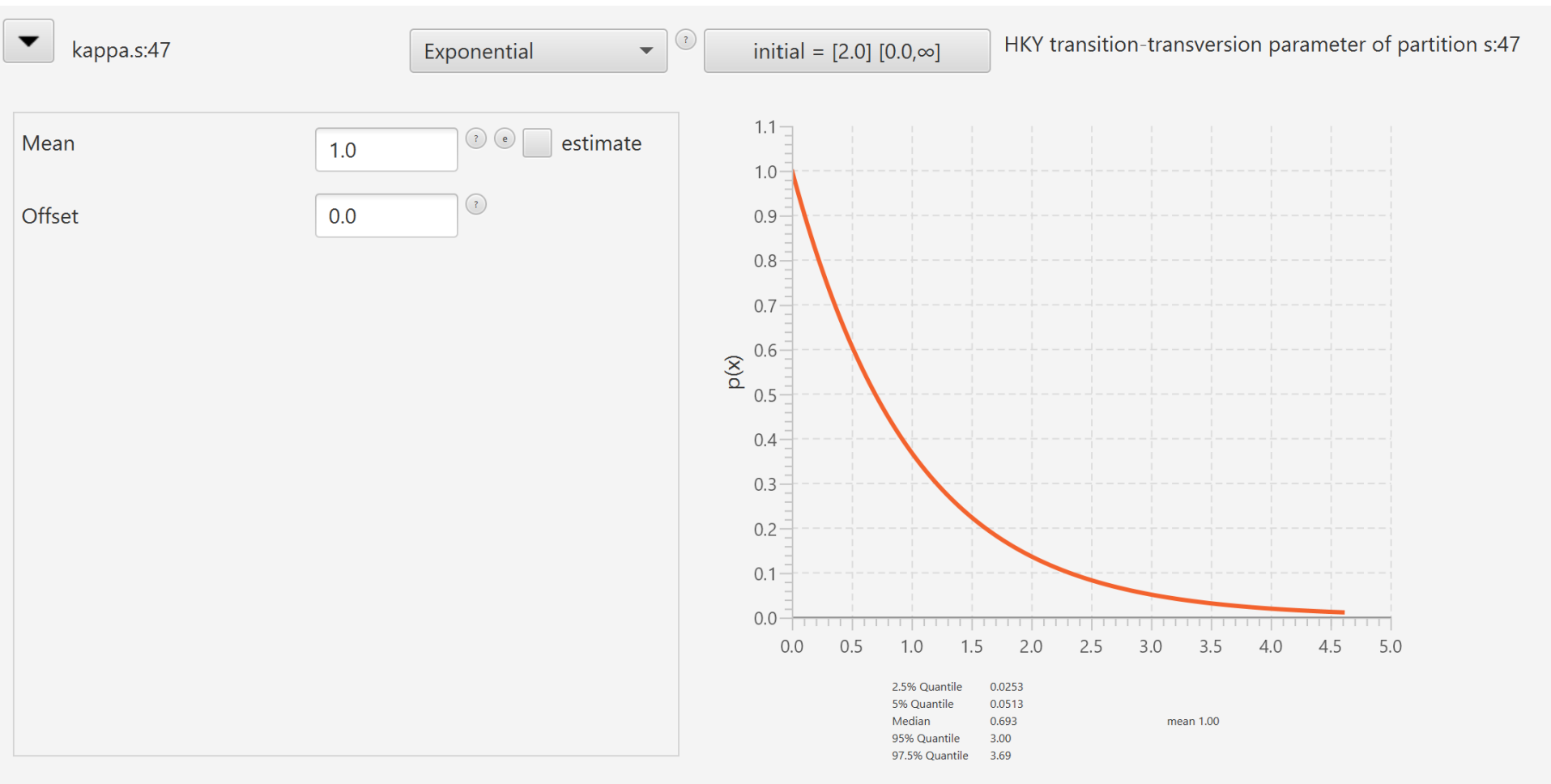
# Species clock model

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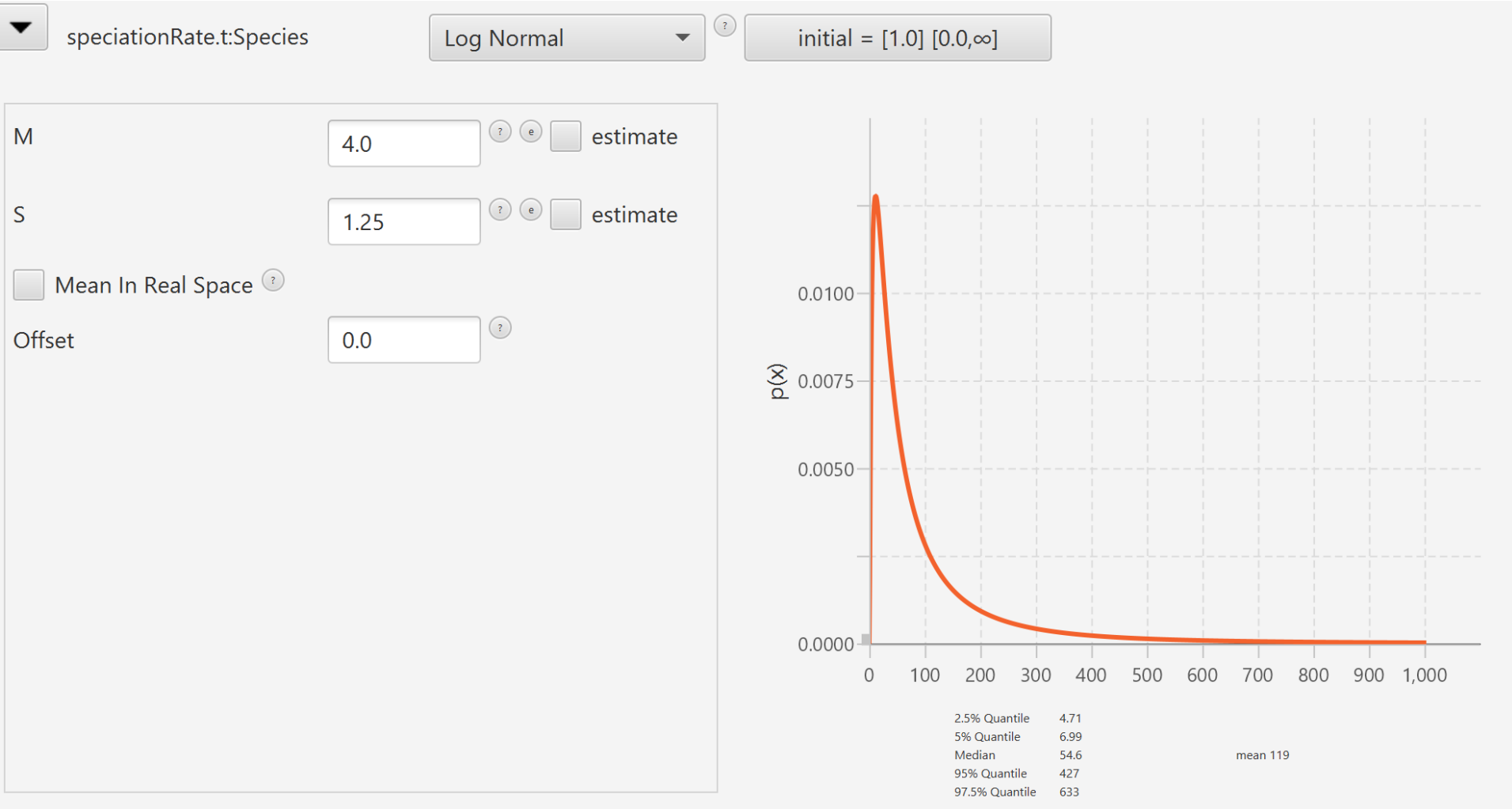
# Priors



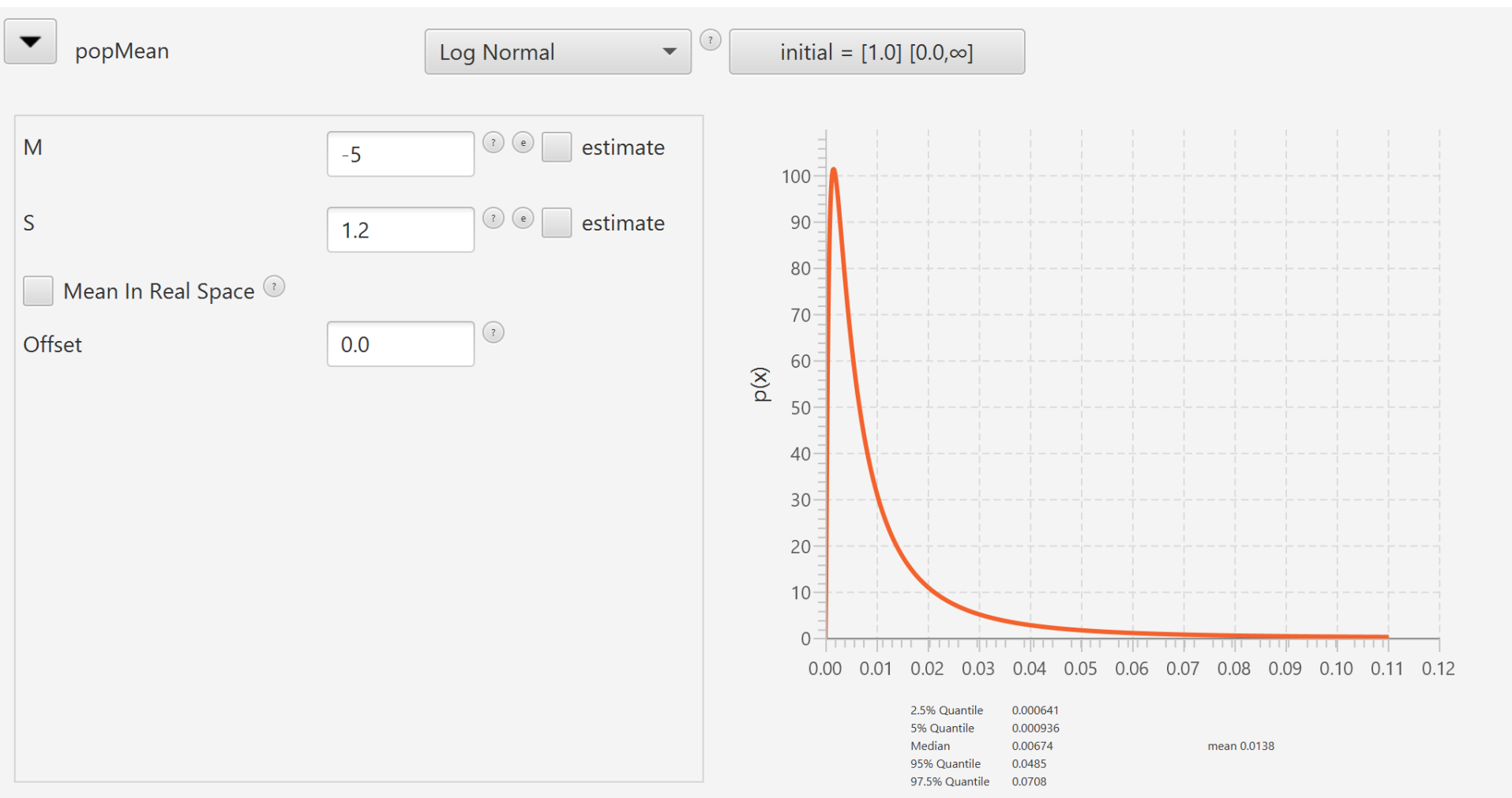
# Priors



# Priors



# Priors





# MCMC

BEAUti 2: StarBeast3

File Mode View Help

Partitions Taxon Sets Tip Dates Gene Ploidy Site Model Gene Clock Model Species Clock Model Priors MCMC ?

Chain Length  ?

Store Every  ?

Pre Burnin  ?

Num Initialization Attempts  ?

▼ tracelog

File Name  ?

Log Every  ?

Mode  ▼ ?

Sort  ▼ ?

500/5000

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# MCMC

---

▼ speciesTreeLogger

File Name

Log Every

Mode

Sort

Sanitise Headers

SpeciesTreeLoggerX

5000

# MCMC

---

▼ screenlog

File Name  ?

Log Every  ?

Mode  ▼ ?

Sort  ▼ ?

5000

# Xml to beast

---

Save xml in folder where results are going to be

# starBeast

Operator	Tuning	#accept	#reject	Pr(m)	Pr(acc m)		
starbeast3.operators.NodeReheight2(Reheight.t:Species)	-	135835	374296	0.10224	0.26627		
starbeast3.operators.CoordinatedExponential(CoordinatedExponential.t:Species)	0.00358	323306	345760	0.05112	0.48322		
starbeast3.operators.CoordinatedUniform(CoordinatedUniform.t:Species)	-	254745	374765	0.10224	0.40467		
kernel.BactrianScaleOperator(TreeRootScaler.t:Species)	0.19119	5548	45552	0.01022	0.10857		
kernel.BactrianNodeOperator(BactrianNodeOperator.t:Species)	0.97070	59922	125784	0.01022	0.32267		
AdaptableOperatorSampler(AdaptableTopologyOperator.lengths.Species)	-	596564	1107649	0.34079	0.35005		
starbeast3.operators.PopSizeGibbsSampler(PopSizeGibbsSampler.Species)	-	851018	0	0.17040	1.00000		
AdaptableOperatorSampler(AdaptableOperatorSampler.popmean:Species)	-	22738	62841	0.01704	0.26570		
kernel.BactrianScaleOperator(clockRateScaler.c:29)	0.31773	447	1217	0.00034	0.26863		
kernel.BactrianScaleOperator(clockRateScaler.c:47)	0.25029	413	1278	0.00034	0.24423		
kernel.BactrianScaleOperator(KappaScaler.s:26)	0.61274	448	1197	0.00034	0.27234		
kernel.BactrianScaleOperator(KappaScaler.s:29)	0.63997	436	1222	0.00034	0.26297		
kernel.BactrianScaleOperator(KappaScaler.s:47)	0.48794	480	1243	0.00034	0.27858		
AdaptableOperatorSampler(AdaptableOperatorSampler.YuleModel.t:Species)	-	25544	59911	0.01704	0.29892		
Uniform(UniformOperator.t:Species)	-	11553	39800	0.01022	0.22497		
WilsonBalding(WilsonBalding.t:Species)	-	2078	254007	0.05112	0.00811		
Exchange(Wide.t:Species)	-	5521	251025	0.05112	0.02152		
Exchange(Narrow.t:Species)	-	3089	14078	0.00341	0.17994		
kernel.BactrianSubtreeSlide(BactrianSubtreeSlide.t:Species)	0.00251	20430	234698	0.05112	0.08008	Try decreasing size to about 0.001	
starbeast3.operators.ParallelMCMCTreeOperator(ParallelMCMCTreeOperator)	-	0	0	0.01000	NaN		

Tuning: The value of the operator's tuning parameter, or '-' if the operator can't be optimized.

#accept: The total number of times a proposal by this operator has been accepted.

#reject: The total number of times a proposal by this operator has been rejected.

Pr(m): The probability this operator is chosen in a step of the MCMC (i.e. the normalized weight).

Pr(acc|m): The acceptance probability (#accept as a fraction of the total proposals for this operator).

Total calculation time: 331.362 seconds

End likelihood: -3937.277984628074

# trace

---

# Treeannotator

TreeAnnotator 2.7.6

Burn in percentage:

Posterior probability limit:

Target tree type:

Node heights:

Target tree file:

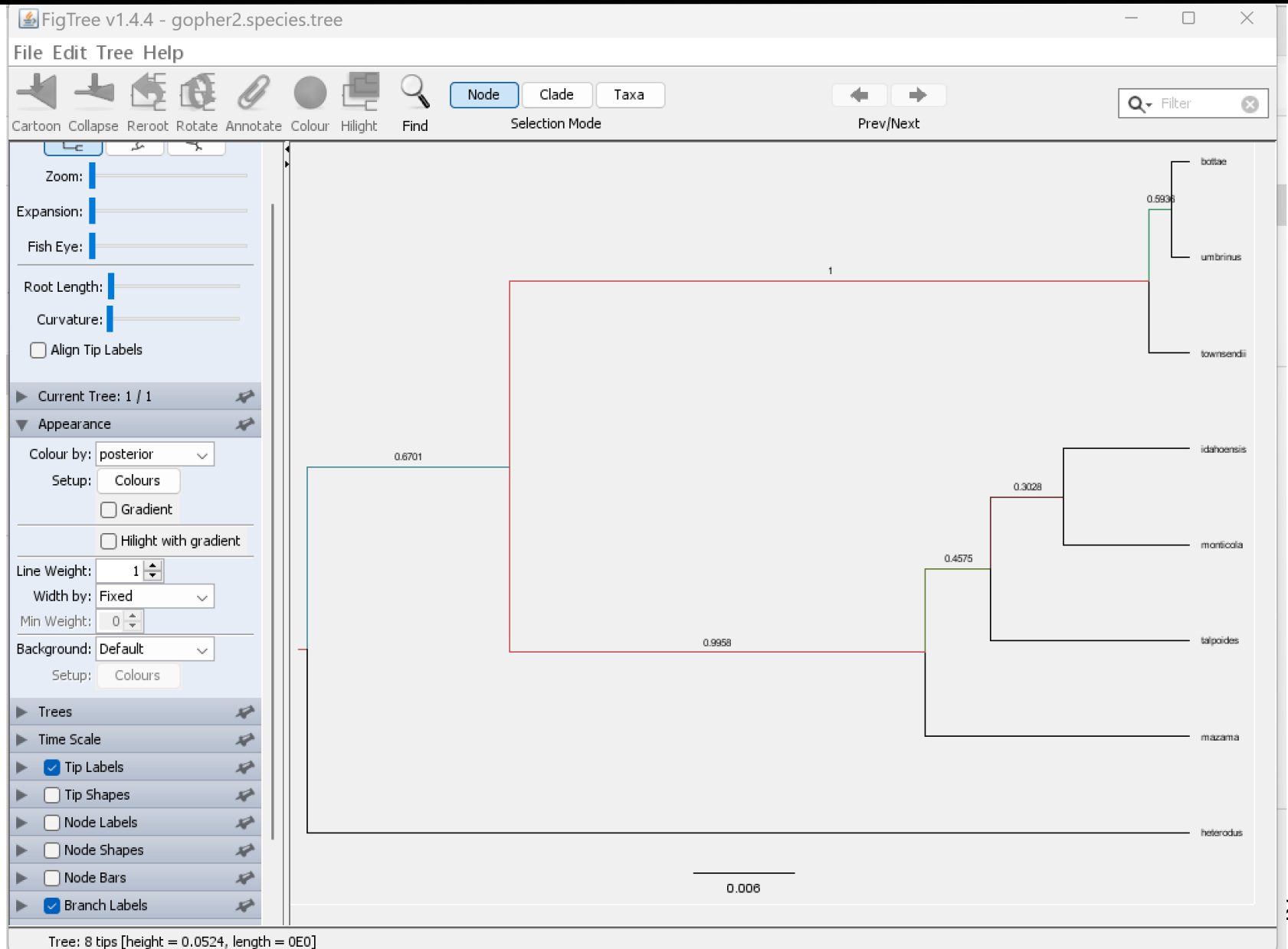
Input Tree File:

Output File:

Low memory:

Input .trees  
Output .tree

# Figtree





# Densitree

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