



# BEAST2 workflow

Jūlija Pečerska & Veronika Bošková



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**FigTree/IcyTree/DensiTree:** Tools for visualisation of trees (.trees)

**R(+RStudio)/Python/Matlab/etc:** Post analysis, plotting, etc.



# Workflow



# Workflow

 ACACACCC  
 TCACACCT  
 ACAGACTT



BEAUi



# Workflow

 ACACACCC  
 TCACACCT  
 ACAGACTT



**BEAUti**



**BEAST2**

xml file

# Workflow

 ACACACCC  
 TCACACCT  
 ACAGACTT



Tracer

log file



BEAUti



BEAST2

xml file

# Workflow

 ACACACCC  
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Tracer



TreeAnnotator



BEAUti



BEAST2

log file

trees file

xml file

# BEAUti



**B**ayesian **E**volutionary **A**nalysis **U**tility

GUI for setting up BEAST2 input file in xml format.

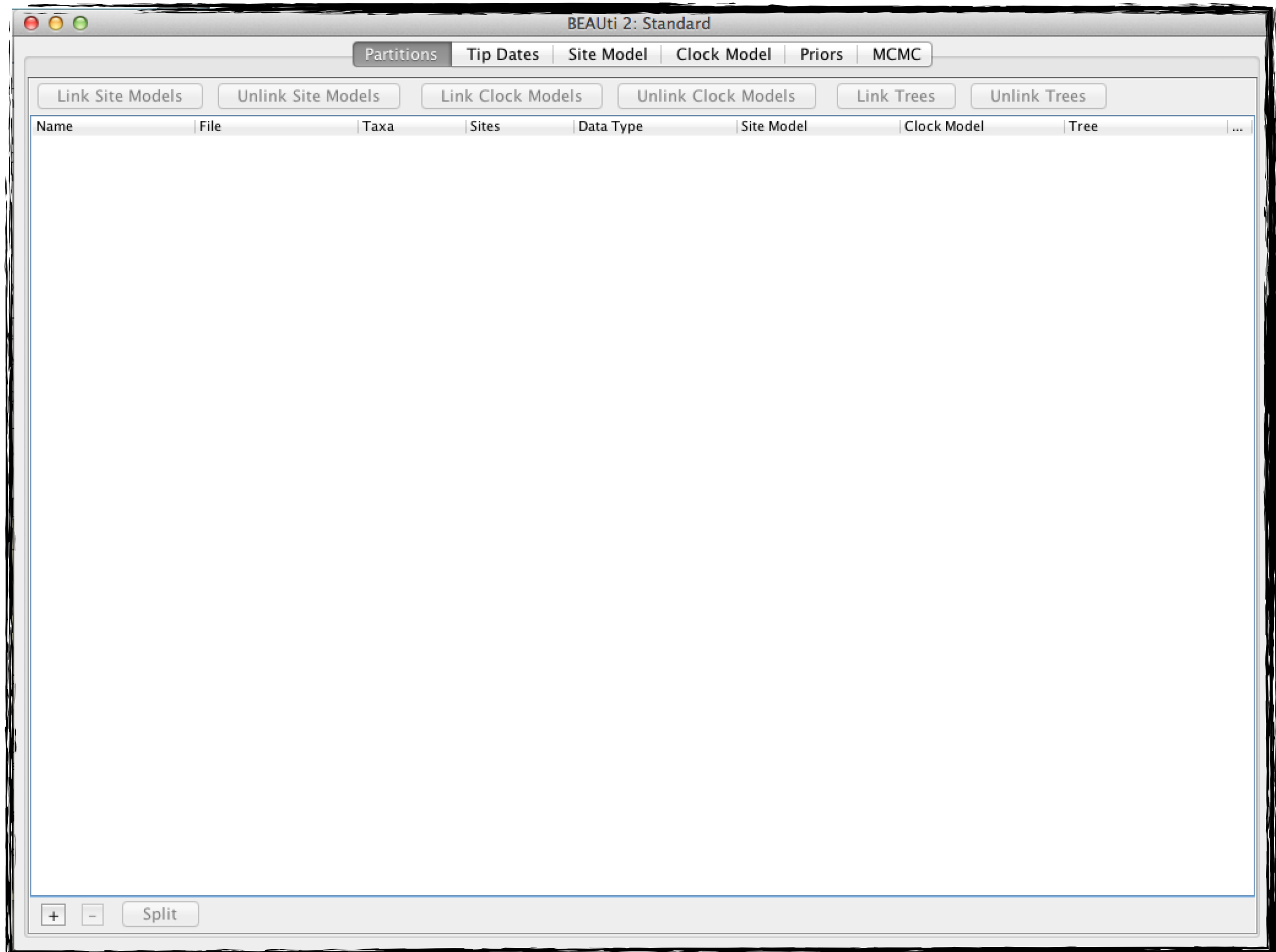
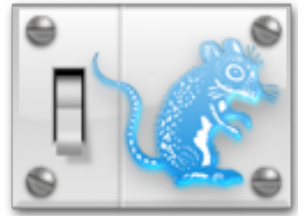
**Input:**

Sequence alignment

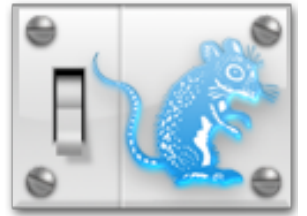
**Output:**

XML file

# BEAUti



# BEAUti



BEAUti 2: Standard

Partitions Tip Dates Site Model Clock Model Priors MCMC

▶ Tree.t:Flu	Birth Death Model		
▶ birthRate2.t:Flu	Log Normal	initial = [1.0] [0.0,10000.0]	Birth-Death speciation process rate of partition t:Flu
▶ clockRate.c:Flu	1/X	initial = [1.0] $[-\infty, \infty]$	substitution rate of partition c:Flu
▶ relativeDeathRate2.t:Flu	Beta	initial = [0.5] [0.0,1.0]	Death/Birth speciation process relative death rate of partition

+



# BEAUti



```
testHKY.xml
<beast version='2.0' namespace='beast.evolution.alignment:beast.core:beast.evolution.tree.coalescent:beast.core.ut...
1 <beast version='2.0'
2   namespace='beast.evolution.alignment:beast.core:beast.evolution.tree.coalescent:beast.core.util:
   beast.evolution.nuc:beast.evolution.operators:beast.evolution.sitemodel:
   beast.evolution.substitutionmodel:beast.evolution.likelihood'>
3
4
5   <!-- The sequence alignment -->
6   <!-- ntax=6 nchar=768 -->
7   <!-- npatterns=69 -->
8   <data id="alignment" dataType="nucleotide">
9     <sequence taxon="human">
10
11       AGAAATATGTCTGATAAAAGAGTTACTTTGATAGAGTAAATAATAGGAGCTTAAACCCCTTATTTCTACTAGGACTATGAGAATCGAACCCAT
12       CCCTGAGAATCCAAAATTCTCCGTGCCACCTATCACACCCCATCCTAAGTAAGGTCAGCTAAATAAGCTATCGGGCCCATACCCCGAAAATGTT
13       GGTATACCCCTTCCCGTACTAAGAAATTTAGGTTAAATACAGACCAAGAGCCTTCAAAGCCCTCAGTAAGTTG-
14       CAATACTTAATTTCTGTAAGGACTGCAAAACCCCACTCTGCATCAACTGAACGCAAAATCAGCCACTTTAATTAAGCTAAGCCCTTCTAGACCAA
15       TGGGACTTAAACCCACAAACACTTAGTTAACAGCTAAGCACCTAATCAAC-TGGCTTCAATCTAAAGCCCCGGCAGG-
16       TTTGAAGCTGCTTCTTGAATTTGCAATTCAATATGAAA-
17       TCACCTCGGAGCTTGGTAAAAAGAGGCTTAACCCCTGTCTTTAGATTTACAGTCCAATGCTTCA-
18       CTCAGCCATTTTACCACAAAAAAGGAAGGAATCGAACCCCTAAAGCTGGTTTCAAGCCAACCCCATGGCCTCCATGACTTTTTCAAAGGTAT
19       TAGAAAAACCATTTTATAAATTTGTCAAAGTTAAATTATAGGCT-AAATCCTATATATCTTA-
20       CACTGTAAAGCTAACTTAGCATTAACTTTTAAGTTAAAGATTAAGAGAACCAACACCTCTTTACAGTGA
21
22     </sequence>
23     <sequence taxon="chimp">
24
25       AGAAATATGTCTGATAAAAGAATTACTTTGATAGAGTAAATAATAGGAGTTCAAATCCCCTTATTTCTACTAGGACTATAAGAATCGAACTCAT
26       CCCTGAGAATCCAAAATTCTCCGTGCCACCTATCACACCCCATCCTAAGTAAGGTCAGCTAAATAAGCTATCGGGCCCATACCCCGAAAATGTT
27       GGTACACCCCTTCCCGTACTAAGAAATTTAGGTTAAGCACAGACCAAGAGCCTTCAAAGCCCTCAGCAAGTTA-
28       CAATACTTAATTTCTGTAAGGACTGCAAAACCCCACTCTGCATCAACTGAACGCAAAATCAGCCACTTTAATTAAGCTAAGCCCTTCTAGATTAA
29       TGGGACTTAAACCCACAAACATTTAGTTAACAGCTAAACACCCTAATCAAC-TGGCTTCAATCTAAAGCCCCGGCAGG-
30       TTTGAAGCTGCTTCTTGAATTTGCAATTCAATATGAAA-
31       TCACCTCAGAGCTTGGTAAAAAGAGGCTTAACCCCTGTCTTTAGATTTACAGTCCAATGCTTCA-
32       CTCAGCCATTTTACCACAAAAAAGGAAGGAATCGAACCCCTAAAGCTGGTTTCAAGCCAACCCCATGACCTCCATGACTTTTTCAAAGATAT
33       TAGAAAAACTATTTTATAAATTTGTCAAAGTTAAATTACAGGTT-AACCCCGTATATCTTA-
34       CACTGTAAAGCTAACCTAGCATTAACTTTTAAGTTAAAGATTAAGAGGACCGACACCTCTTTACAGTGA
35
36     </sequence>
37     <sequence taxon="bonobo">
38
39       AGAAATATGTCTGATAAAAGAATTACTTTGATAGAGTAAATAATAGGAGTTTAAATCCCCTTATTTCTACTAGGACTATGAGAGTCGAACCCAT
40       CCCTGAGAATCCAAAATTCTCCGTGCCACCTATCACACCCCATCCTAAGTAAGGTCAGCTAAATAAGCTATCGGGCCCATACCCCGAAAATGTT
41       GGTATACCCCTTCCCGTACTAAGAAATTTAGGTTAAACACAGACCAAGAGCCTTCAAAGCTCTCAGTAAGTTA-
42       CAATACTTAATTTCTGTAAGGACTGCAAAACCCCACTCTGCATCAACTGAACGCAAAATCAGCCACTTTAATTAAGCTAAGCCCTTCTAGATTAA
43       TGGGACTTAAACCCACAAACATTTAGTTAACAGCTAAACACCCTAATCAGC-TGGCTTCAATCTAAAGCCCCGGCAGG-
44       TTTGAAGCTGCTTCTTGAATTTGCAATTCAATATGAAA-
45       TCACCTCAGAGCTTGGTAAAAAGAGGCTTAACCCCTGTCTTTAGATTTACAGTCCAATGCTTCA-
```

# BEAST2



**B**ayesian **e**volutionary **a**nalysis by **s**ampling **t**rees **2**

Performs MCMC analyses of sequences under selected sequence evolution and tree model;

Planned as an extension of BEAST1, but now a separate package;

Has a modular design that makes it easy to extend.

## **Input:**

XML file

## **Output:**

log file

trees file

# BEAST2




	BEAST 2.1	BEAST 1.8
<b>COALESCENT TREE PRIORS</b>		
Constant size	Drummond 2002	Drummond 2002
Exponential growth	Drummond 2002	Drummond 2002
Bayesian skyline	Drummond 2005	Drummond 2005
Extended Bayesian skyline	Heled 2008	Heled 2008
Bayesian skygrid	X	Gill 2013
Deterministic closed SIR	In preparation	Dearlove 2013
<b>BIRTH-DEATH TREE PRIORS</b>		
Yule	Heled 2012	
Yule with one calibration		
Birth-death		
Calibrated birth-death	Heled 2013	X
Birth-death with incomplete sampling		X
Birth-death serial sampling	Stadler 2012	X
Birth-death serial skyline	Stadler 2013	X
Birth-death SIR	Kuhnert 2013	X
<b>AND MORE</b>		

...

# BEAST2



BEAST v2.4.2

 Bayesian Evolutionary Analysis Sampling Trees  
Version v2.4.2, 2002–2016

BEAST XML File:

Random number seed:

Thread pool size:

☐ Use BEAGLE library if available:

Prefer use of:

Prefer precision:

☐ Show list of available BEAGLE resources and Quit

BEAGLE is a high-performance phylogenetic library that can make use of additional computational resources such as graphics boards. It must be downloaded and installed independently of BEAST:  
<http://beagle-lib.googlecode.com/>

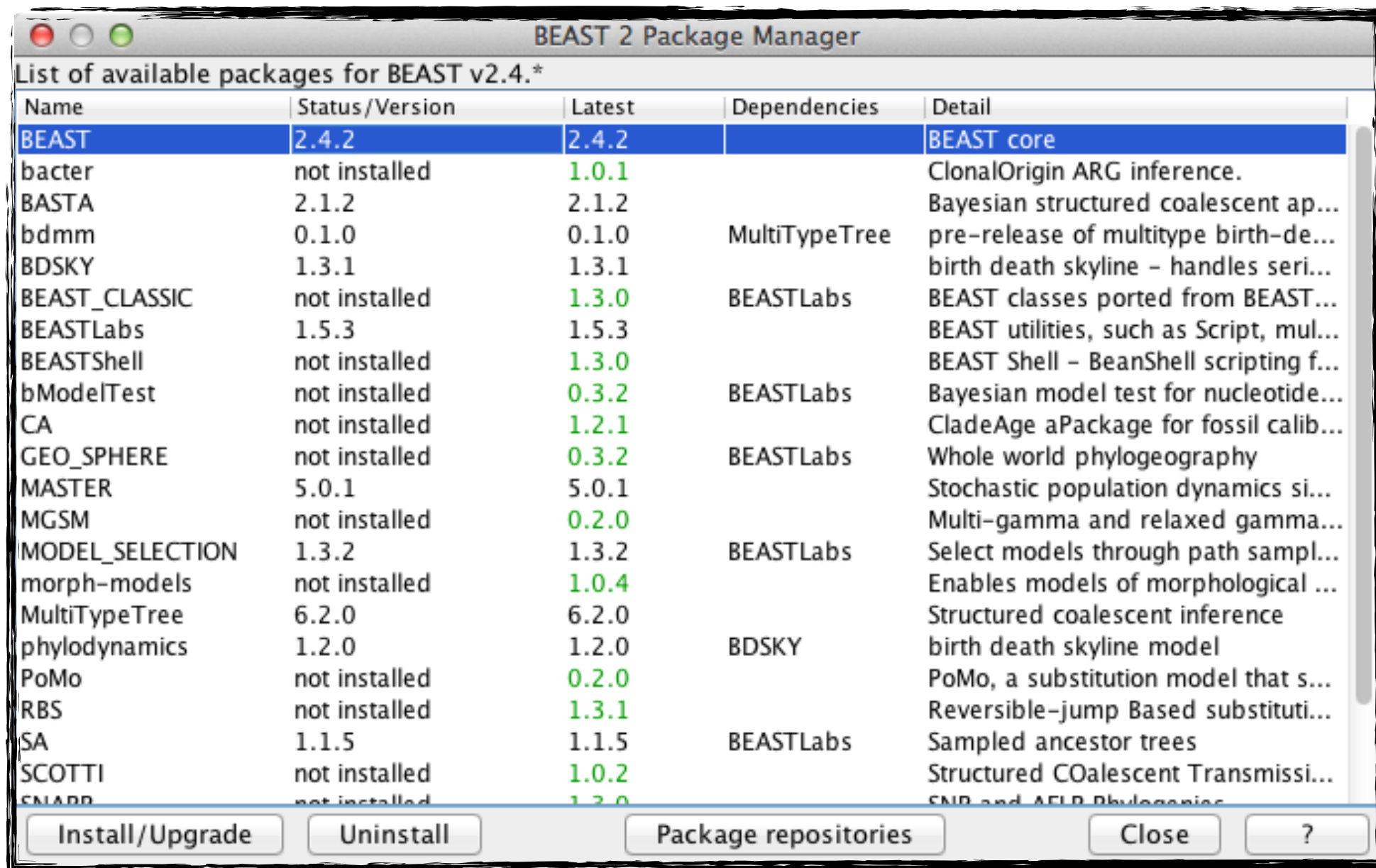
# BEAUti – installing BEAST2 packages

In BEAUti: File > Manage Packages



# BEAUi – installing BEAST2 packages

In BEAUi: File > Manage Packages



Name	Status/Version	Latest	Dependencies	Detail
BEAST	2.4.2	2.4.2		BEAST core
bacter	not installed	1.0.1		ClonalOrigin ARG inference.
BASTA	2.1.2	2.1.2		Bayesian structured coalescent ap...
bdmm	0.1.0	0.1.0	MultiTypeTree	pre-release of multitype birth-de...
BDSKY	1.3.1	1.3.1		birth death skyline – handles seri...
BEAST_CLASSIC	not installed	1.3.0	BEASTLabs	BEAST classes ported from BEAST...
BEASTLabs	1.5.3	1.5.3		BEAST utilities, such as Script, mul...
BEASTShell	not installed	1.3.0		BEAST Shell – BeanShell scripting f...
bModelTest	not installed	0.3.2	BEASTLabs	Bayesian model test for nucleotide...
CA	not installed	1.2.1		CladeAge aPackage for fossil calib...
GEO_SPHERE	not installed	0.3.2	BEASTLabs	Whole world phylogeography
MASTER	5.0.1	5.0.1		Stochastic population dynamics si...
MGSM	not installed	0.2.0		Multi-gamma and relaxed gamma...
MODEL_SELECTION	1.3.2	1.3.2	BEASTLabs	Select models through path sampl...
morph-models	not installed	1.0.4		Enables models of morphological ...
MultiTypeTree	6.2.0	6.2.0		Structured coalescent inference
phylodynamics	1.2.0	1.2.0	BDSKY	birth death skyline model
PoMo	not installed	0.2.0		PoMo, a substitution model that s...
RBS	not installed	1.3.1		Reversible-jump Based substituti...
SA	1.1.5	1.1.5	BEASTLabs	Sampled ancestor trees
SCOTTI	not installed	1.0.2		Structured COalescent Transmissi...
SNAPP	not installed	1.2.0		SNP and AFLP Phylogenies

Install/Upgrade   Uninstall   Package repositories   Close   ?

# Tracer



Summarises log files from BEAST2 runs;

Allows to check mixing, ESS, parameter correlations;

Gives an overview of posterior parameter estimates;

Lets one compare results of several analyses.

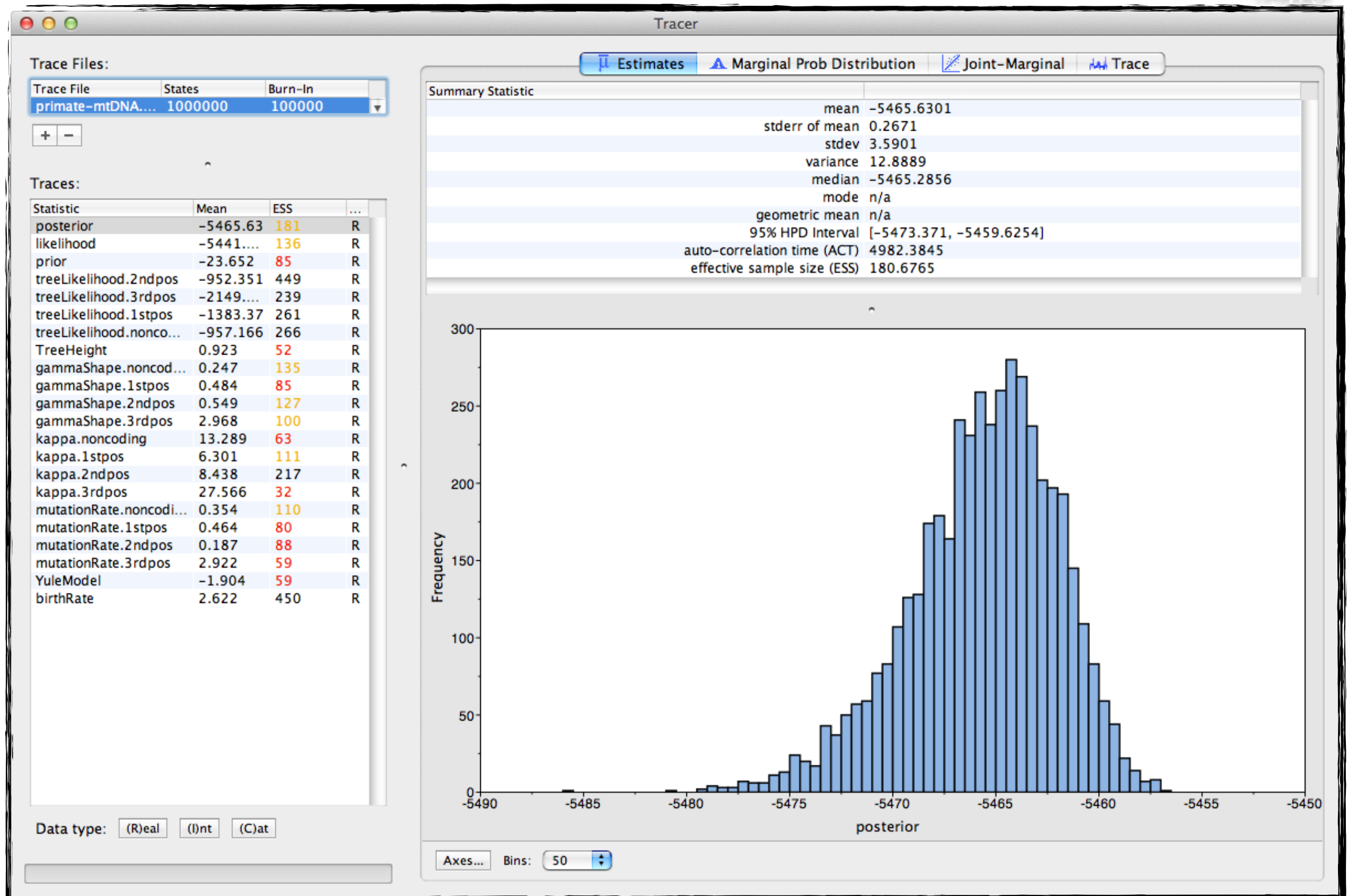
**Input:**

log file

**Output:**

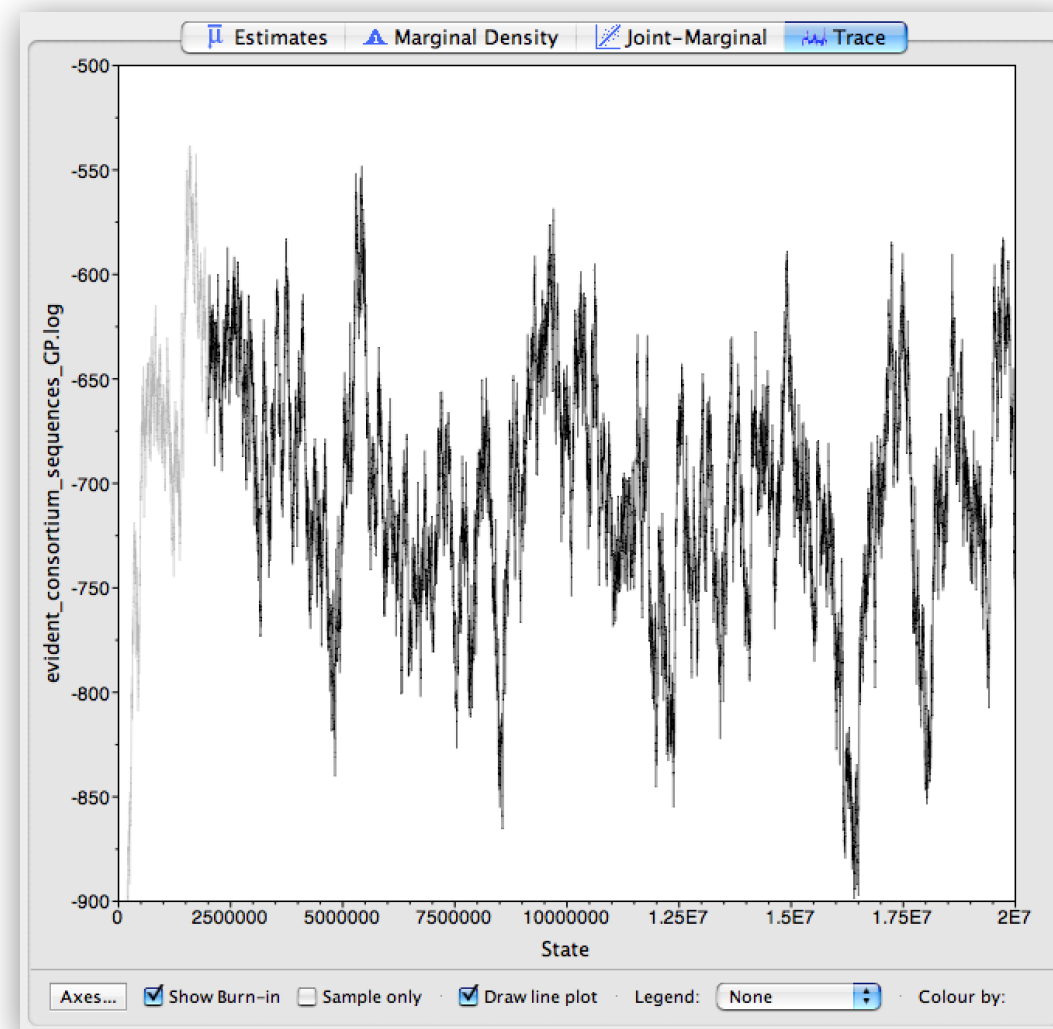
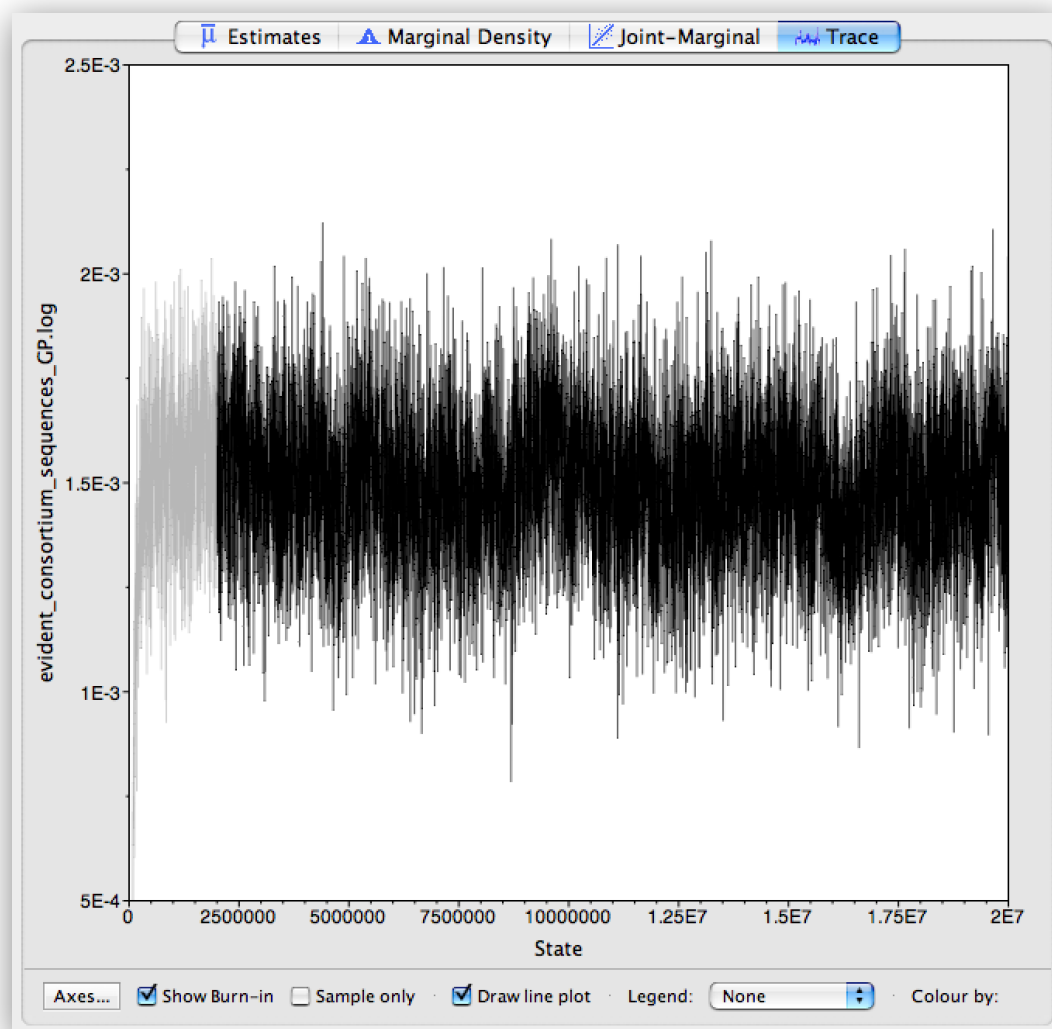
insight

# Tracer

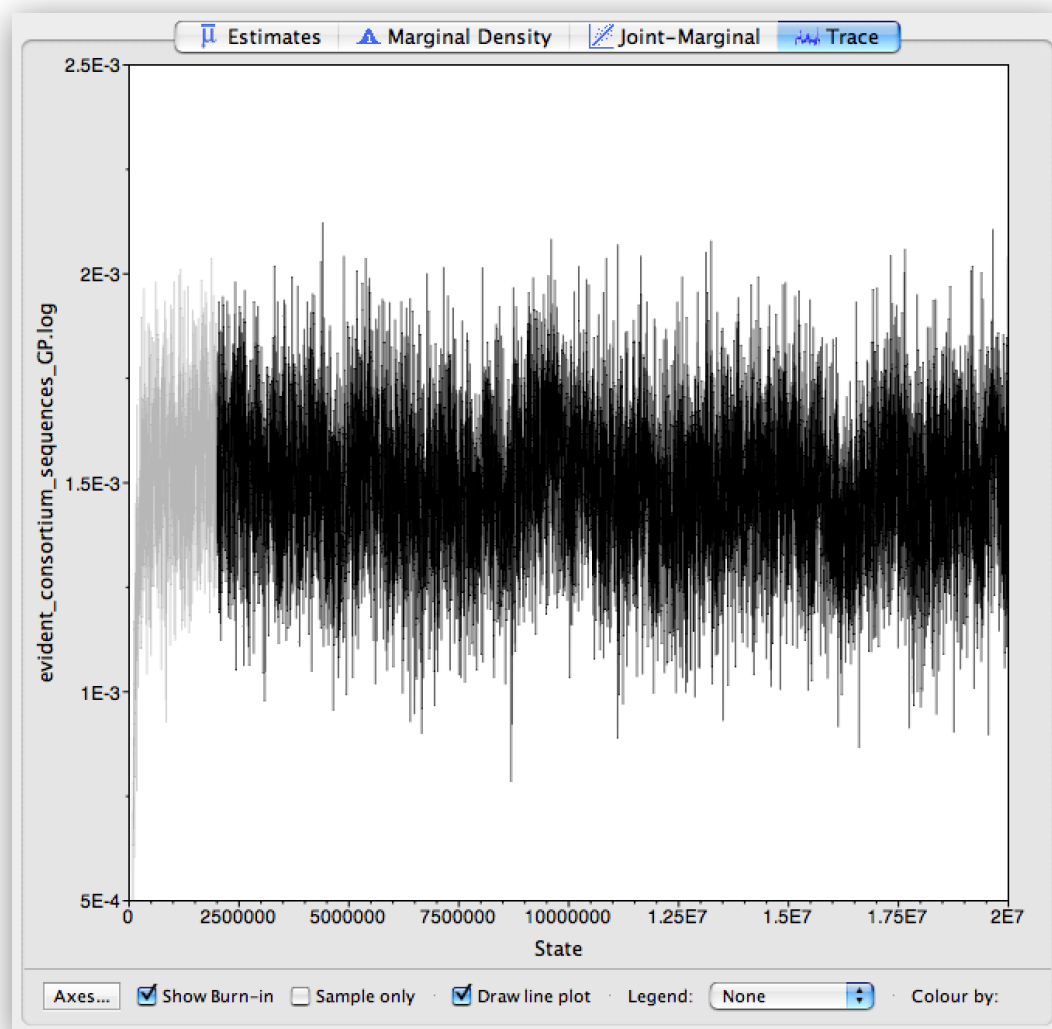




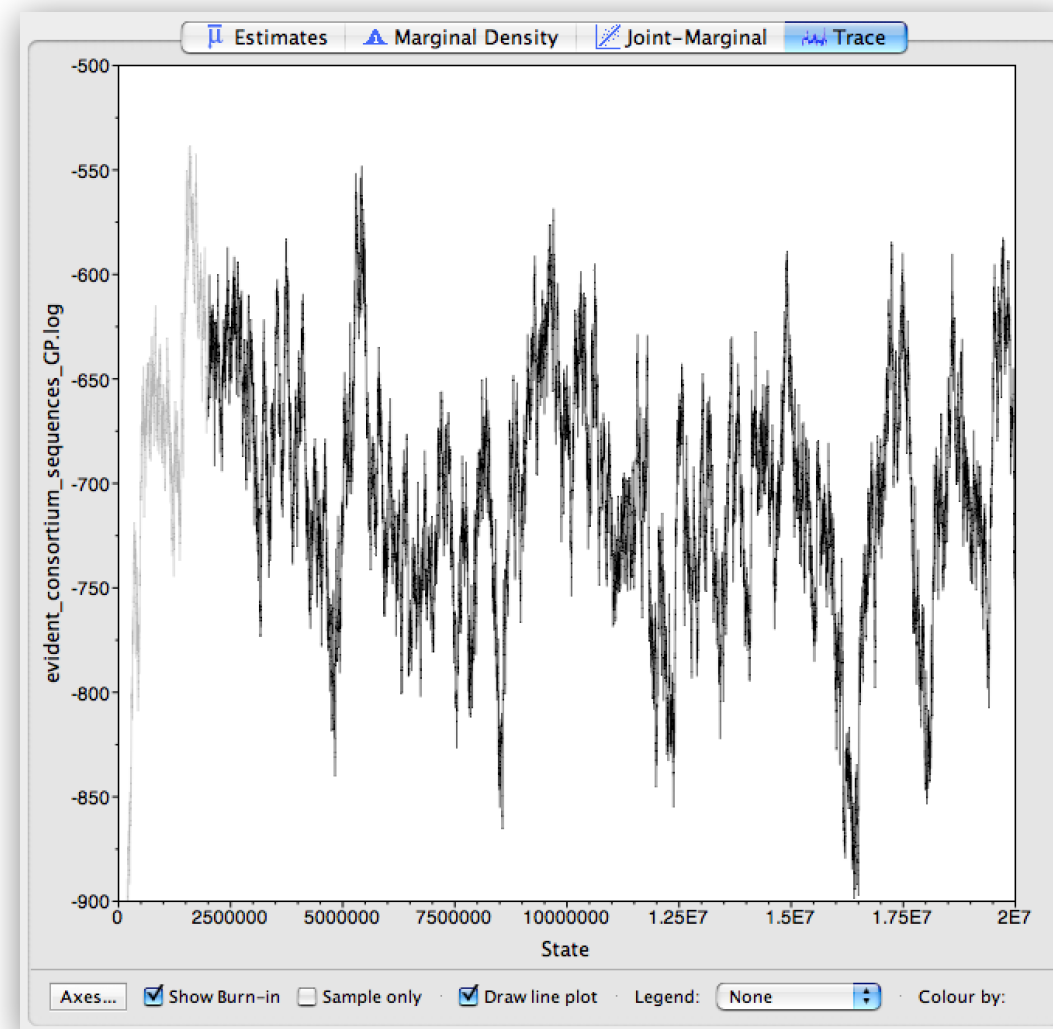
# Tracer



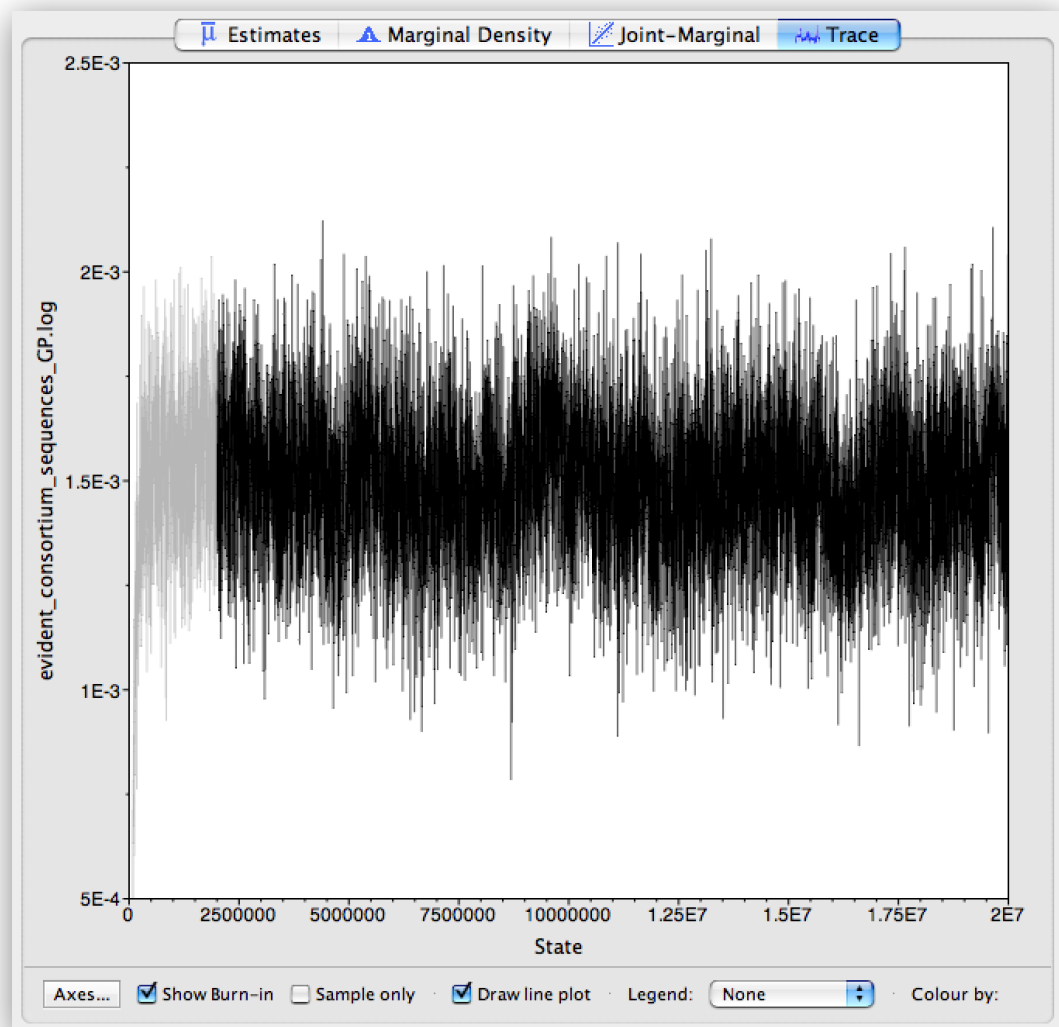
# Tracer



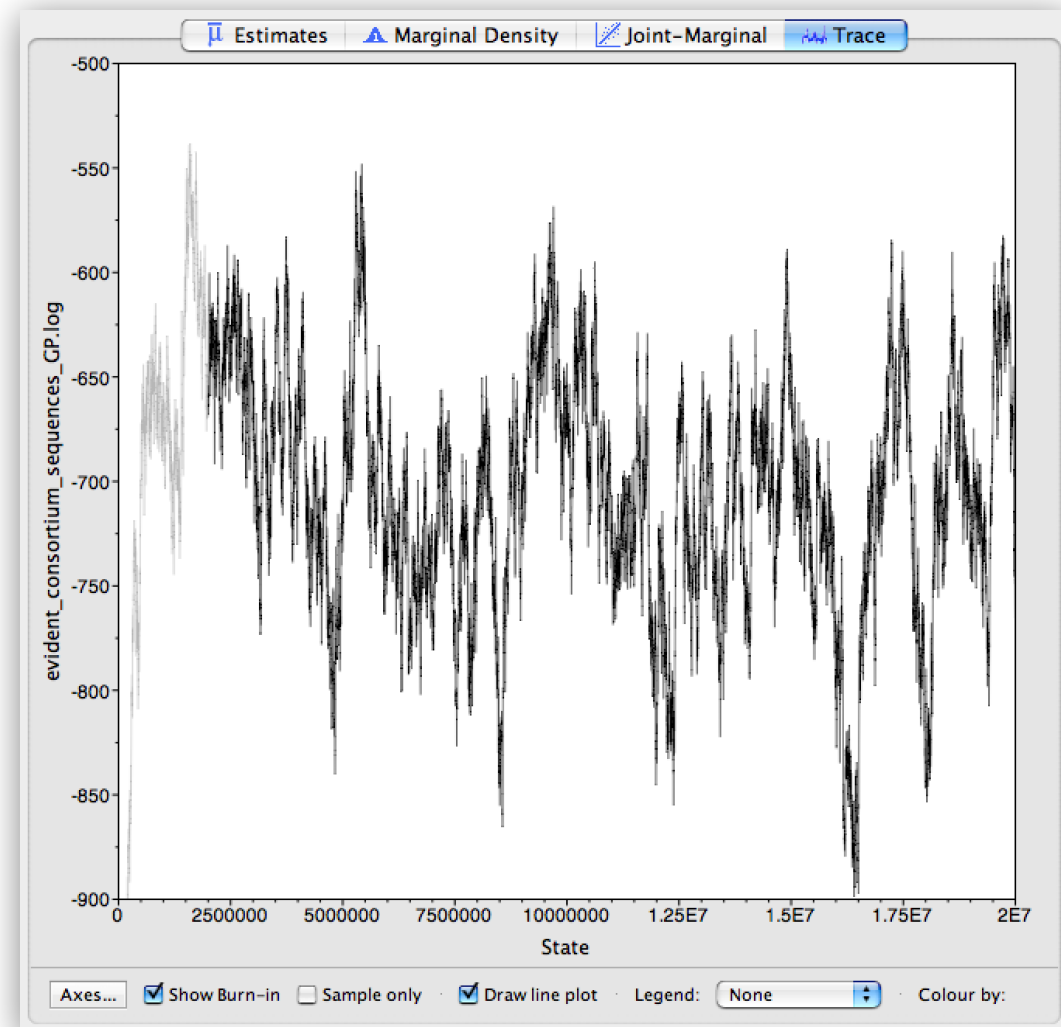
Mixing well! 😊



# Tracer



Mixing well! 😊



Not mixing! 😭

# TreeAnnotator



Analyse trees file from BEAST2 runs;

Produces Maximum Clade Credibility (MCC tree) with node annotations (posterior probability);

## **Input:**

trees file

## **Output:**

summary (MCC) tree

# TreeAnnotator



TreeAnnotator v2.4.2

Burnin percentage:

Posterior probability limit:

Target tree type:

Node heights:

---

Target Tree File:

Input Tree File:

Output File:

Low memory: ☐

# FigTree

View tree sets and summary trees from BEAST2 runs.

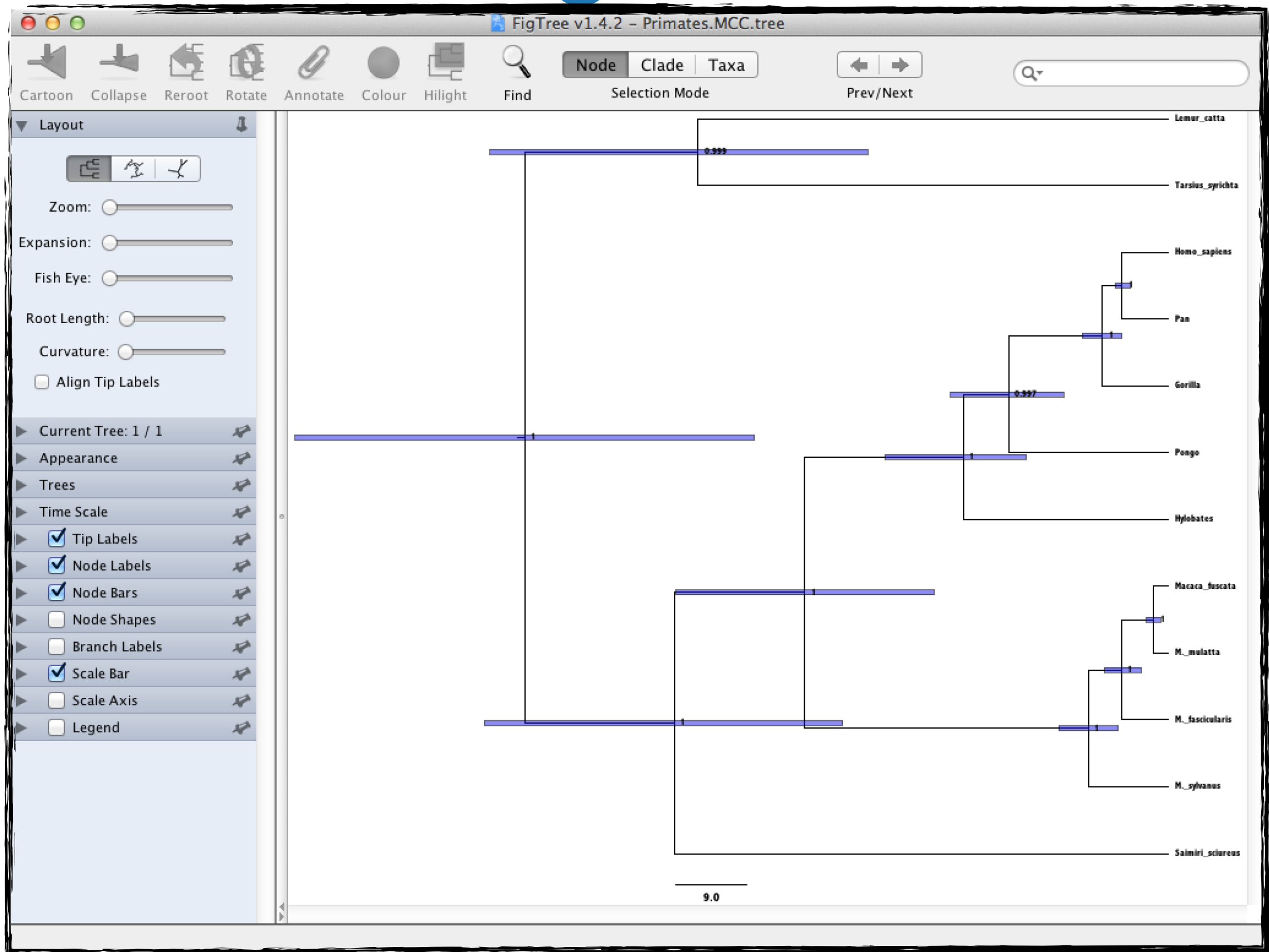
**Input:**

trees file

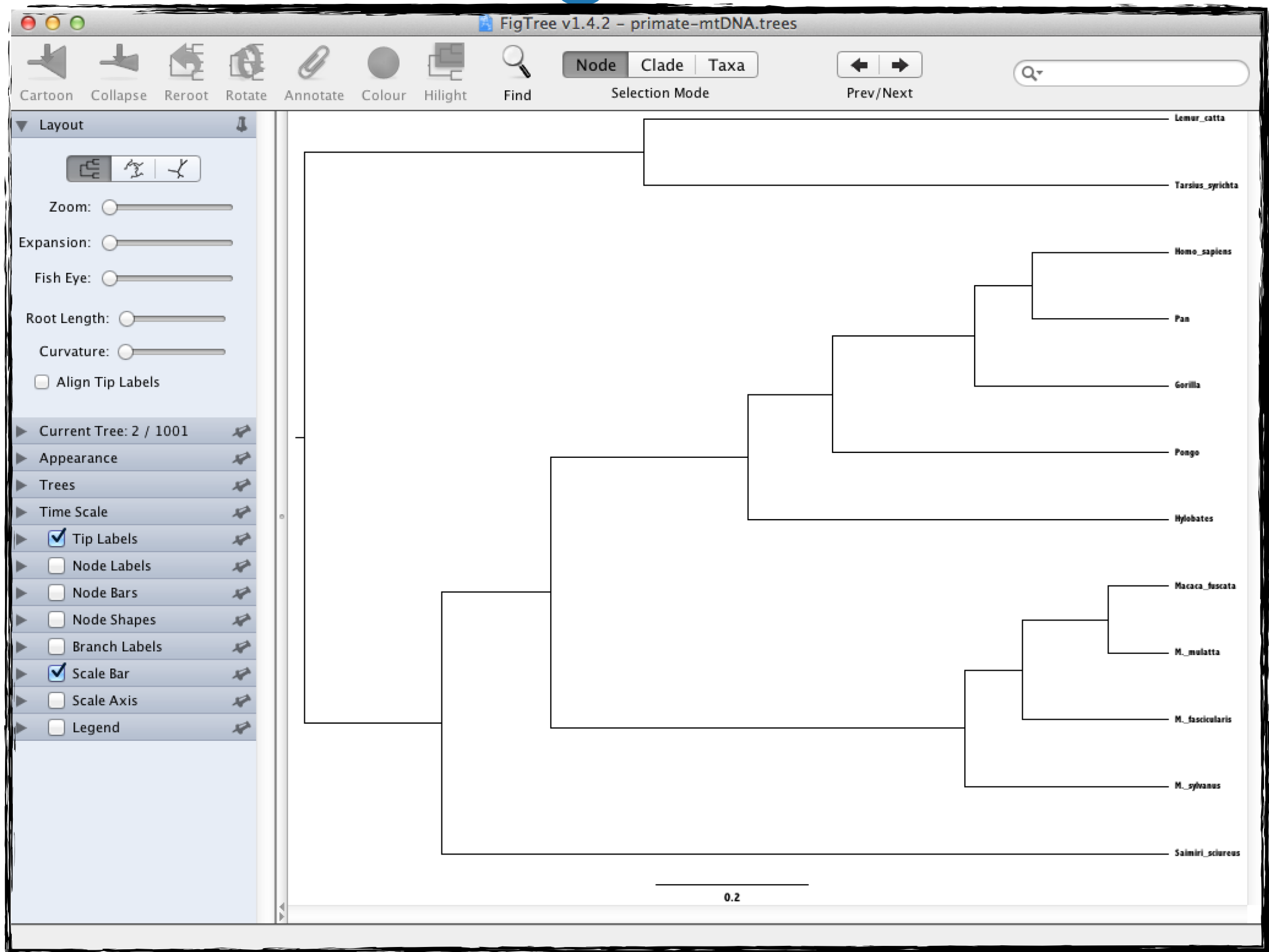
**Output:**

insight

# FigTree



# FigTree





# DensiTree

View the distribution of trees from BEAST2 runs.

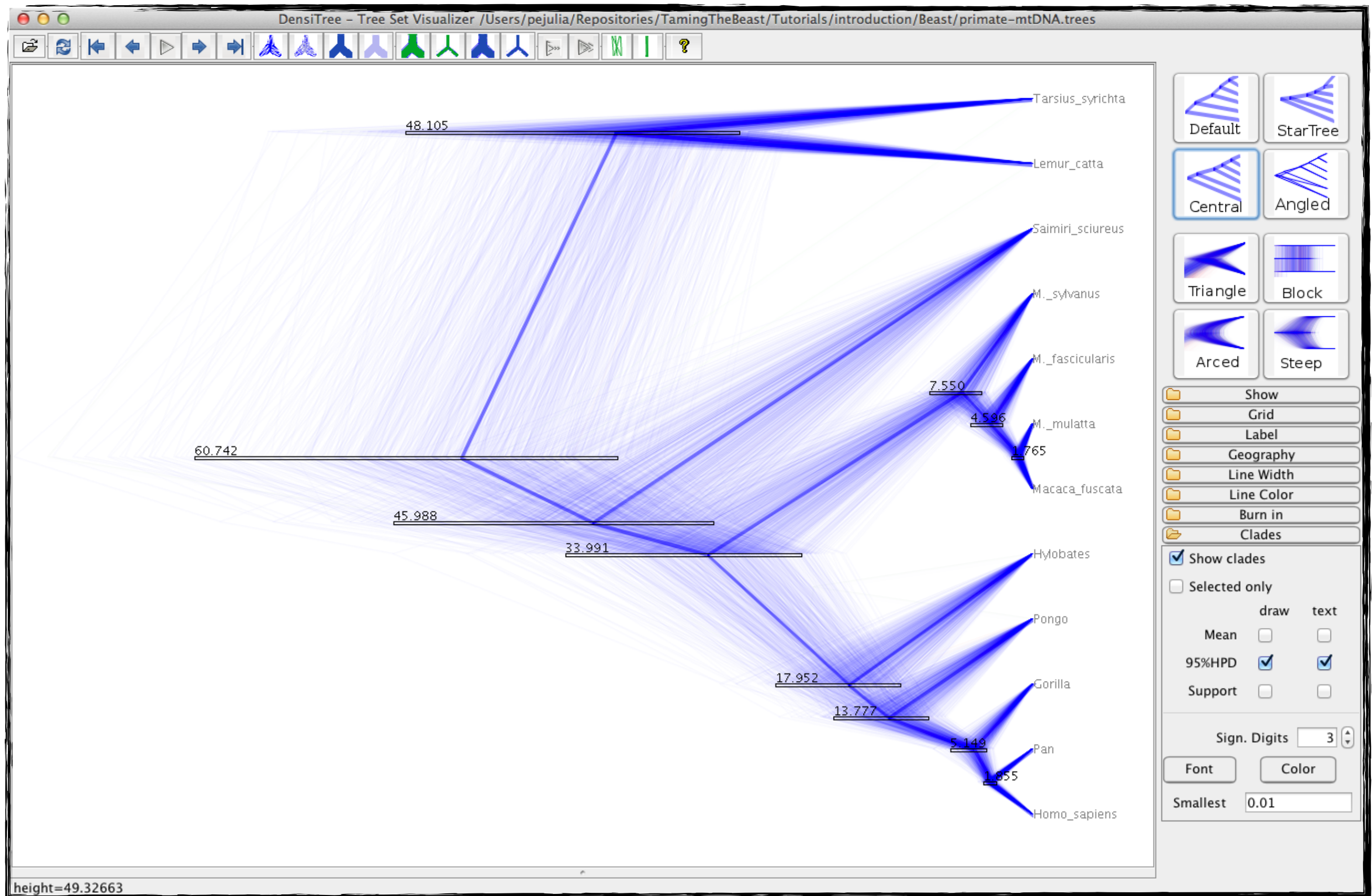
**Input:**

trees file

**Output:**

insight

# DensiTree



# Time to tame!

