

BEAST2

Bayesian Evolutionary Analysis Sampling Trees

BEAUti2 (Bayesian Evolutionary Analysis Utility)

BEAST2

Tracer

TreeAnnotator, FigTree, DensiTree

Partitions Tip Dates Site Model Clock Model Priors MCMC

Link Site Models

Unlink Site Models

Link Clock Models

Unlink Clock Models

Link Trees

Unlink Trees

Name	File	Taxa	Sites	Data Type	Site Model	Clock Model	Tree	...
noncoding	primate-mtDNA	12	205	nucleotide	noncoding	noncoding	noncoding	<input type="checkbox"/>
1stpos	primate-mtDNA	12	231	nucleotide	1stpos	1stpos	1stpos	<input type="checkbox"/>
2ndpos	primate-mtDNA	12	231	nucleotide	2ndpos	2ndpos	2ndpos	<input type="checkbox"/>
3rdpos	primate-mtDNA	12	231	nucleotide	3rdpos	3rdpos	3rdpos	<input type="checkbox"/>

+

-

r

Split

Partitions

Tip Dates

Site Model

Clock Model

Priors

MCMC

Partition

noncoding

1stpos


2ndpos

3rdpos

Gamma Site Model

Substitution Rate

1.0


 estimate 

Gamma Category Count

4


Shape

1.0

 estimate 

Proportion Invariant

0.0


 estimate 

HKY

Subst Model

Kappa

2.0

 estimate 

Frequencies

Empirical

 Fix mean substitution rate

Partitions

Tip Dates

Site Model

Clock Model

Priors

MCMC

▶ Tree.t:tree

Calibrated Yule Model

▼ birthRateY.t:tree

Gamma

initial = [1.0] [-∞, ∞]

Calibrated Yule speciation process birth rate for t:noncoding


Alpha

0.001

 estimate 

Beta

1000

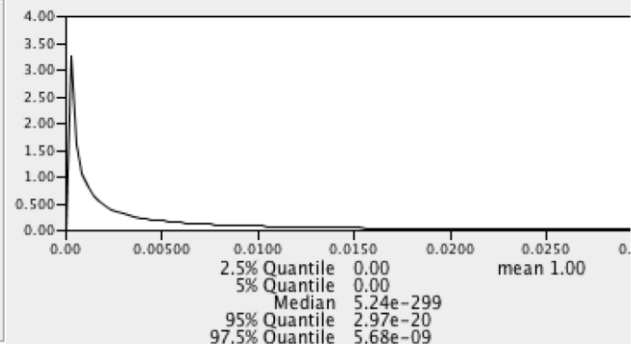
 estimate 

Mode

ShapeScale

Offset

0.0



▶ gammaShape.s:1stpos

Exponential

initial = [1.0] [-∞, ∞]

Prior on gamma shape for partition s:1stpos

▶ gammaShape.s:2ndpos

Exponential

initial = [1.0] [-∞, ∞]

Prior on gamma shape for partition s:2ndpos

▶ gammaShape.s:3rdpos

Exponential

initial = [1.0] [-∞, ∞]

Prior on gamma shape for partition s:3rdpos

▶ gammaShape.s:noncoding

Exponential

initial = [1.0] [-∞, ∞]

Prior on gamma shape for partition s:noncoding

▶ kappa.s:1stpos

Log Normal

initial = [2.0] [0.0, ∞]

▶ kappa.s:2ndpos

Log Normal

initial = [2.0] [0.0, ∞]

▶ kappa.s:3rdpos

Log Normal

initial = [2.0] [0.0, ∞]

▶ kappa.s:noncoding

Log Normal

initial = [2.0] [0.0, ∞]

HKY transition-transversion parameter of partition s:noncoding

+ Add Prior

Partitions

Tip Dates

Site Model

Clock Model

Priors

MCMC

- Calibrated Yule Model
- ▶ birthRateY.t:tree Gamma initial = [1.0] [-∞,∞] Calibrated Yule speciation process birth rate for t:noncodin
 - ▶ clockRate.c:clock Uniform initial = [1.0] [-∞,∞] substitution rate of partition.c:clock
 - ▶ gammaShape.s:1stpos Exponential initial = [1.0] [-∞,∞] Prior on gamma shape for partition s:1stpos
 - ▶ gammaShape.s:2ndpos Exponential initial = [1.0] [-∞,∞] Prior on gamma shape for partition s:2ndpos
 - ▶ gammaShape.s:3rdpos Exponential initial = [1.0] [-∞,∞] Prior on gamma shape for partition s:3rdpos
 - ▶ gammaShape.s:noncoding Exponential initial = [1.0] [-∞,∞] Prior on gamma shape for partition s:noncoding
 - ▶ kappa.s:1stpos Log Normal initial = [2.0] [0.0,∞]
 - ▶ kappa.s:2ndpos Log Normal initial = [2.0] [0.0,∞]
 - ▶ kappa.s:3rdpos Log Normal initial = [2.0] [0.0,∞]
 - ▶ kappa.s:noncoding Log Normal initial = [2.0] [0.0,∞] HKY transition–transversion parameter of partition s:nonco

▼ human-chimp.prior


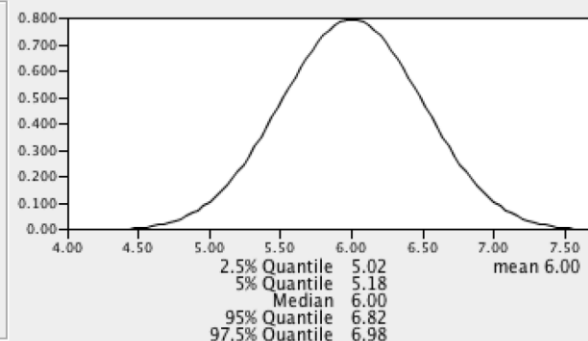
Normal

 monophyletic

Mean

Sigma

Offset

 estimate  estimate  Tiponly Use Originate

Chain Length Store Every Pre Burnin Num Initialization Attempts

▼ tracelog

File Name Log Every Mode Sort Sanitise Headers

posterior
 likelihood
 prior
 treeLikelihood.noncoding
 TreeHeight.t.tree
 treeLikelihood.2ndpos
 treeLikelihood.1stpos
 treeLikelihood.3rdpos
 mutationRate.s.noncoding
 gammaShape.s.noncoding
 kappa.s.noncoding
 kappa.s.1stpos
 mutationRate.s.1stpos
 gammaShape.s.1stpos
 kappa.s.2ndpos
 mutationRate.s.2ndpos
 gammaShape.s.2ndpos
 kappa.s.3rdpos
 mutationRate.s.3rdpos
 gammaShape.s.3rdpos
 CalibratedYuleModel.t.tree
 birthRateY.t.tree
 human-chimp.prior
 clockRate.c.clock

▼ screenlog

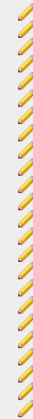
File Name Log Every Mode Sort Sanitise Headers

posterior
 ESS.0
 likelihood
 prior

▼ treelog.t.tree

File Name Log Every Mode Sort Sanitise Headers

TreeWithMetaDataLogger.t.tree



Partitions

Tip Dates

Site Model

Clock Model

Priors

MCMC

Chain Length Store Every Pre Burnin Num Initialization Attempts

▼ tracelog

File Name Log Every Mode Sort Sanitise Headers

posterior
likelihood
prior
treeLikelihood.noncoding
TreeHeight.t:tree
treeLikelihood.2ndpos
treeLikelihood.1stpos
treeLikelihood.3rdpos
mutationRate.s:noncoding
gammaShape.s:noncoding
kappa.s:noncoding
kappa.s:1stpos
mutationRate.s:1stpos
gammaShape.s:1stpos
kappa.s:2ndpos
mutationRate.s:2ndpos
gammaShape.s:2ndpos
kappa.s:3rdpos
mutationRate.s:3rdpos
gammaShape.s:3rdpos
CalibratedYuleModel.t:tree
birthRateY.t:tree
human-chimp.prior
clockRate.c:clock



mutationRate.s:1stpos
gammaShape.s:1stpos
kappa.s:2ndpos
mutationRate.s:2ndpos
gammaShape.s:2ndpos
kappa.s:3rdpos
mutationRate.s:3rdpos
gammaShape.s:3rdpos
CalibratedYuleModel.t:tree
birthRateY.t:tree
human-chimp.prior
clockRate.c:clock

▼ screenlog

File Name

Log Every

Mode ▾

Sort ▾

Sanitise Headers

posterior
ESS.0
likelihood
prior

▼ treelog.t:tree

File Name

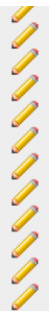
Log Every

Mode ▾

Sort ▾

Sanitise Headers

TreeWithMetaDataLogger.t:tree



Tracer

Trace Files:

Trace File	States	Burn-In
primate-mtDNA....	1000000	100000

+ - Reload

Traces:

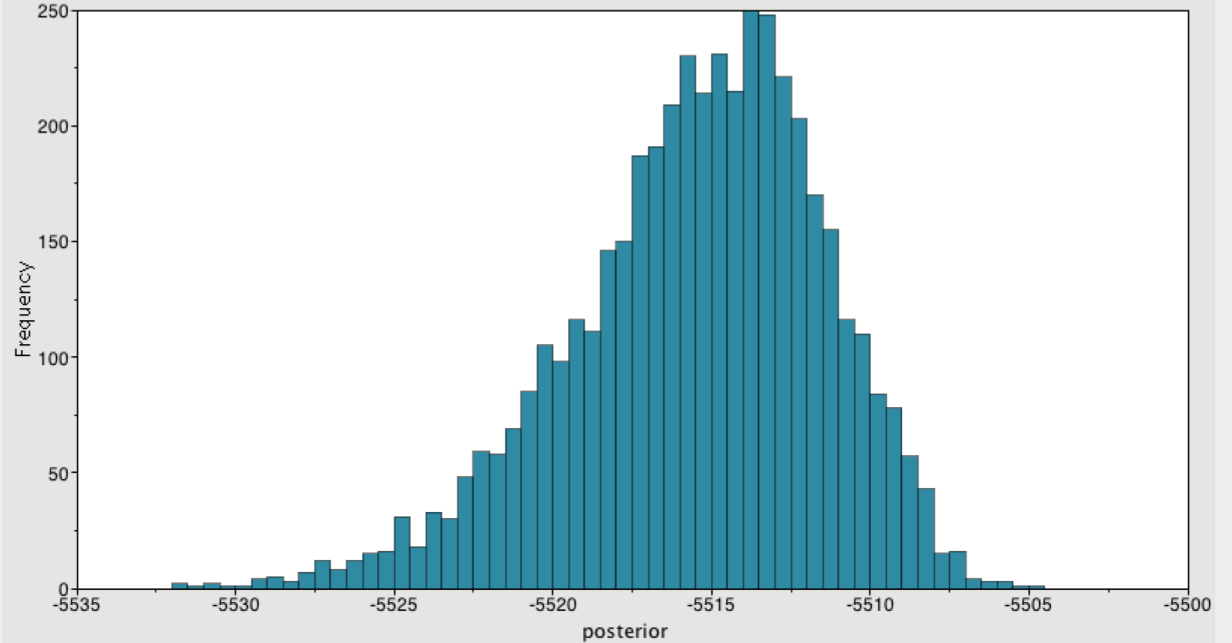
Statistic	Mean	ESS	...
posterior	-5515....	261	R
likelihood	-5442....	335	R
prior	-73.432	113	R
treeLikelihood.1stpos	-1383....	502	R
treeLikelihood.2ndpos	-952.555	321	R
treeLikelihood.3rdpos	-2148....	202	R
treeLikelihood.noncod...	-957.464	192	R
TreeHeight	85.181	235	R
mutationRate.1stpos	0.451	120	R
mutationRate.2ndpos	0.179	124	R
mutationRate.3rdpos	2.955	96	R
mutationRate.noncoding	0.34	180	R
gammaShape.1stpos	0.477	105	R
gammaShape.2ndpos	0.553	76	R
gammaShape.3rdpos	2.998	98	R
gammaShape.noncodi...	0.249	88	R
kappa.1stpos	6.424	86	R
kappa.2ndpos	8.681	79	R
kappa.3rdpos	29.35	42	R
kappa.noncoding	13.619	69	R
CalibratedYuleModel	-47.452	320	R
birthRateY	2.547E-2	731	R
logP(mrca(human-chi...	-0.744	4203	R
mrctime(human-chi...	5.95	2567	R
clockRate	1.165E-2	391	R

Type: (R)real (I)nt (C)at

Estimates Marginal Density Joint-Marginal Trace

Summary Statistic

	posterior
mean	-5515.4884
stderr of mean	0.2487
stdev	4.0176
variance	16.141
median	-5515.0556
value range	[-5531.8494, -5504.8478]
geometric mean	n/a
95% HPD interval	[-5523.3461, -5508.1268]
auto-correlation time (ACT)	3449.4716
effective sample size (ESS)	261
number of samples	4501



Setup... Bins: 50

Tracer

Trace Files:

Trace File	States	Burn-In
primate-mtDNA...	1000000	100000

+ - Reload

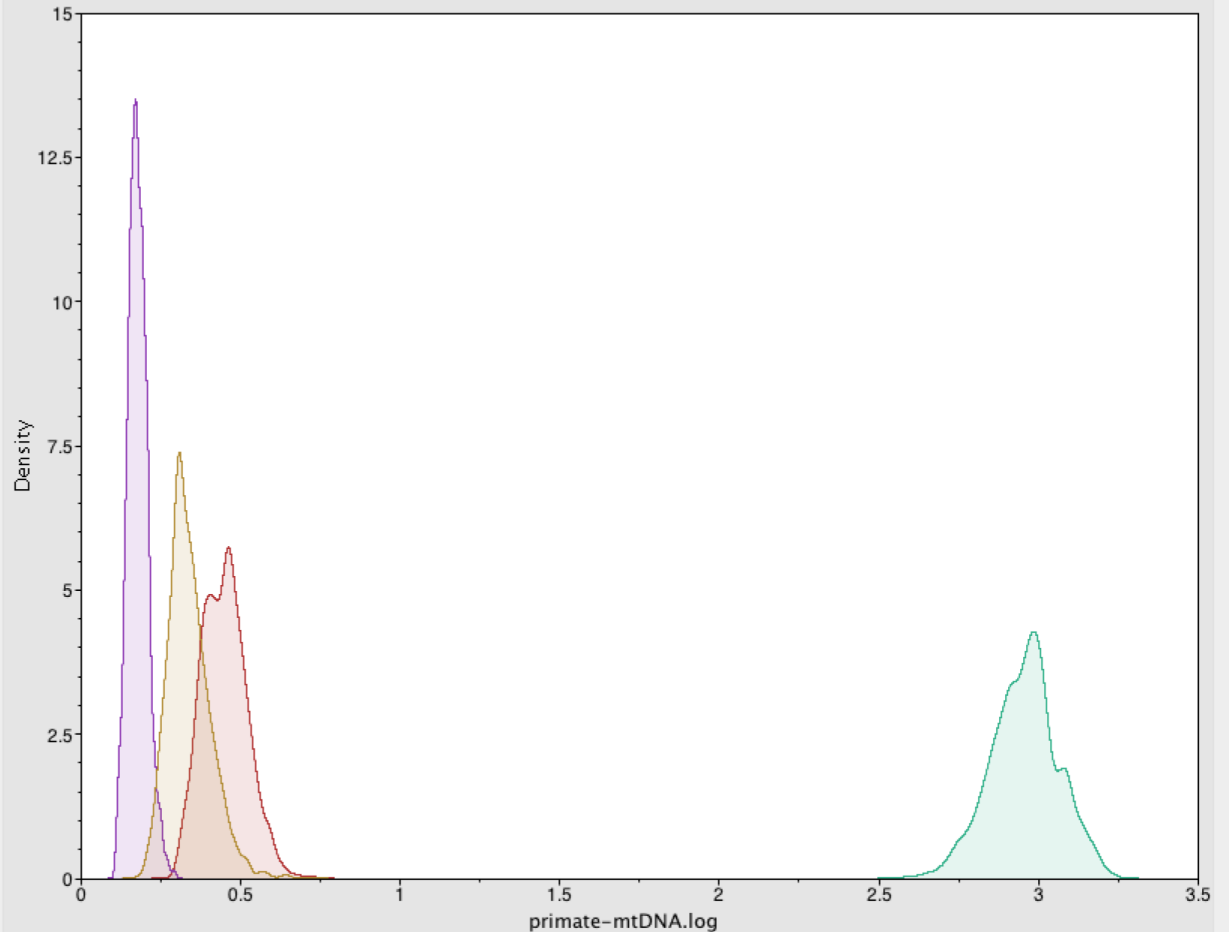
Traces:

Statistic	Mean	ESS	...
posterior	-5515....	261	R
likelihood	-5442....	335	R
prior	-73.432	113	R
treeLikelihood.1stpos	-1383....	502	R
treeLikelihood.2ndpos	-952.555	321	R
treeLikelihood.3rdpos	-2148....	202	R
treeLikelihood.noncod...	-957.464	192	R
TreeHeight	85.181	235	R
mutationRate.1stpos	0.451	120	R
mutationRate.2ndpos	0.179	124	R
mutationRate.3rdpos	2.955	96	R
utationRate.noncoding	0.34	180	R
gammaShape.1stpos	0.477	105	R
gammaShape.2ndpos	0.553	76	R
gammaShape.3rdpos	2.998	98	R
gammaShape.noncodi...	0.249	88	R
kappa.1stpos	6.424	86	R
kappa.2ndpos	8.681	79	R
kappa.3rdpos	29.35	42	R
kappa.noncoding	13.619	69	R
CalibratedYuleModel	-47.452	320	R
birthRateY	2.547E-2	731	R
logP(mrca(human-chi...	-0.744	4203	R
mrcatime(human-chi...	5.95	2567	R
clockRate	1.165E-2	391	R

Type: (R)real (I)nt (C)at

Estimates Marginal Density Joint-Marginal Trace

Display: KDE



Setup... Legend: None Colour by: Trace

Trace Files:

Trace File	States	Burn-In
primate-mtDNA...	1000000	100000

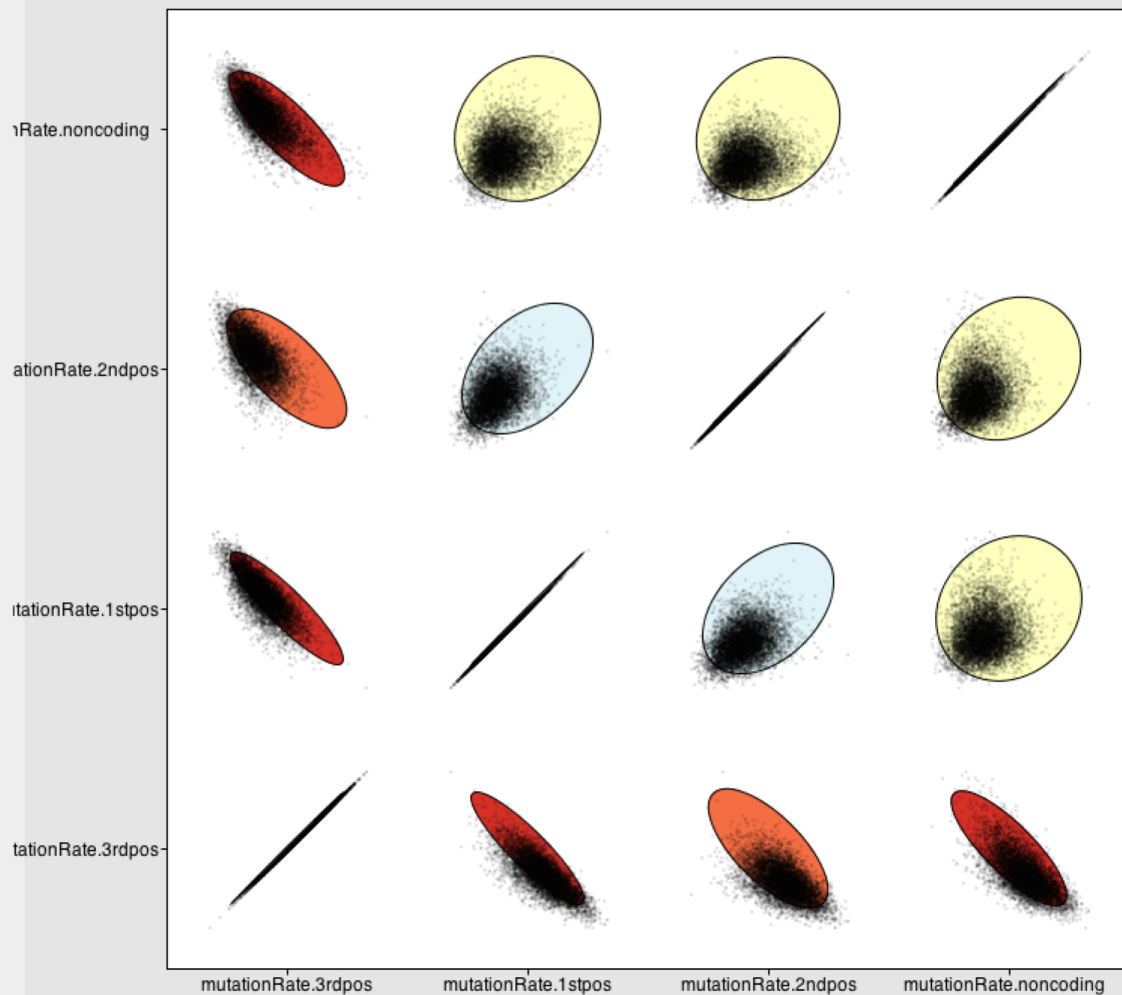
+ -

Reload

Traces:

Statistic	Mean	ESS	...
posterior	-5515....	2387	R
likelihood	-5441....	2349	R
prior	-73.169	1379	R
treeLikelihood.1stpos	-1383....	3189	R
treeLikelihood.2ndpos	-952.37	2885	R
treeLikelihood.3rdpos	-2148....	1687	R
treeLikelihood.noncod...	-957.267	1731	R
TreeHeight	83.827	1409	R
mutationRate.1stpos	0.45	852	R
mutationRate.2ndpos	0.182	714	R
mutationRate.3rdpos	2.949	646	R
mutationRate.noncodi...	0.346	1344	R
gammaShape.1stpos	0.496	889	R
gammaShape.2ndpos	0.575	911	R
gammaShape.3rdpos	3.022	726	R
gammaShape.noncodi...	0.244	1006	R
kappa.1stpos	6.235	719	R
kappa.2ndpos	8.5	1359	R
kappa.3rdpos	28.777	365	R
kappa.noncoding	13.478	875	R
CalibratedYuleModel	-47.285	1755	R
birthRateY	2.561E-2	3805	R
logP(mrca(human-chi...	-0.731	9001	R
mrctime(human-chi...	5.949	8655	R
clockRate	1.161E-2	1836	R

Type: (R)eal (I)nt (C)at

 Estimates
 Marginal Density
 Joint-Marginal
 Trace
 Show points

Cartoon
 Collapse
 Reroot
 Rotate
 Annotate
 Colour
 Highlight
 Find
 Node Clade Taxa

Selection Mode Prev/Next

Layout

Zoom:

Expansion:

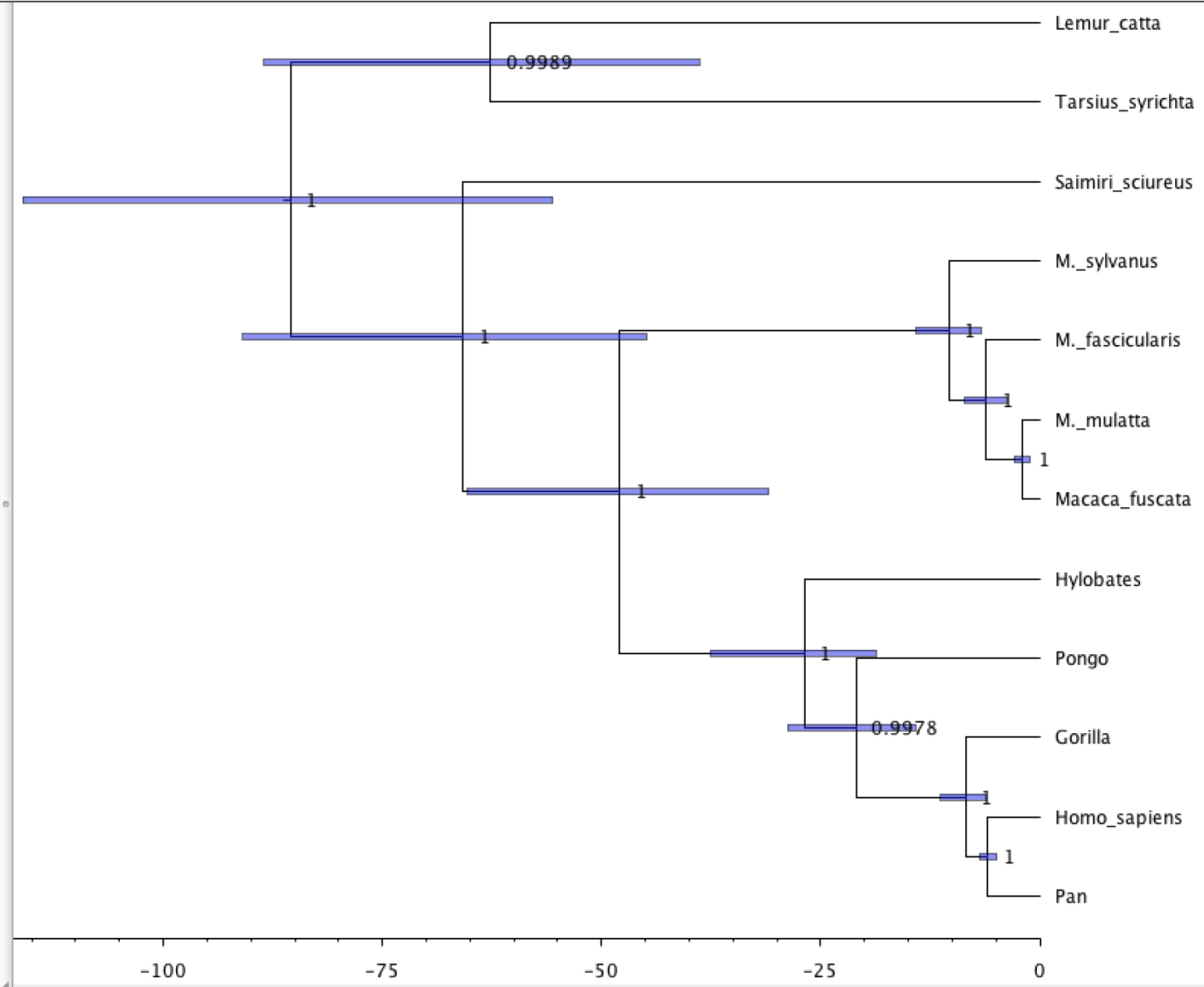
Fish Eye:

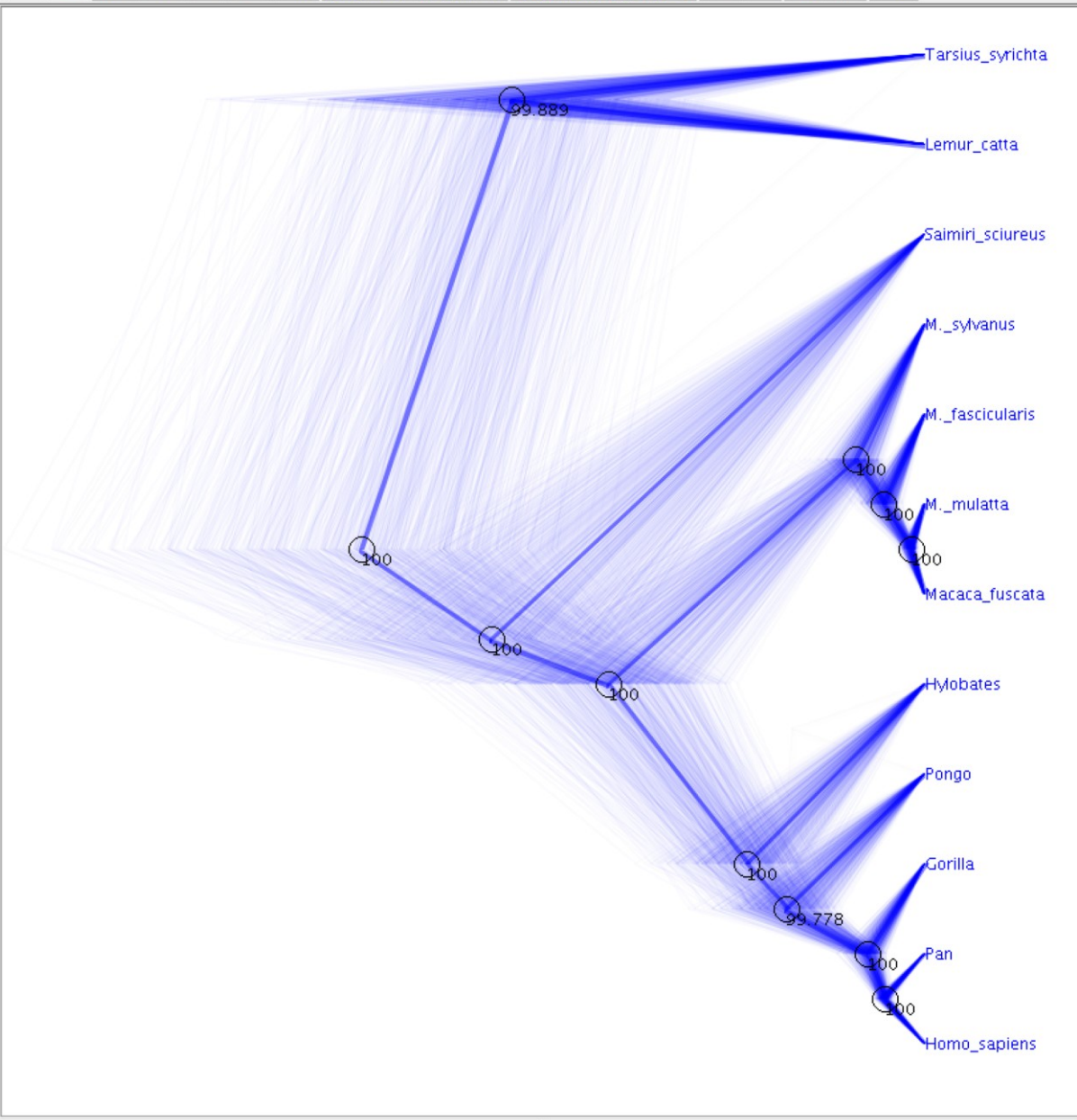
Root Length:

Curvature:

Align Tip Labels

Current Tree: 1 / 1
 Appearance
 Trees
 Time Scale
 Tip Labels
 Tip Shapes
 Node Labels
 Node Shapes
 Node Bars
 Branch Labels
 Scale Bar
 Scale Axis
 Legend





Default StarTree
Central Angled
Triangle Block
Arced Steep

- Show
- Grid
- Label
- Geography
- Line Width
- Line Color
- Burn in
- Clades

Show clades
 Selected only

	draw	text
Mean	<input type="checkbox"/>	<input type="checkbox"/>
95%HPD	<input type="checkbox"/>	<input type="checkbox"/>
Support	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>

Sign. Digits
Font Color
Smallest