

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	clock	tree	
1stpos	primate-mtDNA	12	231	nucleotide	1stpos	clock	tree	
2ndpos	primate-mtDNA	12	231	nucleotide	2ndpos	clock	tree	
3rdpos	primate-mtDNA	12	231	nucleotide	3rdpos	clock	tree	

Partition
noncoding

1stpos
2ndpos
3rdpos

Gamma Site Model

Substitution Rate 1.0 estimate 

Gamma Category Count 4 estimate 

Shape 1.0 estimate 

Proportion Invariant 0.0 estimate 

HKY

Subst Model Kappa 2.0 estimate 

Frequencies Empirical estimate 

Fix mean substitution rate

[Partitions](#) | [Tip Dates](#) [Site Model](#) [Clock Model](#) | [Priors](#) | [MCMC](#)

Partition

noncoding

1stpos

2ndpos

3rdpos

Clone from noncoding ▾

OK

▶ Tree.t:tree	Calibrated Yule Model		▼
▶ birthRateY.t:tree	Gamma	initial = [1.0] $[-\infty, \infty]$	Calibrated Yule speciation process birth rate for t:3rdpos
▶ clockRate.c:clock	Uniform	initial = [1.0] $[-\infty, \infty]$	substitution rate of partition c:3rdpos
▶ gammaShape.s:1stpos	Exponential	initial = [1.0] $[-\infty, \infty]$	Prior on gamma shape for partition s:1stpos
▶ gammaShape.s:2ndpos	Exponential	initial = [1.0] $[-\infty, \infty]$	Prior on gamma shape for partition s:2ndpos
▶ gammaShape.s:3rdpos	Exponential	initial = [1.0] $[-\infty, \infty]$	Prior on gamma shape for partition s:3rdpos
▶ gammaShape.s:noncoding	Exponential	initial = [1.0] $[-\infty, \infty]$	Prior on gamma shape for partition s:noncoding
▶ kappa.s:1stpos	Log Normal	initial = [2.0] $[0.0, \infty]$	HKY transition-transversion parameter of partition s:1stpos
▶ kappa.s:2ndpos	Log Normal	initial = [2.0] $[0.0, \infty]$	HKY transition-transversion parameter of partition s:2ndpos
▶ kappa.s:3rdpos	Log Normal	initial = [2.0] $[0.0, \infty]$	HKY transition-transversion parameter of partition s:3rdpos
▶ kappa.s:noncoding	Log Normal	initial = [2.0] $[0.0, \infty]$	HKY transition-transversion parameter of partition s:noncoding
▶ human-chimp.prior	Normal	▼ <input checked="" type="checkbox"/> monophyletic	-

[+ Add Prior](#)

Chain Length

Store Every

Pre Burnin

Num Initialization Attempts

- ▶ tracelog
- ▶ screenlog
- ▶ treelog.t:tree

Store Every -1
Pre Burnin 0
Num Initialization Attempts 10

▼ tracelog

File Name primate-mtDNA.lo
Log Every 200
Mode autodetect
Sort smart

Sanitise Headers

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

▼ screenlog

File Name

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



▼ screenlog

File Name
Log Every 1000
Mode autodetect
Sort none
 Sanitise Headers



posterior
likelihood
prior

▼ treelog.t:tree

File Name primate-mtDNA.tre
Log Every 1000
Mode tree
Sort none
 Sanitise Headers



TreeWithMetaDataLogger.t:tree

Sample From Prior



Bayesian Evolutionary Analysis Sampling Trees
Version v2.6.6, 2002–2021

BEAST XML File: Primates.xml

[Choose File...](#)

default: only write new log files 

Only load packages and versions specified in XML

Random number seed: 777

Thread pool size:

Automatic 

Use BEAGLE library if available:

Prefer use of: CPU 

Prefer precision: Double 

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/>

Quit

Run

2350000	-5516.7583	-5441.8582	-74.8921 2m18s/Msamples
2351000	-5516.8165	-5442.8565	-73.9600 2m18s/Msamples
2352000	-5512.5075	-5437.5766	-74.9309 2m18s/Msamples
2353000	-5513.1458	-5448.6045	-72.4613 2m18s/Msamples
2354000	-5517.2651	-5439.5458	-77.7193 2m18s/Msamples
2355000	-5512.5341	-5436.3682	-76.1739 2m18s/Msamples
2356000	-5509.5577	-5436.1518	-73.4867 2m18s/Msamples
2357000	-5513.2718	-5448.2269	-73.8448 2m18s/Msamples
2358000	-5511.9083	-5441.5927	-78.3656 2m18s/Msamples
2359000	-5509.8213	-5437.6592	-72.1621 2m18s/Msamples
2360000	-5522.1522	-5453.9289	-68.2312 2m18s/Msamples
2361000	-5514.1499	-5446.1824	-68.8474 2m18s/Msamples
2362000	-5518.9464	-5444.7168	-72.2296 2m18s/Msamples
2363000	-5517.3235	-5449.8365	-68.2738 2m18s/Msamples
2364000	-5516.2776	-5446.8744	-71.4831 2m18s/Msamples
2365000	-5517.5774	-5449.5132	-77.8641 2m18s/Msamples
2366000	-5514.9492	-5443.3812	-71.6479 2m18s/Msamples
2367000	-5512.1883	-5443.8924	-68.6877 2m18s/Msamples
2368000	-5514.6263	-5433.5713	-73.4549 2m18s/Msamples
2369000	-5512.1328	-5443.2325	-68.6993 2m18s/Msamples
2370000	-5514.9362	-5448.5234	-68.4328 2m18s/Msamples
2371000	-5518.5388	-5446.5289	-69.6891 2m18s/Msamples
2372000	-5517.8335	-5444.9513	-72.9621 2m18s/Msamples
2373000	-5514.9282	-5442.4818	-72.4864 2m18s/Msamples
2374000	-5514.8997	-5443.6813	-71.8888 2m18s/Msamples
2375000	-5508.7738	-5439.5121	-71.2618 2m18s/Msamples
2376000	-5513.7653	-5448.3826	-71.3827 2m18s/Msamples
2377000	-5507.8535	-5437.7929	-69.8926 2m18s/Msamples
2378000	-5512.8334	-5438.4775	-73.5618 2m18s/Msamples
2379000	-5518.2584	-5443.5299	-74.7294 2m18s/Msamples
2380000	-5513.7949	-5443.8705	-74.8921 2m18s/Msamples

Tracer



Trace Files:

Trace File	States	Burn-In
primate-mtDNA.log	10000000	1000000
+ -		Reload

Traces:

Statistic	Mean	ESS	...
posterior	-5515.096	2548	R
likelihood	-5441.888	3323	R
prior	-73.208	1281	R
treeLikelihood.1stpos	-1383.392	5726	R
treeLikelihood.2ndpos	-952.378	3822	R
treeLikelihood.3rdpos	-2148.834	2240	R
treeLikelihood.noncoding	-957.285	1611	R
TreeHeight	84.253	2273	R
mutationRate.1stpos	0.449	911	R
mutationRate.2ndpos	0.181	856	R
mutationRate.3rdpos	2.953	636	R
mutationRate.noncoding	0.344	1382	R
gammaShape.1stpos	0.491	951	R
gammaShape.2ndpos	0.567	1169	R
gammaShape.3rdpos	2.991	789	R
gammaShape.noncoding	0.243	951	R
kappa.1stpos	6.251	1082	R
kappa.2ndpos	8.545	1089	R
kappa.3rdpos	28.988	399	R
kappa.noncoding	13.352	1043	R
CalibratedYuleModel	-47.351	2800	R
birthRateY	2.554E-2	8467	R
logP(mrca(human-chimp))	-0.736	41209	R
mrca.age(human-chimp)	5.957	32131	R
clockRate	1.163E-2	2308	R

Type: (R)eal (I)nt (C)at (T)ime * constant

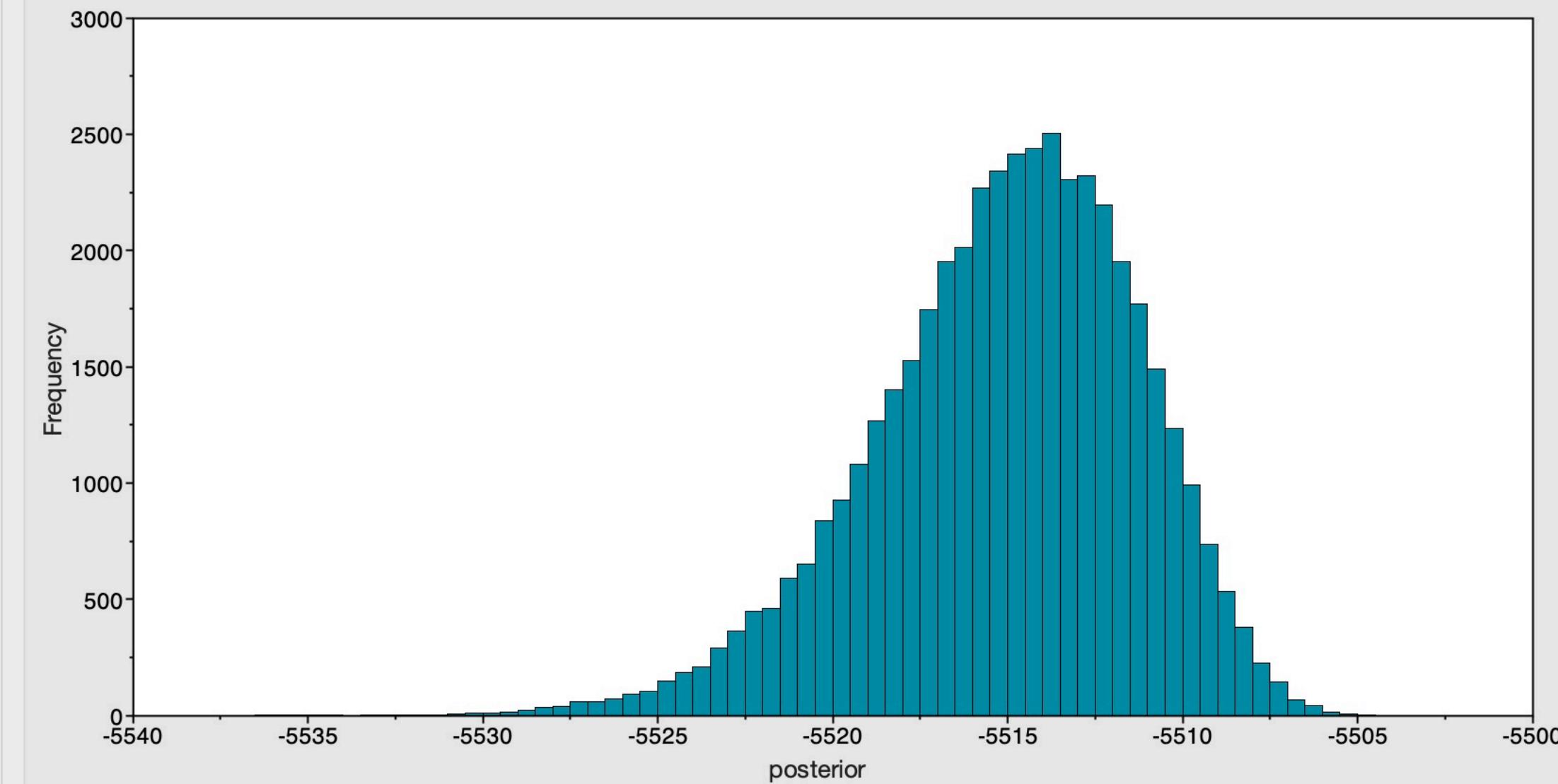
 μ Estimates

Marginal Density

Joint-Marginal

Trace

Summary Statistic	posterior
mean	-5515.0962
stderr of mean	0.0749
stdev	3.7832
variance	14.3125
median	-5514.7385
value range	[-5536.2711, -5504.9608]
geometric mean	n/a
95% HPD interval	[-5522.7729, -5508.3395]
auto-correlation time (ACT)	3532.558
effective sample size (ESS)	2547.8
number of samples	45001



Setup...

Bins: 50



Tracer

Trace File	States	Burn-In
primate-mtDNA.log	10000000	1000000
+ -		Reload

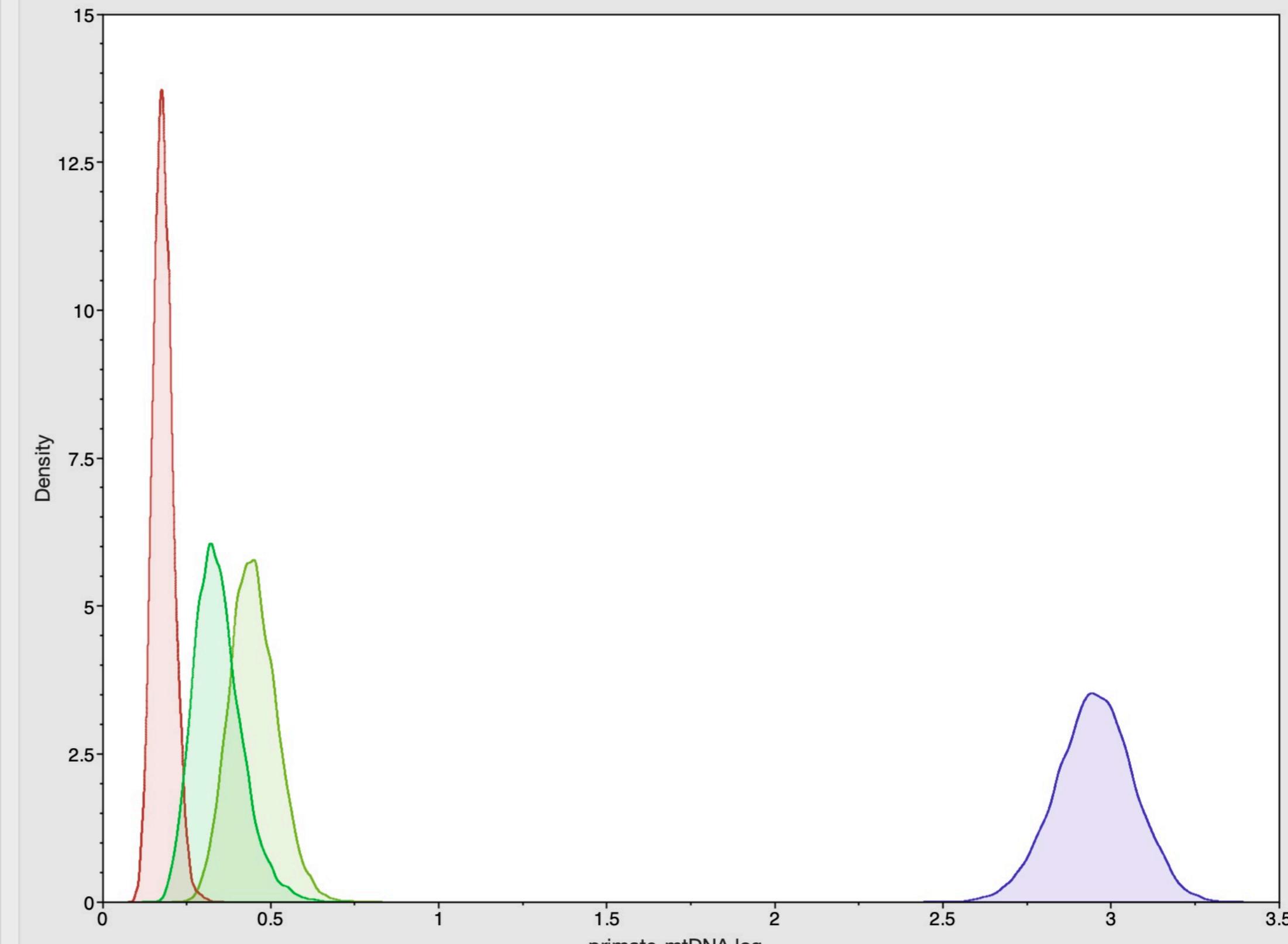
Traces:

Statistic	Mean	ESS	...
posterior	-5515.096	2548	R
likelihood	-5441.888	3323	R
prior	-73.208	1281	R
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mrca.age(human-chimp)	5.957	32131	R
clockRate	1.163E-2	2308	R

Type: (R)eal (I)nt (C)at (T)ime * constant

Estimates Marginal Density Joint-Marginal Trace

Display: KDE



Setup...

Legend: None

Colour by: Trace



Tracer

Trace File	States	Burn-In
primate-mtDNA.log	10000000	1000000
+ -		Reload

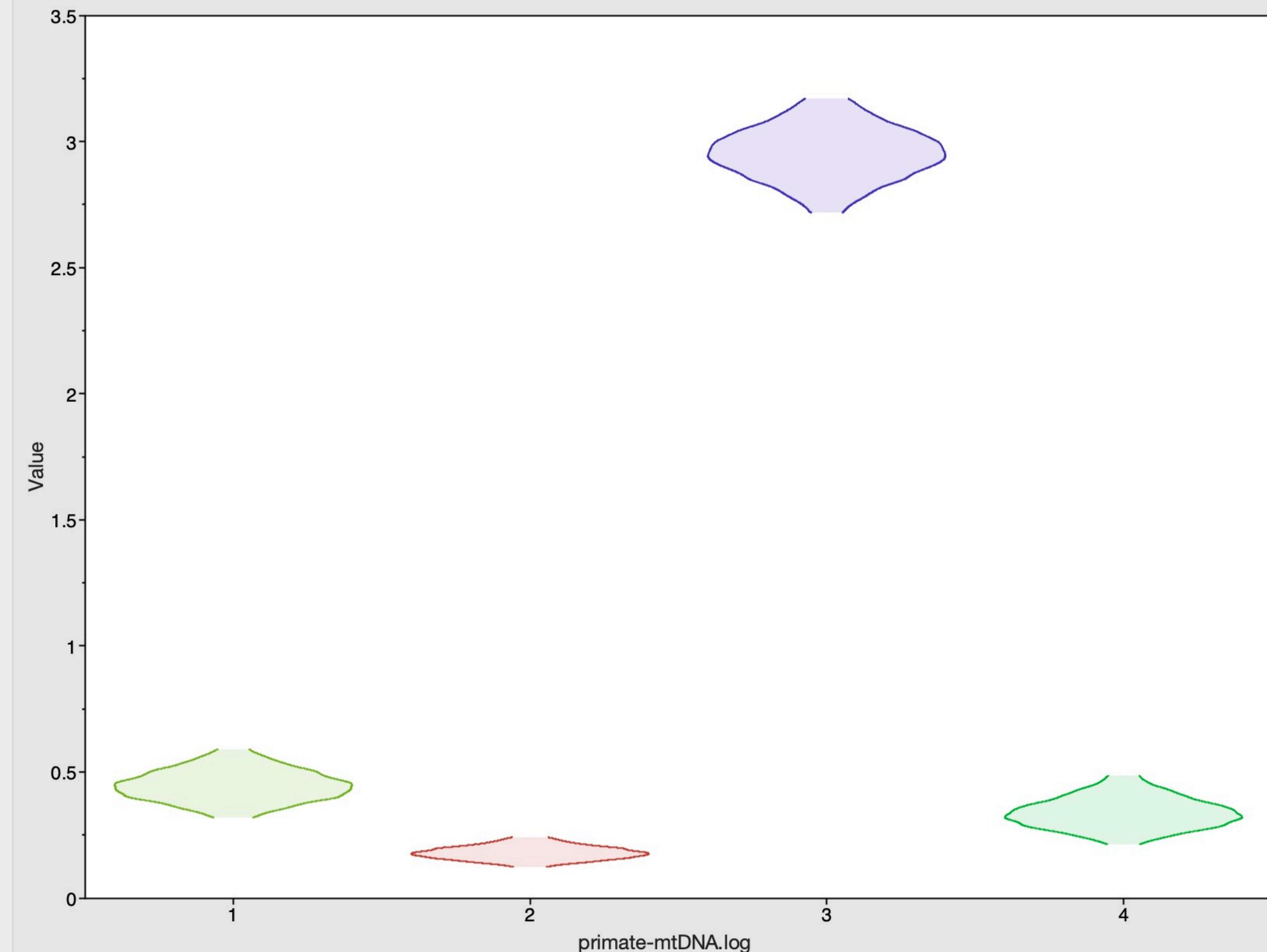
Traces:

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posterior	-5515.096	2548	R
likelihood	-5441.888	3323	R
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mrca.age(human-chimp)	5.957	32131	R
clockRate	1.163E-2	2308	R

Type: (R)eal (I)nt (C)at (T)ime * constant

 Estimates Marginal Density Joint-Marginal Trace

Display: Violin



Setup...

Legend: None

Colour by: Trace



Tracer

Trace Files:

Trace File	States	Burn-In
primate-mtDNA.log	10000000	1000000
+ -		
		Reload

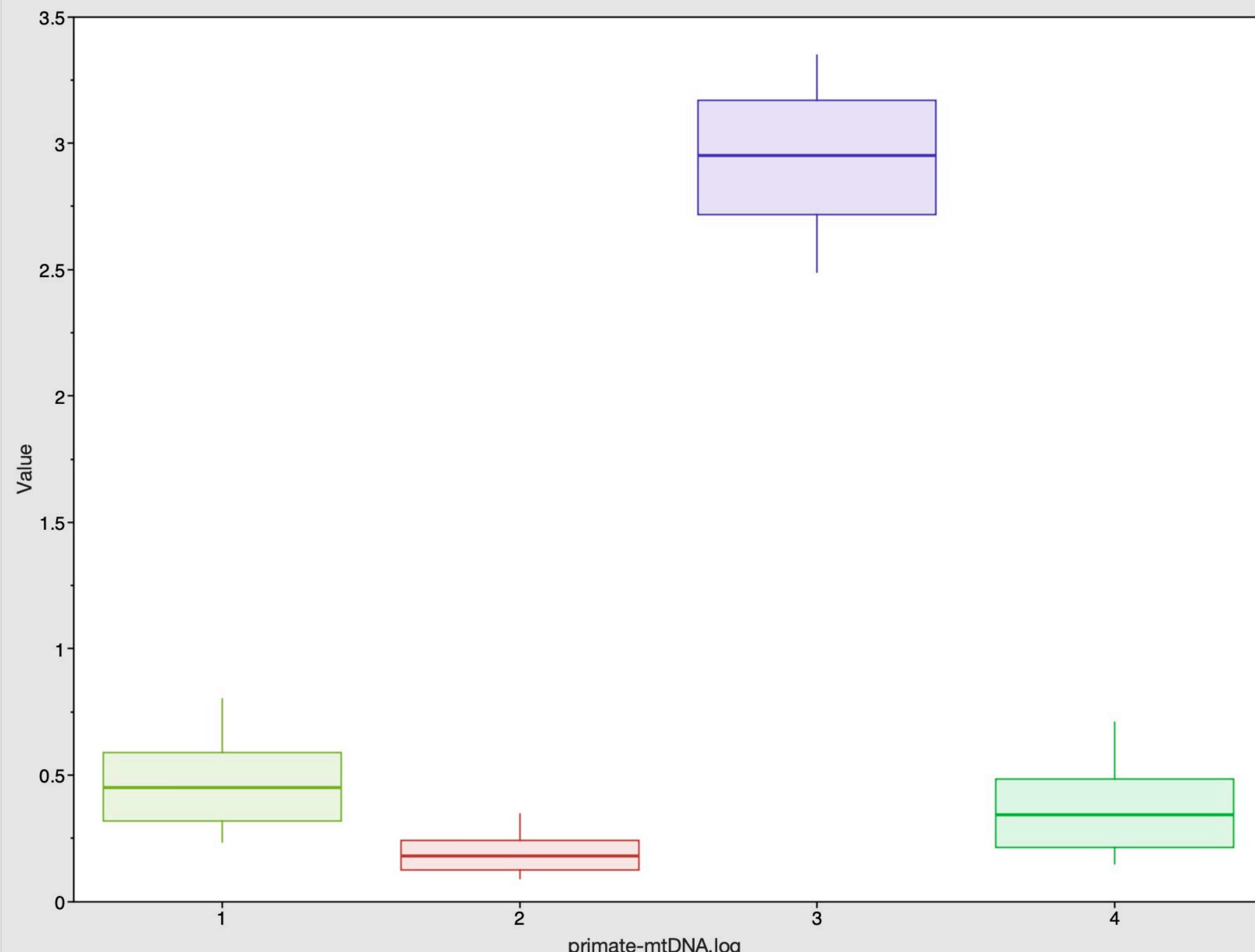
Traces:

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mrca.age(human-chimp)	5.957	32131	R
clockRate	1.163E-2	2308	R

Type: (R)eal (I)nt (C)at (T)ime * constant

Estimates Marginal Density Joint-Marginal Trace

Display: Box and whisker ▾



Setup...

Legend: None ▾

Colour by: Trace ▾

Tracer

Estimates | Marginal Density | Joint-Marginal | Trace

Trace File	States	Burn-In
primate-mtDNA.log	10000000	1000000
+ -		Reload

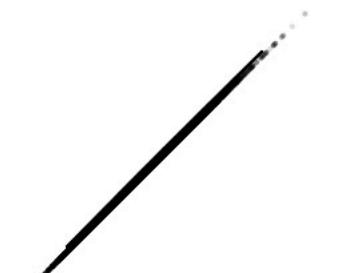
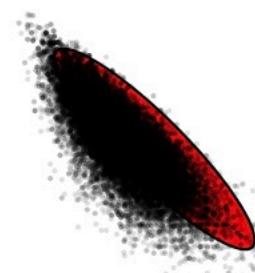
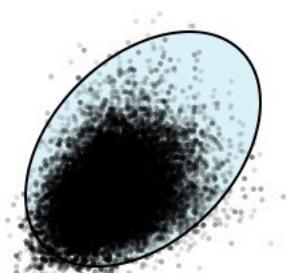
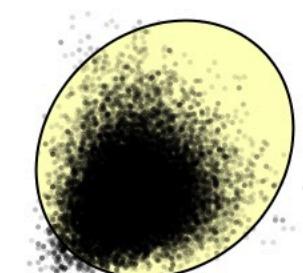
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mrca.age(human-chimp)	5.957	32131	R
clockRate	1.163E-2	2308	R

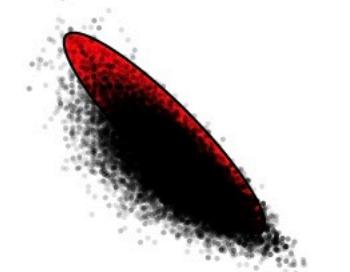
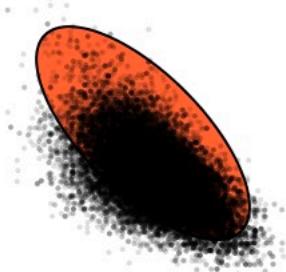
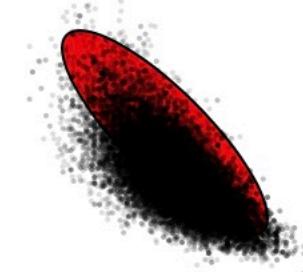
Type: (R)eal (I)nt (C)at (T)ime * constant

Show points

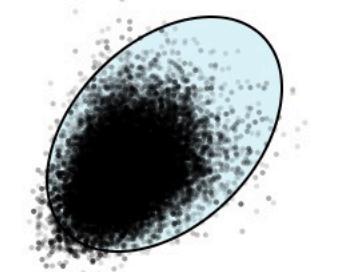
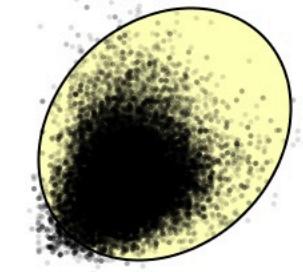
mutationRate.1stpos



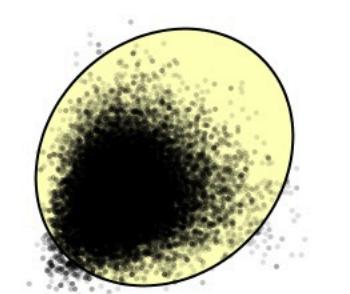
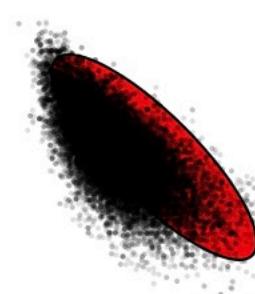
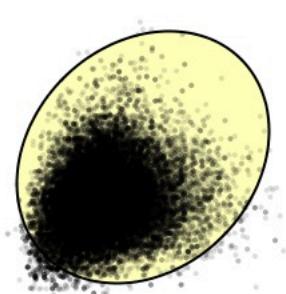
mutationRate.3rdpos



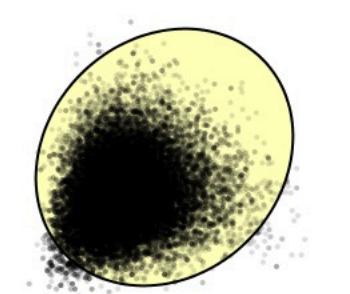
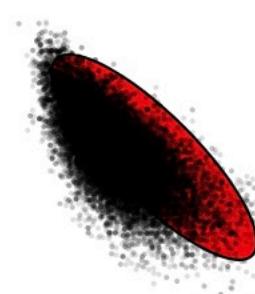
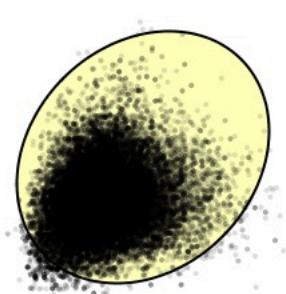
mutationRate.2ndpos



mutationRate.noncoding



mutationRate.noncoding



mutationRate.2ndpos

mutationRate.3rdpos

mutationRate.1stpos

TreeAnnotator v2.6.6

Burnin percentage: 10

Posterior probability limit: 0.0

Target tree type: Maximum clade credibility tree

Node heights: Mean heights

Target Tree File: not selected

Input Tree File: primate-mtDNA.trees

Output File: Primates.MCC.tree

Low memory:

Quit

Run

alexei@cs.auckland.ac.nz

Processing 9001 trees from file after ignoring first 10% = 1000 trees.

Total number of trees 10001, where 9001 are used.

Total unique clades: 17

Finding maximum credibility tree...

Analyzing 9001 trees...

0 25 50 75 100
|-----|-----|-----|-----|

Highest Log Clade Credibility: -0.0031129526052051395

Collecting node information...

0 25 50 75 100
|-----|-----|-----|-----|

Annotating target tree...

Writing annotated tree....

Finished - Quit program to exit.

