

18 · Bayesian evrimsel analizi

BEAUti

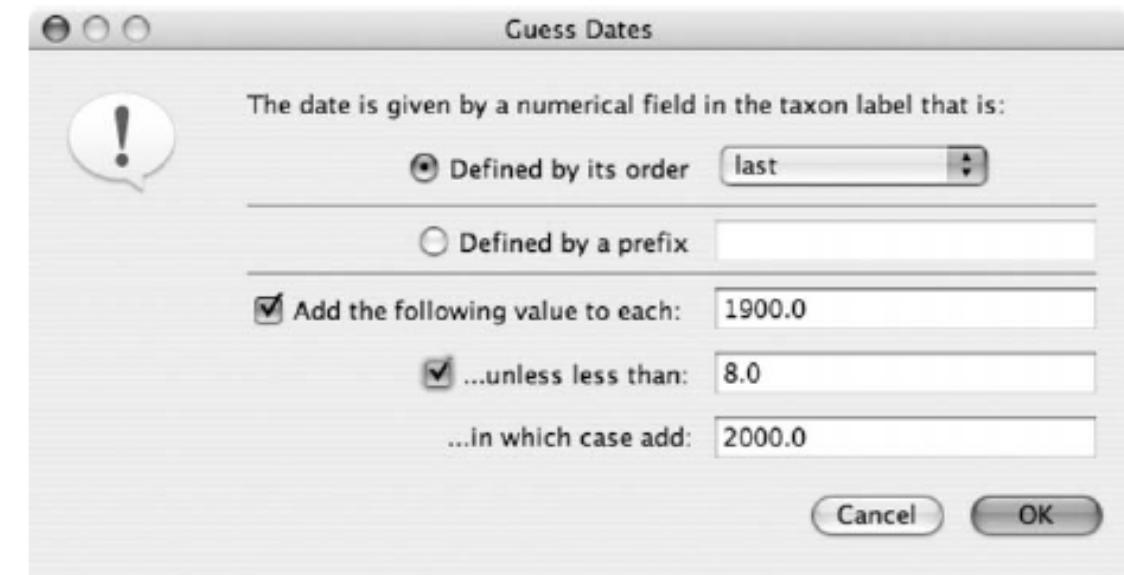
Data Taxa Model Priors Operators MCMC

Clear Dates Guess Dates Dates specified as Years Since some time in the past

Name	Date	Height	Sequence
NYCH09@93	0	0	ACCTCACCCAGAATCCCCAGCTTGAATCAGCTTCTCCAATCTGTCCGAAACTACAT
SE05@91	0	0	ACCTCACCCAGGATCCCCAGCTTGAATCAGCTTCTCCAATCTGTCTGAAACTACAT
BE11600@94	0	0	ACCTGACCCAGAATCCCCAGCTTGAATCAGCTTCTCCAATCTGTCTGAAACTACAT
BE15471@97	0	0	ACCTGACCCAGAATCCCCAGCTTGAATCAGCTTCTCCAATCTGTCTGAAACTACAT
SE03@91	0	0	ACCTGACCCAGAATCCCCAGCTTGAATCAGCTTCTCCAATCTGTCTGAAACTACAT
MAD1@93	0	0	ACCTGACCCAGAATCCCCAGCTTGAATCAGCTTCTCCAATCTGTCTGAAACTACAT
BE1061@00	0	0	ACCTGACCCAGAATCCCCAGCTTGAATCAGCTTCTCCAATCTGTCTGAAACTACAT
BE64@01	0	0	ACCTTACCCAGAATCCCCAGCTTGAATCAGCTTCTCCAATCTGTCTGAAACTACAT
BE14536@98	0	0	ACCTGACCCAGAATCCCCAGCTTGAATCAGCTTCTCCAATCTGTCTGAAACTACAT
BIR6190@89	0	0	ACTTGACCCAAAATCCCCAGCTTGAATCAGCTTCTCCAATCTGTCTGAAACTACAT
WV12342@84	0	0	ACCTGACCCAGAATCCCCAGCTTGAATCAGCTTCTCCAATCTGTCTGAAACTACAT
BE933@88	0	0	ACCTGACCCAGAATCCCCAGCTTGAATCAGCTTCTCCAATCTGTCTGAAACTACAT
BE156@84	0	0	ACCTGACTCAGAATCCCCAGCTTGAATCAGCTTCTCCAATCTGTCTGAAACTACAT
S2@76	0	0	ACCTCACCCAGAATCCCCAGCTTGAATCAGCTTCTCCAATCTGTCTGAAACTACAT
BE004@02	0	0	ACCTCACCCAGAATCCCCAGCTTGAATCAGCTTCTCCAATCTGTCTGAAACTACAT
SE02@98	0	0	ACCTCACCCAGAATCCCCAGCTTGAATCAGCTTCTCCAATCTGTCTGAAACTACAT
BE11@01	0	0	ACCTCACCCAGAATCCCCAGCTTGAATCAGCTTCTCCAATCTGTCTGAAACTACAT
BE332@02	0	0	ACCTCACCCAGAATCCCCAGCTTGAATCAGCTTCTCCAATCTGTCTGAAACTACAT
MON2@88	0	0	ACCTCACCCAGAATCCCCAGCTTGAATCAGCTTCTCCAATCTGTCTGAAACTACAT
BE11465@94	0	0	ACCTCACCCAGAATCCCCAGCTTGAATCAGCTTCTCCAATCTGTCTGAAACCACAT
BE12895@95	0	0	ACCTCACCCAGAATCCCCAGCTTGAATCAGCTTCTCCAATCTGTCTGAAACTACAT
SE10@91	0	0	ACCTCACCCAGAATCCCCAGCTTGAATCAGCTTCAACATCTGTCTGAAACTACAT

Translation: None Ignore data - sample prior only

Alignment: 35 taxa, 629 sites Generate BEAST File...



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Data Taxa Model Priors Operators MCMC

Substitution Model: HKY

Site Heterogeneity Model: None

Number of Gamma Categories: 4

Partition into codon positions: 3 partitions: codon positions 1, 2, 3

Unlink substitution model across codon positions

Unlink rate heterogeneity model across codon positions

Use SRD06 Model

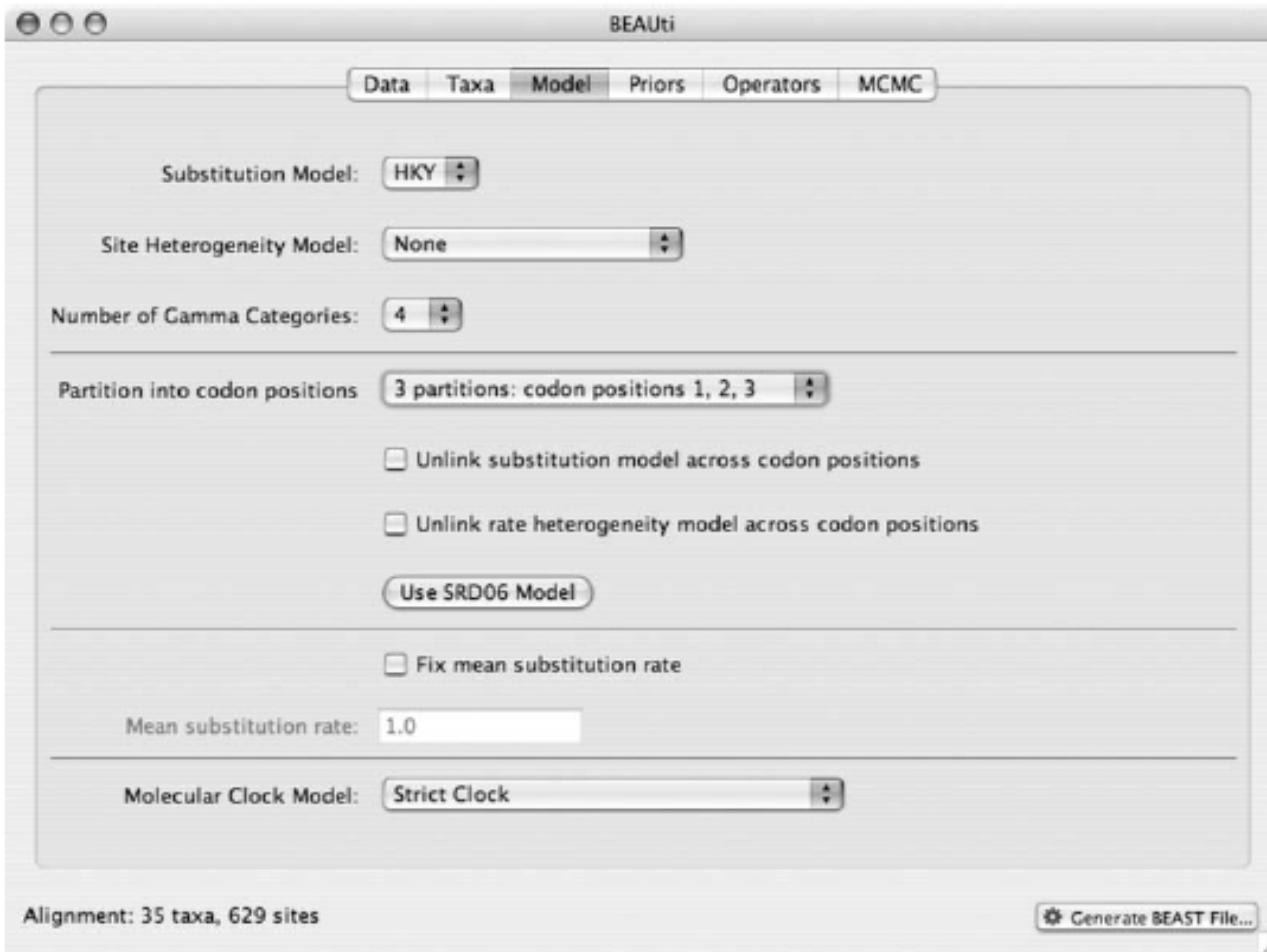
Fix mean substitution rate

Mean substitution rate: 1.0

Molecular Clock Model: Strict Clock

Alignment: 35 taxa, 629 sites

Generate BEAST File...



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Data Taxa Model Priors Operators MCMC

Length of chain: 100000

Echo state to screen every: 100

Log parameters every: 100

Log file name: RSVA.log

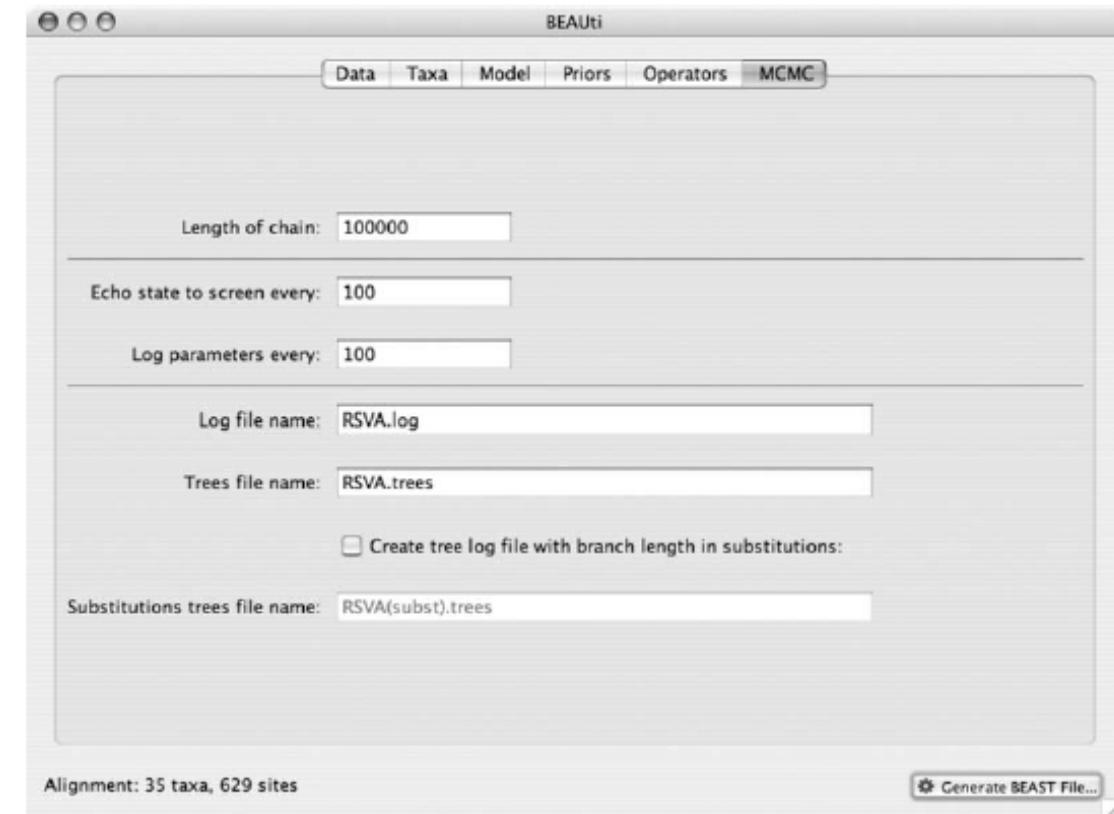
Trees file name: RSVA.trees

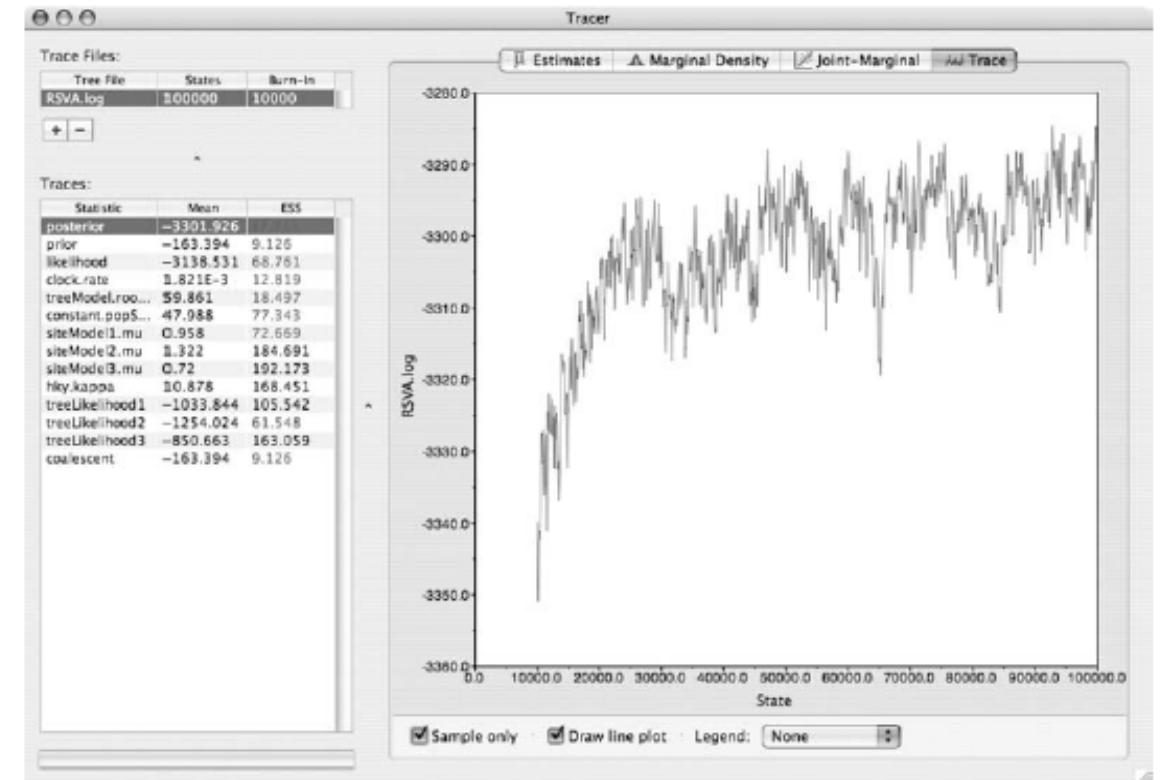
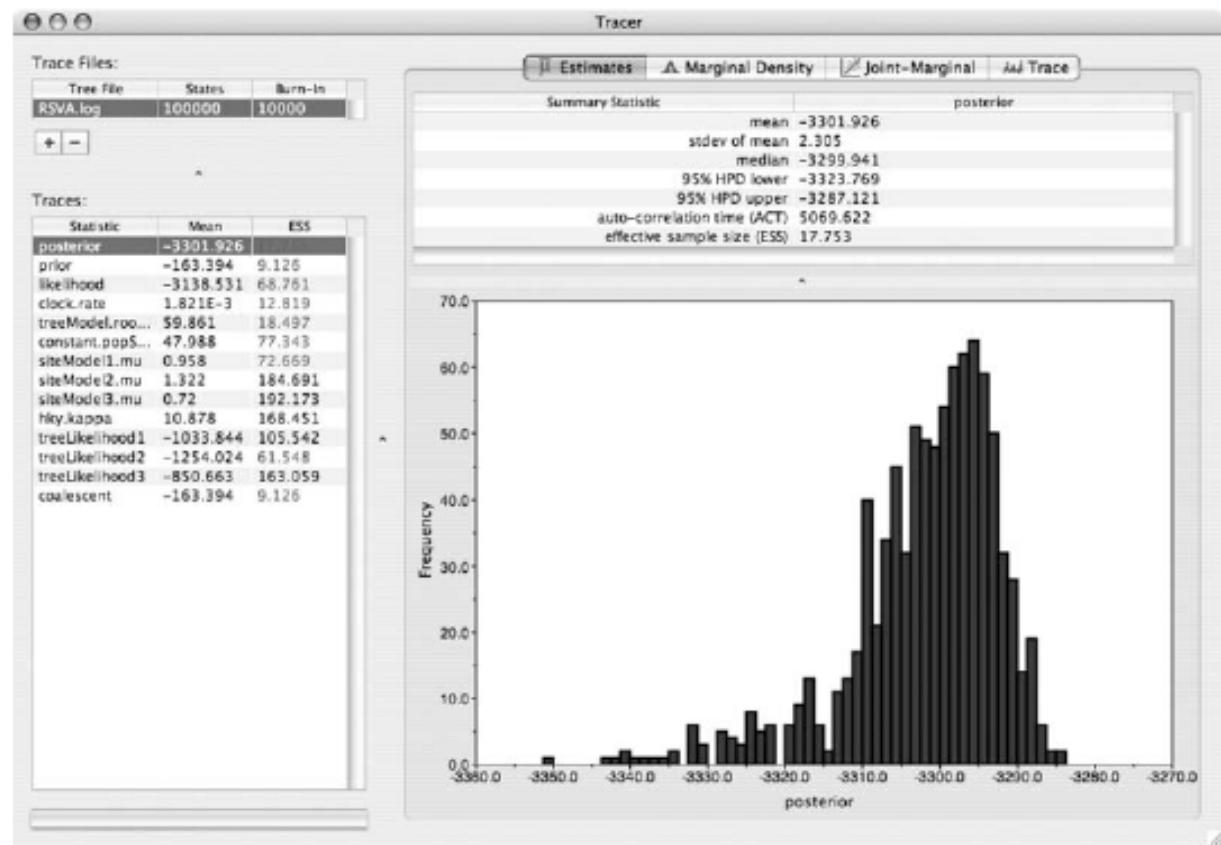
Create tree log file with branch length in substitutions:

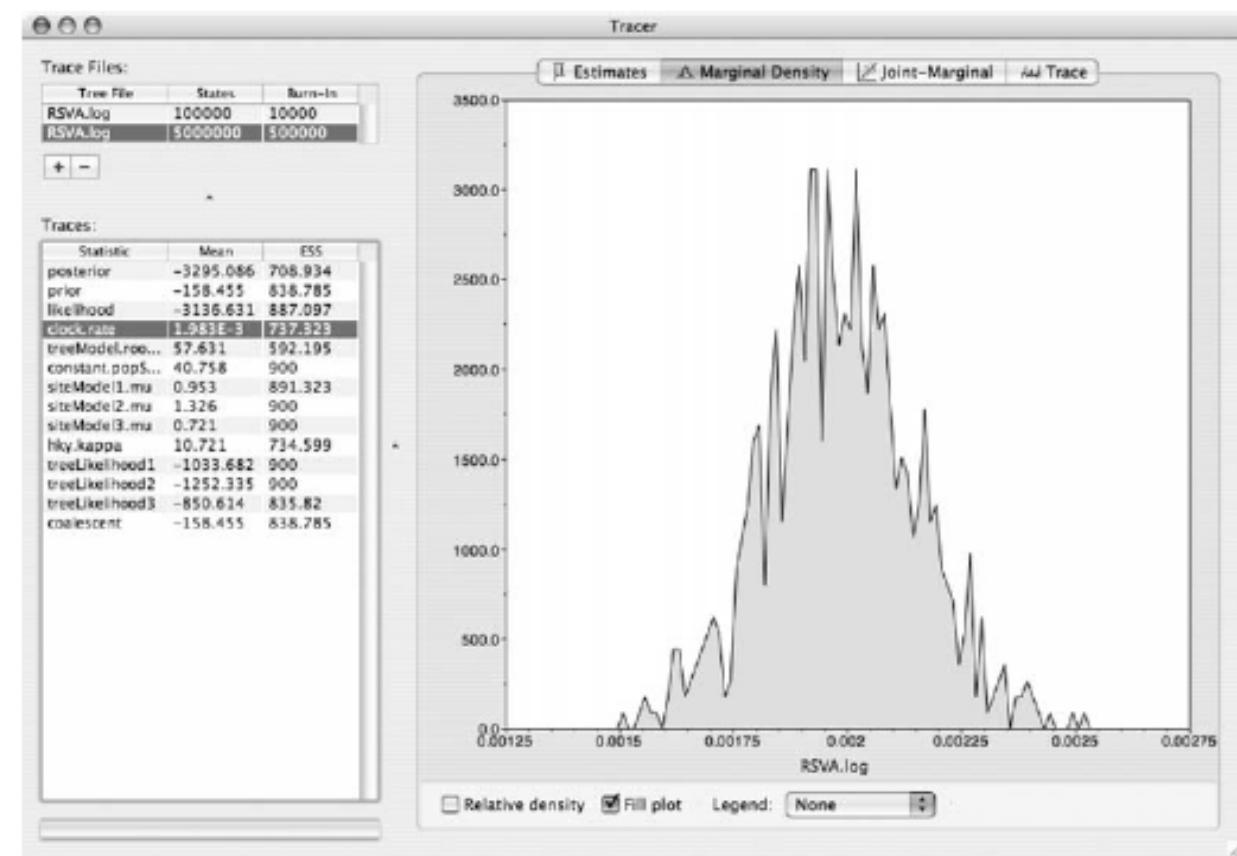
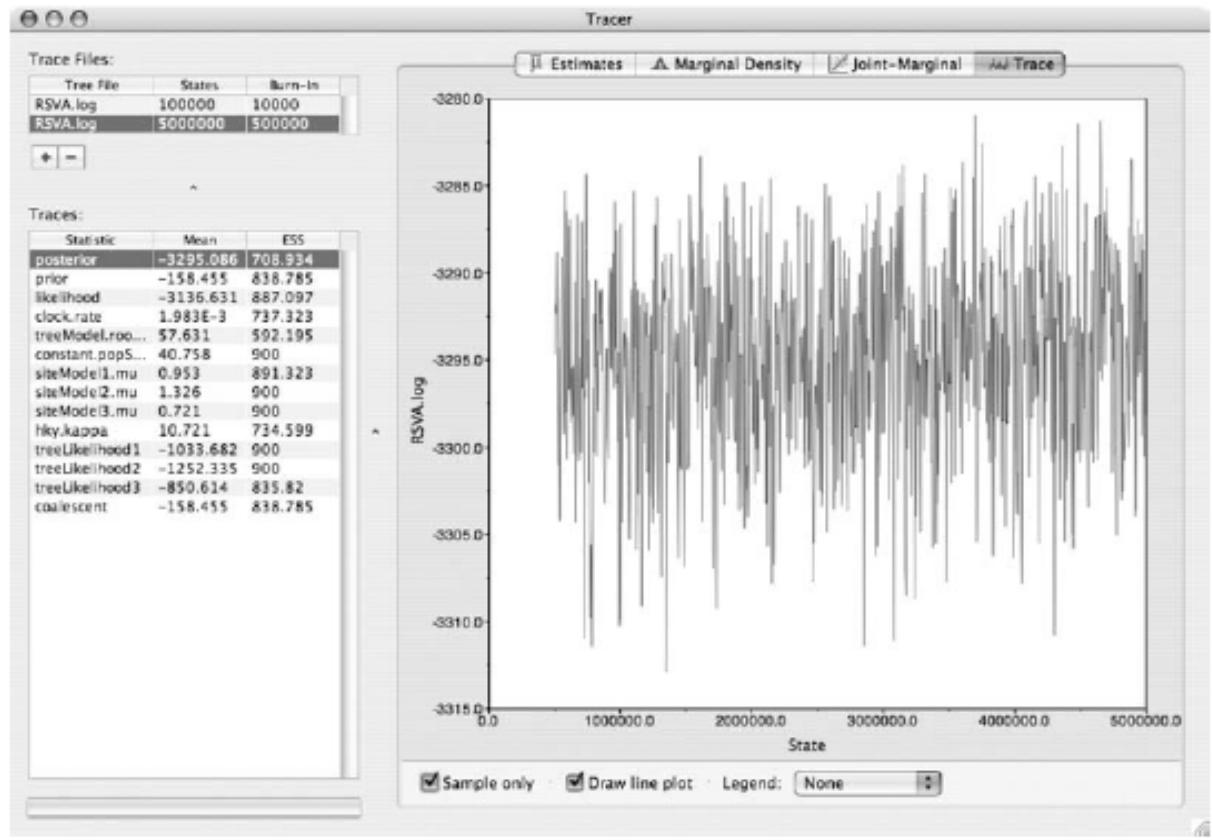
Substitutions trees file name: RSVA(subst).trees

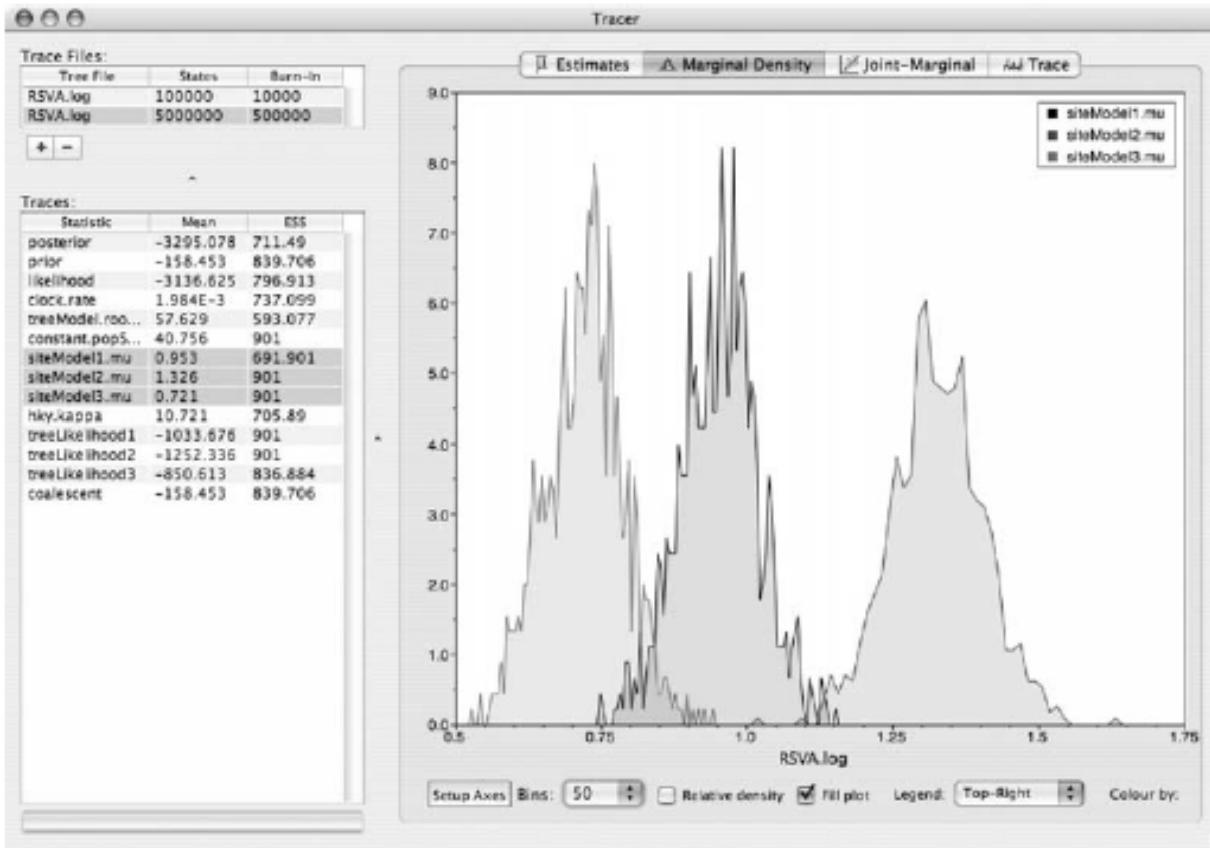
Alignment: 35 taxa, 629 sites

Generate BEAST File...









TreeAnnotator v1.4.6

Burnin:

Posterior probability limit:

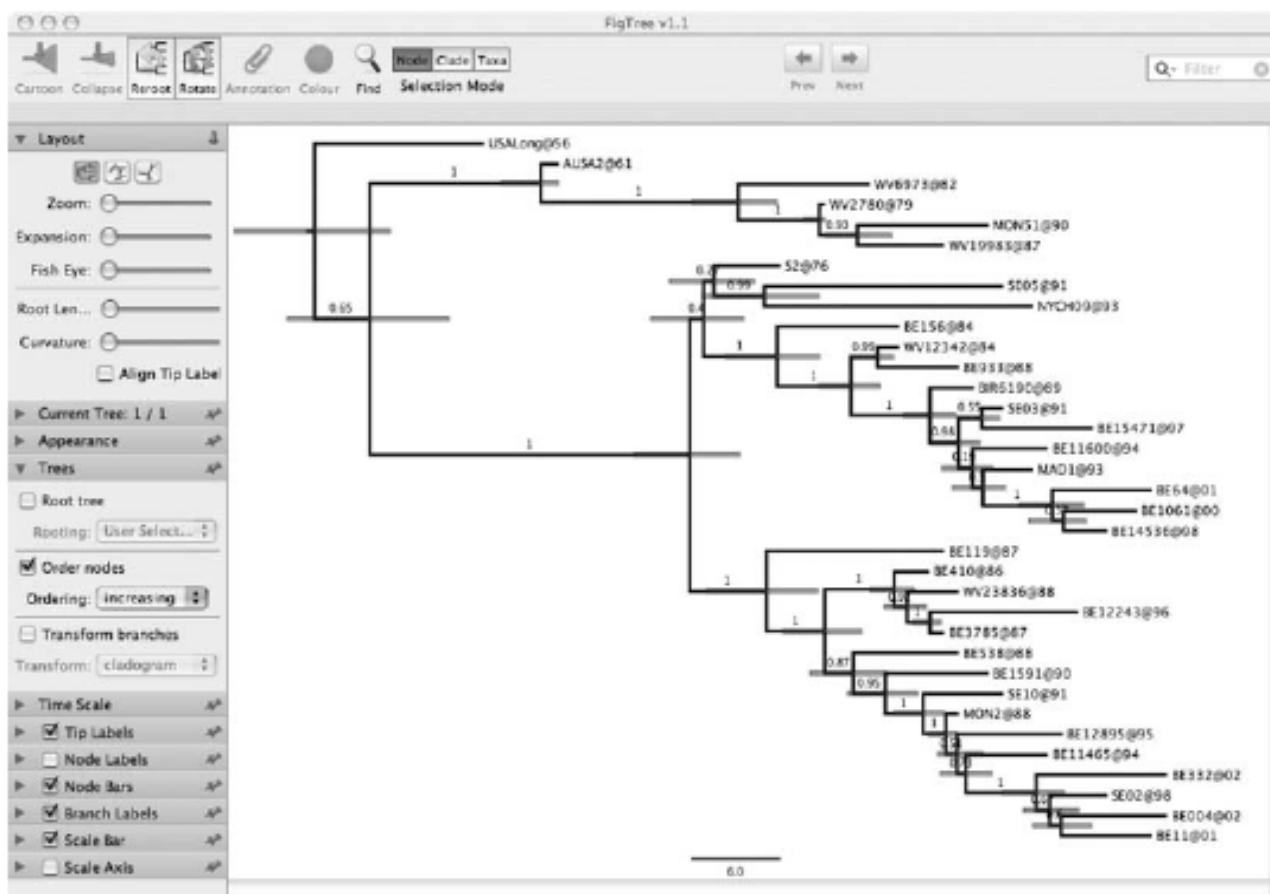
Target tree type:

Node heights:

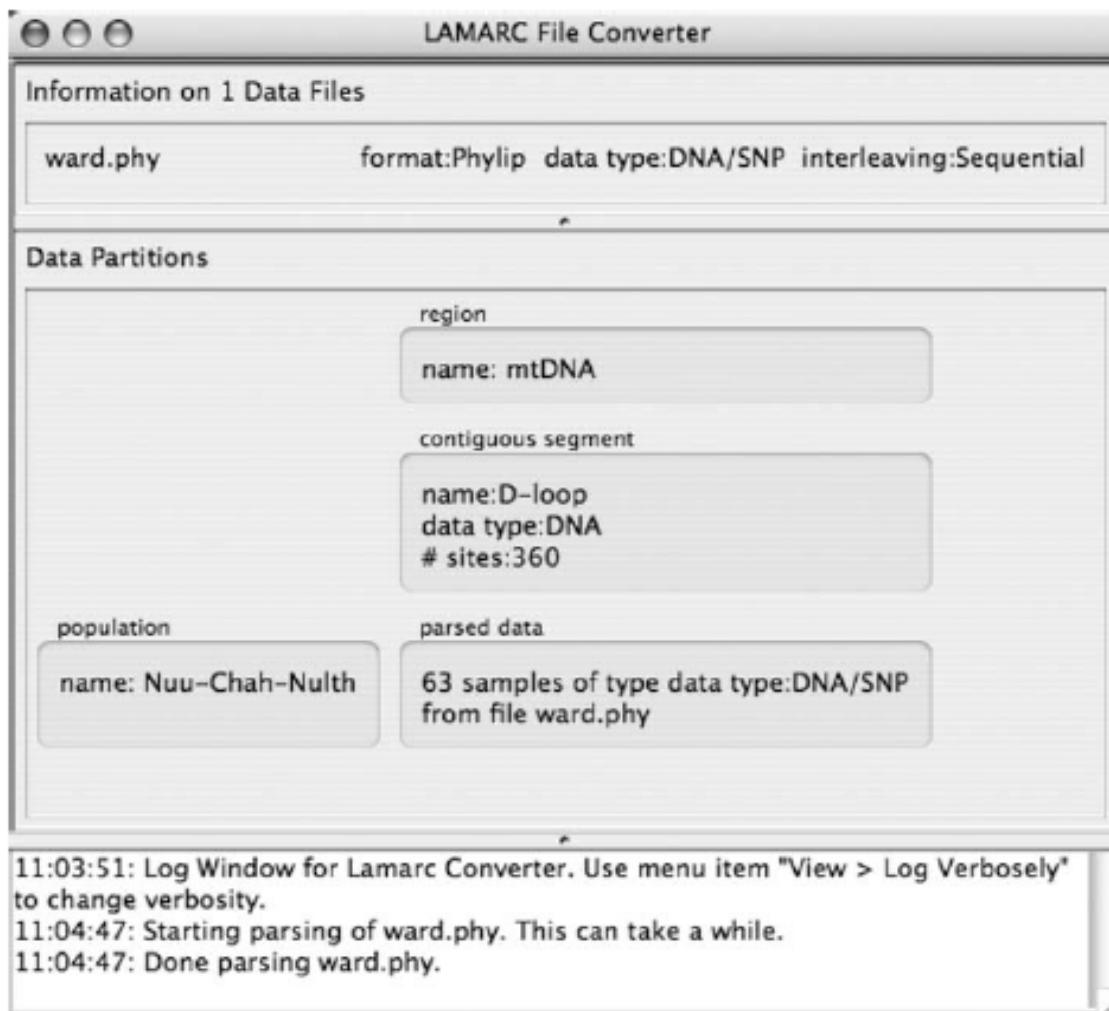
Target Tree File: not selected

Input Tree File: RSVA.trees

Output File: RSA_MCC.tre



19. Populasyon genetiği parametrelerinin tahmini



Edit data model for Region 1: mtDNA

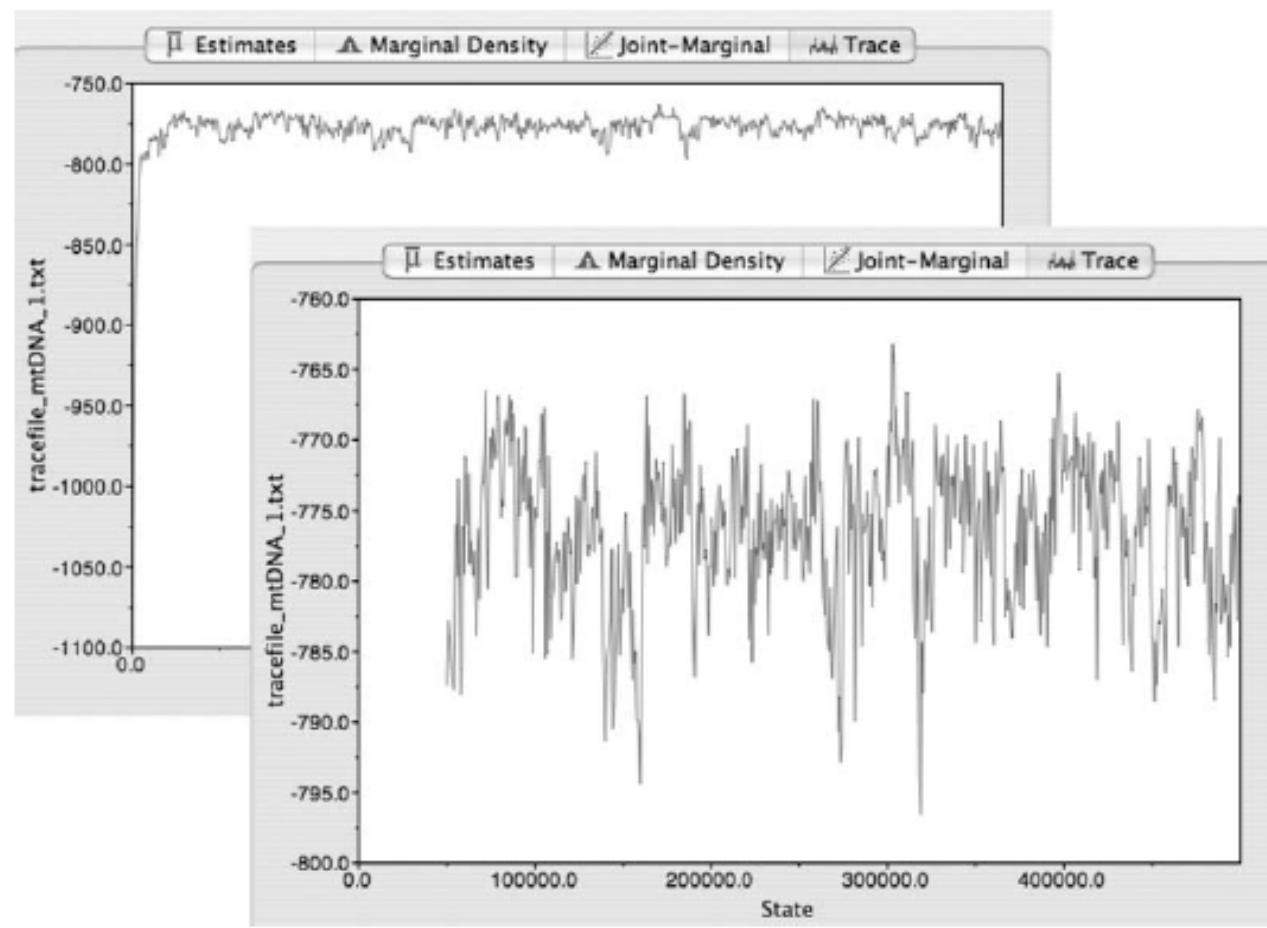
Datatype for this region	DNA
M Data Model	F84
D Use default data model for this region/segment	Yes
C Number of Categories	1
A Auto-Correlation	1
T TT Ratio	2
B Base Frequencies (A C G T)	0.3297 0.3371 0.1120
	0.2213 <calc>
R Relative mutation rate	1

Sampling strategy (chains and replicates)

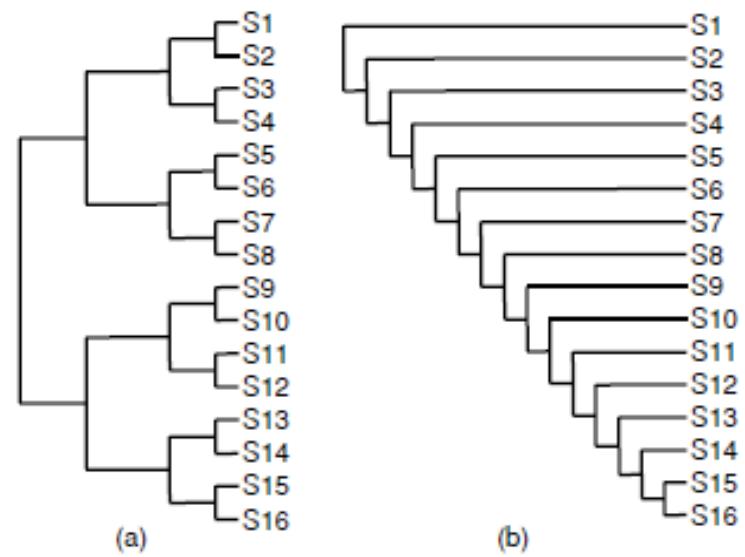
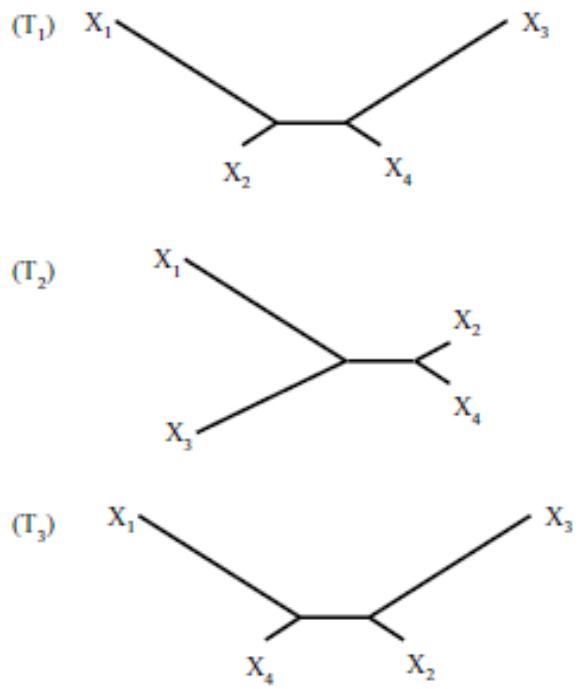
R	Number of replicates	1
	Initial Chains	
1	Number of chains (initial)	10
2	Number of recorded genealogies (initial)	500
3	Interval between recorded items (initial)	20
4	Number of samples to discard (initial burn-in)	1000

	Final Chains	
5	Number of chains (final)	2
6	Number of recorded genealogies (final)	10000
7	Interval between recorded items (final)	20
8	Number of samples to discard (final burn-in)	1000

Population	Theta	GrowthRate
Best Val (MLE)	Theta1	Growth1
Percentile	0.060816	246.0408
99%	0.005	0.033104
95%	0.025	0.037098
90%	0.050	0.039484
75%	0.125	0.043920
50%	0.250	0.049423
MLE	0.060816	246.0408
50%	0.750	0.075975
75%	0.875	0.088914
90%	0.950	0.105897
95%	0.975	0.117563
99%	0.995	0.140588
Theta1: Theta for Nuu-Chah-Nulth		
Growth1: Growth for Nuu-Chah-Nulth		



19. Substitution ile ilişkilendirme



Part II. For an extreme asymmetrical (and generally very unlikely) tree.

```
=====
Iss.c          0.6817
T            11.7056
DF           261
Prob (Two-tailed) 0.0000

95% Lower Limit 0.2749
95% Upper Limit 0.3920
```

Sequences ranked from the best to the worst.

```
=====
Seq_Name      Mean_Phi  Num_Insignif
-----
PanTroglobutesCOX1  0,1584    10
HomoSapiensCOX1    0,1495    12
PongoPygmaeusCOX1  0,1262    12
GallusGallusCOX1   0,1131    20
AlligatorMississippiensis 0,1124    20
BosTauerusCOX1     0,1096    20
BalaenopteraMusculusCOX1 0,1085    20
MasturusLanceolatusCOX1 0,0897    22
=====

Num_Insignif conditional on c > 15.
```

