

# AUTO

POPULATION SIZE, MIGRATION, DIVERGENCE, ASSIGNMENT, HISTORY

Bayesian inference using the structured coalescent

Migrate-n version 5.0.0a [May-20-2017]

Using Intel AVX (Advanced Vector Extensions)

Compiled for PARALLEL computer architectures

One master and 100 compute nodes are available.

Program started at Sun Aug 13 02:00:37 2017

Program finished at Sun Aug 13 03:47:42 2017 [Runtime:0000:01:47:05]



## Options

Datatype:

DNA sequence data

Inheritance scalers in use for Thetas:

All loci use an inheritance scaler of 1.0

[The locus with a scaler of 1.0 used as reference]

Random number seed:

(with internal timer)

1228906688

Start parameters:

Theta values were generated

Using a percent value of the prior

M values were generated

Using a percent value of the prior

Connection matrix:

m = average (average over a group of Thetas or M,

s = symmetric migration M, S = symmetric 4Nm,

0 = zero, and not estimated,

\* = migration free to vary, Thetas are on diagonal

d = row population split off column population, D = split and then migration

Population 1

1 Romanshorn\_0 \*

Order of parameters:

1  $\Theta_1$

<displayed>

Mutation rate among loci:

Mutation rate is constant for all loci

Analysis strategy:

Bayesian inference

-Population size estimation:

Exponential Distribution

Proposal distributions for parameter

Parameter	Proposal
Theta	Metropolis sampling
M	Metropolis sampling
Divergence	Metropolis sampling
Divergence Spread	Metropolis sampling
Genealogy	Metropolis-Hastings

Prior distribution for parameter

Parameter	Prior	Minimum	Mean	Maximum	Delta	Bins	UpdateFreq	
1	Theta -11	Uniform	0.000000	0.050	0.100	0.010	1500	0.20000

[-1 -1 means priors were set globally]

Markov chain settings:

Long chain

Number of chains

1

Recorded steps [a]

50000

Increment (record every x step [b])

200

Number of concurrent chains (replicates) [c]

2

Visited (sampled) parameter values [a\*b\*c]

20000000

Number of discard trees per chain (burn-in)

10000

Multiple Markov chains:

Static heating scheme

4 chains with temperatures

1000000.00

3.00

1.50

1.00

Swapping interval is 1

Print options:

Data file:

infile.0.6

Haplotyping is turned on:

NO

Output file:

outfile\_0.6\_0.4

Posterior distribution raw histogram file:

bayesfile

Raw data from the MCMC run:

bayesallfile\_0.6\_0.4

Print data:

No

Print genealogies [only some for some data type]:

None

## Data summary

Data file: infile.0.6  
 Datatype: Sequence data  
 Number of loci: 100

Mutationmodel:

Locus	Sublocus	Mutationmodel	Mutationmodel parameters
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1	1	Jukes-Cantor	[Basefreq: =0.25]
2	1	Jukes-Cantor	[Basefreq: =0.25]
3	1	Jukes-Cantor	[Basefreq: =0.25]
4	1	Jukes-Cantor	[Basefreq: =0.25]
5	1	Jukes-Cantor	[Basefreq: =0.25]
6	1	Jukes-Cantor	[Basefreq: =0.25]
7	1	Jukes-Cantor	[Basefreq: =0.25]
8	1	Jukes-Cantor	[Basefreq: =0.25]
9	1	Jukes-Cantor	[Basefreq: =0.25]
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12	1	Jukes-Cantor	[Basefreq: =0.25]
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50	1	Jukes-Cantor	[Basefreq: =0.25]
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79	1	Jukes-Cantor	[Basefreq: =0.25]

80	1	Jukes-Cantor	[Basefreq: =0.25]
81	1	Jukes-Cantor	[Basefreq: =0.25]
82	1	Jukes-Cantor	[Basefreq: =0.25]
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86	1	Jukes-Cantor	[Basefreq: =0.25]
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91	1	Jukes-Cantor	[Basefreq: =0.25]
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93	1	Jukes-Cantor	[Basefreq: =0.25]
94	1	Jukes-Cantor	[Basefreq: =0.25]
95	1	Jukes-Cantor	[Basefreq: =0.25]
96	1	Jukes-Cantor	[Basefreq: =0.25]
97	1	Jukes-Cantor	[Basefreq: =0.25]
98	1	Jukes-Cantor	[Basefreq: =0.25]
99	1	Jukes-Cantor	[Basefreq: =0.25]
100	1	Jukes-Cantor	[Basefreq: =0.25]

#### Sites per locus

Locus	Sites
1	10000
2	10000
3	10000
4	10000
5	10000
6	10000
7	10000
8	10000
9	10000
10	10000
11	10000
12	10000
13	10000
14	10000
15	10000
16	10000
17	10000
18	10000
19	10000
20	10000

21	10000
22	10000
23	10000
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90	10000
91	10000
92	10000
93	10000
94	10000
95	10000
96	10000
97	10000
98	10000
99	10000
100	10000

Site rate variation and probabilities:

Locus	Sublocus	Region	type	Rate of change	Probability	Patch size
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1	1	1		1.000	1.000	1.000
2	1	1		1.000	1.000	1.000
3	1	1		1.000	1.000	1.000
4	1	1		1.000	1.000	1.000
5	1	1		1.000	1.000	1.000
6	1	1		1.000	1.000	1.000

7	1	1	1.000	1.000	1.000
8	1	1	1.000	1.000	1.000
9	1	1	1.000	1.000	1.000
10	1	1	1.000	1.000	1.000
11	1	1	1.000	1.000	1.000
12	1	1	1.000	1.000	1.000
13	1	1	1.000	1.000	1.000
14	1	1	1.000	1.000	1.000
15	1	1	1.000	1.000	1.000
16	1	1	1.000	1.000	1.000
17	1	1	1.000	1.000	1.000
18	1	1	1.000	1.000	1.000
19	1	1	1.000	1.000	1.000
20	1	1	1.000	1.000	1.000
21	1	1	1.000	1.000	1.000
22	1	1	1.000	1.000	1.000
23	1	1	1.000	1.000	1.000
24	1	1	1.000	1.000	1.000
25	1	1	1.000	1.000	1.000
26	1	1	1.000	1.000	1.000
27	1	1	1.000	1.000	1.000
28	1	1	1.000	1.000	1.000
29	1	1	1.000	1.000	1.000
30	1	1	1.000	1.000	1.000
31	1	1	1.000	1.000	1.000
32	1	1	1.000	1.000	1.000
33	1	1	1.000	1.000	1.000
34	1	1	1.000	1.000	1.000
35	1	1	1.000	1.000	1.000
36	1	1	1.000	1.000	1.000
37	1	1	1.000	1.000	1.000
38	1	1	1.000	1.000	1.000
39	1	1	1.000	1.000	1.000
40	1	1	1.000	1.000	1.000
41	1	1	1.000	1.000	1.000
42	1	1	1.000	1.000	1.000
43	1	1	1.000	1.000	1.000
44	1	1	1.000	1.000	1.000
45	1	1	1.000	1.000	1.000
46	1	1	1.000	1.000	1.000
47	1	1	1.000	1.000	1.000
48	1	1	1.000	1.000	1.000
49	1	1	1.000	1.000	1.000
50	1	1	1.000	1.000	1.000
51	1	1	1.000	1.000	1.000



52	1	1	1.000	1.000	1.000
53	1	1	1.000	1.000	1.000
54	1	1	1.000	1.000	1.000
55	1	1	1.000	1.000	1.000
56	1	1	1.000	1.000	1.000
57	1	1	1.000	1.000	1.000
58	1	1	1.000	1.000	1.000
59	1	1	1.000	1.000	1.000
60	1	1	1.000	1.000	1.000
61	1	1	1.000	1.000	1.000
62	1	1	1.000	1.000	1.000
63	1	1	1.000	1.000	1.000
64	1	1	1.000	1.000	1.000
65	1	1	1.000	1.000	1.000
66	1	1	1.000	1.000	1.000
67	1	1	1.000	1.000	1.000
68	1	1	1.000	1.000	1.000
69	1	1	1.000	1.000	1.000
70	1	1	1.000	1.000	1.000
71	1	1	1.000	1.000	1.000
72	1	1	1.000	1.000	1.000
73	1	1	1.000	1.000	1.000
74	1	1	1.000	1.000	1.000
75	1	1	1.000	1.000	1.000
76	1	1	1.000	1.000	1.000
77	1	1	1.000	1.000	1.000
78	1	1	1.000	1.000	1.000
79	1	1	1.000	1.000	1.000
80	1	1	1.000	1.000	1.000
81	1	1	1.000	1.000	1.000
82	1	1	1.000	1.000	1.000
83	1	1	1.000	1.000	1.000
84	1	1	1.000	1.000	1.000
85	1	1	1.000	1.000	1.000
86	1	1	1.000	1.000	1.000
87	1	1	1.000	1.000	1.000
88	1	1	1.000	1.000	1.000
89	1	1	1.000	1.000	1.000
90	1	1	1.000	1.000	1.000
91	1	1	1.000	1.000	1.000
92	1	1	1.000	1.000	1.000
93	1	1	1.000	1.000	1.000
94	1	1	1.000	1.000	1.000
95	1	1	1.000	1.000	1.000
96	1	1	1.000	1.000	1.000

97	1	1	1.000	1.000	1.000	
98	1	1	1.000	1.000	1.000	
99	1	1	1.000	1.000	1.000	
100	1	1	1.000	1.000	1.000	
Population			Locus		Gene copies	
1 Romanshorn_0			1		10	
			2		10	
			3		10	
			4		10	
			5		10	
			6		10	
			7		10	
			8		10	
			9		10	
			10		10	
			11		10	
			12		10	
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41	10
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	86	10
	87	10
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	90	10
	91	10
	92	10
	93	10
	94	10
	95	10
	96	10
	97	10
	98	10
	99	10
	100	10
Total of all populations	1	10
	2	10
	3	10
	4	10
	5	10
	6	10
	7	10
	8	10
	9	10
	10	10
	11	10
	12	10
	13	10
	14	10
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93	10
94	10
95	10
96	10
97	10
98	10
99	10
100	10

## *Bayesian Analysis: Posterior distribution table*

Locus	Parameter	2.5%	25.0%	Mode	75.0%	97.5%	Median	Mean
1	$\Theta_1$	0.03047	0.04307	0.04783	0.04973	0.05153	0.04430	0.07992
2	$\Theta_1$	0.03240	0.04393	0.04797	0.04973	0.05167	0.04517	0.08389
3	$\Theta_1$	0.02760	0.04193	0.04777	0.04967	0.05147	0.04317	0.07522
4	$\Theta_1$	0.03240	0.04380	0.04790	0.04967	0.05167	0.04503	0.08435
5	$\Theta_1$	0.03233	0.04500	0.04777	0.04933	0.05160	0.04517	0.08374
6	$\Theta_1$	0.02987	0.04253	0.04777	0.04973	0.05147	0.04377	0.07805
7	$\Theta_1$	0.02967	0.04267	0.04777	0.04960	0.05147	0.04390	0.07827
8	$\Theta_1$	0.03100	0.04453	0.04783	0.04953	0.05160	0.04477	0.08231
9	$\Theta_1$	0.02773	0.04180	0.04770	0.04960	0.05147	0.04310	0.07508
10	$\Theta_1$	0.03173	0.04360	0.04777	0.04973	0.05160	0.04477	0.08191
11	$\Theta_1$	0.03107	0.04340	0.04790	0.04987	0.05160	0.04457	0.08160
12	$\Theta_1$	0.03173	0.04380	0.04803	0.04993	0.05160	0.04497	0.08360
13	$\Theta_1$	0.03127	0.04327	0.04797	0.04980	0.05160	0.04450	0.08124
14	$\Theta_1$	0.03033	0.04300	0.04777	0.04967	0.05147	0.04417	0.07928
15	$\Theta_1$	0.02993	0.04293	0.04777	0.04973	0.05153	0.04417	0.07922
16	$\Theta_1$	0.03027	0.04293	0.04783	0.04973	0.05153	0.04410	0.07941
17	$\Theta_1$	0.03207	0.04373	0.04783	0.04973	0.05153	0.04497	0.08263
18	$\Theta_1$	0.02747	0.04307	0.04783	0.04973	0.05180	0.04430	0.07980

19	$\Theta_1$	0.03067	0.04313	0.04777	0.04967	0.05153	0.04437	0.07985
20	$\Theta_1$	0.02933	0.04293	0.04770	0.04980	0.05147	0.04410	0.07889
21	$\Theta_1$	0.03107	0.04353	0.04783	0.04980	0.05160	0.04470	0.08208
22	$\Theta_1$	0.03420	0.04440	0.04797	0.05000	0.05167	0.04550	0.08589
23	$\Theta_1$	0.03007	0.04293	0.04777	0.04973	0.05153	0.04417	0.08004
24	$\Theta_1$	0.03020	0.04380	0.04777	0.04960	0.05153	0.04443	0.07994
25	$\Theta_1$	0.03200	0.04360	0.04777	0.04967	0.05153	0.04477	0.08254
26	$\Theta_1$	0.03333	0.04453	0.04790	0.04987	0.05173	0.04563	0.08522
27	$\Theta_1$	0.02840	0.04220	0.04770	0.04967	0.05140	0.04343	0.07650
28	$\Theta_1$	0.03153	0.04360	0.04777	0.04980	0.05153	0.04477	0.08209
29	$\Theta_1$	0.03120	0.04367	0.04783	0.04967	0.05160	0.04450	0.08070
30	$\Theta_1$	0.03113	0.04453	0.04790	0.04960	0.05167	0.04470	0.08120
31	$\Theta_1$	0.03047	0.04333	0.04777	0.04980	0.05160	0.04450	0.08166
32	$\Theta_1$	0.02907	0.04207	0.04770	0.04953	0.05153	0.04337	0.07737
33	$\Theta_1$	0.03127	0.04373	0.04797	0.04993	0.05160	0.04477	0.08208
34	$\Theta_1$	0.03020	0.04280	0.04770	0.04953	0.05153	0.04410	0.07839
35	$\Theta_1$	0.03067	0.04327	0.04783	0.04973	0.05153	0.04443	0.08081
36	$\Theta_1$	0.03080	0.04320	0.04783	0.04987	0.05153	0.04437	0.08043
37	$\Theta_1$	0.02807	0.04253	0.04770	0.04940	0.05147	0.04297	0.07503
38	$\Theta_1$	0.03227	0.04400	0.04783	0.04967	0.05167	0.04517	0.08371
39	$\Theta_1$	0.02820	0.04180	0.04763	0.04960	0.05147	0.04310	0.07524
40	$\Theta_1$	0.02853	0.04207	0.04770	0.04960	0.05147	0.04330	0.07646
41	$\Theta_1$	0.03100	0.04327	0.04777	0.04967	0.05153	0.04450	0.08038



Locus	Parameter	2.5%	25.0%	Mode	75.0%	97.5%	Median	Mean
42	$\Theta_1$	0.03027	0.04327	0.04790	0.04987	0.05160	0.04443	0.08171
43	$\Theta_1$	0.03140	0.04353	0.04790	0.04980	0.05153	0.04470	0.08272
44	$\Theta_1$	0.03000	0.04287	0.04783	0.04973	0.05153	0.04403	0.07879
45	$\Theta_1$	0.03080	0.04307	0.04783	0.04967	0.05160	0.04430	0.08012
46	$\Theta_1$	0.02913	0.04247	0.04777	0.04960	0.05153	0.04370	0.07771
47	$\Theta_1$	0.02840	0.04207	0.04770	0.04960	0.05147	0.04337	0.07611
48	$\Theta_1$	0.03247	0.04493	0.04790	0.04953	0.05167	0.04510	0.08262
49	$\Theta_1$	0.02867	0.04213	0.04770	0.04960	0.05147	0.04337	0.07670
50	$\Theta_1$	0.03247	0.04367	0.04783	0.04980	0.05153	0.04483	0.08201
51	$\Theta_1$	0.02980	0.04307	0.04777	0.04973	0.05153	0.04430	0.07854
52	$\Theta_1$	0.03027	0.04400	0.04783	0.04933	0.05153	0.04417	0.08071
53	$\Theta_1$	0.03233	0.04427	0.04783	0.04980	0.05160	0.04537	0.08446
54	$\Theta_1$	0.03227	0.04373	0.04790	0.04987	0.05153	0.04490	0.08379
55	$\Theta_1$	0.02947	0.04280	0.04770	0.04967	0.05147	0.04397	0.07831
56	$\Theta_1$	0.02993	0.04293	0.04777	0.04967	0.05160	0.04423	0.07878
57	$\Theta_1$	0.03340	0.04440	0.04790	0.04987	0.05173	0.04550	0.08595
58	$\Theta_1$	0.03080	0.04313	0.04783	0.04987	0.05153	0.04423	0.08080
59	$\Theta_1$	0.03120	0.04333	0.04777	0.04973	0.05153	0.04457	0.08041
60	$\Theta_1$	0.02853	0.04180	0.04770	0.04967	0.05140	0.04317	0.07605
61	$\Theta_1$	0.02873	0.04233	0.04770	0.04967	0.05147	0.04357	0.07675

62	$\Theta_1$	0.03153	0.04360	0.04790	0.04987	0.05167	0.04470	0.08203
63	$\Theta_1$	0.03073	0.04307	0.04790	0.04980	0.05153	0.04423	0.07934
64	$\Theta_1$	0.02987	0.04313	0.04777	0.04960	0.05160	0.04390	0.07870
65	$\Theta_1$	0.03200	0.04360	0.04777	0.04973	0.05153	0.04477	0.08192
66	$\Theta_1$	0.03040	0.04333	0.04783	0.04987	0.05153	0.04443	0.08197
67	$\Theta_1$	0.03260	0.04413	0.04783	0.04973	0.05160	0.04530	0.08518
68	$\Theta_1$	0.03360	0.04413	0.04797	0.04987	0.05153	0.04530	0.08418
69	$\Theta_1$	0.02913	0.04240	0.04770	0.04960	0.05147	0.04370	0.07723
70	$\Theta_1$	0.02947	0.04260	0.04783	0.04987	0.05153	0.04403	0.07852
71	$\Theta_1$	0.03053	0.04313	0.04770	0.04967	0.05153	0.04437	0.07941
72	$\Theta_1$	0.03027	0.04307	0.04783	0.04973	0.05160	0.04430	0.08146
73	$\Theta_1$	0.03353	0.04520	0.04783	0.04953	0.05153	0.04537	0.08313
74	$\Theta_1$	0.03200	0.04500	0.04803	0.04980	0.05173	0.04517	0.08403
75	$\Theta_1$	0.03147	0.04347	0.04790	0.04987	0.05167	0.04463	0.08323
76	$\Theta_1$	0.03247	0.04427	0.04797	0.04993	0.05160	0.04537	0.08482
77	$\Theta_1$	0.02987	0.04273	0.04763	0.04953	0.05153	0.04403	0.07874
78	$\Theta_1$	0.02920	0.04333	0.04777	0.04933	0.05147	0.04350	0.07684
79	$\Theta_1$	0.03040	0.04340	0.04783	0.04967	0.05160	0.04430	0.08018
80	$\Theta_1$	0.03020	0.04327	0.04777	0.04980	0.05153	0.04443	0.08109
81	$\Theta_1$	0.03007	0.04267	0.04777	0.04967	0.05147	0.04390	0.07877
82	$\Theta_1$	0.03180	0.04373	0.04790	0.04980	0.05167	0.04497	0.08308
83	$\Theta_1$	0.02947	0.04367	0.04777	0.04947	0.05153	0.04383	0.07738
84	$\Theta_1$	0.03147	0.04353	0.04777	0.04973	0.05160	0.04470	0.08259

Locus	Parameter	2.5%	25.0%	Mode	75.0%	97.5%	Median	Mean
85	$\Theta_1$	0.03000	0.04293	0.04777	0.04973	0.05160	0.04417	0.07950
86	$\Theta_1$	0.03233	0.04387	0.04797	0.04973	0.05167	0.04503	0.08332
87	$\Theta_1$	0.02993	0.04253	0.04783	0.04973	0.05153	0.04370	0.07766
88	$\Theta_1$	0.03147	0.04420	0.04777	0.04947	0.05167	0.04470	0.08120
89	$\Theta_1$	0.03153	0.04347	0.04790	0.04987	0.05167	0.04457	0.08073
90	$\Theta_1$	0.03047	0.04340	0.04777	0.04987	0.05153	0.04450	0.08140
91	$\Theta_1$	0.03073	0.04327	0.04790	0.04980	0.05167	0.04450	0.08046
92	$\Theta_1$	0.03067	0.04327	0.04783	0.04973	0.05160	0.04450	0.08194
93	$\Theta_1$	0.03133	0.04367	0.04783	0.04973	0.05160	0.04483	0.08219
94	$\Theta_1$	0.03173	0.04360	0.04783	0.04980	0.05160	0.04477	0.08114
95	$\Theta_1$	0.03173	0.04440	0.04783	0.04927	0.05153	0.04457	0.08138
96	$\Theta_1$	0.03340	0.04453	0.04783	0.04973	0.05180	0.04570	0.08609
97	$\Theta_1$	0.03240	0.04387	0.04797	0.04993	0.05173	0.04497	0.08328
98	$\Theta_1$	0.03273	0.04393	0.04783	0.04973	0.05160	0.04510	0.08343
99	$\Theta_1$	0.03047	0.04267	0.04783	0.04973	0.05153	0.04390	0.07849
100	$\Theta_1$	0.03133	0.04440	0.04783	0.04960	0.05147	0.04457	0.08267
All	$\Theta_1$	0.00860	0.01073	0.01177	0.01380	0.01520	0.01217	0.09936

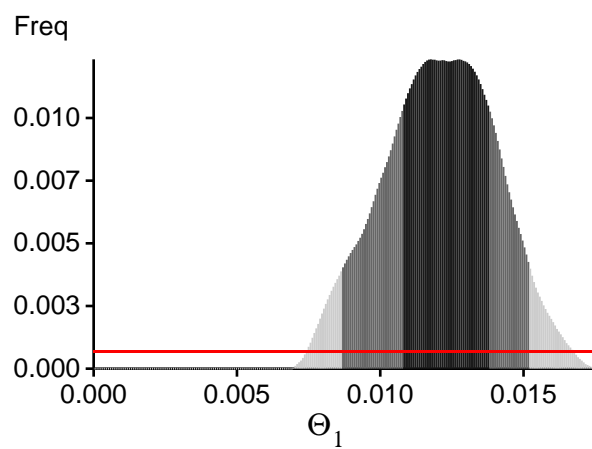
Citation suggestions:

Beerli P., 2006. Comparison of Bayesian and maximum-likelihood inference of population genetic parameters. *Bioinformatics* 22:341-345

Beerli P., 2007. Estimation of the population scaled mutation rate from microsatellite data, *Genetics*, 177:1967-1968.

Beerli P., 2009. How to use MIGRATE or why are Markov chain Monte Carlo programs difficult to use?  
 In Population Genetics for Animal Conservation, G. Bertorelle, M. W. Bruford, H. C. Hauffe, A. Rizzoli,  
 and C. Vernesi, eds., vol. 17 of Conservation Biology, Cambridge University Press, Cambridge UK, pp. 42-79.

# *Bayesian Analysis: Posterior distribution over all loci*



## Log-Probability of the data given the model (marginal likelihood)

Use this value for Bayes factor calculations:

$BF = \text{Exp}[\ln(\text{Prob}(D \mid \text{thisModel}) - \ln(\text{Prob}(D \mid \text{otherModel}))]$

or as  $LBF = 2 (\ln(\text{Prob}(D \mid \text{thisModel}) - \ln(\text{Prob}(D \mid \text{otherModel})))$

shows the support for thisModel]

Locus	TI(1a)	BTI(1b)	SS(2)	HS(3)
1	-13927.20	-13776.37	-13822.81	-13911.62
2	-14789.43	-14410.96	-14432.82	-14510.11
3	-13867.66	-13727.39	-13769.50	-13864.50
4	-14290.52	-14099.41	-14151.90	-14229.03
5	-14466.08	-14189.96	-14228.69	-14305.95
6	-13904.93	-13764.17	-13811.97	-13901.42
7	-13907.86	-13762.87	-13809.35	-13899.32
8	-14223.39	-13971.40	-14007.64	-14089.56
9	-13862.86	-13722.64	-13765.81	-13859.52
10	-14592.12	-14243.17	-14262.37	-14346.48
11	-13987.04	-13824.86	-13874.61	-13958.41
12	-14470.08	-14175.41	-14208.25	-14287.26
13	-13956.52	-13806.97	-13854.93	-13942.79
14	-13952.89	-13797.59	-13844.42	-13933.00
15	-13921.37	-13778.47	-13826.68	-13915.48
16	-13929.48	-13777.09	-13824.14	-13912.82
17	-16409.36	-15771.46	-15753.69	-15836.03
18	-14258.35	-14014.60	-14047.72	-14135.11
19	-13946.14	-13783.13	-13828.78	-13916.29
20	-13912.41	-13767.05	-13813.96	-13902.07
21	-14694.96	-14470.72	-14482.76	-14588.07
22	-17646.43	-15770.43	-15519.52	-15596.00
23	-13936.20	-13791.15	-13837.64	-13926.73
24	-14009.18	-13829.21	-13870.54	-13961.28
25	-14043.28	-13864.51	-13910.61	-13995.20
26	-15461.92	-14793.26	-14767.08	-14840.91
27	-13882.00	-13739.97	-13783.79	-13878.01
28	-17659.34	-15721.15	-15452.20	-15535.30
29	-13990.20	-13815.31	-13859.63	-13946.77

30	-13977.56	-13825.07	-13873.62	-13960.43
31	-13993.54	-13837.79	-13885.42	-13970.72
32	-13893.67	-13752.98	-13799.41	-13890.02
33	-14009.42	-13859.55	-13912.60	-13996.37
34	-13929.02	-13784.54	-13831.52	-13921.40
35	-14272.06	-14082.61	-14129.46	-14214.16
36	-14186.72	-13943.32	-13977.14	-14063.15
37	-13866.53	-13726.27	-13769.89	-13863.25
38	-14283.85	-14035.28	-14074.64	-14154.18
39	-13867.19	-13726.96	-13768.44	-13863.93
40	-13880.56	-13740.17	-13785.15	-13877.38
41	-13967.05	-13799.73	-13845.29	-13931.61
42	-27942.43	-23009.29	-22255.60	-22334.43
43	-14373.53	-14158.45	-14197.30	-14289.41
44	-13920.08	-13772.55	-13819.34	-13908.29
45	-13985.53	-13813.37	-13858.94	-13945.10
46	-13899.20	-13753.92	-13798.82	-13890.69
47	-13881.56	-13741.07	-13785.43	-13878.26
48	-14108.85	-13916.17	-13963.35	-14048.42
49	-13883.35	-13739.53	-13783.22	-13876.48
50	-14036.32	-13858.79	-13906.17	-13989.69
51	-13934.48	-13789.02	-13834.25	-13927.74
52	-13934.53	-13791.40	-13839.26	-13932.86
53	-14190.74	-13976.32	-14022.85	-14101.17
54	-14784.62	-14497.57	-14529.34	-14610.62
55	-13906.74	-13765.88	-13813.73	-13903.14
56	-14016.15	-13829.79	-13870.85	-13959.53
57	-16785.72	-16323.05	-16289.21	-16396.91
58	-13994.83	-13823.55	-13869.77	-13956.93
59	-13953.48	-13796.83	-13844.10	-13930.34
60	-13880.86	-13740.25	-13784.72	-13877.32
61	-13884.80	-13740.31	-13784.11	-13877.02
62	-13992.22	-13834.23	-13884.94	-13971.47
63	-13933.45	-13785.93	-13833.77	-13922.21
64	-13915.58	-13763.14	-13808.79	-13897.66
65	-29234.87	-21120.85	-19727.35	-19808.55
66	-14131.68	-13960.16	-14001.26	-14091.29
67	-15174.96	-14597.41	-14583.45	-14659.62
68	-14221.32	-13974.12	-14013.01	-14092.93
69	-13889.45	-13748.72	-13793.13	-13886.15
70	-13968.45	-13798.85	-13841.57	-13930.90
71	-13964.24	-13799.47	-13844.90	-13932.38
72	-15049.21	-14564.53	-14562.30	-14645.39
73	-14435.08	-14079.81	-14096.94	-14179.37
74	-14117.77	-13934.46	-13983.47	-14064.47

75	-14096.30	-13929.77	-13973.49	-14062.32
76	-14331.75	-14114.93	-14160.83	-14242.66
77	-13939.84	-13783.19	-13829.12	-13917.52
78	-13880.16	-13735.58	-13779.12	-13873.37
79	-13938.20	-13787.59	-13836.36	-13923.35
80	-13969.23	-13811.31	-13859.94	-13945.58
81	-13909.62	-13766.80	-13812.95	-13903.61
82	-20485.43	-18639.41	-18425.89	-18505.60
83	-13899.89	-13751.96	-13796.49	-13887.69
84	-14048.31	-13892.75	-13945.49	-14027.71
85	-13936.43	-13788.63	-13835.92	-13924.85
86	-14084.37	-13913.48	-13963.05	-14045.04
87	-13901.13	-13759.70	-13804.14	-13897.38
88	-13992.61	-13820.69	-13864.46	-13953.89
89	-13966.66	-13811.91	-13860.25	-13948.74
90	-13978.25	-13831.01	-13880.89	-13967.41
91	-13958.16	-13796.45	-13844.08	-13929.92
92	-15009.95	-14668.52	-14686.55	-14772.70
93	-13997.92	-13846.35	-13897.23	-13980.07
94	-13990.32	-13824.50	-13871.65	-13957.41
95	-14135.66	-13914.76	-13953.69	-14040.88
96	-18459.91	-16342.58	-16058.13	-16129.68
97	-15622.76	-14721.03	-14641.42	-14724.08
98	-14374.94	-14049.99	-14074.75	-14154.48
99	-13911.30	-13763.20	-13809.91	-13899.04
100	-16476.27	-15510.20	-15432.11	-15510.57
All	-1465533.37	-1424335.54	-1424685.10	-1433359.42
(1a) TI: Thermodynamic integration: log(Prob(D Model)): Good approximation with many temperatures				
(1b) BTI: Bezier-approximated Thermodynamic integration: when using few temperatures USE THIS!				
(2) SS: Steppingstone Sampling (Xie et al 2011)				
(3) HS: Harmonic mean approximation: Overestimates the marginal likelihood, poor variance				
[Scaling factor = 114.446552]				
Citation suggestions:				
Beerli P. and M. Palczewski, 2010. Unified framework to evaluate panmixia and migration direction among multiple sampling locations, Genetics, 185: 313-326.				
Palczewski M. and P. Beerli, 2014. Population model comparison using multi-locus datasets.				
In M.-H. Chen, L. Kuo, and P. O. Lewis, editors, Bayesian Phylogenetics: Methods, Algorithms, and Applications, pages 187-200. CRC Press, 2014.				
Xie W., P. O. Lewis, Y. Fan, L. Kuo, and M.-H. Chen. 2011. Improving marginal likelihood estimation for Bayesian phylogenetic model selection. Systematic Biology, 60(2):150â 160, 2011.				



*Acceptance ratios for all parameters and the genealogies*

Parameter	Accepted changes	Ratio
$\Theta_1$	381508819/399952863	0.95388
Genealogies	564576689/1600047137	0.35285

### *MCMC-Autocorrelation and Effective MCMC Sample Size*

Parameter	Autocorrelation	Effective Sampe Size
$\Theta_1$	0.54852	2924556.16
Genealogies	0.12936	8048876.63

## *Average temperatures during the run*

Chain	Temperatures
-------	--------------

1	0.00000
2	0.00000
3	0.00000
4	0.00000

Adaptive heating often fails, if the average temperatures are very close together try to rerun using static heating! If you want to compare models using marginal likelihoods then you **MUST** use static heating

## *Potential Problems*

This section reports potential problems with your run, but such reporting is often not very accurate. With many parameters in a multilocus analysis, it is very common that some parameters for some loci will not be very informative, triggering suggestions (for example to increase the prior range) that are not sensible. This suggestion tool will improve with time, therefore do not blindly follow its suggestions. If some parameters are flagged, inspect the tables carefully and judge whether an action is required. For example, if you run a Bayesian inference with sequence data, for macroscopic species there is rarely the need to increase the prior for Theta beyond 0.1; but if you use microsatellites it is rather common that your prior distribution for Theta should have a range from 0.0 to 100 or more. With many populations (>3) it is also very common that some migration routes are estimated poorly because the data contains little or no information for that route. Increasing the range will not help in such situations, reducing number of parameters may help in such situations.

No warning was recorded during the run