

# 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 22:47:14 2017

Program finished at Mon Aug 14 01:09:31 2017 [Runtime:0000:02:22:17]



## 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)

965394430

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.0.4

Haplotyping is turned on:

NO

Output file:

outfile\_0.4\_1.0

Posterior distribution raw histogram file:

bayesfile

Raw data from the MCMC run:

bayesallfile\_0.4\_1.0

Print data:

No

Print genealogies [only some for some data type]:

None

## *Data summary*

Data file:	infile.0.4
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]
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46	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]
87	1	Jukes-Cantor	[Basefreq: =0.25]
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90	1	Jukes-Cantor	[Basefreq: =0.25]
91	1	Jukes-Cantor	[Basefreq: =0.25]
92	1	Jukes-Cantor	[Basefreq: =0.25]
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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81	10000
82	10000
83	10000
84	10000
85	10000
86	10000
87	10000
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89	10000
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	
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			10		10	
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	86	10
	87	10
	88	10
	89	10
	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
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92	10
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	$\Theta_1$	0.00000	0.00000	0.00003	0.00087	0.00220	0.00090	0.00023
2	$\Theta_1$	0.00000	0.00000	0.00003	0.00087	0.00220	0.00090	0.00023
3	$\Theta_1$	0.00000	0.00033	0.00117	0.00193	0.00333	0.00157	0.00119
4	$\Theta_1$	0.00000	0.00000	0.00003	0.00087	0.00220	0.00090	0.00023
5	$\Theta_1$	0.00000	0.00000	0.00003	0.00087	0.00220	0.00090	0.00023
6	$\Theta_1$	0.00000	0.00000	0.00003	0.00087	0.00220	0.00090	0.00023
7	$\Theta_1$	0.00000	0.00000	0.00003	0.00087	0.00220	0.00090	0.00023
8	$\Theta_1$	0.00000	0.00000	0.00003	0.00087	0.00220	0.00090	0.00023
9	$\Theta_1$	0.00000	0.00000	0.00003	0.00087	0.00220	0.00090	0.00023
10	$\Theta_1$	0.00380	0.00687	0.00910	0.01193	0.02080	0.01050	0.01136
11	$\Theta_1$	0.00000	0.00000	0.00003	0.00087	0.00220	0.00090	0.00023
12	$\Theta_1$	0.00000	0.00000	0.00003	0.00087	0.00220	0.00090	0.00023
13	$\Theta_1$	0.00000	0.00000	0.00003	0.00087	0.00220	0.00090	0.00023
14	$\Theta_1$	0.00000	0.00000	0.00003	0.00087	0.00220	0.00090	0.00023
15	$\Theta_1$	0.00000	0.00000	0.00003	0.00087	0.00220	0.00090	0.00023
16	$\Theta_1$	0.00000	0.00000	0.00003	0.00087	0.00220	0.00090	0.00023
17	$\Theta_1$	0.00000	0.00000	0.00010	0.00100	0.00240	0.00103	0.00031
18	$\Theta_1$	0.00000	0.00000	0.00043	0.00113	0.00253	0.00117	0.00047

19	$\Theta_1$	0.00000	0.00000	0.00030	0.00107	0.00247	0.00110	0.00039
20	$\Theta_1$	0.00000	0.00000	0.00003	0.00087	0.00220	0.00090	0.00023
21	$\Theta_1$	0.00000	0.00000	0.00003	0.00087	0.00220	0.00090	0.00023
22	$\Theta_1$	0.00000	0.00000	0.00003	0.00087	0.00220	0.00090	0.00023
23	$\Theta_1$	0.00000	0.00000	0.00003	0.00087	0.00220	0.00090	0.00023
24	$\Theta_1$	0.00000	0.00000	0.00043	0.00113	0.00253	0.00117	0.00044
25	$\Theta_1$	0.00000	0.00000	0.00003	0.00087	0.00220	0.00090	0.00023
26	$\Theta_1$	0.00000	0.00000	0.00003	0.00100	0.00233	0.00103	0.00027
27	$\Theta_1$	0.00000	0.00000	0.00003	0.00087	0.00220	0.00090	0.00023
28	$\Theta_1$	0.00000	0.00000	0.00003	0.00087	0.00220	0.00090	0.00023
29	$\Theta_1$	0.00000	0.00000	0.00003	0.00093	0.00227	0.00097	0.00025
30	$\Theta_1$	0.00000	0.00000	0.00003	0.00087	0.00220	0.00090	0.00023
31	$\Theta_1$	0.00000	0.00067	0.00157	0.00240	0.00387	0.00183	0.00158
32	$\Theta_1$	0.00000	0.00000	0.00003	0.00087	0.00220	0.00090	0.00023
33	$\Theta_1$	0.00000	0.00000	0.00003	0.00087	0.00220	0.00090	0.00023
34	$\Theta_1$	0.00000	0.00053	0.00143	0.00227	0.00373	0.00177	0.00148
35	$\Theta_1$	0.00000	0.00000	0.00003	0.00093	0.00233	0.00097	0.00027
36	$\Theta_1$	0.00000	0.00000	0.00043	0.00113	0.00253	0.00117	0.00044
37	$\Theta_1$	0.00000	0.00000	0.00003	0.00087	0.00220	0.00090	0.00023
38	$\Theta_1$	0.00000	0.00000	0.00003	0.00087	0.00220	0.00090	0.00023
39	$\Theta_1$	0.00000	0.00000	0.00003	0.00087	0.00220	0.00090	0.00023
40	$\Theta_1$	0.00000	0.00000	0.00030	0.00107	0.00247	0.00110	0.00036
41	$\Theta_1$	0.00000	0.00000	0.00003	0.00087	0.00220	0.00090	0.00023



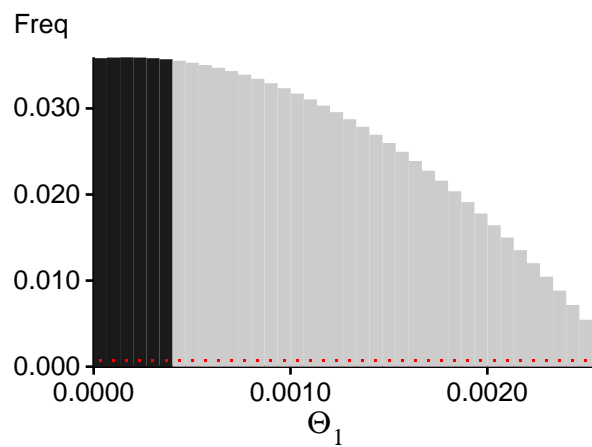
Locus	Parameter	2.5%	25.0%	Mode	75.0%	97.5%	Median	Mean
42	$\Theta_1$	0.00000	0.00000	0.00003	0.00093	0.00227	0.00097	0.00025
43	$\Theta_1$	0.00000	0.00000	0.00003	0.00087	0.00220	0.00090	0.00023
44	$\Theta_1$	0.00000	0.00000	0.00003	0.00087	0.00220	0.00090	0.00023
45	$\Theta_1$	0.00000	0.00013	0.00090	0.00160	0.00307	0.00143	0.00091
46	$\Theta_1$	0.00000	0.00000	0.00003	0.00087	0.00220	0.00090	0.00023
47	$\Theta_1$	0.03220	0.04347	0.04770	0.04907	0.05127	0.04377	0.06438
48	$\Theta_1$	0.00000	0.00000	0.00050	0.00113	0.00260	0.00117	0.00051
49	$\Theta_1$	0.00000	0.00000	0.00003	0.00087	0.00220	0.00090	0.00023
50	$\Theta_1$	0.00000	0.00000	0.00003	0.00100	0.00233	0.00103	0.00027
51	$\Theta_1$	0.04533	0.04687	0.04790	0.04887	0.05040	0.04797	0.08999
52	$\Theta_1$	0.00000	0.00000	0.00003	0.00087	0.00220	0.00090	0.00023
53	$\Theta_1$	0.00000	0.00000	0.00003	0.00087	0.00220	0.00090	0.00023
54	$\Theta_1$	0.00000	0.00000	0.00003	0.00087	0.00220	0.00090	0.00023
55	$\Theta_1$	0.00000	0.00000	0.00003	0.00087	0.00220	0.00090	0.00023
56	$\Theta_1$	0.00000	0.00000	0.00003	0.00087	0.00220	0.00090	0.00023
57	$\Theta_1$	0.00000	0.00000	0.00003	0.00087	0.00220	0.00090	0.00023
58	$\Theta_1$	0.00000	0.00000	0.00003	0.00087	0.00220	0.00090	0.00023
59	$\Theta_1$	0.00273	0.00360	0.00657	0.01080	0.01327	0.00743	0.00799
60	$\Theta_1$	0.00000	0.00000	0.00003	0.00087	0.00220	0.00090	0.00023
61	$\Theta_1$	0.00000	0.00000	0.00003	0.00087	0.00220	0.00090	0.00023

62	$\Theta_1$	0.00000	0.00000	0.00003	0.00087	0.00220	0.00090	0.00023
63	$\Theta_1$	0.00000	0.00000	0.00003	0.00087	0.00220	0.00090	0.00023
64	$\Theta_1$	0.00000	0.00000	0.00003	0.00087	0.00220	0.00090	0.00023
65	$\Theta_1$	0.00000	0.00000	0.00003	0.00087	0.00220	0.00090	0.00023
66	$\Theta_1$	0.00000	0.00000	0.00003	0.00087	0.00220	0.00090	0.00023
67	$\Theta_1$	0.00000	0.00000	0.00003	0.00087	0.00220	0.00090	0.00023
68	$\Theta_1$	0.00000	0.00000	0.00003	0.00087	0.00220	0.00090	0.00023
69	$\Theta_1$	0.00000	0.00000	0.00010	0.00107	0.00240	0.00110	0.00033
70	$\Theta_1$	0.00000	0.00000	0.00003	0.00087	0.00220	0.00090	0.00023
71	$\Theta_1$	0.00000	0.00000	0.00003	0.00087	0.00220	0.00090	0.00023
72	$\Theta_1$	0.00000	0.00000	0.00003	0.00087	0.00220	0.00090	0.00023
73	$\Theta_1$	0.00000	0.00000	0.00003	0.00087	0.00220	0.00090	0.00023
74	$\Theta_1$	0.00000	0.00000	0.00003	0.00087	0.00220	0.00090	0.00023
75	$\Theta_1$	0.00000	0.00000	0.00003	0.00087	0.00220	0.00090	0.00023
76	$\Theta_1$	0.00000	0.00000	0.00003	0.00087	0.00220	0.00090	0.00023
77	$\Theta_1$	0.00000	0.00000	0.00003	0.00100	0.00233	0.00103	0.00030
78	$\Theta_1$	0.00000	0.00000	0.00003	0.00087	0.00220	0.00090	0.00023
79	$\Theta_1$	0.00000	0.00000	0.00003	0.00100	0.00233	0.00103	0.00027
80	$\Theta_1$	0.00000	0.00000	0.00003	0.00087	0.00220	0.00090	0.00023
81	$\Theta_1$	0.00060	0.00213	0.00290	0.00360	0.00507	0.00310	0.00315
82	$\Theta_1$	0.00000	0.00000	0.00003	0.00093	0.00227	0.00097	0.00026
83	$\Theta_1$	0.00000	0.00000	0.00023	0.00107	0.00240	0.00110	0.00033
84	$\Theta_1$	0.00280	0.00560	0.00763	0.01007	0.01747	0.00877	0.00943

Locus	Parameter	2.5%	25.0%	Mode	75.0%	97.5%	Median	Mean
85	$\Theta_1$	0.00000	0.00000	0.00003	0.00087	0.00220	0.00090	0.00023
86	$\Theta_1$	0.00000	0.00000	0.00003	0.00087	0.00220	0.00090	0.00023
87	$\Theta_1$	0.00000	0.00000	0.00003	0.00087	0.00220	0.00090	0.00023
88	$\Theta_1$	0.00000	0.00000	0.00003	0.00087	0.00220	0.00090	0.00023
89	$\Theta_1$	0.00000	0.00000	0.00003	0.00087	0.00220	0.00090	0.00023
90	$\Theta_1$	0.00000	0.00000	0.00003	0.00087	0.00220	0.00090	0.00023
91	$\Theta_1$	0.00000	0.00000	0.00017	0.00107	0.00240	0.00110	0.00032
92	$\Theta_1$	0.00000	0.00000	0.00003	0.00087	0.00220	0.00090	0.00023
93	$\Theta_1$	0.00000	0.00000	0.00003	0.00087	0.00220	0.00090	0.00023
94	$\Theta_1$	0.00000	0.00000	0.00003	0.00087	0.00220	0.00090	0.00023
95	$\Theta_1$	0.00000	0.00000	0.00003	0.00100	0.00233	0.00103	0.00029
96	$\Theta_1$	0.02560	0.03633	0.04123	0.04787	0.05060	0.03930	0.05088
97	$\Theta_1$	0.00000	0.00000	0.00003	0.00087	0.00220	0.00090	0.00023
98	$\Theta_1$	0.00000	0.00000	0.00003	0.00100	0.00233	0.00103	0.00029
99	$\Theta_1$	0.00000	0.00000	0.00003	0.00087	0.00220	0.00090	0.00022
100	$\Theta_1$	0.00000	0.00000	0.00003	0.00087	0.00220	0.00090	0.00023
All	$\Theta_1$	0.00000	0.00000	0.00017	0.00040	0.00040	0.00103	0.00017
Citation suggestions:								
Beerli P., 2006. Comparison of Bayesian and maximum-likelihood inference of population genetic parameters. <i>Bioinformatics</i> 22:341-345								
Beerli P., 2007. Estimation of the population scaled mutation rate from microsatellite data, <i>Genetics</i> , 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	-14122.04	-13773.37	-13776.40	-13870.06
2	-14123.27	-13772.61	-13775.95	-13869.18
3	-14608.95	-14249.71	-14281.44	-14350.97
4	-14123.37	-13773.92	-13777.61	-13869.65
5	-14120.68	-13772.12	-13775.87	-13869.22
6	-14120.85	-13771.64	-13775.60	-13867.85
7	-14123.26	-13773.79	-13776.65	-13869.82
8	-14125.44	-13774.28	-13777.38	-13870.34
9	-14121.58	-13771.35	-13774.48	-13866.79
10	-20693.09	-17973.43	-17611.82	-17662.28
11	-14123.10	-13773.82	-13777.79	-13870.06
12	-14120.31	-13770.41	-13774.10	-13866.63
13	-14120.41	-13772.81	-13776.54	-13869.77
14	-14125.41	-13774.31	-13777.10	-13870.13
15	-14121.03	-13772.80	-13775.78	-13870.16
16	-14124.27	-13773.36	-13776.65	-13869.18
17	-14148.57	-13799.04	-13806.12	-13894.48
18	-14297.55	-13915.65	-13929.56	-14007.52
19	-14156.40	-13809.02	-13820.54	-13905.93
20	-14119.14	-13770.58	-13774.20	-13868.16
21	-14123.35	-13774.13	-13777.84	-13870.55
22	-14121.52	-13770.71	-13773.83	-13866.50
23	-14125.17	-13774.05	-13777.10	-13870.62
24	-14193.74	-13845.44	-13860.76	-13941.84
25	-14122.06	-13774.04	-13778.39	-13870.33
26	-14145.80	-13793.10	-13799.14	-13889.09
27	-14124.13	-13773.20	-13775.73	-13869.23
28	-14124.80	-13774.24	-13777.37	-13870.58
29	-14133.82	-13785.59	-13788.94	-13880.49

30	-14123.36	-13773.89	-13776.76	-13870.34
31	-14483.06	-14110.38	-14139.91	-14205.72
32	-14122.21	-13773.92	-13777.77	-13870.02
33	-14122.04	-13773.04	-13776.19	-13869.66
34	-14471.52	-14088.71	-14115.82	-14182.35
35	-14133.76	-13784.63	-13790.49	-13881.35
36	-14271.11	-13897.19	-13911.92	-13990.57
37	-14121.50	-13773.01	-13777.28	-13869.37
38	-14124.11	-13772.99	-13776.12	-13869.21
39	-14122.12	-13773.03	-13776.74	-13869.32
40	-14171.57	-13819.10	-13828.51	-13915.79
41	-14123.21	-13773.41	-13776.84	-13869.61
42	-14138.79	-13786.81	-13789.59	-13881.07
43	-14121.91	-13773.77	-13777.46	-13870.36
44	-14123.70	-13773.50	-13776.62	-13869.43
45	-14272.20	-13920.29	-13944.22	-14016.85
46	-14123.15	-13773.23	-13775.66	-13869.21
47	-37039.93	-26600.69	-24869.33	-24902.45
48	-14228.12	-13873.08	-13891.80	-13969.57
49	-14120.89	-13772.66	-13776.01	-13869.71
50	-14142.49	-13790.84	-13797.60	-13886.96
51	-33730.37	-30195.87	-29850.08	-29871.81
52	-14120.86	-13772.15	-13775.34	-13868.50
53	-14122.47	-13772.47	-13775.93	-13868.51
54	-14124.28	-13774.15	-13777.44	-13870.06
55	-14121.54	-13772.87	-13776.26	-13870.26
56	-14123.52	-13773.27	-13776.71	-13869.54
57	-14125.41	-13774.53	-13778.02	-13871.40
58	-14121.44	-13771.21	-13774.74	-13867.10
59	-17955.85	-16794.29	-16716.33	-16769.25
60	-14121.40	-13772.35	-13776.14	-13869.18
61	-14122.86	-13772.65	-13776.10	-13868.49
62	-14119.20	-13769.73	-13773.06	-13867.16
63	-14120.67	-13773.18	-13777.21	-13869.58
64	-14121.79	-13773.70	-13776.83	-13871.03
65	-14121.93	-13773.43	-13777.34	-13870.17
66	-14119.27	-13771.19	-13774.75	-13867.83
67	-14121.38	-13772.95	-13776.03	-13870.56
68	-14120.69	-13772.15	-13775.08	-13868.03
69	-14141.61	-13793.88	-13803.19	-13891.46
70	-14121.00	-13773.10	-13776.72	-13869.31
71	-14124.41	-13774.41	-13777.93	-13874.64
72	-14127.58	-13774.52	-13777.36	-13869.83
73	-14117.62	-13769.77	-13772.70	-13866.29
74	-14121.54	-13772.78	-13773.90	-13869.10

75	-14123.91	-13774.10	-13777.78	-13870.39
76	-14122.60	-13773.39	-13776.52	-13869.57
77	-14163.06	-13811.39	-13819.48	-13908.44
78	-14123.14	-13772.40	-13775.51	-13868.37
79	-14135.07	-13785.51	-13791.10	-13881.60
80	-14120.38	-13771.93	-13775.28	-13868.44
81	-14553.03	-14201.11	-14240.73	-14301.23
82	-14131.64	-13784.65	-13788.58	-13882.32
83	-14183.75	-13826.20	-13834.96	-13920.67
84	-15259.56	-14878.88	-14930.96	-14981.20
85	-14122.58	-13773.47	-13776.91	-13869.46
86	-14121.23	-13771.14	-13774.17	-13867.15
87	-14126.94	-13774.67	-13778.20	-13870.64
88	-14122.43	-13773.88	-13777.77	-13871.19
89	-14124.49	-13774.32	-13777.36	-13872.29
90	-14122.61	-13772.94	-13776.35	-13869.15
91	-14172.26	-13816.47	-13823.95	-13912.67
92	-14119.51	-13771.42	-13775.00	-13869.23
93	-14122.07	-13771.70	-13775.58	-13867.62
94	-14122.58	-13774.00	-13777.96	-13870.29
95	-14169.37	-13812.64	-13821.59	-13908.25
96	-35496.64	-25260.00	-23547.34	-23585.51
97	-14122.30	-13773.71	-13777.71	-13871.85
98	-14155.38	-13805.74	-13813.38	-13902.48
99	-14120.63	-13772.48	-13776.11	-13871.09
100	-14121.80	-13773.97	-13777.58	-13870.69
All	-1489910.96	-1428432.75	-1424815.74	-1433566.61
(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 = 510.581572]				
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
$\Theta_1$	44773313/399978944	0.11194
Genealogies	1047317148/1600021056	0.65456

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

Parameter	Autocorrelation	Effective Sampe Size
$\Theta_1$	0.09434	8337250.83
Genealogies	0.12527	7896825.52

## *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