

# 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 09:22:39 2017

Program finished at Sun Aug 13 10:02:35 2017 [Runtime:0000:00:39:56]



## 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)

3719965653

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

1000000.00	4 chains with temperatures	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_1.0
Posterior distribution raw histogram file:	bayesfile
Raw data from the MCMC run:	bayesallfile_0.6_1.0
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]
10	1	Jukes-Cantor	[Basefreq: =0.25]
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12	1	Jukes-Cantor	[Basefreq: =0.25]
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45	1	Jukes-Cantor	[Basefreq: =0.25]
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50	1	Jukes-Cantor	[Basefreq: =0.25]
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80	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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27	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
	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
	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	$\Theta_1$	0.00000	0.00000	0.00070	0.00133	0.00280	0.00130	0.00069
2	$\Theta_1$	0.00000	0.00000	0.00030	0.00107	0.00247	0.00110	0.00039
3	$\Theta_1$	0.00000	0.00000	0.00043	0.00113	0.00253	0.00117	0.00046
4	$\Theta_1$	0.00000	0.00000	0.00003	0.00093	0.00227	0.00097	0.00025
5	$\Theta_1$	0.00000	0.00000	0.00043	0.00113	0.00253	0.00117	0.00046
6	$\Theta_1$	0.00000	0.00000	0.00037	0.00107	0.00247	0.00110	0.00038
7	$\Theta_1$	0.00000	0.00000	0.00043	0.00113	0.00253	0.00117	0.00046
8	$\Theta_1$	0.00000	0.00000	0.00050	0.00113	0.00260	0.00117	0.00052
9	$\Theta_1$	0.00000	0.00000	0.00003	0.00087	0.00220	0.00090	0.00023
10	$\Theta_1$	0.00000	0.00000	0.00037	0.00107	0.00247	0.00110	0.00038
11	$\Theta_1$	0.00000	0.00073	0.00170	0.00253	0.00413	0.00197	0.00173
12	$\Theta_1$	0.00000	0.00000	0.00017	0.00107	0.00240	0.00110	0.00033
13	$\Theta_1$	0.00000	0.00000	0.00003	0.00100	0.00233	0.00103	0.00027
14	$\Theta_1$	0.00000	0.00000	0.00030	0.00107	0.00240	0.00110	0.00035
15	$\Theta_1$	0.00000	0.00013	0.00090	0.00160	0.00307	0.00143	0.00092
16	$\Theta_1$	0.00000	0.00000	0.00010	0.00100	0.00240	0.00103	0.00031
17	$\Theta_1$	0.00000	0.00013	0.00083	0.00153	0.00300	0.00137	0.00086
18	$\Theta_1$	0.00000	0.00013	0.00090	0.00160	0.00313	0.00143	0.00095

19	$\Theta_1$	0.00000	0.00113	0.00217	0.00313	0.00493	0.00237	0.00228
20	$\Theta_1$	0.00000	0.00013	0.00090	0.00160	0.00307	0.00143	0.00093
21	$\Theta_1$	0.00000	0.00000	0.00043	0.00113	0.00253	0.00117	0.00046
22	$\Theta_1$	0.00000	0.00000	0.00003	0.00100	0.00233	0.00103	0.00027
23	$\Theta_1$	0.00000	0.00000	0.00037	0.00107	0.00247	0.00110	0.00038
24	$\Theta_1$	0.00000	0.00000	0.00070	0.00133	0.00287	0.00130	0.00073
25	$\Theta_1$	0.00000	0.00000	0.00003	0.00093	0.00227	0.00097	0.00025
26	$\Theta_1$	0.00000	0.00040	0.00123	0.00200	0.00347	0.00163	0.00126
27	$\Theta_1$	0.00000	0.00000	0.00037	0.00113	0.00253	0.00117	0.00042
28	$\Theta_1$	0.00000	0.00000	0.00030	0.00107	0.00247	0.00110	0.00038
29	$\Theta_1$	0.00000	0.00000	0.00063	0.00127	0.00273	0.00123	0.00066
30	$\Theta_1$	0.00000	0.00073	0.00170	0.00253	0.00407	0.00197	0.00173
31	$\Theta_1$	0.00000	0.00013	0.00090	0.00160	0.00307	0.00143	0.00092
32	$\Theta_1$	0.00000	0.00020	0.00097	0.00167	0.00320	0.00150	0.00101
33	$\Theta_1$	0.00000	0.00000	0.00003	0.00100	0.00233	0.00103	0.00028
34	$\Theta_1$	0.00380	0.00693	0.00923	0.01213	0.02120	0.01063	0.01153
35	$\Theta_1$	0.00000	0.00000	0.00003	0.00087	0.00220	0.00090	0.00023
36	$\Theta_1$	0.00000	0.00040	0.00123	0.00200	0.00347	0.00163	0.00127
37	$\Theta_1$	0.00000	0.00000	0.00057	0.00120	0.00267	0.00123	0.00056
38	$\Theta_1$	0.00000	0.00133	0.00243	0.00347	0.00527	0.00263	0.00257
39	$\Theta_1$	0.00000	0.00033	0.00117	0.00187	0.00333	0.00157	0.00117
40	$\Theta_1$	0.00000	0.00000	0.00050	0.00113	0.00260	0.00117	0.00052
41	$\Theta_1$	0.00000	0.00000	0.00010	0.00107	0.00240	0.00110	0.00033



Locus	Parameter	2.5%	25.0%	Mode	75.0%	97.5%	Median	Mean
42	$\Theta_1$	0.00000	0.00140	0.00257	0.00360	0.00560	0.00277	0.00275
43	$\Theta_1$	0.00000	0.00000	0.00023	0.00107	0.00240	0.00110	0.00034
44	$\Theta_1$	0.00000	0.00067	0.00157	0.00240	0.00387	0.00183	0.00159
45	$\Theta_1$	0.00000	0.00000	0.00037	0.00107	0.00247	0.00110	0.00036
46	$\Theta_1$	0.00000	0.00000	0.00003	0.00093	0.00227	0.00097	0.00025
47	$\Theta_1$	0.00000	0.00000	0.00003	0.00100	0.00233	0.00103	0.00027
48	$\Theta_1$	0.00000	0.00000	0.00003	0.00100	0.00233	0.00103	0.00027
49	$\Theta_1$	0.00000	0.00000	0.00003	0.00100	0.00233	0.00103	0.00027
50	$\Theta_1$	0.00000	0.00000	0.00057	0.00120	0.00267	0.00123	0.00057
51	$\Theta_1$	0.00000	0.00000	0.00043	0.00113	0.00253	0.00117	0.00043
52	$\Theta_1$	0.00000	0.00047	0.00130	0.00207	0.00353	0.00163	0.00130
53	$\Theta_1$	0.00000	0.00000	0.00050	0.00120	0.00260	0.00123	0.00053
54	$\Theta_1$	0.00267	0.00540	0.00730	0.00960	0.01667	0.00837	0.00900
55	$\Theta_1$	0.00313	0.00613	0.00817	0.01080	0.01940	0.00943	0.01019
56	$\Theta_1$	0.00000	0.00000	0.00063	0.00120	0.00267	0.00123	0.00062
57	$\Theta_1$	0.00000	0.00000	0.00023	0.00107	0.00247	0.00110	0.00036
58	$\Theta_1$	0.00000	0.00167	0.00290	0.00393	0.00613	0.00310	0.00311
59	$\Theta_1$	0.00000	0.00000	0.00003	0.00087	0.00220	0.00090	0.00022
60	$\Theta_1$	0.00787	0.00980	0.01277	0.01673	0.02133	0.01490	0.01624
61	$\Theta_1$	0.00000	0.00000	0.00070	0.00133	0.00280	0.00130	0.00068

62	$\Theta_1$	0.00047	0.00247	0.00383	0.00513	0.00853	0.00417	0.00435
63	$\Theta_1$	0.00000	0.00000	0.00037	0.00113	0.00253	0.00117	0.00042
64	$\Theta_1$	0.00000	0.00000	0.00063	0.00127	0.00280	0.00130	0.00066
65	$\Theta_1$	0.00000	0.00000	0.00057	0.00120	0.00267	0.00123	0.00057
66	$\Theta_1$	0.00000	0.00000	0.00037	0.00107	0.00247	0.00110	0.00036
67	$\Theta_1$	0.00000	0.00000	0.00030	0.00107	0.00247	0.00110	0.00038
68	$\Theta_1$	0.00000	0.00000	0.00043	0.00113	0.00253	0.00117	0.00045
69	$\Theta_1$	0.00000	0.00000	0.00023	0.00107	0.00240	0.00110	0.00034
70	$\Theta_1$	0.00000	0.00000	0.00003	0.00100	0.00233	0.00103	0.00028
71	$\Theta_1$	0.00000	0.00000	0.00037	0.00107	0.00247	0.00110	0.00038
72	$\Theta_1$	0.00000	0.00000	0.00037	0.00107	0.00247	0.00110	0.00040
73	$\Theta_1$	0.00000	0.00040	0.00123	0.00200	0.00347	0.00163	0.00123
74	$\Theta_1$	0.00073	0.00293	0.00437	0.00580	0.00967	0.00477	0.00503
75	$\Theta_1$	0.00087	0.00300	0.00450	0.00593	0.01000	0.00497	0.00520
76	$\Theta_1$	0.00000	0.00000	0.00057	0.00120	0.00267	0.00123	0.00056
77	$\Theta_1$	0.00000	0.00000	0.00043	0.00113	0.00253	0.00117	0.00045
78	$\Theta_1$	0.00500	0.00860	0.01130	0.01487	0.02627	0.01323	0.01437
79	$\Theta_1$	0.00000	0.00053	0.00137	0.00220	0.00373	0.00177	0.00142
80	$\Theta_1$	0.00000	0.00127	0.00243	0.00340	0.00533	0.00257	0.00254
81	$\Theta_1$	0.00000	0.00027	0.00103	0.00180	0.00320	0.00150	0.00106
82	$\Theta_1$	0.00000	0.00000	0.00037	0.00107	0.00247	0.00110	0.00039
83	$\Theta_1$	0.00000	0.00020	0.00097	0.00167	0.00307	0.00143	0.00094
84	$\Theta_1$	0.00000	0.00000	0.00057	0.00120	0.00260	0.00123	0.00054

Locus	Parameter	2.5%	25.0%	Mode	75.0%	97.5%	Median	Mean
85	$\Theta_1$	0.00000	0.00033	0.00117	0.00187	0.00333	0.00157	0.00115
86	$\Theta_1$	0.00000	0.00000	0.00037	0.00113	0.00247	0.00117	0.00040
87	$\Theta_1$	0.00000	0.00000	0.00037	0.00113	0.00247	0.00117	0.00040
88	$\Theta_1$	0.00000	0.00000	0.00063	0.00127	0.00273	0.00123	0.00065
89	$\Theta_1$	0.00987	0.01287	0.01750	0.02467	0.03420	0.02043	0.02244
90	$\Theta_1$	0.03207	0.04267	0.04763	0.04940	0.05133	0.04397	0.06545
91	$\Theta_1$	0.00000	0.00000	0.00003	0.00100	0.00233	0.00103	0.00028
92	$\Theta_1$	0.00000	0.00000	0.00003	0.00100	0.00233	0.00103	0.00028
93	$\Theta_1$	0.00000	0.00000	0.00003	0.00093	0.00227	0.00097	0.00025
94	$\Theta_1$	0.00000	0.00000	0.00037	0.00113	0.00247	0.00117	0.00040
95	$\Theta_1$	0.00000	0.00000	0.00003	0.00100	0.00233	0.00103	0.00028
96	$\Theta_1$	0.00000	0.00000	0.00063	0.00127	0.00273	0.00130	0.00066
97	$\Theta_1$	0.00000	0.00000	0.00050	0.00113	0.00260	0.00117	0.00051
98	$\Theta_1$	0.00000	0.00000	0.00003	0.00100	0.00233	0.00103	0.00028
99	$\Theta_1$	0.00000	0.00000	0.00017	0.00107	0.00240	0.00110	0.00034
100	$\Theta_1$	0.00000	0.00000	0.00003	0.00100	0.00233	0.00103	0.00028
All	$\Theta_1$	0.00000	0.00000	0.00037	0.00107	0.00240	0.00110	0.00037

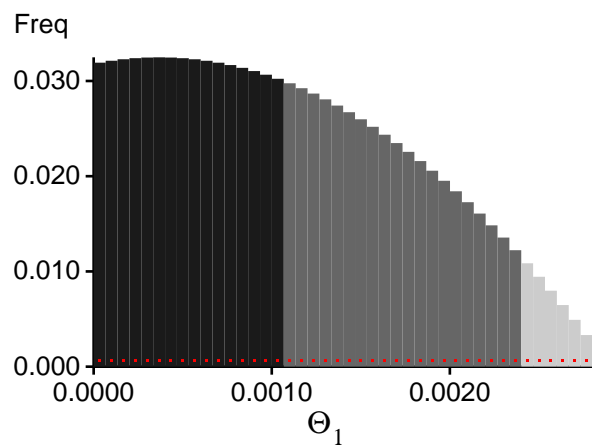
Citation suggestions:

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	-14237.02	-13884.35	-13907.09	-13985.12
2	-14169.57	-13822.46	-13831.51	-13918.54
3	-14235.68	-13879.41	-13895.35	-13973.90
4	-14136.84	-13786.73	-13790.04	-13882.27
5	-14202.41	-13851.62	-13863.67	-13946.60
6	-14226.75	-13860.78	-13874.42	-13955.70
7	-14179.11	-13832.74	-13846.32	-13930.53
8	-14274.23	-13902.15	-13918.98	-13995.88
9	-14118.86	-13772.99	-13777.29	-13869.89
10	-14242.94	-13866.69	-13878.01	-13958.79
11	-14531.86	-14150.67	-14180.20	-14244.64
12	-14147.24	-13798.28	-13807.49	-13894.82
13	-14148.06	-13794.16	-13799.18	-13889.86
14	-14211.23	-13846.63	-13858.78	-13941.80
15	-14311.59	-13950.16	-13974.66	-14046.88
16	-14161.62	-13813.59	-13822.47	-13910.17
17	-14339.97	-13970.36	-13993.80	-14064.91
18	-14274.19	-13922.03	-13947.72	-14019.77
19	-14494.78	-14132.67	-14166.33	-14229.63
20	-14285.50	-13930.87	-13954.29	-14028.87
21	-14220.36	-13858.97	-13873.03	-13955.26
22	-14133.50	-13783.95	-13789.69	-13880.88
23	-14203.31	-13854.72	-13870.15	-13951.09
24	-14293.19	-13925.24	-13946.50	-14019.83
25	-14137.22	-13786.88	-13789.52	-13882.87
26	-14626.25	-14212.15	-14233.93	-14301.62
27	-14169.59	-13820.44	-13830.52	-13915.55
28	-14180.16	-13827.92	-13839.43	-13925.11
29	-14443.27	-14020.08	-14031.25	-14105.33

30	-14598.47	-14189.71	-14214.94	-14279.38
31	-14345.57	-14000.29	-14028.98	-14099.33
32	-14278.79	-13928.65	-13953.42	-14024.77
33	-14133.09	-13784.16	-13790.44	-13880.99
34	-15837.63	-15366.80	-15405.71	-15457.75
35	-14123.51	-13773.40	-13776.49	-13869.53
36	-14517.64	-14114.45	-14137.22	-14204.37
37	-14307.63	-13934.40	-13952.59	-14028.26
38	-15221.64	-14830.57	-14867.70	-14929.87
39	-14448.61	-14101.28	-14133.24	-14200.53
40	-14225.85	-13869.13	-13884.72	-13964.76
41	-14146.36	-13798.12	-13806.19	-13895.00
42	-15091.67	-14575.59	-14588.81	-14649.51
43	-14179.25	-13825.51	-13836.85	-13921.42
44	-14597.45	-14183.12	-14206.31	-14273.93
45	-14215.72	-13854.00	-13866.98	-13948.90
46	-14139.85	-13787.58	-13790.79	-13883.56
47	-14148.93	-13795.46	-13800.90	-13893.24
48	-14129.52	-13781.95	-13788.20	-13878.39
49	-14133.76	-13786.51	-13792.57	-13885.38
50	-14225.54	-13873.02	-13892.26	-13969.81
51	-14241.49	-13874.15	-13887.63	-13967.52
52	-14550.70	-14133.10	-14153.07	-14221.15
53	-14299.46	-13920.39	-13935.60	-14012.36
54	-16304.23	-15695.68	-15713.49	-15766.85
55	-16498.20	-15875.80	-15892.39	-15943.01
56	-14400.11	-13992.31	-14005.70	-14080.19
57	-14157.59	-13809.89	-13819.10	-13906.38
58	-15196.29	-14733.27	-14759.29	-14819.83
59	-14124.24	-13774.11	-13777.71	-13870.31
60	-22996.16	-19264.16	-18725.99	-18772.27
61	-14318.09	-13952.94	-13975.14	-14048.62
62	-14970.61	-14549.70	-14581.84	-14640.71
63	-14163.74	-13817.21	-13829.89	-13915.90
64	-14243.12	-13885.90	-13906.26	-13983.58
65	-14231.76	-13878.22	-13897.15	-13974.39
66	-14227.73	-13857.13	-13869.19	-13950.33
67	-14182.38	-13829.19	-13839.60	-13924.30
68	-14190.16	-13838.82	-13851.47	-13935.28
69	-14159.14	-13809.37	-13816.67	-13904.10
70	-14149.45	-13797.28	-13802.11	-13891.91
71	-14180.20	-13827.49	-13839.87	-13924.42
72	-14162.05	-13814.07	-13823.06	-13909.24
73	-14334.94	-13976.07	-14002.63	-14072.18
74	-14904.55	-14518.26	-14559.42	-14614.93

75	-15138.41	-14723.03	-14758.92	-14820.68
76	-14197.95	-13851.10	-13866.55	-13951.63
77	-14233.64	-13867.73	-13882.89	-13962.06
78	-15845.78	-15417.96	-15467.30	-15515.40
79	-14308.54	-13965.34	-13995.29	-14063.49
80	-14565.49	-14191.39	-14222.97	-14286.68
81	-14656.90	-14183.06	-14190.55	-14259.56
82	-14179.05	-13828.01	-13840.12	-13924.65
83	-14525.32	-14111.77	-14128.33	-14199.51
84	-14222.45	-13869.85	-13886.58	-13966.06
85	-14376.38	-14007.38	-14034.52	-14105.86
86	-14196.05	-13840.99	-13853.35	-13935.96
87	-14209.52	-13856.54	-13872.20	-13954.23
88	-14342.15	-13974.60	-13996.65	-14070.39
89	-24931.94	-20435.31	-19768.99	-19811.56
90	-33468.92	-26183.75	-25047.02	-25089.87
91	-14157.45	-13803.40	-13811.15	-13899.22
92	-14132.41	-13785.14	-13791.05	-13881.65
93	-14139.37	-13787.87	-13791.53	-13886.51
94	-14251.73	-13879.37	-13891.03	-13971.83
95	-14148.22	-13796.70	-13802.07	-13893.80
96	-14368.66	-13994.55	-14014.77	-14087.90
97	-14224.24	-13864.83	-13882.45	-13960.22
98	-14143.07	-13794.29	-13800.42	-13891.41
99	-14158.47	-13808.96	-13816.17	-13907.41
100	-14144.45	-13795.04	-13801.36	-13891.88
All	-1476480.89	-1424700.94	-1423930.61	-1431649.07
(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 = 354.875106]				
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
$\Theta_1$	76480965/400000561	0.19120
Genealogies	483195917/1599999439	0.30200

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

Parameter	Autocorrelation	Effective Sampe Size
$\Theta_1$	0.06879	8767672.58
Genealogies	0.11010	8197993.06

## *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