

# 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 03:48:36 2017

Program finished at Sun Aug 13 05:37:06 2017 [Runtime:0000:01:48:30]



## 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)

3067184943

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\_0.7

Posterior distribution raw histogram file:

bayesfile

Raw data from the MCMC run:

bayesallfile\_0.6\_0.7

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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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
24	10000
25	10000
26	10000
27	10000
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31	10000
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81	10000
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88	10000
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	
			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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	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	$\Theta_1$	0.00240	0.00240	0.00570	0.01087	0.01087	0.00710	0.00792
2	$\Theta_1$	0.00533	0.00887	0.01317	0.01887	0.02907	0.01643	0.01863
3	$\Theta_1$	0.00000	0.00207	0.00370	0.00547	0.01080	0.00450	0.00495
4	$\Theta_1$	0.00667	0.01113	0.01703	0.02487	0.03913	0.02043	0.02329
5	$\Theta_1$	0.00473	0.01047	0.01290	0.01673	0.03307	0.01703	0.01960
6	$\Theta_1$	0.00060	0.00333	0.00537	0.00813	0.01687	0.00683	0.00773
7	$\Theta_1$	0.00047	0.00307	0.00497	0.00747	0.01513	0.00623	0.00700
8	$\Theta_1$	0.00167	0.00807	0.00890	0.00967	0.02927	0.01117	0.01259
9	$\Theta_1$	0.00107	0.00273	0.00370	0.00473	0.00720	0.00450	0.00496
10	$\Theta_1$	0.00287	0.00840	0.00937	0.01047	0.02433	0.01217	0.01384
11	$\Theta_1$	0.00193	0.00547	0.00817	0.01207	0.02407	0.01037	0.01165
12	$\Theta_1$	0.00407	0.00933	0.01437	0.02080	0.04133	0.01790	0.02050
13	$\Theta_1$	0.00133	0.00447	0.00683	0.01007	0.02040	0.00863	0.00967
14	$\Theta_1$	0.00080	0.00353	0.00550	0.00813	0.01613	0.00683	0.00760
15	$\Theta_1$	0.00120	0.00387	0.00617	0.00913	0.01720	0.00777	0.00878
16	$\Theta_1$	0.00073	0.00353	0.00557	0.00827	0.01653	0.00697	0.00778
17	$\Theta_1$	0.00113	0.00753	0.00910	0.01080	0.03980	0.01237	0.01445
18	$\Theta_1$	0.00260	0.00393	0.00623	0.00933	0.01233	0.00790	0.00885

19	$\Theta_1$	0.00113	0.00247	0.00543	0.00993	0.01387	0.00670	0.00746
20	$\Theta_1$	0.00060	0.00333	0.00530	0.00787	0.01587	0.00663	0.00742
21	$\Theta_1$	0.00640	0.00867	0.01437	0.02347	0.03020	0.01983	0.02530
22	$\Theta_1$	0.00600	0.01087	0.01910	0.03467	0.05013	0.02370	0.02792
23	$\Theta_1$	0.00120	0.00427	0.00670	0.00987	0.02020	0.00843	0.00950
24	$\Theta_1$	0.00233	0.00353	0.00583	0.00907	0.01167	0.00723	0.00805
25	$\Theta_1$	0.00387	0.00640	0.00803	0.01013	0.01560	0.01017	0.01135
26	$\Theta_1$	0.00573	0.01060	0.01670	0.02493	0.04307	0.02050	0.02414
27	$\Theta_1$	0.00013	0.00247	0.00417	0.00620	0.01227	0.00510	0.00567
28	$\Theta_1$	0.00287	0.00353	0.00717	0.01360	0.01580	0.00977	0.01144
29	$\Theta_1$	0.00133	0.00400	0.00610	0.00893	0.01620	0.00757	0.00838
30	$\Theta_1$	0.00300	0.00587	0.00763	0.00980	0.01653	0.00970	0.01088
31	$\Theta_1$	0.00213	0.00593	0.00897	0.01300	0.02593	0.01117	0.01254
32	$\Theta_1$	0.00093	0.00287	0.00470	0.00713	0.01173	0.00597	0.00668
33	$\Theta_1$	0.00240	0.00640	0.00950	0.01387	0.02867	0.01197	0.01347
34	$\Theta_1$	0.00047	0.00300	0.00483	0.00713	0.01413	0.00597	0.00664
35	$\Theta_1$	0.00147	0.00480	0.00750	0.01120	0.02287	0.00963	0.01082
36	$\Theta_1$	0.00233	0.00533	0.00683	0.00853	0.01520	0.00850	0.00951
37	$\Theta_1$	0.00000	0.00207	0.00370	0.00547	0.01080	0.00450	0.00496
38	$\Theta_1$	0.00353	0.00553	0.01123	0.02173	0.03000	0.01417	0.01594
39	$\Theta_1$	0.00000	0.00213	0.00370	0.00553	0.01087	0.00450	0.00498
40	$\Theta_1$	0.00007	0.00247	0.00417	0.00627	0.01253	0.00517	0.00577
41	$\Theta_1$	0.00207	0.00380	0.00583	0.00860	0.01247	0.00723	0.00809



Locus	Parameter	2.5%	25.0%	Mode	75.0%	97.5%	Median	Mean
42	$\Theta_1$	0.00207	0.00547	0.00983	0.01713	0.03533	0.01383	0.01687
43	$\Theta_1$	0.00813	0.01440	0.01717	0.02113	0.03480	0.02217	0.02673
44	$\Theta_1$	0.00193	0.00380	0.00497	0.00627	0.00960	0.00617	0.00684
45	$\Theta_1$	0.00107	0.00400	0.00617	0.00900	0.01800	0.00763	0.00855
46	$\Theta_1$	0.00167	0.00240	0.00463	0.00767	0.00907	0.00577	0.00641
47	$\Theta_1$	0.00007	0.00247	0.00417	0.00627	0.01253	0.00517	0.00577
48	$\Theta_1$	0.00367	0.00780	0.01030	0.01320	0.02480	0.01270	0.01434
49	$\Theta_1$	0.00007	0.00240	0.00410	0.00613	0.01207	0.00503	0.00560
50	$\Theta_1$	0.00173	0.00500	0.00750	0.01087	0.02133	0.00930	0.01038
51	$\Theta_1$	0.00147	0.00360	0.00497	0.00653	0.01080	0.00610	0.00681
52	$\Theta_1$	0.00207	0.00453	0.00650	0.00887	0.01500	0.00817	0.00918
53	$\Theta_1$	0.00500	0.01000	0.01190	0.01393	0.02620	0.01463	0.01639
54	$\Theta_1$	0.00807	0.01140	0.01710	0.02733	0.03727	0.02250	0.02747
55	$\Theta_1$	0.00060	0.00333	0.00537	0.00813	0.01693	0.00683	0.00775
56	$\Theta_1$	0.00067	0.00333	0.00530	0.00780	0.01527	0.00657	0.00726
57	$\Theta_1$	0.01160	0.01713	0.02337	0.03313	0.04813	0.02803	0.03686
58	$\Theta_1$	0.00307	0.00567	0.00723	0.00893	0.01427	0.00903	0.01009
59	$\Theta_1$	0.00093	0.00380	0.00597	0.00873	0.01760	0.00743	0.00826
60	$\Theta_1$	0.00007	0.00247	0.00417	0.00627	0.01253	0.00517	0.00577
61	$\Theta_1$	0.00007	0.00240	0.00410	0.00607	0.01193	0.00503	0.00553

62	$\Theta_1$	0.00280	0.00427	0.00763	0.01307	0.01733	0.00957	0.01076
63	$\Theta_1$	0.00247	0.00247	0.00583	0.01140	0.01140	0.00737	0.00830
64	$\Theta_1$	0.00047	0.00300	0.00483	0.00720	0.01433	0.00597	0.00668
65	$\Theta_1$	0.00287	0.00500	0.00710	0.01007	0.01560	0.00970	0.01144
66	$\Theta_1$	0.00353	0.00967	0.01317	0.01733	0.03767	0.01683	0.01954
67	$\Theta_1$	0.00820	0.01520	0.01823	0.02347	0.04160	0.02297	0.02680
68	$\Theta_1$	0.00420	0.00820	0.01117	0.01533	0.02747	0.01397	0.01565
69	$\Theta_1$	0.00153	0.00340	0.00437	0.00553	0.00867	0.00550	0.00613
70	$\Theta_1$	0.00053	0.00307	0.00490	0.00720	0.01433	0.00603	0.00671
71	$\Theta_1$	0.00100	0.00427	0.00543	0.00680	0.01447	0.00670	0.00748
72	$\Theta_1$	0.00373	0.00440	0.00850	0.01567	0.01760	0.01150	0.01338
73	$\Theta_1$	0.00307	0.00807	0.00963	0.01127	0.02453	0.01190	0.01325
74	$\Theta_1$	0.00560	0.00920	0.01337	0.01900	0.03007	0.01650	0.01861
75	$\Theta_1$	0.00320	0.01100	0.01397	0.01767	0.04613	0.01757	0.02006
76	$\Theta_1$	0.00773	0.01260	0.01617	0.02187	0.03413	0.02023	0.02298
77	$\Theta_1$	0.00060	0.00327	0.00517	0.00767	0.01527	0.00643	0.00718
78	$\Theta_1$	0.00007	0.00240	0.00410	0.00607	0.01193	0.00497	0.00553
79	$\Theta_1$	0.00100	0.00387	0.00597	0.00887	0.01793	0.00757	0.00845
80	$\Theta_1$	0.00327	0.00327	0.00750	0.01473	0.01473	0.00937	0.01050
81	$\Theta_1$	0.00053	0.00313	0.00510	0.00760	0.01567	0.00643	0.00723
82	$\Theta_1$	0.00167	0.00447	0.00877	0.01627	0.03187	0.01170	0.01381
83	$\Theta_1$	0.00020	0.00253	0.00430	0.00633	0.01260	0.00530	0.00585
84	$\Theta_1$	0.00293	0.00667	0.00983	0.01420	0.02680	0.01230	0.01376

Locus	Parameter	2.5%	25.0%	Mode	75.0%	97.5%	Median	Mean
85	$\Theta_1$	0.00193	0.00373	0.00583	0.00873	0.01307	0.00737	0.00829
86	$\Theta_1$	0.00533	0.00780	0.01143	0.01660	0.02307	0.01437	0.01625
87	$\Theta_1$	0.00027	0.00273	0.00450	0.00667	0.01333	0.00557	0.00617
88	$\Theta_1$	0.00133	0.00427	0.00657	0.00953	0.01900	0.00817	0.00910
89	$\Theta_1$	0.00127	0.00427	0.00657	0.00967	0.01960	0.00830	0.00930
90	$\Theta_1$	0.00173	0.00513	0.00783	0.01147	0.02327	0.00990	0.01112
91	$\Theta_1$	0.00107	0.00400	0.00617	0.00907	0.01827	0.00770	0.00859
92	$\Theta_1$	0.00487	0.00853	0.01217	0.01760	0.02907	0.01690	0.02051
93	$\Theta_1$	0.00240	0.00680	0.00950	0.01340	0.02853	0.01210	0.01358
94	$\Theta_1$	0.00320	0.00480	0.00737	0.01073	0.01467	0.00923	0.01036
95	$\Theta_1$	0.00160	0.00487	0.00737	0.01067	0.02087	0.00910	0.01015
96	$\Theta_1$	0.00853	0.01480	0.02030	0.02627	0.04447	0.02410	0.02863
97	$\Theta_1$	0.00400	0.00820	0.00997	0.01187	0.02220	0.01290	0.01471
98	$\Theta_1$	0.00380	0.00773	0.00943	0.01140	0.02067	0.01170	0.01306
99	$\Theta_1$	0.00047	0.00300	0.00483	0.00720	0.01433	0.00603	0.00668
100	$\Theta_1$	0.00467	0.00980	0.01237	0.01607	0.03187	0.01690	0.02024
All	$\Theta_1$	0.00487	0.00613	0.00710	0.00800	0.00933	0.00717	0.00712

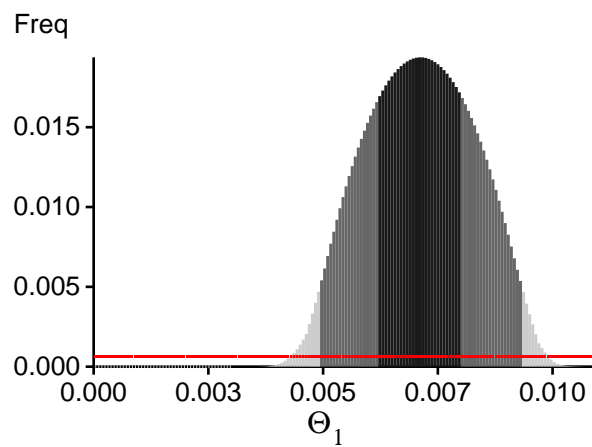
Citation suggestions:

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	-13961.62	-13784.37	-13826.89	-13913.10
2	-14721.89	-14402.46	-14441.97	-14512.50
3	-13910.60	-13738.15	-13775.14	-13869.55
4	-14291.99	-14096.04	-14157.78	-14225.22
5	-14440.50	-14187.50	-14236.66	-14308.20
6	-13943.40	-13771.30	-13816.44	-13904.24
7	-13945.92	-13771.04	-13813.24	-13901.34
8	-14215.48	-13972.71	-14015.39	-14092.28
9	-13905.32	-13733.34	-13769.99	-13863.29
10	-14540.29	-14238.18	-14273.41	-14349.80
11	-14014.38	-13828.64	-13880.19	-13957.49
12	-14439.30	-14172.78	-14218.25	-14289.78
13	-13989.82	-13813.41	-13859.39	-13941.89
14	-13986.14	-13805.49	-13849.61	-13934.91
15	-13957.36	-13784.78	-13831.17	-13916.24
16	-13964.18	-13784.44	-13828.00	-13913.58
17	-16197.03	-15739.63	-15763.90	-15839.43
18	-14253.33	-14017.44	-14056.03	-14139.00
19	-13977.06	-13790.86	-13833.80	-13919.93
20	-13950.51	-13775.83	-13816.42	-13904.62
21	-14645.69	-14433.08	-14487.64	-14562.45
22	-16991.13	-15662.39	-15527.80	-15593.32
23	-13972.07	-13797.48	-13842.71	-13926.68
24	-14032.84	-13835.69	-13877.86	-13962.03
25	-14063.64	-13868.13	-13917.23	-13995.31
26	-15277.11	-14767.22	-14777.21	-14848.83
27	-13922.58	-13750.00	-13787.43	-13880.47
28	-16995.81	-15618.36	-15460.11	-15538.58
29	-14016.00	-13822.21	-13866.63	-13951.15

30	-14007.50	-13829.36	-13879.13	-13958.63
31	-14022.33	-13841.87	-13892.73	-13971.02
32	-13933.35	-13761.32	-13803.61	-13891.88
33	-14039.02	-13863.82	-13919.01	-13995.09
34	-13967.67	-13794.59	-13836.69	-13925.44
35	-14281.94	-14086.65	-14137.42	-14219.19
36	-14183.46	-13945.18	-13984.47	-14065.62
37	-13909.81	-13737.08	-13773.80	-13866.79
38	-14274.54	-14035.64	-14083.11	-14157.42
39	-13910.10	-13737.72	-13773.85	-13867.70
40	-13921.42	-13749.70	-13788.87	-13881.02
41	-13995.59	-13806.33	-13849.60	-13933.79
42	-25974.11	-22713.96	-22268.61	-22357.35
43	-14362.91	-14150.55	-14205.41	-14277.93
44	-13957.32	-13781.11	-13823.21	-13910.54
45	-14011.10	-13818.74	-13862.92	-13945.93
46	-13938.23	-13763.34	-13802.95	-13891.61
47	-13922.47	-13750.59	-13790.21	-13880.94
48	-14117.62	-13914.19	-13966.91	-14040.42
49	-13924.43	-13749.81	-13786.92	-13878.82
50	-14058.69	-13863.34	-13911.83	-13990.72
51	-13971.84	-13798.83	-13842.07	-13929.77
52	-13970.53	-13797.88	-13843.73	-13927.66
53	-14192.01	-13974.52	-14026.94	-14099.21
54	-14733.98	-14481.19	-14537.06	-14605.58
55	-13944.12	-13772.83	-13817.35	-13903.37
56	-14037.75	-13836.55	-13877.04	-13962.98
57	-16548.66	-16223.99	-16285.53	-16352.59
58	-14021.12	-13830.07	-13876.70	-13958.18
59	-13986.13	-13804.61	-13848.29	-13932.34
60	-13921.64	-13749.77	-13789.13	-13880.48
61	-13925.47	-13750.74	-13787.07	-13879.63
62	-14021.21	-13839.96	-13889.51	-13968.48
63	-13968.46	-13792.66	-13837.94	-13923.27
64	-13951.48	-13771.60	-13812.43	-13900.28
65	-26253.43	-20647.02	-19736.36	-19811.06
66	-14145.38	-13956.70	-14008.89	-14087.20
67	-15023.29	-14569.69	-14590.53	-14657.74
68	-14210.17	-13970.26	-14018.74	-14089.96
69	-13929.84	-13757.78	-13797.13	-13888.24
70	-13997.73	-13806.90	-13847.06	-13934.54
71	-13994.14	-13806.72	-13849.92	-13934.39
72	-14939.28	-14550.85	-14571.89	-14649.45
73	-14386.10	-14072.98	-14103.48	-14181.17
74	-14129.09	-13931.83	-13988.04	-14059.85

75	-14111.19	-13925.08	-13981.82	-14055.27
76	-14324.99	-14110.38	-14168.48	-14237.07
77	-13973.09	-13790.89	-13833.38	-13919.66
78	-13920.56	-13745.96	-13781.51	-13874.19
79	-13972.94	-13794.75	-13840.98	-13924.72
80	-13999.92	-13817.44	-13866.06	-13945.91
81	-13948.80	-13775.29	-13816.29	-13904.50
82	-19753.70	-18525.44	-18434.95	-18507.97
83	-13938.71	-13761.38	-13800.17	-13891.54
84	-14076.06	-13898.06	-13952.73	-14028.27
85	-13971.04	-13795.28	-13840.46	-13925.79
86	-14101.19	-13911.75	-13967.63	-14040.56
87	-13940.57	-13768.73	-13808.58	-13898.62
88	-14018.08	-13826.12	-13871.29	-13952.92
89	-13998.51	-13818.04	-13864.15	-13946.77
90	-14010.31	-13835.88	-13885.86	-13965.56
91	-13988.22	-13803.21	-13848.74	-13931.61
92	-14934.24	-14649.08	-14694.66	-14768.49
93	-14027.48	-13851.21	-13903.09	-13980.87
94	-14016.03	-13827.98	-13876.18	-13956.04
95	-14140.92	-13917.48	-13959.43	-14039.95
96	-17712.36	-16224.52	-16067.49	-16131.09
97	-15354.45	-14679.29	-14649.07	-14723.84
98	-14337.53	-14045.98	-14081.26	-14158.56
99	-13948.67	-13771.68	-13813.65	-13903.55
100	-16158.13	-15462.11	-15441.27	-15511.86
All	-1457948.65	-1423118.27	-1425213.05	-1433337.19
(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 = 168.490386]				
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
$\Theta_1$	286665230/400021023	0.71663
Genealogies	515579144/1599978977	0.32224

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

Parameter	Autocorrelation	Effective Sample Size
$\Theta_1$	0.23676	6462019.70
Genealogies	0.06804	8858776.74

## *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