

# 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 40 compute nodes are available.

Program started at Mon Jul 24 14:46:08 2017

Program finished at Mon Jul 24 18:39:56 2017 [Runtime:0000:03:53:48]



## 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)

1400104014

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.0.8  
 Haplotyping is turned on: NO  
 Output file: outfile\_0.8\_0.5  
 Posterior distribution raw histogram file: bayesfile  
 Raw data from the MCMC run: bayesallfile\_0.8\_0.5  
 Print data: No  
 Print genealogies [only some for some data type]: None

## Data summary

Data file: infile.0.8  
 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]
11	1	Jukes-Cantor	[Basefreq: =0.25]
12	1	Jukes-Cantor	[Basefreq: =0.25]
13	1	Jukes-Cantor	[Basefreq: =0.25]
14	1	Jukes-Cantor	[Basefreq: =0.25]
15	1	Jukes-Cantor	[Basefreq: =0.25]
16	1	Jukes-Cantor	[Basefreq: =0.25]
17	1	Jukes-Cantor	[Basefreq: =0.25]
18	1	Jukes-Cantor	[Basefreq: =0.25]
19	1	Jukes-Cantor	[Basefreq: =0.25]
20	1	Jukes-Cantor	[Basefreq: =0.25]
21	1	Jukes-Cantor	[Basefreq: =0.25]
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28	1	Jukes-Cantor	[Basefreq: =0.25]
29	1	Jukes-Cantor	[Basefreq: =0.25]
30	1	Jukes-Cantor	[Basefreq: =0.25]
31	1	Jukes-Cantor	[Basefreq: =0.25]
32	1	Jukes-Cantor	[Basefreq: =0.25]
33	1	Jukes-Cantor	[Basefreq: =0.25]
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35	1	Jukes-Cantor	[Basefreq: =0.25]
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37	1	Jukes-Cantor	[Basefreq: =0.25]
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39	1	Jukes-Cantor	[Basefreq: =0.25]
40	1	Jukes-Cantor	[Basefreq: =0.25]
41	1	Jukes-Cantor	[Basefreq: =0.25]
42	1	Jukes-Cantor	[Basefreq: =0.25]
43	1	Jukes-Cantor	[Basefreq: =0.25]
44	1	Jukes-Cantor	[Basefreq: =0.25]
45	1	Jukes-Cantor	[Basefreq: =0.25]
46	1	Jukes-Cantor	[Basefreq: =0.25]
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48	1	Jukes-Cantor	[Basefreq: =0.25]
49	1	Jukes-Cantor	[Basefreq: =0.25]
50	1	Jukes-Cantor	[Basefreq: =0.25]
51	1	Jukes-Cantor	[Basefreq: =0.25]
52	1	Jukes-Cantor	[Basefreq: =0.25]
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54	1	Jukes-Cantor	[Basefreq: =0.25]
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61	1	Jukes-Cantor	[Basefreq: =0.25]
62	1	Jukes-Cantor	[Basefreq: =0.25]
63	1	Jukes-Cantor	[Basefreq: =0.25]
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69	1	Jukes-Cantor	[Basefreq: =0.25]
70	1	Jukes-Cantor	[Basefreq: =0.25]
71	1	Jukes-Cantor	[Basefreq: =0.25]
72	1	Jukes-Cantor	[Basefreq: =0.25]
73	1	Jukes-Cantor	[Basefreq: =0.25]
74	1	Jukes-Cantor	[Basefreq: =0.25]
75	1	Jukes-Cantor	[Basefreq: =0.25]
76	1	Jukes-Cantor	[Basefreq: =0.25]
77	1	Jukes-Cantor	[Basefreq: =0.25]
78	1	Jukes-Cantor	[Basefreq: =0.25]
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]
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
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24	10000
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26	10000
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28	10000
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79	10000
80	10000
81	10000
82	10000
83	10000
84	10000
85	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	
			13		10	
			14		10	
			15		10	
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			25		10	
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			31		10	
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			37		10	
			38		10	
			39		10	
			40		10	

41	10
42	10
43	10
44	10
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79	10
80	10
81	10
82	10
83	10
84	10
85	10

	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
	15	10
	16	10
	17	10
	18	10
	19	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

## *Bayesian Analysis: Posterior distribution table*

Locus	Parameter	2.5%	25.0%	Mode	75.0%	97.5%	Median	Mean
1	$\Theta_1$	0.03200	0.04353	0.04790	0.04980	0.05160	0.04470	0.08165
2	$\Theta_1$	0.02493	0.04033	0.04763	0.04947	0.05133	0.04170	0.07116
3	$\Theta_1$	0.02927	0.04287	0.04777	0.04960	0.05153	0.04357	0.07829
4	$\Theta_1$	0.02967	0.04267	0.04777	0.04967	0.05153	0.04390	0.07839
5	$\Theta_1$	0.02820	0.04160	0.04763	0.04947	0.05140	0.04290	0.07278
6	$\Theta_1$	0.03013	0.04260	0.04770	0.04960	0.05153	0.04383	0.07784
7	$\Theta_1$	0.02493	0.04040	0.04763	0.04940	0.05133	0.04170	0.07103
8	$\Theta_1$	0.03120	0.04340	0.04770	0.04967	0.05147	0.04457	0.07954
9	$\Theta_1$	0.03040	0.04300	0.04770	0.04967	0.05147	0.04417	0.07810
10	$\Theta_1$	0.03267	0.04407	0.04797	0.04993	0.05153	0.04517	0.08456
11	$\Theta_1$	0.03233	0.04400	0.04783	0.04980	0.05153	0.04517	0.08302
12	$\Theta_1$	0.02807	0.03447	0.04777	0.05060	0.05133	0.04290	0.07340
13	$\Theta_1$	0.03093	0.04300	0.04783	0.04973	0.05147	0.04417	0.07853
14	$\Theta_1$	0.02940	0.04267	0.04783	0.04967	0.05160	0.04390	0.07807
15	$\Theta_1$	0.02827	0.04293	0.04770	0.04933	0.05140	0.04310	0.07403
16	$\Theta_1$	0.02847	0.04227	0.04777	0.04967	0.05147	0.04350	0.07570
17	$\Theta_1$	0.02993	0.04300	0.04777	0.04960	0.05153	0.04423	0.07824
18	$\Theta_1$	0.02933	0.04213	0.04777	0.04960	0.05140	0.04343	0.07598

19	$\Theta_1$	0.02993	0.04367	0.04777	0.04940	0.05153	0.04383	0.07799
20	$\Theta_1$	0.02800	0.04200	0.04770	0.04960	0.05147	0.04330	0.07606
21	$\Theta_1$	0.03007	0.04280	0.04783	0.04967	0.05153	0.04403	0.07894
22	$\Theta_1$	0.03153	0.04347	0.04777	0.04967	0.05160	0.04470	0.08169
23	$\Theta_1$	0.02887	0.04233	0.04770	0.04960	0.05147	0.04363	0.07854
24	$\Theta_1$	0.02953	0.04360	0.04783	0.04940	0.05153	0.04377	0.07642
25	$\Theta_1$	0.02813	0.04180	0.04777	0.04967	0.05147	0.04303	0.07393
26	$\Theta_1$	0.03000	0.04400	0.04783	0.04953	0.05153	0.04417	0.07885
27	$\Theta_1$	0.03113	0.04347	0.04777	0.04967	0.05160	0.04470	0.08116
28	$\Theta_1$	0.03373	0.04413	0.04783	0.04967	0.05160	0.04537	0.08501
29	$\Theta_1$	0.03033	0.04287	0.04777	0.04960	0.05153	0.04417	0.07917
30	$\Theta_1$	0.02927	0.04333	0.04777	0.04947	0.05153	0.04350	0.07724
31	$\Theta_1$	0.03127	0.04360	0.04783	0.04987	0.05153	0.04470	0.08159
32	$\Theta_1$	0.03147	0.04313	0.04783	0.04967	0.05153	0.04443	0.08110
33	$\Theta_1$	0.03233	0.04507	0.04803	0.04967	0.05167	0.04523	0.08353
34	$\Theta_1$	0.02880	0.04227	0.04777	0.04960	0.05153	0.04357	0.07781
35	$\Theta_1$	0.02727	0.04167	0.04770	0.04967	0.05140	0.04290	0.07470
36	$\Theta_1$	0.02767	0.04193	0.04763	0.04947	0.05147	0.04323	0.07514
37	$\Theta_1$	0.03060	0.04420	0.04790	0.04947	0.05153	0.04437	0.07999
38	$\Theta_1$	0.02587	0.04080	0.04770	0.04960	0.05140	0.04210	0.07356
39	$\Theta_1$	0.02653	0.04087	0.04763	0.04940	0.05133	0.04230	0.06956
40	$\Theta_1$	0.03020	0.04407	0.04777	0.04940	0.05153	0.04423	0.08018
41	$\Theta_1$	0.03293	0.04373	0.04777	0.04960	0.05160	0.04497	0.08351



Locus	Parameter	2.5%	25.0%	Mode	75.0%	97.5%	Median	Mean
42	$\Theta_1$	0.02680	0.04207	0.04757	0.04920	0.05133	0.04223	0.07014
43	$\Theta_1$	0.03040	0.04320	0.04790	0.04973	0.05160	0.04443	0.08066
44	$\Theta_1$	0.02753	0.04187	0.04777	0.04967	0.05147	0.04310	0.07448
45	$\Theta_1$	0.02740	0.04173	0.04770	0.04953	0.05147	0.04297	0.07428
46	$\Theta_1$	0.02600	0.04133	0.04763	0.04933	0.05133	0.04203	0.07111
47	$\Theta_1$	0.03173	0.04360	0.04783	0.04980	0.05147	0.04477	0.08079
48	$\Theta_1$	0.02813	0.04180	0.04770	0.04953	0.05140	0.04310	0.07592
49	$\Theta_1$	0.03147	0.04333	0.04790	0.04973	0.05160	0.04450	0.08113
50	$\Theta_1$	0.02900	0.04273	0.04783	0.04973	0.05153	0.04390	0.07940
51	$\Theta_1$	0.02773	0.04173	0.04770	0.04960	0.05147	0.04303	0.07452
52	$\Theta_1$	0.02800	0.04293	0.04770	0.04933	0.05140	0.04310	0.07486
53	$\Theta_1$	0.03067	0.04433	0.04777	0.04933	0.05153	0.04450	0.08167
54	$\Theta_1$	0.03093	0.04373	0.04777	0.04987	0.05160	0.04483	0.08258
55	$\Theta_1$	0.02740	0.04280	0.04770	0.04927	0.05140	0.04297	0.07335
56	$\Theta_1$	0.02813	0.04173	0.04770	0.04953	0.05140	0.04303	0.07469
57	$\Theta_1$	0.02620	0.04140	0.04770	0.04967	0.05140	0.04263	0.07284
58	$\Theta_1$	0.02980	0.04373	0.04770	0.04933	0.05147	0.04390	0.07775
59	$\Theta_1$	0.03293	0.04513	0.04790	0.04960	0.05153	0.04537	0.08438
60	$\Theta_1$	0.03000	0.04340	0.04777	0.04980	0.05160	0.04457	0.08031
61	$\Theta_1$	0.03427	0.04467	0.04790	0.04993	0.05167	0.04577	0.08491

62	$\Theta_1$	0.02960	0.04280	0.04777	0.04967	0.05153	0.04403	0.07842
63	$\Theta_1$	0.03080	0.04327	0.04777	0.04980	0.05160	0.04443	0.08212
64	$\Theta_1$	0.02853	0.04207	0.04770	0.04960	0.05147	0.04330	0.07423
65	$\Theta_1$	0.03273	0.04373	0.04790	0.04980	0.05167	0.04490	0.08255
66	$\Theta_1$	0.02800	0.03933	0.04770	0.04987	0.05140	0.04283	0.07206
67	$\Theta_1$	0.02987	0.04300	0.04777	0.04967	0.05160	0.04423	0.08036
68	$\Theta_1$	0.02653	0.04113	0.04770	0.04953	0.05140	0.04243	0.07244
69	$\Theta_1$	0.03033	0.04413	0.04777	0.04947	0.05153	0.04430	0.07837
70	$\Theta_1$	0.02987	0.04307	0.04783	0.04987	0.05160	0.04423	0.07916
71	$\Theta_1$	0.03080	0.04400	0.04783	0.04940	0.05153	0.04423	0.07979
72	$\Theta_1$	0.02687	0.04133	0.04763	0.04940	0.05147	0.04277	0.07338
73	$\Theta_1$	0.03000	0.04373	0.04777	0.04947	0.05153	0.04403	0.07913
74	$\Theta_1$	0.03127	0.04073	0.04783	0.05027	0.05153	0.04450	0.07981
75	$\Theta_1$	0.03180	0.04393	0.04797	0.04993	0.05167	0.04503	0.08212
76	$\Theta_1$	0.02873	0.04207	0.04770	0.04953	0.05147	0.04337	0.07492
77	$\Theta_1$	0.02807	0.04193	0.04770	0.04960	0.05147	0.04323	0.07374
78	$\Theta_1$	0.02740	0.04220	0.04763	0.04940	0.05140	0.04283	0.07411
79	$\Theta_1$	0.03567	0.04580	0.04777	0.04920	0.05153	0.04597	0.08757
80	$\Theta_1$	0.03307	0.04440	0.04790	0.04987	0.05167	0.04550	0.08398
81	$\Theta_1$	0.02927	0.04307	0.04777	0.04953	0.05147	0.04377	0.07637
82	$\Theta_1$	0.03120	0.04367	0.04777	0.04973	0.05167	0.04483	0.08150
83	$\Theta_1$	0.02787	0.04167	0.04770	0.04960	0.05140	0.04297	0.07337
84	$\Theta_1$	0.03247	0.04427	0.04783	0.04973	0.05160	0.04543	0.08491

Locus	Parameter	2.5%	25.0%	Mode	75.0%	97.5%	Median	Mean
85	$\Theta_1$	0.02927	0.04273	0.04770	0.04967	0.05147	0.04390	0.07731
86	$\Theta_1$	0.03107	0.04320	0.04777	0.04973	0.05147	0.04437	0.08109
87	$\Theta_1$	0.02813	0.04280	0.04770	0.04940	0.05140	0.04310	0.07357
88	$\Theta_1$	0.02833	0.04320	0.04777	0.04933	0.05153	0.04337	0.07708
89	$\Theta_1$	0.03067	0.04427	0.04783	0.04953	0.05160	0.04443	0.08135
90	$\Theta_1$	0.03000	0.04300	0.04783	0.04987	0.05153	0.04417	0.08033
91	$\Theta_1$	0.03113	0.04353	0.04783	0.04973	0.05160	0.04470	0.08130
92	$\Theta_1$	0.02887	0.04287	0.04770	0.04967	0.05153	0.04397	0.07791
93	$\Theta_1$	0.02660	0.04100	0.04770	0.04947	0.05140	0.04237	0.07121
94	$\Theta_1$	0.03093	0.04320	0.04783	0.04973	0.05160	0.04443	0.08042
95	$\Theta_1$	0.03060	0.04327	0.04777	0.04967	0.05167	0.04450	0.08242
96	$\Theta_1$	0.02680	0.04153	0.04770	0.04933	0.05133	0.04237	0.07096
97	$\Theta_1$	0.03073	0.04373	0.04783	0.04960	0.05147	0.04430	0.08140
98	$\Theta_1$	0.02887	0.04233	0.04770	0.04973	0.05147	0.04350	0.07729
99	$\Theta_1$	0.02920	0.04213	0.04777	0.04960	0.05147	0.04343	0.07670
100	$\Theta_1$	0.02920	0.04267	0.04777	0.04973	0.05160	0.04390	0.07953
All	$\Theta_1$	0.00527	0.00820	0.00950	0.01100	0.01287	0.00950	0.09909

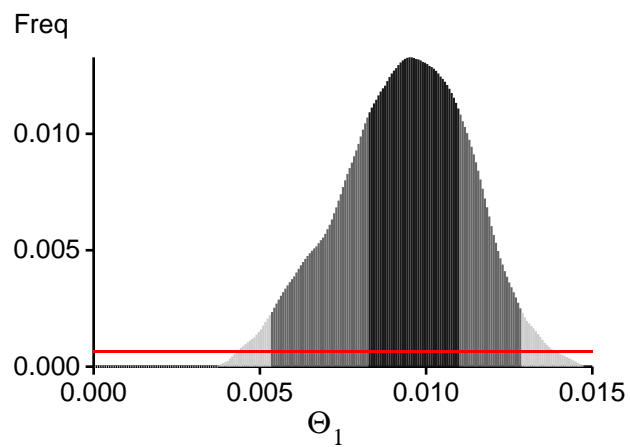
Citation suggestions:

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	-15019.26	-14546.80	-14563.97	-14628.29
2	-14092.21	-13934.42	-13987.65	-14067.15
3	-14980.33	-14732.31	-14778.47	-14853.39
4	-14337.38	-14125.10	-14185.27	-14252.40
5	-14508.04	-14264.50	-14314.27	-14387.60
6	-14182.07	-13994.18	-14053.18	-14123.69
7	-14056.67	-13904.44	-13960.14	-14039.08
8	-14433.11	-14164.95	-14212.01	-14280.32
9	-14662.05	-14337.78	-14376.81	-14446.55
10	-41569.93	-28764.04	-26579.57	-26637.44
11	-16238.41	-15391.66	-15352.79	-15412.25
12	-14342.19	-14137.59	-14193.80	-14266.60
13	-14391.80	-14130.55	-14178.78	-14248.19
14	-14606.40	-14342.73	-14391.45	-14461.73
15	-14247.12	-14020.23	-14068.61	-14144.62
16	-15794.95	-15082.37	-15055.02	-15125.69
17	-14587.22	-14316.00	-14366.99	-14433.74
18	-14157.13	-13962.27	-14018.76	-14090.99
19	-14882.18	-14479.35	-14506.67	-14575.19
20	-14568.23	-14246.80	-14283.17	-14355.87
21	-14255.24	-14066.73	-14128.61	-14198.55
22	-14637.49	-14293.30	-14330.72	-14398.05
23	-23204.07	-21262.69	-21053.57	-21122.95
24	-14774.09	-14382.53	-14407.82	-14479.81
25	-14244.92	-14004.84	-14050.60	-14126.15
26	-14379.11	-14148.92	-14200.97	-14270.77
27	-17295.52	-15821.77	-15660.78	-15725.78
28	-15994.99	-15332.22	-15329.79	-15387.12
29	-15302.75	-14611.26	-14583.11	-14651.57

30	-14399.68	-14194.77	-14253.03	-14324.10
31	-15018.80	-14643.15	-14683.58	-14745.30
32	-15612.18	-14826.95	-14784.57	-14851.30
33	-20399.77	-18757.56	-18602.17	-18663.78
34	-14570.26	-14260.48	-14302.33	-14372.21
35	-14275.92	-14076.34	-14132.00	-14206.15
36	-14349.52	-14106.67	-14155.31	-14227.61
37	-15511.30	-15130.80	-15167.58	-15234.64
38	-22043.21	-20688.38	-20535.75	-20638.36
39	-14199.46	-13987.00	-14038.52	-14113.09
40	-18250.92	-16893.77	-16762.19	-16831.88
41	-14991.57	-14572.87	-14010.79	-14662.85
42	-14127.69	-13962.90	-13959.45	-14099.38
43	-20788.89	-19227.73	-14083.02	-19155.91
44	-14673.29	-14301.77	-14025.16	-14400.67
45	-14518.05	-14243.32	-14052.11	-14364.61
46	-14030.95	-13874.40	-13932.12	-14008.13
47	-14622.50	-14305.68	-14184.25	-14415.06
48	-14193.30	-14024.95	-14058.68	-14157.96
49	-15829.44	-15361.12	-15389.92	-15453.86
50	-17031.63	-15719.18	-14585.92	-15649.93
51	-14130.41	-13952.03	-14011.54	-14083.83
52	-14293.12	-14057.44	-14106.75	-14179.65
53	-14437.72	-14202.17	-14209.02	-14325.63
54	-18353.76	-17065.88	-14216.98	-17020.50
55	-14410.25	-14155.30	-14199.88	-14275.37
56	-14184.04	-13974.21	-14025.16	-14098.63
57	-14056.31	-13901.42	-13959.45	-14034.66
58	-14321.83	-14111.44	-14168.13	-14238.32
59	-14986.34	-14568.37	-14175.16	-14659.21
60	-16182.09	-15561.76	-14374.17	-15626.38
61	-17820.21	-16407.72	-16264.69	-16330.73
62	-14283.63	-14069.55	-14124.54	-14196.23
63	-14738.24	-14477.82	-14195.57	-14598.73
64	-14126.75	-13942.16	-13999.39	-14071.91
65	-15041.08	-14555.88	-14329.16	-14636.47
66	-14174.79	-14002.45	-14058.19	-14135.37
67	-15813.82	-15124.41	-14568.62	-15165.57
68	-15193.22	-14754.19	-14383.12	-14845.49
69	-17166.20	-15596.08	-14257.92	-15480.02
70	-14649.45	-14286.64	-14318.74	-14387.45
71	-14577.04	-14293.77	-14341.08	-14409.01
72	-14071.86	-13907.75	-13968.39	-14040.50
73	-14299.70	-14089.85	-14150.47	-14217.69
74	-15119.16	-14661.60	-14681.40	-14747.45

75	-27720.01	-21695.02	-15171.20	-20791.61
76	-14594.06	-14283.80	-14321.49	-14394.24
77	-14207.65	-13982.89	-14032.84	-14106.72
78	-14161.03	-13974.08	-14031.67	-14104.04
79	-86398.40	-52701.19	-13966.95	-46827.00
80	-14762.74	-14495.53	-14554.09	-14613.93
81	-16808.61	-15731.64	-14029.10	-15711.61
82	-15140.26	-14701.55	-14021.31	-14792.15
83	-14501.28	-14200.91	-14087.94	-14312.08
84	-15280.00	-14803.05	-13984.83	-14888.51
85	-14343.17	-14105.61	-14025.57	-14226.88
86	-15152.58	-14732.22	-14359.76	-14822.70
87	-14243.70	-14004.08	-14052.32	-14124.86
88	-14349.78	-14133.76	-14190.75	-14262.36
89	-14493.69	-14227.05	-14281.36	-14345.66
90	-14624.37	-14349.68	-14116.05	-14465.87
91	-14856.36	-14412.05	-14009.18	-14498.37
92	-15982.64	-14969.48	-14255.66	-14951.39
93	-14176.77	-13963.41	-14013.04	-14088.99
94	-16100.69	-15320.07	-14131.36	-15352.56
95	-15024.16	-14669.75	-14302.70	-14774.77
96	-14133.04	-13966.24	-14025.14	-14100.10
97	-14582.80	-14318.04	-14342.39	-14435.02
98	-14456.74	-14246.10	-14172.22	-14371.41
99	-14576.55	-14267.42	-14308.89	-14377.46
100	-14477.29	-14245.49	-13978.11	-14370.62
All	-1626668.38	-1530087.91	-1462631.01	-1529589.78
(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 = 94.219646]				
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
$\Theta_1$	384020349/399988535	0.96008
Genealogies	185592184/1600011465	0.11599

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

Parameter	Autocorrelation	Effective Sample Size
$\Theta_1$	0.57875	6935275.21
Genealogies	0.25421	16050650.85

## *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