

# 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 03:51:21 2017

Program finished at Sun Aug 13 05:23:00 2017 [Runtime:0000:01:31:39]



## 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)

136131862

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.0.7
Haplotyping is turned on:	NO
Output file:	outfile_0.7_0.6
Posterior distribution raw histogram file:	bayesfile
Raw data from the MCMC run:	bayesallfile_0.7_0.6
Print data:	No
Print genealogies [only some for some data type]:	None

## Data summary

Data file: infile.0.7  
 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]
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18	1	Jukes-Cantor	[Basefreq: =0.25]
19	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]
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35	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]
47	1	Jukes-Cantor	[Basefreq: =0.25]
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]
53	1	Jukes-Cantor	[Basefreq: =0.25]
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61	1	Jukes-Cantor	[Basefreq: =0.25]
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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]
83	1	Jukes-Cantor	[Basefreq: =0.25]
84	1	Jukes-Cantor	[Basefreq: =0.25]
85	1	Jukes-Cantor	[Basefreq: =0.25]
86	1	Jukes-Cantor	[Basefreq: =0.25]
87	1	Jukes-Cantor	[Basefreq: =0.25]
88	1	Jukes-Cantor	[Basefreq: =0.25]
89	1	Jukes-Cantor	[Basefreq: =0.25]
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
24	10000
25	10000
26	10000
27	10000
28	10000
29	10000
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31	10000
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36	10000
37	10000
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43	10000
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46	10000
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51	10000
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81	10000
82	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	
			9		10	
			10		10	
			11		10	
			12		10	
			13		10	
			14		10	
			15		10	
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			39		10	
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41	10
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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
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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	$\Theta_1$	0.01733	0.03080	0.03990	0.04813	0.05040	0.03530	0.05139
2	$\Theta_1$	0.02333	0.03953	0.04757	0.04933	0.05127	0.04090	0.06939
3	$\Theta_1$	0.01413	0.01973	0.02803	0.04027	0.04920	0.03063	0.03943
4	$\Theta_1$	0.01960	0.03640	0.04197	0.04780	0.05060	0.03690	0.05217
5	$\Theta_1$	0.01520	0.02300	0.03257	0.03867	0.04947	0.03183	0.04112
6	$\Theta_1$	0.01907	0.02593	0.03863	0.04900	0.05053	0.03617	0.04917
7	$\Theta_1$	0.02147	0.03773	0.04750	0.04893	0.05093	0.03903	0.06095
8	$\Theta_1$	0.00540	0.00887	0.01530	0.02527	0.03953	0.01897	0.02167
9	$\Theta_1$	0.01500	0.01933	0.02923	0.04240	0.04927	0.03110	0.03881
10	$\Theta_1$	0.02067	0.03547	0.04177	0.04807	0.05067	0.03743	0.05319
11	$\Theta_1$	0.00607	0.01313	0.01610	0.01940	0.04087	0.02010	0.02339
12	$\Theta_1$	0.02033	0.03613	0.04070	0.04687	0.05060	0.03717	0.05205
13	$\Theta_1$	0.01900	0.03293	0.03970	0.04593	0.05040	0.03597	0.04898
14	$\Theta_1$	0.01647	0.02487	0.03230	0.04033	0.04960	0.03283	0.04196
15	$\Theta_1$	0.00900	0.01327	0.01863	0.02733	0.03973	0.02383	0.02957
16	$\Theta_1$	0.01233	0.01440	0.02450	0.03900	0.04507	0.02743	0.03315
17	$\Theta_1$	0.00500	0.00860	0.01630	0.02807	0.04447	0.01957	0.02262
18	$\Theta_1$	0.02047	0.03800	0.04623	0.04853	0.05087	0.03817	0.05806

19	$\Theta_1$	0.01713	0.02833	0.03317	0.04147	0.04993	0.03390	0.04480
20	$\Theta_1$	0.01773	0.02927	0.03477	0.04420	0.05020	0.03477	0.04695
21	$\Theta_1$	0.01553	0.02373	0.02970	0.03707	0.04920	0.03150	0.03968
22	$\Theta_1$	0.02007	0.03653	0.04617	0.04827	0.05067	0.03737	0.05413
23	$\Theta_1$	0.01340	0.02167	0.02590	0.03333	0.04887	0.02983	0.03759
24	$\Theta_1$	0.01820	0.03033	0.03650	0.04407	0.05027	0.03523	0.04708
25	$\Theta_1$	0.02040	0.03700	0.04277	0.04847	0.05080	0.03770	0.05513
26	$\Theta_1$	0.02187	0.03907	0.04750	0.04887	0.05107	0.03930	0.06190
27	$\Theta_1$	0.02453	0.04000	0.04757	0.04927	0.05133	0.04143	0.06722
28	$\Theta_1$	0.01860	0.03280	0.03877	0.04687	0.05040	0.03583	0.04982
29	$\Theta_1$	0.01273	0.02000	0.02503	0.03393	0.04887	0.02917	0.03605
30	$\Theta_1$	0.02127	0.03840	0.04497	0.04847	0.05093	0.03890	0.05880
31	$\Theta_1$	0.01453	0.02193	0.02783	0.03580	0.04893	0.03057	0.03862
32	$\Theta_1$	0.01767	0.02807	0.03443	0.04800	0.05033	0.03503	0.04781
33	$\Theta_1$	0.01387	0.02093	0.02717	0.03447	0.04880	0.02997	0.03743
34	$\Theta_1$	0.01907	0.03593	0.04637	0.04827	0.05073	0.03710	0.05501
35	$\Theta_1$	0.00400	0.01267	0.01763	0.02420	0.05093	0.02163	0.02533
36	$\Theta_1$	0.01627	0.02620	0.03257	0.04120	0.04993	0.03337	0.04362
37	$\Theta_1$	0.01093	0.01507	0.02237	0.03293	0.04447	0.02637	0.03213
38	$\Theta_1$	0.02193	0.03840	0.04757	0.04893	0.05107	0.03943	0.06164
39	$\Theta_1$	0.01613	0.02480	0.03090	0.03880	0.04967	0.03250	0.04179
40	$\Theta_1$	0.01653	0.02720	0.03410	0.04367	0.05020	0.03403	0.04538
41	$\Theta_1$	0.02507	0.03967	0.04750	0.04913	0.05120	0.04117	0.06751



Locus	Parameter	2.5%	25.0%	Mode	75.0%	97.5%	Median	Mean
42	$\Theta_1$	0.02347	0.03920	0.04750	0.04920	0.05113	0.04063	0.06431
43	$\Theta_1$	0.02113	0.03913	0.04750	0.04907	0.05120	0.03970	0.06728
44	$\Theta_1$	0.01093	0.01227	0.02150	0.03867	0.04260	0.02597	0.03108
45	$\Theta_1$	0.01300	0.01840	0.02470	0.03220	0.04527	0.02810	0.03434
46	$\Theta_1$	0.01973	0.03447	0.04050	0.04773	0.05060	0.03677	0.05080
47	$\Theta_1$	0.01660	0.02520	0.03230	0.04167	0.04987	0.03323	0.04349
48	$\Theta_1$	0.01127	0.01640	0.02190	0.02920	0.04227	0.02623	0.03286
49	$\Theta_1$	0.02220	0.03800	0.04750	0.04873	0.05093	0.03923	0.05990
50	$\Theta_1$	0.00793	0.00820	0.01570	0.02660	0.02733	0.01903	0.02216
51	$\Theta_1$	0.01860	0.03413	0.04017	0.04780	0.05053	0.03623	0.05114
52	$\Theta_1$	0.00800	0.01347	0.01883	0.02673	0.04380	0.02337	0.02772
53	$\Theta_1$	0.01587	0.01753	0.02923	0.04900	0.04953	0.03230	0.04126
54	$\Theta_1$	0.01293	0.02000	0.02683	0.03347	0.04893	0.02943	0.03646
55	$\Theta_1$	0.00913	0.01567	0.02050	0.02700	0.04493	0.02463	0.02938
56	$\Theta_1$	0.01520	0.02273	0.02970	0.03967	0.04933	0.03170	0.04068
57	$\Theta_1$	0.01687	0.02580	0.03330	0.04460	0.05000	0.03377	0.04491
58	$\Theta_1$	0.01213	0.01553	0.02323	0.03367	0.04240	0.02663	0.03184
59	$\Theta_1$	0.01973	0.03553	0.04163	0.04827	0.05067	0.03723	0.05470
60	$\Theta_1$	0.00427	0.01000	0.01410	0.01913	0.04067	0.01783	0.02068
61	$\Theta_1$	0.01487	0.02207	0.02650	0.03407	0.04860	0.03017	0.03733

62	$\Theta_1$	0.02053	0.03767	0.04757	0.04907	0.05120	0.03917	0.06153
63	$\Theta_1$	0.02080	0.03587	0.04417	0.04840	0.05073	0.03777	0.05443
64	$\Theta_1$	0.01267	0.01733	0.02303	0.03087	0.04220	0.02710	0.03263
65	$\Theta_1$	0.01307	0.01753	0.02423	0.03400	0.04480	0.02797	0.03384
66	$\Theta_1$	0.02060	0.03600	0.04670	0.04853	0.05073	0.03777	0.05475
67	$\Theta_1$	0.01387	0.01993	0.02643	0.03547	0.04860	0.02977	0.03755
68	$\Theta_1$	0.02547	0.04060	0.04763	0.04947	0.05133	0.04177	0.06976
69	$\Theta_1$	0.01947	0.02700	0.04123	0.04907	0.05047	0.03650	0.05056
70	$\Theta_1$	0.01033	0.01633	0.02143	0.02873	0.04440	0.02563	0.03106
71	$\Theta_1$	0.01407	0.01980	0.02783	0.03580	0.04813	0.02957	0.03634
72	$\Theta_1$	0.01653	0.02773	0.03370	0.04360	0.05020	0.03403	0.04737
73	$\Theta_1$	0.00687	0.01067	0.01530	0.02240	0.03340	0.01963	0.02287
74	$\Theta_1$	0.02407	0.03913	0.04757	0.04913	0.05120	0.04063	0.06389
75	$\Theta_1$	0.01113	0.01673	0.02343	0.03147	0.04693	0.02690	0.03242
76	$\Theta_1$	0.00393	0.01080	0.01303	0.01540	0.03780	0.01657	0.01901
77	$\Theta_1$	0.01633	0.02867	0.03290	0.03980	0.05007	0.03357	0.04465
78	$\Theta_1$	0.02500	0.04093	0.04763	0.04913	0.05120	0.04110	0.06492
79	$\Theta_1$	0.01440	0.01440	0.02763	0.04873	0.04873	0.03037	0.03829
80	$\Theta_1$	0.01527	0.02420	0.03037	0.04013	0.04973	0.03237	0.04173
81	$\Theta_1$	0.01880	0.02853	0.03717	0.04680	0.05020	0.03530	0.04731
82	$\Theta_1$	0.01553	0.02107	0.02970	0.04047	0.04907	0.03130	0.03935
83	$\Theta_1$	0.02340	0.03880	0.04750	0.04907	0.05113	0.04030	0.06170
84	$\Theta_1$	0.01867	0.03340	0.03857	0.04807	0.05053	0.03623	0.05134

Locus	Parameter	2.5%	25.0%	Mode	75.0%	97.5%	Median	Mean
85	$\Theta_1$	0.02413	0.04067	0.04763	0.04913	0.05120	0.04090	0.06774
86	$\Theta_1$	0.02553	0.04067	0.04763	0.04947	0.05140	0.04203	0.07148
87	$\Theta_1$	0.02080	0.03627	0.04517	0.04813	0.05067	0.03757	0.05309
88	$\Theta_1$	0.01887	0.03247	0.04010	0.04593	0.05040	0.03577	0.04929
89	$\Theta_1$	0.01533	0.02187	0.03330	0.04640	0.04993	0.03290	0.04361
90	$\Theta_1$	0.00827	0.01320	0.01637	0.02140	0.03300	0.02077	0.02408
91	$\Theta_1$	0.02527	0.04027	0.04763	0.04940	0.05127	0.04150	0.06869
92	$\Theta_1$	0.01913	0.03433	0.04110	0.04780	0.05060	0.03657	0.05086
93	$\Theta_1$	0.01287	0.01913	0.02570	0.03533	0.04887	0.02943	0.03897
94	$\Theta_1$	0.02220	0.03793	0.04757	0.04913	0.05100	0.03950	0.06202
95	$\Theta_1$	0.01500	0.02333	0.03023	0.03960	0.04973	0.03190	0.04117
96	$\Theta_1$	0.00547	0.01047	0.01343	0.01707	0.03113	0.01703	0.01957
97	$\Theta_1$	0.01620	0.02140	0.03397	0.04580	0.04960	0.03257	0.04231
98	$\Theta_1$	0.00867	0.01433	0.02057	0.02840	0.04513	0.02430	0.02891
99	$\Theta_1$	0.01687	0.02767	0.03383	0.04280	0.05013	0.03403	0.04596
100	$\Theta_1$	0.00740	0.01680	0.01830	0.01940	0.03953	0.02177	0.02555
All	$\Theta_1$	0.02913	0.03193	0.03337	0.03500	0.03733	0.03343	0.03336

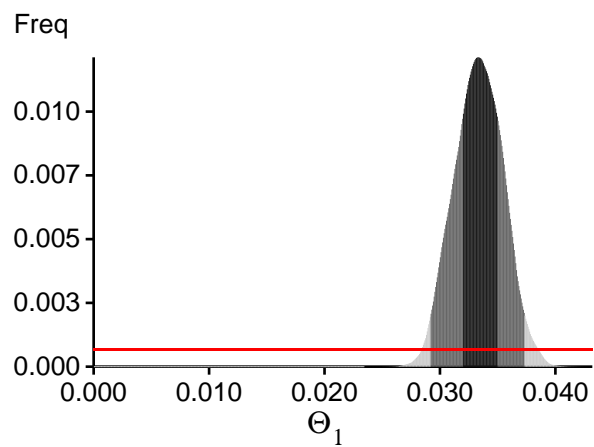
Citation suggestions:

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	-15079.49	-14780.31	-14826.41	-14899.01
2	-16387.54	-15908.47	-15949.15	-16005.91
3	-16977.24	-15539.47	-15373.80	-15447.67
4	-14230.74	-14029.00	-14088.34	-14157.36
5	-14030.42	-13861.07	-13918.35	-13992.13
6	-14288.32	-14039.15	-14089.34	-14159.09
7	-22106.25	-20479.43	-20350.25	-20413.31
8	-13956.55	-13792.19	-13837.13	-13926.39
9	-14184.48	-13961.36	-14011.46	-14085.91
10	-15130.59	-14597.44	-14601.42	-14668.66
11	-13945.82	-13781.10	-13828.28	-13913.59
12	-14257.24	-14024.35	-14077.80	-14146.66
13	-14200.87	-14006.96	-14067.32	-14137.90
14	-14280.96	-14024.91	-14070.08	-14142.36
15	-23086.64	-18376.74	-17608.45	-17687.43
16	-14035.85	-13860.15	-13912.81	-13990.61
17	-14045.45	-13861.95	-13906.67	-13992.19
18	-14222.46	-14040.10	-14102.81	-14171.38
19	-14170.29	-13997.84	-14058.53	-14131.90
20	-14636.60	-14325.17	-14364.87	-14435.75
21	-14758.17	-14304.75	-14313.69	-14388.04
22	-14196.95	-13999.58	-14059.88	-14128.34
23	-14096.82	-13911.55	-13964.96	-14041.95
24	-15019.57	-14523.04	-14530.49	-14600.09
25	-15838.70	-15090.49	-15059.19	-15126.88
26	-15614.89	-15237.47	-15279.93	-15344.25
27	-15415.72	-14910.13	-14930.05	-14991.52
28	-14292.61	-14069.34	-14125.03	-14194.12
29	-14101.27	-13910.40	-13962.98	-14040.67

30	-14224.54	-14037.42	-14102.01	-14167.57
31	-14150.27	-13948.29	-13999.77	-14075.91
32	-14687.42	-14424.25	-14476.38	-14547.60
33	-14036.19	-13860.26	-13916.26	-13991.06
34	-14185.48	-14012.25	-14072.80	-14145.08
35	-13943.26	-13783.26	-13832.01	-13915.14
36	-14096.39	-13911.45	-13969.44	-14041.64
37	-13973.49	-13814.05	-13867.56	-13947.90
38	-15462.48	-14860.92	-14857.67	-14922.04
39	-14783.08	-14357.30	-14374.65	-14446.39
40	-14084.93	-13910.41	-13969.64	-14041.94
41	-16786.93	-15955.83	-15924.98	-15986.09
42	-15034.87	-14722.52	-14776.10	-14838.69
43	-16487.10	-15997.95	-16035.41	-16092.26
44	-14037.86	-13877.63	-13930.40	-14012.34
45	-14086.76	-13889.62	-13940.51	-14017.65
46	-14353.49	-14094.90	-14144.36	-14214.08
47	-14281.71	-14035.64	-14081.67	-14155.03
48	-16145.04	-15650.45	-15661.81	-15741.70
49	-14289.07	-14111.50	-14179.18	-14244.38
50	-13925.35	-13769.47	-13814.74	-13903.17
51	-14149.14	-13975.01	-14037.67	-14108.75
52	-13952.14	-13794.97	-13844.66	-13927.99
53	-14102.95	-13905.53	-13960.10	-14033.60
54	-14076.72	-13885.29	-13937.71	-14013.44
55	-13967.81	-13803.37	-13853.28	-13935.95
56	-15479.10	-14697.50	-14648.27	-14721.72
57	-14082.84	-13905.97	-13964.69	-14037.41
58	-14014.89	-13845.03	-13897.18	-13976.31
59	-14985.37	-14608.06	-14643.05	-14710.10
60	-13911.12	-13756.92	-13801.44	-13892.47
61	-14093.26	-13891.49	-13944.12	-14018.05
62	-15014.53	-14694.39	-14742.06	-14807.27
63	-14702.80	-14381.40	-14422.57	-14491.27
64	-14024.79	-13847.95	-13899.25	-13978.09
65	-14013.56	-13843.81	-13898.22	-13976.21
66	-15715.59	-14955.85	-14919.19	-14987.21
67	-14014.32	-13846.82	-13902.47	-13979.04
68	-14941.78	-14585.17	-14629.02	-14689.66
69	-14149.93	-13956.05	-14015.60	-14084.51
70	-14018.94	-13841.73	-13893.70	-13973.32
71	-14296.26	-14036.15	-14076.58	-14152.43
72	-24157.20	-19014.60	-18180.28	-18249.91
73	-13923.58	-13768.98	-13816.75	-13903.64
74	-19179.29	-17289.19	-17069.50	-17132.48

75	-14000.07	-13832.12	-13886.01	-13965.47
76	-13925.08	-13766.58	-13809.95	-13899.68
77	-14195.99	-14018.65	-14077.84	-14152.00
78	-14536.76	-14268.00	-14323.84	-14386.62
79	-14060.50	-13877.24	-13931.43	-14007.30
80	-14048.16	-13874.77	-13932.29	-14008.89
81	-14272.72	-14087.67	-14148.83	-14219.56
82	-14230.66	-14051.28	-14110.97	-14184.08
83	-14375.88	-14130.10	-14185.50	-14250.75
84	-14187.05	-13994.31	-14052.56	-14123.82
85	-15076.56	-14807.84	-14869.44	-14930.82
86	-15628.28	-15099.43	-15116.18	-15176.50
87	-14742.28	-14375.89	-14409.57	-14476.45
88	-14533.16	-14217.46	-14256.22	-14325.81
89	-14036.82	-13869.69	-13929.26	-14001.73
90	-13969.75	-13797.30	-13844.09	-13928.93
91	-17118.55	-16486.35	-16503.65	-16560.78
92	-14291.79	-14054.97	-14108.58	-14180.85
93	-22976.58	-19640.51	-19156.41	-19231.56
94	-15216.97	-14891.37	-14942.69	-15006.00
95	-14201.78	-13972.22	-14019.46	-14094.70
96	-13919.71	-13759.01	-13801.94	-13892.72
97	-14056.54	-13880.17	-13938.23	-14010.78
98	-14516.38	-14143.60	-14160.18	-14240.58
99	-14125.23	-13941.77	-13998.56	-14072.23
100	-13944.08	-13785.18	-13833.68	-13918.01
All	-1490762.38	-1446986.94	-1448504.44	-1455799.17
(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 = 37.068993]				
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
$\Theta_1$	372882677/399998168	0.93221
Genealogies	275890222/1600001832	0.17243

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

Parameter	Autocorrelation	Effective Sampe Size
$\Theta_1$	0.65451	2104760.99
Genealogies	0.10864	8134353.78

## *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