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 21:07:57 2017
Program finished at Sun Aug 13 22:38:59 2017 [Runtime:0000:01:31:02]

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) 369822670
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	Θ_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	-1-1	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
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]
22	1	Jukes-Cantor	[Basefreq: =0.25]
23	1	Jukes-Cantor	[Basefreq: =0.25]
24	1	Jukes-Cantor	[Basefreq: =0.25]
25	1	Jukes-Cantor	[Basefreq: =0.25]
26	1	Jukes-Cantor	[Basefreq: =0.25]
27	1	Jukes-Cantor	[Basefreq: =0.25]
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]
34	1	Jukes-Cantor	[Basefreq: =0.25]

35	1	Jukes-Cantor	[Basefreq: =0.25]
36	1	Jukes-Cantor	[Basefreq: =0.25]
37	1	Jukes-Cantor	[Basefreq: =0.25]
38	1	Jukes-Cantor	[Basefreq: =0.25]
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]
54	1	Jukes-Cantor	[Basefreq: =0.25]
55	1	Jukes-Cantor	[Basefreq: =0.25]
56	1	Jukes-Cantor	[Basefreq: =0.25]
57	1	Jukes-Cantor	[Basefreq: =0.25]
58	1	Jukes-Cantor	[Basefreq: =0.25]
59	1	Jukes-Cantor	[Basefreq: =0.25]
60	1	Jukes-Cantor	[Basefreq: =0.25]
61	1	Jukes-Cantor	[Basefreq: =0.25]
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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]
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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
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39	10000
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42	10000
43	10000
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45	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
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
	16	10
	17	10
	18	10
	19	10
	20	10
	21	10
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	30	10
	31	10
	32	10
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	35	10
	36	10
	37	10
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	39	10
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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
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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

Bayesian Analysis: Posterior distribution table

Locus	Parameter	2.5%	25.0%	Mode	75.0%	97.5%	Median	Mean
1	Θ_1	0.03147	0.04347	0.04790	0.04980	0.05160	0.04470	0.08149
2	Θ_1	0.03033	0.04307	0.04777	0.04967	0.05160	0.04430	0.07953
3	Θ_1	0.02927	0.04240	0.04770	0.04960	0.05147	0.04363	0.07637
4	Θ_1	0.02953	0.04260	0.04783	0.04967	0.05153	0.04383	0.07724
5	Θ_1	0.03067	0.04427	0.04777	0.04947	0.05153	0.04443	0.08040
6	Θ_1	0.03087	0.04300	0.04777	0.04960	0.05153	0.04423	0.07912
7	Θ_1	0.03100	0.04360	0.04783	0.04980	0.05160	0.04477	0.08188
8	Θ_1	0.03160	0.04333	0.04777	0.04973	0.05160	0.04457	0.08059
9	Θ_1	0.03313	0.04407	0.04790	0.04980	0.05160	0.04523	0.08442
10	Θ_1	0.03227	0.04427	0.04797	0.04980	0.05173	0.04543	0.08470
11	Θ_1	0.03047	0.04307	0.04797	0.04967	0.05160	0.04417	0.07953
12	Θ_1	0.02727	0.04147	0.04770	0.04953	0.05140	0.04277	0.07433
13	Θ_1	0.02627	0.04160	0.04763	0.04927	0.05127	0.04183	0.06889
14	Θ_1	0.03307	0.04427	0.04783	0.04980	0.05167	0.04543	0.08419
15	Θ_1	0.02927	0.04327	0.04777	0.04953	0.05153	0.04370	0.07866
16	Θ_1	0.03180	0.04353	0.04803	0.04980	0.05160	0.04477	0.08426
17	Θ_1	0.02387	0.03933	0.04757	0.04920	0.05120	0.04083	0.06823
18	Θ_1	0.03293	0.04400	0.04790	0.04980	0.05167	0.04523	0.08317

19	Θ_1	0.02740	0.04147	0.04770	0.04947	0.05140	0.04277	0.07285
20	Θ_1	0.02880	0.04267	0.04777	0.04967	0.05153	0.04390	0.07988
21	Θ_1	0.02627	0.04087	0.04763	0.04940	0.05140	0.04223	0.07114
22	Θ_1	0.02947	0.04353	0.04770	0.04947	0.05147	0.04370	0.07891
23	Θ_1	0.03147	0.04333	0.04783	0.04973	0.05167	0.04457	0.08300
24	Θ_1	0.02740	0.04160	0.04770	0.04953	0.05140	0.04290	0.07221
25	Θ_1	0.03247	0.04407	0.04783	0.04980	0.05167	0.04523	0.08251
26	Θ_1	0.03153	0.04373	0.04783	0.04987	0.05160	0.04490	0.08207
27	Θ_1	0.02860	0.04253	0.04777	0.04973	0.05153	0.04370	0.07701
28	Θ_1	0.03093	0.04327	0.04783	0.04973	0.05160	0.04443	0.08005
29	Θ_1	0.02873	0.04213	0.04763	0.04953	0.05147	0.04343	0.07637
30	Θ_1	0.03020	0.04387	0.04777	0.04933	0.05153	0.04403	0.07785
31	Θ_1	0.03360	0.04407	0.04783	0.04973	0.05167	0.04523	0.08460
32	Θ_1	0.02880	0.04247	0.04770	0.04960	0.05153	0.04370	0.07832
33	Θ_1	0.03213	0.04413	0.04783	0.04993	0.05153	0.04523	0.08352
34	Θ_1	0.03020	0.04300	0.04783	0.04967	0.05160	0.04430	0.07854
35	Θ_1	0.03260	0.04380	0.04783	0.04987	0.05153	0.04490	0.08361
36	Θ_1	0.02807	0.04207	0.04770	0.04947	0.05147	0.04337	0.07817
37	Θ_1	0.02640	0.04127	0.04763	0.04940	0.05127	0.04210	0.07070
38	Θ_1	0.03107	0.04353	0.04783	0.04973	0.05160	0.04470	0.08297
39	Θ_1	0.02800	0.04213	0.04763	0.04960	0.05140	0.04337	0.07415
40	Θ_1	0.02933	0.04260	0.04770	0.04967	0.05147	0.04377	0.07681
41	Θ_1	0.03013	0.04300	0.04783	0.04973	0.05160	0.04423	0.07843

Locus	Parameter	2.5%	25.0%	Mode	75.0%	97.5%	Median	Mean
42	Θ_1	0.02873	0.04220	0.04763	0.04940	0.05147	0.04357	0.07712
43	Θ_1	0.02933	0.04280	0.04783	0.04967	0.05160	0.04403	0.07899
44	Θ_1	0.03347	0.04440	0.04790	0.04987	0.05167	0.04557	0.08528
45	Θ_1	0.03060	0.04307	0.04777	0.04967	0.05153	0.04430	0.07908
46	Θ_1	0.02993	0.04367	0.04783	0.04947	0.05147	0.04390	0.07749
47	Θ_1	0.02607	0.03773	0.04763	0.04987	0.05127	0.04203	0.07138
48	Θ_1	0.03240	0.04473	0.04790	0.04940	0.05153	0.04490	0.08295
49	Θ_1	0.03240	0.04380	0.04783	0.04980	0.05160	0.04497	0.08287
50	Θ_1	0.03067	0.04327	0.04783	0.04967	0.05160	0.04450	0.08026
51	Θ_1	0.03033	0.04280	0.04777	0.04960	0.05153	0.04403	0.07937
52	Θ_1	0.02967	0.04280	0.04777	0.04960	0.05153	0.04410	0.07941
53	Θ_1	0.02940	0.04253	0.04770	0.04967	0.05147	0.04377	0.07833
54	Θ_1	0.02633	0.04093	0.04770	0.04947	0.05140	0.04230	0.07078
55	Θ_1	0.02953	0.04367	0.04777	0.04947	0.05153	0.04383	0.07967
56	Θ_1	0.03140	0.04333	0.04777	0.04973	0.05153	0.04450	0.07986
57	Θ_1	0.02893	0.04180	0.04770	0.04973	0.05153	0.04363	0.07661
58	Θ_1	0.03207	0.03893	0.04783	0.05060	0.05160	0.04477	0.08215
59	Θ_1	0.03287	0.04400	0.04790	0.04973	0.05173	0.04517	0.08499
60	Θ_1	0.03100	0.04333	0.04783	0.04973	0.05160	0.04450	0.08198
61	Θ_1	0.03220	0.04360	0.04803	0.04980	0.05167	0.04483	0.08509

62	Θ_1	0.03267	0.04407	0.04777	0.04973	0.05147	0.04523	0.08410
63	Θ_1	0.03040	0.04320	0.04777	0.04967	0.05160	0.04443	0.08085
64	Θ_1	0.03033	0.04293	0.04770	0.04960	0.05147	0.04417	0.07774
65	Θ_1	0.03080	0.04413	0.04783	0.04947	0.05147	0.04430	0.07996
66	Θ_1	0.02927	0.04260	0.04777	0.04967	0.05147	0.04383	0.07765
67	Θ_1	0.02973	0.04293	0.04783	0.04980	0.05153	0.04417	0.08017
68	Θ_1	0.03433	0.04420	0.04790	0.04967	0.05160	0.04550	0.08471
69	Θ_1	0.02873	0.04313	0.04777	0.04947	0.05147	0.04330	0.07614
70	Θ_1	0.03140	0.04333	0.04790	0.04980	0.05160	0.04457	0.08012
71	Θ_1	0.03440	0.04413	0.04777	0.04953	0.05160	0.04543	0.08563
72	Θ_1	0.02940	0.04260	0.04770	0.04960	0.05153	0.04383	0.07702
73	Θ_1	0.03100	0.04333	0.04777	0.04967	0.05160	0.04457	0.08011
74	Θ_1	0.03067	0.04307	0.04777	0.04967	0.05147	0.04423	0.07936
75	Θ_1	0.03047	0.04333	0.04790	0.04980	0.05160	0.04457	0.08227
76	Θ_1	0.02747	0.04147	0.04777	0.04960	0.05140	0.04277	0.07379
77	Θ_1	0.02920	0.04280	0.04777	0.04973	0.05153	0.04397	0.07875
78	Θ_1	0.02933	0.04273	0.04783	0.04980	0.05147	0.04390	0.07813
79	Θ_1	0.03153	0.04467	0.04783	0.04940	0.05160	0.04483	0.08320
80	Θ_1	0.03080	0.04320	0.04777	0.04980	0.05147	0.04437	0.08061
81	Θ_1	0.03007	0.04307	0.04777	0.04967	0.05147	0.04423	0.07842
82	Θ_1	0.03133	0.04227	0.04783	0.05007	0.05160	0.04457	0.07978
83	Θ_1	0.03220	0.04360	0.04777	0.04973	0.05160	0.04477	0.08124
84	Θ_1	0.03100	0.04347	0.04783	0.04967	0.05160	0.04470	0.08045

Locus	Parameter	2.5%	25.0%	Mode	75.0%	97.5%	Median	Mean
85	Θ_1	0.02913	0.04347	0.04770	0.04940	0.05147	0.04370	0.07611
86	Θ_1	0.03060	0.04333	0.04783	0.04973	0.05153	0.04457	0.08157
87	Θ_1	0.03347	0.04427	0.04797	0.04987	0.05160	0.04537	0.08430
88	Θ_1	0.03133	0.04293	0.04783	0.04967	0.05153	0.04417	0.08165
89	Θ_1	0.02900	0.04227	0.04777	0.04960	0.05147	0.04350	0.07656
90	Θ_1	0.03393	0.04427	0.04783	0.04980	0.05160	0.04543	0.08535
91	Θ_1	0.03307	0.04420	0.04783	0.04987	0.05167	0.04530	0.08382
92	Θ_1	0.03000	0.04307	0.04770	0.04967	0.05153	0.04430	0.07828
93	Θ_1	0.03160	0.04353	0.04783	0.04973	0.05160	0.04477	0.08072
94	Θ_1	0.03113	0.04360	0.04770	0.04973	0.05160	0.04470	0.08207
95	Θ_1	0.02693	0.04173	0.04770	0.04967	0.05147	0.04297	0.07582
96	Θ_1	0.03327	0.04420	0.04797	0.04987	0.05160	0.04537	0.08322
97	Θ_1	0.02860	0.03627	0.04777	0.05060	0.05140	0.04330	0.07356
98	Θ_1	0.02887	0.04193	0.04770	0.04947	0.05140	0.04323	0.07512
99	Θ_1	0.03140	0.04307	0.04777	0.04960	0.05153	0.04437	0.08102
100	Θ_1	0.03093	0.04320	0.04783	0.04973	0.05160	0.04443	0.08019
All	Θ_1	0.00733	0.00940	0.01070	0.01207	0.01420	0.01090	0.09935

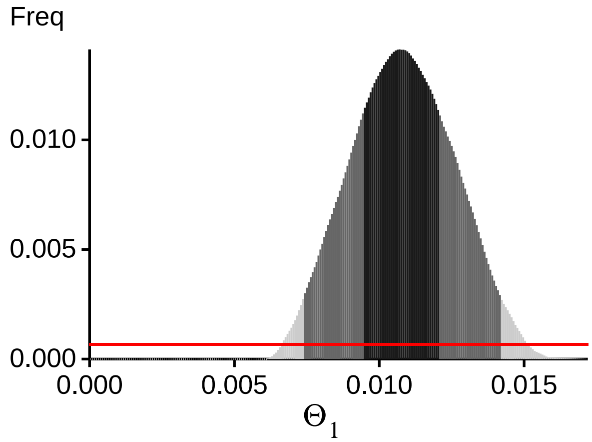
Citation suggestions:

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 = Exp[ln(Prob(D | thisModel) - ln(Prob(D | otherModel)
or as LBF = 2 (ln(Prob(D | thisModel) - ln(Prob(D | otherModel))
shows the support for thisModel]

Locus	TI(1a)	BTI(1b)	SS(2)	HS(3)
1	-16236.46	-15750.00	-15777.04	-15840.38
2	-17565.91	-15828.97	-15614.18	-15682.65
3	-14355.53	-14122.88	-14176.50	-14246.76
4	-14325.10	-14132.88	-14193.97	-14264.05
5	-14396.69	-14153.67	-14209.40	-14274.54
6	-14408.03	-14126.00	-14171.67	-14238.48
7	-14832.06	-14491.44	-14530.94	-14596.08
8	-15346.16	-14668.91	-14646.45	-14714.64
9	-18424.49	-16338.74	-16068.17	-16130.13
10	-16844.13	-15840.63	-15775.14	-15835.35
11	-14395.02	-14135.75	-14187.85	-14253.41
12	-14268.81	-14063.91	-14117.87	-14192.10
13	-14045.40	-13873.26	-13928.66	-14005.31
14	-15244.65	-14767.83	-14789.91	-14850.78
15	-20157.67	-18564.20	-18415.87	-18477.53
16	-16564.88	-15701.56	-15663.31	-15722.73
17	-17241.67	-16377.31	-16331.70	-16405.14
18	-15699.60	-14919.54	-14885.43	-14946.86
19	-14250.93	-14007.20	-14053.84	-14127.77
20	-15734.59	-15384.31	-15415.93	-15485.38
21	-15229.35	-14646.37	-14635.43	-14709.99
22	-14266.28	-14074.75	-14134.31	-14205.65
23	-16474.39	-15746.96	-15727.66	-15789.93
24	-14713.63	-14263.38	-14273.54	-14346.92
25	-14778.87	-14445.58	-14486.35	-14554.50
26	-17383.05	-15713.32	-15514.29	-15578.78
27	-14269.32	-14046.75	-14101.59	-14171.20
28	-14620.84	-14396.04	-14452.30	-14521.80
29	-14577.32	-14225.08	-14251.77	-14325.33

30	-14510.53	-14181.40	-14217.24	-14286.78
31	-14992.62	-14608.98	-14647.56	-14710.16
32	-14253.66	-14061.81	-14120.62	-14189.71
33	-16256.61	-15462.38	-15429.48	-15491.89
34	-14398.33	-14122.77	-14169.24	-14240.64
35	-16197.68	-15286.37	-15222.94	-15286.45
36	-16709.91	-15662.49	-15567.98	-15641.67
37	-14948.87	-14498.20	-14509.72	-14583.87
38	-15375.73	-14829.61	-14840.64	-14901.69
39	-14297.18	-14046.03	-14092.29	-14165.46
40	-14442.73	-14175.30	-14223.66	-14292.25
41	-15446.78	-15065.28	-15101.01	-15172.53
42	-14178.53	-13999.56	-14059.67	-14132.35
43	-20734.84	-19042.27	-18878.52	-18940.76
44	-15397.71	-14871.44	-14889.66	-14945.85
45	-14403.00	-14162.97	-14215.28	-14286.17
46	-14533.42	-14253.96	-14295.38	-14368.37
47	-14063.57	-13904.26	-13960.84	-14040.27
48	-14691.03	-14400.05	-14452.53	-14511.87
49	-14905.84	-14581.66	-14629.69	-14692.15
50	-15432.34	-14725.60	-14698.08	-14764.14
51	-15349.55	-14704.03	-14686.98	-14756.26
52	-14440.66	-14198.42	-14254.44	-14320.61
53	-14319.49	-14130.06	-14188.50	-14260.07
54	-14099.42	-13914.57	-13970.43	-14046.32
55	-17032.85	-16205.56	-16171.28	-16236.35
56	-15200.73	-14708.83	-14719.79	-14789.43
57	-14207.83	-14004.08	-14059.62	-14131.69
58	-14882.89	-14528.18	-14568.58	-14632.57
59	-15803.08	-15135.98	-15126.17	-15185.36
60	-14724.16	-14472.31	-14528.59	-14592.11
61	-21991.74	-19980.28	-19773.58	-19830.83
62	-16979.91	-15591.42	-15447.97	-15514.73
63	-14410.23	-14152.30	-14206.57	-14271.35
64	-15443.71	-14755.25	-14728.51	-14798.72
65	-14361.81	-14152.20	-14214.29	-14281.90
66	-14288.40	-14079.87	-14137.66	-14206.17
67	-17323.77	-16711.31	-16713.12	-16779.81
68	-16429.90	-15546.15	-15502.17	-15560.01
69	-15429.24	-14920.71	-14930.69	-14999.66
70	-26859.85	-20006.90	-18858.66	-18923.44
71	-16976.69	-16058.48	-16013.47	-16072.58
72	-14640.06	-14363.96	-14412.92	-14481.47
73	-14577.19	-14286.13	-14335.72	-14400.24
74	-16208.20	-15118.84	-15019.55	-15087.52

75	-24654.38	-21708.39	-21343.53	-21397.94
76	-14412.00	-14118.05	-14153.22	-14229.79
77	-14328.56	-14131.25	-14188.81	-14258.12
78	-14254.84	-14049.58	-14106.84	-14176.23
79	-14900.22	-14567.99	-14612.88	-14676.59
80	-14330.88	-14105.52	-14163.14	-14228.74
81	-14474.89	-14222.71	-14274.83	-14346.58
82	-14424.74	-14162.23	-14212.59	-14280.26
83	-14459.36	-14219.56	-14271.13	-14340.07
84	-14524.57	-14256.37	-14307.21	-14372.94
85	-20450.39	-17404.07	-16953.95	-17024.69
86	-22650.83	-18841.69	-18268.70	-18331.13
87	-35397.20	-28243.98	-26499.13	-27299.51
88	-15087.10	-14772.29	-14821.33	-14883.42
89	-14250.68	-14024.85	-14078.89	-14148.24
90	-15736.93	-15147.91	-15159.61	-15212.10
91	-16347.21	-15236.91	-15143.29	-15203.77
92	-14932.09	-14437.14	-14446.56	-14513.91
93	-14381.33	-14166.27	-14226.33	-14296.35
94	-14988.55	-14549.24	-14572.88	-14642.25
95	-14363.37	-14154.09	-14209.37	-14282.61
96	-15514.59	-14808.75	-14784.32	-14848.65
97	-14149.42	-13970.10	-14029.58	-14101.76
98	-14218.42	-14012.86	-14066.81	-14139.38
99	-14565.84	-14290.71	-14342.68	-14408.21
100	-15426.44	-14778.83	-14762.35	-14831.12
All	-1583922.80	-1510751.60	-1507217.24	-1514667.66

(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 = 105.119348]

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
Θ_1	382578640/399990894	0.95647
Genealogies	159598537/1600009106	0.09975

MCMC-Autocorrelation and Effective MCMC Sample Size

Parameter	Autocorrelation	Effective Sampe Size
Θ_1	0.56002	2833966.99
Genealogies	0.27374	5867482.39

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. Whith many parameters in a multilocus analysi s, it is very common that some parameters for some loci will not be very informative, triggering suggestions (for example to increase the prior ran ge) that are not sensible. This suggestion tool will improve with time, therefore do not blindly follow its suggestions. If some parameters are fla gged, inspect the tables carefully and judge wether an action is required. For example, if you run a Bayesian inference with sequence data, for mac roscopic 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 rou tes 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