

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 39 compute nodes are available.

Program started at Fri Aug 11 02:10:48 2017

Program finished at Fri Aug 11 17:32:25 2017 [Runtime:0000:15:21:37]



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)

1749442872

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 -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_0.4

Posterior distribution raw histogram file:

bayesfile

Raw data from the MCMC run:

bayesallfile_0.6_0.4

Print data:

No

Print genealogies [only some for some data type]:

None

Data summary

Data file: infile.0.6
 Datatype: Sequence data
 Number of loci: 100

Mutationmodel:

Locus	Sublocus	Mutationmodel	Mutationmodel parameters
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1	1	Jukes-Cantor	[Basefreq: =0.25]
2	1	Jukes-Cantor	[Basefreq: =0.25]
3	1	Jukes-Cantor	[Basefreq: =0.25]
4	1	Jukes-Cantor	[Basefreq: =0.25]
5	1	Jukes-Cantor	[Basefreq: =0.25]
6	1	Jukes-Cantor	[Basefreq: =0.25]
7	1	Jukes-Cantor	[Basefreq: =0.25]
8	1	Jukes-Cantor	[Basefreq: =0.25]
9	1	Jukes-Cantor	[Basefreq: =0.25]
10	1	Jukes-Cantor	[Basefreq: =0.25]
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12	1	Jukes-Cantor	[Basefreq: =0.25]
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30	1	Jukes-Cantor	[Basefreq: =0.25]
31	1	Jukes-Cantor	[Basefreq: =0.25]
32	1	Jukes-Cantor	[Basefreq: =0.25]
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36	1	Jukes-Cantor	[Basefreq: =0.25]
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40	1	Jukes-Cantor	[Basefreq: =0.25]
41	1	Jukes-Cantor	[Basefreq: =0.25]
42	1	Jukes-Cantor	[Basefreq: =0.25]
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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]
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50	1	Jukes-Cantor	[Basefreq: =0.25]
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68	1	Jukes-Cantor	[Basefreq: =0.25]
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]
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74	1	Jukes-Cantor	[Basefreq: =0.25]
75	1	Jukes-Cantor	[Basefreq: =0.25]
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80	1	Jukes-Cantor	[Basefreq: =0.25]
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82	1	Jukes-Cantor	[Basefreq: =0.25]
83	1	Jukes-Cantor	[Basefreq: =0.25]
84	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
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21	10000
22	10000
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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	
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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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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	0.03113	0.04453	0.04783	0.04947	0.05160	0.04477	0.08111
2	Θ_1	0.03273	0.04367	0.04790	0.04980	0.05160	0.04490	0.08357
3	Θ_1	0.03167	0.04427	0.04783	0.04967	0.05160	0.04477	0.08138
4	Θ_1	0.03627	0.04627	0.04803	0.04940	0.05167	0.04643	0.08900
5	Θ_1	0.03160	0.04380	0.04770	0.04960	0.05167	0.04510	0.08343
6	Θ_1	0.03153	0.04387	0.04783	0.04980	0.05153	0.04503	0.08318
7	Θ_1	0.02973	0.04313	0.04777	0.04980	0.05167	0.04437	0.07978
8	Θ_1	0.03000	0.04320	0.04777	0.04973	0.05153	0.04437	0.08097
9	Θ_1	0.03153	0.04387	0.04783	0.04980	0.05160	0.04510	0.08311
10	Θ_1	0.02993	0.04307	0.04777	0.04973	0.05160	0.04430	0.07997
11	Θ_1	0.03233	0.04467	0.04783	0.04933	0.05160	0.04490	0.08283
12	Θ_1	0.03140	0.04353	0.04803	0.04980	0.05160	0.04477	0.08303
13	Θ_1	0.03273	0.04400	0.04783	0.04973	0.05160	0.04517	0.08308
14	Θ_1	0.03033	0.04327	0.04783	0.04987	0.05153	0.04443	0.07907
15	Θ_1	0.03333	0.04500	0.04783	0.04947	0.05147	0.04517	0.08344
16	Θ_1	0.02827	0.04207	0.04770	0.04953	0.05147	0.04337	0.07672
17	Θ_1	0.03007	0.04287	0.04777	0.04967	0.05153	0.04410	0.07897
18	Θ_1	0.02353	0.04173	0.04763	0.04953	0.05180	0.04303	0.07534

19	Θ_1	0.03027	0.04407	0.04777	0.04940	0.05160	0.04423	0.07951
20	Θ_1	0.03200	0.04433	0.04790	0.04993	0.05173	0.04543	0.08454
21	Θ_1	0.03107	0.04427	0.04790	0.04953	0.05153	0.04443	0.08084
22	Θ_1	0.03213	0.04367	0.04777	0.04960	0.05167	0.04497	0.08313
23	Θ_1	0.03093	0.04460	0.04777	0.04947	0.05167	0.04477	0.08139
24	Θ_1	0.03027	0.04380	0.04777	0.04947	0.05153	0.04403	0.07934
25	Θ_1	0.03140	0.04327	0.04783	0.04980	0.05153	0.04450	0.08101
26	Θ_1	0.03260	0.04473	0.04783	0.04947	0.05167	0.04523	0.08552
27	Θ_1	0.02993	0.04293	0.04777	0.04980	0.05160	0.04410	0.08102
28	Θ_1	0.03060	0.04400	0.04783	0.04960	0.05153	0.04443	0.08089
29	Θ_1	0.03000	0.04407	0.04777	0.04953	0.05153	0.04423	0.08111
30	Θ_1	0.03067	0.04327	0.04783	0.04980	0.05153	0.04443	0.08072
31	Θ_1	0.02993	0.04307	0.04777	0.04967	0.05160	0.04423	0.08055
32	Θ_1	0.03173	0.04387	0.04790	0.04980	0.05160	0.04503	0.08364
33	Θ_1	0.02880	0.04220	0.04770	0.04953	0.05153	0.04350	0.07735
34	Θ_1	0.03233	0.04453	0.04797	0.04980	0.05160	0.04503	0.08311
35	Θ_1	0.03133	0.04447	0.04763	0.04927	0.05153	0.04463	0.08066
36	Θ_1	0.02887	0.04220	0.04770	0.04960	0.05147	0.04350	0.07625
37	Θ_1	0.03253	0.04387	0.04777	0.04960	0.05160	0.04510	0.08353
38	Θ_1	0.03227	0.04387	0.04790	0.04987	0.05160	0.04503	0.08283
39	Θ_1	0.03247	0.04407	0.04797	0.04987	0.05167	0.04523	0.08407
40	Θ_1	0.03287	0.04420	0.04777	0.04980	0.05160	0.04530	0.08444
41	Θ_1	0.03400	0.04420	0.04790	0.04967	0.05153	0.04543	0.08574

Locus	Parameter	2.5%	25.0%	Mode	75.0%	97.5%	Median	Mean
42	Θ_1	0.02920	0.04240	0.04777	0.04973	0.05147	0.04363	0.07771
43	Θ_1	0.03153	0.04467	0.04797	0.04967	0.05160	0.04483	0.08266
44	Θ_1	0.03213	0.04393	0.04790	0.04980	0.05167	0.04510	0.08356
45	Θ_1	0.03167	0.04460	0.04790	0.04927	0.05167	0.04477	0.08248
46	Θ_1	0.03027	0.04313	0.04777	0.04980	0.05147	0.04430	0.07974
47	Θ_1	0.02780	0.04180	0.04770	0.04960	0.05147	0.04310	0.07500
48	Θ_1	0.03153	0.04360	0.04770	0.04967	0.05153	0.04483	0.08122
49	Θ_1	0.03060	0.04300	0.04770	0.04960	0.05147	0.04430	0.08037
50	Θ_1	0.03107	0.04340	0.04777	0.04967	0.05153	0.04457	0.08074
51	Θ_1	0.02760	0.04167	0.04777	0.04960	0.05153	0.04297	0.07514
52	Θ_1	0.03087	0.04360	0.04790	0.04980	0.05160	0.04477	0.08213
53	Θ_1	0.03093	0.04360	0.04777	0.04960	0.05147	0.04437	0.07989
54	Θ_1	0.02900	0.04240	0.04770	0.04967	0.05153	0.04363	0.07662
55	Θ_1	0.03260	0.04500	0.04783	0.04953	0.05160	0.04517	0.08362
56	Θ_1	0.03293	0.04433	0.04797	0.04993	0.05167	0.04550	0.08587
57	Θ_1	0.03080	0.04300	0.04777	0.04967	0.05147	0.04423	0.08103
58	Θ_1	0.03033	0.04273	0.04777	0.04967	0.05153	0.04403	0.07845
59	Θ_1	0.03133	0.04400	0.04797	0.05000	0.05167	0.04510	0.08329
60	Θ_1	0.03200	0.04373	0.04783	0.04973	0.05167	0.04497	0.08353
61	Θ_1	0.02967	0.04287	0.04777	0.04973	0.05153	0.04410	0.07826

62	Θ_1	0.03167	0.04353	0.04783	0.04973	0.05160	0.04470	0.08194
63	Θ_1	0.02767	0.04180	0.04770	0.04960	0.05147	0.04310	0.07515
64	Θ_1	0.02940	0.04273	0.04777	0.04967	0.05153	0.04390	0.07779
65	Θ_1	0.03047	0.04313	0.04777	0.04960	0.05147	0.04437	0.08162
66	Θ_1	0.03120	0.04373	0.04790	0.04987	0.05153	0.04490	0.08365
67	Θ_1	0.03187	0.04387	0.04790	0.04980	0.05167	0.04510	0.08443
68	Θ_1	0.03120	0.04327	0.04783	0.04973	0.05160	0.04450	0.08051
69	Θ_1	0.03160	0.04340	0.04783	0.04980	0.05153	0.04457	0.08135
70	Θ_1	0.03080	0.04320	0.04777	0.04973	0.05160	0.04443	0.08003
71	Θ_1	0.03093	0.04333	0.04783	0.04973	0.05160	0.04457	0.08095
72	Θ_1	0.03167	0.04473	0.04783	0.04947	0.05167	0.04490	0.08352
73	Θ_1	0.02987	0.04280	0.04790	0.04967	0.05167	0.04417	0.08093
74	Θ_1	0.03033	0.04353	0.04777	0.04980	0.05160	0.04470	0.08291
75	Θ_1	0.03233	0.04487	0.04797	0.04960	0.05160	0.04503	0.08210
76	Θ_1	0.03000	0.04373	0.04777	0.04933	0.05153	0.04390	0.07855
77	Θ_1	0.02993	0.04307	0.04783	0.04973	0.05167	0.04430	0.07998
78	Θ_1	0.03167	0.04367	0.04790	0.04987	0.05167	0.04483	0.08257
79	Θ_1	0.02880	0.04240	0.04777	0.04967	0.05153	0.04363	0.07722
80	Θ_1	0.03033	0.04300	0.04783	0.04967	0.05160	0.04417	0.08148
81	Θ_1	0.03260	0.04487	0.04783	0.04933	0.05167	0.04503	0.08501
82	Θ_1	0.02947	0.04293	0.04777	0.04973	0.05153	0.04410	0.07992
83	Θ_1	0.03193	0.04387	0.04783	0.04980	0.05167	0.04503	0.08370
84	Θ_1	0.02853	0.04220	0.04783	0.04967	0.05153	0.04343	0.07642

Locus	Parameter	2.5%	25.0%	Mode	75.0%	97.5%	Median	Mean
85	Θ_1	0.02927	0.04300	0.04770	0.04940	0.05140	0.04357	0.07719
86	Θ_1	0.03253	0.04500	0.04790	0.04940	0.05160	0.04517	0.08351
87	Θ_1	0.02827	0.04293	0.04763	0.04920	0.05140	0.04310	0.07521
88	Θ_1	0.02853	0.04227	0.04777	0.04973	0.05153	0.04350	0.07742
89	Θ_1	0.03387	0.04420	0.04790	0.04980	0.05160	0.04537	0.08547
90	Θ_1	0.03267	0.04427	0.04783	0.04980	0.05173	0.04543	0.08478
91	Θ_1	0.03313	0.04407	0.04783	0.04960	0.05153	0.04530	0.08471
92	Θ_1	0.03040	0.04340	0.04777	0.04973	0.05160	0.04457	0.08003
93	Θ_1	0.03087	0.04353	0.04777	0.04987	0.05153	0.04463	0.08319
94	Θ_1	0.03133	0.04453	0.04783	0.04947	0.05160	0.04470	0.08131
95	Θ_1	0.03133	0.04353	0.04777	0.04967	0.05167	0.04477	0.08357
96	Θ_1	0.03027	0.04293	0.04777	0.04960	0.05153	0.04423	0.07919
97	Θ_1	0.02960	0.04380	0.04770	0.04947	0.05153	0.04397	0.07799
98	Θ_1	0.03133	0.04327	0.04777	0.04967	0.05153	0.04450	0.08121
99	Θ_1	0.03267	0.04407	0.04790	0.04980	0.05153	0.04523	0.08366
100	Θ_1	0.02993	0.04293	0.04770	0.04967	0.05153	0.04417	0.07857
All	Θ_1	0.00733	0.01047	0.01257	0.01380	0.01647	0.01210	0.09964

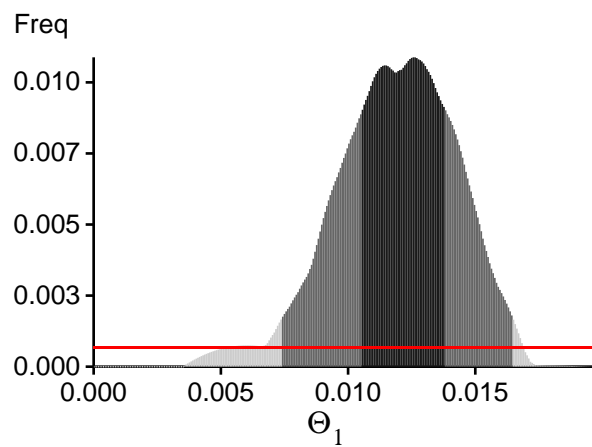
Citation suggestions:

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	-13976.00	-13813.53	-13861.60	-13946.91
2	-14117.69	-13940.96	-13987.99	-14069.16
3	-13965.60	-13817.28	-13866.80	-13955.09
4	-134364.72	-82889.38	-73874.26	-73953.36
5	-14434.41	-14147.92	-14181.66	-14261.66
6	-14077.55	-13899.19	-13949.94	-14030.12
7	-13923.32	-13776.86	-13824.03	-13913.13
8	-14224.91	-13992.36	-14030.41	-14115.10
9	-14037.00	-13883.65	-13933.71	-14018.13
10	-13971.58	-13803.21	-13848.46	-13936.40
11	-15079.25	-14432.84	-14399.21	-14480.95
12	-14270.74	-14033.11	-14075.21	-14154.35
13	-14620.10	-14180.38	-14183.41	-14264.63
14	-13925.04	-13771.33	-13817.08	-13906.14
15	-14594.14	-14174.59	-14179.93	-14262.95
16	-13882.01	-13740.06	-13783.17	-13875.94
17	-13910.51	-13765.12	-13811.79	-13905.52
18	-13867.09	-13726.81	-13770.08	-13863.69
19	-13922.90	-13777.18	-13823.98	-13913.05
20	-14966.76	-14414.43	-14396.05	-14477.87
21	-14045.92	-13865.81	-13911.52	-13997.13
22	-14432.45	-14208.22	-14253.82	-14334.00
23	-15855.49	-14800.75	-14690.58	-14774.02
24	-13924.91	-13780.84	-13827.04	-13916.50
25	-14017.13	-13843.92	-13891.03	-13976.50
26	-14511.73	-14201.80	-14238.80	-14313.49
27	-18789.95	-17039.80	-16815.41	-16914.85
28	-13945.45	-13790.52	-13837.92	-13924.59
29	-13960.04	-13813.71	-13862.35	-13950.57

30	-14124.54	-13911.21	-13951.04	-14036.04
31	-13949.07	-13803.46	-13851.37	-13940.41
32	-14080.39	-13919.71	-13967.82	-14053.61
33	-13898.92	-13751.03	-13795.62	-13886.80
34	-14051.83	-13890.16	-13944.23	-14024.48
35	-14489.86	-14130.01	-14144.64	-14229.48
36	-13881.63	-13741.14	-13785.81	-13878.18
37	-14144.38	-13972.47	-14022.36	-14104.95
38	-19518.81	-17204.21	-16882.73	-16963.30
39	-14456.72	-14265.07	-14299.85	-14389.28
40	-14124.76	-13932.53	-13940.21	-14061.26
41	-15273.19	-14735.88	-13955.43	-14806.30
42	-13895.75	-13753.52	-13799.75	-13889.47
43	-14144.28	-13930.39	-13866.83	-14055.86
44	-14190.82	-13986.25	-13986.29	-14114.15
45	-14786.98	-14316.91	-13844.31	-14397.89
46	-14019.54	-13836.98	-13860.33	-13966.99
47	-13864.08	-13723.84	-13766.89	-13860.77
48	-13973.44	-13820.34	-13827.27	-13956.36
49	-13958.96	-13801.76	-13827.26	-13935.79
50	-14020.99	-13841.04	-13850.80	-13970.96
51	-13867.88	-13727.53	-13771.21	-13864.43
52	-15163.87	-14636.35	-13821.43	-14709.74
53	-14007.94	-13838.70	-13884.85	-13971.35
54	-13883.56	-13741.42	-13783.87	-13877.78
55	-16542.87	-15491.06	-13873.87	-15473.29
56	-19192.62	-17968.23	-13872.87	-17925.06
57	-14212.41	-14025.01	-13803.44	-14156.23
58	-13996.78	-13809.30	-13848.90	-13938.34
59	-14042.86	-13869.98	-13920.61	-14001.35
60	-14206.13	-14008.86	-13842.51	-14135.26
61	-13929.43	-13776.54	-13789.30	-13912.52
62	-14009.41	-13836.45	-13883.32	-13968.01
63	-13865.12	-13724.97	-13767.76	-13862.00
64	-13930.53	-13769.68	-13812.75	-13903.32
65	-17981.78	-16572.08	-13802.84	-16500.37
66	-15533.36	-14880.94	-14189.99	-14934.34
67	-14731.33	-14269.62	-13790.63	-14349.41
68	-14892.24	-14590.78	-14150.97	-14707.30
69	-14183.04	-13970.37	-14012.47	-14096.28
70	-14355.05	-14151.46	-14194.96	-14281.65
71	-14022.69	-13846.95	-13892.97	-13978.34
72	-14965.62	-14683.75	-14309.32	-14796.93
73	-14091.46	-13897.24	-13941.08	-14026.21
74	-21728.84	-19824.16	-14241.17	-19659.83

75	-14094.07	-13891.98	-13935.13	-14018.91
76	-13917.11	-13763.37	-13808.72	-13897.61
77	-14520.07	-14144.70	-14155.14	-14241.19
78	-14124.87	-13930.14	-13975.63	-14057.85
79	-13890.56	-13749.93	-13796.08	-13887.11
80	-20783.52	-18179.47	-13876.61	-17899.02
81	-15020.06	-14525.08	-13927.08	-14601.93
82	-13929.82	-13785.19	-13831.62	-13921.25
83	-14380.88	-14087.70	-14119.97	-14199.32
84	-13882.34	-13740.03	-13784.35	-13876.23
85	-13891.85	-13751.11	-13795.12	-13888.41
86	-14081.90	-13912.47	-13894.84	-14045.85
87	-13865.05	-13724.86	-13766.94	-13861.82
88	-13893.93	-13753.28	-13787.45	-13890.39
89	-46094.97	-29783.71	-14275.11	-26945.73
90	-14203.42	-14002.05	-14043.02	-14128.37
91	-14580.36	-14311.88	-14323.85	-14429.84
92	-13957.64	-13793.07	-13838.72	-13925.64
93	-14187.65	-13991.26	-13787.72	-14118.58
94	-14533.04	-14156.37	-14168.49	-14252.86
95	-15004.95	-14669.85	-14059.95	-14772.75
96	-14009.11	-13855.49	-13778.17	-13991.14
97	-13899.58	-13752.58	-13797.18	-13888.58
98	-14005.73	-13834.97	-13823.42	-13967.42
99	-14172.40	-13974.20	-13902.79	-14102.14
100	-13947.70	-13801.20	-13827.03	-13937.80
All	-1608553.41	-1507251.50	-1460261.97	-1505585.88
(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 = 119.317967]				
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	380725044/399995364	0.95182
Genealogies	537426124/1600004636	0.33589

MCMC-Autocorrelation and Effective MCMC Sample Size

Parameter	Autocorrelation	Effective Sampe Size
Θ_1	0.53971	8010594.49
Genealogies	0.18406	20146560.09

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