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 00:34:39 2017
Program finished at Sun Aug 13 04:10:15 2017 [Runtime:0000:03:35:36]

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) 2576299313
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.0.6
Haplotyping is turned on:	NO
Output file:	outfile_0.6_1.0
Posterior distribution raw histogram file:	bayesfile
Raw data from the MCMC run:	bayesallfile_0.6_1.0
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
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]
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22	1	Jukes-Cantor	[Basefreq: =0.25]
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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]
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80	1	Jukes-Cantor	[Basefreq: =0.25]
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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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28	10000
29	10000
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34	10000
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36	10000
37	10000
38	10000
39	10000
40	10000
41	10000
42	10000
43	10000
44	10000
45	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
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
	22	10
	23	10
	24	10
	25	10
	26	10
	27	10
	28	10
	29	10
	30	10
	31	10
	32	10
	33	10
	34	10
	35	10
	36	10
	37	10
	38	10
	39	10
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	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
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92	10
93	10
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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	0.00093	0.00307	0.00457	0.00600	0.01013	0.00497	0.00527
2	Θ_1	0.00000	0.00000	0.00010	0.00107	0.00240	0.00110	0.00033
3	Θ_1	0.00000	0.00000	0.00003	0.00100	0.00233	0.00103	0.00029
4	Θ_1	0.00000	0.00000	0.00043	0.00113	0.00253	0.00117	0.00045
5	Θ_1	0.00000	0.00000	0.00043	0.00113	0.00247	0.00117	0.00042
6	Θ_1	0.00000	0.00040	0.00130	0.00207	0.00360	0.00170	0.00133
7	Θ_1	0.00000	0.00000	0.00037	0.00107	0.00247	0.00110	0.00040
8	Θ_1	0.00000	0.00053	0.00143	0.00220	0.00380	0.00177	0.00146
9	Θ_1	0.00480	0.00813	0.01077	0.01407	0.02393	0.01243	0.01350
10	Θ_1	0.00000	0.00000	0.00003	0.00100	0.00240	0.00103	0.00030
11	Θ_1	0.00020	0.00207	0.00337	0.00453	0.00720	0.00357	0.00367
12	Θ_1	0.00000	0.00000	0.00050	0.00113	0.00260	0.00117	0.00050
13	Θ_1	0.00000	0.00000	0.00037	0.00107	0.00247	0.00110	0.00039
14	Θ_1	0.00080	0.00293	0.00437	0.00580	0.00980	0.00477	0.00504
15	Θ_1	0.00000	0.00000	0.00023	0.00107	0.00240	0.00110	0.00034
16	Θ_1	0.00260	0.00527	0.00710	0.00940	0.01613	0.00810	0.00873
17	Θ_1	0.00000	0.00000	0.00030	0.00107	0.00240	0.00110	0.00035
18	Θ_1	0.00000	0.00000	0.00017	0.00107	0.00240	0.00110	0.00033

19	Θ_1	0.00100	0.00313	0.00457	0.00607	0.00993	0.00503	0.00529
20	Θ_1	0.00000	0.00073	0.00170	0.00260	0.00427	0.00197	0.00179
21	Θ_1	0.00000	0.00000	0.00050	0.00113	0.00260	0.00117	0.00053
22	Θ_1	0.00000	0.00000	0.00037	0.00113	0.00247	0.00117	0.00041
23	Θ_1	0.00000	0.00000	0.00003	0.00100	0.00233	0.00103	0.00030
24	Θ_1	0.00000	0.00080	0.00177	0.00267	0.00427	0.00203	0.00182
25	Θ_1	0.00000	0.00000	0.00010	0.00107	0.00240	0.00110	0.00032
26	Θ_1	0.00000	0.00000	0.00050	0.00113	0.00260	0.00117	0.00052
27	Θ_1	0.00140	0.00373	0.00530	0.00700	0.01193	0.00590	0.00627
28	Θ_1	0.00000	0.00000	0.00010	0.00100	0.00240	0.00103	0.00030
29	Θ_1	0.00000	0.00000	0.00003	0.00100	0.00233	0.00103	0.00027
30	Θ_1	0.00000	0.00000	0.00043	0.00113	0.00253	0.00117	0.00043
31	Θ_1	0.00000	0.00027	0.00103	0.00180	0.00327	0.00150	0.00107
32	Θ_1	0.00000	0.00007	0.00077	0.00147	0.00293	0.00137	0.00079
33	Θ_1	0.00000	0.00100	0.00203	0.00300	0.00480	0.00230	0.00216
34	Θ_1	0.00000	0.00053	0.00143	0.00220	0.00373	0.00177	0.00146
35	Θ_1	0.00000	0.00013	0.00090	0.00160	0.00307	0.00143	0.00094
36	Θ_1	0.00000	0.00027	0.00103	0.00173	0.00320	0.00150	0.00104
37	Θ_1	0.00273	0.00540	0.00730	0.00960	0.01660	0.00837	0.00899
38	Θ_1	0.00000	0.00013	0.00090	0.00160	0.00307	0.00143	0.00094
39	Θ_1	0.00000	0.00000	0.00043	0.00113	0.00253	0.00117	0.00044
40	Θ_1	0.00000	0.00000	0.00003	0.00100	0.00233	0.00103	0.00030
41	Θ_1	0.00000	0.00000	0.00003	0.00100	0.00233	0.00103	0.00029

Locus	Parameter	2.5%	25.0%	Mode	75.0%	97.5%	Median	Mean
42	Θ_1	0.00000	0.00013	0.00083	0.00153	0.00300	0.00137	0.00087
43	Θ_1	0.00000	0.00000	0.00003	0.00100	0.00233	0.00103	0.00029
44	Θ_1	0.00000	0.00000	0.00043	0.00113	0.00253	0.00117	0.00047
45	Θ_1	0.00000	0.00013	0.00083	0.00153	0.00300	0.00137	0.00086
46	Θ_1	0.00000	0.00013	0.00090	0.00153	0.00300	0.00137	0.00089
47	Θ_1	0.00000	0.00000	0.00057	0.00120	0.00267	0.00123	0.00055
48	Θ_1	0.00000	0.00073	0.00170	0.00253	0.00407	0.00197	0.00172
49	Θ_1	0.00000	0.00000	0.00030	0.00107	0.00247	0.00110	0.00038
50	Θ_1	0.00813	0.01160	0.01357	0.01580	0.02313	0.01583	0.01722
51	Θ_1	0.00487	0.00847	0.01123	0.01473	0.02573	0.01297	0.01413
52	Θ_1	0.00000	0.00000	0.00010	0.00100	0.00240	0.00103	0.00032
53	Θ_1	0.00000	0.00000	0.00003	0.09993	0.09993	0.00003	0.09486
54	Θ_1	0.00000	0.00020	0.00097	0.00167	0.00320	0.00150	0.00101
55	Θ_1	0.00000	0.00000	0.00037	0.00107	0.00247	0.00110	0.00040
56	Θ_1	0.00000	0.00133	0.00243	0.00347	0.00540	0.00263	0.00259
57	Θ_1	0.00000	0.00000	0.00003	0.00100	0.00233	0.00103	0.00028
58	Θ_1	0.00000	0.00147	0.00263	0.00367	0.00567	0.00283	0.00282
59	Θ_1	0.00000	0.00000	0.00070	0.00133	0.00280	0.00130	0.00072
60	Θ_1	0.00000	0.00000	0.00030	0.00107	0.00240	0.00110	0.00035
61	Θ_1	0.00000	0.00133	0.00243	0.00347	0.00533	0.00263	0.00257

62	Θ_1	0.00000	0.00000	0.00003	0.00100	0.00233	0.00103	0.00028
63	Θ_1	0.00000	0.00180	0.00303	0.00413	0.00660	0.00323	0.00330
64	Θ_1	0.00000	0.00000	0.00003	0.00093	0.00227	0.00097	0.00026
65	Θ_1	0.00000	0.00020	0.00097	0.00167	0.00307	0.00143	0.00096
66	Θ_1	0.00000	0.00013	0.00083	0.00153	0.00300	0.00137	0.00087
67	Θ_1	0.00000	0.00000	0.00017	0.00100	0.00240	0.00103	0.00030
68	Θ_1	0.00000	0.00000	0.00003	0.00100	0.00233	0.00103	0.00027
69	Θ_1	0.00000	0.00000	0.00003	0.00100	0.00233	0.00103	0.00027
70	Θ_1	0.00000	0.00000	0.00003	0.00093	0.00227	0.00097	0.00026
71	Θ_1	0.00000	0.00000	0.00010	0.00107	0.00240	0.00110	0.00033
72	Θ_1	0.00200	0.00453	0.00630	0.00833	0.01433	0.00717	0.00767
73	Θ_1	0.00000	0.00020	0.00097	0.00167	0.00313	0.00143	0.00097
74	Θ_1	0.00000	0.00000	0.00037	0.00113	0.00247	0.00117	0.00041
75	Θ_1	0.00000	0.00167	0.00290	0.00400	0.00627	0.00310	0.00315
76	Θ_1	0.00000	0.00000	0.00003	0.00093	0.00227	0.00097	0.00026
77	Θ_1	0.00000	0.00000	0.00063	0.00120	0.00273	0.00123	0.00061
78	Θ_1	0.00000	0.00000	0.00043	0.00113	0.00253	0.00117	0.00045
79	Θ_1	0.00000	0.00000	0.00003	0.00093	0.00227	0.00097	0.00026
80	Θ_1	0.00000	0.00000	0.00057	0.00120	0.00267	0.00123	0.00059
81	Θ_1	0.00027	0.00227	0.00363	0.00487	0.00793	0.00390	0.00404
82	Θ_1	0.01313	0.01753	0.02030	0.02340	0.03313	0.02357	0.02610
83	Θ_1	0.00000	0.00000	0.00003	0.00087	0.00220	0.00090	0.00023
84	Θ_1	0.00000	0.00000	0.00003	0.00093	0.00227	0.00097	0.00026

Locus	Parameter	2.5%	25.0%	Mode	75.0%	97.5%	Median	Mean
85	Θ_1	0.00000	0.00020	0.00097	0.00167	0.00313	0.00143	0.00098
86	Θ_1	0.00000	0.00000	0.00037	0.00107	0.00247	0.00110	0.00039
87	Θ_1	0.00000	0.00027	0.00103	0.00173	0.00313	0.00150	0.00102
88	Θ_1	0.00000	0.00000	0.00070	0.00133	0.00287	0.00130	0.00073
89	Θ_1	0.00027	0.00227	0.00357	0.00487	0.00793	0.00390	0.00403
90	Θ_1	0.00000	0.00153	0.00270	0.00373	0.00567	0.00283	0.00283
91	Θ_1	0.00000	0.00000	0.00070	0.00133	0.00280	0.00130	0.00069
92	Θ_1	0.00053	0.00253	0.00397	0.00520	0.00860	0.00423	0.00444
93	Θ_1	0.00000	0.00027	0.00110	0.00180	0.00327	0.00150	0.00110
94	Θ_1	0.00000	0.00000	0.00017	0.00107	0.00240	0.00110	0.00033
95	Θ_1	0.00000	0.00133	0.00243	0.00347	0.00533	0.00263	0.00259
96	Θ_1	0.00000	0.00000	0.00050	0.00113	0.00260	0.00117	0.00049
97	Θ_1	0.00000	0.00000	0.00010	0.00107	0.00240	0.00110	0.00031
98	Θ_1	0.00000	0.00040	0.00123	0.00200	0.00353	0.00163	0.00126
99	Θ_1	0.00000	0.00000	0.00003	0.00087	0.00220	0.00090	0.00023
100	Θ_1	0.00000	0.00053	0.00137	0.00220	0.00367	0.00170	0.00142
All	Θ_1	0.00000	0.00000	0.00037	0.00107	0.00240	0.00110	0.00039

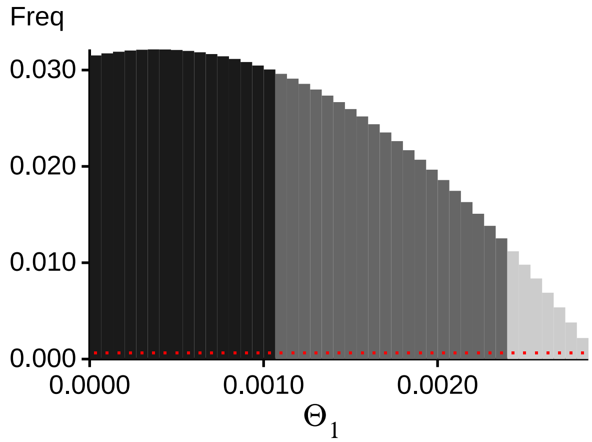
Citation suggestions:

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	-15432.58	-14897.39	-14914.30	-14970.17
2	-14147.09	-13797.99	-13806.81	-13894.83
3	-14151.51	-13800.05	-13805.54	-13896.21
4	-14181.58	-13832.18	-13845.12	-13926.38
5	-14223.65	-13874.85	-13892.97	-13972.06
6	-14388.95	-14024.90	-14054.34	-14121.27
7	-14190.18	-13835.40	-13847.05	-13932.86
8	-14363.84	-14010.15	-14041.45	-14109.12
9	-15807.95	-15441.62	-15503.28	-15551.60
10	-14151.61	-13803.68	-13810.77	-13900.20
11	-15998.78	-15231.76	-15206.65	-15264.64
12	-14196.25	-13846.07	-13860.08	-13942.32
13	-14171.97	-13821.94	-13832.24	-13925.65
14	-15809.76	-15109.20	-15098.34	-15153.98
15	-14184.57	-13827.29	-13837.11	-13922.33
16	-17148.89	-16119.70	-16060.78	-16111.63
17	-14165.84	-13815.63	-13824.50	-13910.63
18	-14158.17	-13807.21	-13816.10	-13903.33
19	-15987.40	-15269.54	-15256.32	-15312.29
20	-14381.81	-14028.16	-14061.70	-14126.67
21	-14318.93	-13939.43	-13954.92	-14032.63
22	-14218.56	-13856.62	-13869.25	-13950.66
23	-14147.94	-13798.62	-13804.11	-13894.85
24	-14489.53	-14112.85	-14144.31	-14208.22
25	-14158.96	-13806.77	-13814.75	-13902.44
26	-14269.41	-13900.00	-13917.33	-13993.91
27	-15313.42	-14850.49	-14882.34	-14936.86
28	-14179.93	-13821.54	-13830.94	-13916.90
29	-14133.38	-13785.01	-13791.13	-13881.39

30	-14184.03	-13833.03	-13843.47	-13928.20
31	-14343.75	-13982.53	-14007.77	-14078.87
32	-14279.76	-13920.09	-13943.09	-14016.08
33	-14435.55	-14086.10	-14118.74	-14184.51
34	-14532.19	-14175.09	-14208.18	-14274.58
35	-14295.30	-13941.61	-13966.66	-14039.30
36	-14595.51	-14162.31	-14177.95	-14246.82
37	-17207.68	-16180.73	-16122.49	-16174.46
38	-14337.83	-13979.09	-14004.67	-14077.17
39	-14223.52	-13875.15	-13891.45	-13972.15
40	-14149.92	-13799.12	-13804.95	-13895.78
41	-14153.14	-13802.08	-13808.21	-13898.16
42	-14417.39	-14027.82	-14048.40	-14120.74
43	-14166.17	-13812.32	-13821.41	-13909.02
44	-14243.07	-13877.69	-13893.78	-13972.39
45	-14360.90	-14011.52	-14037.62	-14110.10
46	-14261.83	-13909.33	-13933.86	-14005.74
47	-14284.18	-13916.18	-13933.87	-14011.05
48	-14487.35	-14111.91	-14142.33	-14206.74
49	-14171.18	-13818.65	-13828.75	-13915.67
50	-15757.72	-15387.23	-15449.02	-15495.73
51	-15389.18	-15050.51	-15113.32	-15164.84
52	-14149.71	-13799.65	-13806.17	-13896.30
53	-40262.40	-36252.00	-35884.51	-35907.98
54	-14272.99	-13925.06	-13948.25	-14020.92
55	-14170.04	-13821.27	-13830.66	-13917.19
56	-14465.14	-14113.54	-14150.62	-14215.34
57	-14142.75	-13793.98	-13800.77	-13890.37
58	-15724.69	-15002.18	-14979.41	-15041.10
59	-14295.94	-13936.58	-13958.22	-14032.32
60	-14183.02	-13827.16	-13837.56	-13924.24
61	-14849.01	-14409.82	-14436.18	-14497.65
62	-14149.02	-13796.99	-13803.19	-13893.11
63	-14657.95	-14285.77	-14324.61	-14384.30
64	-14140.00	-13787.91	-13791.00	-13883.50
65	-14394.93	-14033.45	-14060.69	-14130.56
66	-14283.60	-13930.10	-13953.78	-14025.64
67	-14176.15	-13821.53	-13831.48	-13917.19
68	-14149.92	-13796.07	-13801.00	-13891.68
69	-14132.23	-13784.37	-13790.50	-13882.33
70	-14136.46	-13786.07	-13789.03	-13881.05
71	-14146.57	-13797.34	-13805.51	-13893.83
72	-15334.50	-14893.42	-14934.15	-14987.19
73	-14358.16	-13986.21	-14007.86	-14080.47
74	-14187.39	-13835.93	-13848.47	-13931.74

75	-14758.68	-14376.66	-14414.79	-14474.47
76	-14136.89	-13787.59	-13791.42	-13885.27
77	-14250.72	-13894.03	-13914.09	-13989.96
78	-14206.50	-13859.98	-13876.22	-13956.68
79	-14134.51	-13787.07	-13792.10	-13882.51
80	-14304.35	-13932.97	-13951.18	-14026.13
81	-14662.99	-14305.94	-14349.72	-14406.92
82	-17115.62	-16599.18	-16652.05	-16696.51
83	-14119.81	-13772.11	-13776.08	-13868.53
84	-14137.17	-13787.37	-13791.64	-13882.61
85	-14300.69	-13944.72	-13970.45	-14041.36
86	-14183.71	-13830.64	-13842.06	-13926.27
87	-14592.61	-14185.03	-14205.32	-14275.10
88	-14279.62	-13920.11	-13940.01	-14015.20
89	-14635.86	-14282.54	-14322.52	-14381.97
90	-15832.07	-15015.15	-14975.50	-15035.86
91	-14284.59	-13917.92	-13937.55	-14012.88
92	-15618.99	-15038.11	-15047.07	-15105.27
93	-14325.85	-13969.58	-13995.10	-14067.85
94	-14157.50	-13806.12	-13813.16	-13901.08
95	-15015.00	-14634.40	-14673.87	-14736.87
96	-14205.16	-13850.67	-13865.51	-13947.15
97	-14161.21	-13808.26	-13816.12	-13907.38
98	-14315.08	-13969.40	-13998.22	-14069.50
99	-14116.05	-13768.93	-13772.29	-13866.60
100	-14686.49	-14326.27	-14358.41	-14427.91
All	-1479750.77	-1436214.14	-1437401.45	-1444878.87

(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 = 299.120598]

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	90065214/400010010	0.22516
Genealogies	435915422/1599989990	0.27245

MCMC-Autocorrelation and Effective MCMC Sample Size

Parameter	Autocorrelation	Effective Sampe Size
Θ_1	0.06239	8858813.41
Genealogies	0.12399	7970410.03

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