

# AUTO

POPULATION SIZE, MIGRATION, DIVERGENCE, ASSIGNMENT, HISTORY

Bayesian inference using the structured coalescent

Migrate-n version 5.0.0a [May-20-2017]

Using Intel AVX (Advanced Vector Extensions)

Compiled for PARALLEL computer architectures

One master and 40 compute nodes are available.

Program started at Sun Jul 23 19:32:30 2017

Program finished at Sun Jul 23 22:07:48 2017 [Runtime:0000:02:35:18]



## 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)

1892270635

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.0.4
Haplotyping is turned on:	NO
Output file:	outfile_0.4_0.7
Posterior distribution raw histogram file:	bayesfile
Raw data from the MCMC run:	bayesallfile_0.4_0.7
Print data:	No
Print genealogies [only some for some data type]:	None

## *Data summary*

Data file:	infile.0.4
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]
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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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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]
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50	1	Jukes-Cantor	[Basefreq: =0.25]
51	1	Jukes-Cantor	[Basefreq: =0.25]
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79	1	Jukes-Cantor	[Basefreq: =0.25]

80	1	Jukes-Cantor	[Basefreq: =0.25]
81	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
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21	10000
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85	10000
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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	
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			39		10	
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41	10
42	10
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83	10
84	10
85	10

	86	10
	87	10
	88	10
	89	10
	90	10
	91	10
	92	10
	93	10
	94	10
	95	10
	96	10
	97	10
	98	10
	99	10
	100	10
Total of all populations	1	10
	2	10
	3	10
	4	10
	5	10
	6	10
	7	10
	8	10
	9	10
	10	10
	11	10
	12	10
	13	10
	14	10
	15	10
	16	10
	17	10
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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	$\Theta_1$	0.00000	0.00207	0.00370	0.00547	0.01080	0.00450	0.00496
2	$\Theta_1$	0.00127	0.00473	0.00517	0.00553	0.01240	0.00637	0.00710
3	$\Theta_1$	0.00027	0.00207	0.00370	0.00547	0.00920	0.00450	0.00495
4	$\Theta_1$	0.00000	0.00207	0.00370	0.00547	0.01080	0.00450	0.00496
5	$\Theta_1$	0.00000	0.00207	0.00370	0.00547	0.01080	0.00450	0.00496
6	$\Theta_1$	0.00000	0.00207	0.00370	0.00547	0.01073	0.00450	0.00493
7	$\Theta_1$	0.00000	0.00207	0.00370	0.00547	0.01080	0.00450	0.00497
8	$\Theta_1$	0.00240	0.00460	0.00637	0.00860	0.01380	0.00830	0.00945
9	$\Theta_1$	0.00007	0.00247	0.00417	0.00627	0.01240	0.00517	0.00574
10	$\Theta_1$	0.00000	0.00207	0.00370	0.00547	0.01073	0.00450	0.00494
11	$\Theta_1$	0.00000	0.00207	0.00370	0.00547	0.01073	0.00450	0.00495
12	$\Theta_1$	0.00007	0.00247	0.00410	0.00613	0.01200	0.00503	0.00558
13	$\Theta_1$	0.00000	0.00207	0.00370	0.00547	0.01080	0.00450	0.00496
14	$\Theta_1$	0.00300	0.00907	0.01130	0.01467	0.03767	0.01617	0.01935
15	$\Theta_1$	0.00000	0.00207	0.00370	0.00547	0.01073	0.00450	0.00493
16	$\Theta_1$	0.00107	0.00193	0.00370	0.00573	0.00720	0.00450	0.00496
17	$\Theta_1$	0.00000	0.00253	0.00423	0.00627	0.02013	0.00523	0.00579
18	$\Theta_1$	0.00000	0.00207	0.00370	0.00547	0.01073	0.00450	0.00495

19	$\Theta_1$	0.00107	0.00127	0.00370	0.00693	0.00720	0.00450	0.00496
20	$\Theta_1$	0.00000	0.00207	0.00370	0.00547	0.01080	0.00450	0.00495
21	$\Theta_1$	0.00067	0.00333	0.00530	0.00773	0.01520	0.00643	0.00717
22	$\Theta_1$	0.00033	0.00280	0.00457	0.00673	0.01313	0.00557	0.00618
23	$\Theta_1$	0.00000	0.00207	0.00370	0.00547	0.01080	0.00450	0.00496
24	$\Theta_1$	0.00000	0.00207	0.00370	0.00547	0.01073	0.00450	0.00495
25	$\Theta_1$	0.00020	0.00267	0.00443	0.00660	0.01327	0.00550	0.00613
26	$\Theta_1$	0.00007	0.00240	0.00410	0.00607	0.01200	0.00503	0.00558
27	$\Theta_1$	0.00227	0.00400	0.00610	0.00907	0.01353	0.00830	0.00975
28	$\Theta_1$	0.00547	0.01013	0.01470	0.02140	0.03773	0.01997	0.02477
29	$\Theta_1$	0.00000	0.00207	0.00370	0.00547	0.01080	0.00450	0.00494
30	$\Theta_1$	0.00000	0.00213	0.00370	0.00553	0.01080	0.00450	0.00497
31	$\Theta_1$	0.00000	0.00213	0.00370	0.00553	0.01073	0.00450	0.00496
32	$\Theta_1$	0.00000	0.00207	0.00370	0.00547	0.01080	0.00450	0.00496
33	$\Theta_1$	0.00000	0.00207	0.00370	0.00547	0.01080	0.00450	0.00495
34	$\Theta_1$	0.00000	0.00207	0.00370	0.00547	0.01080	0.00450	0.00496
35	$\Theta_1$	0.00000	0.00207	0.00370	0.00547	0.01080	0.00450	0.00496
36	$\Theta_1$	0.00020	0.00253	0.00423	0.00627	0.01240	0.00523	0.00577
37	$\Theta_1$	0.00000	0.00207	0.00370	0.00547	0.01073	0.00450	0.00494
38	$\Theta_1$	0.00000	0.00213	0.00370	0.00553	0.01080	0.00450	0.00497
39	$\Theta_1$	0.00093	0.00393	0.00617	0.00913	0.01840	0.00770	0.00863
40	$\Theta_1$	0.00000	0.00207	0.00370	0.00547	0.01080	0.00450	0.00497
41	$\Theta_1$	0.00000	0.00207	0.00370	0.00547	0.01413	0.00450	0.00497



Locus	Parameter	2.5%	25.0%	Mode	75.0%	97.5%	Median	Mean
42	$\Theta_1$	0.00167	0.00280	0.00463	0.00693	0.00920	0.00577	0.00646
43	$\Theta_1$	0.00213	0.00460	0.00750	0.01193	0.02047	0.01037	0.01223
44	$\Theta_1$	0.00000	0.00207	0.00370	0.00547	0.01073	0.00450	0.00494
45	$\Theta_1$	0.00007	0.00240	0.00410	0.00607	0.01213	0.00503	0.00559
46	$\Theta_1$	0.00100	0.00473	0.00737	0.01120	0.02607	0.00957	0.01087
47	$\Theta_1$	0.00000	0.00207	0.00370	0.00547	0.01080	0.00450	0.00495
48	$\Theta_1$	0.00000	0.00207	0.00370	0.00547	0.01080	0.00450	0.00496
49	$\Theta_1$	0.00000	0.00207	0.00370	0.00547	0.01080	0.00450	0.00496
50	$\Theta_1$	0.00193	0.00193	0.00637	0.01580	0.01580	0.00863	0.01007
51	$\Theta_1$	0.00000	0.00207	0.00370	0.00547	0.01080	0.00450	0.00495
52	$\Theta_1$	0.00033	0.00280	0.00457	0.00673	0.01333	0.00557	0.00621
53	$\Theta_1$	0.00000	0.00207	0.00370	0.00547	0.01080	0.00450	0.00496
54	$\Theta_1$	0.00000	0.00207	0.00370	0.00547	0.01073	0.00450	0.00495
55	$\Theta_1$	0.00547	0.00740	0.01350	0.02413	0.03053	0.01797	0.02116
56	$\Theta_1$	0.00007	0.00247	0.00417	0.00620	0.01227	0.00510	0.00569
57	$\Theta_1$	0.00007	0.00240	0.00410	0.00607	0.01187	0.00503	0.00553
58	$\Theta_1$	0.00007	0.00247	0.00417	0.00627	0.01253	0.00517	0.00577
59	$\Theta_1$	0.00000	0.00207	0.00370	0.00547	0.01080	0.00450	0.00496
60	$\Theta_1$	0.00000	0.00207	0.00370	0.00547	0.01073	0.00450	0.00494
61	$\Theta_1$	0.00007	0.00247	0.00417	0.00620	0.01227	0.00510	0.00568

62	$\Theta_1$	0.00000	0.00207	0.00370	0.00547	0.01080	0.00450	0.00495
63	$\Theta_1$	0.00000	0.00207	0.00370	0.00547	0.01080	0.00450	0.00496
64	$\Theta_1$	0.00000	0.00207	0.00370	0.00547	0.01073	0.00450	0.00495
65	$\Theta_1$	0.00107	0.00193	0.00370	0.00573	0.00720	0.00450	0.00496
66	$\Theta_1$	0.00007	0.00247	0.00417	0.00627	0.01247	0.00517	0.00577
67	$\Theta_1$	0.00000	0.00213	0.00370	0.00553	0.01080	0.00450	0.00495
68	$\Theta_1$	0.00080	0.00473	0.00657	0.00907	0.02367	0.00890	0.01026
69	$\Theta_1$	0.00000	0.00207	0.00370	0.00547	0.01080	0.00450	0.00495
70	$\Theta_1$	0.00067	0.00320	0.00510	0.00747	0.01427	0.00630	0.00698
71	$\Theta_1$	0.00033	0.00287	0.00470	0.00700	0.01407	0.00590	0.00656
72	$\Theta_1$	0.00000	0.00207	0.00370	0.00547	0.01087	0.00450	0.00497
73	$\Theta_1$	0.00000	0.00207	0.00370	0.00547	0.01073	0.00450	0.00494
74	$\Theta_1$	0.00000	0.00207	0.00370	0.00547	0.01080	0.00450	0.00496
75	$\Theta_1$	0.00007	0.00247	0.00417	0.00627	0.01233	0.00517	0.00572
76	$\Theta_1$	0.00107	0.00107	0.00370	0.00720	0.00720	0.00450	0.00495
77	$\Theta_1$	0.00080	0.00380	0.00617	0.01000	0.02273	0.00857	0.01003
78	$\Theta_1$	0.00000	0.00207	0.00370	0.00547	0.01080	0.00450	0.00496
79	$\Theta_1$	0.00060	0.00327	0.00523	0.00773	0.01560	0.00650	0.00728
80	$\Theta_1$	0.00000	0.00207	0.00370	0.00547	0.01073	0.00450	0.00494
81	$\Theta_1$	0.00000	0.00207	0.00370	0.00547	0.01073	0.00450	0.00495
82	$\Theta_1$	0.00000	0.00213	0.00370	0.00553	0.01073	0.00450	0.00495
83	$\Theta_1$	0.00000	0.00207	0.00370	0.00547	0.01080	0.00450	0.00497
84	$\Theta_1$	0.00000	0.00207	0.00370	0.00547	0.01080	0.00450	0.00494

Locus	Parameter	2.5%	25.0%	Mode	75.0%	97.5%	Median	Mean
85	$\Theta_1$	0.00000	0.00207	0.00370	0.00547	0.01073	0.00450	0.00494
86	$\Theta_1$	0.00007	0.00247	0.00417	0.00627	0.01253	0.00517	0.00577
87	$\Theta_1$	0.00160	0.00453	0.00710	0.01047	0.01947	0.00897	0.01001
88	$\Theta_1$	0.00000	0.00207	0.00370	0.00547	0.01080	0.00450	0.00496
89	$\Theta_1$	0.00547	0.01387	0.01757	0.02167	0.04747	0.02110	0.02412
90	$\Theta_1$	0.00087	0.00393	0.00650	0.01033	0.02340	0.00890	0.01041
91	$\Theta_1$	0.00107	0.00207	0.00370	0.00547	0.00720	0.00450	0.00497
92	$\Theta_1$	0.00000	0.00207	0.00370	0.00547	0.01080	0.00450	0.00496
93	$\Theta_1$	0.00000	0.00207	0.00370	0.00547	0.01067	0.00450	0.00493
94	$\Theta_1$	0.00033	0.00287	0.00477	0.00713	0.01453	0.00597	0.00672
95	$\Theta_1$	0.00000	0.00207	0.00370	0.00547	0.01080	0.00450	0.00495
96	$\Theta_1$	0.00000	0.00247	0.00417	0.00627	0.01533	0.00517	0.00576
97	$\Theta_1$	0.00000	0.00207	0.00370	0.00547	0.01080	0.00450	0.00496
98	$\Theta_1$	0.00147	0.00260	0.00430	0.00647	0.00853	0.00537	0.00594
99	$\Theta_1$	0.00047	0.00380	0.00597	0.00887	0.02007	0.00750	0.00838
100	$\Theta_1$	0.00173	0.00353	0.00470	0.00607	0.00913	0.00583	0.00650
All	$\Theta_1$	0.00167	0.00287	0.00383	0.00473	0.00593	0.00390	0.00383

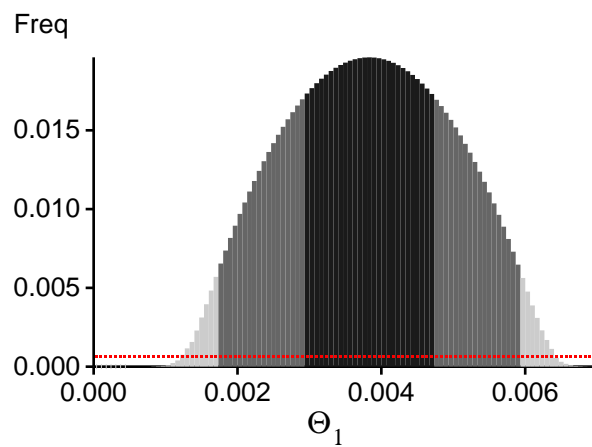
Citation suggestions:

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	-13908.90	-13737.18	-13773.60	-13867.81
2	-13955.20	-13780.80	-13821.25	-13912.70
3	-13902.69	-13730.44	-13767.15	-13860.35
4	-13908.68	-13736.19	-13772.52	-13865.91
5	-13910.38	-13737.89	-13774.74	-13868.64
6	-13907.26	-13734.50	-13771.27	-13864.04
7	-13910.57	-13737.99	-13774.61	-13867.93
8	-14623.78	-14249.53	-14264.92	-14346.96
9	-13921.36	-13748.97	-13787.59	-13879.30
10	-13907.44	-13735.45	-13769.52	-13866.84
11	-13911.18	-13738.23	-13774.86	-13868.49
12	-13925.32	-13751.19	-13787.20	-13880.00
13	-13906.31	-13734.32	-13771.33	-13865.02
14	-14371.29	-14161.76	-14213.71	-14289.73
15	-13911.22	-13738.21	-13774.93	-13870.36
16	-13908.50	-13736.28	-13773.17	-13866.18
17	-13938.99	-13760.09	-13798.72	-13892.27
18	-13910.31	-13737.32	-13773.80	-13867.69
19	-13910.75	-13738.40	-13775.16	-13868.46
20	-13909.53	-13736.89	-13773.74	-13866.80
21	-14012.75	-13824.81	-13867.17	-13952.92
22	-13964.53	-13778.93	-13818.55	-13907.06
23	-13910.78	-13738.13	-13773.21	-13867.88
24	-13910.58	-13738.22	-13774.67	-13869.00
25	-13933.06	-13760.60	-13799.63	-13890.95
26	-13926.71	-13752.03	-13789.28	-13881.36
27	-26596.89	-20334.96	-19291.65	-19369.17
28	-26805.00	-24366.08	-24118.77	-24186.87
29	-13909.42	-13737.21	-13774.00	-13868.22

30	-13910.72	-13738.15	-13774.93	-13867.96
31	-13911.08	-13738.39	-13774.96	-13868.08
32	-13909.27	-13737.32	-13774.46	-13867.39
33	-13909.37	-13736.93	-13773.85	-13866.42
34	-13909.95	-13737.50	-13774.25	-13867.61
35	-13911.12	-13738.44	-13774.39	-13868.59
36	-13940.16	-13760.95	-13799.30	-13890.16
37	-13909.40	-13736.73	-13773.14	-13866.39
38	-13909.53	-13737.11	-13773.88	-13868.09
39	-14264.49	-13999.99	-14032.59	-14115.98
40	-13910.29	-13738.08	-13774.43	-13867.85
41	-13908.18	-13736.10	-13773.14	-13866.17
42	-13938.32	-13763.65	-13792.62	-13893.73
43	-20712.60	-18162.97	-13834.31	-17886.73
44	-13909.58	-13737.48	-13773.36	-13867.21
45	-13927.35	-13752.31	-13789.78	-13881.64
46	-14637.49	-14229.82	-13806.57	-14320.81
47	-13910.75	-13737.88	-13774.05	-13867.54
48	-13909.64	-13736.94	-13772.96	-13866.66
49	-13909.27	-13736.89	-13773.64	-13867.10
50	-16653.03	-15533.43	-13793.18	-15502.57
51	-13908.18	-13736.54	-13773.68	-13867.36
52	-13956.13	-13778.25	-13794.30	-13907.52
53	-13902.38	-13730.15	-13767.07	-13861.62
54	-13909.87	-13737.99	-13775.05	-13868.67
55	-14128.97	-13956.68	-13799.05	-14089.34
56	-13922.77	-13749.97	-13784.95	-13879.30
57	-13925.93	-13750.70	-13779.28	-13879.59
58	-13922.01	-13749.39	-13777.81	-13881.05
59	-13908.82	-13736.81	-13773.87	-13866.89
60	-13907.66	-13735.11	-13771.87	-13865.46
61	-13922.09	-13749.60	-13782.73	-13879.95
62	-13907.61	-13734.69	-13770.00	-13864.37
63	-13908.35	-13735.84	-13772.88	-13866.35
64	-13909.60	-13737.19	-13774.39	-13868.10
65	-13907.41	-13735.15	-13771.64	-13864.98
66	-13921.04	-13749.03	-13778.36	-13879.38
67	-13909.30	-13736.49	-13772.85	-13866.47
68	-14883.92	-14621.22	-13789.82	-14744.36
69	-13909.64	-13737.28	-13774.20	-13867.40
70	-13983.34	-13809.25	-13806.94	-13941.11
71	-13939.03	-13764.42	-13782.04	-13893.79
72	-13907.77	-13735.77	-13772.70	-13865.87
73	-13909.59	-13737.08	-13774.09	-13866.90
74	-13909.62	-13737.56	-13772.81	-13867.84

75	-13924.29	-13750.72	-13779.35	-13882.99
76	-13909.33	-13736.97	-13773.29	-13867.38
77	-16542.09	-15470.33	-15367.89	-15448.43
78	-13910.30	-13737.56	-13774.27	-13867.73
79	-13947.20	-13770.18	-13812.40	-13899.16
80	-13909.59	-13737.60	-13774.34	-13867.62
81	-13908.38	-13736.39	-13772.61	-13866.52
82	-13910.58	-13738.15	-13774.67	-13868.04
83	-13910.33	-13737.26	-13773.90	-13866.88
84	-13910.09	-13737.58	-13774.66	-13867.46
85	-13910.50	-13738.11	-13775.35	-13867.93
86	-13918.46	-13746.27	-13786.01	-13876.31
87	-14112.33	-13893.49	-13800.54	-14017.59
88	-13910.69	-13738.19	-13775.43	-13868.23
89	-15059.05	-14574.85	-13804.05	-14655.58
90	-15498.74	-15150.07	-13831.05	-15263.75
91	-13910.05	-13738.07	-13774.78	-13868.40
92	-13905.30	-13732.88	-13767.92	-13863.10
93	-13909.92	-13737.44	-13774.81	-13867.49
94	-13933.79	-13761.79	-13780.36	-13892.43
95	-13906.65	-13734.16	-13770.50	-13864.23
96	-13920.02	-13747.81	-13787.41	-13879.18
97	-13910.79	-13738.26	-13774.14	-13868.55
98	-13934.51	-13759.71	-13782.72	-13889.95
99	-14195.49	-13951.44	-13785.45	-14072.16
100	-13938.94	-13763.92	-13778.34	-13892.83
All	-1435872.52	-1404714.07	-1396556.20	-1415430.25
(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 = 246.930589]				
Citation suggestions:				
Beerli P. and M. Palczewski, 2010. Unified framework to evaluate panmixia and migration direction among multiple sampling locations, <i>Genetics</i> , 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, <i>Bayesian Phylogenetics: Methods, Algorithms, and Applications</i> , 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. <i>Systematic Biology</i> , 60(2):150â 160, 2011.				



*Acceptance ratios for all parameters and the genealogies*

Parameter	Accepted changes	Ratio
$\Theta_1$	234651422/400036343	0.58658
Genealogies	1052079638/1599963657	0.65756

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

Parameter	Autocorrelation	Effective Sampe Size
$\Theta_1$	0.09117	22536252.67
Genealogies	0.03270	24814324.39

## *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. 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