

# *Palythoa tuberculosa - Hawaii*

POPULATION SIZE, MIGRATION, DIVERGENCE, ASSIGNMENT, HISTORY

Bayesian inference using the structured coalescent

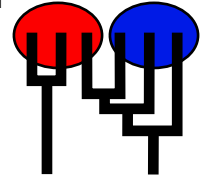
Migrate-n version 4.4.4(git:) [June-1-2019]

Compiled for PARALLEL computer architectures

One master and 31 compute nodes are available.

Program started at Sun Jan 23 11:46:22 2022

Program finished at Sun Jan 23 13:25:05 2022 [Runtime:0000:01:38:43]



## *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)

3611595333

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	2	3	4	5	6	7	8	9	10
1 Pop_Kure	*	*	0	0	0	0	0	0	0	0
2 Pop_P&H	*	*	*	0	0	0	0	0	0	0
3 Pop_Pbanks	0	*	*	*	0	0	0	0	0	0
4 Pop_MaroReef	0	0	*	*	*	0	0	0	0	0
5 Pop_Maui	0	0	0	*	*	*	0	0	0	0
6 Pop_FFS	0	0	0	0	*	*	*	0	0	0
7 Pop_Kauai	0	0	0	0	0	*	*	*	0	0

8 Pop_Oahu	0	0	0	0	0	0	*	*	*	0
9 Pop_Molokai	0	0	0	0	0	0	0	*	*	*
10 Pop_BigIsland	0	0	0	0	0	0	0	0	*	*

Order of parameters:

1	$\Theta_1$	<displayed>
2	$\Theta_2$	<displayed>
3	$\Theta_3$	<displayed>
4	$\Theta_4$	<displayed>
5	$\Theta_5$	<displayed>
6	$\Theta_6$	<displayed>
7	$\Theta_7$	<displayed>
8	$\Theta_8$	<displayed>
9	$\Theta_9$	<displayed>
10	$\Theta_{10}$	<displayed>
11	$M_{2 \rightarrow 1}$	<displayed>
12	$M_{1 \rightarrow 2}$	<displayed>
13	$M_{3 \rightarrow 2}$	<displayed>
14	$M_{2 \rightarrow 3}$	<displayed>
15	$M_{4 \rightarrow 3}$	<displayed>
16	$M_{3 \rightarrow 4}$	<displayed>
17	$M_{5 \rightarrow 4}$	<displayed>
18	$M_{4 \rightarrow 5}$	<displayed>
19	$M_{6 \rightarrow 5}$	<displayed>
20	$M_{5 \rightarrow 6}$	<displayed>
21	$M_{7 \rightarrow 6}$	<displayed>
22	$M_{6 \rightarrow 7}$	<displayed>
23	$M_{8 \rightarrow 7}$	<displayed>
24	$M_{7 \rightarrow 8}$	<displayed>
25	$M_{9 \rightarrow 8}$	<displayed>
26	$M_{8 \rightarrow 9}$	<displayed>
27	$M_{10 \rightarrow 9}$	<displayed>
28	$M_{9 \rightarrow 10}$	<displayed>

Mutation rate among loci:

Mutation rate is constant for all loci

Analysis strategy:

Bayesian inference

-Population size estimation:

Exponential Distribution

-Geneflow estimation:

Exponential Distribution

Proposal distributions for parameter

Parameter	Proposal
Theta	Metropolis sampling

M Slice 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 *Exp window	0.000000	0.001	0.100	0.010	500	0.01190
2	Theta *Exp window	0.000000	0.001	0.100	0.010	500	0.01190
3	Theta *Exp window	0.000000	0.001	0.100	0.010	500	0.01190
4	Theta *Exp window	0.000000	0.001	0.100	0.010	500	0.01190
5	Theta *Exp window	0.000000	0.001	0.100	0.010	500	0.01190
6	Theta *Exp window	0.000000	0.001	0.100	0.010	500	0.01190
7	Theta *Exp window	0.000000	0.001	0.100	0.010	500	0.01190
8	Theta *Exp window	0.000000	0.001	0.100	0.010	500	0.01190
9	Theta *Exp window	0.000000	0.001	0.100	0.010	500	0.01190
10	Theta *Exp window	0.000000	0.001	0.100	0.010	500	0.01190
11	M *Exp window	0.000100	1000.	10000	100.0	500	0.01190
12	M *Exp window	0.000100	1000.	10000	100.0	500	0.01190
13	M *Exp window	0.000100	1000.	10000	100.0	500	0.01190
14	M *Exp window	0.000100	1000.	10000	100.0	500	0.01190
15	M *Exp window	0.000100	1000.	10000	100.0	500	0.01190
16	M *Exp window	0.000100	1000.	10000	100.0	500	0.01190
17	M *Exp window	0.000100	1000.	10000	100.0	500	0.01190
18	M *Exp window	0.000100	1000.	10000	100.0	500	0.01190
19	M *Exp window	0.000100	1000.	10000	100.0	500	0.01190
20	M *Exp window	0.000100	1000.	10000	100.0	500	0.01190
21	M *Exp window	0.000100	1000.	10000	100.0	500	0.01190
22	M *Exp window	0.000100	1000.	10000	100.0	500	0.01190
23	M *Exp window	0.000100	1000.	10000	100.0	500	0.01190
24	M *Exp window	0.000100	1000.	10000	100.0	500	0.01190
25	M *Exp window	0.000100	1000.	10000	100.0	500	0.01190
26	M *Exp window	0.000100	1000.	10000	100.0	500	0.01190
27	M *Exp window	0.000100	1000.	10000	100.0	500	0.01190
28	M *Exp window	0.000100	1000.	10000	100.0	500	0.01190

[\* \* means priors were set globally]

## Markov chain settings:

Long chain

Number of chains	1
Recorded steps [a]	10000
Increment (record every x step [b])	100
Number of concurrent chains (replicates) [c]	1
Visited (sampled) parameter values [a*b*c]	1000000
Number of discard trees per chain (burn-in)	2000

## 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:

../ptuberculosa.mig

Haplotyping is turned on:

YES: NO report of haplotype probabilities

Output file:

outfile.txt

Posterior distribution raw histogram file:

bayesfile

Raw data from the MCMC run:

bayesallfile

Print data:

No

Print genealogies [only some for some data type]:

None

## *Data summary*

Data file: ../../ptuberculosa.mig  
 Datatype: Sequence data  
 Number of loci: 109

### Mutationmodel:

Locus	Sublocus	Mutationmodel	Mutationmodel parameters
1	1	HKY	[Bf:0.31 0.21 0.18 0.29, kappa=1.000]
2	1	HKY	[Bf:0.29 0.20 0.23 0.28, kappa=1.000]
3	1	HKY	[Bf:0.26 0.29 0.23 0.22, kappa=1.000]
4	1	HKY	[Bf:0.32 0.22 0.21 0.25, kappa=1.000]
5	1	HKY	[Bf:0.33 0.19 0.23 0.24, kappa=1.000]
6	1	HKY	[Bf:0.26 0.20 0.19 0.35, kappa=1.000]
7	1	HKY	[Bf:0.25 0.18 0.22 0.35, kappa=1.000]
8	1	HKY	[Bf:0.27 0.19 0.18 0.36, kappa=1.000]
9	1	HKY	[Bf:0.30 0.24 0.24 0.22, kappa=1.000]
10	1	HKY	[Bf:0.31 0.23 0.23 0.24, kappa=1.000]
11	1	HKY	[Bf:0.33 0.20 0.23 0.24, kappa=1.000]
12	1	HKY	[Bf:0.21 0.24 0.22 0.32, kappa=1.000]
13	1	HKY	[Bf:0.28 0.17 0.21 0.35, kappa=1.000]
14	1	HKY	[Bf:0.22 0.23 0.27 0.29, kappa=1.000]
15	1	HKY	[Bf:0.29 0.23 0.28 0.21, kappa=1.000]
16	1	HKY	[Bf:0.32 0.14 0.27 0.27, kappa=1.000]
17	1	HKY	[Bf:0.35 0.21 0.13 0.31, kappa=1.000]
18	1	HKY	[Bf:0.27 0.25 0.25 0.23, kappa=1.000]
19	1	HKY	[Bf:0.32 0.19 0.27 0.22, kappa=1.000]
20	1	HKY	[Bf:0.25 0.21 0.21 0.33, kappa=1.000]
21	1	HKY	[Bf:0.20 0.31 0.23 0.26, kappa=1.000]
22	1	HKY	[Bf:0.32 0.18 0.18 0.31, kappa=1.000]
23	1	HKY	[Bf:0.28 0.16 0.14 0.42, kappa=1.000]
24	1	HKY	[Bf:0.28 0.26 0.24 0.23, kappa=1.000]
25	1	HKY	[Bf:0.32 0.21 0.24 0.23, kappa=1.000]
26	1	HKY	[Bf:0.35 0.22 0.27 0.16, kappa=1.000]
27	1	HKY	[Bf:0.26 0.27 0.16 0.31, kappa=1.000]
28	1	HKY	[Bf:0.33 0.26 0.21 0.19, kappa=1.000]
29	1	HKY	[Bf:0.36 0.23 0.19 0.22, kappa=1.000]
30	1	HKY	[Bf:0.32 0.14 0.25 0.28, kappa=1.000]
31	1	HKY	[Bf:0.29 0.27 0.23 0.22, kappa=1.000]
32	1	HKY	[Bf:0.28 0.22 0.17 0.33, kappa=1.000]
33	1	HKY	[Bf:0.35 0.15 0.20 0.30, kappa=1.000]
34	1	HKY	[Bf:0.22 0.22 0.22 0.34, kappa=1.000]

35	1	HKY	[Bf:0.35 0.14 0.17 0.33, kappa=1.000]
36	1	HKY	[Bf:0.31 0.19 0.28 0.23, kappa=1.000]
37	1	HKY	[Bf:0.27 0.18 0.27 0.28, kappa=1.000]
38	1	HKY	[Bf:0.40 0.21 0.24 0.14, kappa=1.000]
39	1	HKY	[Bf:0.37 0.22 0.20 0.21, kappa=1.000]
40	1	HKY	[Bf:0.30 0.19 0.18 0.32, kappa=1.000]
41	1	HKY	[Bf:0.27 0.24 0.20 0.29, kappa=1.000]
42	1	HKY	[Bf:0.34 0.19 0.15 0.32, kappa=1.000]
43	1	HKY	[Bf:0.29 0.15 0.25 0.31, kappa=1.000]
44	1	HKY	[Bf:0.27 0.18 0.18 0.37, kappa=1.000]
45	1	HKY	[Bf:0.30 0.19 0.22 0.28, kappa=1.000]
46	1	HKY	[Bf:0.38 0.19 0.30 0.13, kappa=1.000]
47	1	HKY	[Bf:0.18 0.28 0.21 0.32, kappa=1.000]
48	1	HKY	[Bf:0.24 0.28 0.33 0.15, kappa=1.000]
49	1	HKY	[Bf:0.27 0.21 0.21 0.31, kappa=1.000]
50	1	HKY	[Bf:0.27 0.20 0.21 0.32, kappa=1.000]
51	1	HKY	[Bf:0.29 0.16 0.25 0.29, kappa=1.000]
52	1	HKY	[Bf:0.32 0.12 0.24 0.32, kappa=1.000]
53	1	HKY	[Bf:0.19 0.27 0.21 0.33, kappa=1.000]
54	1	HKY	[Bf:0.28 0.21 0.21 0.30, kappa=1.000]
55	1	HKY	[Bf:0.36 0.18 0.27 0.19, kappa=1.000]
56	1	HKY	[Bf:0.31 0.23 0.25 0.21, kappa=1.000]
57	1	HKY	[Bf:0.20 0.23 0.18 0.39, kappa=1.000]
58	1	HKY	[Bf:0.28 0.23 0.26 0.24, kappa=1.000]
59	1	HKY	[Bf:0.28 0.20 0.17 0.36, kappa=1.000]
60	1	HKY	[Bf:0.36 0.21 0.16 0.28, kappa=1.000]
61	1	HKY	[Bf:0.35 0.22 0.18 0.25, kappa=1.000]
62	1	HKY	[Bf:0.27 0.24 0.20 0.29, kappa=1.000]
63	1	HKY	[Bf:0.28 0.23 0.24 0.25, kappa=1.000]
64	1	HKY	[Bf:0.29 0.25 0.22 0.23, kappa=1.000]
65	1	HKY	[Bf:0.28 0.22 0.22 0.28, kappa=1.000]
66	1	HKY	[Bf:0.24 0.26 0.21 0.30, kappa=1.000]
67	1	HKY	[Bf:0.24 0.25 0.24 0.28, kappa=1.000]
68	1	HKY	[Bf:0.21 0.21 0.25 0.33, kappa=1.000]
69	1	HKY	[Bf:0.20 0.22 0.21 0.37, kappa=1.000]
70	1	HKY	[Bf:0.21 0.19 0.22 0.38, kappa=1.000]
71	1	HKY	[Bf:0.30 0.23 0.14 0.33, kappa=1.000]
72	1	HKY	[Bf:0.30 0.24 0.23 0.24, kappa=1.000]
73	1	HKY	[Bf:0.31 0.23 0.22 0.25, kappa=1.000]
74	1	HKY	[Bf:0.31 0.18 0.25 0.25, kappa=1.000]
75	1	HKY	[Bf:0.25 0.27 0.22 0.26, kappa=1.000]
76	1	HKY	[Bf:0.32 0.22 0.25 0.20, kappa=1.000]
77	1	HKY	[Bf:0.30 0.19 0.23 0.28, kappa=1.000]
78	1	HKY	[Bf:0.25 0.20 0.24 0.30, kappa=1.000]
79	1	HKY	[Bf:0.30 0.20 0.21 0.29, kappa=1.000]

80	1	HKY	[Bf:0.32 0.20 0.22 0.27, kappa=1.000]
81	1	HKY	[Bf:0.20 0.23 0.33 0.24, kappa=1.000]
82	1	HKY	[Bf:0.29 0.22 0.26 0.23, kappa=1.000]
83	1	HKY	[Bf:0.27 0.27 0.21 0.25, kappa=1.000]
84	1	HKY	[Bf:0.34 0.19 0.16 0.31, kappa=1.000]
85	1	HKY	[Bf:0.28 0.24 0.18 0.30, kappa=1.000]
86	1	HKY	[Bf:0.22 0.33 0.25 0.20, kappa=1.000]
87	1	HKY	[Bf:0.30 0.18 0.19 0.32, kappa=1.000]
88	1	HKY	[Bf:0.33 0.22 0.24 0.21, kappa=1.000]
89	1	HKY	[Bf:0.35 0.18 0.13 0.34, kappa=1.000]
90	1	HKY	[Bf:0.31 0.21 0.23 0.26, kappa=1.000]
91	1	HKY	[Bf:0.21 0.22 0.25 0.32, kappa=1.000]
92	1	HKY	[Bf:0.22 0.20 0.22 0.36, kappa=1.000]
93	1	HKY	[Bf:0.32 0.27 0.20 0.21, kappa=1.000]
94	1	HKY	[Bf:0.22 0.27 0.25 0.25, kappa=1.000]
95	1	HKY	[Bf:0.25 0.21 0.20 0.35, kappa=1.000]
96	1	HKY	[Bf:0.28 0.22 0.19 0.32, kappa=1.000]
97	1	HKY	[Bf:0.23 0.23 0.23 0.30, kappa=1.000]
98	1	HKY	[Bf:0.20 0.23 0.22 0.34, kappa=1.000]
99	1	HKY	[Bf:0.25 0.20 0.24 0.31, kappa=1.000]
100	1	HKY	[Bf:0.33 0.22 0.26 0.19, kappa=1.000]
101	1	HKY	[Bf:0.30 0.18 0.20 0.32, kappa=1.000]
102	1	HKY	[Bf:0.32 0.15 0.24 0.29, kappa=1.000]
103	1	HKY	[Bf:0.29 0.25 0.17 0.29, kappa=1.000]
104	1	HKY	[Bf:0.29 0.17 0.24 0.30, kappa=1.000]
105	1	HKY	[Bf:0.27 0.23 0.26 0.25, kappa=1.000]
106	1	HKY	[Bf:0.32 0.21 0.28 0.19, kappa=1.000]
107	1	HKY	[Bf:0.26 0.24 0.20 0.30, kappa=1.000]
108	1	HKY	[Bf:0.39 0.19 0.12 0.30, kappa=1.000]
109	1	HKY	[Bf:0.33 0.22 0.22 0.23, kappa=1.000]

## Sites per locus

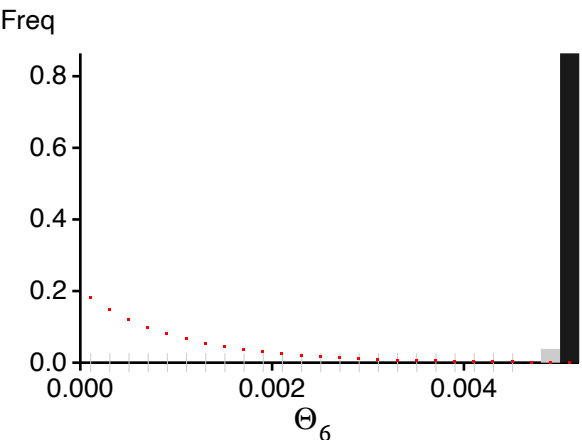
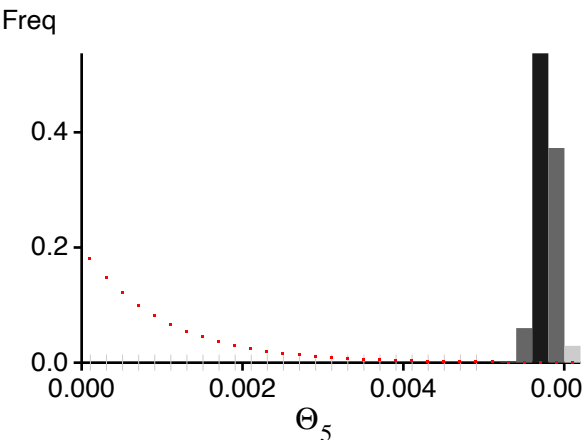
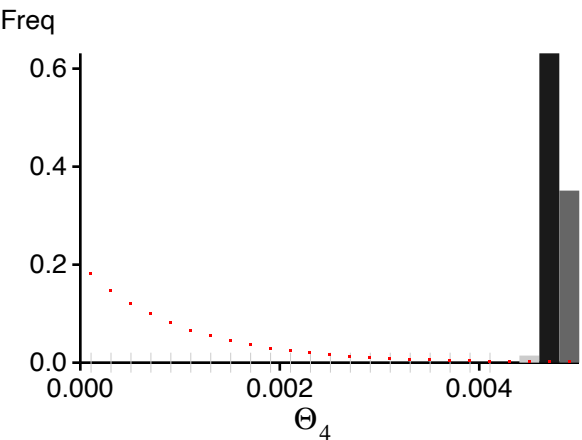
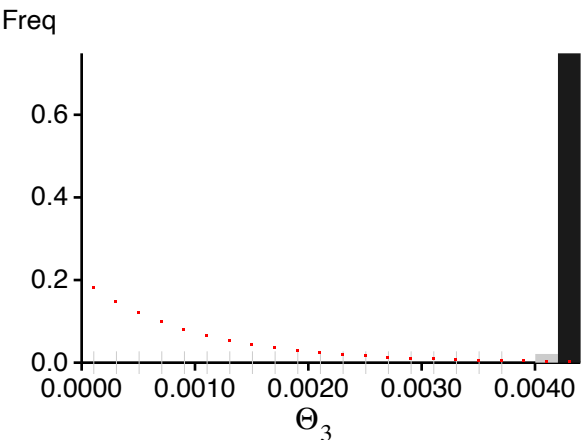
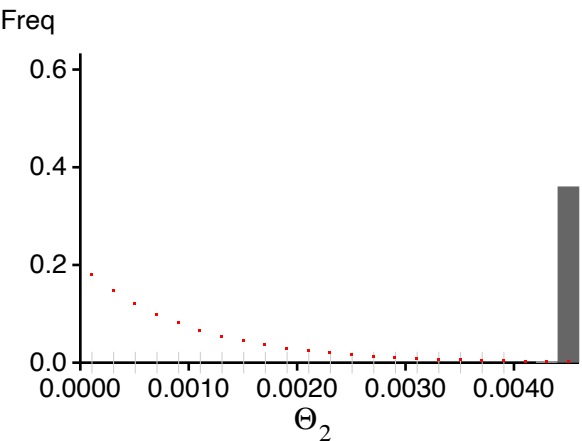
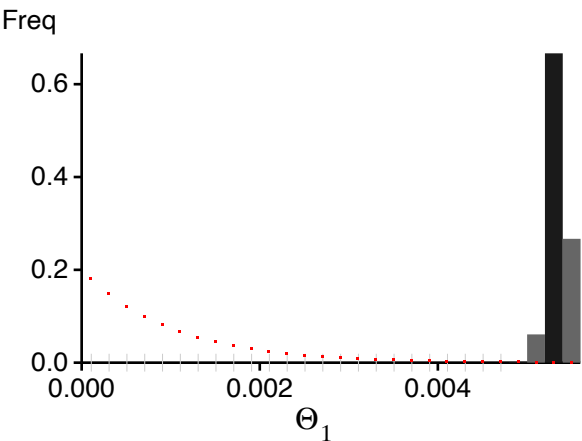
Locus	Sites
1	411
2	388
3	472
4	468
5	499
6	516
7	496
8	337
9	512
10	618
11	387

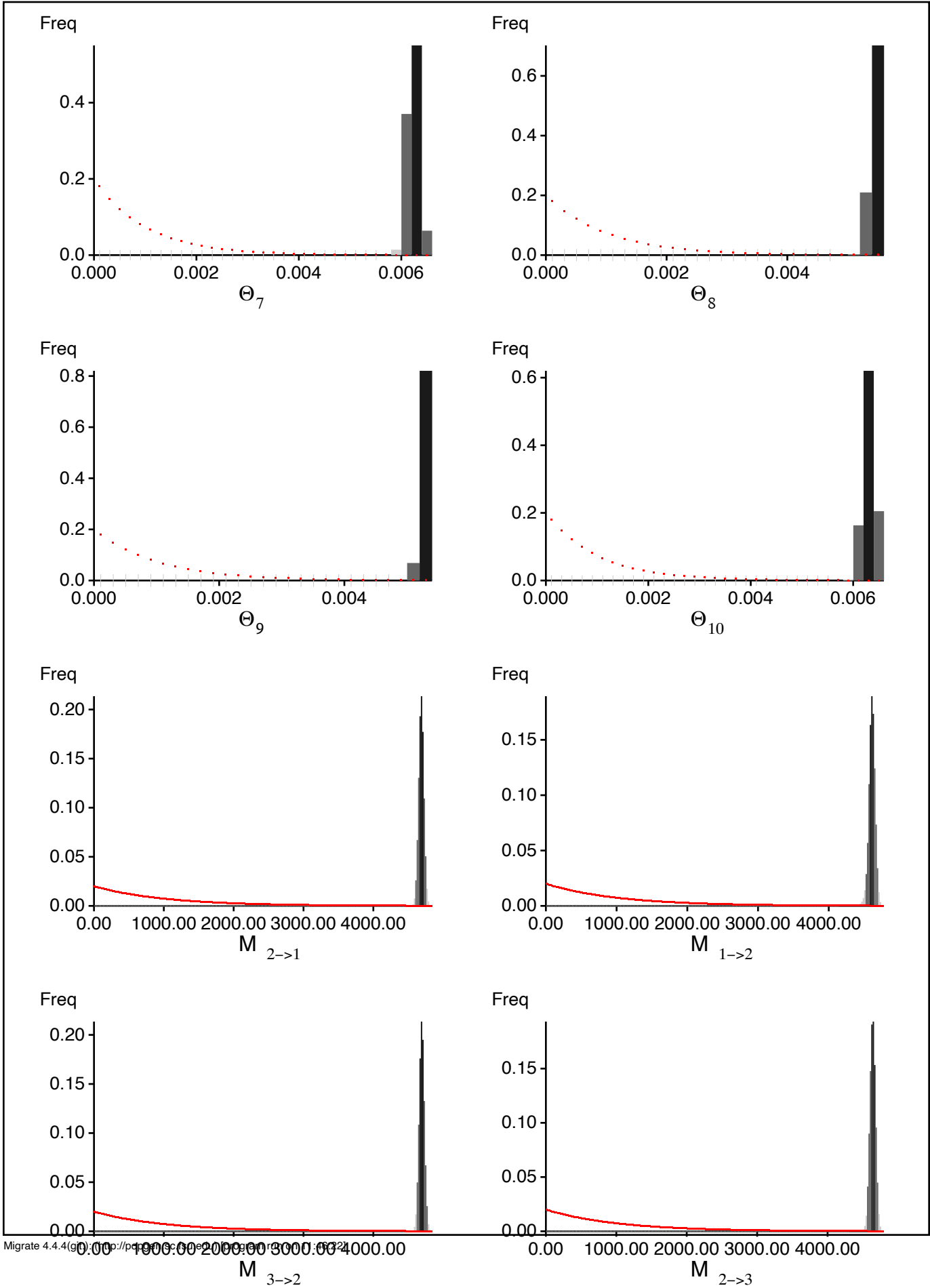
12	394
13	500
14	726
15	479
16	338
17	382
18	316
19	659
20	478
21	446
22	353
23	397
24	729
25	269
26	413
27	463
28	741
29	701
30	370
31	725
32	470
33	335
34	261
35	433
36	328
37	313
38	314
39	678
40	455
41	338
42	462
43	784
44	325
45	489
46	370
47	316
48	505
49	437
50	264
51	340
52	345
53	369
54	433
55	273
56	469

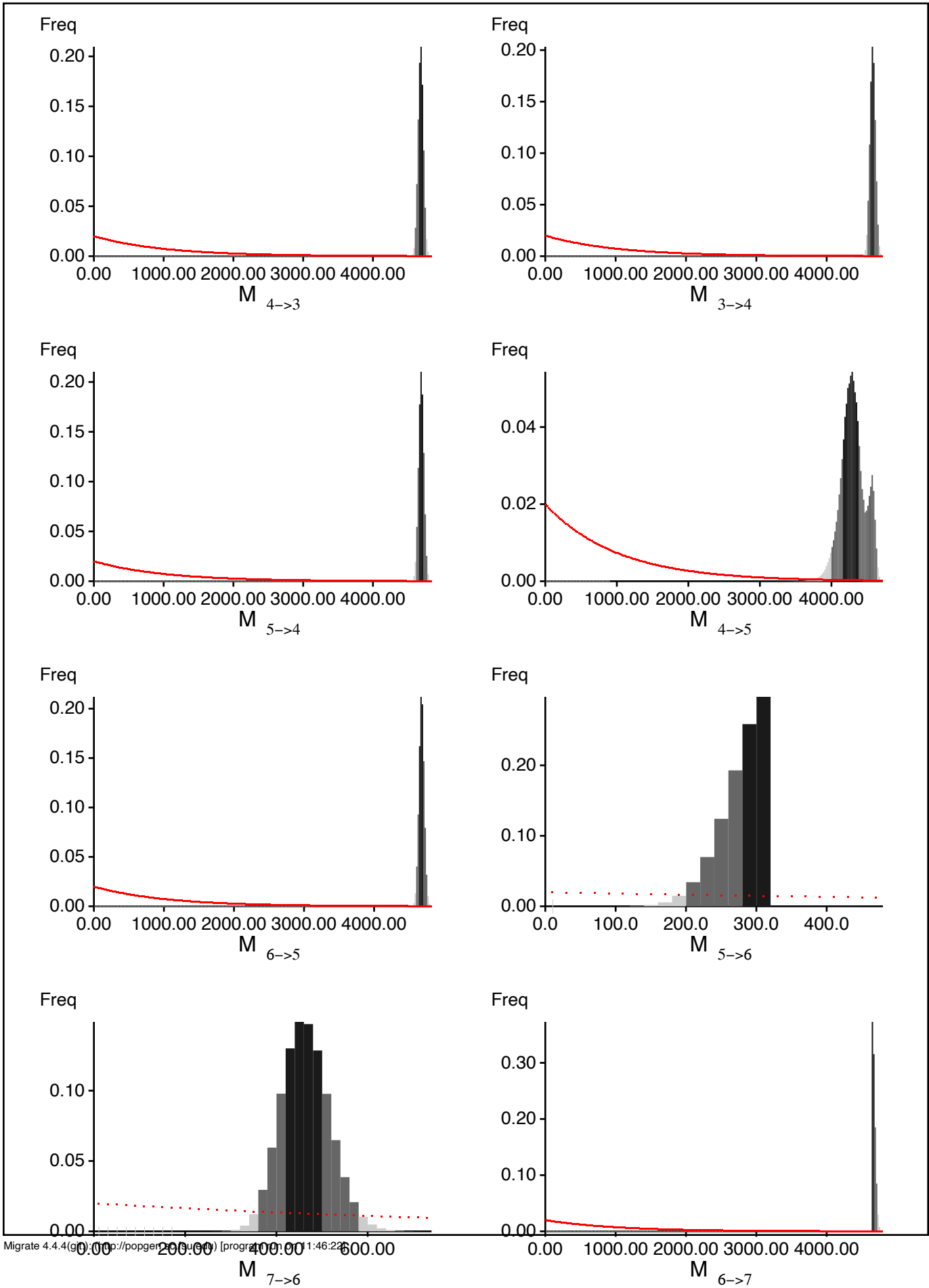


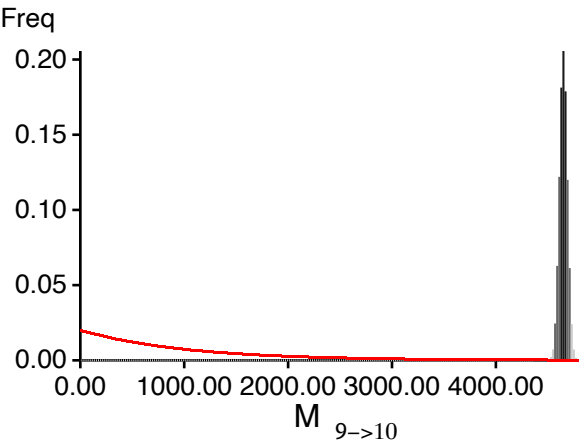
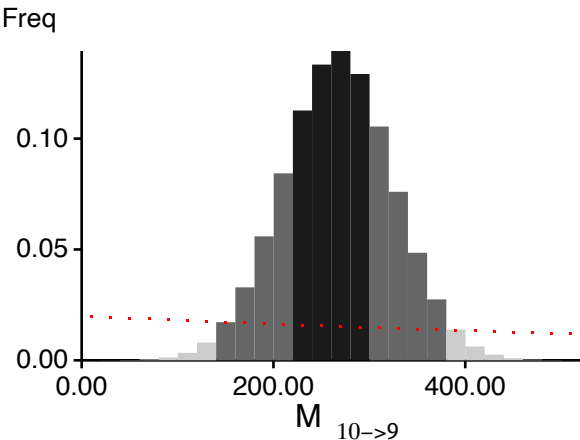
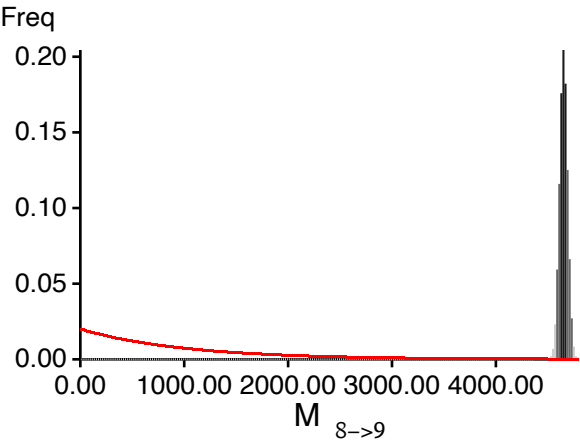
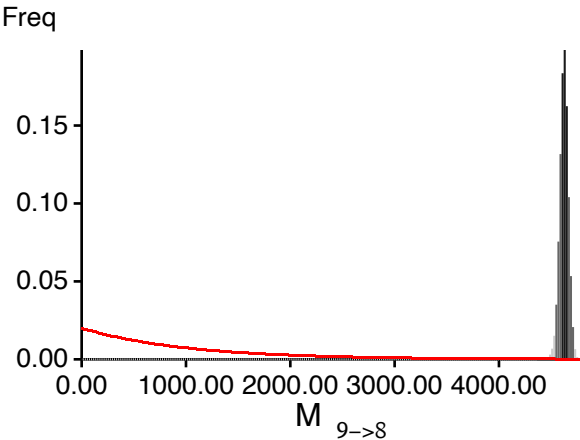
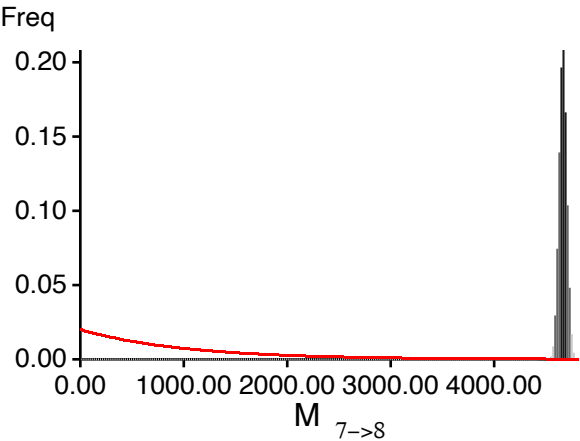
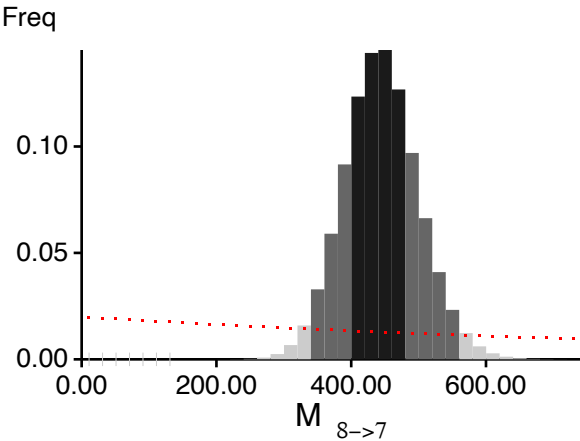
57	275
58	409
59	471
60	379
61	621
62	473
63	579
64	302
65	634
66	782
67	454
68	541
69	411
70	534
71	349
72	399
73	242
74	505
75	398
76	308
77	469
78	338
79	429
80	433
81	395
82	376
83	473
84	524
85	427
86	650
87	428
88	419
89	194
90	699
91	621
92	515
93	494
94	502
95	305
96	382
97	338
98	572
99	324
100	439
101	596

*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	Raw thermodynamic score(1a)	Bezier approximation score(1b)	Harmonic mean(2)
1	-585.38	-579.53	-587.95
2	-627.54	-620.81	-628.03
3	-708.78	-701.60	-713.50
4	-682.26	-675.42	-686.59
5	-767.60	-759.76	-770.53
6	-726.19	-718.94	-731.08
7	-757.37	-749.20	-761.03
8	-486.21	-481.28	-489.80
9	-899.65	-828.59	-794.55
10	-885.11	-876.30	-890.33
11	-588.48	-582.21	-594.07
12	-586.21	-580.25	-588.03
13	-743.04	-735.39	-745.81
14	-1027.71	-1017.51	-1036.33
15	-698.87	-691.85	-702.30
16	-488.85	-483.84	-490.81
17	-540.27	-534.82	-543.57
18	-500.52	-495.28	-502.46
19	-926.85	-917.65	-930.01
20	-692.12	-685.19	-696.76
21	-679.35	-672.19	-681.49
22	-619.78	-611.15	-611.90
23	-537.02	-531.64	-540.17
24	-1066.82	-1056.14	-1075.25
25	-379.28	-375.52	-381.60
26	-631.87	-621.27	-620.57
27	-744.16	-732.33	-724.18
28	-1058.29	-1047.72	-1066.45
29	-986.11	-976.30	-990.63

30	-537.97	-532.14	-541.51
31	-1026.07	-1015.88	-1032.31
32	-664.96	-658.32	-667.22
33	-557.02	-549.60	-543.82
34	-378.05	-374.25	-379.00
35	-584.76	-578.95	-587.41
36	-510.06	-504.75	-514.84
37	-462.29	-457.61	-463.68
38	-510.58	-499.89	-486.30
39	-961.35	-951.74	-967.89
40	-654.17	-647.60	-657.63
41	-535.87	-528.62	-533.10
42	-746.81	-737.31	-732.20
43	-1107.08	-1095.98	-1111.17
44	-468.28	-463.55	-470.85
45	-771.41	-760.53	-755.27
46	-507.25	-502.19	-509.22
47	-463.69	-458.99	-465.62
48	-707.92	-700.85	-709.63
49	-627.20	-620.94	-629.82
50	-394.90	-390.68	-395.74
51	-486.21	-481.35	-488.45
52	-470.94	-466.27	-473.28
53	-597.02	-589.54	-585.98
54	-706.14	-698.54	-708.56
55	-473.22	-468.08	-460.58
56	-692.45	-685.47	-697.80
57	-402.70	-398.41	-405.31
58	-602.54	-596.48	-606.49
59	-691.64	-684.31	-691.34
60	-534.32	-528.98	-537.04
61	-898.69	-889.66	-903.52
62	-710.03	-702.82	-714.85
63	-1066.68	-1033.74	-968.64
64	-477.81	-472.66	-478.32
65	-957.07	-947.26	-961.98
66	-1105.55	-1094.57	-1109.58
67	-654.76	-648.22	-658.85
68	-757.84	-750.32	-762.14
69	-568.92	-563.28	-572.86
70	-769.81	-761.33	-770.71
71	-538.00	-531.29	-535.60
72	-762.88	-752.61	-733.80
73	-400.77	-393.46	-379.79
74	-735.37	-727.89	-739.94

75	-576.16	-570.41	-578.04
76	-484.67	-479.56	-484.90
77	-660.18	-653.63	-664.51
78	-488.71	-483.82	-491.01
79	-614.09	-607.96	-616.09
80	-650.99	-644.34	-654.57
81	-655.50	-647.86	-638.47
82	-609.27	-602.75	-607.96
83	-691.53	-684.57	-693.38
84	-764.25	-756.30	-767.59
85	-736.61	-727.92	-720.24
86	-913.55	-904.47	-920.04
87	-606.45	-600.39	-608.53
88	-681.45	-673.55	-678.01
89	-282.80	-279.89	-283.47
90	-1025.28	-1014.98	-1031.10
91	-897.02	-888.04	-904.14
92	-727.69	-720.42	-731.16
93	-695.45	-688.55	-699.83
94	-723.71	-716.49	-728.94
95	-425.02	-420.80	-426.90
96	-597.47	-591.19	-600.58
97	-519.78	-514.37	-521.65
98	-833.32	-824.93	-836.38
99	-518.78	-508.78	-493.54
100	-683.71	-676.74	-685.66
101	-830.15	-821.91	-835.53
102	-477.00	-472.23	-479.28
103	-535.02	-529.67	-536.70
104	-825.90	-815.96	-815.44
105	-519.84	-514.68	-521.90
106	-482.10	-476.98	-485.14
107	-563.35	-557.77	-566.77
108	-453.46	-448.91	-455.17
109	-518.61	-513.33	-521.09
All	-65831.15	-64972.23	-65660.69
<p>(1a, 1b and 2) are approximations to the marginal likelihood, make sure that the program run long enough!  (1a, 1b) and (2) should give similar results, in principle.  But (2) is overestimating the likelihood, it is presented for historical reasons and should not be used  (1a, 1b) needs heating with chains that span a temperature range of 1.0 to at least 100,000.  (1b) is using a Bezier-curve to get better approximations for runs with low number of heated chains  [Scaling factor = 6298.471288]  Citation suggestions:</p>			



Beerli P. and M. Palczewski, 2010. Unified framework to evaluate panmixia and migration direction among multiple sampling locations, *Genetics*, 185: 313-326.

# *Acceptance ratios for all parameters and the genealogies*

Parameter	Accepted changes	Ratio
$\Theta_1$	328648/1296377	0.25351
$\Theta_2$	471007/1298611	0.36270
$\Theta_3$	507867/1295359	0.39207
$\Theta_4$	483565/1298556	0.37239
$\Theta_5$	256379/1295098	0.19796
$\Theta_6$	239063/1298020	0.18418
$\Theta_7$	149012/1295786	0.11500
$\Theta_8$	269392/1298384	0.20748
$\Theta_9$	248916/1297400	0.19186
$\Theta_{10}$	161284/1296350	0.12441
M <sub>2→1</sub>	1299340/1299340	1.00000
M <sub>1→2</sub>	1298321/1298321	1.00000
M <sub>3→2</sub>	1297564/1297564	1.00000
M <sub>2→3</sub>	1297381/1297381	1.00000
M <sub>4→3</sub>	1296743/1296743	1.00000
M <sub>3→4</sub>	1297976/1297976	1.00000
M <sub>5→4</sub>	1297056/1297056	1.00000
M <sub>4→5</sub>	1298153/1298153	1.00000
M <sub>6→5</sub>	1296900/1296900	1.00000
M <sub>5→6</sub>	1297508/1297508	1.00000
M <sub>7→6</sub>	1299116/1299116	1.00000
M <sub>6→7</sub>	1299410/1299410	1.00000
M <sub>8→7</sub>	1297622/1297622	1.00000
M <sub>7→8</sub>	1296394/1296394	1.00000
M <sub>9→8</sub>	1299687/1299687	1.00000
M <sub>8→9</sub>	1298109/1298109	1.00000
M <sub>10→9</sub>	1297210/1297210	1.00000
M <sub>9→10</sub>	1298255/1298255	1.00000
Genealogies	28812889/36331610	0.79305

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

Parameter	Autocorrelation	Effective Sample Size
$\Theta_1$	0.79628	456240.45
$\Theta_2$	0.71684	663498.52
$\Theta_3$	0.67793	767915.38
$\Theta_4$	0.71603	664643.31
$\Theta_5$	0.84072	348373.31
$\Theta_6$	0.84480	337752.76
$\Theta_7$	0.90066	210412.47
$\Theta_8$	0.83205	368273.85
$\Theta_9$	0.84383	341294.06
$\Theta_{10}$	0.89250	227957.40
$M_{2 \rightarrow 1}$	0.59445	1016569.94
$M_{1 \rightarrow 2}$	0.62452	916993.15
$M_{3 \rightarrow 2}$	0.63692	889013.66
$M_{2 \rightarrow 3}$	0.67193	782575.54
$M_{4 \rightarrow 3}$	0.64915	850004.81
$M_{3 \rightarrow 4}$	0.67393	773163.49
$M_{5 \rightarrow 4}$	0.61843	942431.27
$M_{4 \rightarrow 5}$	0.65974	817487.77
$M_{6 \rightarrow 5}$	0.65657	831870.37
$M_{5 \rightarrow 6}$	0.67439	778938.16
$M_{7 \rightarrow 6}$	0.67236	786061.61
$M_{6 \rightarrow 7}$	0.68066	766771.69
$M_{8 \rightarrow 7}$	0.67930	768327.35
$M_{7 \rightarrow 8}$	0.69275	732784.04
$M_{9 \rightarrow 8}$	0.71906	652477.54
$M_{8 \rightarrow 9}$	0.74318	590302.01
$M_{10 \rightarrow 9}$	0.62524	914305.88
$M_{9 \rightarrow 10}$	0.63591	890415.63
Genealogies	0.78531	494706.05

## *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