

Palythoa tuberculosa - Hawaii

POPULATION SIZE, MIGRATION, DIVERGENCE, ASSIGNMENT, HISTORY

Bayesian inference using the structured coalescent

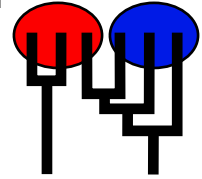
Migrate-n version 4.4.4(git:) [June-1-2019]

Compiled for PARALLEL computer architectures

One master and 31 compute nodes are available.

Program started at Sun Jan 23 14:21:54 2022

Program finished at Sun Jan 23 14:45:54 2022 [Runtime:0000:00:24:00]



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)

266050072

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	1	1	1	1	1	1	1	1
1 Pop_Kure	*	*	*	*	*	*	*	*	*	*
1 Pop_P&H	*	*	*	*	*	*	*	*	*	*
1 Pop_Pbanks	*	*	*	*	*	*	*	*	*	*
1 Pop_MaroReef	*	*	*	*	*	*	*	*	*	*
1 Pop_Maui	*	*	*	*	*	*	*	*	*	*
1 Pop_FFS	*	*	*	*	*	*	*	*	*	*
1 Pop_Kauai	*	*	*	*	*	*	*	*	*	*

1 Pop_Oahu	*	*	*	*	*	*	*	*	*	*
1 Pop_Molokai	*	*	*	*	*	*	*	*	*	*
1 Pop_BigIsland	*	*	*	*	*	*	*	*	*	*

Order of parameters:

1	Θ_1	<displayed>
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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	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	0.33333

[* * 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

4 chains with temperatures
1000000.00 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

102	337
103	374
104	487
105	366
106	317
107	399
108	333
109	347

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
101	1	1	1.000	1.000	1.000
102	1	1	1.000	1.000	1.000
103	1	1	1.000	1.000	1.000
104	1	1	1.000	1.000	1.000
105	1	1	1.000	1.000	1.000
106	1	1	1.000	1.000	1.000
107	1	1	1.000	1.000	1.000
108	1	1	1.000	1.000	1.000
109	1	1	1.000	1.000	1.000
Population			Locus		Gene copies
1 Pop_Kure			1		20
			2		20
			3		20
			4		20
			5		20
			6		20
			7		20
			8		20
			9		20
			10		20
			11		20
			12		20
			13		20

14	20
15	20
16	20
17	20
18	20
19	20
20	20
21	20
22	20
23	20
24	20
25	20
26	20
27	20
28	20
29	20
30	20
31	20
32	20
33	20
34	20
35	20
36	20
37	20
38	20
39	20
40	20
41	20
42	20
43	20
44	20
45	20
46	20
47	20
48	20
49	20
50	20
51	20
52	20
53	20
54	20
55	20
56	20
57	20
58	20

59	20
60	20
61	20
62	20
63	20
64	20
65	20
66	20
67	20
68	20
69	20
70	20
71	20
72	20
73	20
74	20
75	20
76	20
77	20
78	20
79	20
80	20
81	20
82	20
83	20
84	20
85	20
86	20
87	20
88	20
89	20
90	20
91	20
92	20
93	20
94	20
95	20
96	20
97	20
98	20
99	20
100	20
101	20
102	20
103	20

1 Pop_P&H

104	20
105	20
106	20
107	20
108	20
109	20
1	8
2	8
3	8
4	8
5	8
6	8
7	8
8	8
9	8
10	8
11	8
12	8
13	8
14	8
15	8
16	8
17	8
18	8
19	8
20	8
21	8
22	8
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1 Pop_Molokai	106	20
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Total of all populations	1	186
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Bayesian Analysis: Posterior distribution table

Locus	Parameter	2.5%	25.0%	Mode	75.0%	97.5%	Median	Mean
1	Θ_1	0.00240	0.00300	0.00370	0.00420	0.00520	0.00390	0.00380
2	Θ_1	0.00280	0.00300	0.00370	0.00440	0.00700	0.00450	0.00469
3	Θ_1	0.00380	0.00540	0.00610	0.00700	0.00800	0.00650	0.00651
4	Θ_1	0.00240	0.00320	0.00390	0.00440	0.00560	0.00430	0.00411
5	Θ_1	0.00260	0.00280	0.00350	0.00380	0.00480	0.00410	0.00555
6	Θ_1	0.00260	0.00320	0.00370	0.00420	0.00540	0.00410	0.00396
7	Θ_1	0.00240	0.00300	0.00370	0.00440	0.00580	0.00450	0.00553
8	Θ_1	0.00220	0.00300	0.00350	0.00420	0.00560	0.00410	0.00396
9	Θ_1	0.00660	0.00740	0.00810	0.00840	0.00920	0.00830	0.00807
10	Θ_1	0.00260	0.00320	0.00390	0.00420	0.00520	0.00410	0.00396
11	Θ_1	0.00260	0.00380	0.00470	0.00540	0.00600	0.00530	0.00620
12	Θ_1	0.00280	0.00340	0.00430	0.00460	0.00600	0.00450	0.00432
13	Θ_1	0.00260	0.00300	0.00370	0.00440	0.00660	0.00430	0.00436
14	Θ_1	0.00280	0.00340	0.00390	0.00440	0.00520	0.00430	0.00411
15	Θ_1	0.00260	0.00340	0.00410	0.00460	0.00580	0.00430	0.00415
16	Θ_1	0.00220	0.00320	0.00410	0.00440	0.00580	0.00430	0.00409
17	Θ_1	0.00260	0.00340	0.00410	0.00460	0.00580	0.00430	0.00424
18	Θ_1	0.00240	0.00280	0.00350	0.00440	0.00680	0.00450	0.00477

19	Θ_1	0.00260	0.00320	0.00370	0.00420	0.00500	0.00390	0.00382
20	Θ_1	0.00240	0.00320	0.00390	0.00420	0.00560	0.00410	0.00403
21	Θ_1	0.00220	0.00320	0.00390	0.00480	0.00660	0.00450	0.00439
22	Θ_1	0.00780	0.00880	0.00950	0.00980	0.01060	0.00970	0.00953
23	Θ_1	0.00260	0.00320	0.00390	0.00420	0.00560	0.00410	0.00403
24	Θ_1	0.00220	0.00300	0.00370	0.00420	0.00520	0.00390	0.00381
25	Θ_1	0.00220	0.00280	0.00350	0.00400	0.00520	0.00390	0.00370
26	Θ_1	0.00740	0.00800	0.00870	0.00880	0.01000	0.00910	0.00892
27	Θ_1	0.00640	0.00900	0.00930	0.00940	0.00980	0.00850	0.00835
28	Θ_1	0.00280	0.00320	0.00370	0.00440	0.00660	0.00430	0.00429
29	Θ_1	0.00240	0.00320	0.00370	0.00420	0.00500	0.00390	0.00383
30	Θ_1	0.00340	0.00380	0.00470	0.00520	0.00680	0.00510	0.00539
31	Θ_1	0.00320	0.00360	0.00410	0.00460	0.00560	0.00450	0.00431
32	Θ_1	0.00240	0.00320	0.00370	0.00420	0.00540	0.00390	0.00383
33	Θ_1	0.01080	0.01080	0.01110	0.01120	0.01140	0.00970	0.00982
34	Θ_1	0.00260	0.00300	0.00370	0.00420	0.00480	0.00410	0.00389
35	Θ_1	0.00280	0.00340	0.00390	0.00440	0.00540	0.00430	0.00420
36	Θ_1	0.00240	0.00480	0.00550	0.00640	0.00740	0.00590	0.00547
37	Θ_1	0.00240	0.00320	0.00410	0.00440	0.00580	0.00410	0.00406
38	Θ_1	0.01040	0.01040	0.01070	0.01080	0.01100	0.00990	0.00956
39	Θ_1	0.00260	0.00320	0.00390	0.00420	0.00520	0.00410	0.00397
40	Θ_1	0.00280	0.00360	0.00410	0.00480	0.00580	0.00450	0.00429
41	Θ_1	0.00940	0.00940	0.01010	0.01020	0.01060	0.00930	0.00834

Locus	Parameter	2.5%	25.0%	Mode	75.0%	97.5%	Median	Mean
42	Θ_1	0.00820	0.00880	0.00910	0.00940	0.00940	0.00870	0.00718
43	Θ_1	0.00240	0.00300	0.00370	0.00400	0.00520	0.00390	0.00381
44	Θ_1	0.00200	0.00260	0.00330	0.00400	0.00560	0.00390	0.00375
45	Θ_1	0.00820	0.00880	0.00910	0.00920	0.01000	0.00930	0.00930
46	Θ_1	0.00260	0.00340	0.00410	0.00440	0.00560	0.00410	0.00406
47	Θ_1	0.00240	0.00300	0.00370	0.00420	0.00580	0.00410	0.00399
48	Θ_1	0.00260	0.00320	0.00390	0.00420	0.00520	0.00410	0.00394
49	Θ_1	0.00220	0.00300	0.00350	0.00400	0.00520	0.00390	0.00376
50	Θ_1	0.00320	0.00420	0.00510	0.00560	0.00760	0.00570	0.00568
51	Θ_1	0.00240	0.00300	0.00370	0.00420	0.00560	0.00410	0.00391
52	Θ_1	0.00260	0.00320	0.00370	0.00420	0.00540	0.00410	0.00394
53	Θ_1	0.00940	0.00940	0.00970	0.00980	0.01060	0.00830	0.00674
54	Θ_1	0.00220	0.00280	0.00350	0.00460	0.00660	0.00450	0.00488
55	Θ_1	0.00980	0.00980	0.01010	0.01020	0.01020	0.00850	0.00768
56	Θ_1	0.00260	0.00320	0.00390	0.00440	0.00520	0.00410	0.00401
57	Θ_1	0.00300	0.00340	0.00430	0.00480	0.00640	0.00470	0.00519
58	Θ_1	0.00220	0.00300	0.00350	0.00420	0.00560	0.00390	0.00386
59	Θ_1	0.00260	0.00320	0.00370	0.00420	0.00580	0.00410	0.00437
60	Θ_1	0.00240	0.00320	0.00370	0.00420	0.00540	0.00410	0.00393
61	Θ_1	0.00260	0.00340	0.00390	0.00440	0.00540	0.00410	0.00405

62	Θ_1	0.00220	0.00320	0.00370	0.00460	0.00600	0.00410	0.00409
63	Θ_1	0.00880	0.00940	0.00970	0.00980	0.00980	0.00990	0.00998
64	Θ_1	0.00300	0.00300	0.00370	0.00480	0.00520	0.00490	0.00530
65	Θ_1	0.00300	0.00320	0.00410	0.00480	0.00540	0.00470	0.00487
66	Θ_1	0.00280	0.00340	0.00390	0.00440	0.00520	0.00430	0.00411
67	Θ_1	0.00240	0.00300	0.00390	0.00420	0.00540	0.00390	0.00384
68	Θ_1	0.00260	0.00320	0.00390	0.00420	0.00520	0.00410	0.00390
69	Θ_1	0.00200	0.00260	0.00330	0.00360	0.00480	0.00350	0.00349
70	Θ_1	0.00320	0.00320	0.00430	0.00560	0.00560	0.00510	0.00612
71	Θ_1	0.00420	0.00440	0.00530	0.00560	0.00780	0.00670	0.00703
72	Θ_1	0.00800	0.00880	0.00930	0.00940	0.01020	0.00970	0.00973
73	Θ_1	0.00720	0.00920	0.00950	0.00960	0.01000	0.00890	0.00875
74	Θ_1	0.00300	0.00360	0.00430	0.00480	0.00660	0.00470	0.00471
75	Θ_1	0.00260	0.00360	0.00390	0.00460	0.00560	0.00450	0.00428
76	Θ_1	0.00240	0.00300	0.00350	0.00460	0.00760	0.00470	0.00488
77	Θ_1	0.00240	0.00300	0.00370	0.00400	0.00500	0.00390	0.00379
78	Θ_1	0.00240	0.00300	0.00370	0.00400	0.00540	0.00410	0.00389
79	Θ_1	0.00240	0.00320	0.00390	0.00420	0.00540	0.00410	0.00397
80	Θ_1	0.00220	0.00320	0.00390	0.00460	0.00580	0.00430	0.00415
81	Θ_1	0.00920	0.00940	0.00970	0.00980	0.01000	0.00890	0.00890
82	Θ_1	0.00300	0.00360	0.00450	0.00480	0.00640	0.00470	0.00500
83	Θ_1	0.00220	0.00280	0.00350	0.00400	0.00540	0.00390	0.00375
84	Θ_1	0.00260	0.00260	0.00350	0.00420	0.00680	0.00430	0.00496

Locus	Parameter	2.5%	25.0%	Mode	75.0%	97.5%	Median	Mean
85	Θ_1	0.00840	0.01000	0.01030	0.01040	0.01040	0.00990	0.00954
86	Θ_1	0.00280	0.00320	0.00390	0.00420	0.00520	0.00410	0.00394
87	Θ_1	0.00220	0.00280	0.00350	0.00380	0.00520	0.00370	0.00361
88	Θ_1	0.00320	0.00320	0.00530	0.00600	0.00600	0.00610	0.00663
89	Θ_1	0.00240	0.00340	0.00370	0.00460	0.00620	0.00430	0.00417
90	Θ_1	0.00260	0.00300	0.00350	0.00400	0.00780	0.00530	0.00510
91	Θ_1	0.00300	0.00340	0.00410	0.00460	0.00620	0.00450	0.00440
92	Θ_1	0.00280	0.00340	0.00410	0.00440	0.00540	0.00430	0.00414
93	Θ_1	0.00280	0.00340	0.00390	0.00440	0.00540	0.00430	0.00407
94	Θ_1	0.00260	0.00340	0.00370	0.00440	0.00540	0.00430	0.00406
95	Θ_1	0.00240	0.00280	0.00330	0.00380	0.00460	0.00370	0.00368
96	Θ_1	0.00260	0.00360	0.00450	0.00520	0.00680	0.00470	0.00468
97	Θ_1	0.00260	0.00340	0.00430	0.00480	0.00600	0.00450	0.00443
98	Θ_1	0.00260	0.00320	0.00390	0.00440	0.00560	0.00430	0.00407
99	Θ_1	0.00720	0.00860	0.00890	0.00920	0.01020	0.00890	0.00843
100	Θ_1	0.00260	0.00500	0.00550	0.00620	0.00720	0.00570	0.00570
101	Θ_1	0.00260	0.00320	0.00390	0.00420	0.00500	0.00410	0.00388
102	Θ_1	0.00240	0.00320	0.00390	0.00440	0.00540	0.00410	0.00398
103	Θ_1	0.00260	0.00340	0.00410	0.00460	0.00560	0.00430	0.00420
104	Θ_1	0.00960	0.00960	0.01010	0.01020	0.01020	0.00630	0.00668

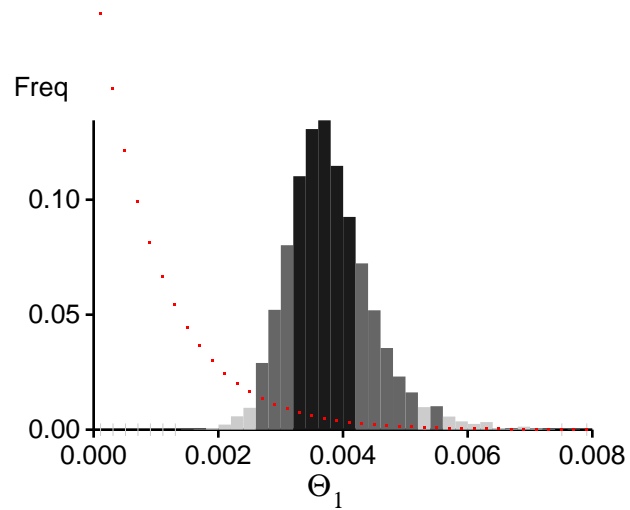
105	Θ_1	0.00260	0.00340	0.00390	0.00440	0.00520	0.00410	0.00404
106	Θ_1	0.00340	0.00400	0.00490	0.00520	0.00660	0.00510	0.00501
107	Θ_1	0.00280	0.00320	0.00390	0.00420	0.00540	0.00410	0.00401
108	Θ_1	0.00260	0.00340	0.00390	0.00460	0.00580	0.00430	0.00422
109	Θ_1	0.00260	0.00340	0.00430	0.00460	0.00580	0.00430	0.00422
All	Θ_1	0.00760	0.00780	0.00810	0.00820	0.00840	0.00830	0.00808

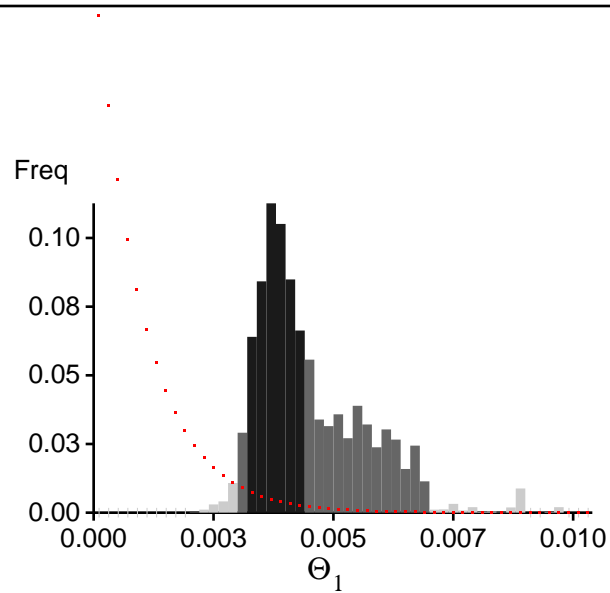
Citation suggestions:

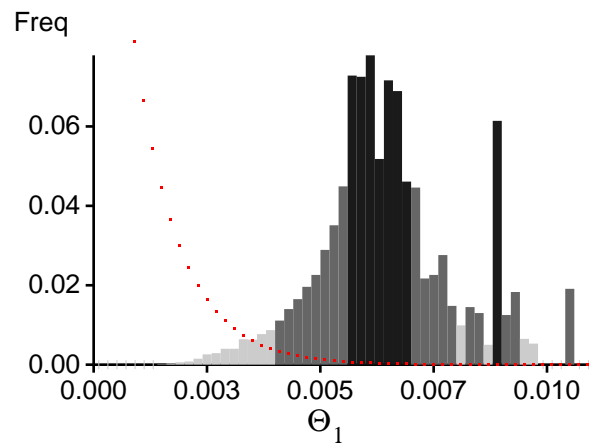
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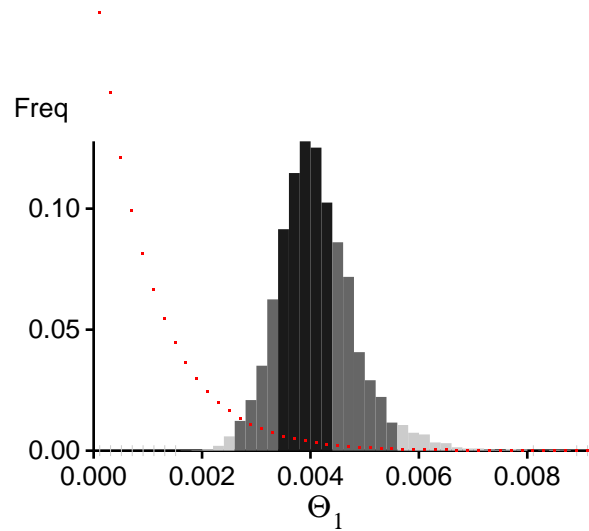
Beerli P., 2007. Estimation of the population scaled mutation rate from microsatellite data,
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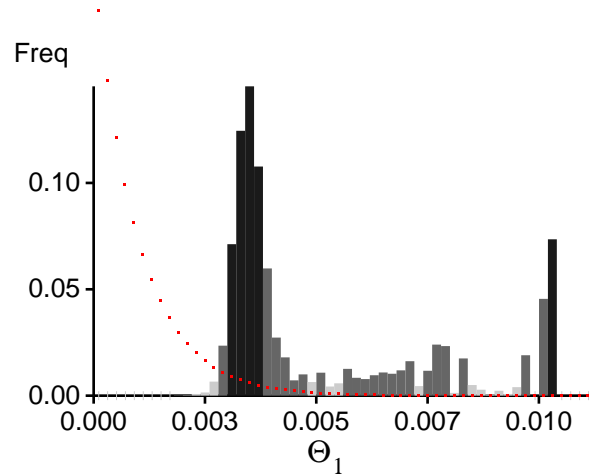
Beerli P., 2009. How to use MIGRATE or why are Markov chain Monte Carlo programs difficult to use?
In Population Genetics for Animal Conservation, G. Bertorelle, M. W. Bruford, H. C. Hauffe, A. Rizzoli,
and C. Vernesi, eds., vol. 17 of Conservation Biology, Cambridge University Press, Cambridge UK, pp. 42-79.

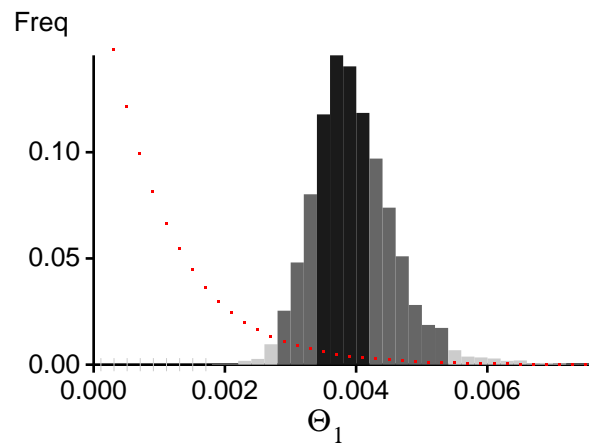
Bayesian Analysis: Posterior distribution for locus 1

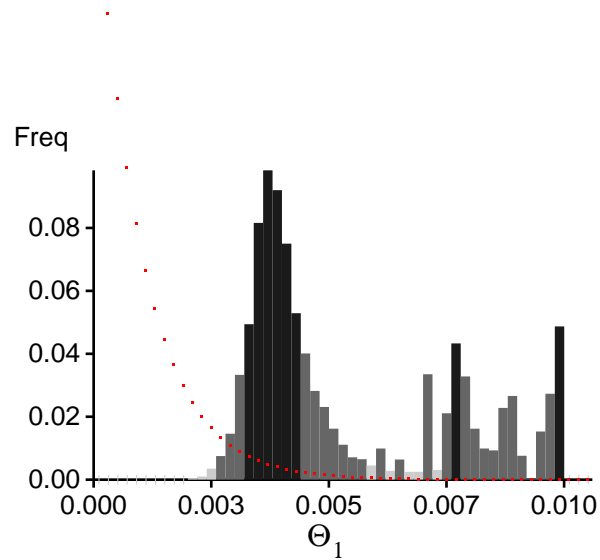
Bayesian Analysis: Posterior distribution for locus 2

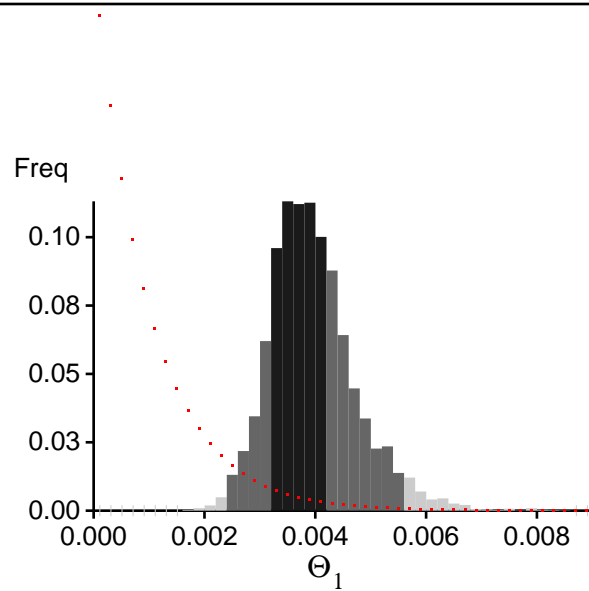
Bayesian Analysis: Posterior distribution for locus 3

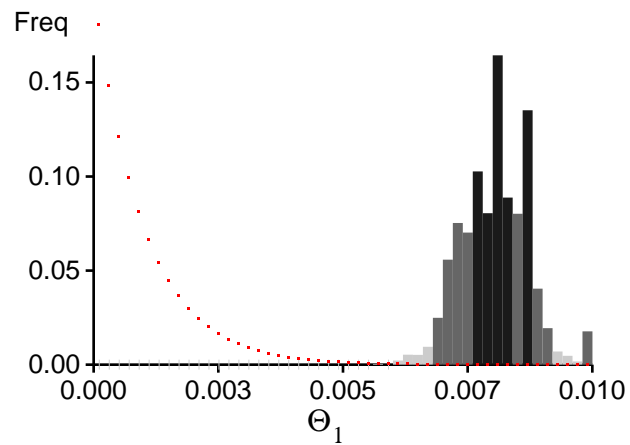
Bayesian Analysis: Posterior distribution for locus 4

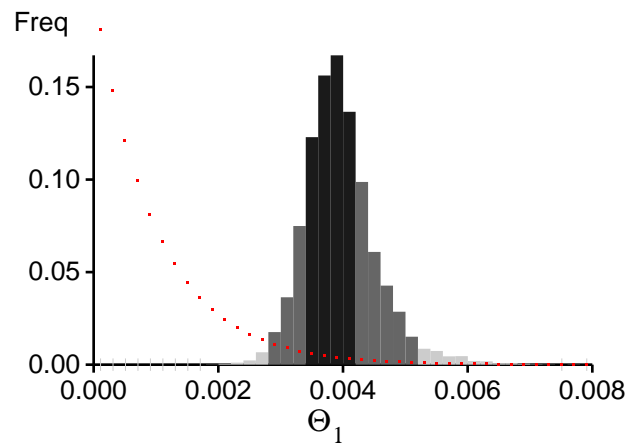
Bayesian Analysis: Posterior distribution for locus 5

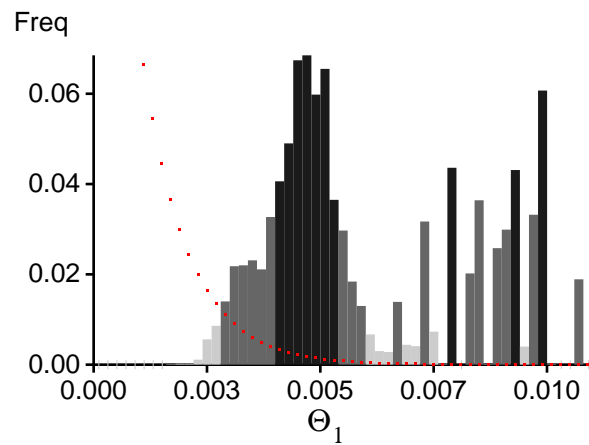
Bayesian Analysis: Posterior distribution for locus 6

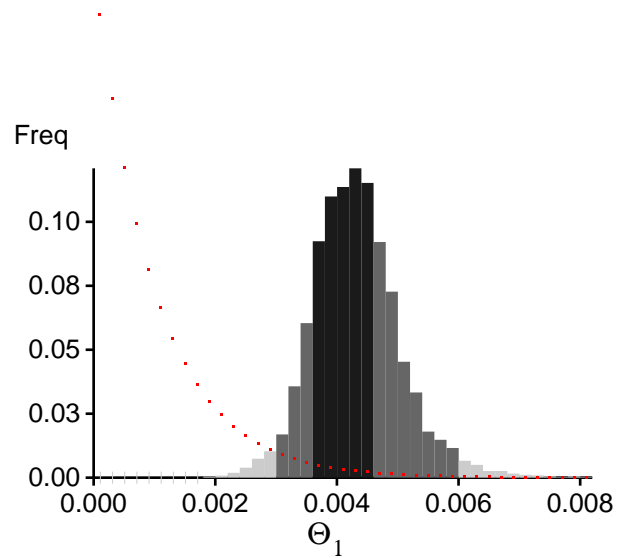
Bayesian Analysis: Posterior distribution for locus 7

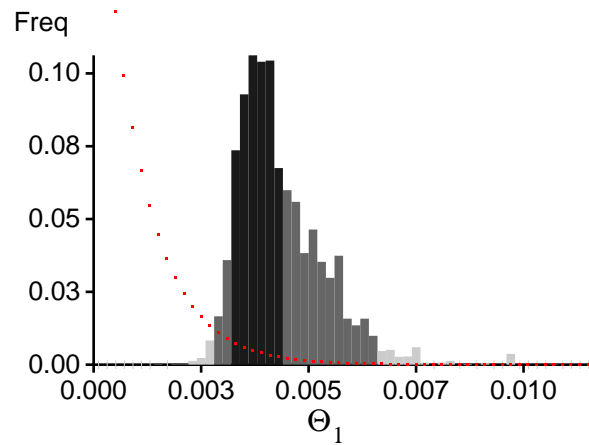
Bayesian Analysis: Posterior distribution for locus 8

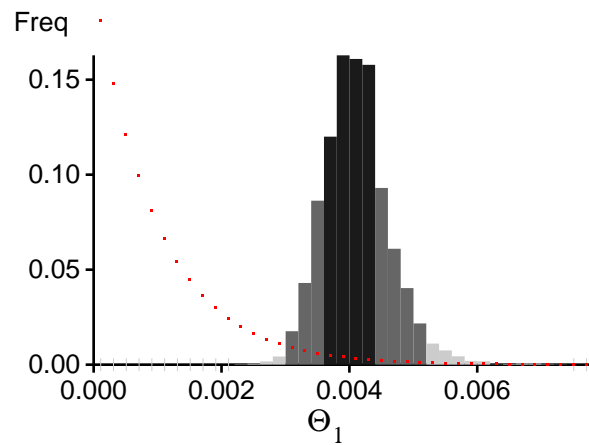
Bayesian Analysis: Posterior distribution for locus 9

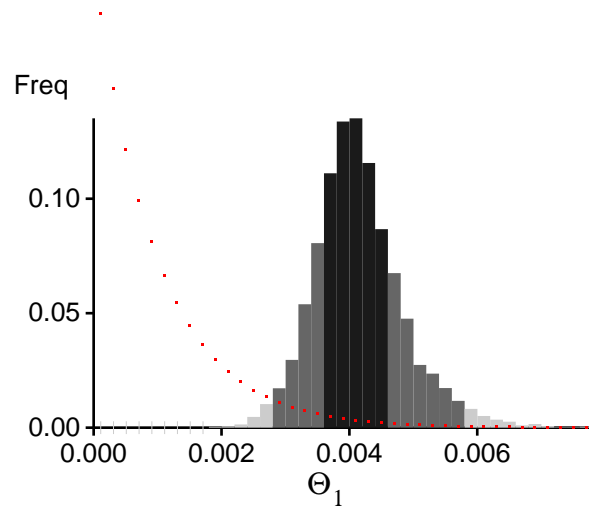
Bayesian Analysis: Posterior distribution for locus 10

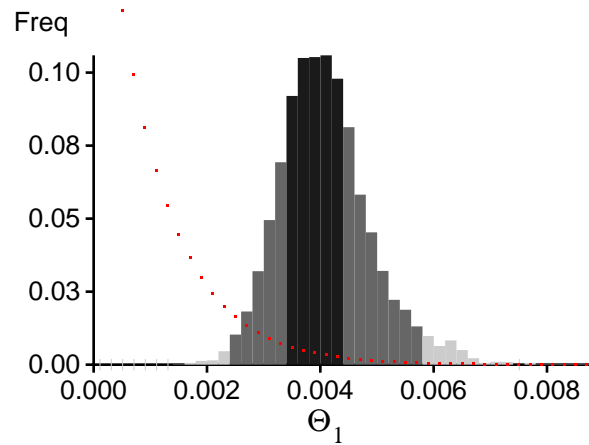
Bayesian Analysis: Posterior distribution for locus 11

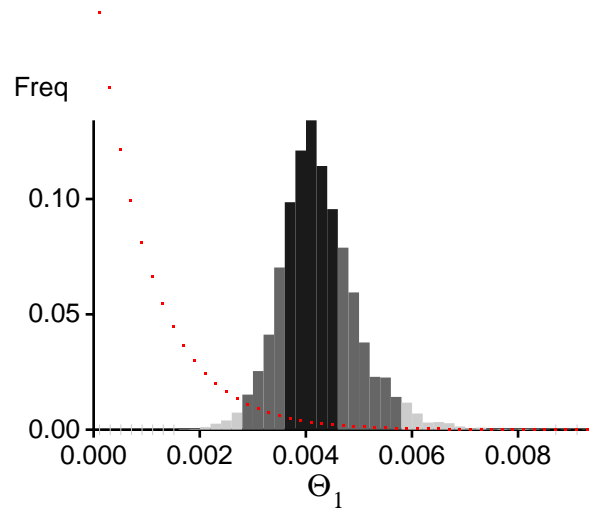
Bayesian Analysis: Posterior distribution for locus 12

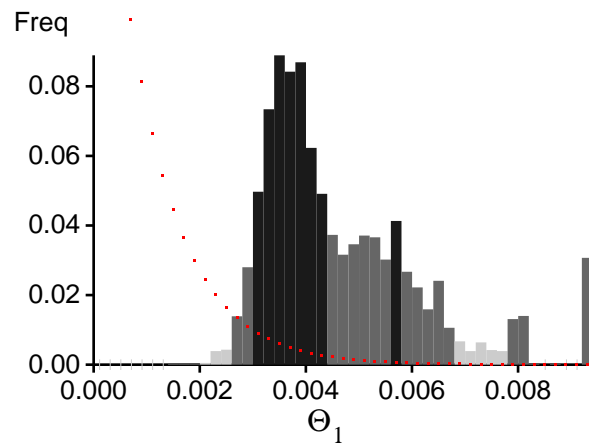
Bayesian Analysis: Posterior distribution for locus 13

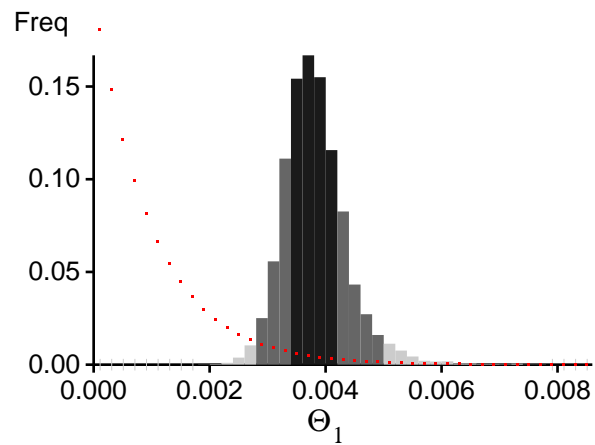
Bayesian Analysis: Posterior distribution for locus 14

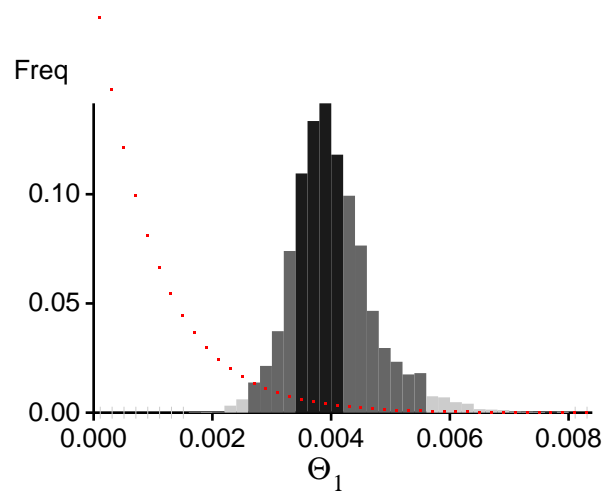
Bayesian Analysis: Posterior distribution for locus 15

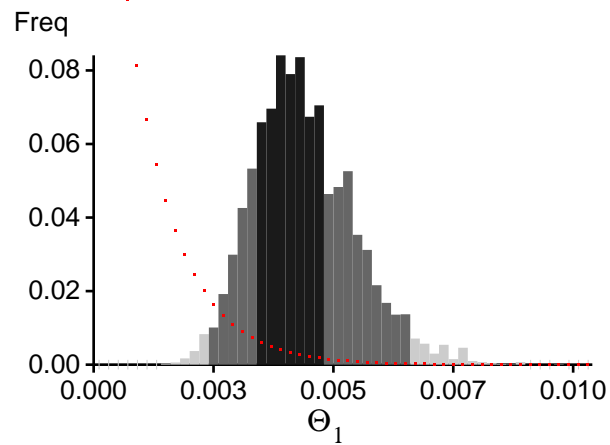
Bayesian Analysis: Posterior distribution for locus 16

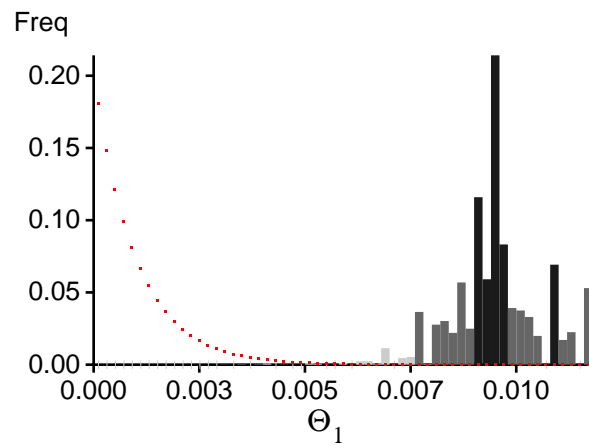
Bayesian Analysis: Posterior distribution for locus 17

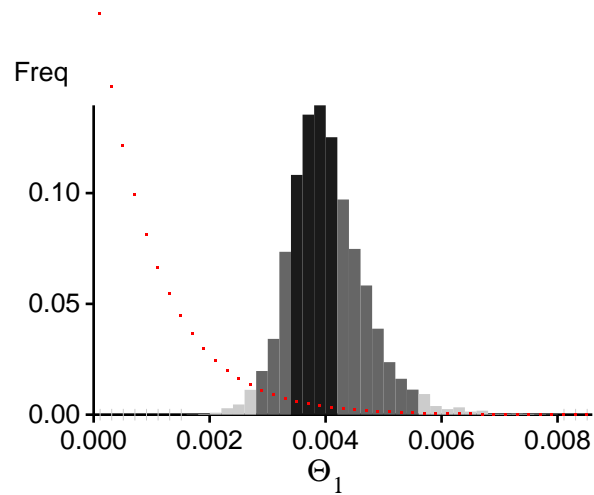
Bayesian Analysis: Posterior distribution for locus 18

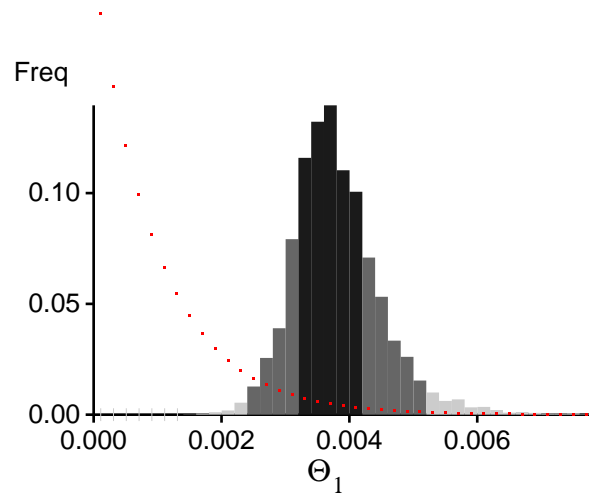
Bayesian Analysis: Posterior distribution for locus 19

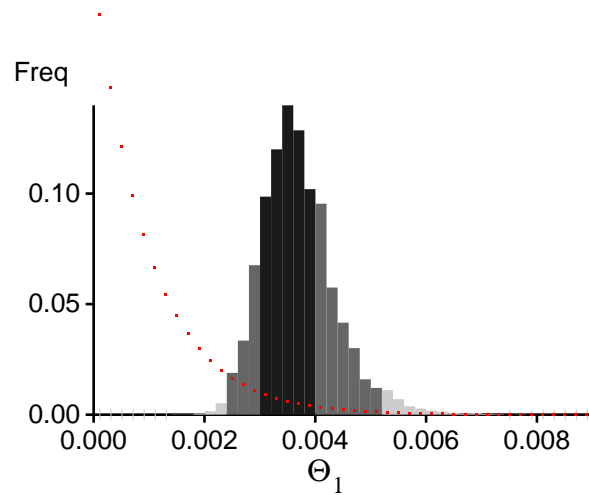
Bayesian Analysis: Posterior distribution for locus 20

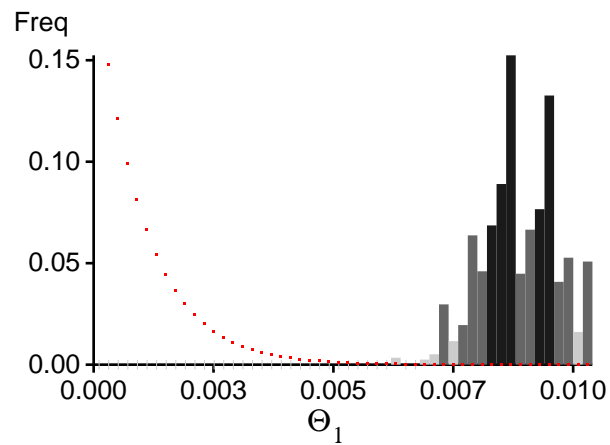
Bayesian Analysis: Posterior distribution for locus 21

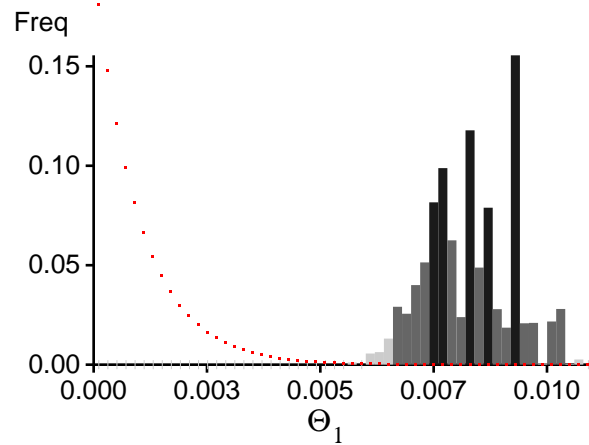
Bayesian Analysis: Posterior distribution for locus 22

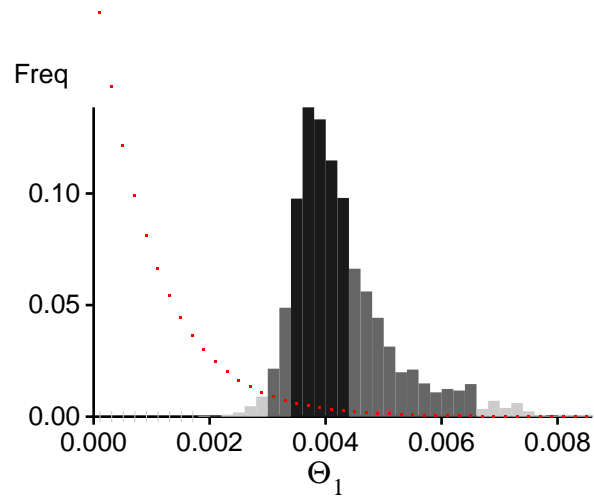
Bayesian Analysis: Posterior distribution for locus 23

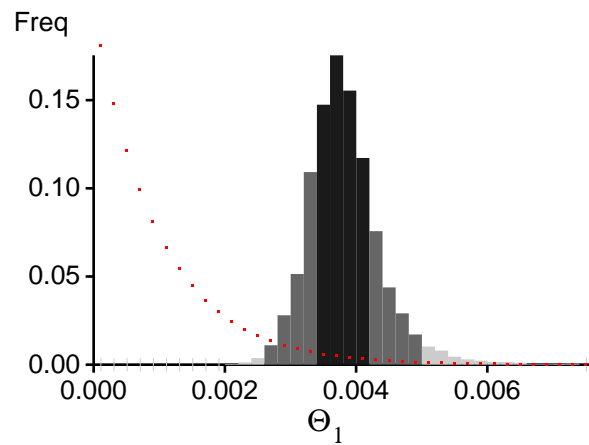
Bayesian Analysis: Posterior distribution for locus 24

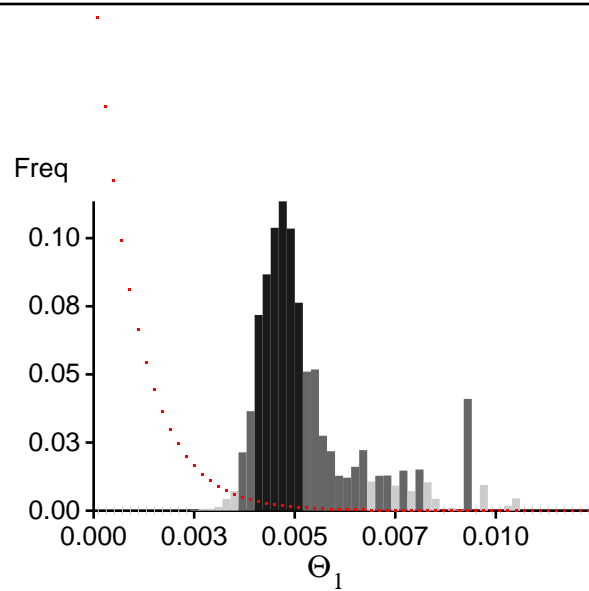
Bayesian Analysis: Posterior distribution for locus 25

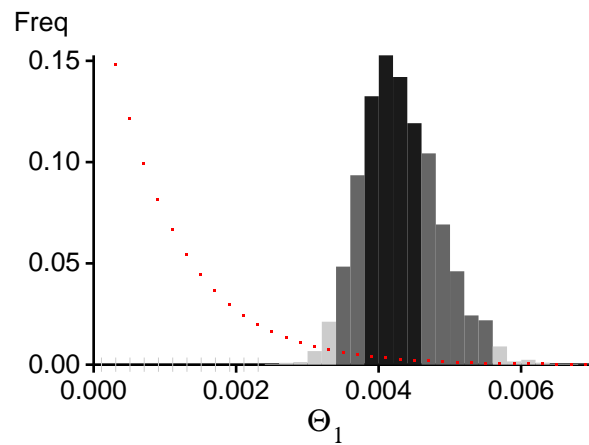
Bayesian Analysis: Posterior distribution for locus 26

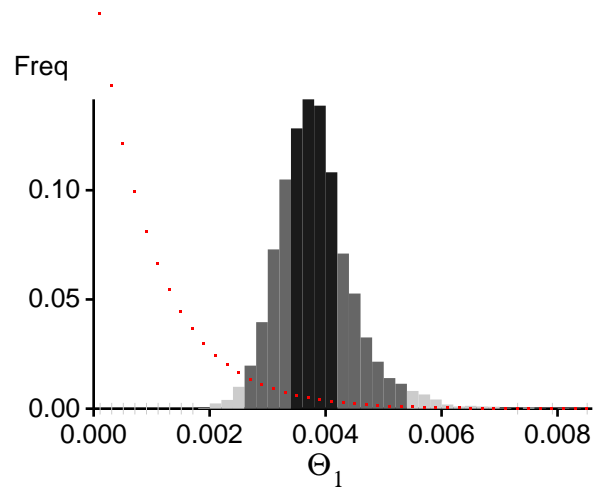
Bayesian Analysis: Posterior distribution for locus 27

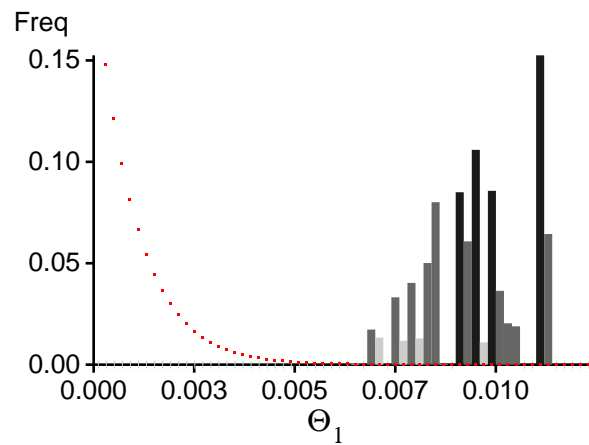
Bayesian Analysis: Posterior distribution for locus 28

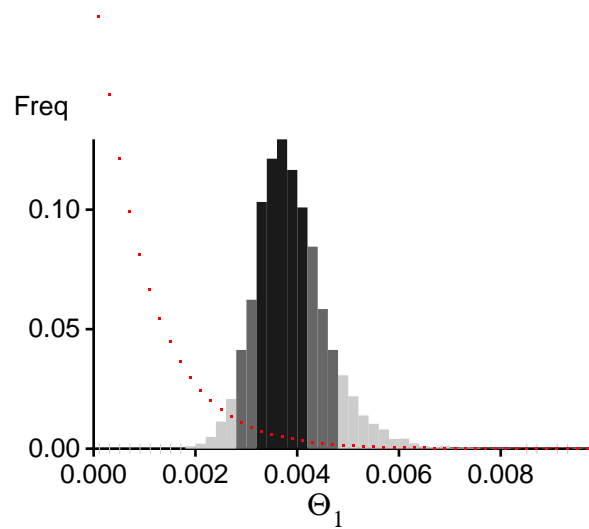
Bayesian Analysis: Posterior distribution for locus 29

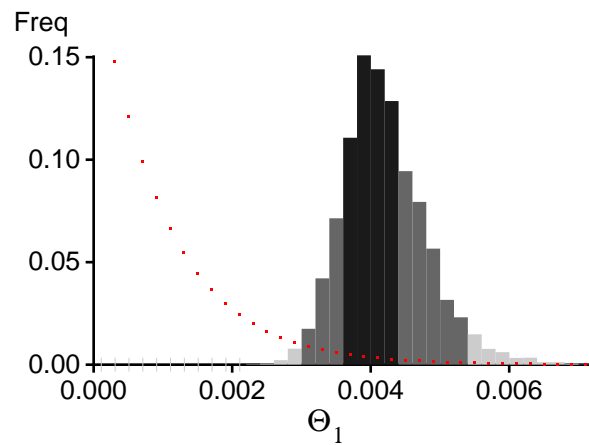
Bayesian Analysis: Posterior distribution for locus 30

Bayesian Analysis: Posterior distribution for locus 31

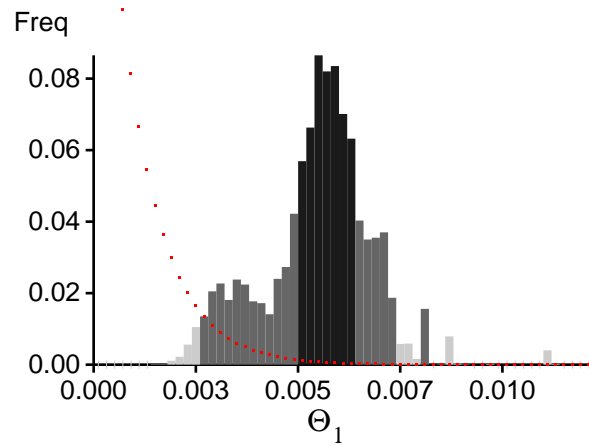
Bayesian Analysis: Posterior distribution for locus 32

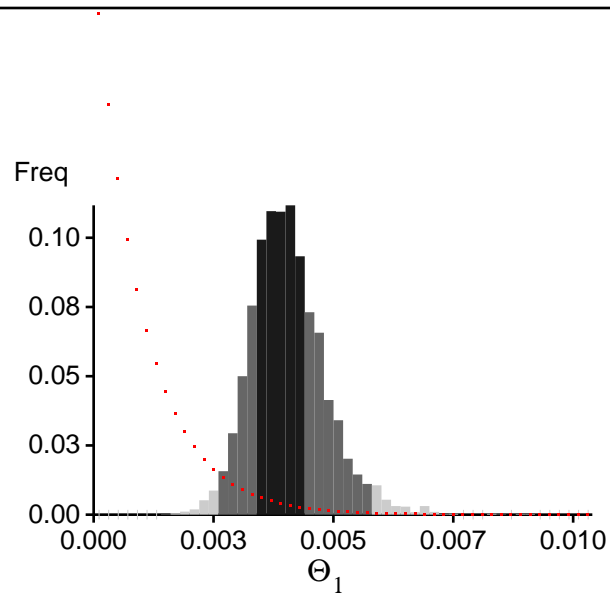
Bayesian Analysis: Posterior distribution for locus 33

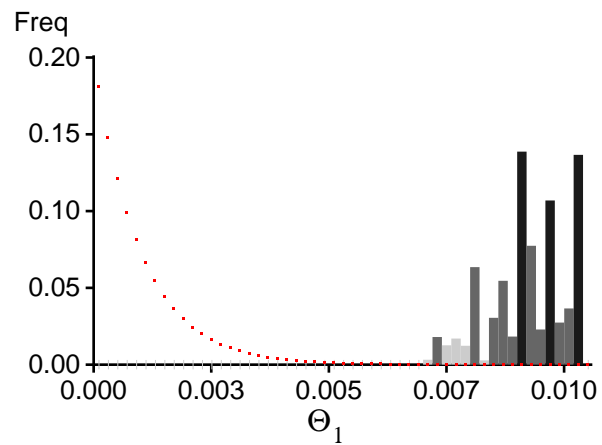
Bayesian Analysis: Posterior distribution for locus 34

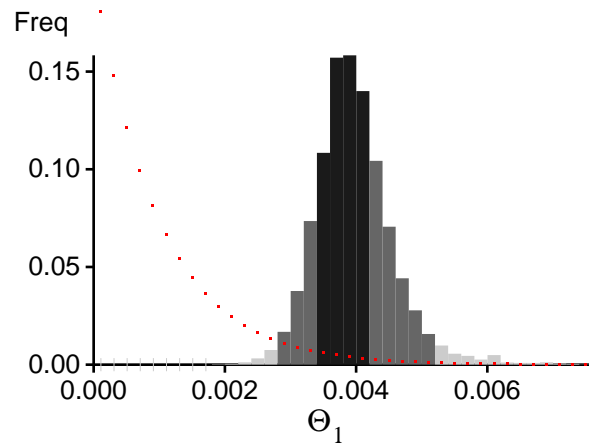
Bayesian Analysis: Posterior distribution for locus 35

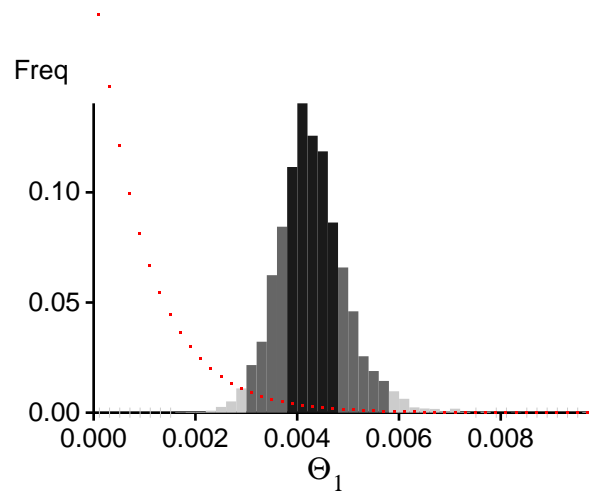
Bayesian Analysis: Posterior distribution for locus 36



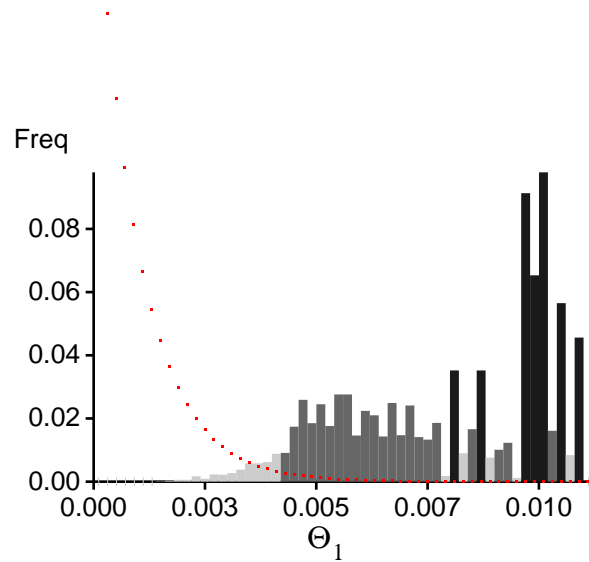
Bayesian Analysis: Posterior distribution for locus 37

Bayesian Analysis: Posterior distribution for locus 38

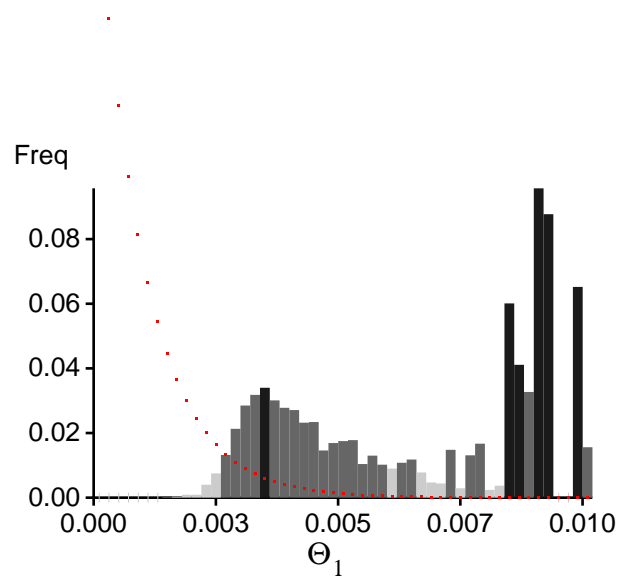
Bayesian Analysis: Posterior distribution for locus 39

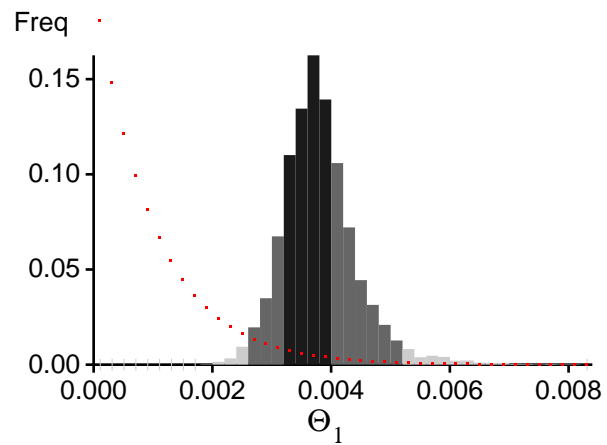
Bayesian Analysis: Posterior distribution for locus 40

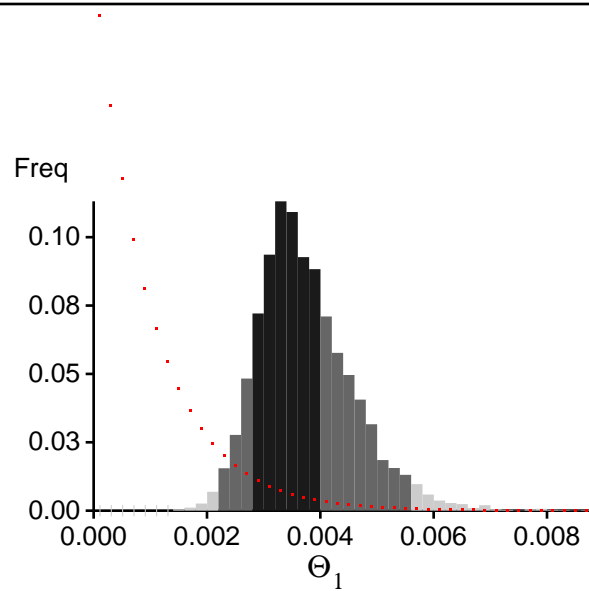
Bayesian Analysis: Posterior distribution for locus 41

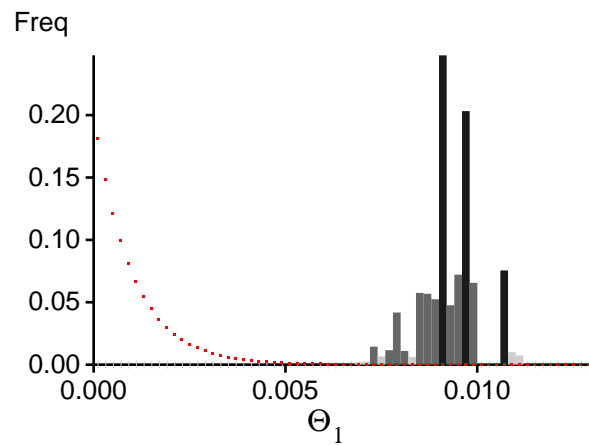


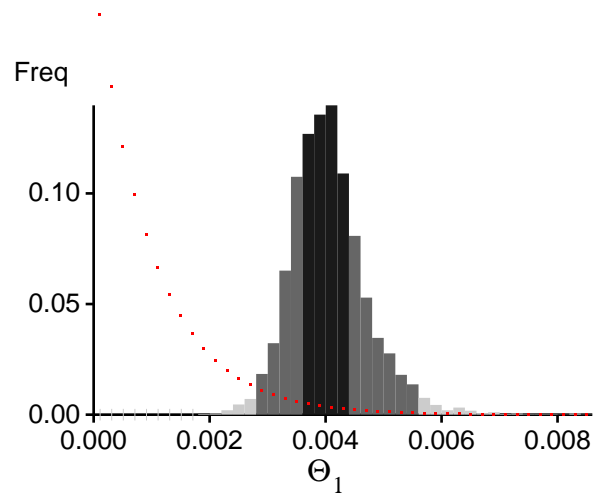
Bayesian Analysis: Posterior distribution for locus 42

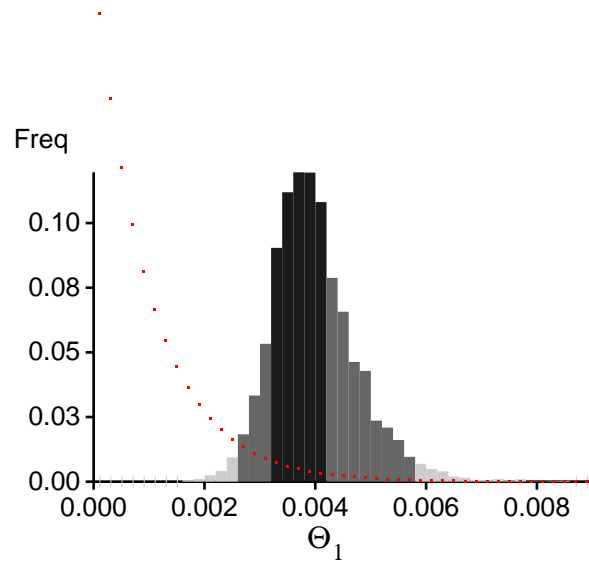


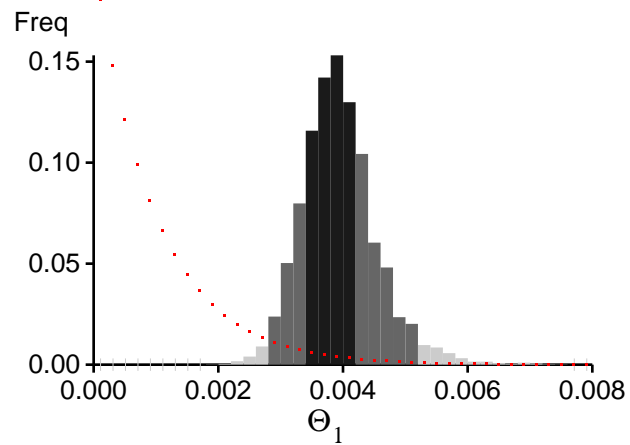
Bayesian Analysis: Posterior distribution for locus 43

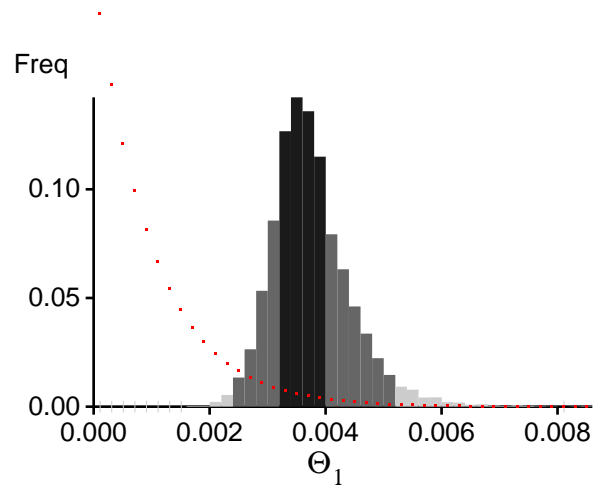
Bayesian Analysis: Posterior distribution for locus 44

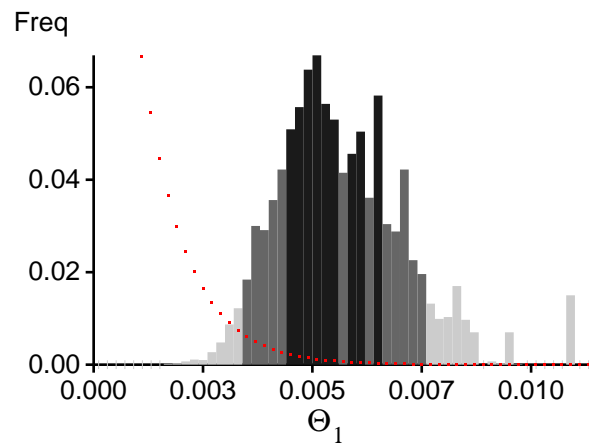
Bayesian Analysis: Posterior distribution for locus 45

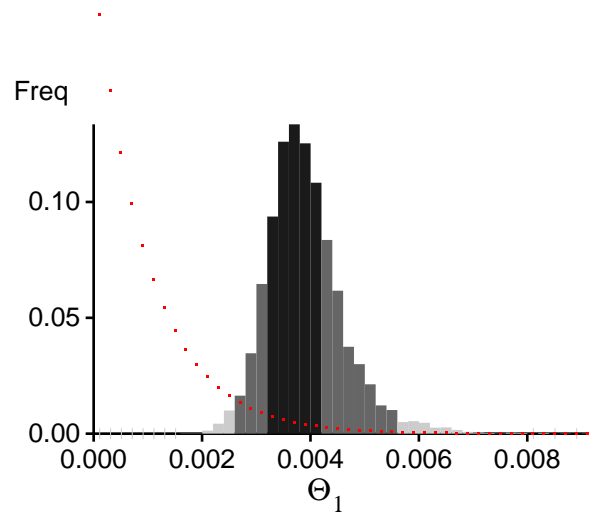
Bayesian Analysis: Posterior distribution for locus 46

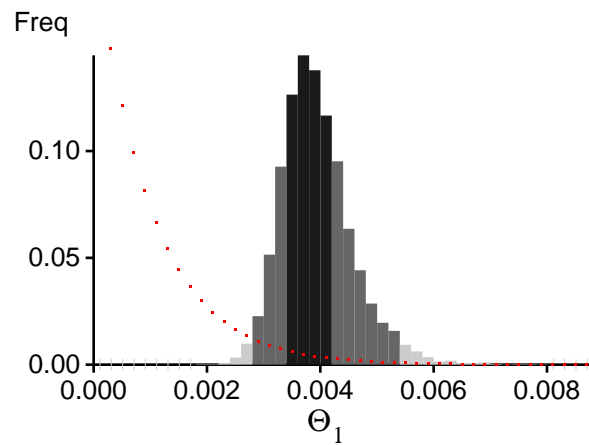
Bayesian Analysis: Posterior distribution for locus 47

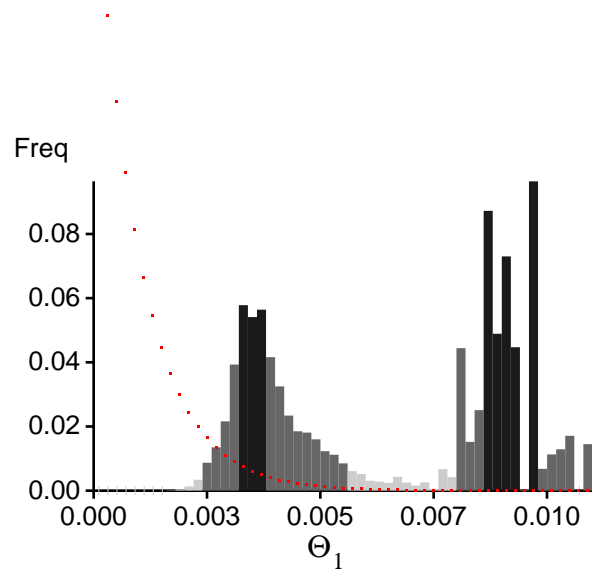
Bayesian Analysis: Posterior distribution for locus 48

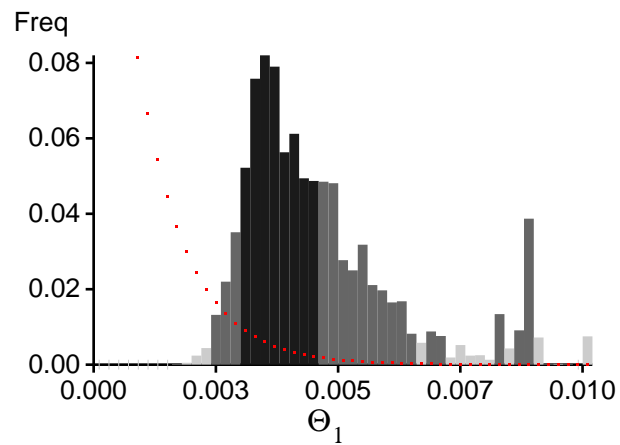
Bayesian Analysis: Posterior distribution for locus 49

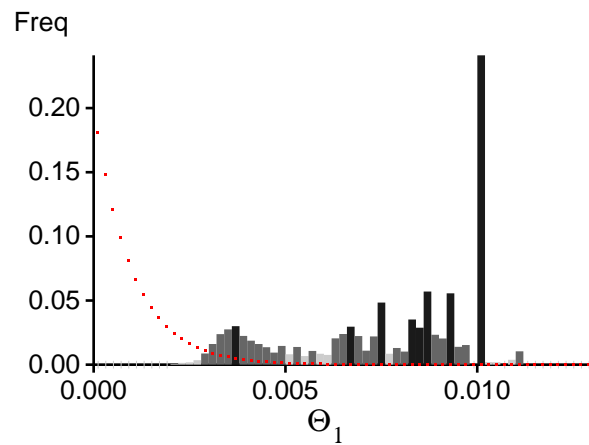
Bayesian Analysis: Posterior distribution for locus 50

Bayesian Analysis: Posterior distribution for locus 51

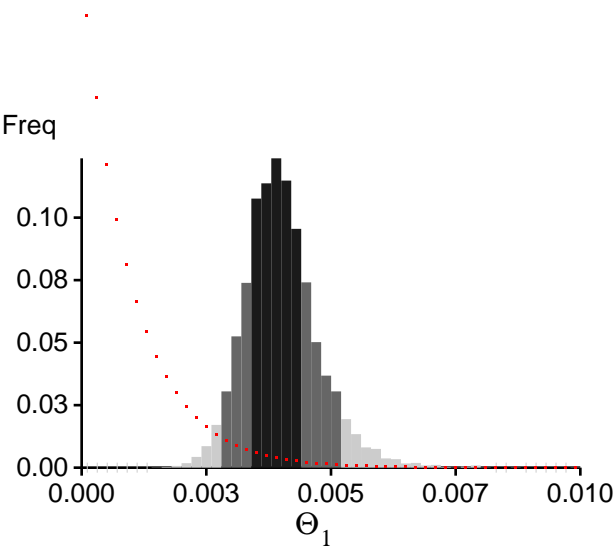
Bayesian Analysis: Posterior distribution for locus 52

Bayesian Analysis: Posterior distribution for locus 53

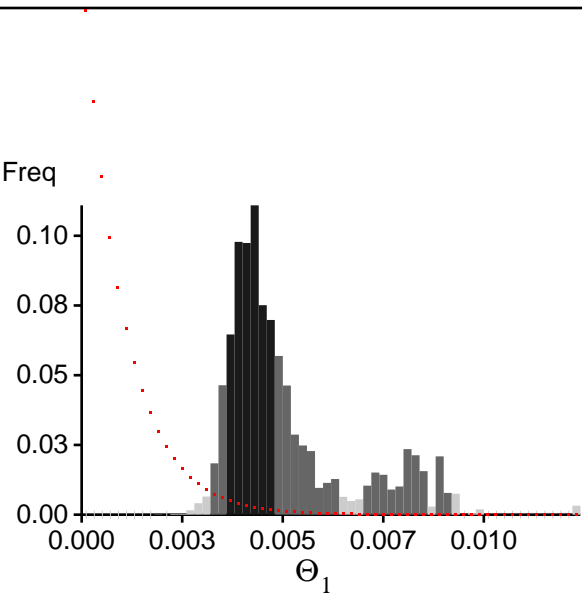
Bayesian Analysis: Posterior distribution for locus 54

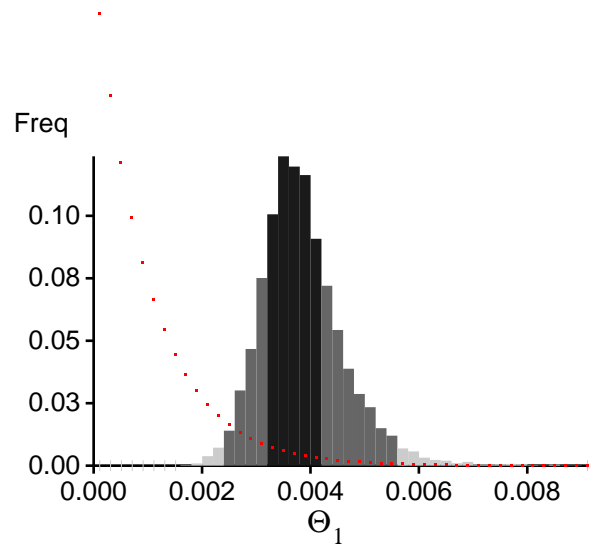
Bayesian Analysis: Posterior distribution for locus 55

Bayesian Analysis: Posterior distribution for locus 56

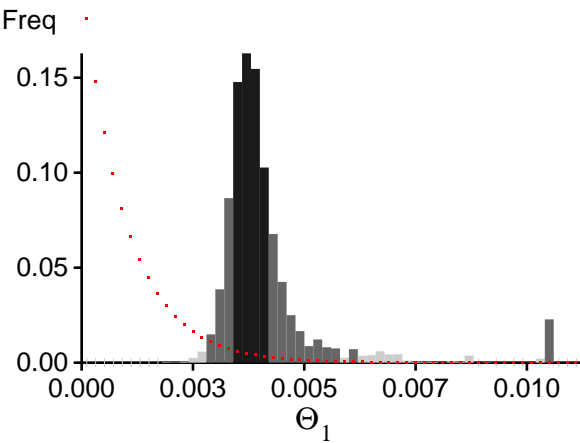


Bayesian Analysis: Posterior distribution for locus 57

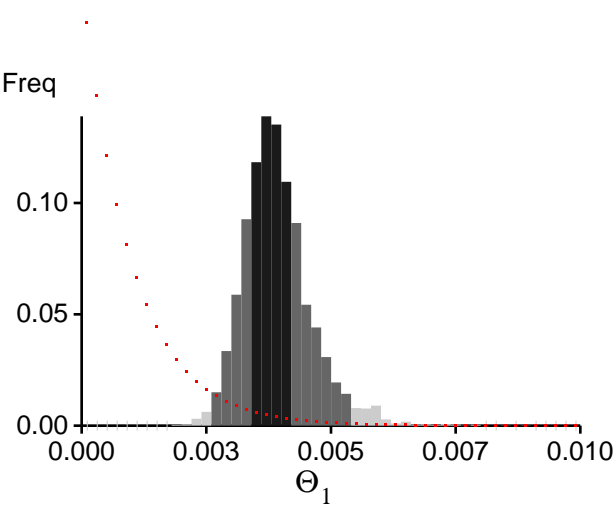


Bayesian Analysis: Posterior distribution for locus 58

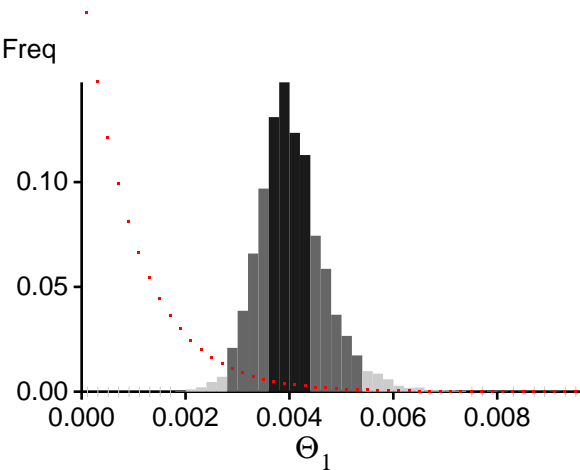
Bayesian Analysis: Posterior distribution for locus 59



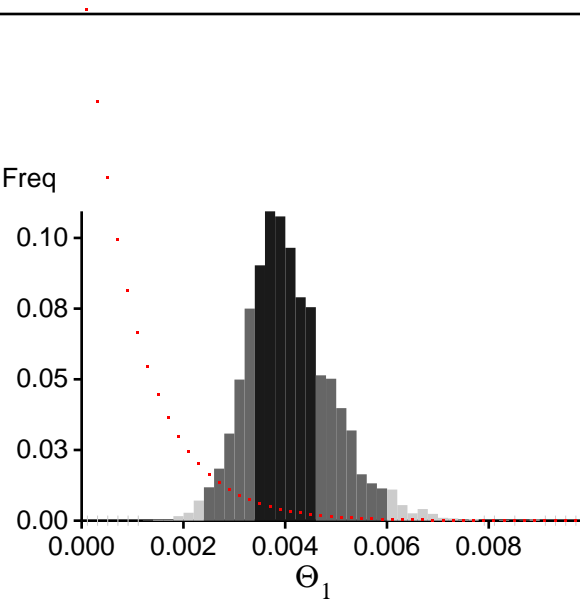
Bayesian Analysis: Posterior distribution for locus 60



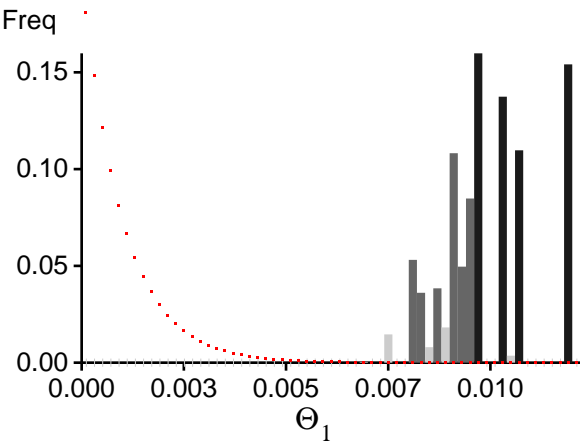
Bayesian Analysis: Posterior distribution for locus 61



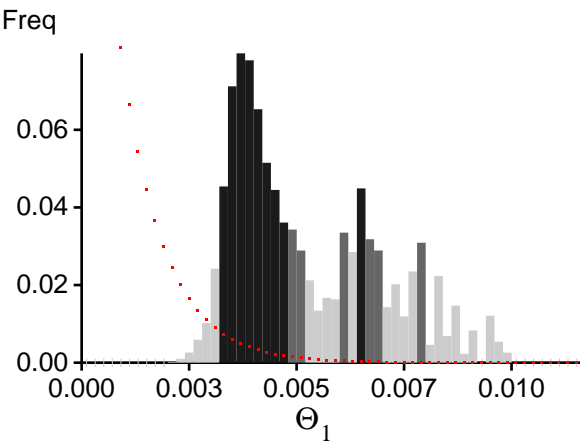
Bayesian Analysis: Posterior distribution for locus 62



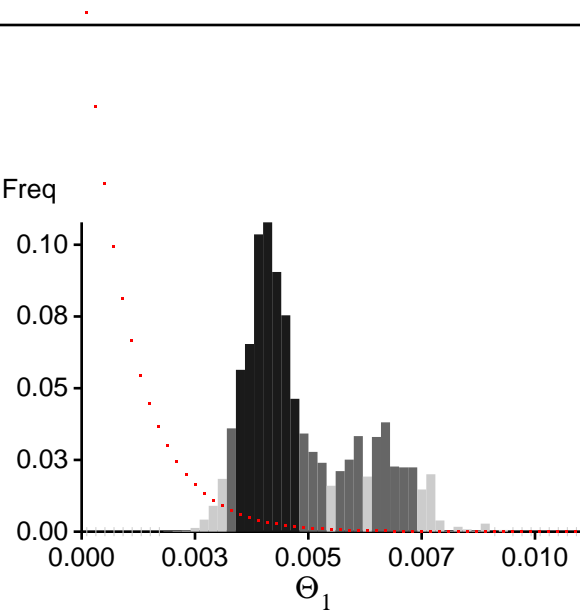
Bayesian Analysis: Posterior distribution for locus 63

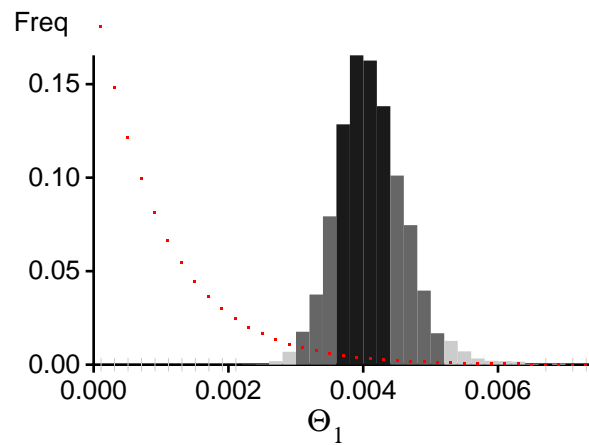


Bayesian Analysis: Posterior distribution for locus 64

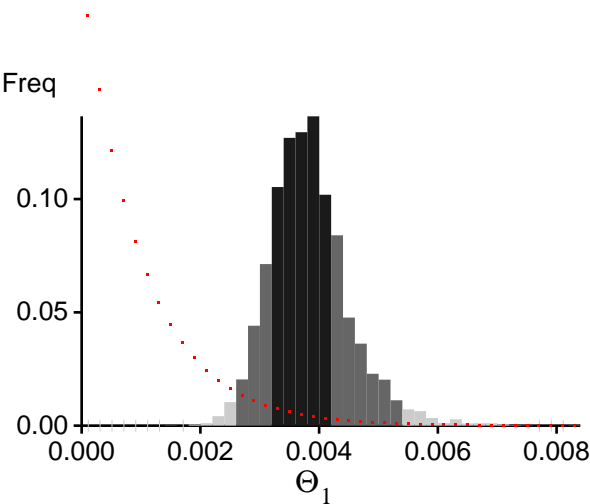


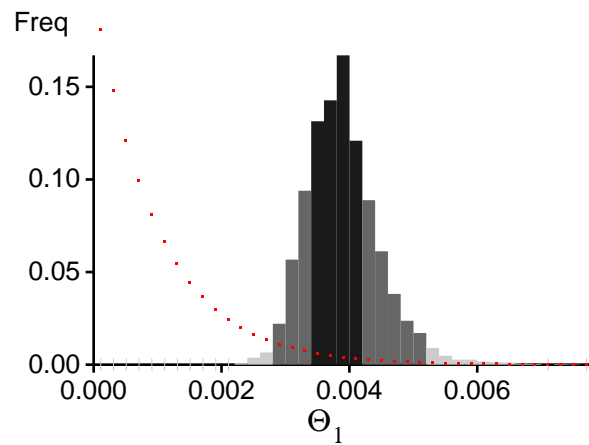
Bayesian Analysis: Posterior distribution for locus 65

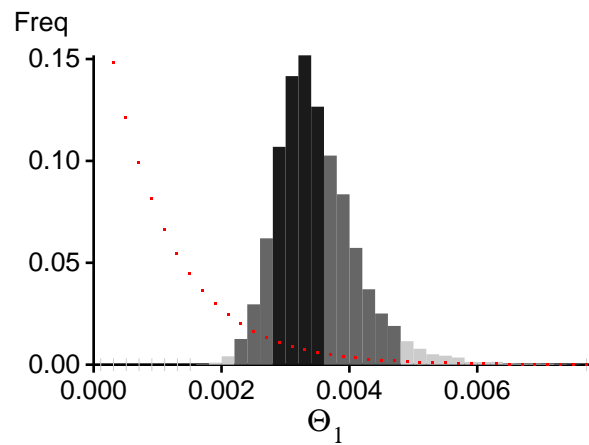


Bayesian Analysis: Posterior distribution for locus 66

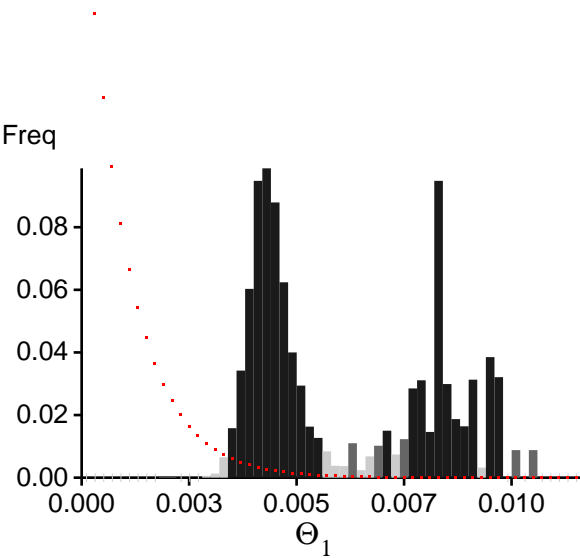
Bayesian Analysis: Posterior distribution for locus 67



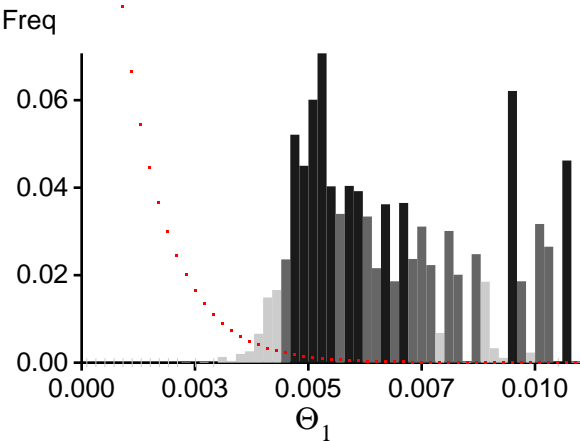
Bayesian Analysis: Posterior distribution for locus 68

Bayesian Analysis: Posterior distribution for locus 69

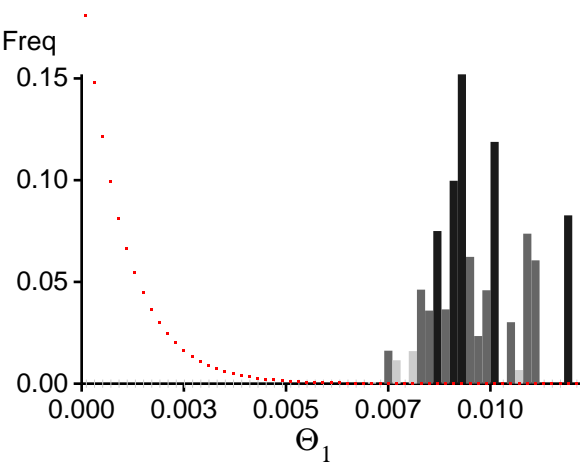
Bayesian Analysis: Posterior distribution for locus 70



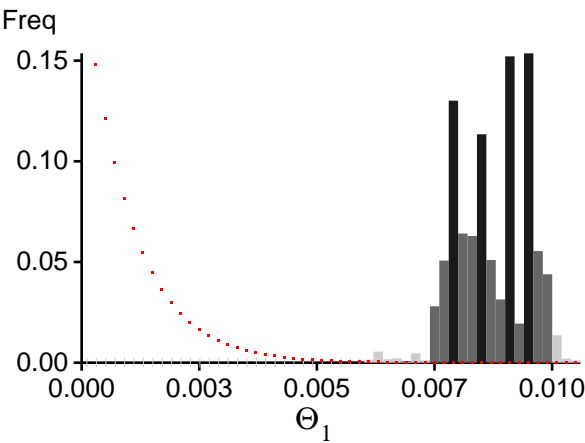
Bayesian Analysis: Posterior distribution for locus 71



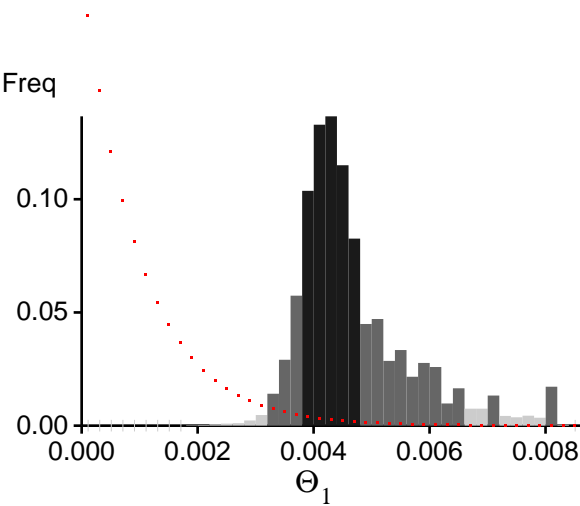
Bayesian Analysis: Posterior distribution for locus 72

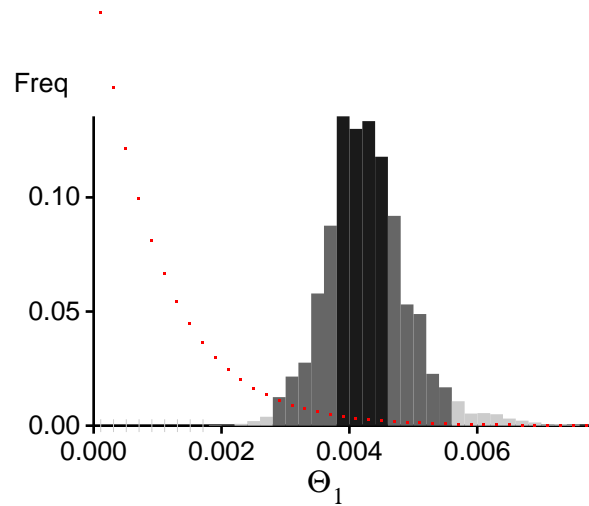


Bayesian Analysis: Posterior distribution for locus 73

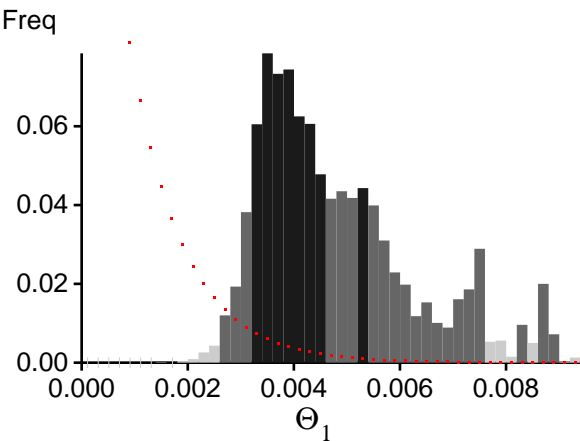


Bayesian Analysis: Posterior distribution for locus 74

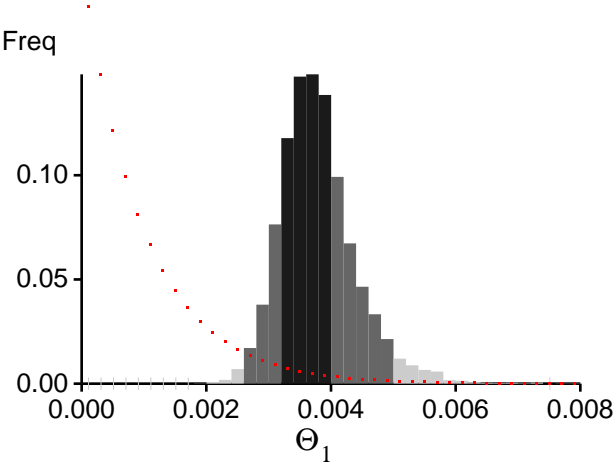


Bayesian Analysis: Posterior distribution for locus 75

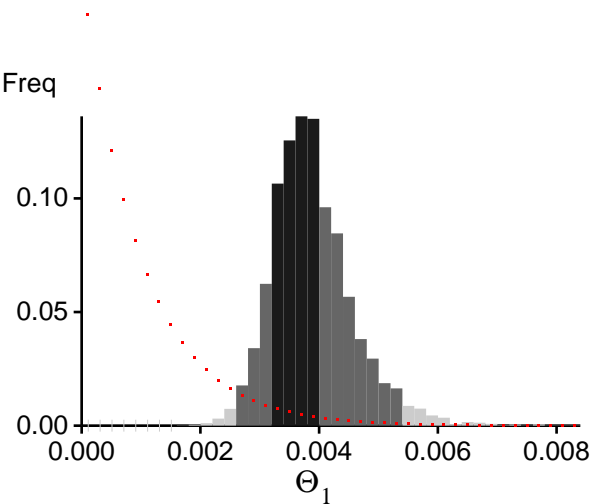
Bayesian Analysis: Posterior distribution for locus 76

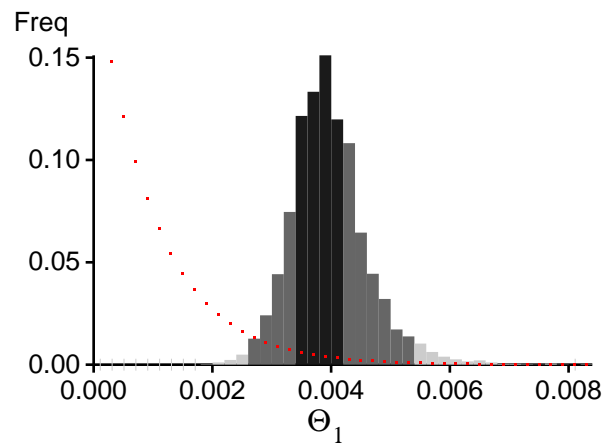


Bayesian Analysis: Posterior distribution for locus 77

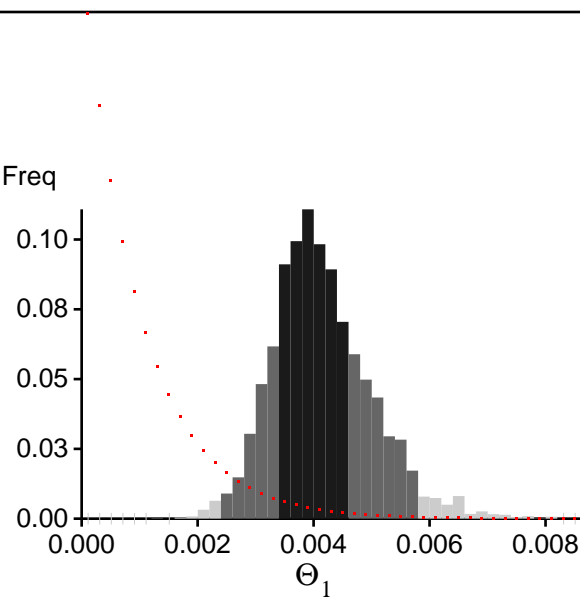


Bayesian Analysis: Posterior distribution for locus 78

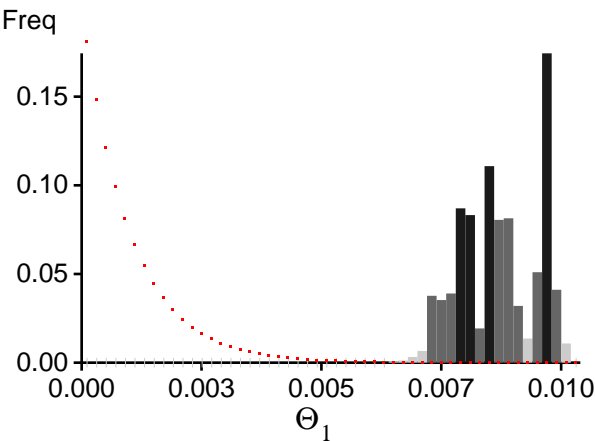


Bayesian Analysis: Posterior distribution for locus 79

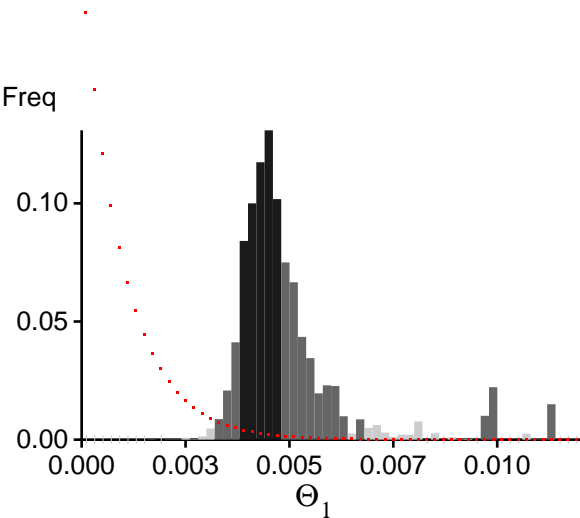
Bayesian Analysis: Posterior distribution for locus 80



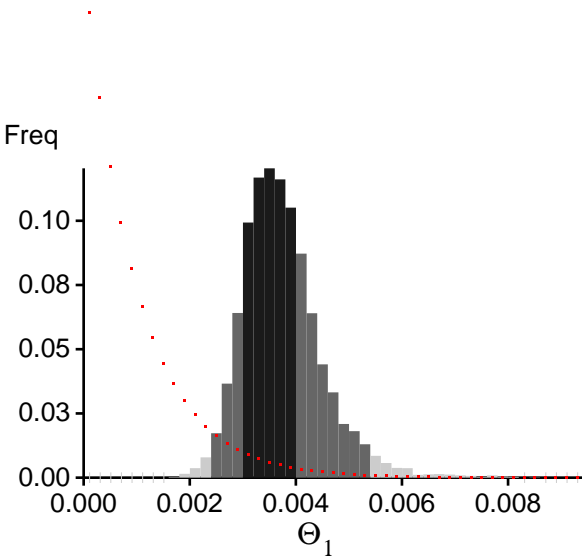
Bayesian Analysis: Posterior distribution for locus 81



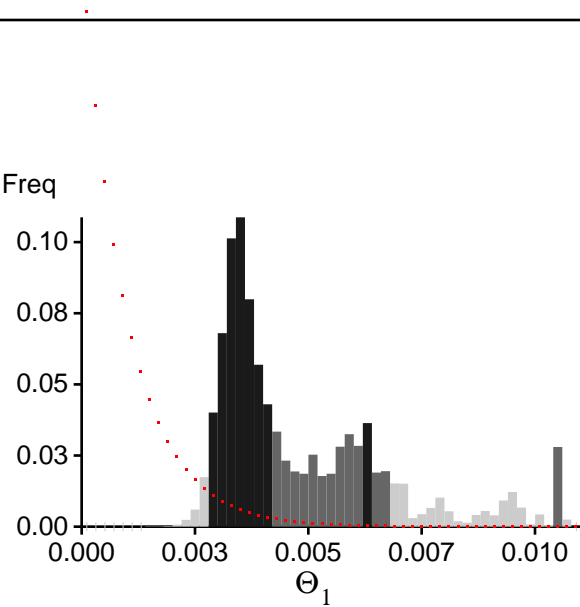
Bayesian Analysis: Posterior distribution for locus 82



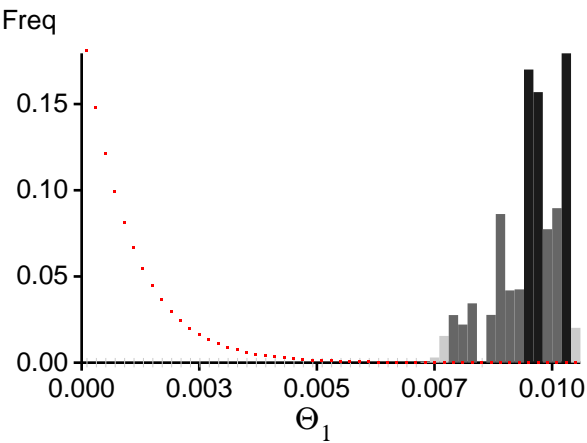
Bayesian Analysis: Posterior distribution for locus 83

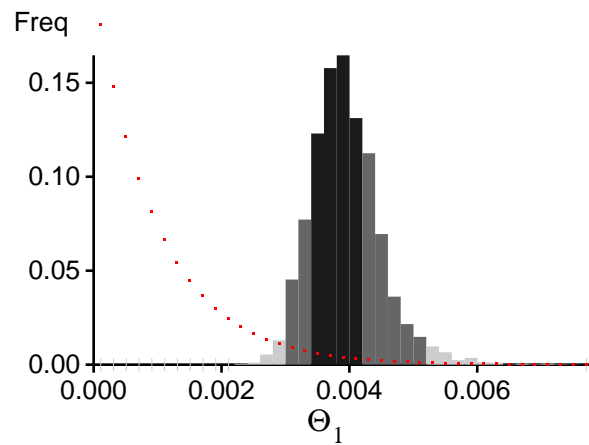


Bayesian Analysis: Posterior distribution for locus 84

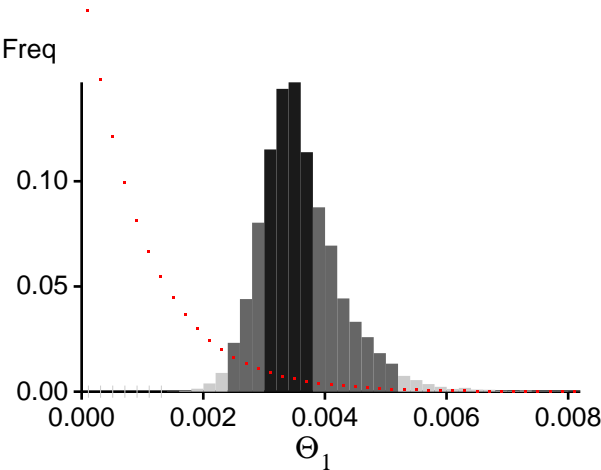


Bayesian Analysis: Posterior distribution for locus 85

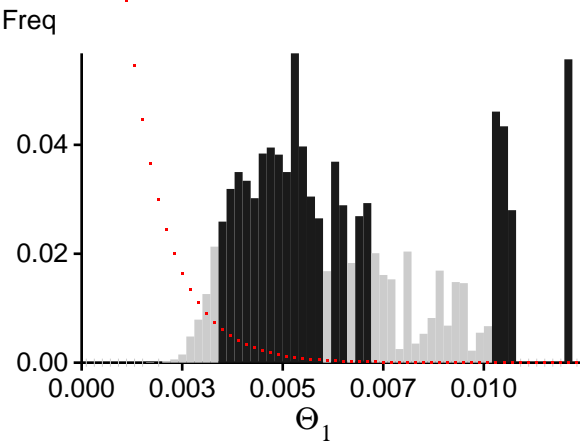


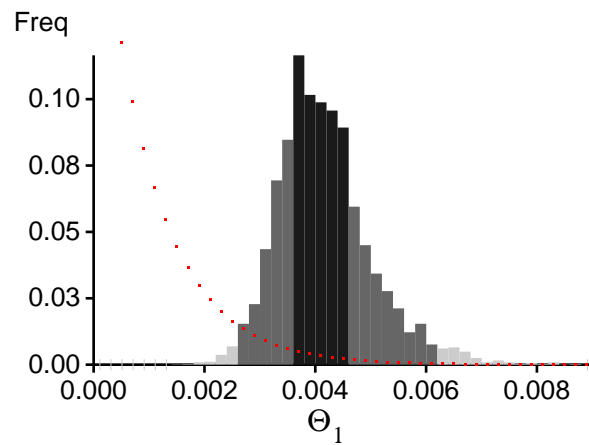
Bayesian Analysis: Posterior distribution for locus 86

Bayesian Analysis: Posterior distribution for locus 87

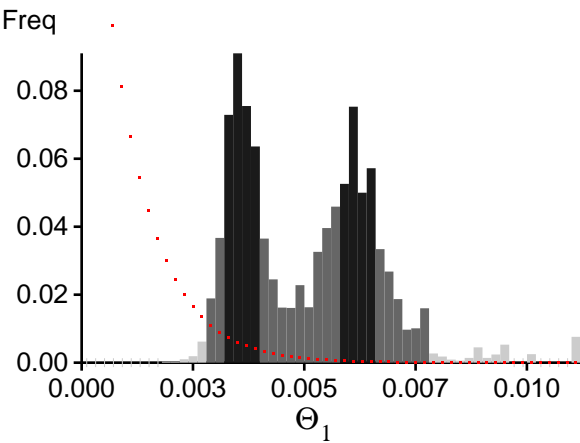


Bayesian Analysis: Posterior distribution for locus 88

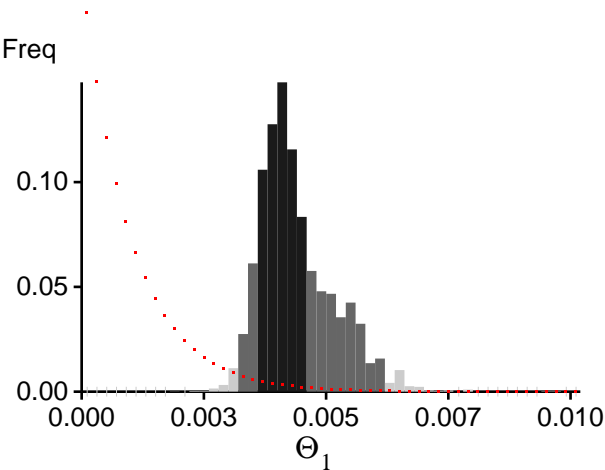


Bayesian Analysis: Posterior distribution for locus 89

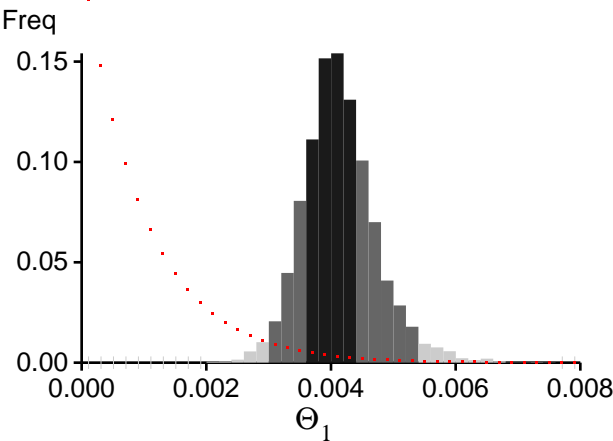
Bayesian Analysis: Posterior distribution for locus 90



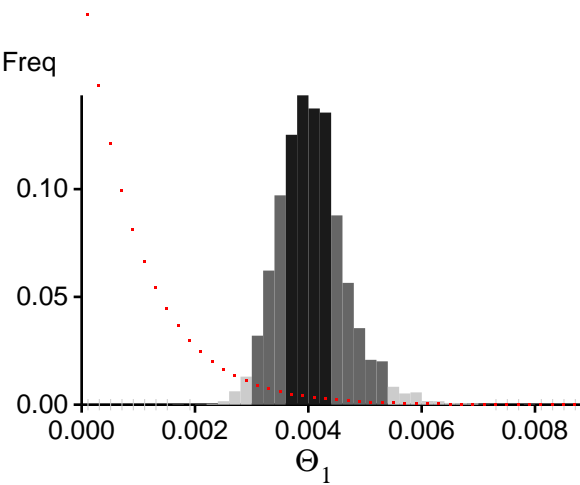
Bayesian Analysis: Posterior distribution for locus 91

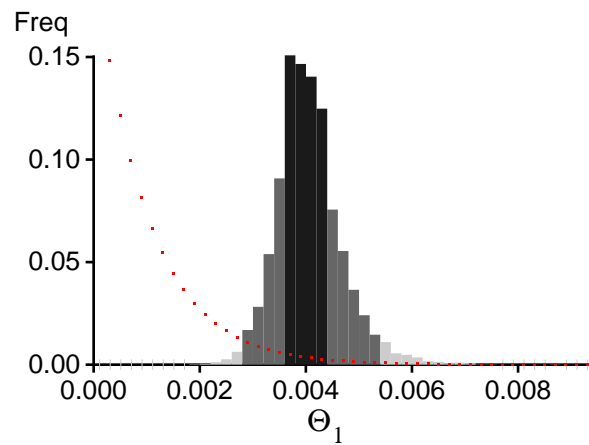


Bayesian Analysis: Posterior distribution for locus 92

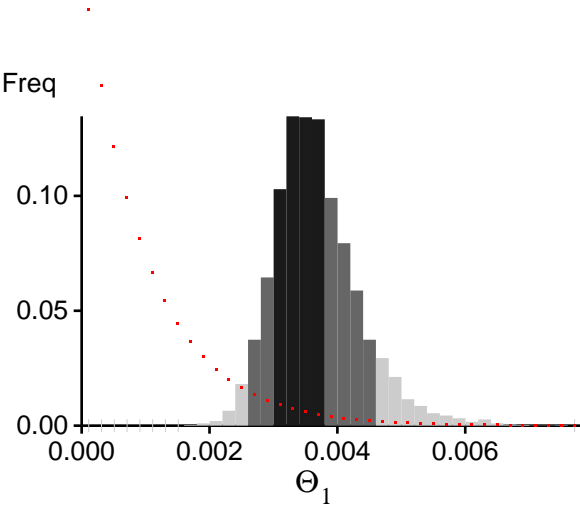


Bayesian Analysis: Posterior distribution for locus 93

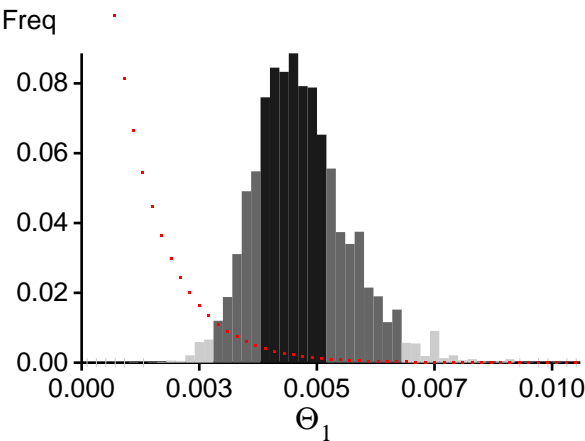


Bayesian Analysis: Posterior distribution for locus 94

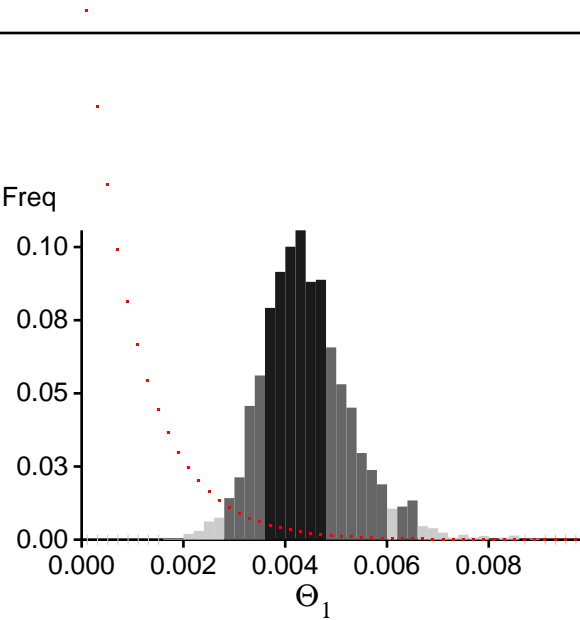
Bayesian Analysis: Posterior distribution for locus 95



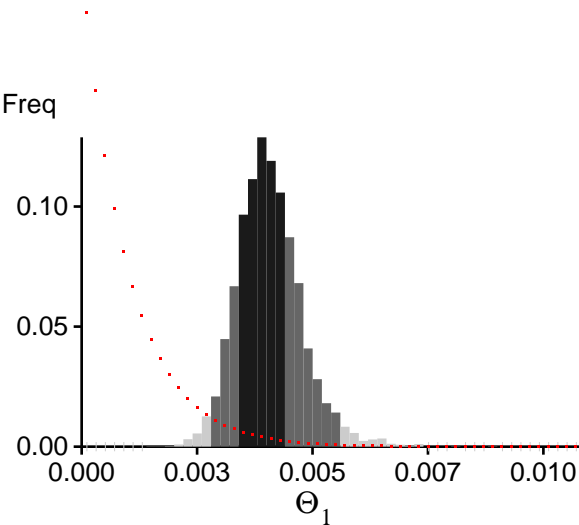
Bayesian Analysis: Posterior distribution for locus 96



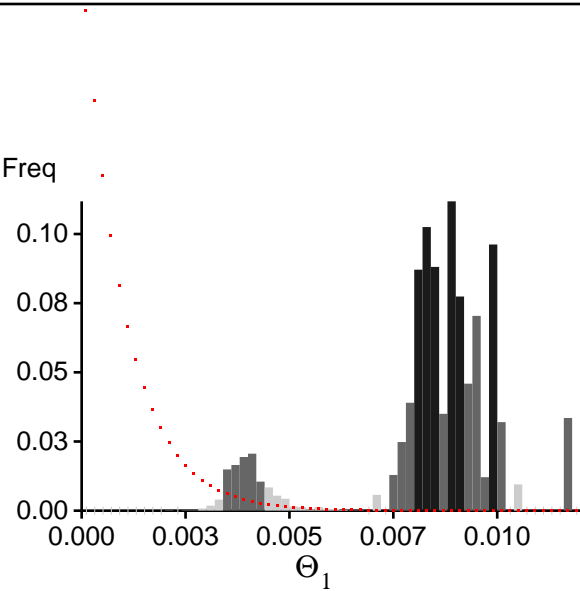
Bayesian Analysis: Posterior distribution for locus 97



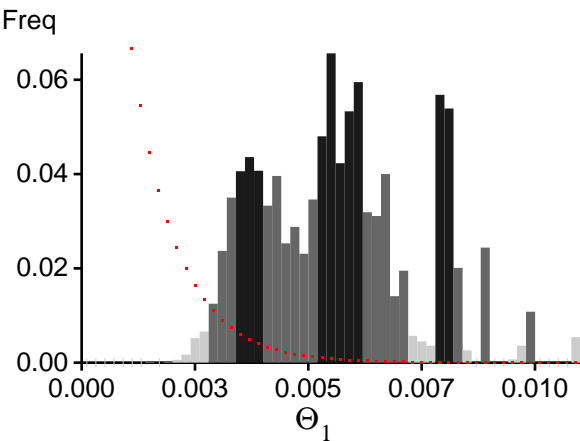
Bayesian Analysis: Posterior distribution for locus 98

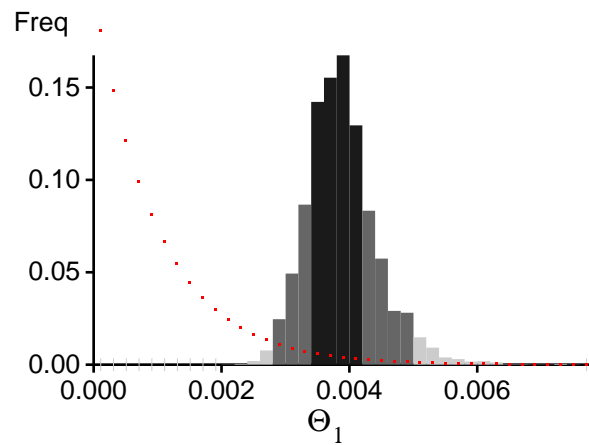


Bayesian Analysis: Posterior distribution for locus 99

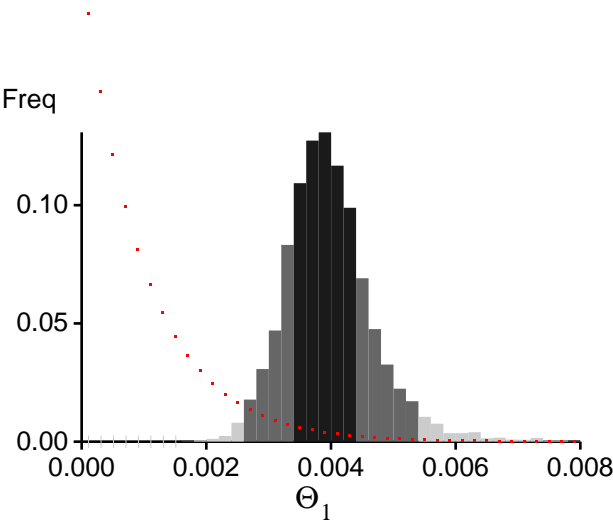


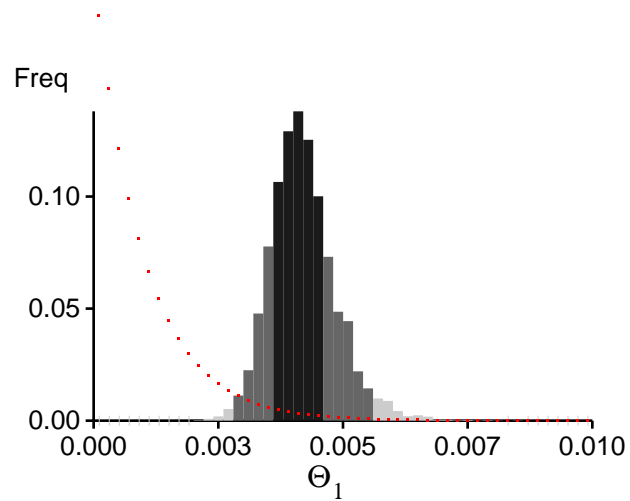
Bayesian Analysis: Posterior distribution for locus 100



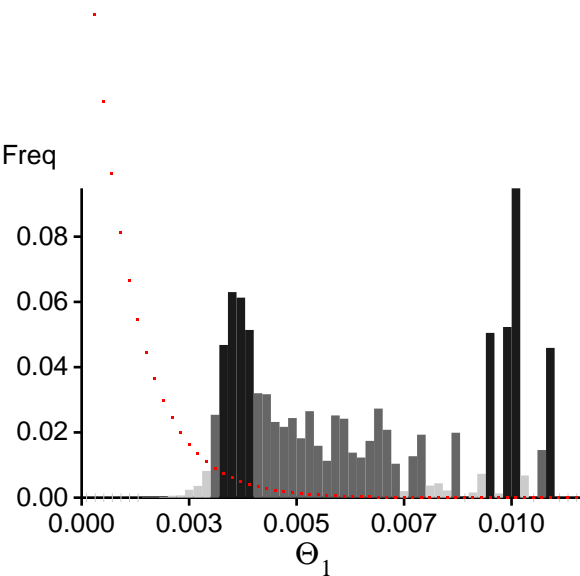
Bayesian Analysis: Posterior distribution for locus 101

Bayesian Analysis: Posterior distribution for locus 102

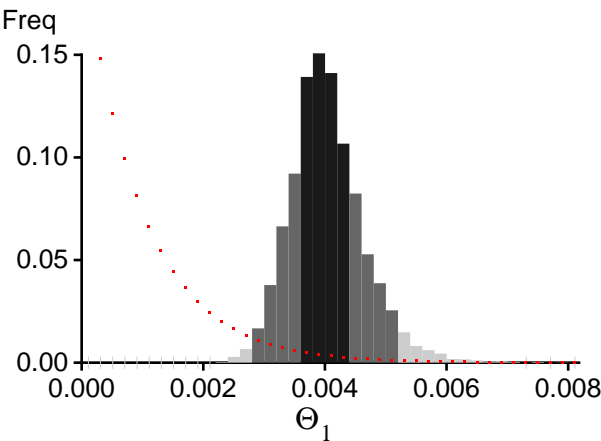


Bayesian Analysis: Posterior distribution for locus 103

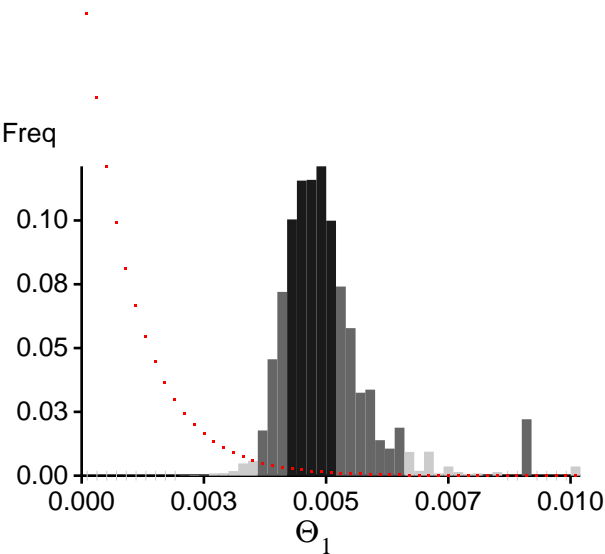
Bayesian Analysis: Posterior distribution for locus 104

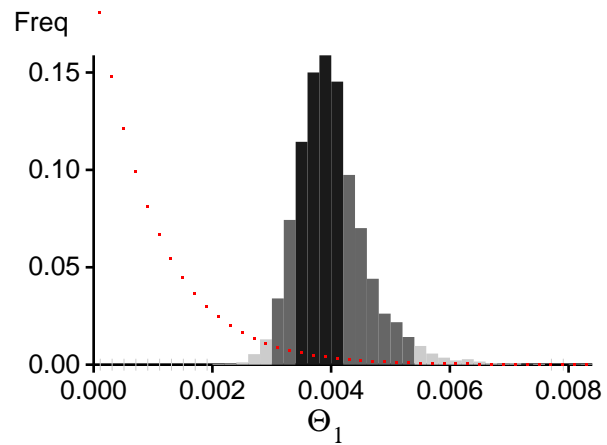


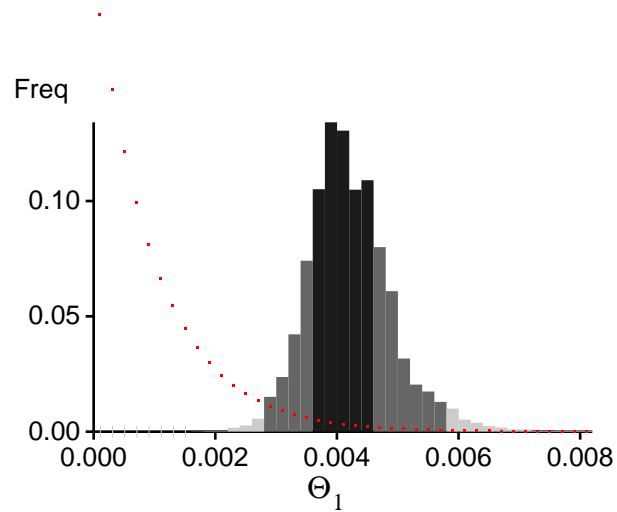
Bayesian Analysis: Posterior distribution for locus 105



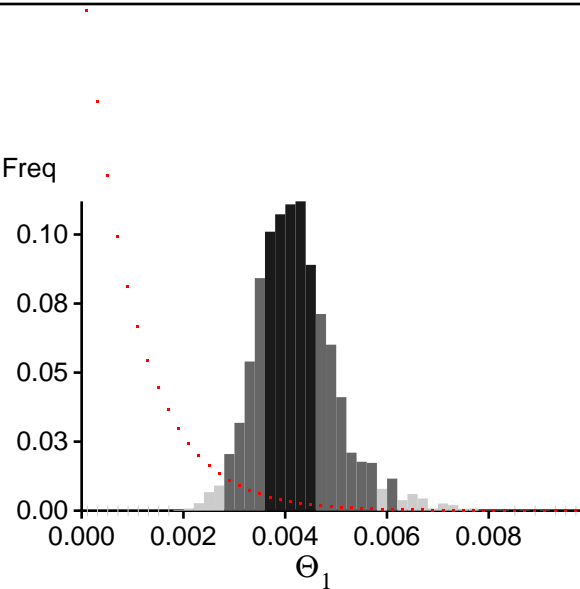
Bayesian Analysis: Posterior distribution for locus 106



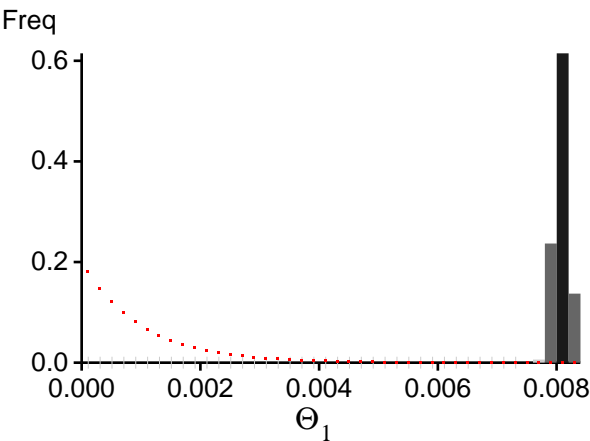
Bayesian Analysis: Posterior distribution for locus 107

Bayesian Analysis: Posterior distribution for locus 108

Bayesian Analysis: Posterior distribution for locus 109



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	-575.50	-569.75	-575.55
2	-620.70	-613.88	-617.83
3	-691.52	-684.45	-686.02
4	-671.13	-664.38	-671.19
5	-750.32	-742.26	-743.94
6	-713.79	-706.67	-713.93
7	-744.97	-737.65	-737.80
8	-478.62	-473.76	-478.57
9	-906.04	-809.25	-759.82
10	-869.62	-860.96	-869.77
11	-574.48	-567.45	-568.78
12	-578.55	-572.64	-578.55
13	-730.75	-723.19	-729.63
14	-1008.94	-998.95	-1009.21
15	-687.58	-680.66	-687.56
16	-481.72	-476.73	-481.90
17	-532.71	-527.31	-532.77
18	-490.98	-485.92	-490.24
19	-908.60	-899.60	-908.87
20	-681.31	-674.45	-681.42
21	-673.37	-666.13	-672.76
22	-625.11	-617.03	-616.72
23	-528.08	-522.80	-528.09
24	-1050.76	-1040.19	-1051.04
25	-371.52	-367.84	-371.53
26	-623.17	-613.20	-594.73
27	-734.95	-723.09	-703.11
28	-1035.00	-1024.84	-1035.37
29	-967.71	-958.08	-968.00

30	-524.98	-519.62	-520.95
31	-1007.33	-997.35	-1007.67
32	-652.83	-646.31	-652.89
33	-541.43	-533.17	-510.90
34	-370.76	-367.03	-370.80
35	-573.72	-568.04	-573.86
36	-501.69	-496.54	-500.77
37	-455.16	-450.53	-455.09
38	-504.40	-492.04	-472.06
39	-945.84	-936.37	-946.12
40	-644.51	-638.02	-644.61
41	-529.45	-521.64	-522.14
42	-733.26	-722.95	-704.87
43	-1088.32	-1077.34	-1088.41
44	-461.32	-456.63	-461.32
45	-760.10	-749.56	-739.10
46	-498.28	-493.30	-498.40
47	-456.72	-452.07	-456.60
48	-695.59	-688.66	-695.79
49	-615.73	-609.58	-615.76
50	-391.83	-387.85	-391.04
51	-478.26	-473.47	-478.29
52	-461.18	-456.61	-461.23
53	-581.26	-571.67	-561.24
54	-698.02	-690.43	-692.91
55	-461.33	-450.23	-453.17
56	-684.02	-677.07	-684.06
57	-398.40	-394.43	-398.05
58	-592.88	-586.90	-592.84
59	-675.31	-668.48	-666.74
60	-524.35	-519.11	-524.46
61	-885.02	-876.09	-884.97
62	-701.71	-694.48	-701.57
63	-1032.27	-984.44	-922.36
64	-470.79	-465.73	-469.32
65	-942.66	-933.09	-941.17
66	-1084.32	-1073.58	-1084.78
67	-643.84	-637.41	-643.89
68	-743.97	-736.60	-744.17
69	-557.38	-551.86	-557.42
70	-758.40	-750.81	-752.34
71	-532.21	-526.54	-521.38
72	-737.34	-723.39	-688.06
73	-393.94	-384.81	-364.51
74	-724.15	-716.96	-725.35

75	-566.38	-560.73	-566.48
76	-474.10	-469.18	-473.22
77	-647.27	-640.85	-647.42
78	-480.21	-475.39	-480.22
79	-603.17	-597.15	-603.27
80	-642.86	-636.24	-642.66
81	-639.75	-630.87	-610.89
82	-606.07	-599.59	-604.66
83	-680.81	-673.96	-680.81
84	-749.42	-741.62	-745.81
85	-715.61	-701.37	-702.35
86	-896.02	-887.14	-896.46
87	-594.79	-588.86	-594.79
88	-679.55	-671.66	-674.12
89	-280.13	-277.22	-280.09
90	-1002.67	-992.73	-997.18
91	-876.34	-867.90	-875.79
92	-715.31	-708.17	-715.50
93	-681.02	-674.27	-681.18
94	-710.81	-703.72	-710.99
95	-416.94	-412.80	-416.95
96	-592.89	-586.55	-592.70
97	-514.82	-509.34	-514.75
98	-821.06	-812.75	-821.17
99	-511.22	-499.15	-479.11
100	-677.64	-670.55	-676.83
101	-815.05	-806.98	-815.23
102	-468.58	-463.88	-468.63
103	-525.63	-520.37	-525.69
104	-819.24	-808.96	-800.45
105	-510.29	-505.24	-510.37
106	-475.21	-470.37	-473.82
107	-552.49	-547.01	-552.59
108	-445.72	-441.25	-445.77
109	-511.83	-506.57	-511.80
All	-70394.23	-69481.85	-69667.50
<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 = 530.397711] 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
Θ_1	710835/36330283	0.01957
Genealogies	21135161/36331607	0.58173

MCMC-Autocorrelation and Effective MCMC Sample Size

Parameter	Autocorrelation	Effective Sample Size
Θ_1	0.61638	1082064.29
Genealogies	0.38966	1836042.73

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