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 Tue Jan 25 15:52:31 2022
Program finished at Tue Jan 25 17:13:35 2022 [Runtime:0000:01:21:04]

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) 2803505854
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	m	m	m	m	m	m	m	m	m	m
2 Pop_P&H	m	m	m	m	m	m	m	m	m	m
3 Pop_Pbanks	m	m	m	m	m	m	m	m	m	m
4 Pop_MaroReef	m	m	m	m	m	m	m	m	m	m
5 Pop_FFS	m	m	m	m	m	m	m	m	m	m
6 Pop_Kauai	m	m	m	m	m	m	m	m	m	m
7 Pop_Oahu	m	m	m	m	m	m	m	m	m	m

8 Pop_Molokai	m	m	m	m	m	m	m	m	m	m
9 Pop_Maui	m	m	m	m	m	m	m	m	m	m
10 Pop_BigIsland	m	m	m	m	m	m	m	m	m	m

Order of parameters:

1	Θ_1	=	Θ_1	[m]	<displayed>
2	$M_{2->1}$	=	$M_{2->1}$	[m]	<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	0.16667
2	M	* * Exp window	0.000100	1000.	10000	100.0	500	0.16667

[* * 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
Log file:	logfile.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
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

	104	20
	105	20
	106	20
	107	20
	108	20
	109	20
2 Pop_P&H	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
	23	8
	24	8
	25	8
	26	8
	27	8
	28	8
	29	8
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9 Pop_Maui	1	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
All	Θ_1	0.00500	0.00500	0.00530	0.00540	0.00560	0.00550	0.00531
All	$M_{2->1}$	140.0	180.0	210.0	240.0	280.0	230.0	210.9

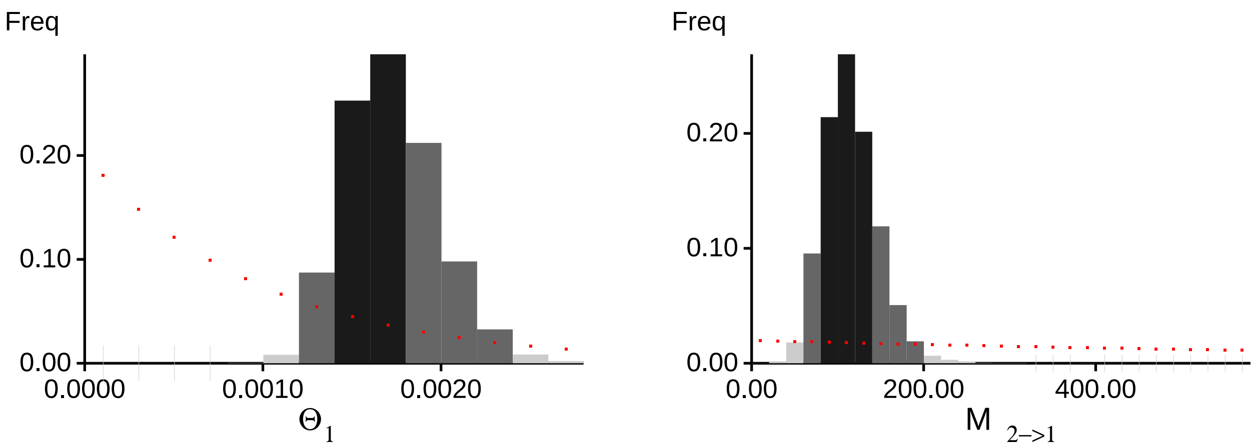
Citation suggestions:

Beerli P., 2006. Comparison of Bayesian and maximum-likelihood inference of population genetic parameters. Bioinformatics 22:341-345

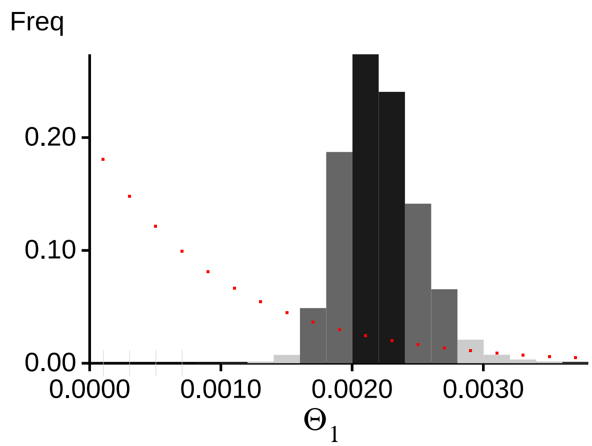
Beerli P., 2007. Estimation of the population scaled mutation rate from microsatellite data, Genetics, 177:1967-1968.

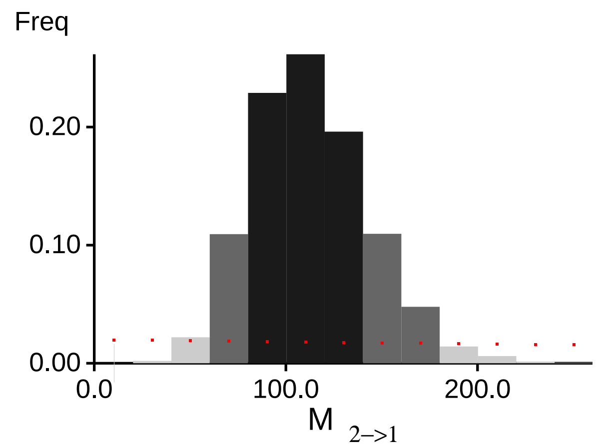
Beerli P., 2009. How to use MIGRATE or why are Markov chain Monte Carlo programs difficult to use? In Population Genetics for Animal Conservation, G. Bertorelle, M. W. Bruford, H. C. Hauffe, A. Rizzoli, and C. Vernesi, eds., vol. 17 of Conservation Biology, Cambridge University Press, Cambridge UK, pp.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

Bayesian Analysis: Posterior distribution for locus 1

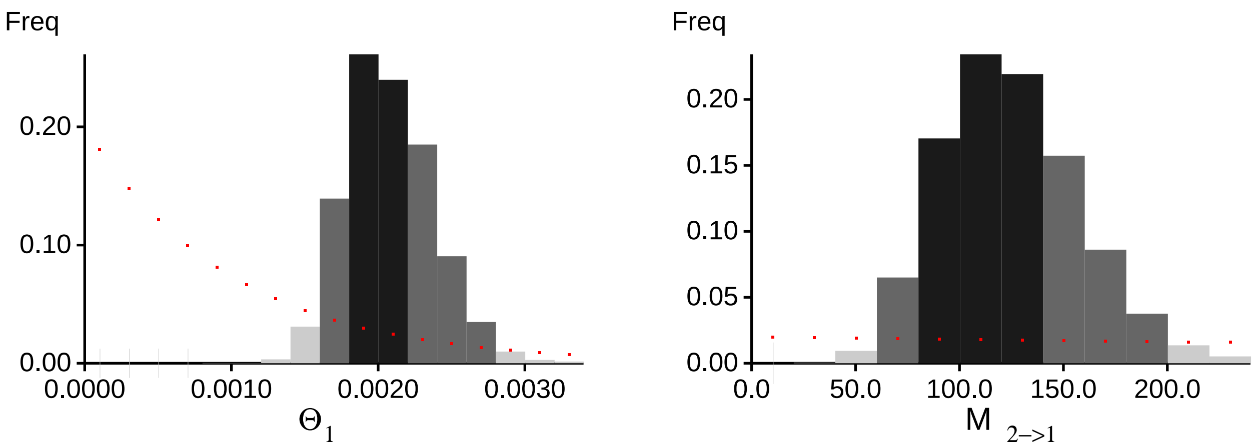


Bayesian Analysis: Posterior distribution for locus 2

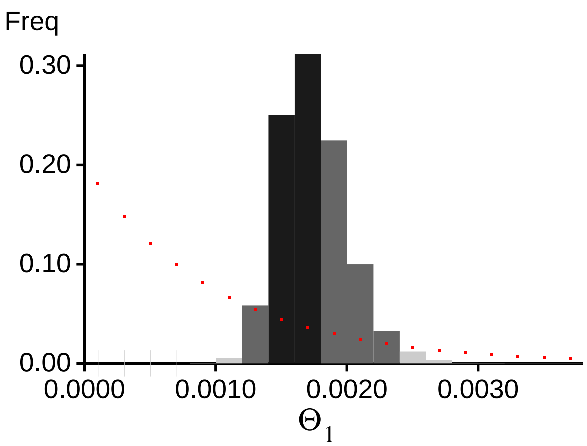


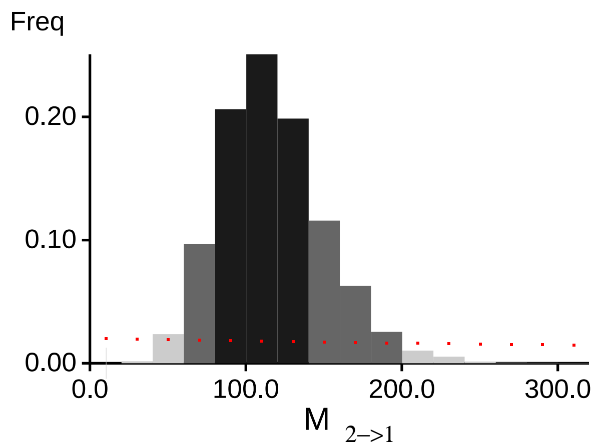


Bayesian Analysis: Posterior distribution for locus 3

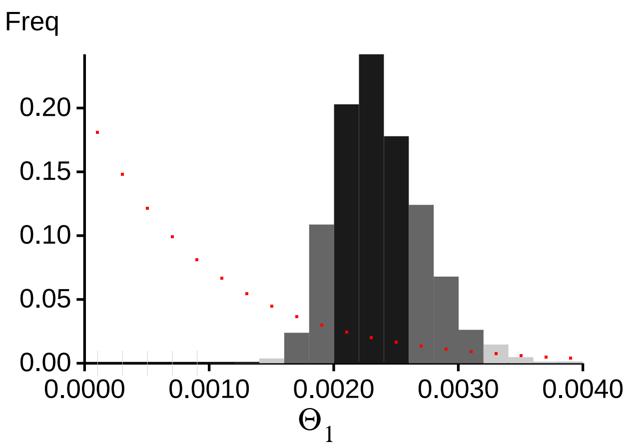


Bayesian Analysis: Posterior distribution for locus 4

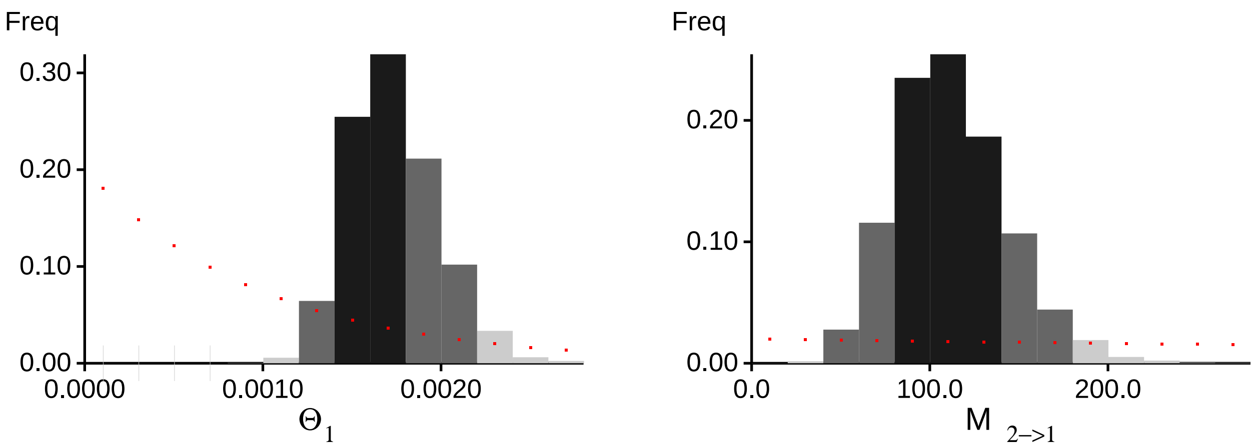




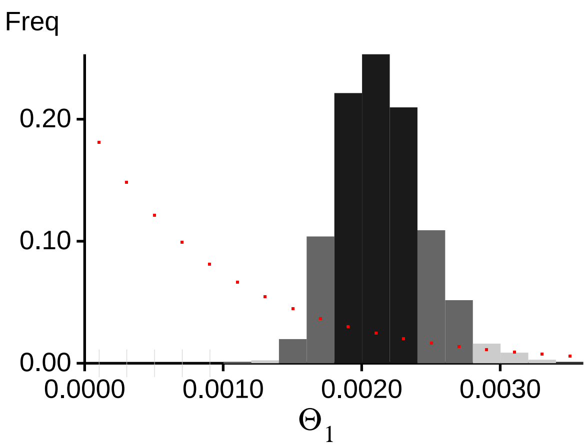
Bayesian Analysis: Posterior distribution for locus 5

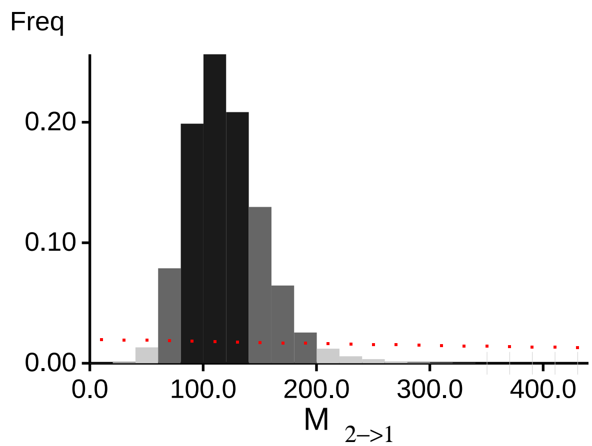


Bayesian Analysis: Posterior distribution for locus 6

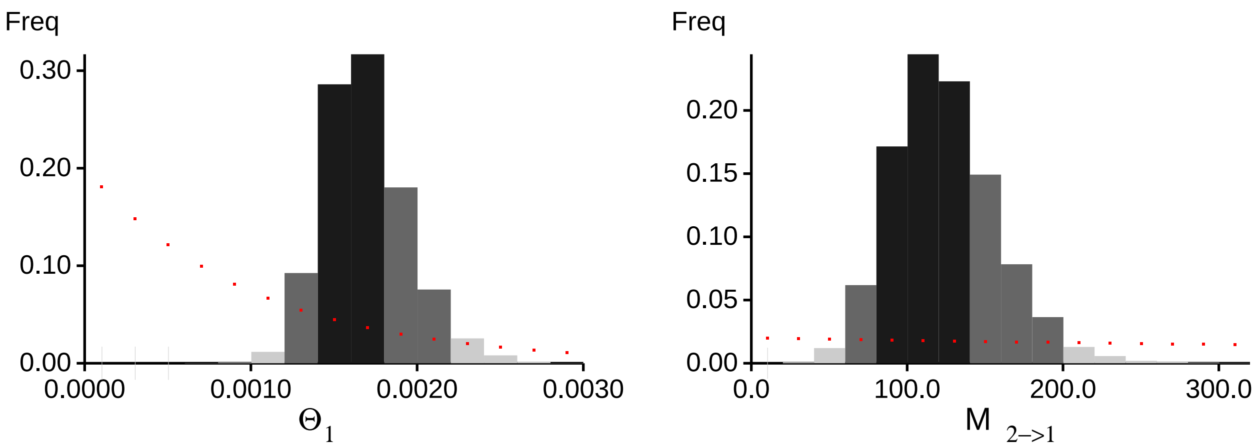


Bayesian Analysis: Posterior distribution for locus 7

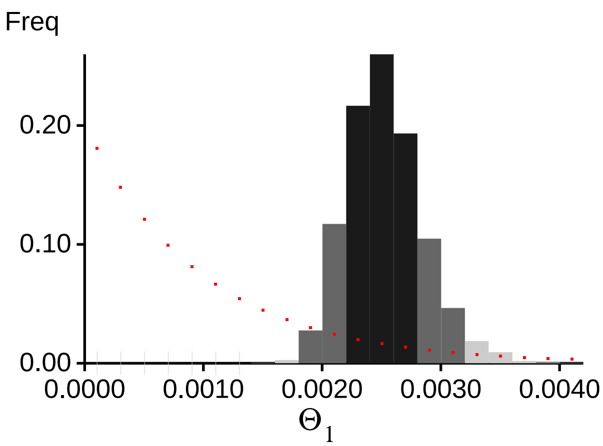


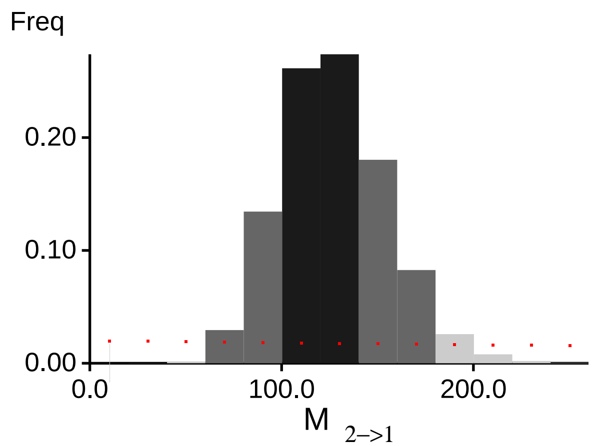


Bayesian Analysis: Posterior distribution for locus 8

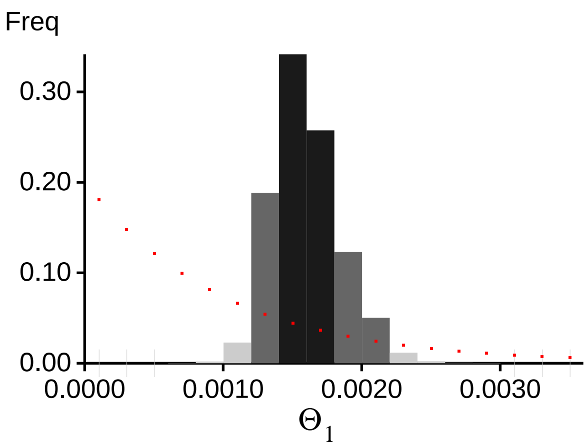


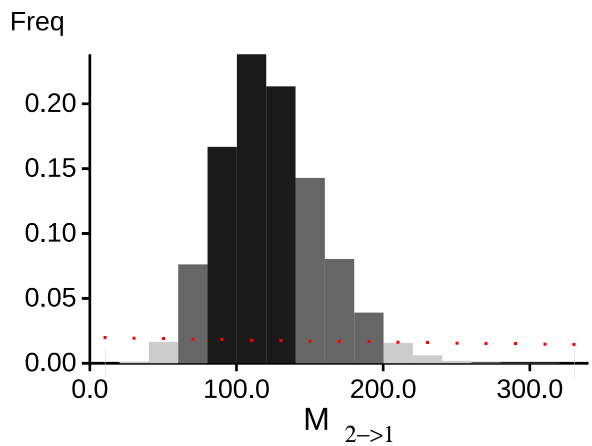
Bayesian Analysis: Posterior distribution for locus 9



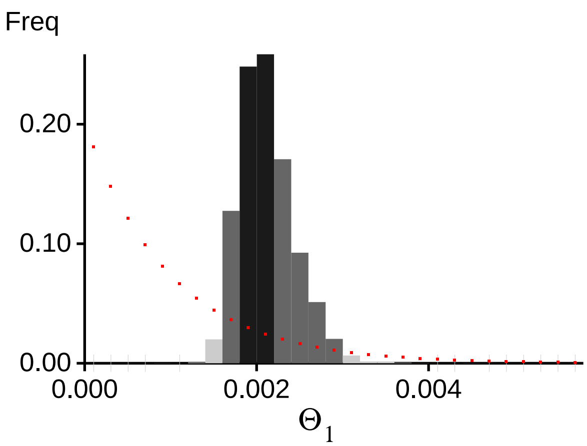


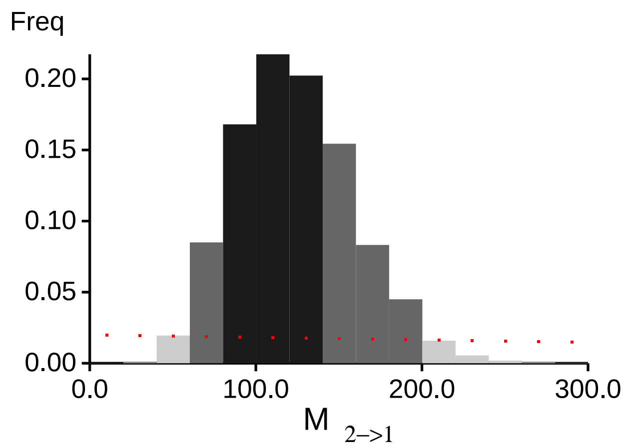
Bayesian Analysis: Posterior distribution for locus 10



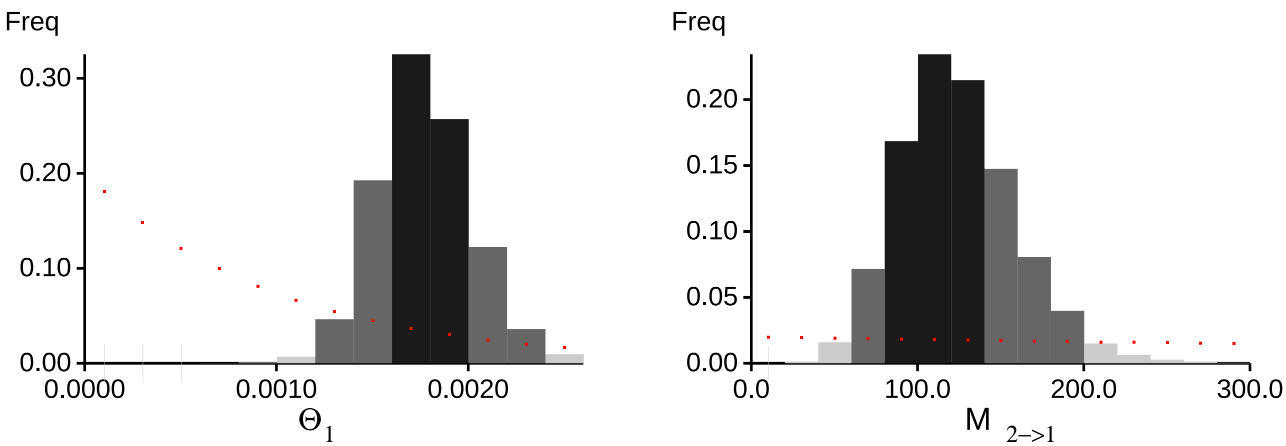


Bayesian Analysis: Posterior distribution for locus 11

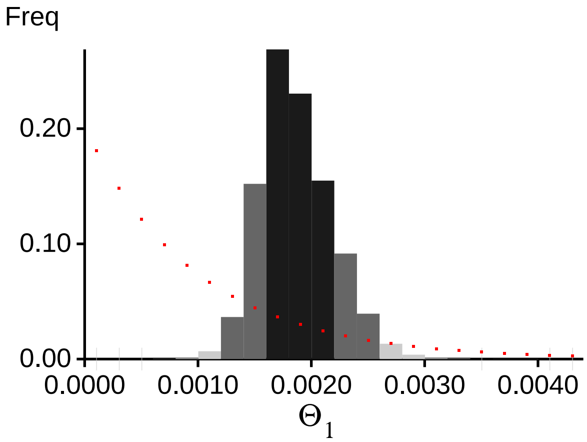


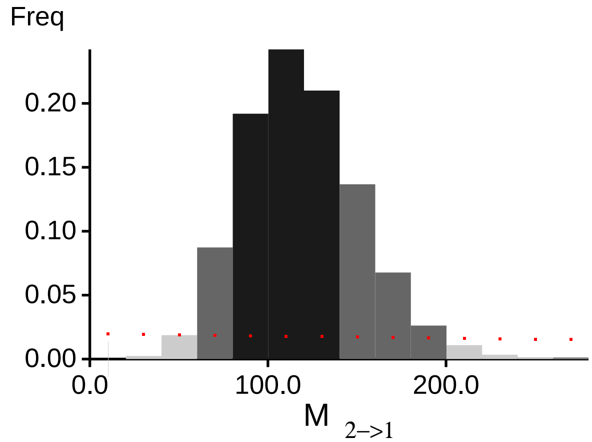


Bayesian Analysis: Posterior distribution for locus 12

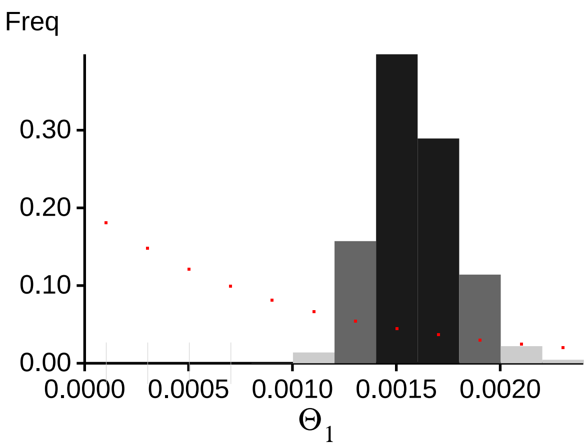


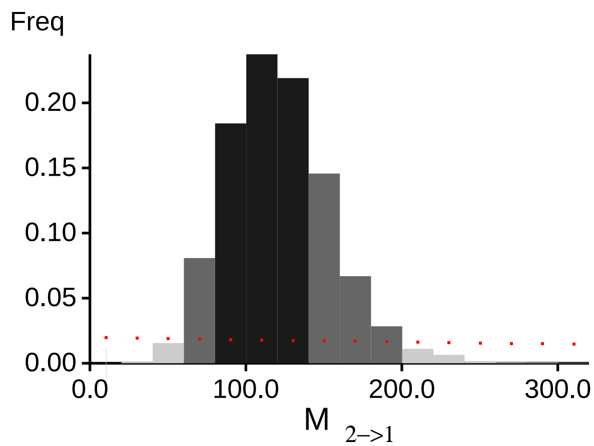
Bayesian Analysis: Posterior distribution for locus 13



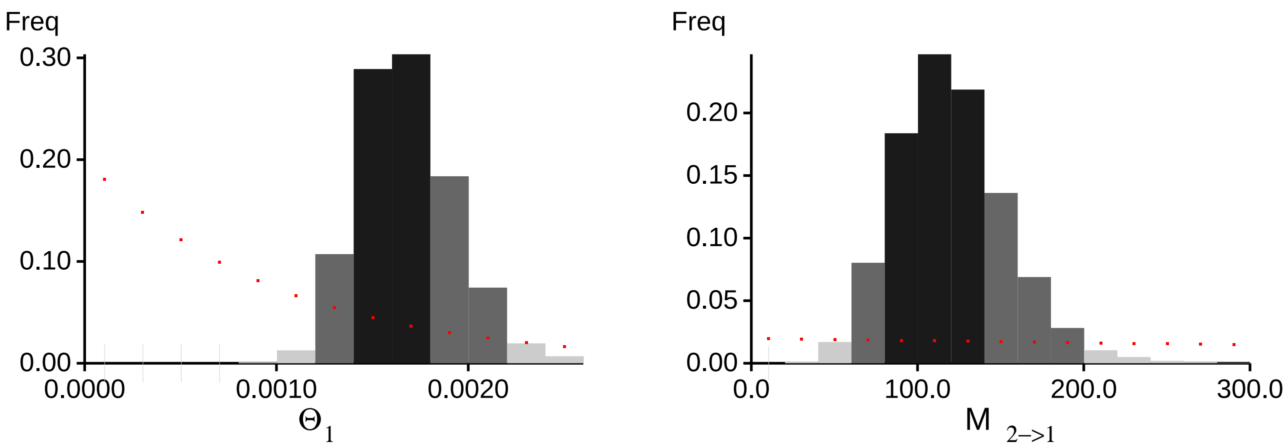


Bayesian Analysis: Posterior distribution for locus 14

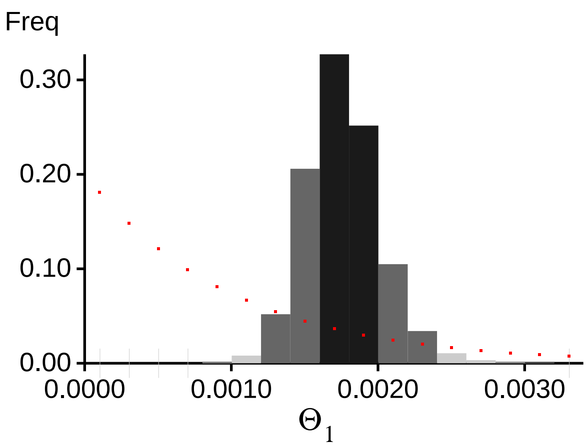


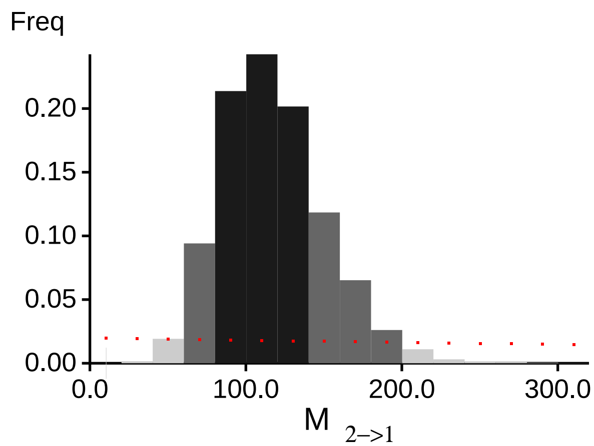


Bayesian Analysis: Posterior distribution for locus 15

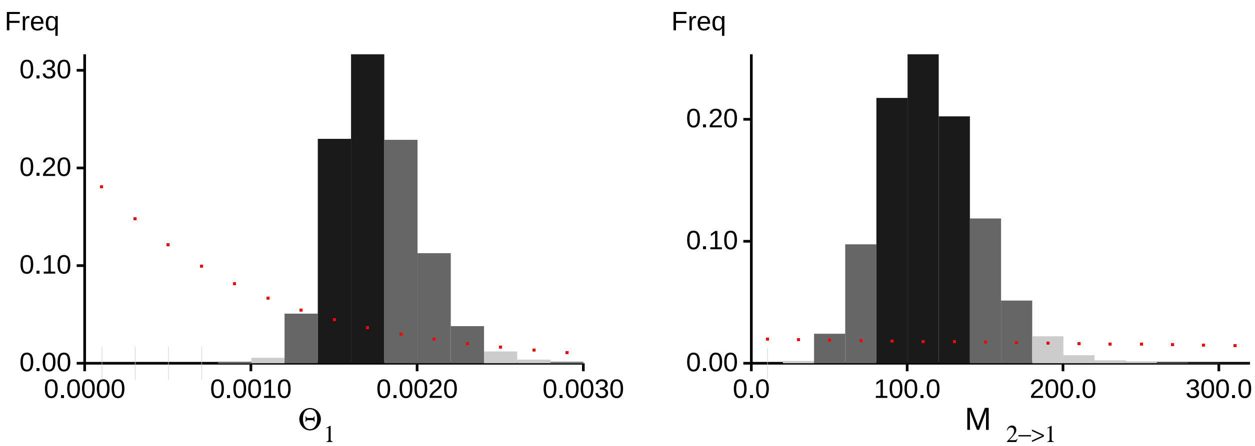


Bayesian Analysis: Posterior distribution for locus 16

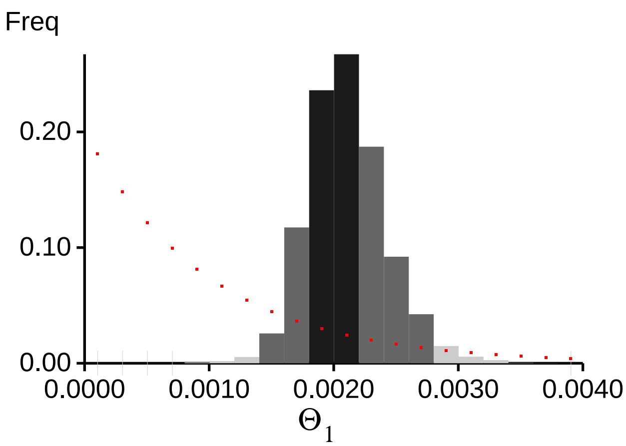




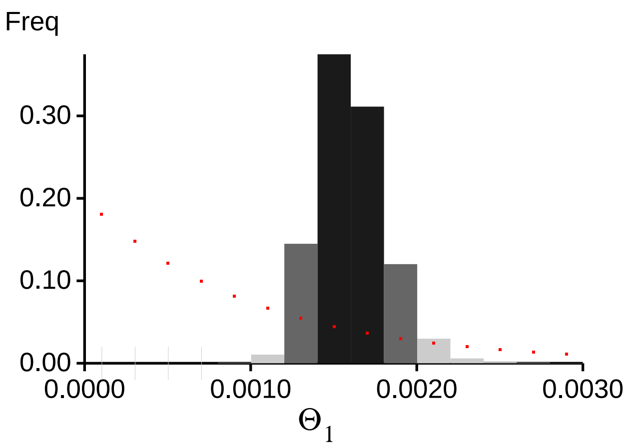
Bayesian Analysis: Posterior distribution for locus 17

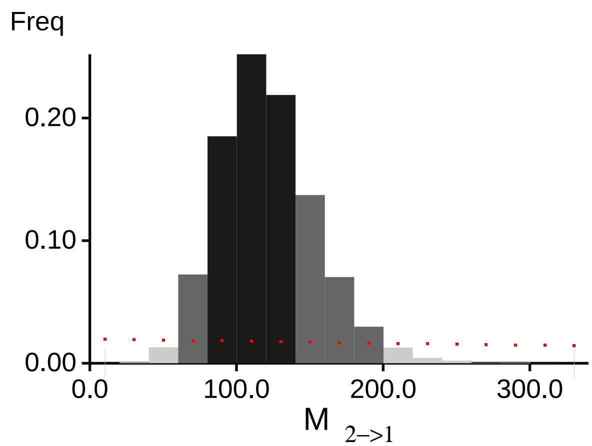


Bayesian Analysis: Posterior distribution for locus 18

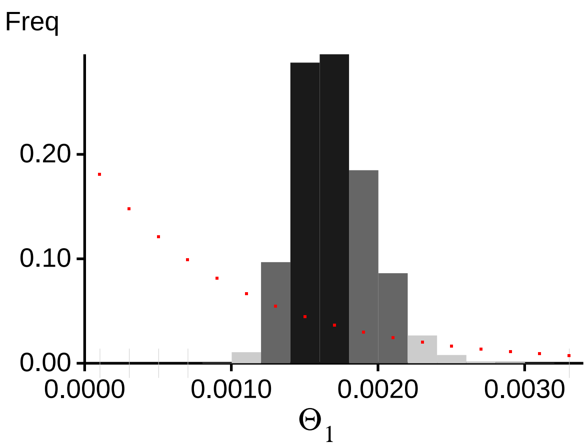


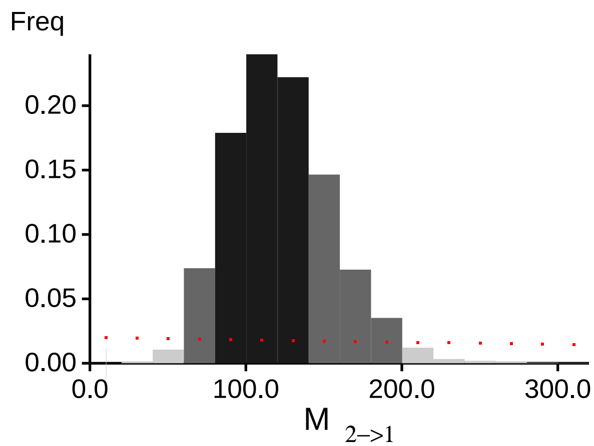
Bayesian Analysis: Posterior distribution for locus 19



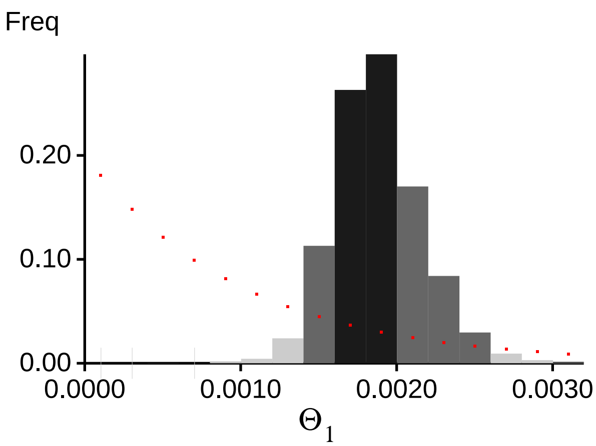


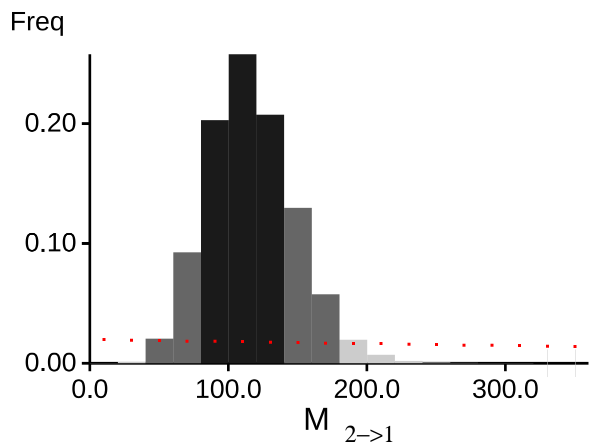
Bayesian Analysis: Posterior distribution for locus 20



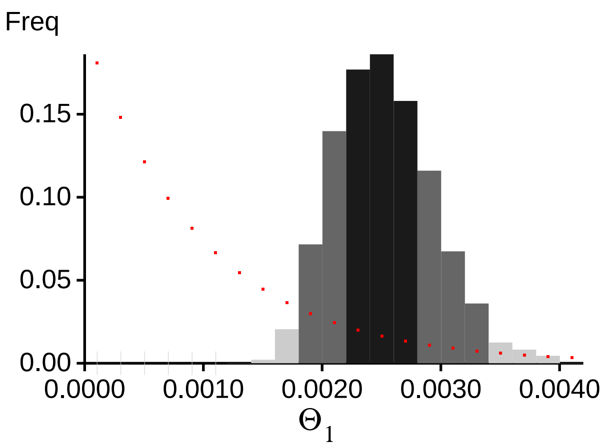


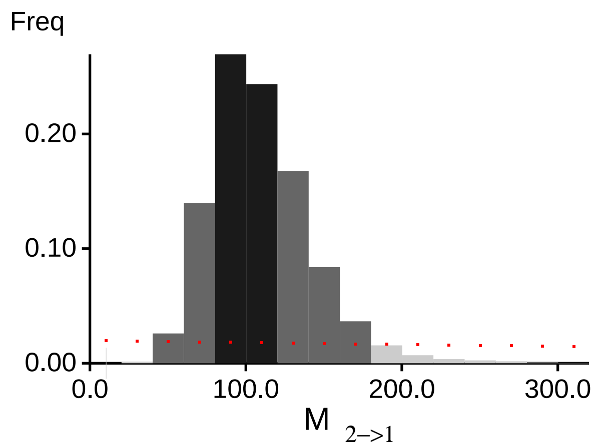
Bayesian Analysis: Posterior distribution for locus 21



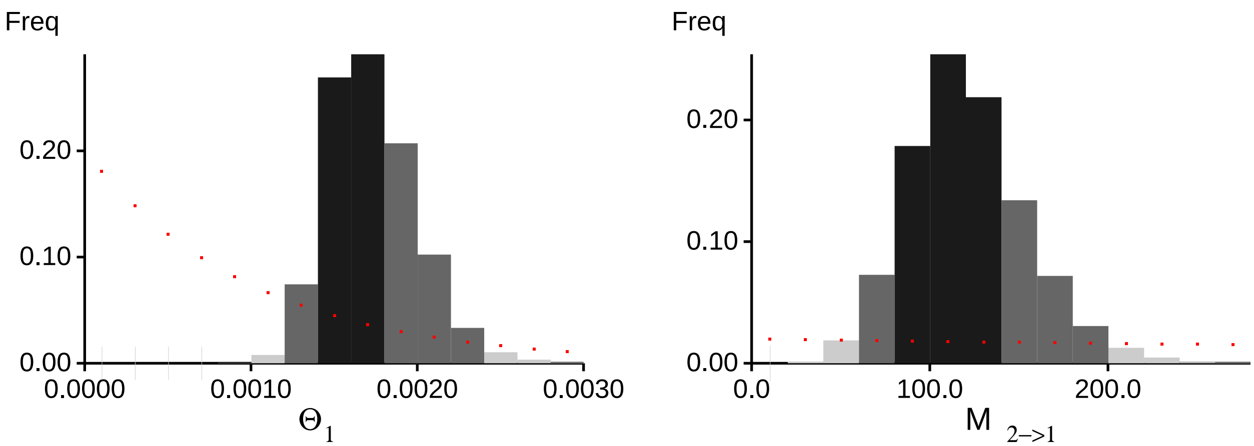


Bayesian Analysis: Posterior distribution for locus 22

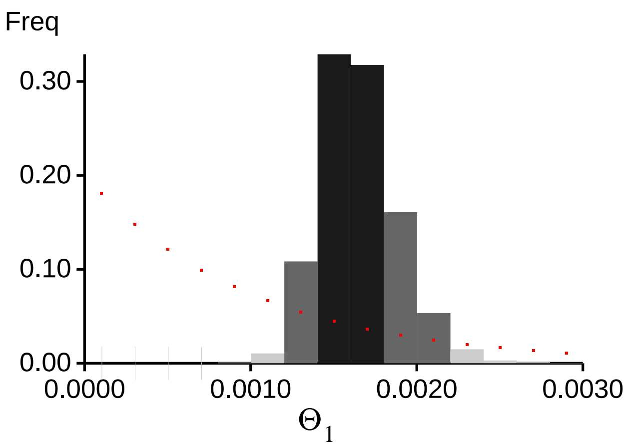


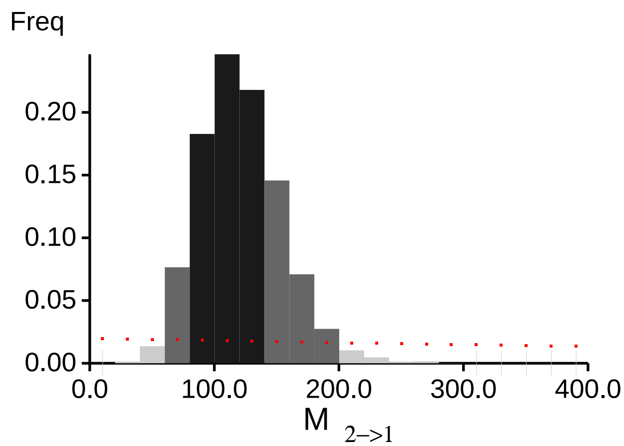


Bayesian Analysis: Posterior distribution for locus 23

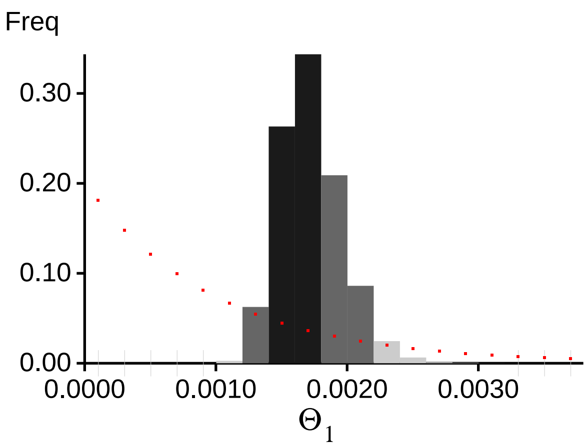


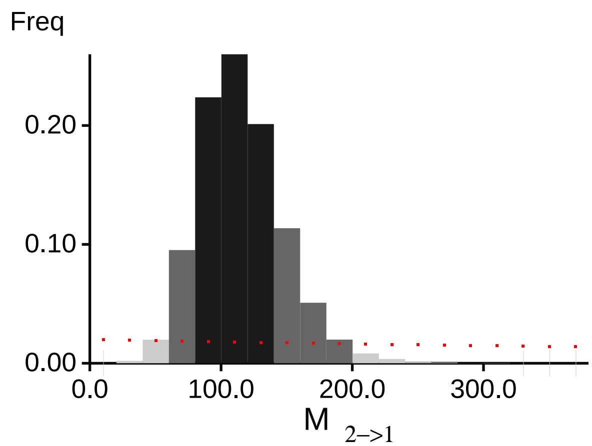
Bayesian Analysis: Posterior distribution for locus 24



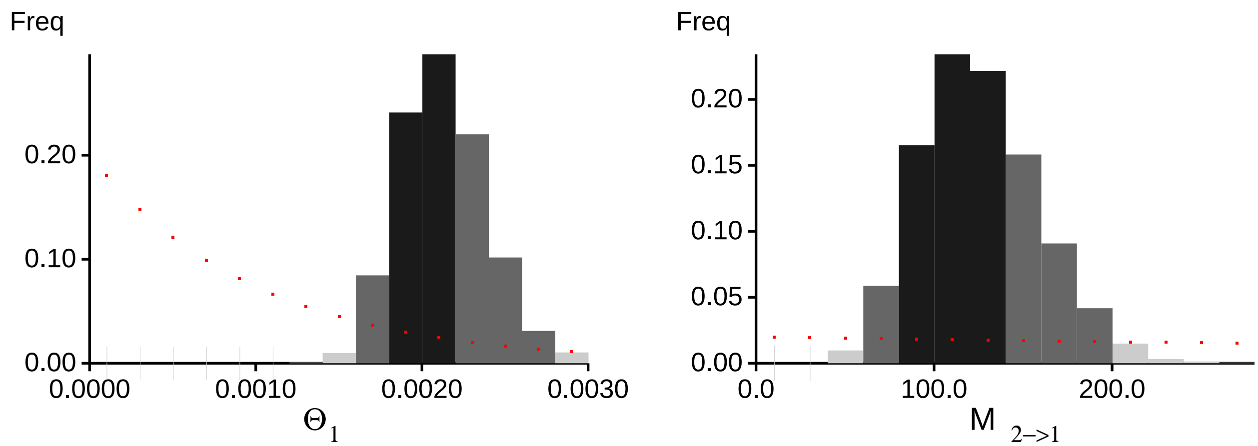


Bayesian Analysis: Posterior distribution for locus 25

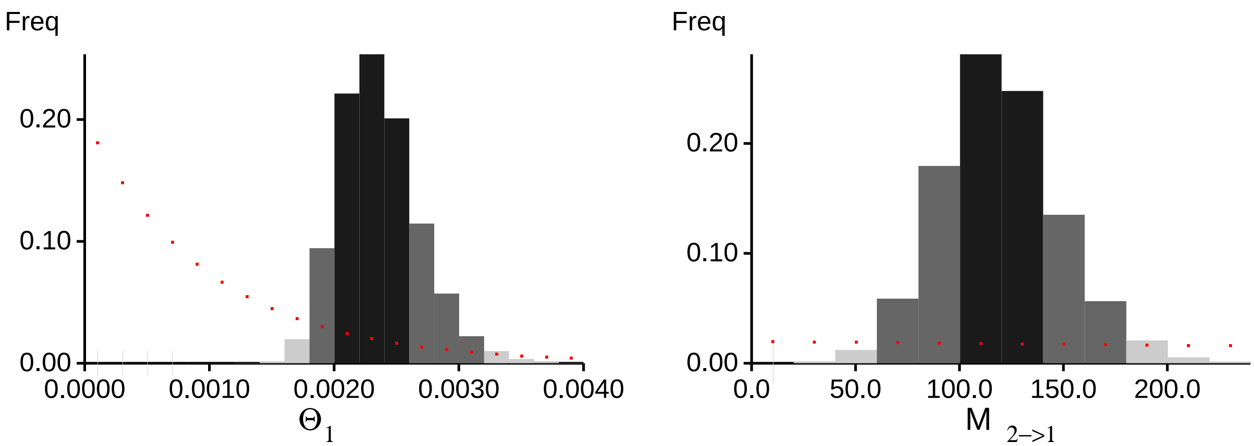




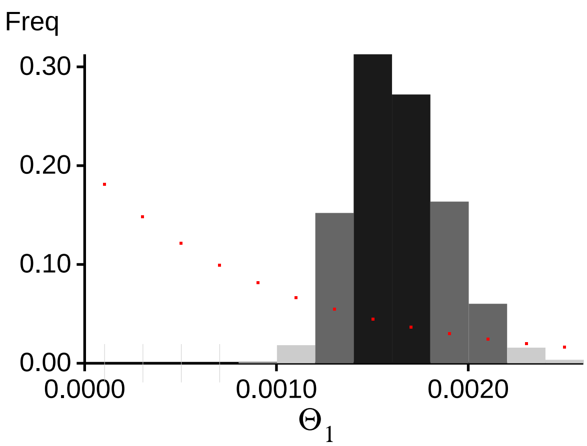
Bayesian Analysis: Posterior distribution for locus 26

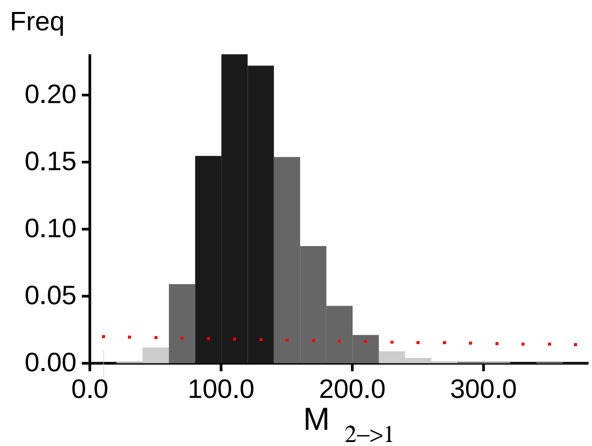


Bayesian Analysis: Posterior distribution for locus 27

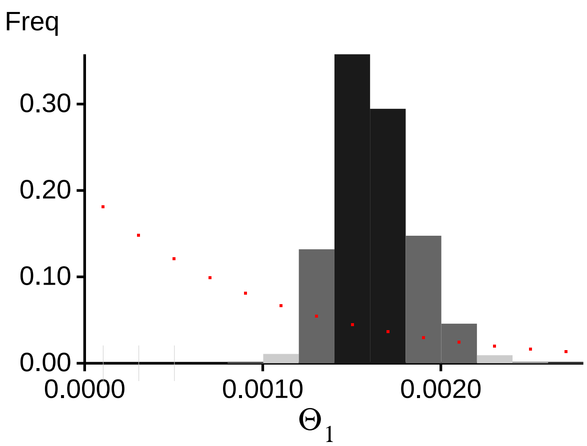


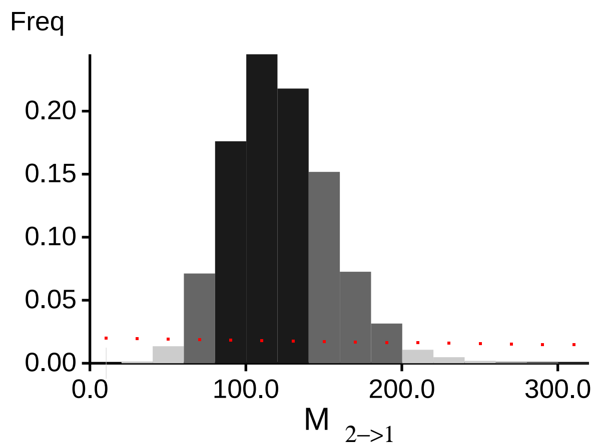
Bayesian Analysis: Posterior distribution for locus 28



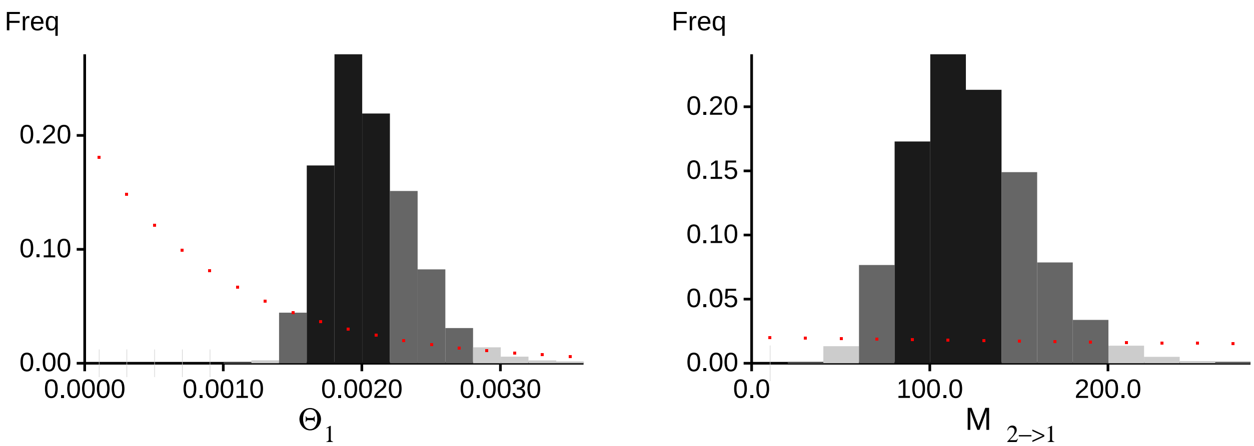


Bayesian Analysis: Posterior distribution for locus 29

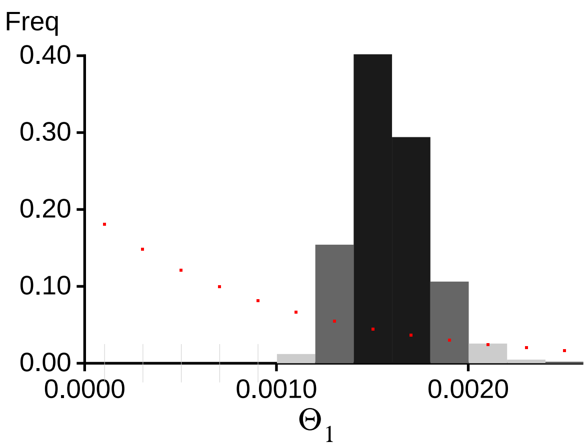


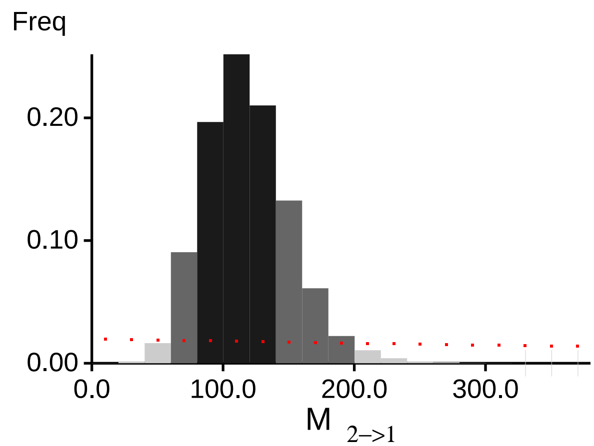


Bayesian Analysis: Posterior distribution for locus 30

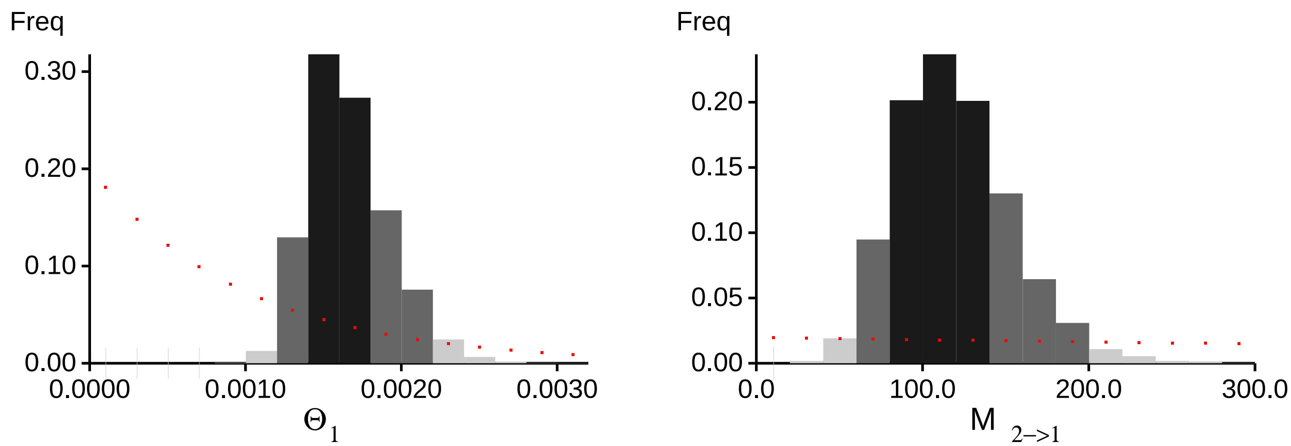


Bayesian Analysis: Posterior distribution for locus 31

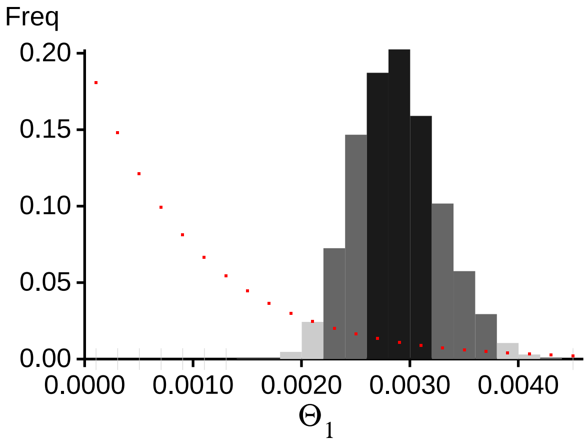


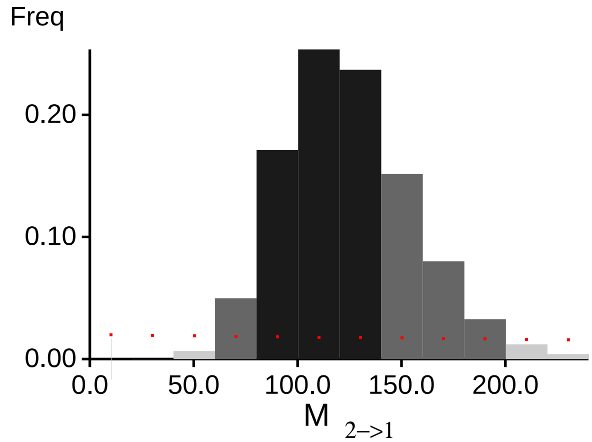


Bayesian Analysis: Posterior distribution for locus 32

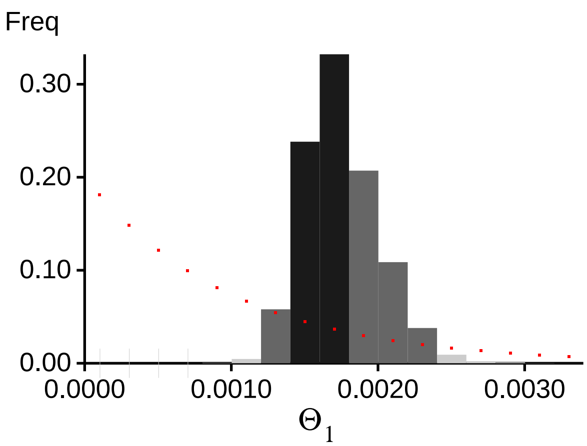


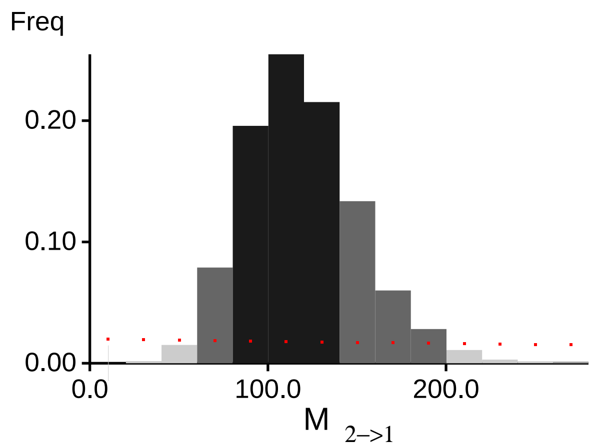
Bayesian Analysis: Posterior distribution for locus 33



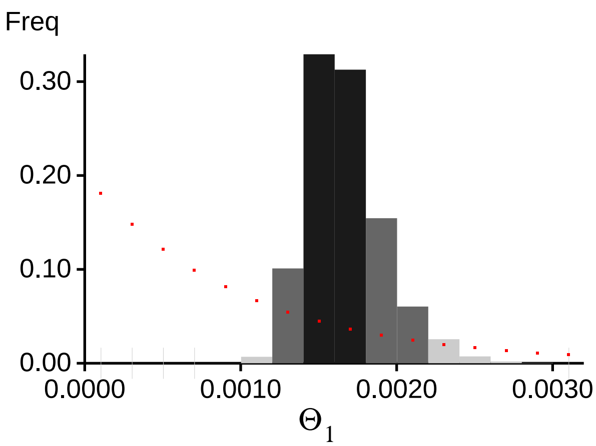


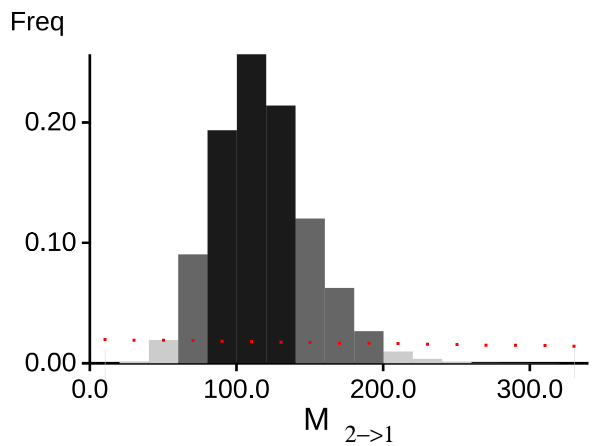
Bayesian Analysis: Posterior distribution for locus 34



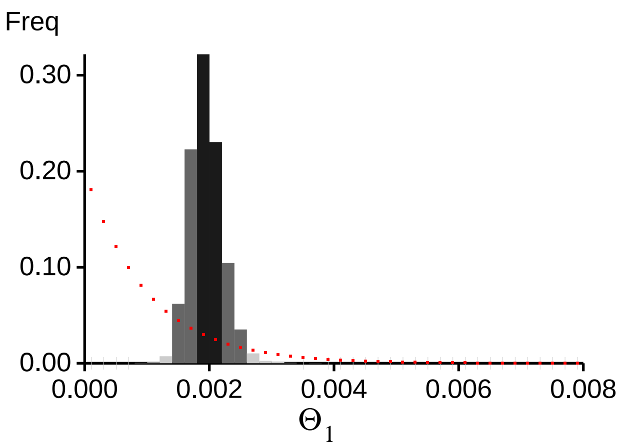


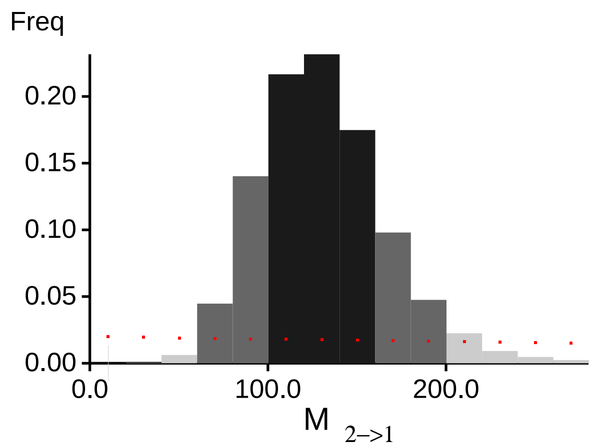
Bayesian Analysis: Posterior distribution for locus 35



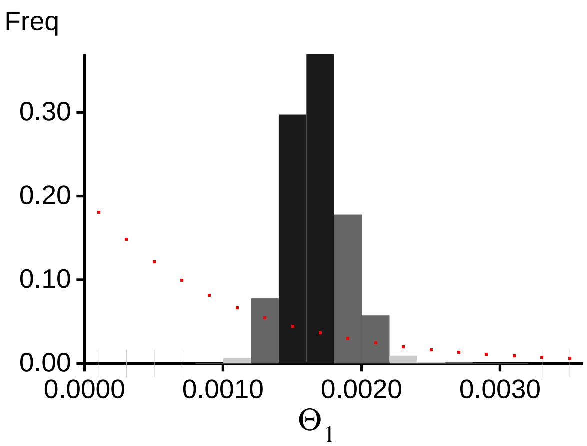


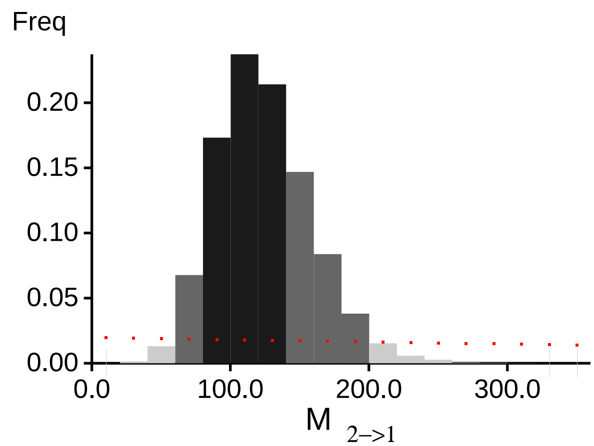
Bayesian Analysis: Posterior distribution for locus 36



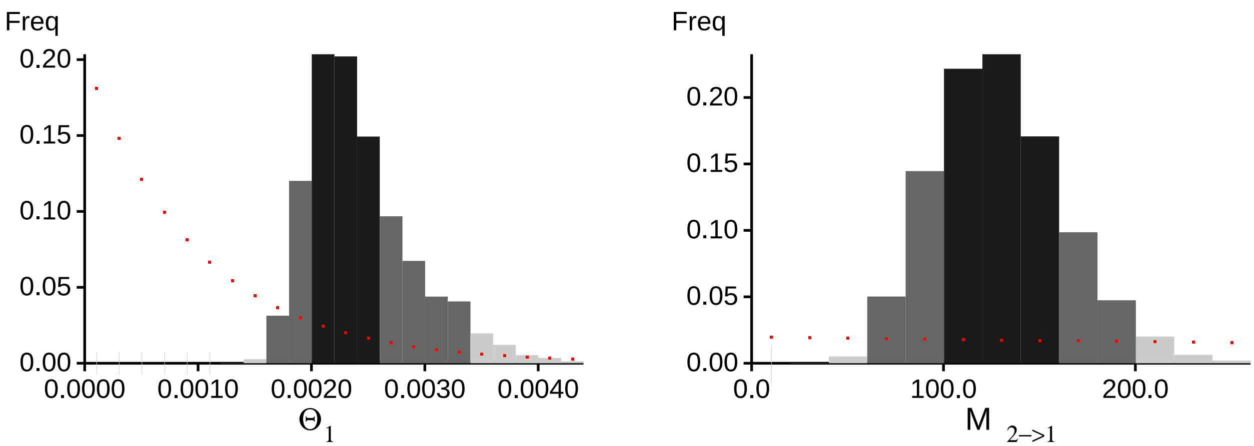


Bayesian Analysis: Posterior distribution for locus 37

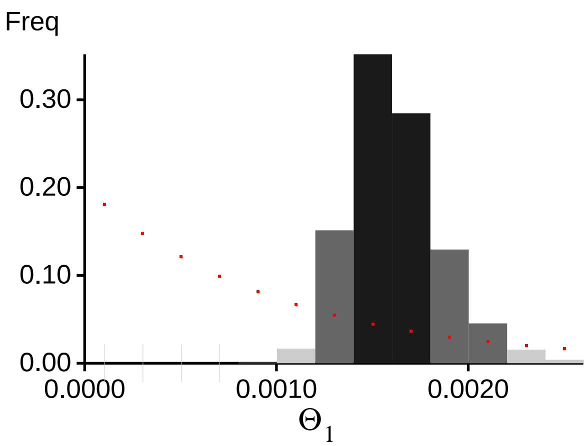


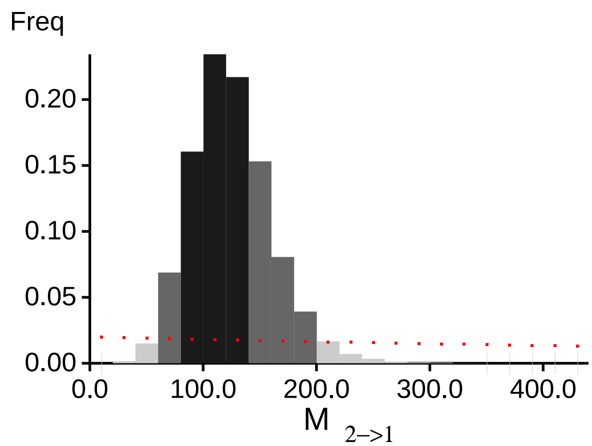


Bayesian Analysis: Posterior distribution for locus 38

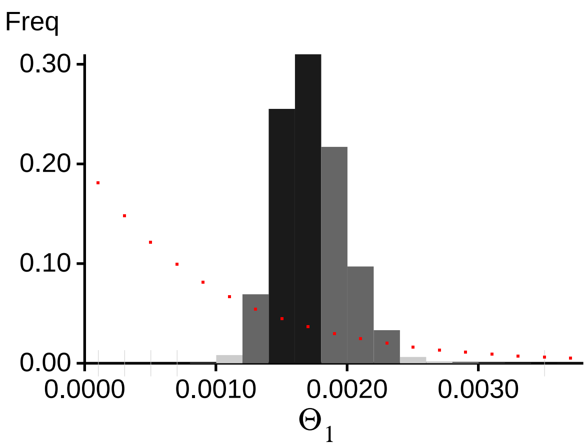


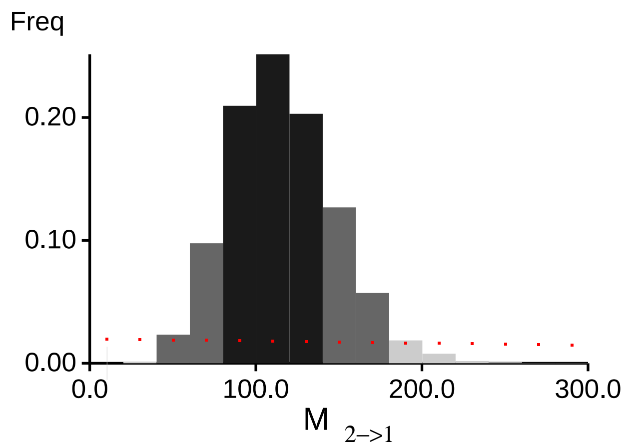
Bayesian Analysis: Posterior distribution for locus 39



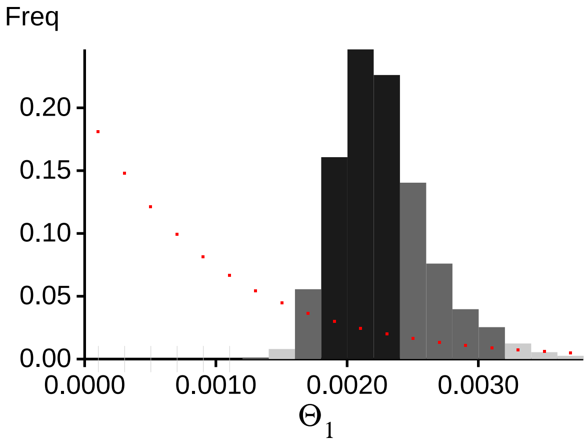


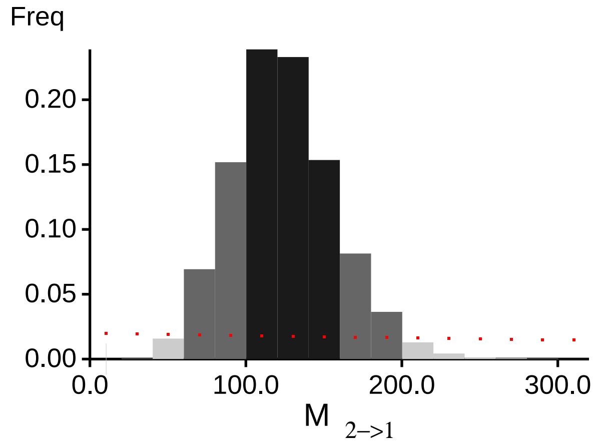
Bayesian Analysis: Posterior distribution for locus 40



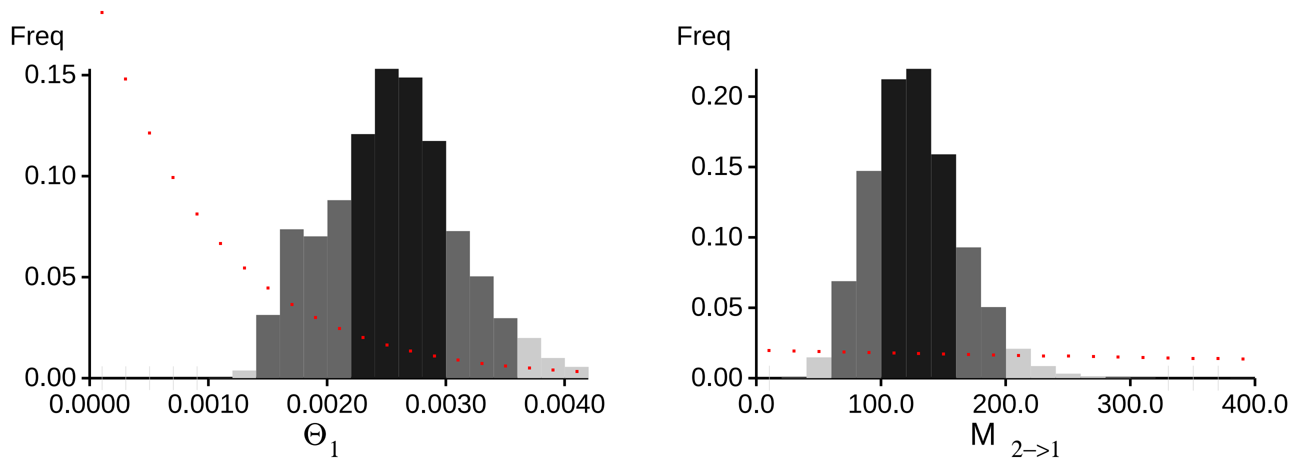


Bayesian Analysis: Posterior distribution for locus 41

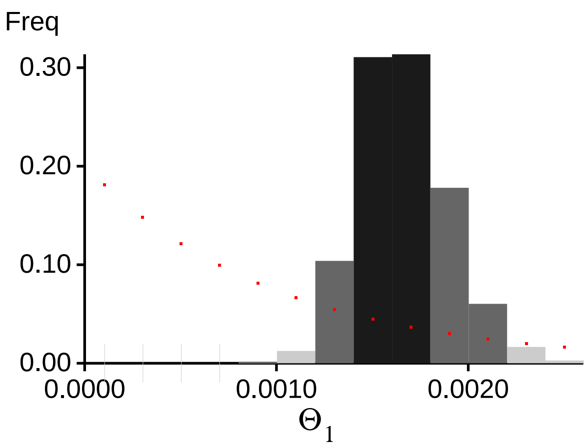


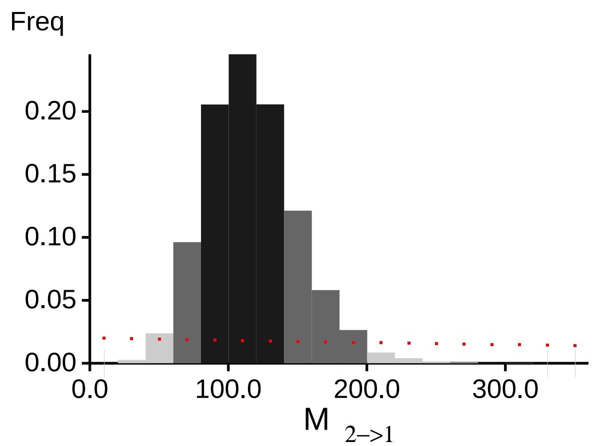


Bayesian Analysis: Posterior distribution for locus 42

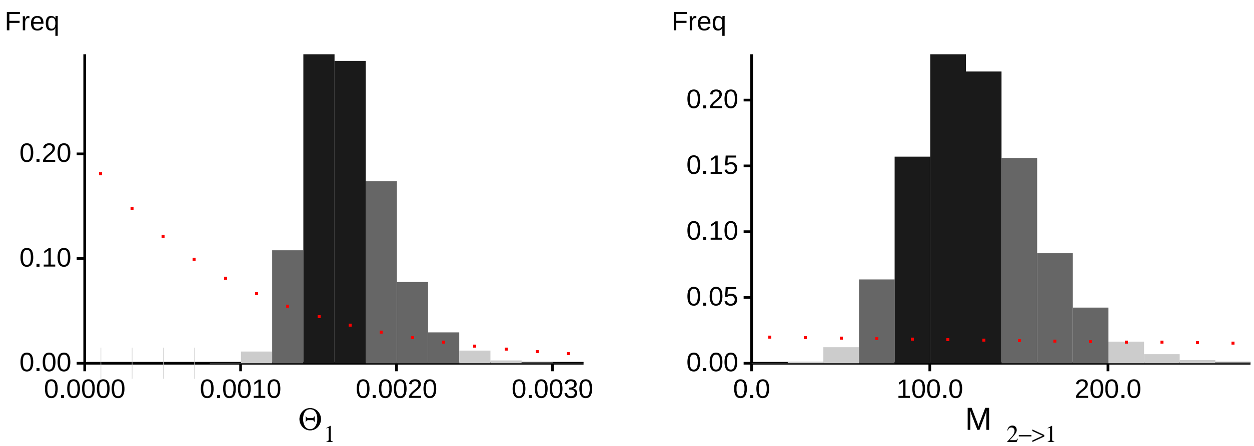


Bayesian Analysis: Posterior distribution for locus 43

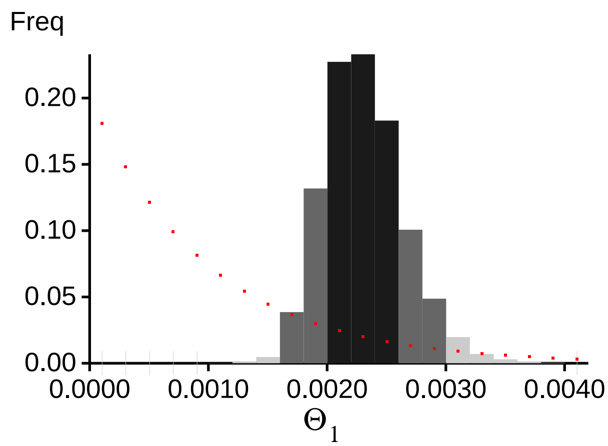


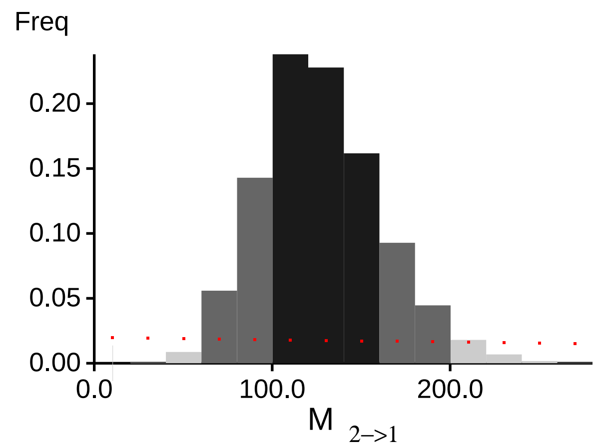


Bayesian Analysis: Posterior distribution for locus 44

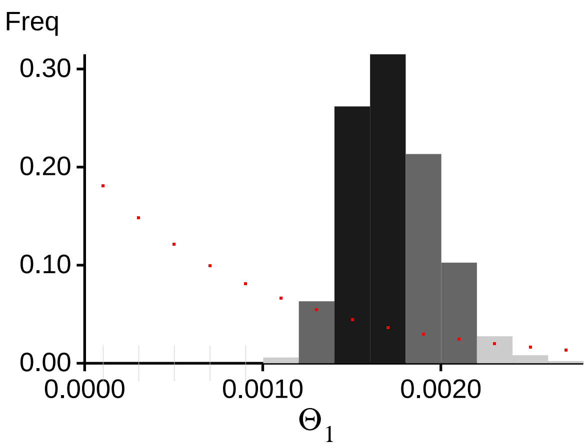


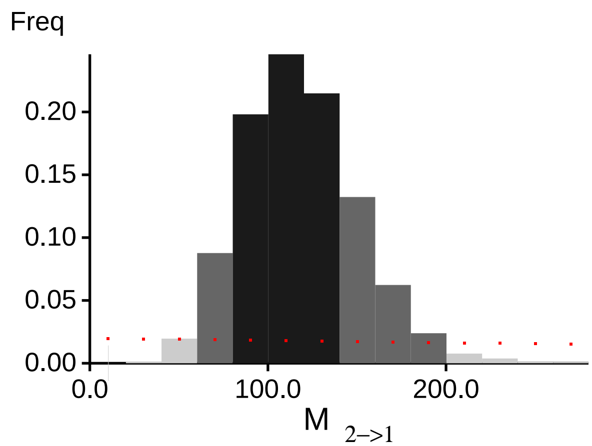
Bayesian Analysis: Posterior distribution for locus 45



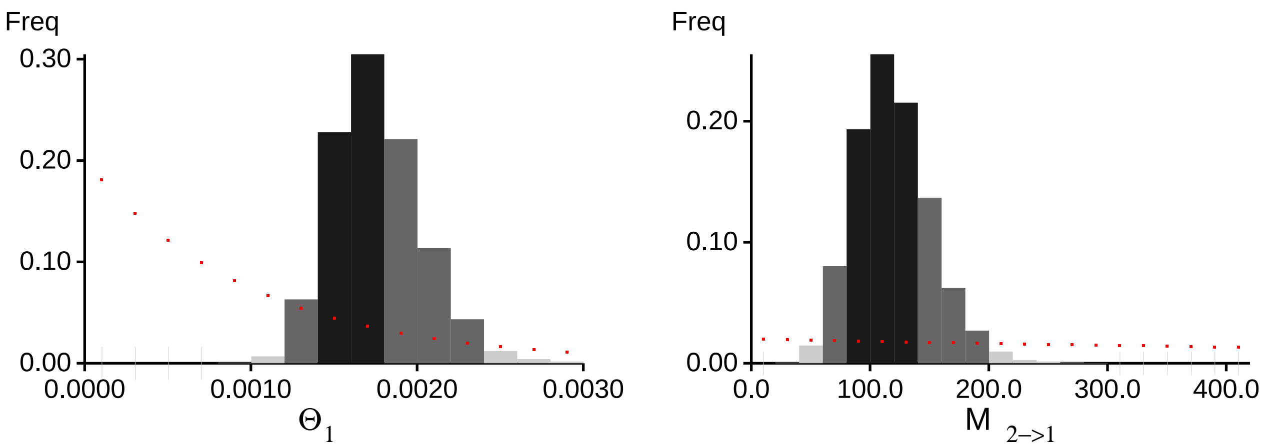


Bayesian Analysis: Posterior distribution for locus 46

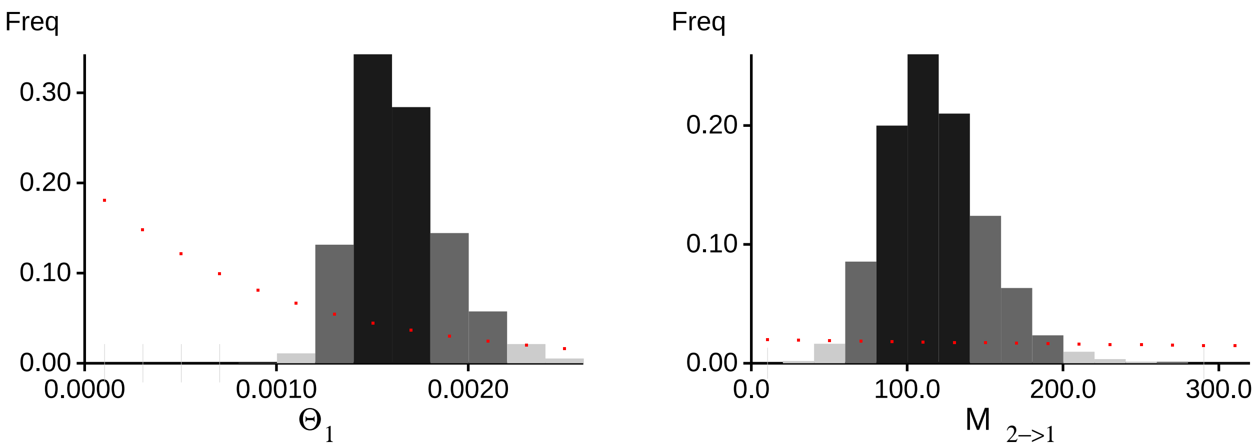




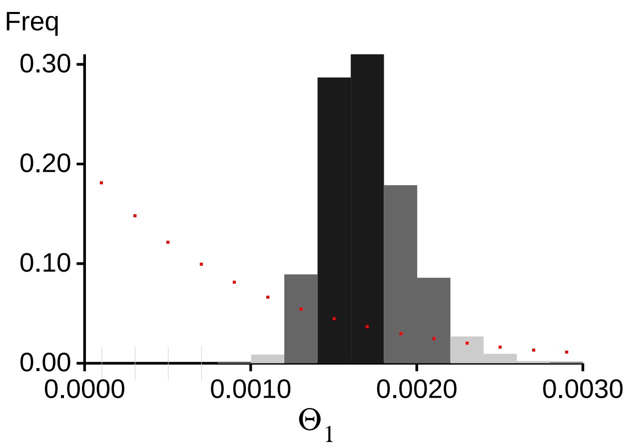
Bayesian Analysis: Posterior distribution for locus 47

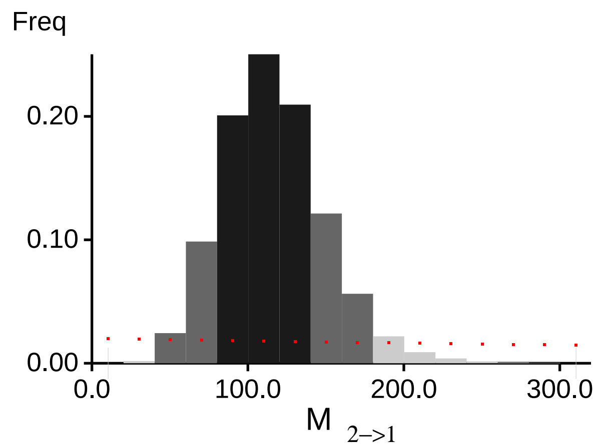


Bayesian Analysis: Posterior distribution for locus 48

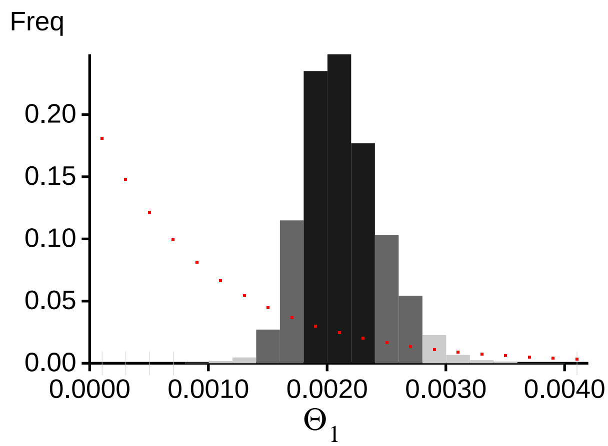


Bayesian Analysis: Posterior distribution for locus 49

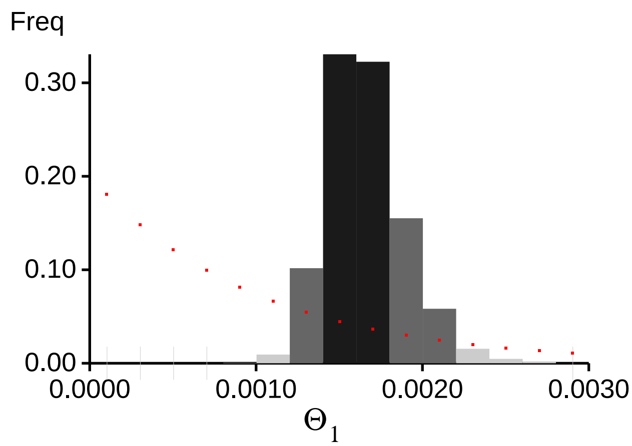


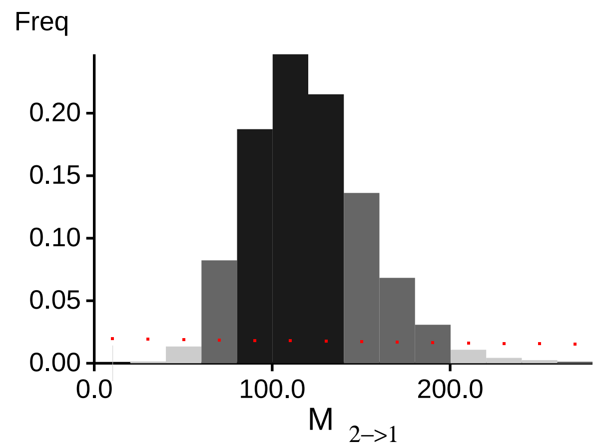


Bayesian Analysis: Posterior distribution for locus 50

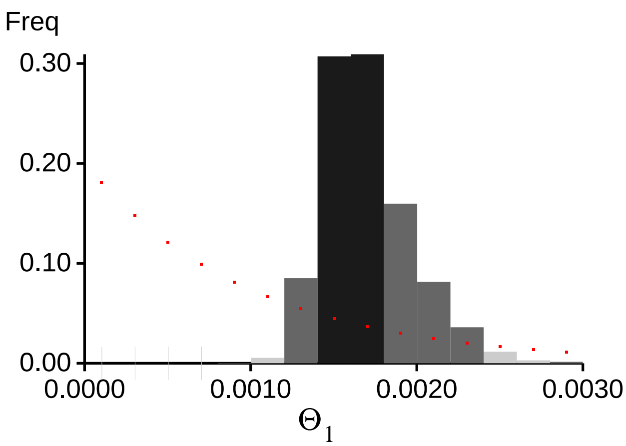


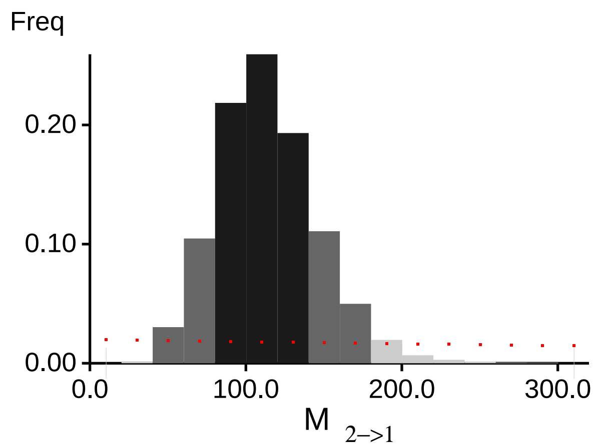
Bayesian Analysis: Posterior distribution for locus 51



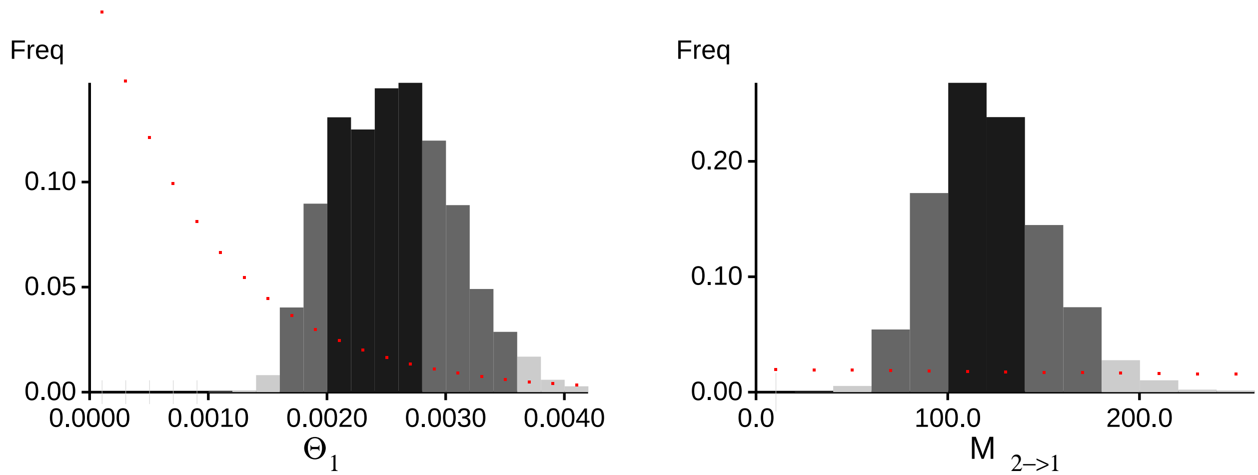


Bayesian Analysis: Posterior distribution for locus 52

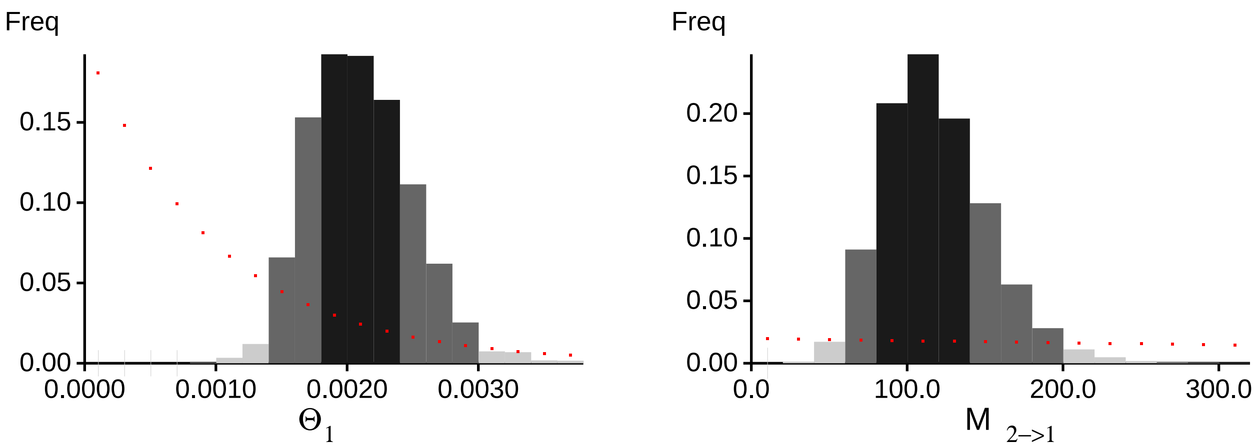




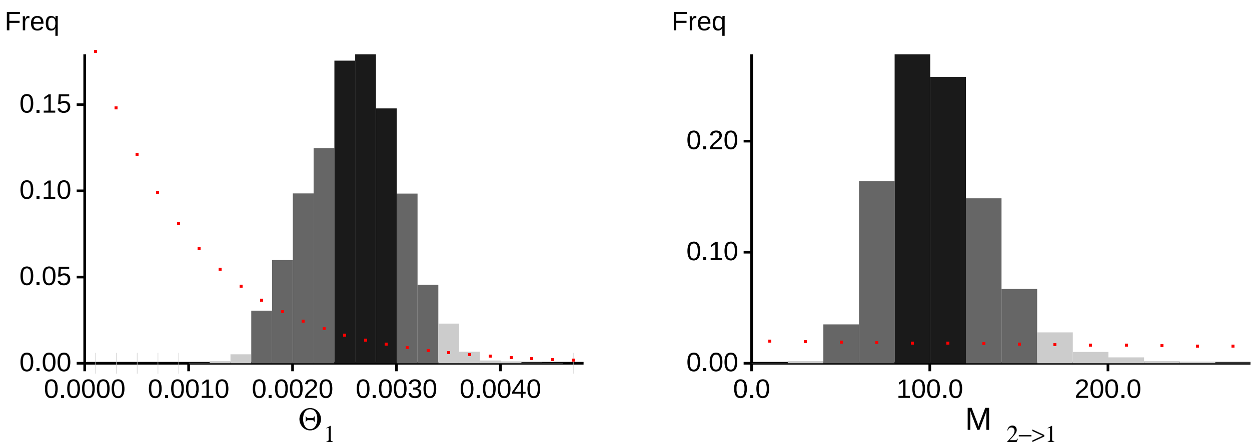
Bayesian Analysis: Posterior distribution for locus 53



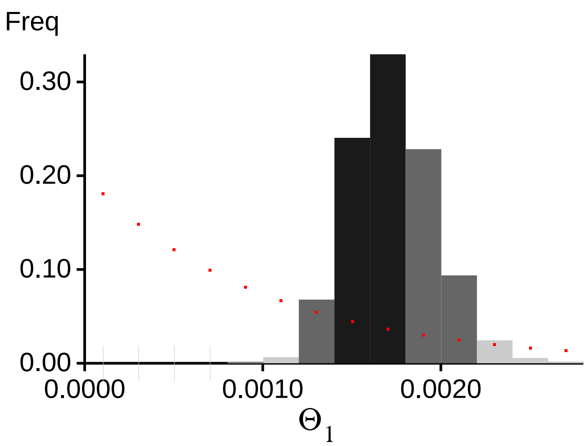
Bayesian Analysis: Posterior distribution for locus 54

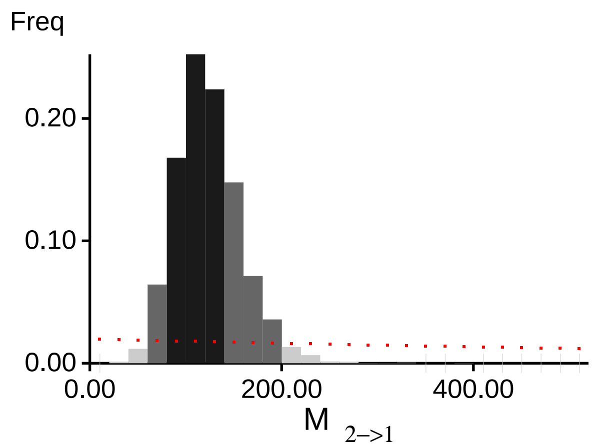


Bayesian Analysis: Posterior distribution for locus 55

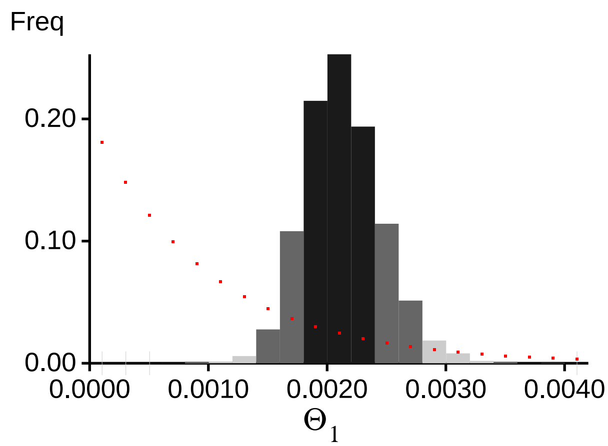


Bayesian Analysis: Posterior distribution for locus 56

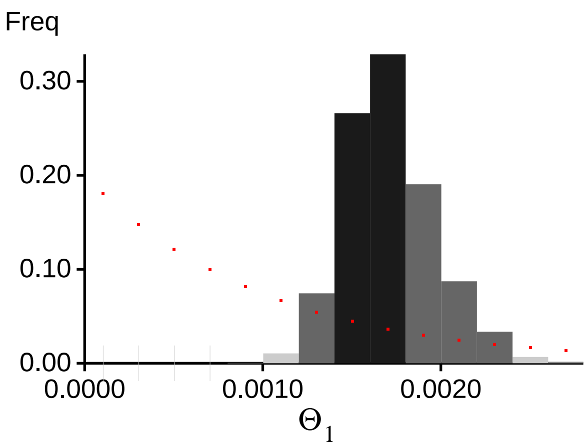


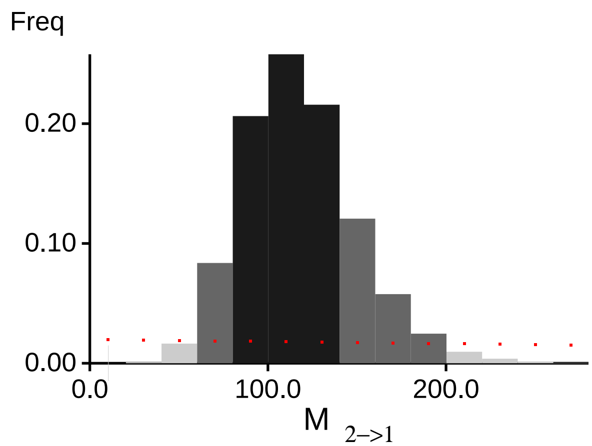


Bayesian Analysis: Posterior distribution for locus 57

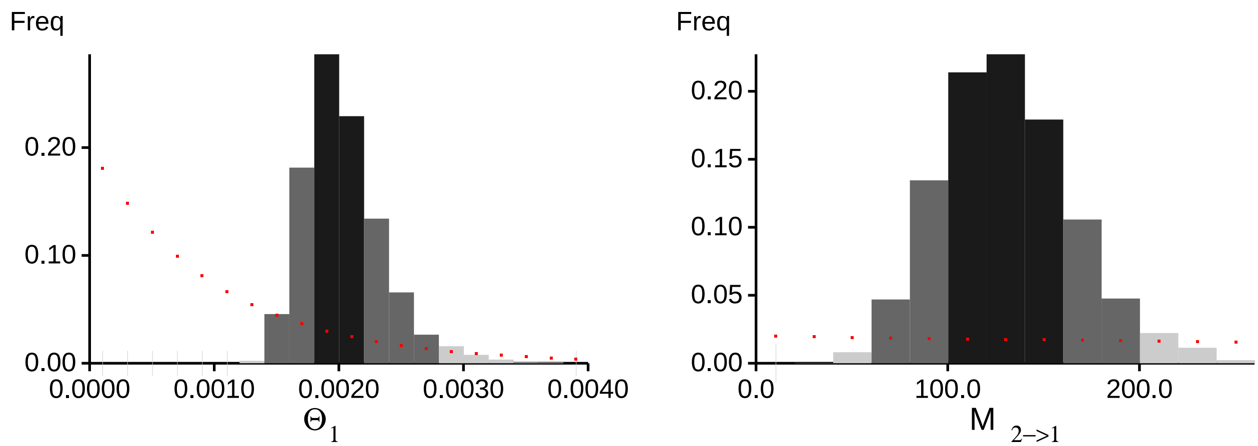


Bayesian Analysis: Posterior distribution for locus 58

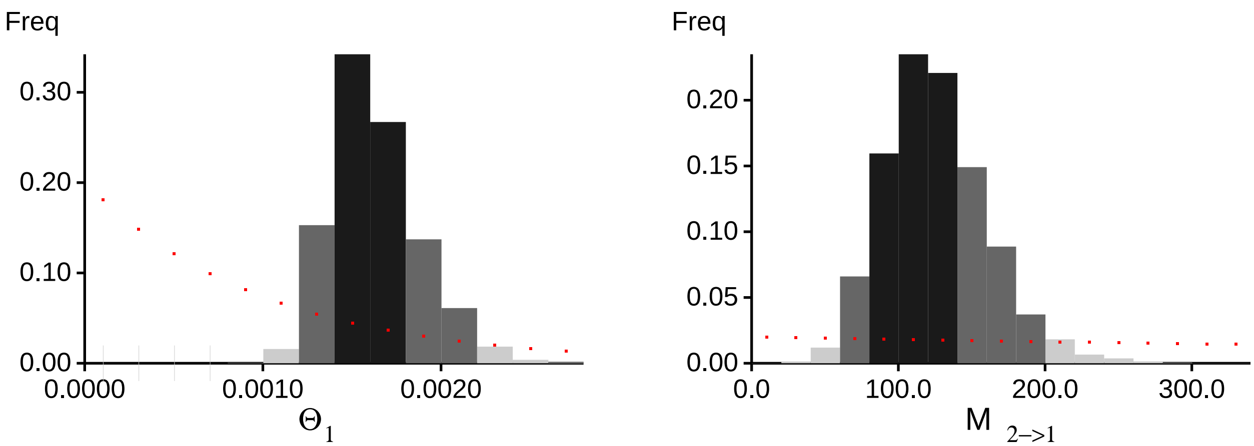




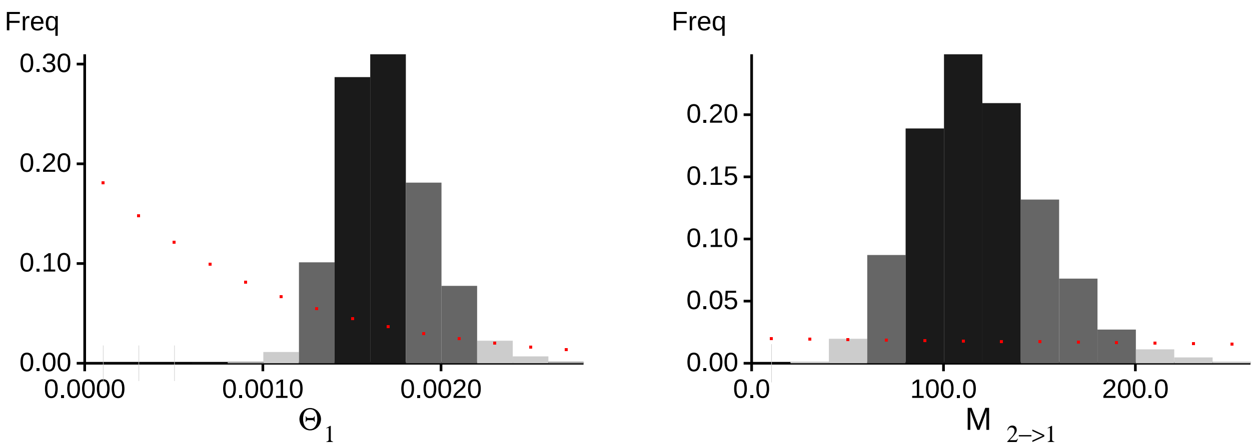
Bayesian Analysis: Posterior distribution for locus 59



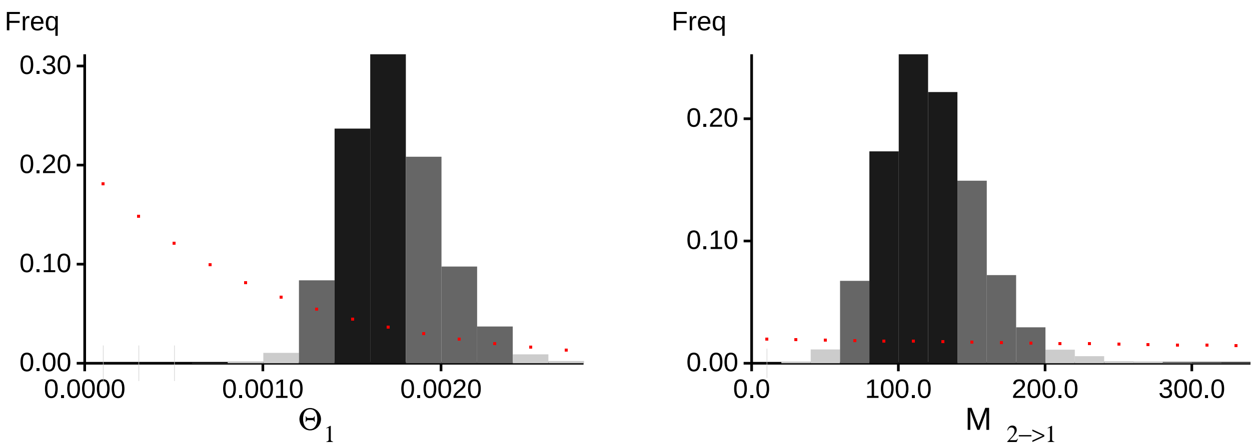
Bayesian Analysis: Posterior distribution for locus 60



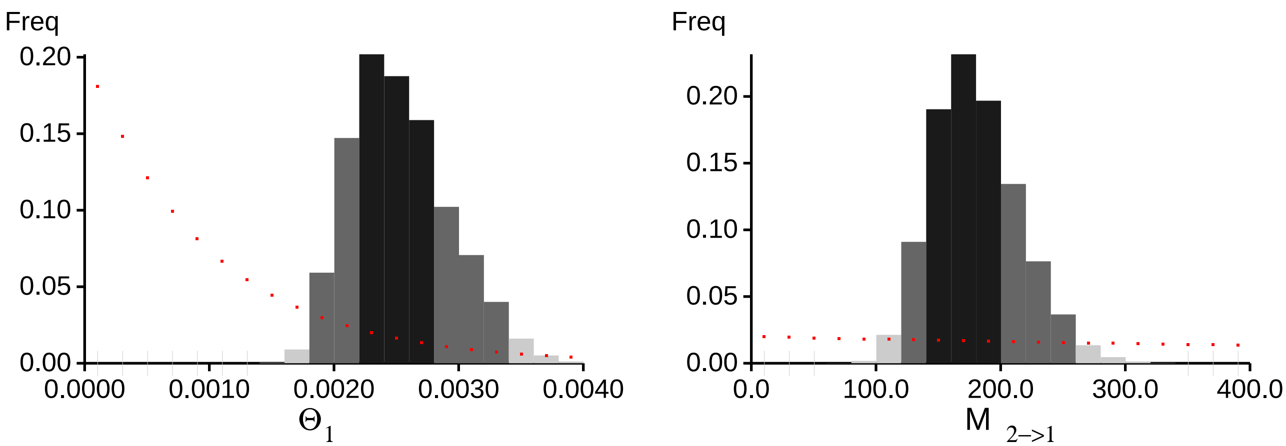
Bayesian Analysis: Posterior distribution for locus 61



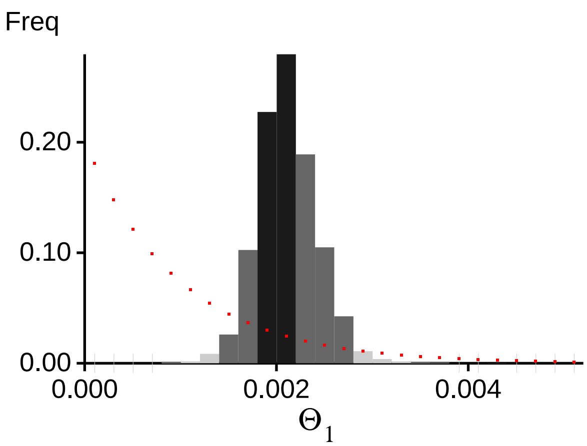
Bayesian Analysis: Posterior distribution for locus 62

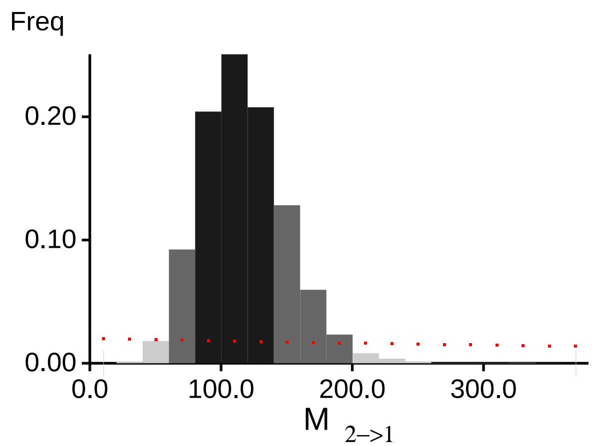


Bayesian Analysis: Posterior distribution for locus 63

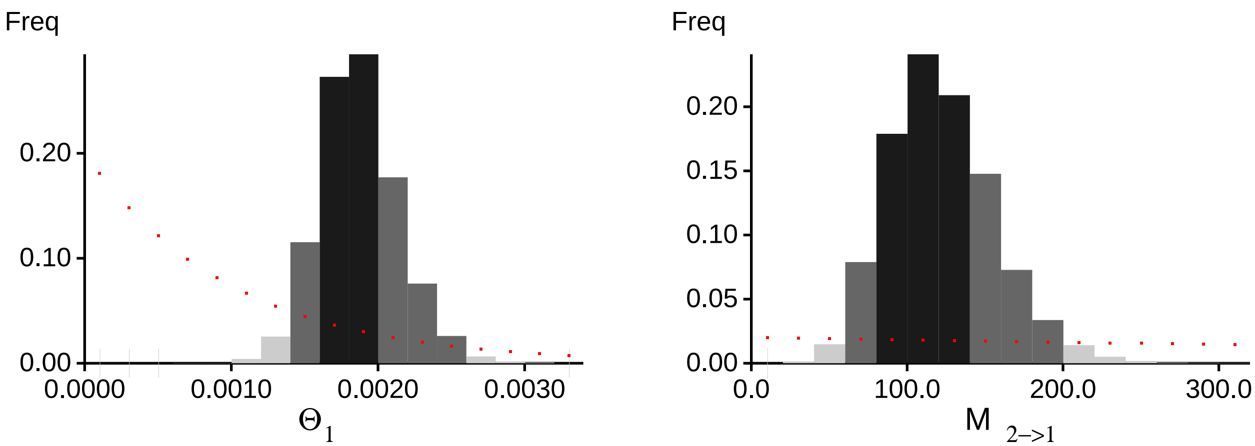


Bayesian Analysis: Posterior distribution for locus 64

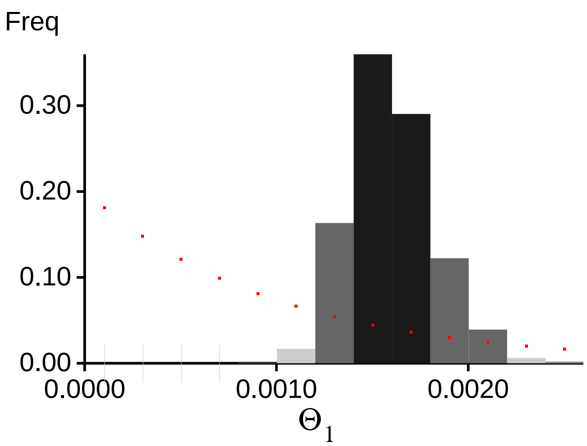


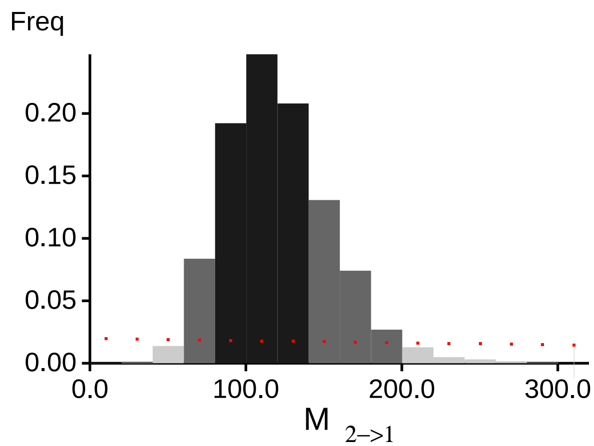


Bayesian Analysis: Posterior distribution for locus 65

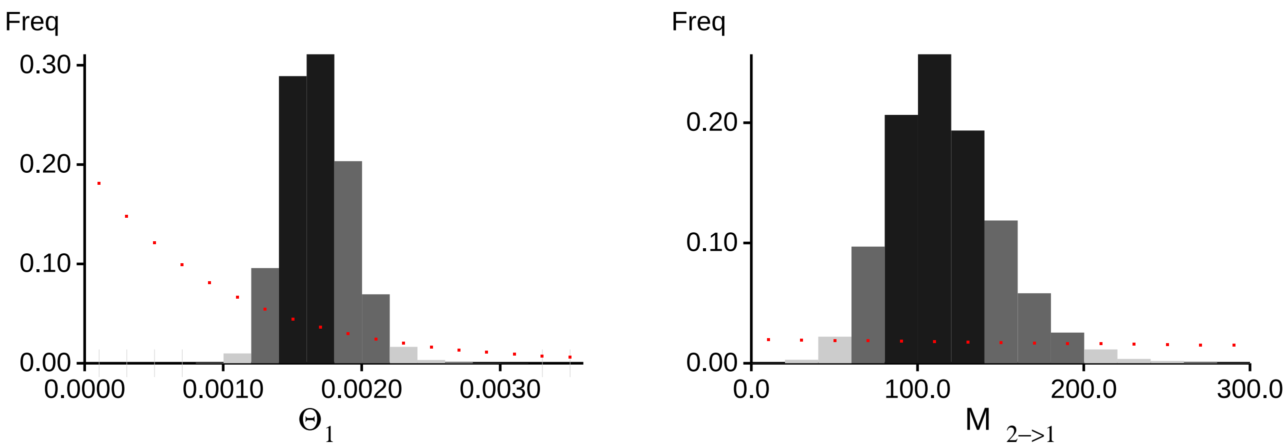


Bayesian Analysis: Posterior distribution for locus 66

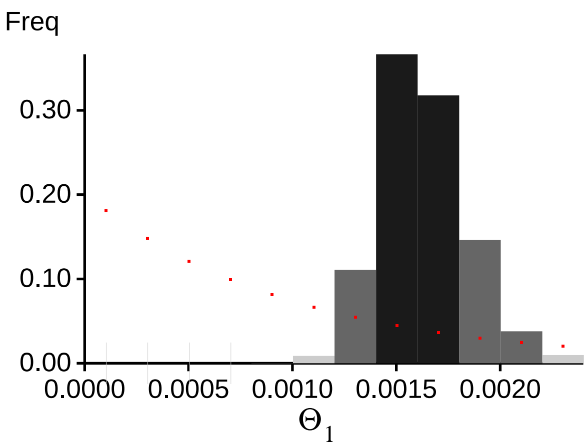


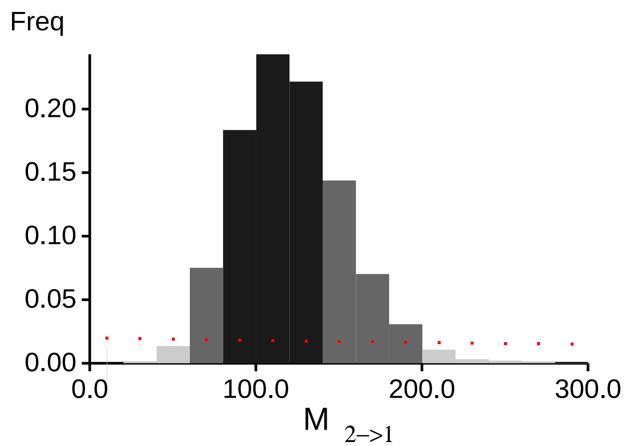


Bayesian Analysis: Posterior distribution for locus 67

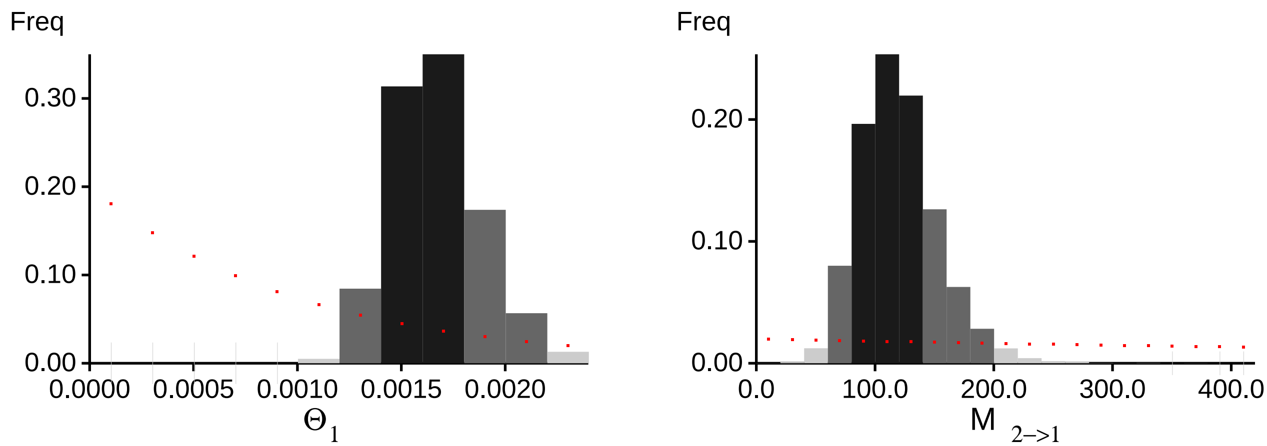


Bayesian Analysis: Posterior distribution for locus 68

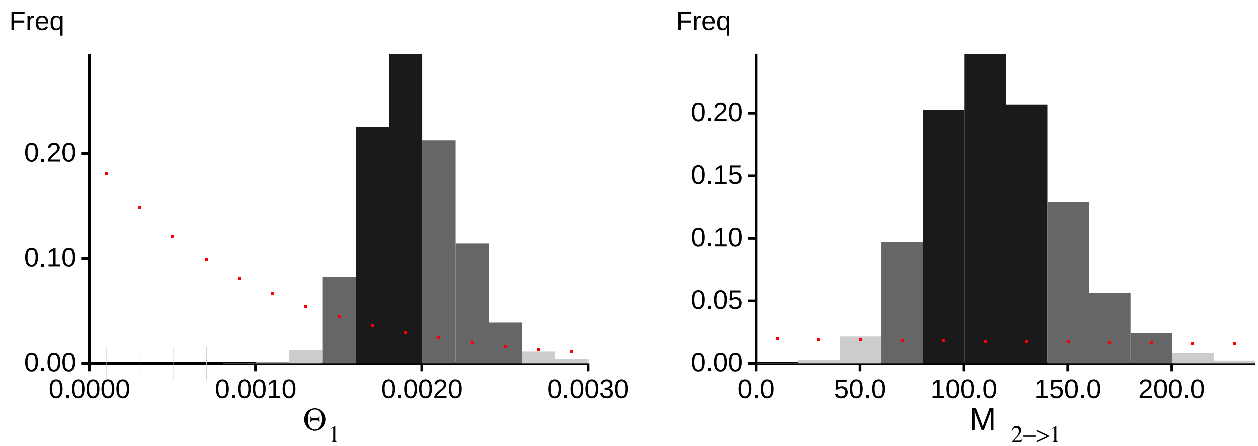




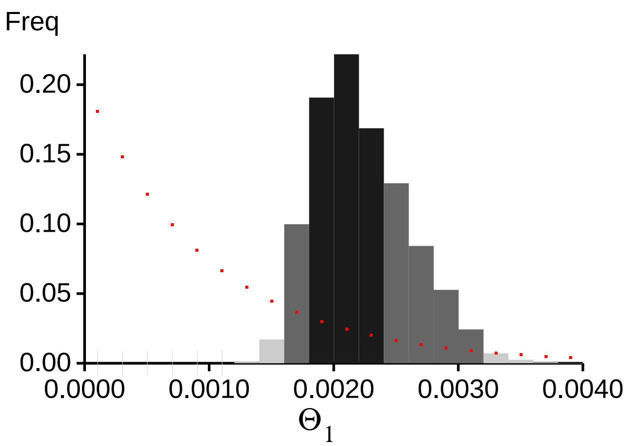
Bayesian Analysis: Posterior distribution for locus 69

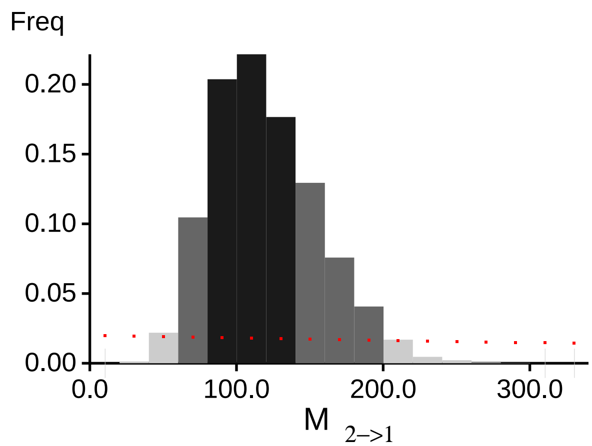


Bayesian Analysis: Posterior distribution for locus 70

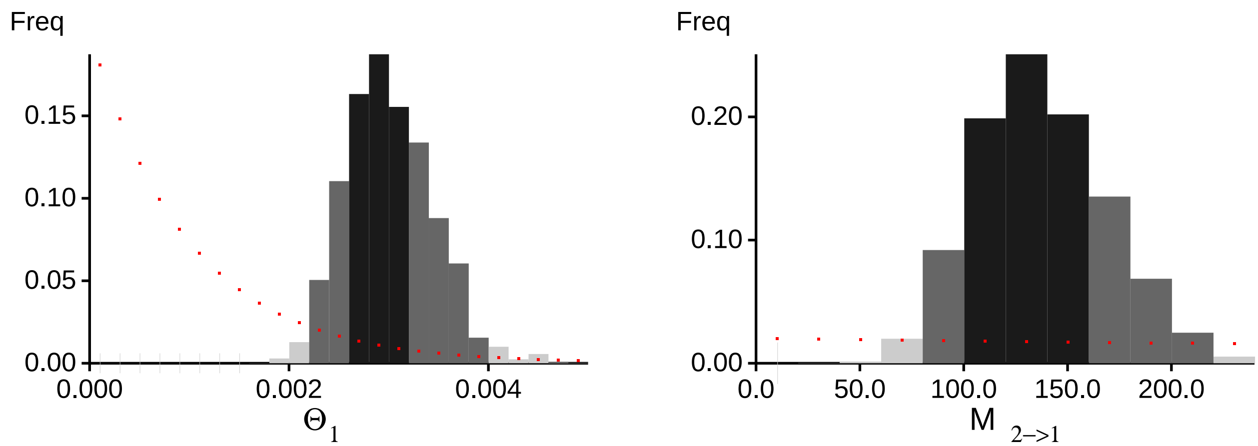


Bayesian Analysis: Posterior distribution for locus 71

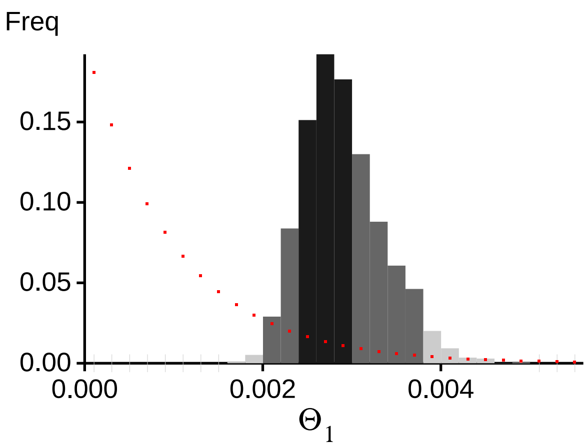


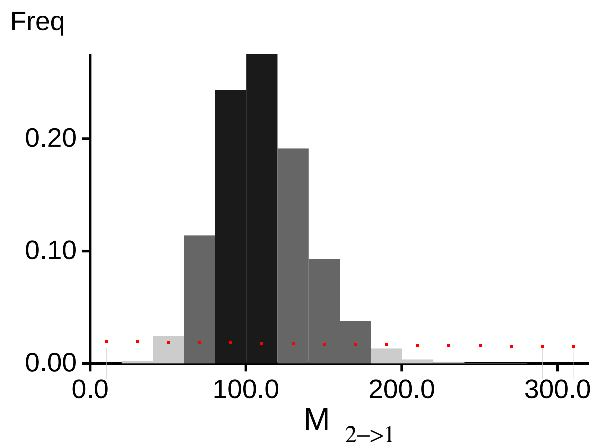


Bayesian Analysis: Posterior distribution for locus 72

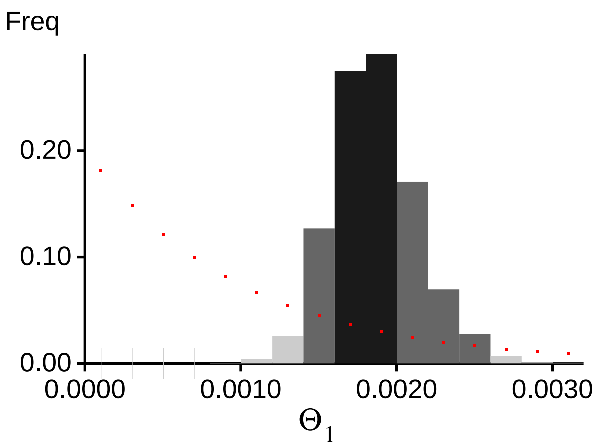


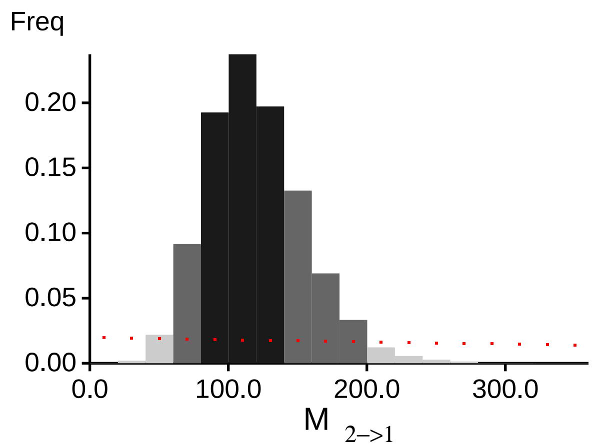
Bayesian Analysis: Posterior distribution for locus 73



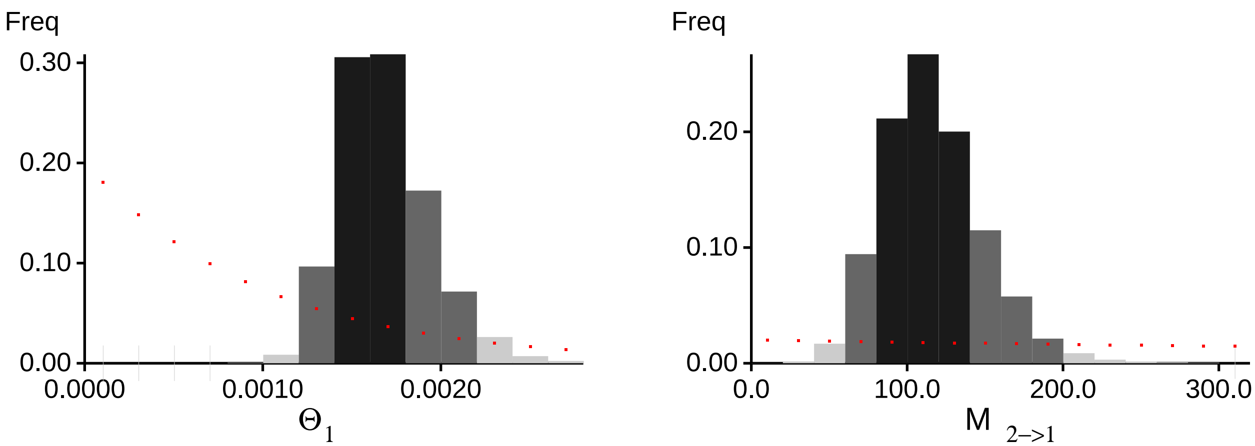


Bayesian Analysis: Posterior distribution for locus 74

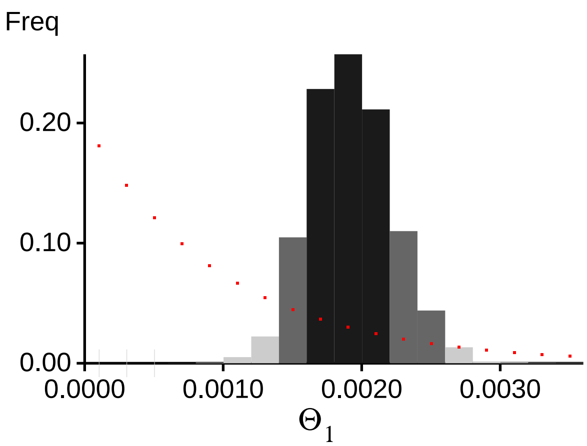


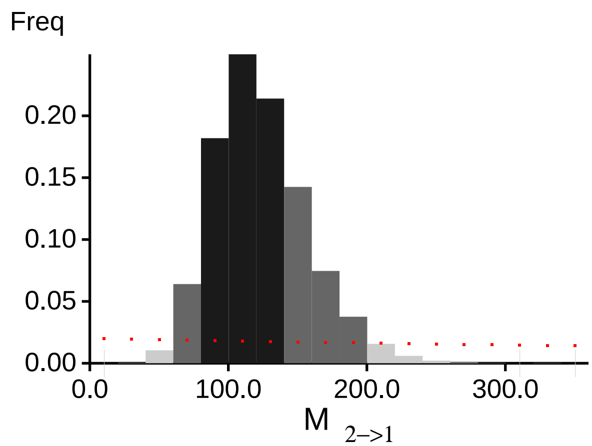


Bayesian Analysis: Posterior distribution for locus 75

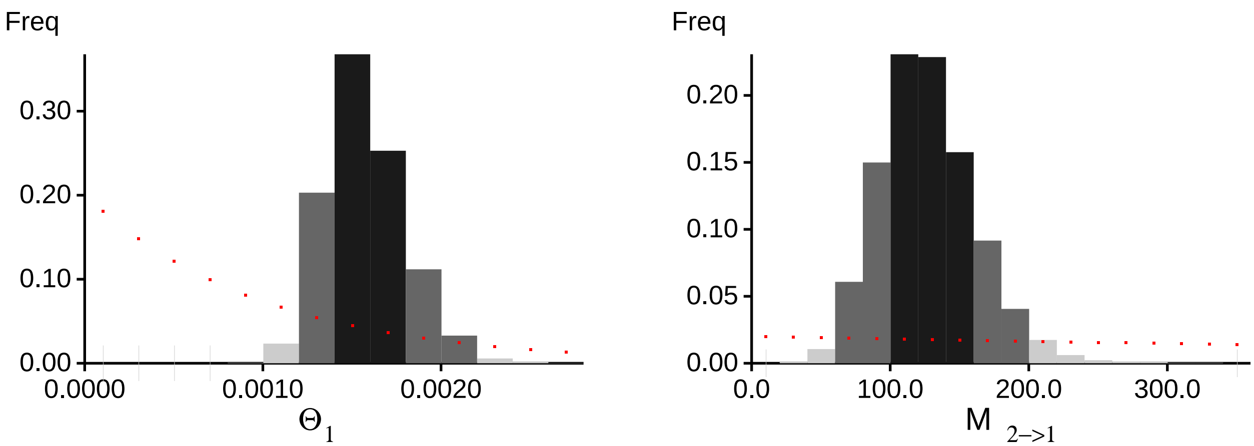


Bayesian Analysis: Posterior distribution for locus 76

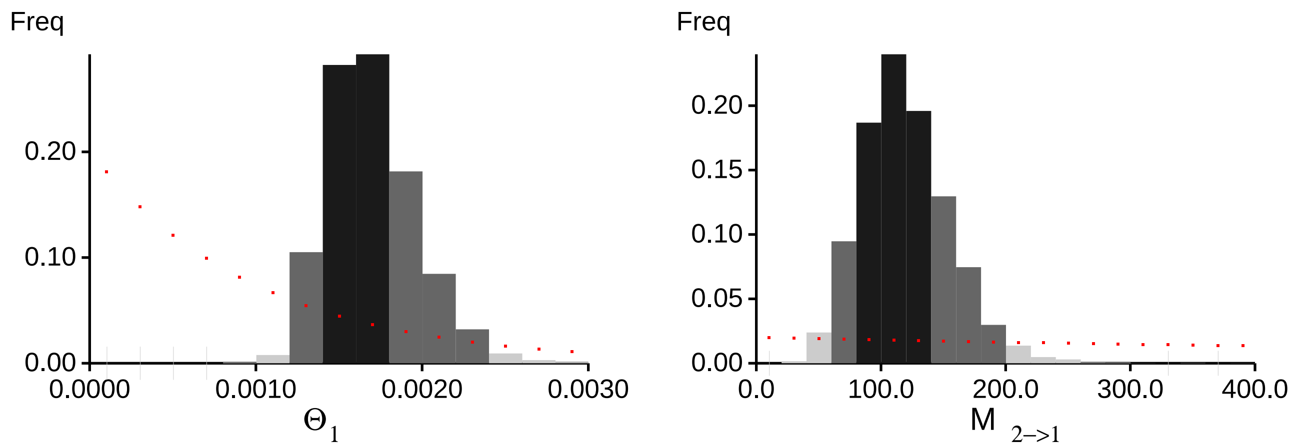




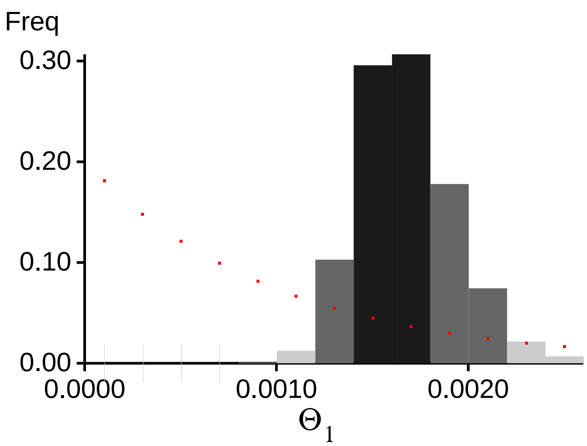
Bayesian Analysis: Posterior distribution for locus 77

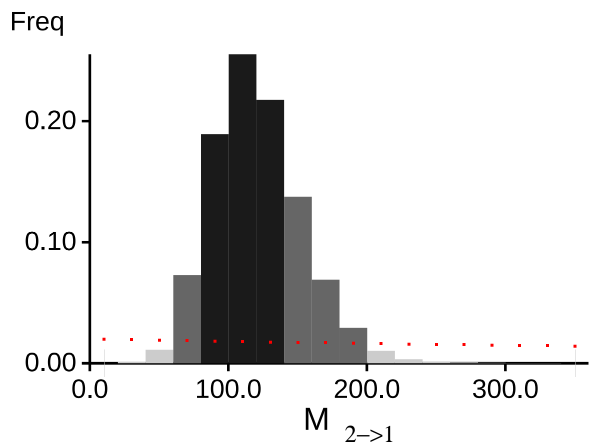


Bayesian Analysis: Posterior distribution for locus 78

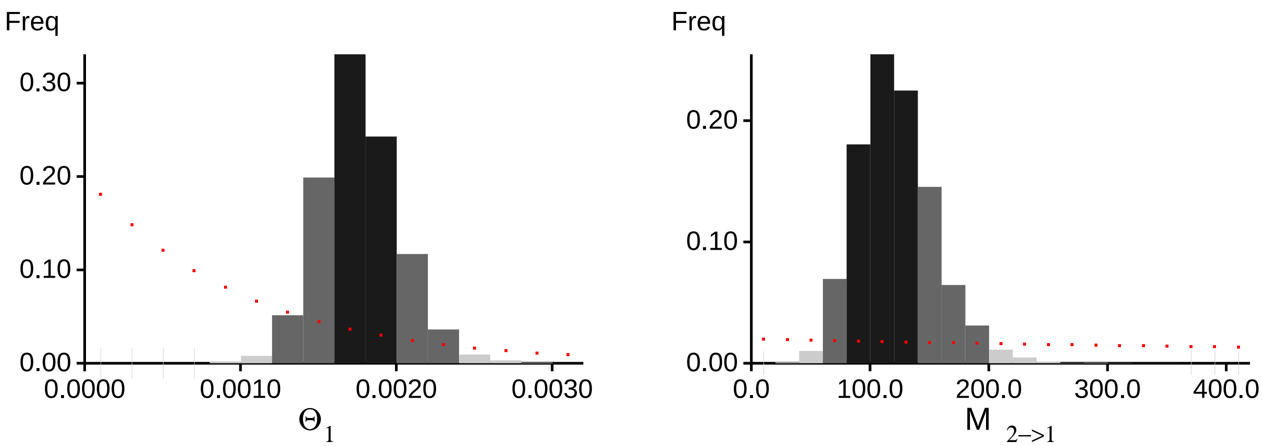


Bayesian Analysis: Posterior distribution for locus 79

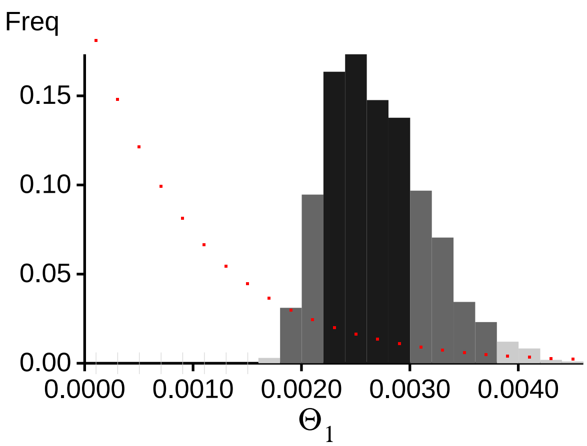


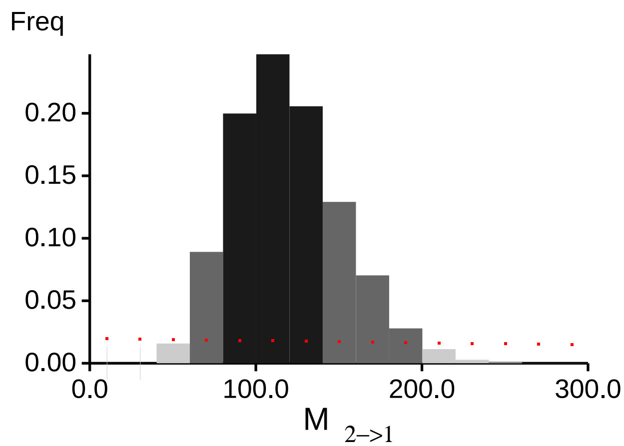


Bayesian Analysis: Posterior distribution for locus 80

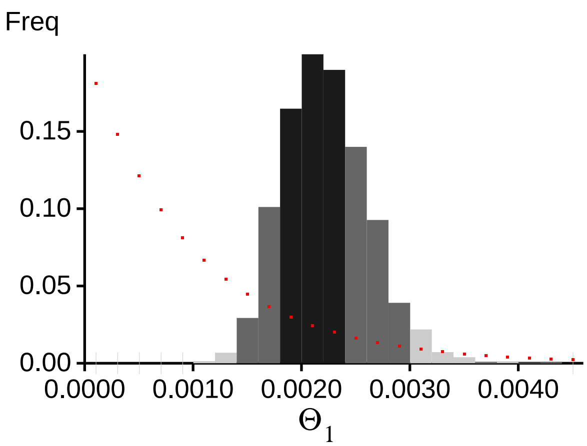


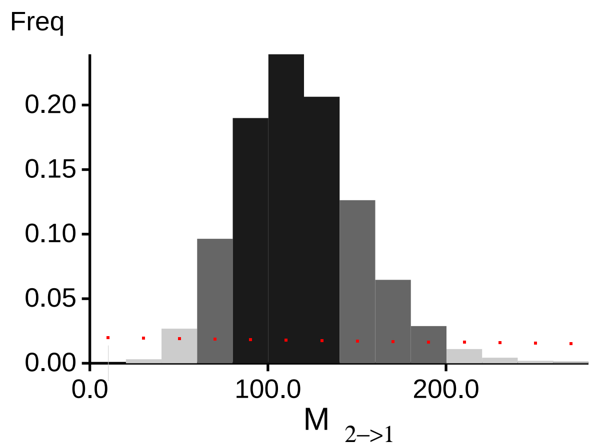
Bayesian Analysis: Posterior distribution for locus 81



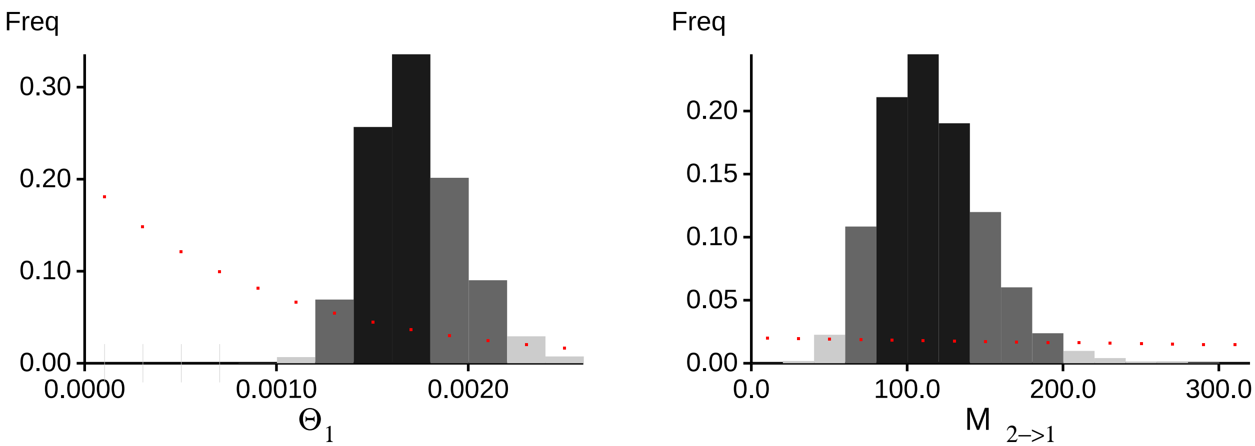


Bayesian Analysis: Posterior distribution for locus 82

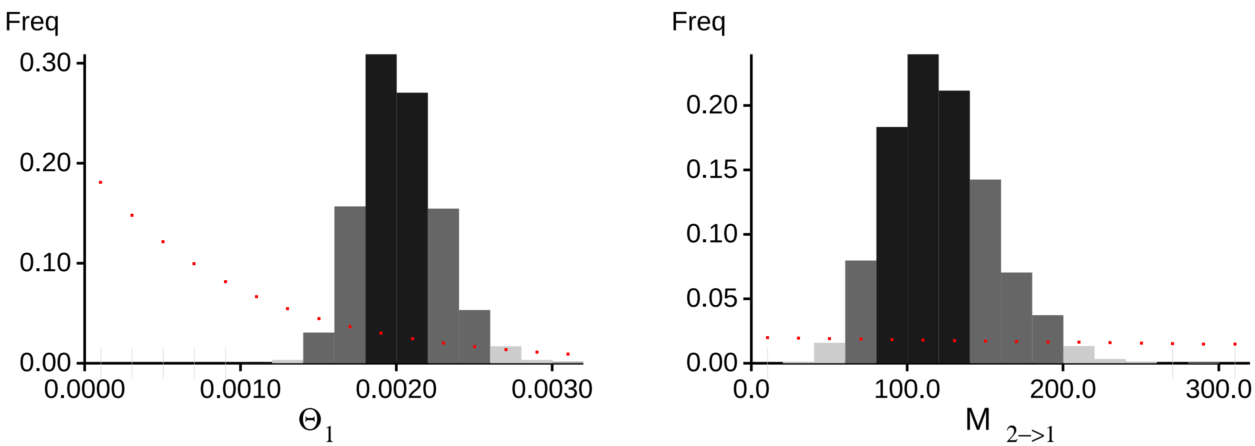




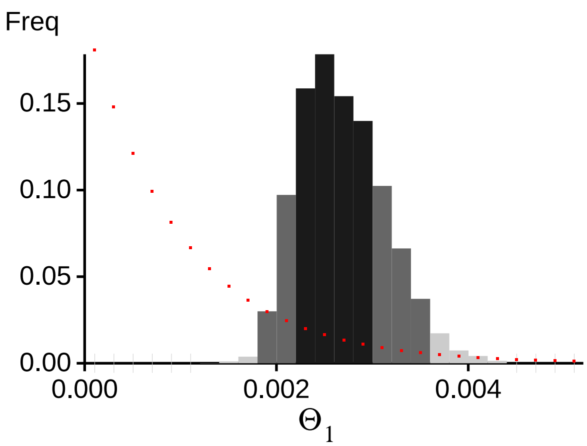
Bayesian Analysis: Posterior distribution for locus 83

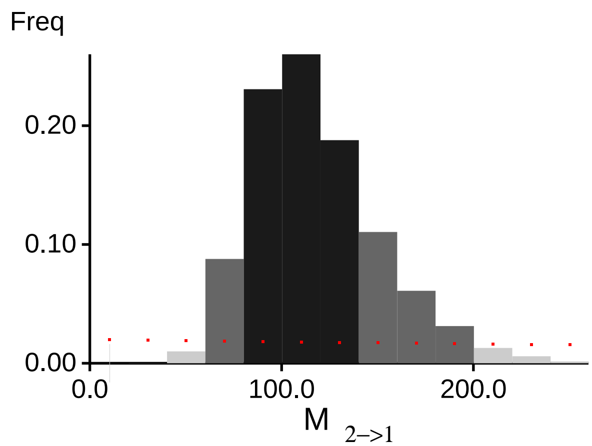


Bayesian Analysis: Posterior distribution for locus 84

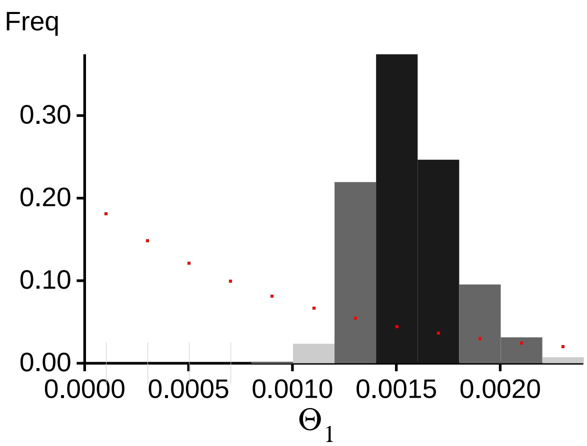


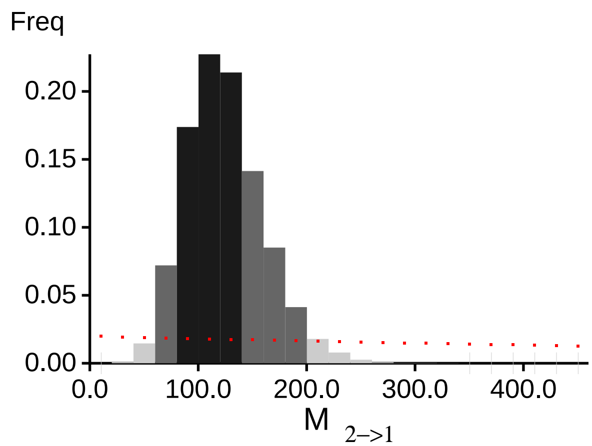
Bayesian Analysis: Posterior distribution for locus 85



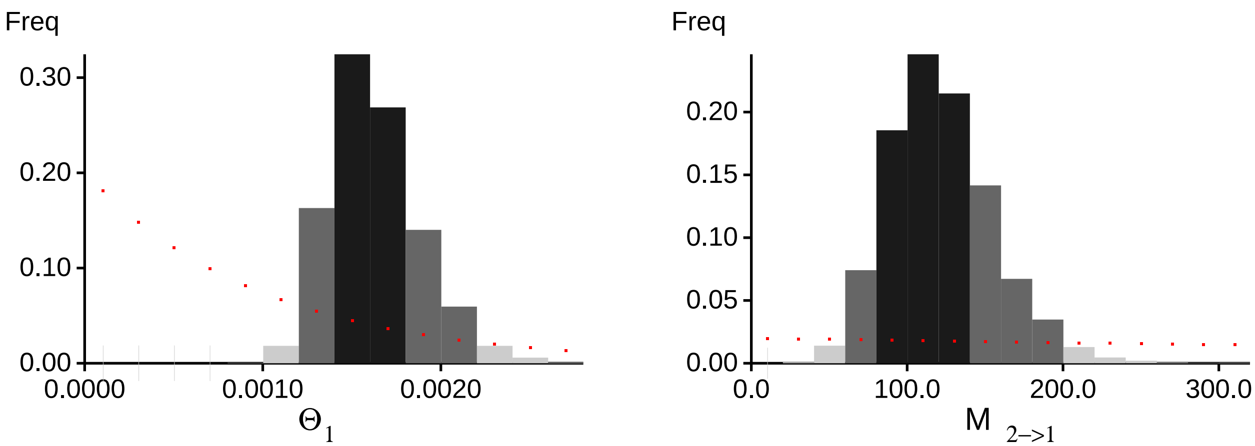


Bayesian Analysis: Posterior distribution for locus 86

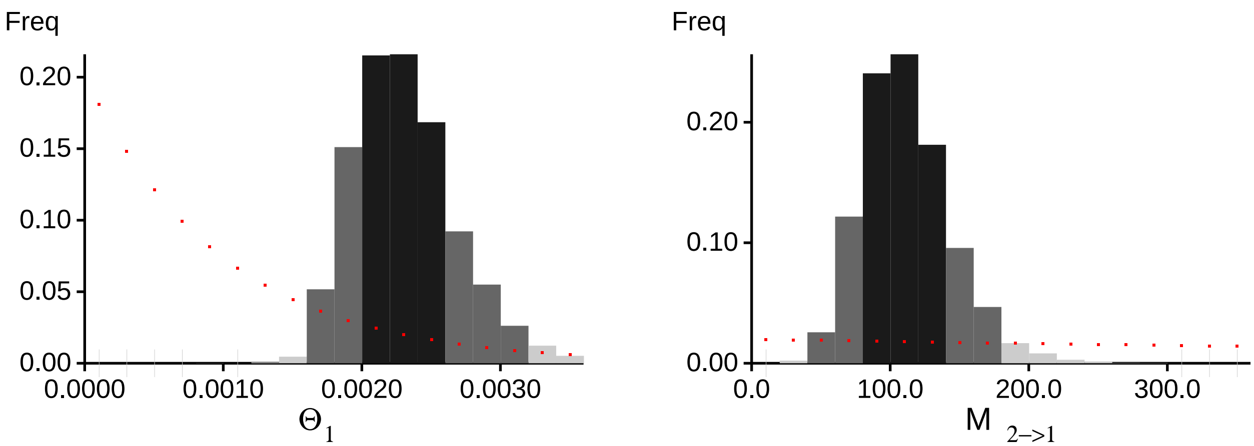




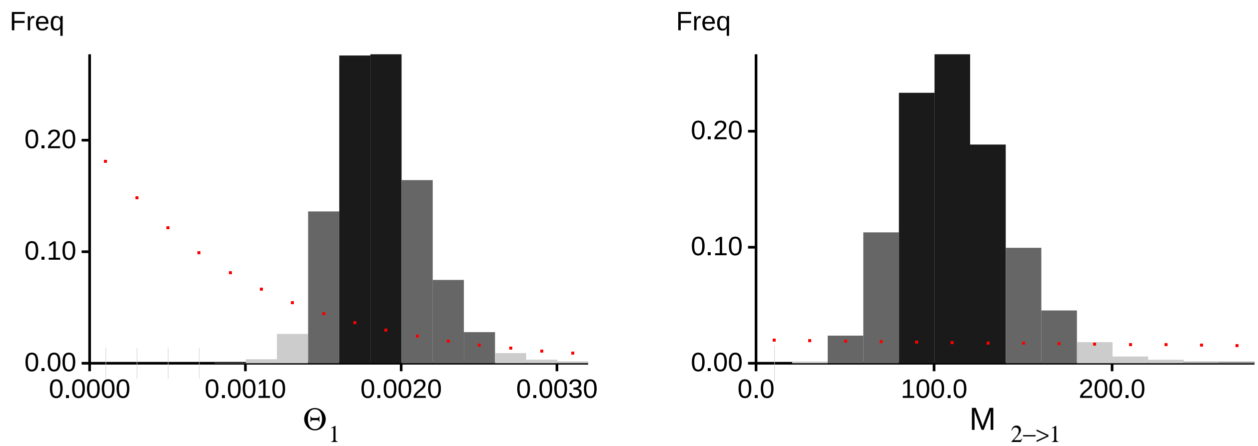
Bayesian Analysis: Posterior distribution for locus 87



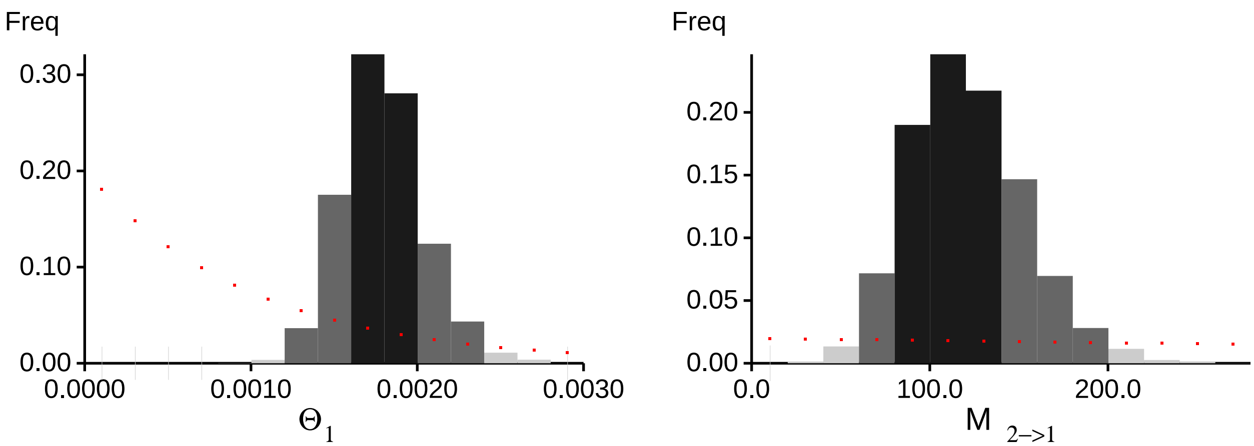
Bayesian Analysis: Posterior distribution for locus 88



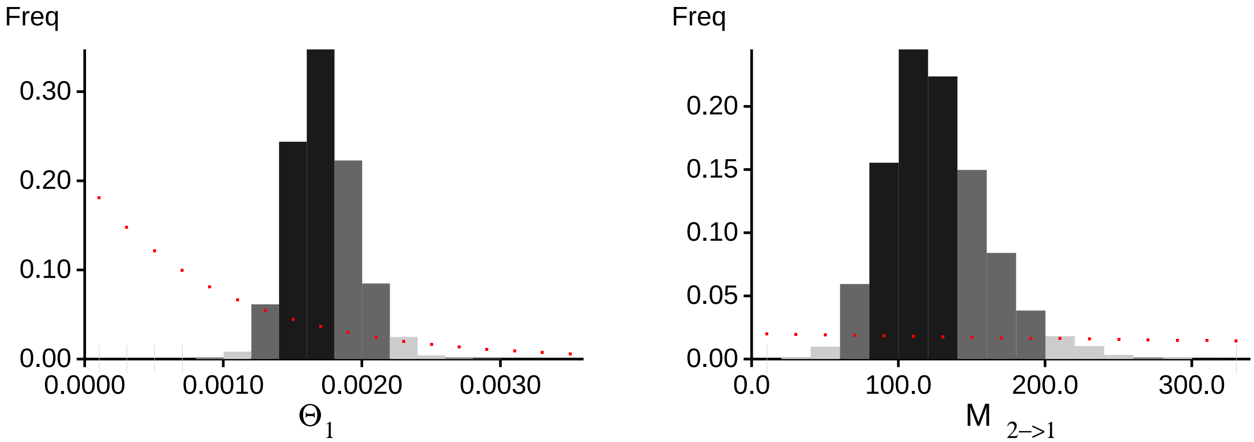
Bayesian Analysis: Posterior distribution for locus 89



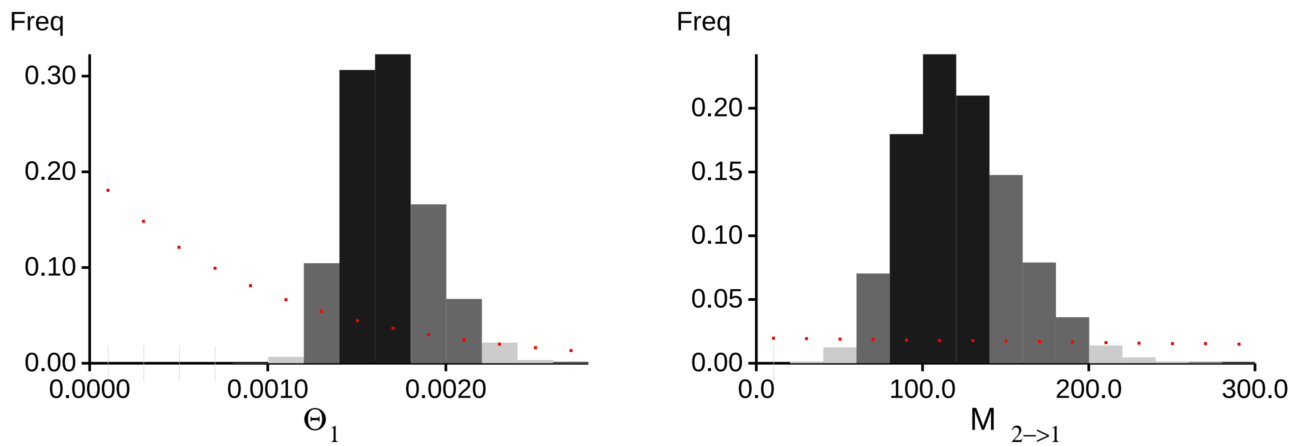
Bayesian Analysis: Posterior distribution for locus 90



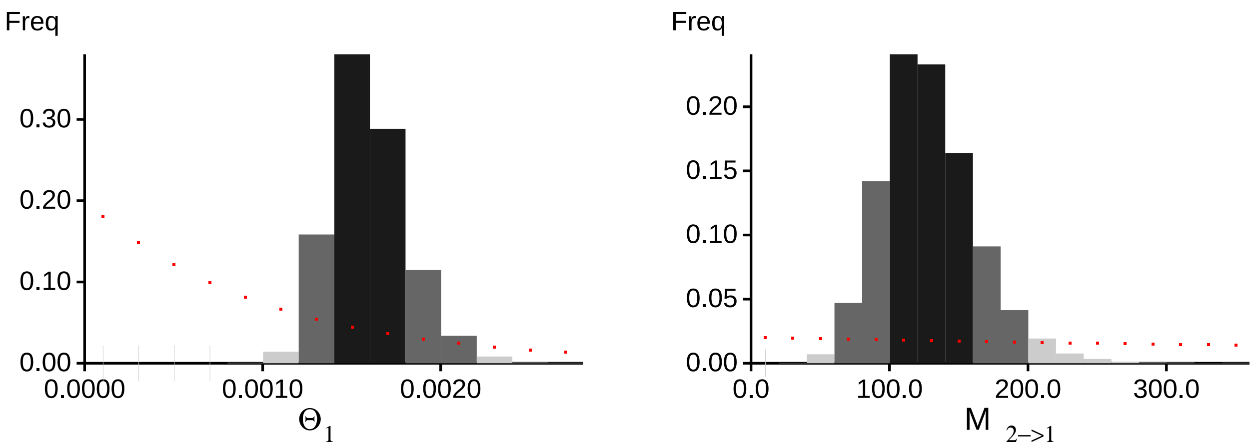
Bayesian Analysis: Posterior distribution for locus 91



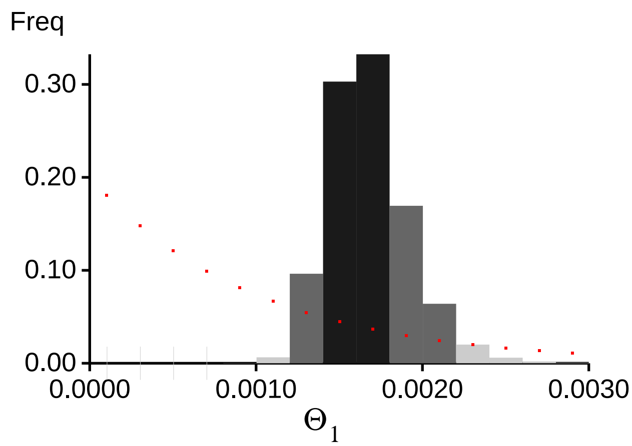
Bayesian Analysis: Posterior distribution for locus 92



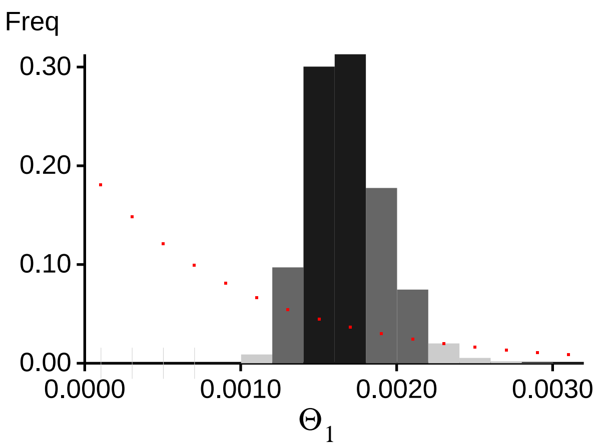
Bayesian Analysis: Posterior distribution for locus 93

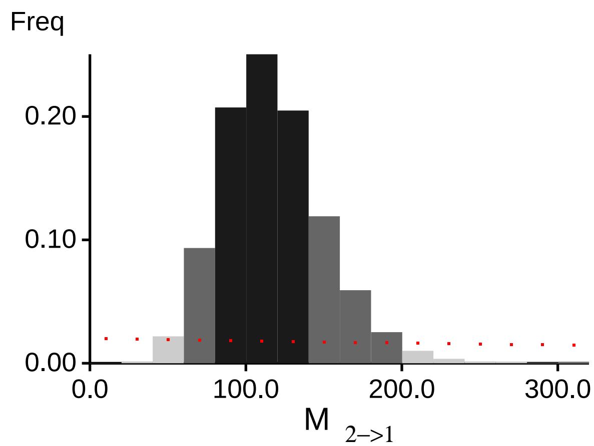


Bayesian Analysis: Posterior distribution for locus 94

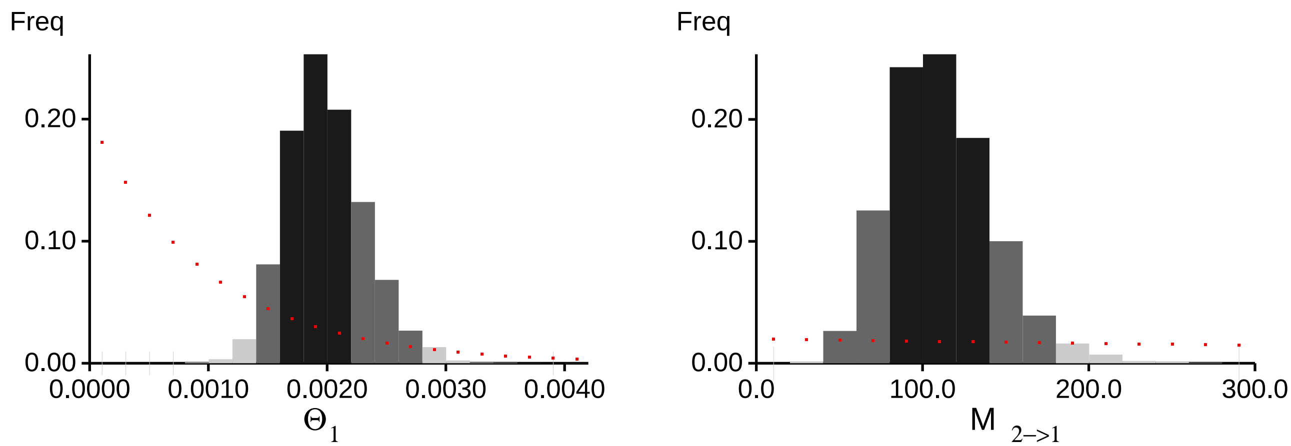


Bayesian Analysis: Posterior distribution for locus 95

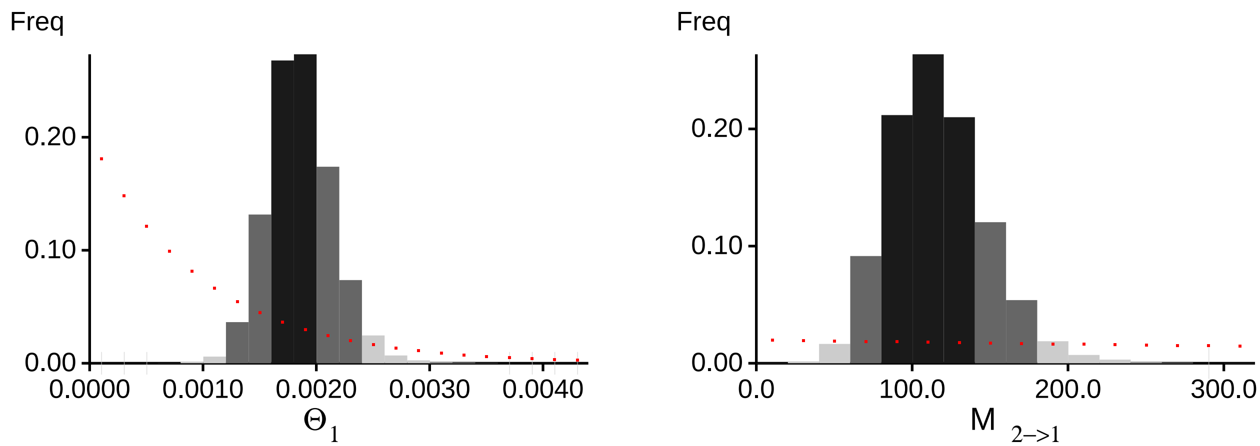




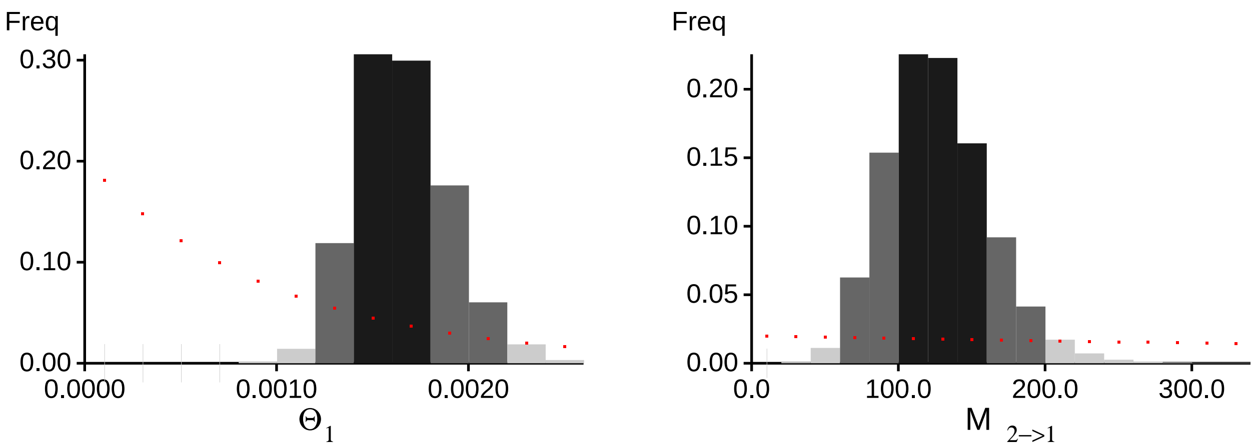
Bayesian Analysis: Posterior distribution for locus 96



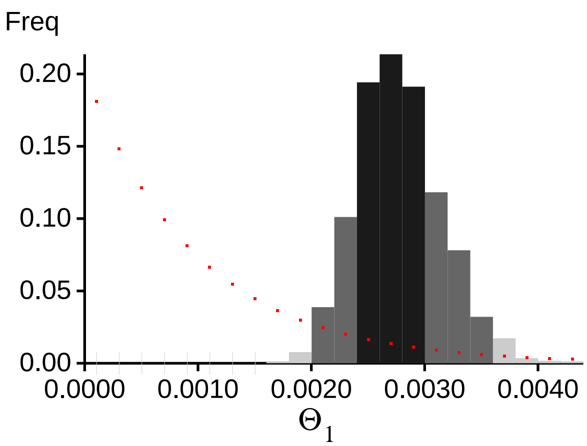
Bayesian Analysis: Posterior distribution for locus 97

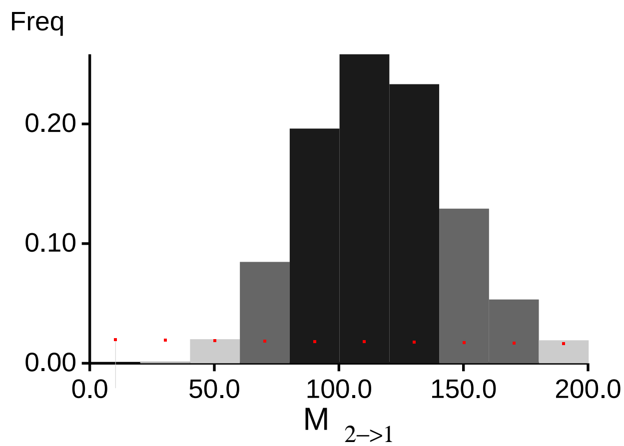


Bayesian Analysis: Posterior distribution for locus 98

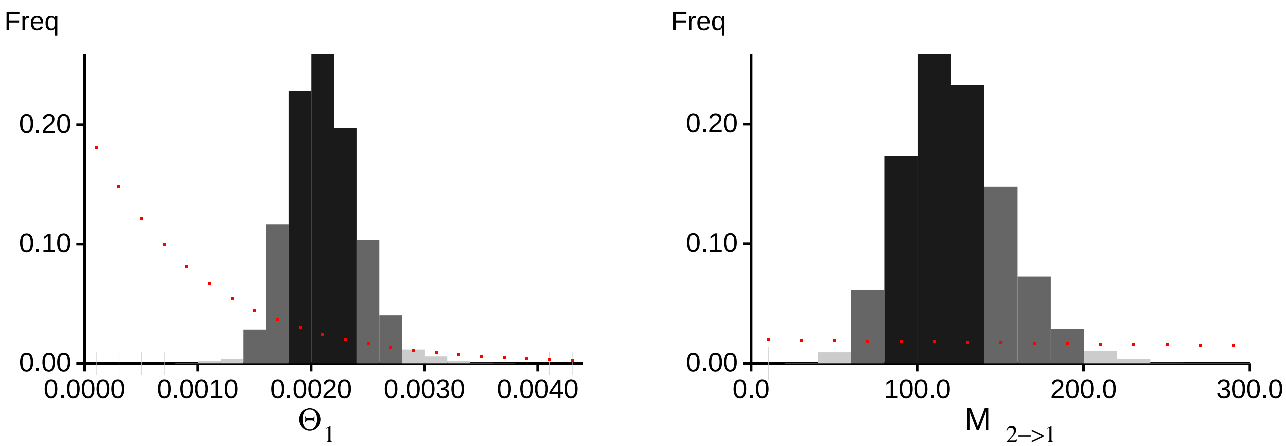


Bayesian Analysis: Posterior distribution for locus 99

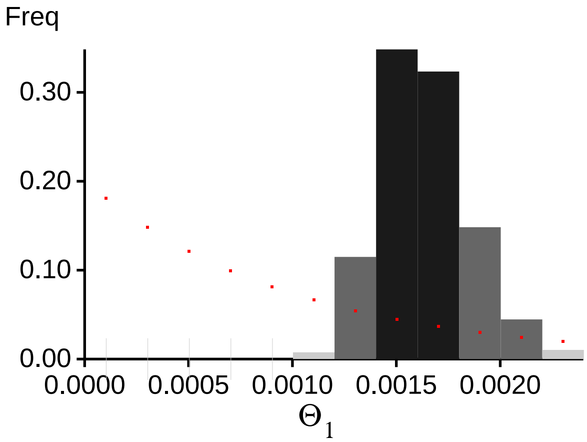


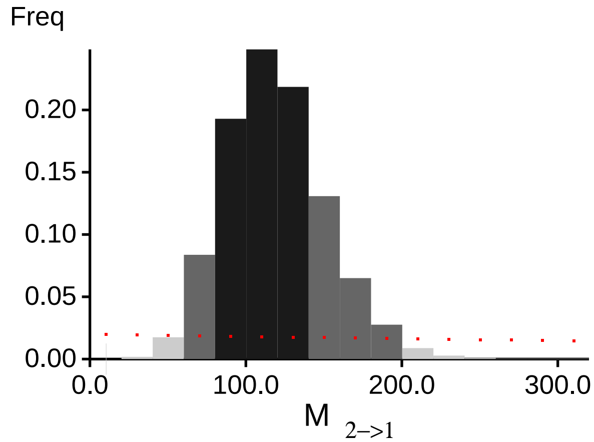


Bayesian Analysis: Posterior distribution for locus 100

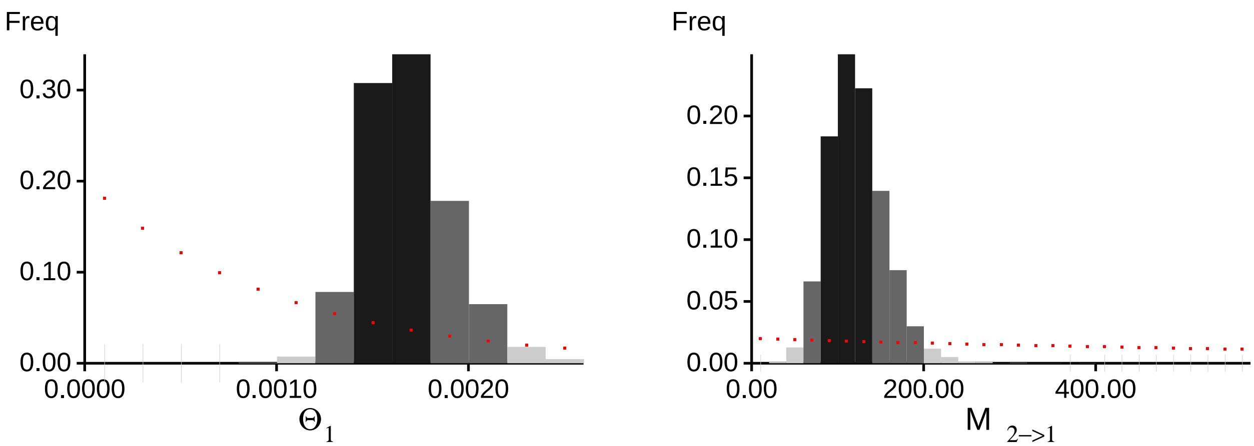


Bayesian Analysis: Posterior distribution for locus 101

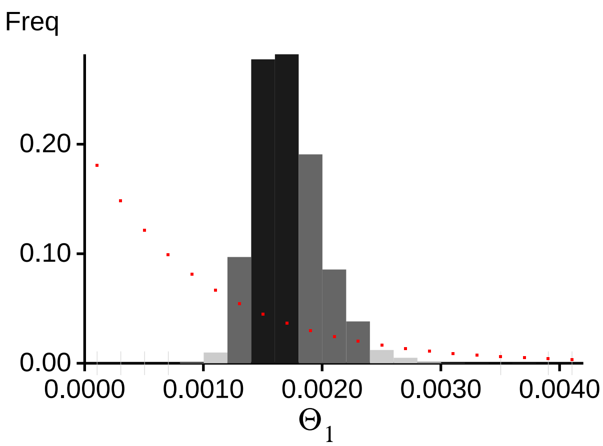


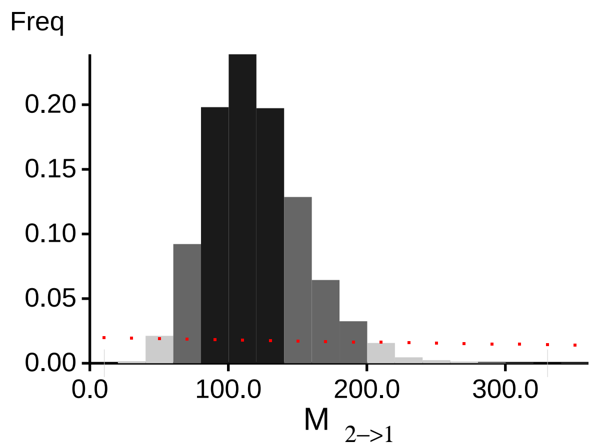


Bayesian Analysis: Posterior distribution for locus 102

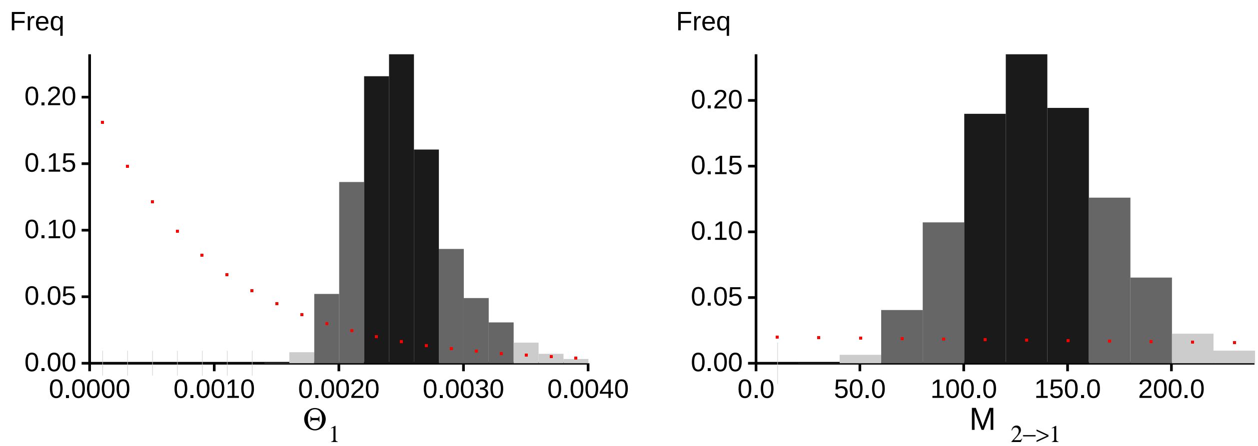


Bayesian Analysis: Posterior distribution for locus 103

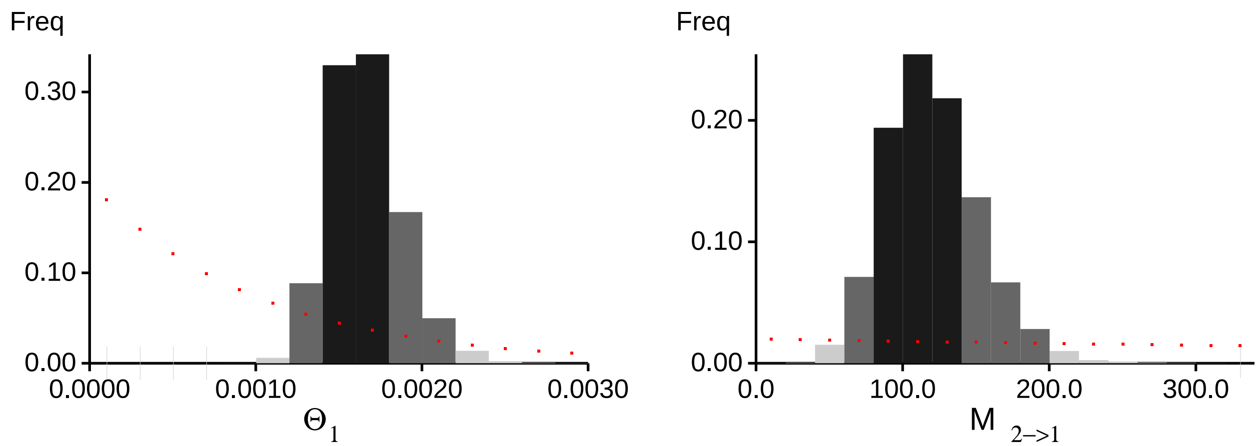




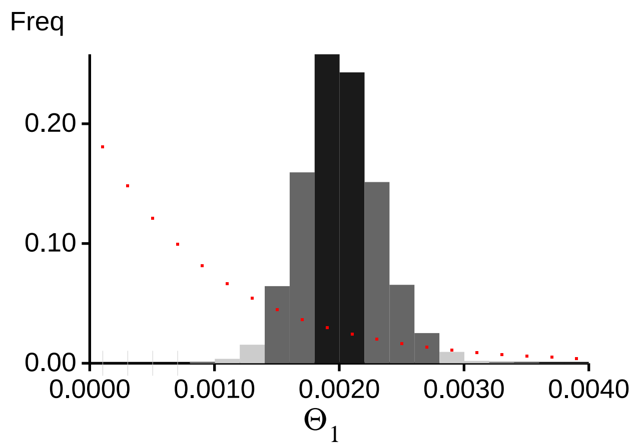
Bayesian Analysis: Posterior distribution for locus 104



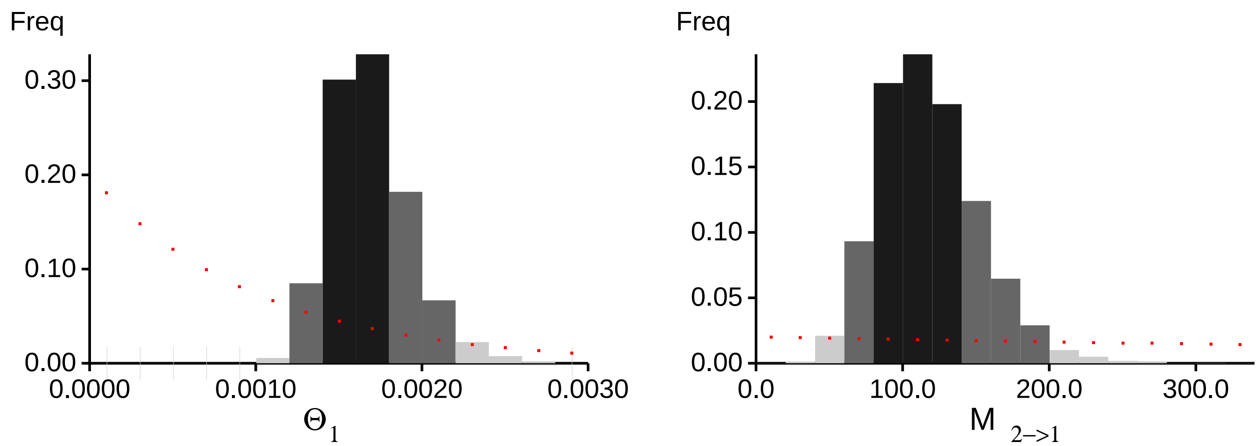
Bayesian Analysis: Posterior distribution for locus 105



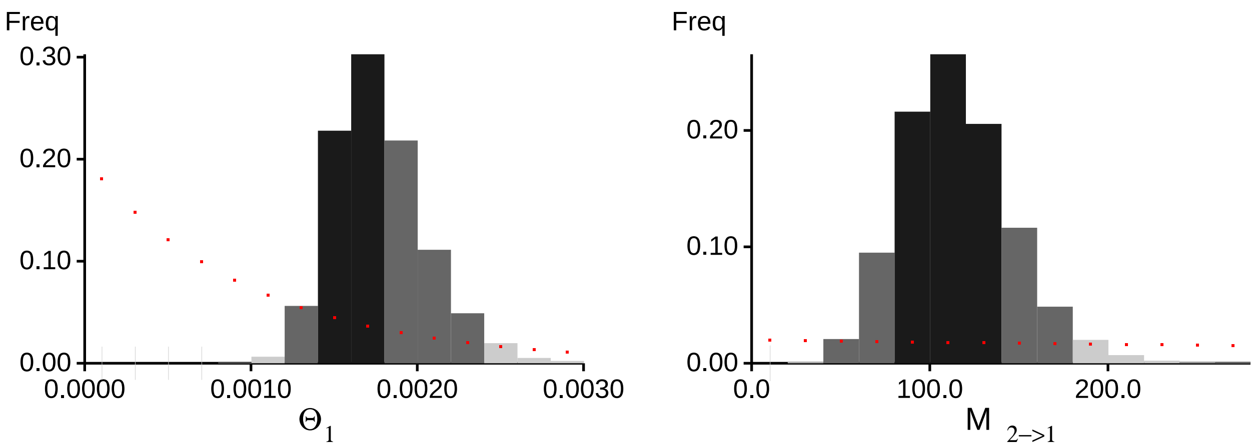
Bayesian Analysis: Posterior distribution for locus 106



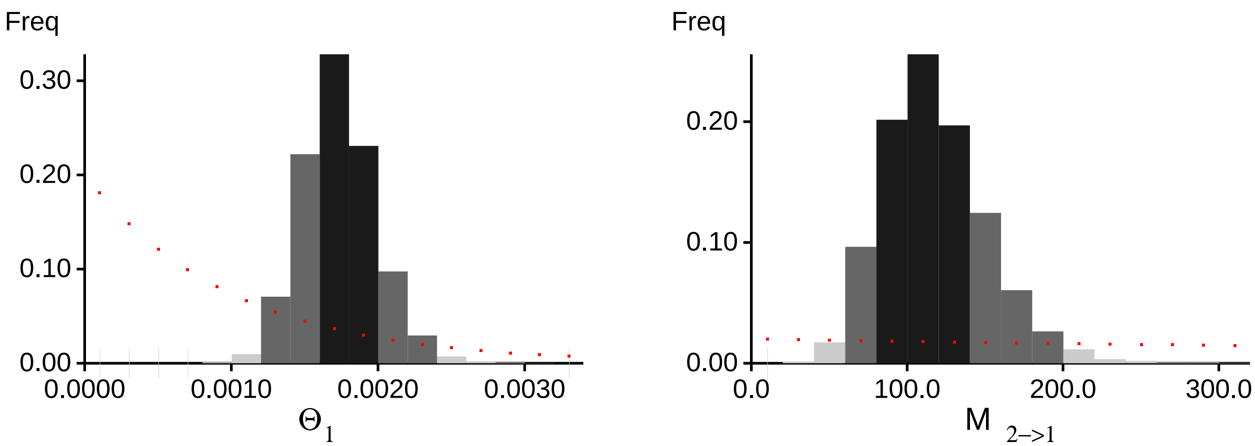
Bayesian Analysis: Posterior distribution for locus 107



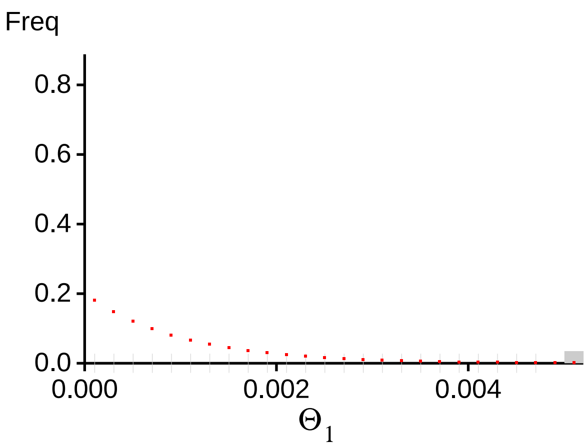
Bayesian Analysis: Posterior distribution for locus 108

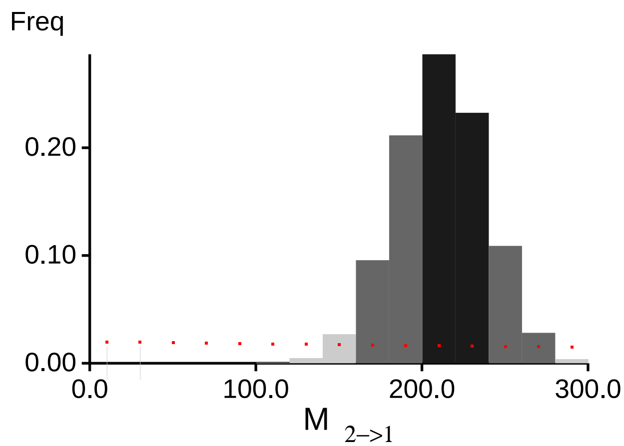


Bayesian Analysis: Posterior distribution for locus 109



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 = Exp[ln(Prob(D | thisModel) - ln(Prob(D | otherModel)
or as LBF = 2 (ln(Prob(D | thisModel) - ln(Prob(D | otherModel))
shows the support for thisModel]

Locus	Raw thermodynamic score(1a)	Bezier approximation score(1b)	Harmonic mean(2)
1	-588.83	-582.94	-593.08
2	-629.22	-622.56	-633.03
3	-709.25	-702.16	-712.75
4	-685.52	-678.64	-689.89
5	-768.62	-760.66	-765.64
6	-731.02	-723.72	-735.84
7	-759.14	-751.15	-758.31
8	-486.99	-482.08	-489.40
9	-904.83	-835.41	-783.21
10	-888.41	-879.55	-894.20
11	-590.97	-585.13	-595.93
12	-589.04	-583.05	-594.95
13	-747.10	-739.37	-750.66
14	-1032.44	-1022.17	-1037.63
15	-700.88	-693.83	-704.62
16	-490.64	-485.60	-492.99
17	-543.23	-537.75	-545.51
18	-499.75	-494.55	-500.80
19	-930.86	-921.61	-936.96
20	-694.61	-687.64	-700.31
21	-682.30	-675.08	-688.21
22	-628.09	-619.66	-623.18
23	-539.93	-534.52	-543.32
24	-1071.83	-1061.10	-1077.55
25	-381.38	-377.58	-383.27
26	-634.90	-624.27	-623.27
27	-743.73	-731.71	-725.76
28	-1061.51	-1050.91	-1069.42
29	-989.29	-979.44	-996.92

30	-538.06	-532.37	-539.28
31	-1030.48	-1020.25	-1035.39
32	-667.33	-660.67	-672.71
33	-554.79	-547.66	-534.19
34	-379.07	-375.26	-381.50
35	-587.63	-581.80	-592.00
36	-508.57	-503.39	-507.62
37	-463.60	-458.90	-464.98
38	-513.92	-504.94	-481.16
39	-964.97	-955.33	-971.67
40	-657.51	-650.90	-661.38
41	-541.62	-536.19	-545.00
42	-745.51	-736.34	-731.44
43	-1111.18	-1100.04	-1118.73
44	-469.50	-464.75	-473.19
45	-773.68	-762.43	-762.02
46	-509.87	-504.78	-513.30
47	-465.78	-461.07	-468.07
48	-710.73	-703.64	-716.36
49	-629.64	-623.35	-635.59
50	-397.86	-393.65	-401.75
51	-487.96	-483.07	-491.45
52	-472.97	-468.27	-477.13
53	-596.52	-589.63	-580.25
54	-707.95	-700.35	-710.31
55	-468.12	-460.86	-455.61
56	-695.65	-688.61	-698.10
57	-405.47	-401.20	-406.83
58	-605.11	-599.02	-609.65
59	-692.63	-685.29	-691.45
60	-534.68	-529.33	-537.83
61	-902.57	-893.50	-908.68
62	-712.38	-705.13	-716.07
63	-1066.73	-1037.31	-953.19
64	-479.02	-473.94	-482.86
65	-959.94	-950.08	-965.94
66	-1109.96	-1098.92	-1119.00
67	-658.66	-652.08	-663.01
68	-761.70	-754.12	-765.99
69	-571.71	-566.02	-575.13
70	-771.92	-763.44	-775.69
71	-538.77	-532.20	-536.08
72	-751.97	-741.94	-720.35
73	-405.78	-399.35	-382.83
74	-738.24	-730.72	-741.09

75	-578.47	-572.70	-582.77
76	-484.08	-479.00	-483.77
77	-661.39	-654.82	-665.33
78	-490.94	-486.03	-496.07
79	-616.49	-610.34	-619.83
80	-653.37	-646.67	-657.57
81	-657.09	-649.73	-636.76
82	-615.91	-609.27	-615.73
83	-695.05	-688.07	-700.20
84	-765.96	-758.08	-766.67
85	-732.97	-723.72	-725.06
86	-916.21	-907.11	-924.07
87	-606.88	-600.82	-612.09
88	-687.13	-679.26	-686.17
89	-284.07	-281.15	-284.96
90	-1026.81	-1016.54	-1034.61
91	-898.42	-889.42	-904.20
92	-732.13	-724.81	-737.60
93	-696.76	-689.84	-702.26
94	-727.60	-720.33	-732.21
95	-427.81	-423.56	-432.12
96	-600.91	-594.60	-603.45
97	-521.53	-516.05	-523.54
98	-835.31	-826.90	-838.91
99	-523.61	-513.96	-499.92
100	-688.74	-681.51	-691.18
101	-835.36	-827.06	-841.63
102	-478.30	-473.49	-479.97
103	-537.59	-532.20	-541.77
104	-828.59	-818.66	-814.10
105	-522.70	-517.50	-525.00
106	-484.39	-479.29	-487.67
107	-566.46	-560.83	-569.96
108	-455.69	-451.12	-459.09
109	-519.86	-514.56	-522.57
All	-71971.81	-71120.19	-71812.53

(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 = 404.751246]
Citation suggestions:

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	1361883/18164269	0.07498
Θ_2	1361883/18164269	0.07498
Θ_3	1361883/18164269	0.07498
Θ_4	1361883/18164269	0.07498
Θ_5	1361883/18164269	0.07498
Θ_6	1361883/18164269	0.07498
Θ_7	1361883/18164269	0.07498
Θ_8	1361883/18164269	0.07498
Θ_9	1361883/18164269	0.07498
Θ_{10}	1361883/18164269	0.07498
$M_{2->1}$	18166221/18166221	1.00000
$M_{3->1}$	18166221/18166221	1.00000
$M_{4->1}$	18166221/18166221	1.00000
$M_{5->1}$	18166221/18166221	1.00000
$M_{6->1}$	18166221/18166221	1.00000
$M_{7->1}$	18166221/18166221	1.00000
$M_{8->1}$	18166221/18166221	1.00000
$M_{9->1}$	18166221/18166221	1.00000
$M_{10->1}$	18166221/18166221	1.00000
$M_{1->2}$	18166221/18166221	1.00000
$M_{3->2}$	18166221/18166221	1.00000
$M_{4->2}$	18166221/18166221	1.00000
$M_{5->2}$	18166221/18166221	1.00000
$M_{6->2}$	18166221/18166221	1.00000
$M_{7->2}$	18166221/18166221	1.00000
$M_{8->2}$	18166221/18166221	1.00000
$M_{9->2}$	18166221/18166221	1.00000
$M_{10->2}$	18166221/18166221	1.00000
$M_{1->3}$	18166221/18166221	1.00000
$M_{2->3}$	18166221/18166221	1.00000
$M_{4->3}$	18166221/18166221	1.00000
$M_{5->3}$	18166221/18166221	1.00000
$M_{6->3}$	18166221/18166221	1.00000
$M_{7->3}$	18166221/18166221	1.00000
$M_{8->3}$	18166221/18166221	1.00000
$M_{9->3}$	18166221/18166221	1.00000
$M_{10->3}$	18166221/18166221	1.00000

$M_{1->4}$	18166221/18166221	1.00000
$M_{2->4}$	18166221/18166221	1.00000
$M_{3->4}$	18166221/18166221	1.00000
$M_{5->4}$	18166221/18166221	1.00000
$M_{6->4}$	18166221/18166221	1.00000
$M_{7->4}$	18166221/18166221	1.00000
$M_{8->4}$	18166221/18166221	1.00000
$M_{9->4}$	18166221/18166221	1.00000
$M_{10->4}$	18166221/18166221	1.00000
$M_{1->5}$	18166221/18166221	1.00000
$M_{2->5}$	18166221/18166221	1.00000
$M_{3->5}$	18166221/18166221	1.00000
$M_{4->5}$	18166221/18166221	1.00000
$M_{6->5}$	18166221/18166221	1.00000
$M_{7->5}$	18166221/18166221	1.00000
$M_{8->5}$	18166221/18166221	1.00000
$M_{9->5}$	18166221/18166221	1.00000
$M_{10->5}$	18166221/18166221	1.00000
$M_{1->6}$	18166221/18166221	1.00000
$M_{2->6}$	18166221/18166221	1.00000
$M_{3->6}$	18166221/18166221	1.00000
$M_{4->6}$	18166221/18166221	1.00000
$M_{5->6}$	18166221/18166221	1.00000
$M_{7->6}$	18166221/18166221	1.00000
$M_{8->6}$	18166221/18166221	1.00000
$M_{9->6}$	18166221/18166221	1.00000
$M_{10->6}$	18166221/18166221	1.00000
$M_{1->7}$	18166221/18166221	1.00000
$M_{2->7}$	18166221/18166221	1.00000
$M_{3->7}$	18166221/18166221	1.00000
$M_{4->7}$	18166221/18166221	1.00000
$M_{5->7}$	18166221/18166221	1.00000
$M_{6->7}$	18166221/18166221	1.00000
$M_{8->7}$	18166221/18166221	1.00000
$M_{9->7}$	18166221/18166221	1.00000
$M_{10->7}$	18166221/18166221	1.00000
$M_{1->8}$	18166221/18166221	1.00000
$M_{2->8}$	18166221/18166221	1.00000
$M_{3->8}$	18166221/18166221	1.00000
$M_{4->8}$	18166221/18166221	1.00000
$M_{5->8}$	18166221/18166221	1.00000
$M_{6->8}$	18166221/18166221	1.00000
$M_{7->8}$	18166221/18166221	1.00000
$M_{9->8}$	18166221/18166221	1.00000
$M_{10->8}$	18166221/18166221	1.00000

$M_{1\to 9}$	18166221/18166221	1.00000
$M_{2\to 9}$	18166221/18166221	1.00000
$M_{3\to 9}$	18166221/18166221	1.00000
$M_{4\to 9}$	18166221/18166221	1.00000
$M_{5\to 9}$	18166221/18166221	1.00000
$M_{6\to 9}$	18166221/18166221	1.00000
$M_{7\to 9}$	18166221/18166221	1.00000
$M_{8\to 9}$	18166221/18166221	1.00000
$M_{10\to 9}$	18166221/18166221	1.00000
$M_{1\to 10}$	18166221/18166221	1.00000
$M_{2\to 10}$	18166221/18166221	1.00000
$M_{3\to 10}$	18166221/18166221	1.00000
$M_{4\to 10}$	18166221/18166221	1.00000
$M_{5\to 10}$	18166221/18166221	1.00000
$M_{6\to 10}$	18166221/18166221	1.00000
$M_{7\to 10}$	18166221/18166221	1.00000
$M_{8\to 10}$	18166221/18166221	1.00000
$M_{9\to 10}$	18166221/18166221	1.00000
Genealogies	28707420/36334671	0.79008

MCMC-Autocorrelation and Effective MCMC Sample Size

Parameter	Autocorrelation	Effective Sampe Size
Θ_1	0.94292	116382.37
Θ_2	0.94292	116382.37
Θ_3	0.94292	116382.37
Θ_4	0.94292	116382.37
Θ_5	0.94292	116382.37
Θ_6	0.94292	116382.37
Θ_7	0.94292	116382.37
Θ_8	0.94292	116382.37
Θ_9	0.94292	116382.37
Θ_{10}	0.94292	116382.37
$M_{2\rightarrow1}$	0.99163	16532.69
$M_{3\rightarrow1}$	0.99163	16532.69
$M_{4\rightarrow1}$	0.99163	16532.69
$M_{5\rightarrow1}$	0.99163	16532.69
$M_{6\rightarrow1}$	0.99163	16532.69
$M_{7\rightarrow1}$	0.99163	16532.69
$M_{8\rightarrow1}$	0.99163	16532.69
$M_{9\rightarrow1}$	0.99163	16532.69
$M_{10\rightarrow1}$	0.99163	16532.69
$M_{1\rightarrow2}$	0.99163	16532.69
$M_{3\rightarrow2}$	0.99163	16532.69
$M_{4\rightarrow2}$	0.99163	16532.69
$M_{5\rightarrow2}$	0.99163	16532.69
$M_{6\rightarrow2}$	0.99163	16532.69
$M_{7\rightarrow2}$	0.99163	16532.69
$M_{8\rightarrow2}$	0.99163	16532.69
$M_{9\rightarrow2}$	0.99163	16532.69
$M_{10\rightarrow2}$	0.99163	16532.69
$M_{1\rightarrow3}$	0.99163	16532.69
$M_{2\rightarrow3}$	0.99163	16532.69
$M_{4\rightarrow3}$	0.99163	16532.69
$M_{5\rightarrow3}$	0.99163	16532.69
$M_{6\rightarrow3}$	0.99163	16532.69
$M_{7\rightarrow3}$	0.99163	16532.69
$M_{8\rightarrow3}$	0.99163	16532.69
$M_{9\rightarrow3}$	0.99163	16532.69
$M_{10\rightarrow3}$	0.99163	16532.69

$M_{1->4}$	0.99163	16532.69
$M_{2->4}$	0.99163	16532.69
$M_{3->4}$	0.99163	16532.69
$M_{5->4}$	0.99163	16532.69
$M_{6->4}$	0.99163	16532.69
$M_{7->4}$	0.99163	16532.69
$M_{8->4}$	0.99163	16532.69
$M_{9->4}$	0.99163	16532.69
$M_{10->4}$	0.99163	16532.69
$M_{1->5}$	0.99163	16532.69
$M_{2->5}$	0.99163	16532.69
$M_{3->5}$	0.99163	16532.69
$M_{4->5}$	0.99163	16532.69
$M_{6->5}$	0.99163	16532.69
$M_{7->5}$	0.99163	16532.69
$M_{8->5}$	0.99163	16532.69
$M_{9->5}$	0.99163	16532.69
$M_{10->5}$	0.99163	16532.69
$M_{1->6}$	0.99163	16532.69
$M_{2->6}$	0.99163	16532.69
$M_{3->6}$	0.99163	16532.69
$M_{4->6}$	0.99163	16532.69
$M_{5->6}$	0.99163	16532.69
$M_{7->6}$	0.99163	16532.69
$M_{8->6}$	0.99163	16532.69
$M_{9->6}$	0.99163	16532.69
$M_{10->6}$	0.99163	16532.69
$M_{1->7}$	0.99163	16532.69
$M_{2->7}$	0.99163	16532.69
$M_{3->7}$	0.99163	16532.69
$M_{4->7}$	0.99163	16532.69
$M_{5->7}$	0.99163	16532.69
$M_{6->7}$	0.99163	16532.69
$M_{8->7}$	0.99163	16532.69
$M_{9->7}$	0.99163	16532.69
$M_{10->7}$	0.99163	16532.69
$M_{1->8}$	0.99163	16532.69
$M_{2->8}$	0.99163	16532.69
$M_{3->8}$	0.99163	16532.69
$M_{4->8}$	0.99163	16532.69
$M_{5->8}$	0.99163	16532.69
$M_{6->8}$	0.99163	16532.69
$M_{7->8}$	0.99163	16532.69
$M_{9->8}$	0.99163	16532.69
$M_{10->8}$	0.99163	16532.69

$M_{1->9}$	0.99163	16532.69
$M_{2->9}$	0.99163	16532.69
$M_{3->9}$	0.99163	16532.69
$M_{4->9}$	0.99163	16532.69
$M_{5->9}$	0.99163	16532.69
$M_{6->9}$	0.99163	16532.69
$M_{7->9}$	0.99163	16532.69
$M_{8->9}$	0.99163	16532.69
$M_{10->9}$	0.99163	16532.69
$M_{1->10}$	0.99163	16532.69
$M_{2->10}$	0.99163	16532.69
$M_{3->10}$	0.99163	16532.69
$M_{4->10}$	0.99163	16532.69
$M_{5->10}$	0.99163	16532.69
$M_{6->10}$	0.99163	16532.69
$M_{7->10}$	0.99163	16532.69
$M_{8->10}$	0.99163	16532.69
$M_{9->10}$	0.99163	16532.69
Genealogies	0.83091	383296.47

Potential Problems

This section reports potential problems with your run, but such reporting is often not very accurate. Whith many parameters in a multilocus analysi s, it is very common that some parameters for some loci will not be very informative, triggering suggestions (for example to increase the prior ran ge) that are not sensible. This suggestion tool will improve with time, therefore do not blindly follow its suggestions. If some parameters are fla gged, inspect the tables carefully and judge wether an action is required. For example, if you run a Bayesian inference with sequence data, for mac roscopic species there is rarely the need to increase the prior for Theta beyond 0.1; but if you use microsatellites it is rather common that your prior distribution for Theta should have a range from 0.0 to 100 or more. With many populations (>3) it is also very common that some migration rou tes are estimated poorly because the data contains little or no information for that route. Increasing the range will not help in such situations, reducing number of parameters may help in such situations.

No warning was recorded during the run