

Translated from VCF 2020-07-20

POPULATION SIZE, MIGRATION, DIVERGENCE, ASSIGNMENT, HISTORY

Bayesian inference using the structured coalescent

Migrate-n version 4.5.1(git:4.5-2-g6c1d014-dirty) [July-4-2020]

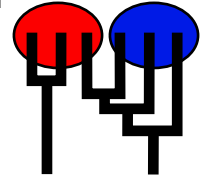
Compiled for PARALLEL computer architectures

One master and 8 compute nodes are available.

Compiled for a SYMMETRIC multiprocessors (Grandcentral)

Program started at Fri Jul 24 14:23:40 2020

Program finished at Fri Jul 24 14:38:46 2020 [Runtime:0000:00:15:06]



Options

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) 1184853818

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
1 Pop1	*	*
2 Pop2	*	*

Order of parameters:

1 Θ_1 <displayed>

2 Θ_2 <displayed>

3 M $2 \rightarrow 1$ <displayed>
 4 M $1 \rightarrow 2$ <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	Metropolis sampling
Divergence	Metropolis sampling
Divergence Spread	Metropolis sampling
Genealogy	Metropolis-Hastings

Prior distribution for parameter

Parameter	Prior	Minimum	Mean	Maximum	Delta	Bins	UpdateFreq
1 Theta **	Gamma	0.000000	0.010	0.100	0.010	1500	0.12500
2 Theta **	Gamma	0.000000	0.010	0.100	0.010	1500	0.12500
3 M **	Gamma	0.000000	500.0	10000	1000.	1500	0.12500
4 M **	Gamma	0.000000	500.0	10000	1000.	1500	0.12500

[* * means priors were set globally]

Posterior distribution:

Parameter values were collected using MCMC, these values

were then used to generate the posterior histograms using KERNEL SMOOTHING (window=41)

and subsequent MOVING AVERAGE SMOOTHING (window=11) for combination over loci

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)

1000

Multiple Markov chains:

Static heating scheme

4 chains with temperatures

1000000.00

3.00

1.50

1.00

Swapping interval is 1

Print options:

Data file:	infile
	parmfile
Haplotyping is turned on:	NO
Output file:	outfile
Posterior distribution raw histogram file:	bayesfile
Raw data from the MCMC run:	bayesallfile.gz
Print data:	No
Print genealogies [only some for some data type]:	None

Data summary

Data file: infile
 Datatype: Haplotype data
 Number of loci: 20

Mutationmodel:

Locus	Sublocus	Mutationmodel	Mutationmodel parameters
1	1	Felsenstein 84	[Bf:0.95 0.00 0.00 0.05, t/t ratio=2.000]
2	1	Felsenstein 84	[Bf:0.95 0.00 0.00 0.05, t/t ratio=2.000]
3	1	Felsenstein 84	[Bf:0.95 0.00 0.00 0.05, t/t ratio=2.000]
4	1	Felsenstein 84	[Bf:0.95 0.00 0.00 0.05, t/t ratio=2.000]
5	1	Felsenstein 84	[Bf:0.95 0.00 0.00 0.05, t/t ratio=2.000]
6	1	Felsenstein 84	[Bf:0.95 0.00 0.00 0.05, t/t ratio=2.000]
7	1	Felsenstein 84	[Bf:0.95 0.00 0.00 0.05, t/t ratio=2.000]
8	1	Felsenstein 84	[Bf:0.95 0.00 0.00 0.05, t/t ratio=2.000]
9	1	Felsenstein 84	[Bf:0.95 0.00 0.00 0.05, t/t ratio=2.000]
10	1	Felsenstein 84	[Bf:0.95 0.00 0.00 0.05, t/t ratio=2.000]
11	1	Felsenstein 84	[Bf:0.95 0.00 0.00 0.05, t/t ratio=2.000]
12	1	Felsenstein 84	[Bf:0.95 0.00 0.00 0.05, t/t ratio=2.000]
13	1	Felsenstein 84	[Bf:0.95 0.00 0.00 0.05, t/t ratio=2.000]
14	1	Felsenstein 84	[Bf:0.95 0.00 0.00 0.05, t/t ratio=2.000]
15	1	Felsenstein 84	[Bf:0.95 0.00 0.00 0.05, t/t ratio=2.000]
16	1	Felsenstein 84	[Bf:0.95 0.00 0.00 0.05, t/t ratio=2.000]
17	1	Felsenstein 84	[Bf:0.95 0.00 0.00 0.05, t/t ratio=2.000]
18	1	Felsenstein 84	[Bf:0.94 0.00 0.00 0.06, t/t ratio=2.000]
19	1	Felsenstein 84	[Bf:0.95 0.00 0.00 0.05, t/t ratio=2.000]
20	1	Felsenstein 84	[Bf:0.95 0.00 0.00 0.05, t/t ratio=2.000]

Sites per locus

Locus	Sites
1	10000
2	10000
3	10000
4	10000
5	10000
6	10000
7	10000
8	10000
9	10000
10	10000

11	10000
12	10000
13	10000
14	10000
15	10000
16	10000
17	10000
18	10000
19	10000
20	10000

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

Population

Locus

Gene copies

data

(missing)

1 Pop1

1	10
2	10
3	10
4	10
5	10
6	10
7	10
8	10
9	10

2 Pop2	10	10	
	11	10	
	12	10	
	13	10	
	14	10	
	15	10	
	16	10	
	17	10	
	18	10	
	19	10	
	20	10	
	1	10	
	2	10	
	3	10	
	4	10	
	5	10	
	6	10	
	7	10	
	8	10	
	9	10	
	10	10	
	11	10	
	12	10	
	13	10	
	14	10	
	15	10	
	16	10	
	17	10	
	18	10	
	19	10	
	20	10	
Total of all populations	1	20	(0)
	2	20	(0)
	3	20	(0)
	4	20	(0)
	5	20	(0)
	6	20	(0)
	7	20	(0)
	8	20	(0)
	9	20	(0)
	10	20	(0)
	11	20	(0)
	12	20	(0)
	13	20	(0)
	14	20	(0)

15	20	(0)
16	20	(0)
17	20	(0)
18	20	(0)
19	20	(0)
20	20	(0)

Bayesian Analysis: Posterior distribution table

Locus	Parameter	2.5%	25.0%	Mode	75.0%	97.5%	Median	Mean
1	Θ_1	0.00447	0.00847	0.01137	0.01480	0.02420	0.01283	0.01436
1	Θ_2	0.00867	0.01180	0.01497	0.01793	0.02340	0.01610	0.00880
1	$M_{2 \rightarrow 1}$	0.000	60.000	123.333	180.000	326.667	150.000	37.818
1	$M_{1 \rightarrow 2}$	0.000	26.667	56.667	93.333	146.667	76.667	5.401
2	Θ_1	0.00093	0.00373	0.00530	0.00727	0.01133	0.00583	0.00679
2	Θ_2	0.00360	0.00820	0.00883	0.00987	0.01827	0.01023	0.00575
2	$M_{2 \rightarrow 1}$	0.000	33.333	76.667	120.000	226.667	103.333	17.539
2	$M_{1 \rightarrow 2}$	0.000	60.000	116.667	166.667	286.667	136.667	24.043
3	Θ_1	0.00393	0.00753	0.01030	0.01293	0.02113	0.01123	0.01260
3	Θ_2	0.01000	0.01433	0.01823	0.02213	0.03240	0.01970	0.01069
3	$M_{2 \rightarrow 1}$	0.000	53.333	96.667	140.000	220.000	110.000	20.511
3	$M_{1 \rightarrow 2}$	0.000	26.667	56.667	93.333	153.333	76.667	5.799
4	Θ_1	0.01167	0.01793	0.02157	0.02627	0.03947	0.02363	0.02541
4	Θ_2	0.00907	0.01633	0.01717	0.01747	0.02953	0.01857	0.01012
4	$M_{2 \rightarrow 1}$	0.000	20.000	50.000	86.667	140.000	70.000	5.161
4	$M_{1 \rightarrow 2}$	0.000	53.333	96.667	133.333	220.000	110.000	14.953
5	Θ_1	0.01187	0.01713	0.02077	0.02553	0.03420	0.02243	0.02405
5	Θ_2	0.01327	0.01807	0.02417	0.03207	0.04207	0.02650	0.01450
5	$M_{2 \rightarrow 1}$	0.000	33.333	70.000	106.667	173.333	90.000	11.226
5	$M_{1 \rightarrow 2}$	13.333	73.333	123.333	166.667	266.667	136.667	22.186
6	Θ_1	0.00740	0.01173	0.01437	0.01853	0.02833	0.01643	0.01794
6	Θ_2	0.00513	0.01033	0.01257	0.01633	0.02867	0.01450	0.00801
6	$M_{2 \rightarrow 1}$	0.000	20.000	56.667	86.667	146.667	76.667	6.359
6	$M_{1 \rightarrow 2}$	0.000	53.333	103.333	140.000	233.333	116.667	16.884
7	Θ_1	0.00460	0.00700	0.00970	0.01207	0.01633	0.01037	0.01171
7	Θ_2	0.00827	0.01420	0.01477	0.01687	0.02873	0.01723	0.00947
7	$M_{2 \rightarrow 1}$	0.000	33.333	70.000	106.667	173.333	83.333	10.761
7	$M_{1 \rightarrow 2}$	0.000	46.667	83.333	126.667	200.000	103.333	12.334
8	Θ_1	0.00560	0.00980	0.01017	0.01040	0.01700	0.01150	0.01293

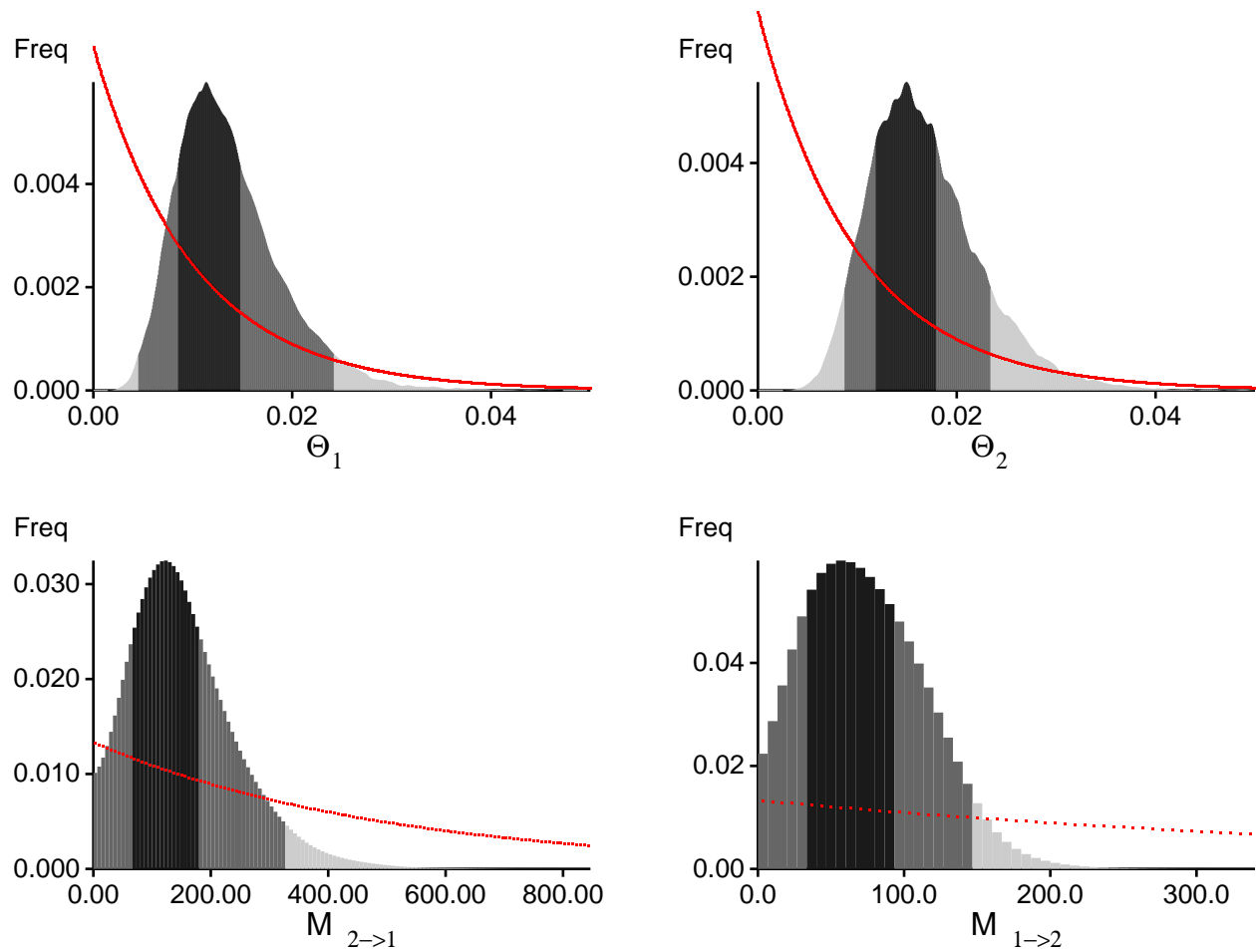
Locus	Parameter	2.5%	25.0%	Mode	75.0%	97.5%	Median	Mean
8	Θ_2	0.00747	0.01253	0.01550	0.02000	0.03180	0.01750	0.00954
8	$M_{2 \rightarrow 1}$	0.000	26.667	63.333	93.333	153.333	76.667	8.122
8	$M_{1 \rightarrow 2}$	0.000	46.667	83.333	120.000	193.333	103.333	11.646
9	Θ_1	0.00787	0.00993	0.01470	0.02373	0.02873	0.01710	0.01864
9	Θ_2	0.01353	0.01380	0.02430	0.03967	0.04073	0.02557	0.01373
9	$M_{2 \rightarrow 1}$	0.000	26.667	56.667	93.333	153.333	76.667	7.419
9	$M_{1 \rightarrow 2}$	0.000	40.000	83.333	120.000	200.000	103.333	12.287
10	Θ_1	0.00227	0.00513	0.00770	0.00940	0.01473	0.00790	0.00910
10	Θ_2	0.00413	0.00773	0.01010	0.01280	0.02000	0.01097	0.00615
10	$M_{2 \rightarrow 1}$	0.000	60.000	116.667	166.667	286.667	136.667	30.984
10	$M_{1 \rightarrow 2}$	0.000	33.333	70.000	113.333	193.333	90.000	10.009
11	Θ_1	0.00467	0.00873	0.00997	0.01193	0.01907	0.01143	0.01284
11	Θ_2	0.01220	0.01800	0.02223	0.02740	0.03927	0.02410	0.01292
11	$M_{2 \rightarrow 1}$	0.000	53.333	96.667	140.000	233.333	116.667	21.703
11	$M_{1 \rightarrow 2}$	0.000	26.667	56.667	93.333	146.667	76.667	4.930
12	Θ_1	0.00793	0.01267	0.01563	0.01820	0.02853	0.01690	0.01857
12	Θ_2	0.00913	0.01393	0.01763	0.02147	0.03240	0.01903	0.01034
12	$M_{2 \rightarrow 1}$	0.000	60.000	103.333	146.667	246.667	123.333	23.691
12	$M_{1 \rightarrow 2}$	0.000	20.000	56.667	86.667	146.667	76.667	4.642
13	Θ_1	0.00440	0.00760	0.01037	0.01340	0.02033	0.01163	0.01315
13	Θ_2	0.00087	0.00360	0.00563	0.00713	0.01120	0.00577	0.00334
13	$M_{2 \rightarrow 1}$	0.000	53.333	130.000	226.667	520.000	190.000	63.002
13	$M_{1 \rightarrow 2}$	0.000	40.000	83.333	126.667	240.000	103.333	14.636
14	Θ_1	0.02647	0.03453	0.04243	0.04340	0.04993	0.03877	0.04393
14	Θ_2	0.00593	0.01220	0.01437	0.01767	0.03167	0.01650	0.00909
14	$M_{2 \rightarrow 1}$	0.000	13.333	43.333	80.000	133.333	63.333	3.286
14	$M_{1 \rightarrow 2}$	0.000	60.000	116.667	166.667	313.333	136.667	25.288
15	Θ_1	0.01120	0.01560	0.01803	0.02273	0.03220	0.02083	0.02252
15	Θ_2	0.00393	0.00773	0.01043	0.01347	0.02200	0.01170	0.00654
15	$M_{2 \rightarrow 1}$	0.000	20.000	56.667	86.667	146.667	76.667	6.412
15	$M_{1 \rightarrow 2}$	0.000	60.000	110.000	160.000	280.000	130.000	22.058
16	Θ_1	0.00267	0.00580	0.00757	0.01007	0.01580	0.00850	0.00965
16	Θ_2	0.00827	0.01240	0.01530	0.01913	0.02873	0.01723	0.00944

Locus	Parameter	2.5%	25.0%	Mode	75.0%	97.5%	Median	Mean
16	$M_{2 \rightarrow 1}$	0.000	33.333	76.667	113.333	200.000	96.667	14.625
16	$M_{1 \rightarrow 2}$	0.000	53.333	90.000	133.333	213.333	110.000	14.016
17	Θ_1	0.00760	0.01133	0.01497	0.01947	0.02760	0.01683	0.01865
17	Θ_2	0.02007	0.02427	0.03050	0.03773	0.04527	0.03217	0.01735
17	$M_{2 \rightarrow 1}$	0.000	66.667	123.333	173.333	286.667	143.333	33.545
17	$M_{1 \rightarrow 2}$	0.000	33.333	63.333	100.000	153.333	83.333	6.611
18	Θ_1	0.00360	0.00667	0.00963	0.01147	0.01747	0.00990	0.01111
18	Θ_2	0.00573	0.00993	0.01250	0.01660	0.02633	0.01450	0.00804
18	$M_{2 \rightarrow 1}$	0.000	33.333	70.000	106.667	173.333	83.333	10.629
18	$M_{1 \rightarrow 2}$	0.000	46.667	90.000	126.667	206.667	103.333	13.266
19	Θ_1	0.00067	0.00320	0.00490	0.00633	0.00933	0.00490	0.00574
19	Θ_2	0.00120	0.00287	0.00663	0.01187	0.01747	0.00777	0.00466
19	$M_{2 \rightarrow 1}$	0.000	33.333	90.000	133.333	293.333	116.667	24.922
19	$M_{1 \rightarrow 2}$	0.000	126.667	283.333	480.000	953.333	390.000	114.530
20	Θ_1	0.01267	0.01707	0.02277	0.02967	0.03940	0.02477	0.02676
20	Θ_2	0.00840	0.01540	0.01923	0.02193	0.03380	0.01997	0.01077
20	$M_{2 \rightarrow 1}$	0.000	40.000	90.000	133.333	253.333	110.000	22.392
20	$M_{1 \rightarrow 2}$	6.667	53.333	90.000	126.667	200.000	103.333	12.810
All	Θ_1	0.01140	0.01260	0.01303	0.01327	0.01353	0.01290	0.01279
All	Θ_2	0.02367	0.02387	0.02423	0.02453	0.02480	0.02410	0.02247
All	$M_{2 \rightarrow 1}$	40.000	66.667	90.000	106.667	126.667	96.667	86.740
All	$M_{1 \rightarrow 2}$	46.667	66.667	90.000	106.667	133.333	96.667	93.275

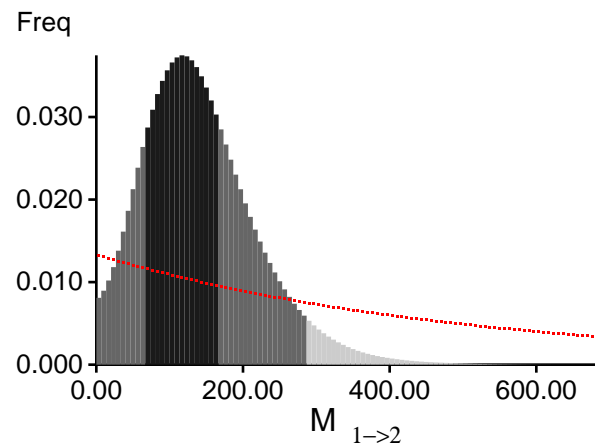
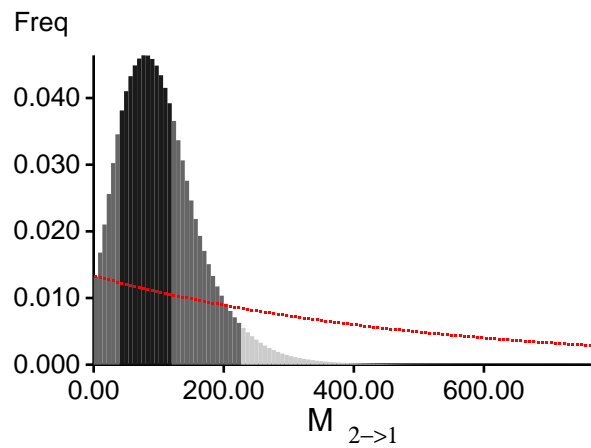
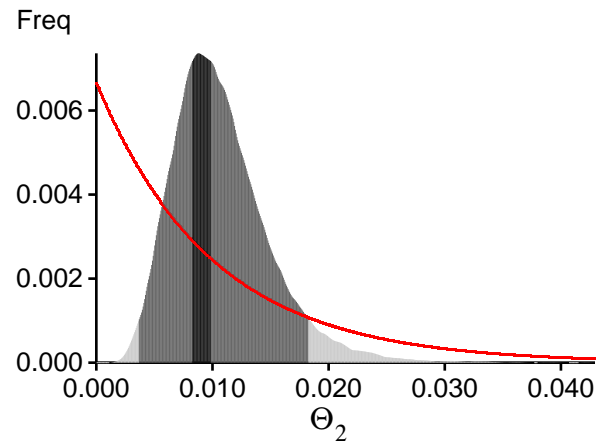
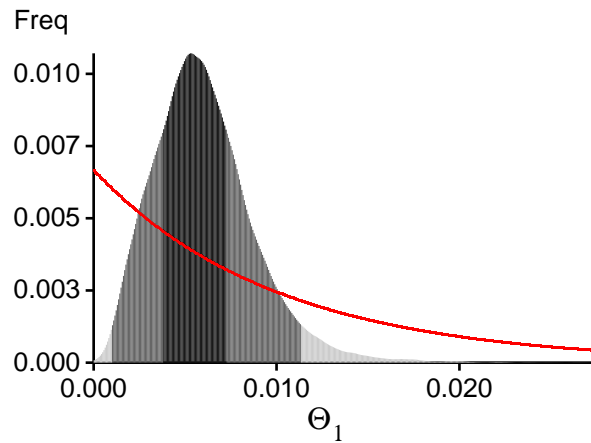
Citation suggestions:

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

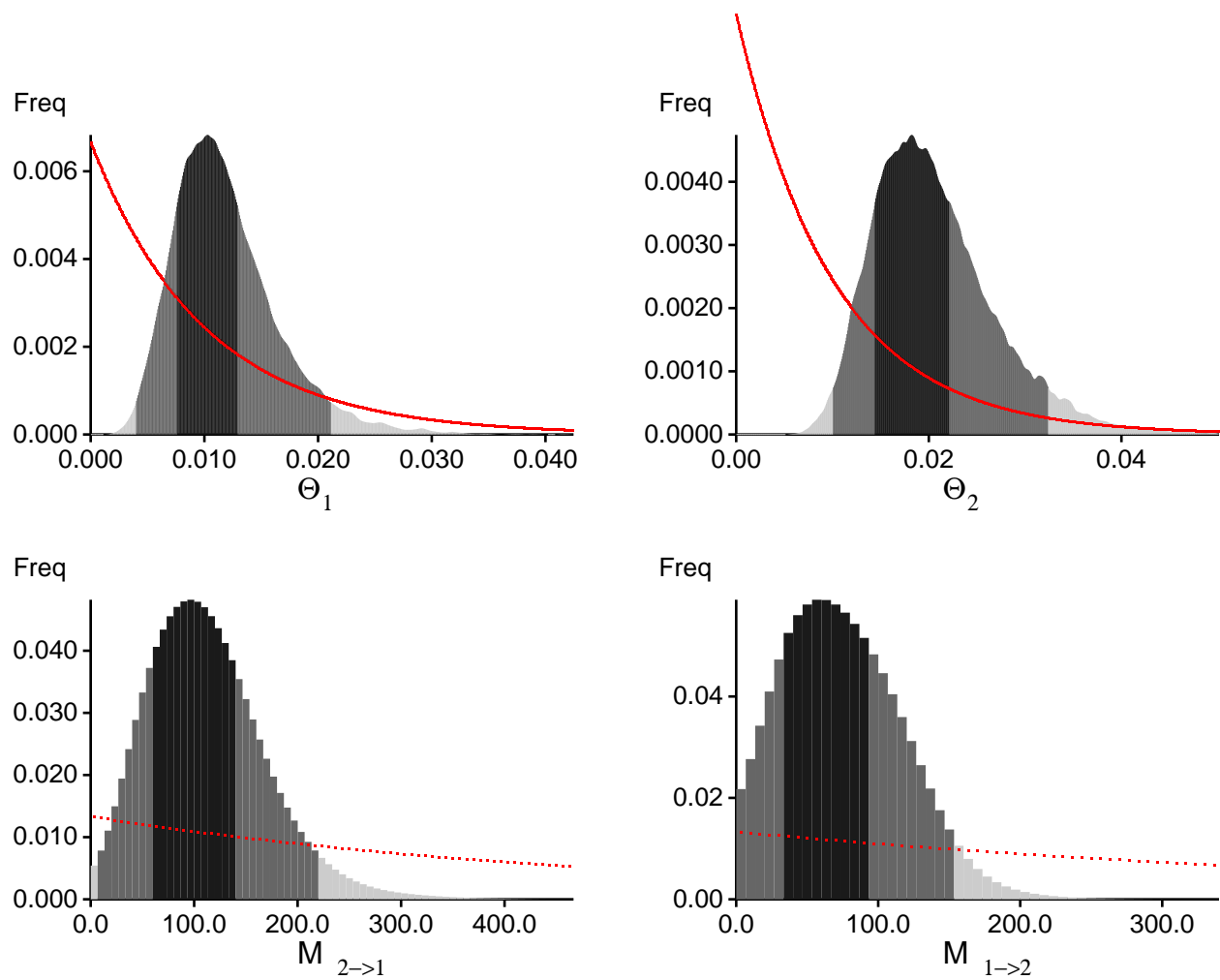
Beerli P., 2009. How to use MIGRATE or why are Markov chain Monte Carlo programs difficult to use? In *Population Genetics for Animal Conservation*, G. Bertorelle, M. W. Bruford, H. C. Hauffe, A. Rizzoli, and C. Vernesi, eds., vol. 17 of *Conservation Biology*, Cambridge University Press, Cambridge UK,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

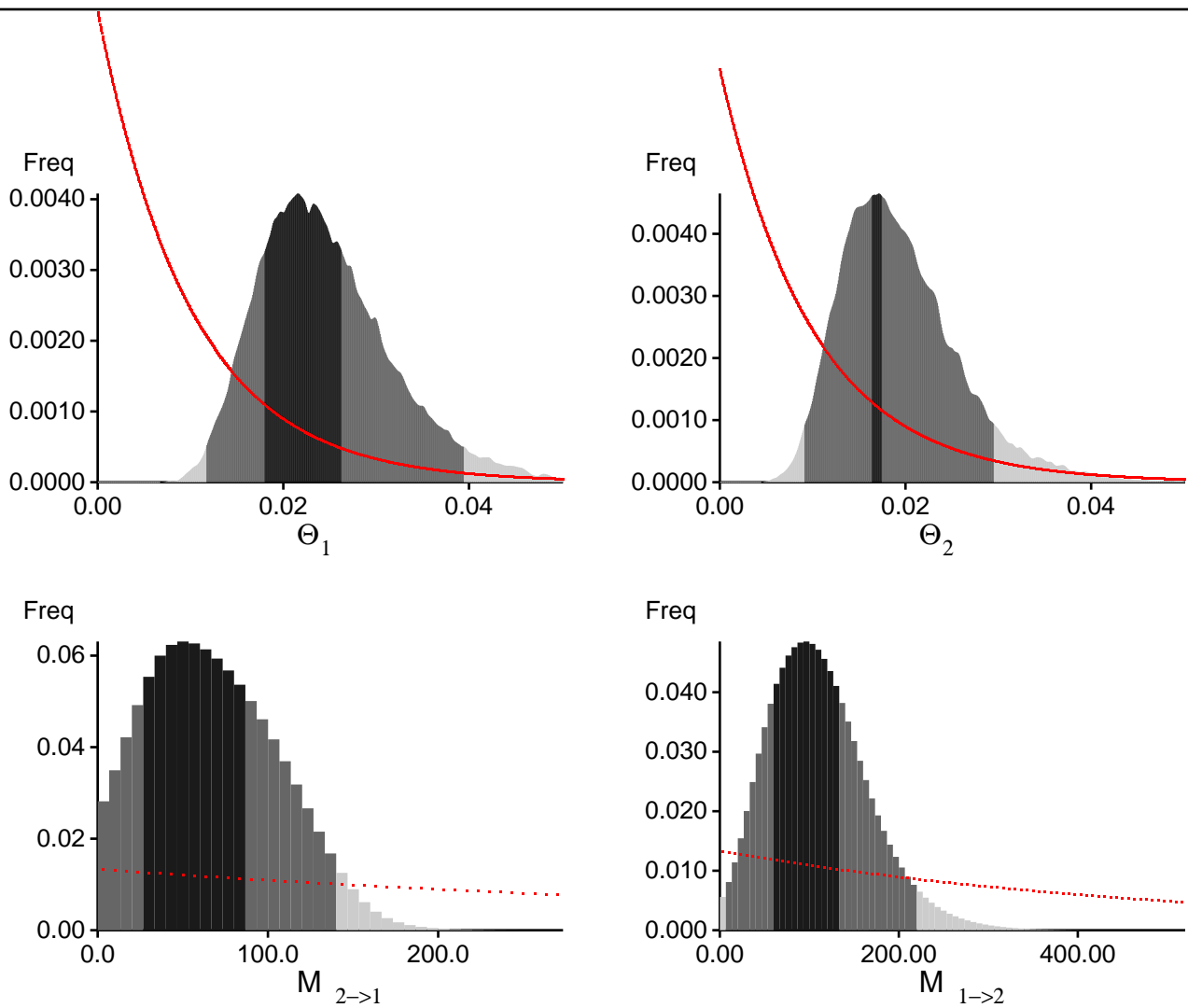
Bayesian Analysis: Posterior distribution for locus 1

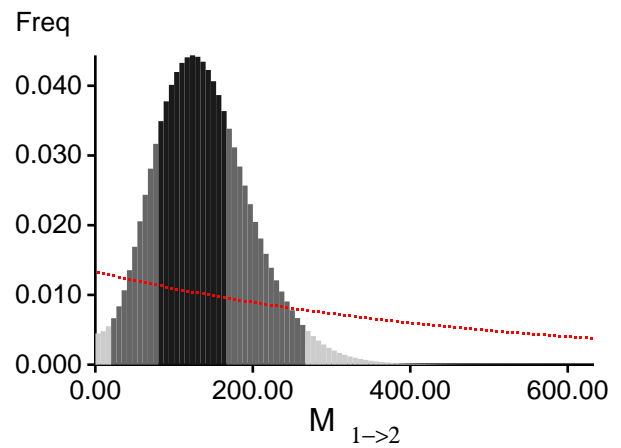
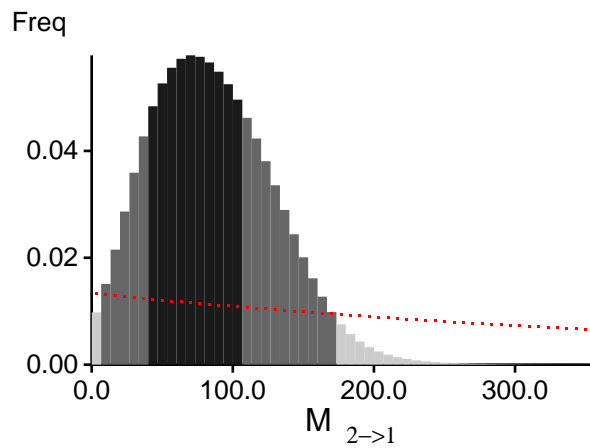
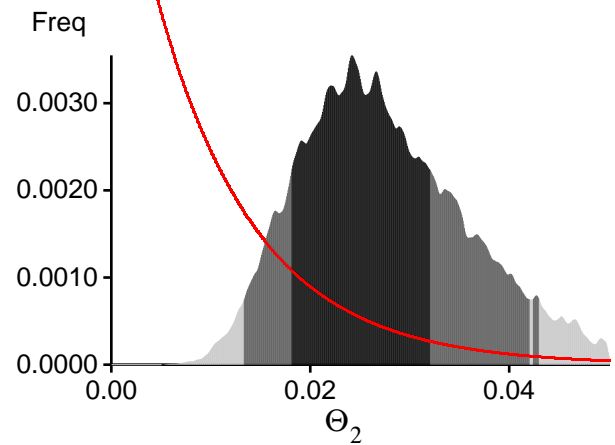
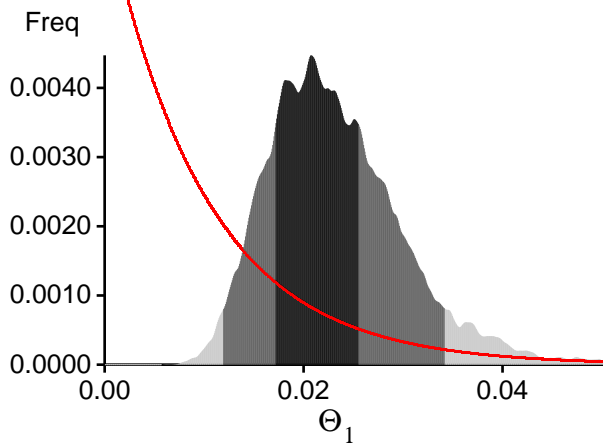
Bayesian Analysis: Posterior distribution for locus 2



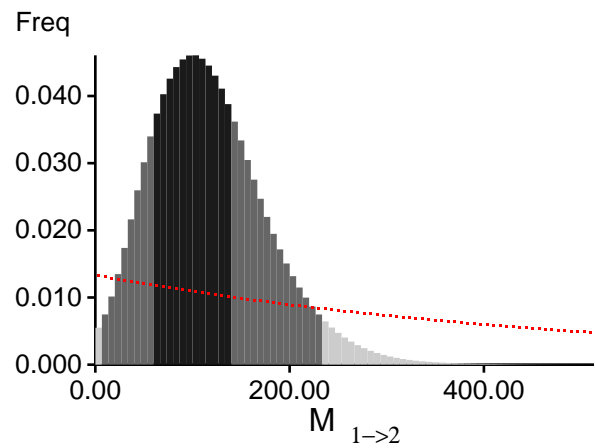
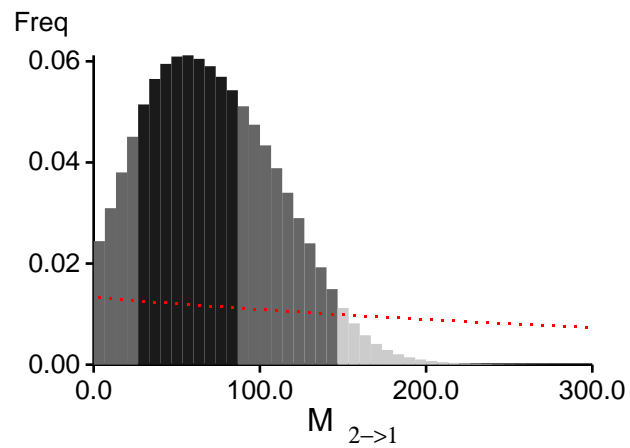
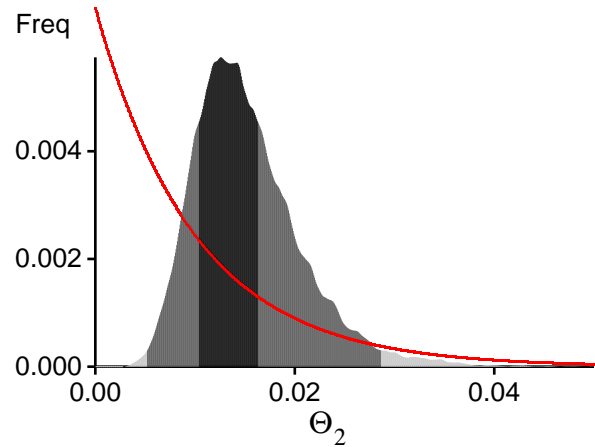
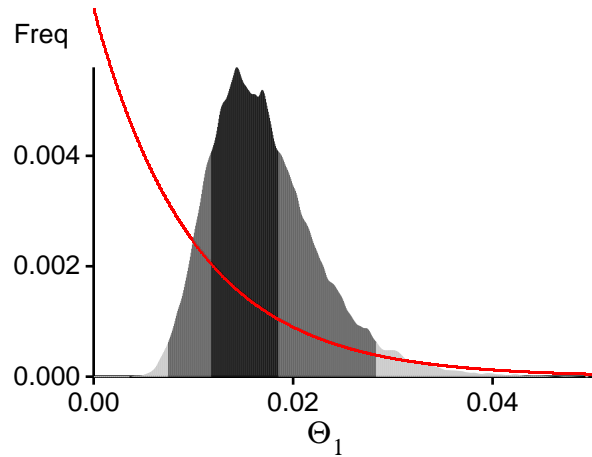
Bayesian Analysis: Posterior distribution for locus 3



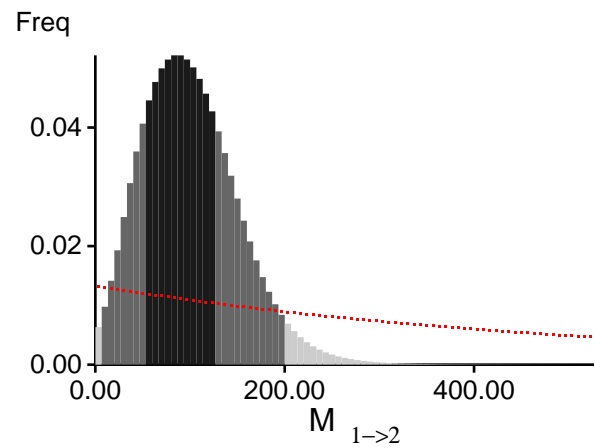
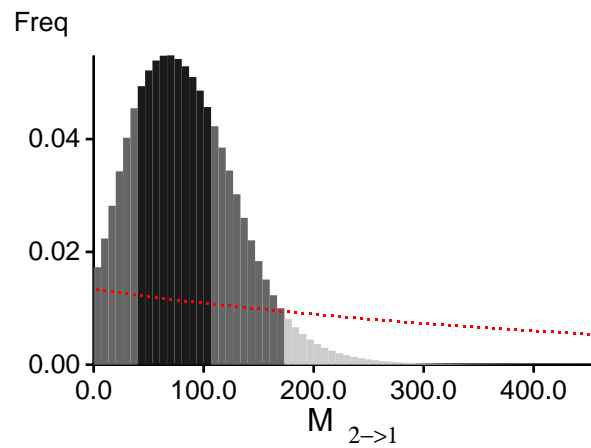
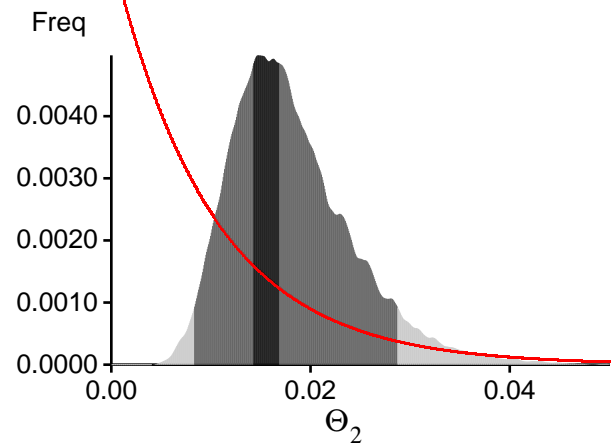
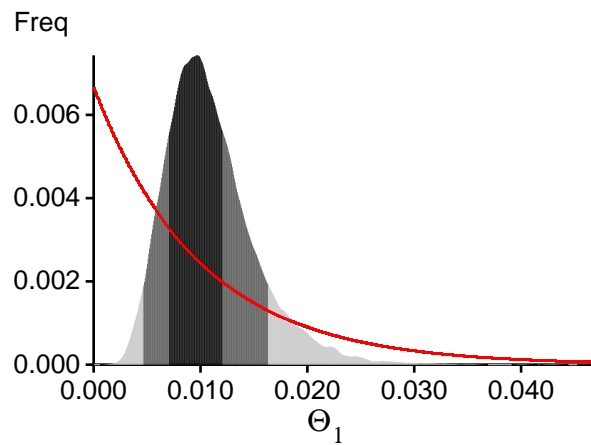
Bayesian Analysis: Posterior distribution for locus 4

Bayesian Analysis: Posterior distribution for locus 5

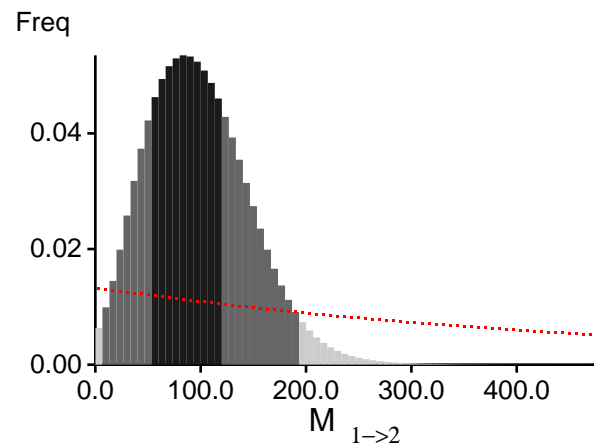
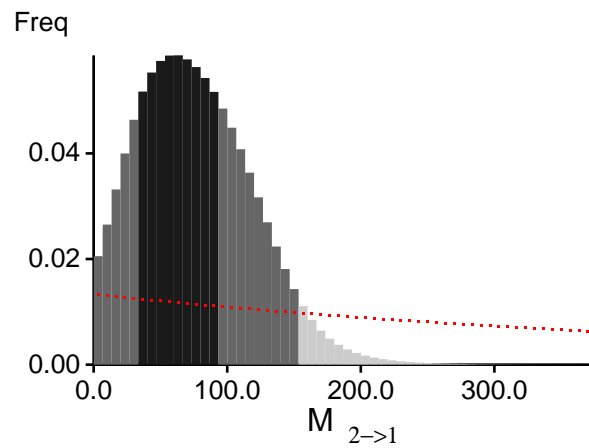
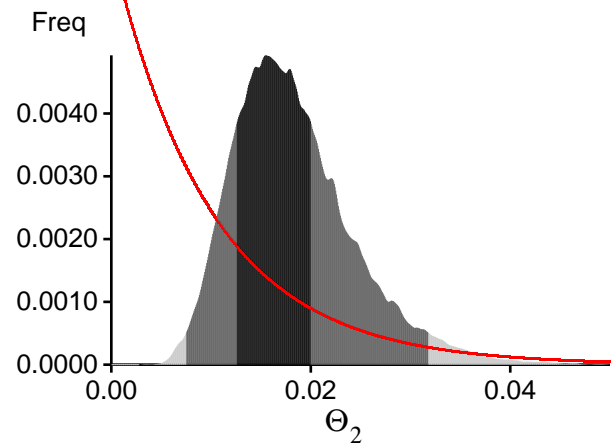
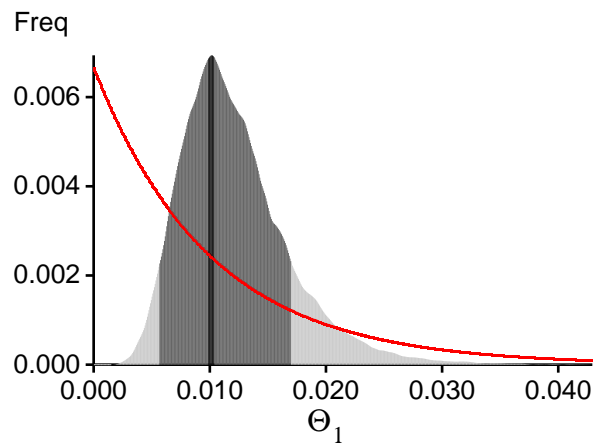
Bayesian Analysis: Posterior distribution for locus 6

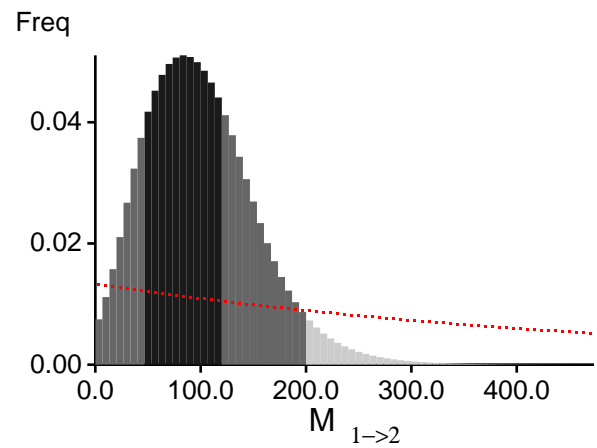
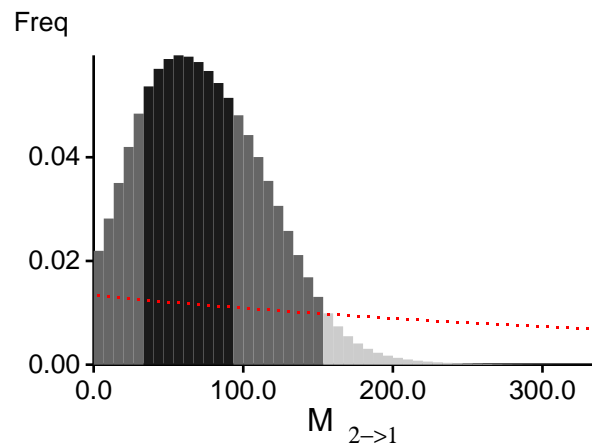
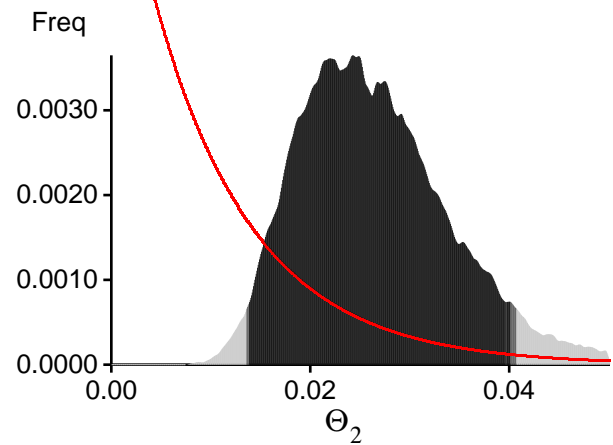
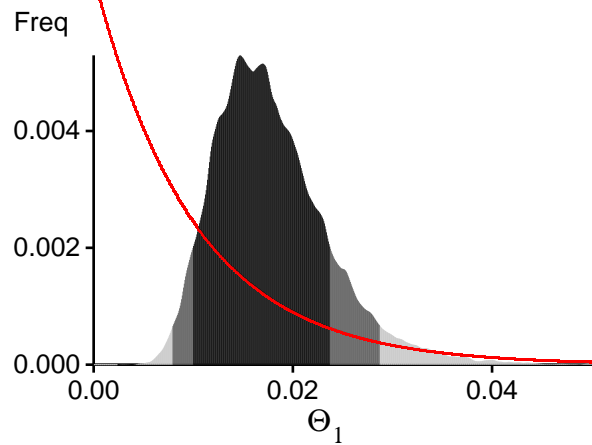


Bayesian Analysis: Posterior distribution for locus 7

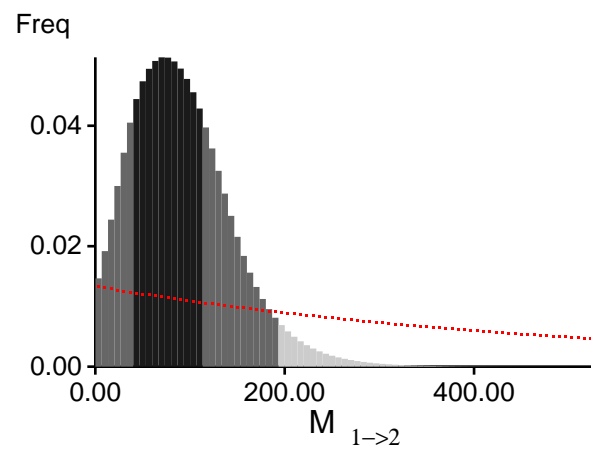
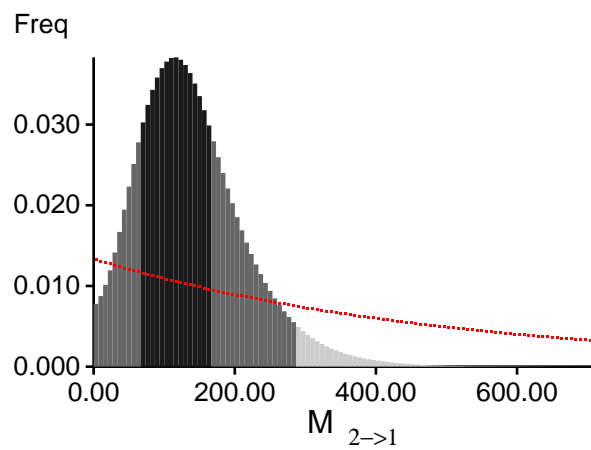
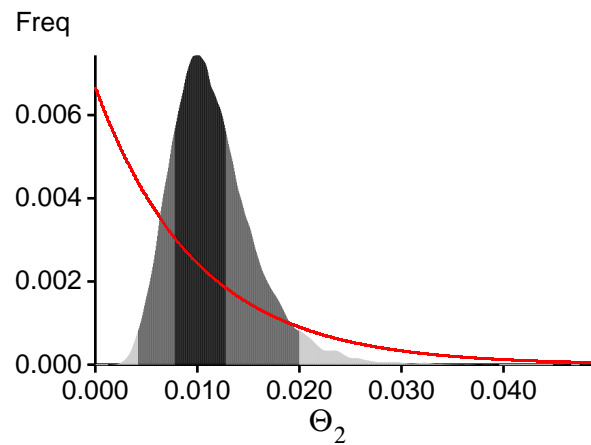
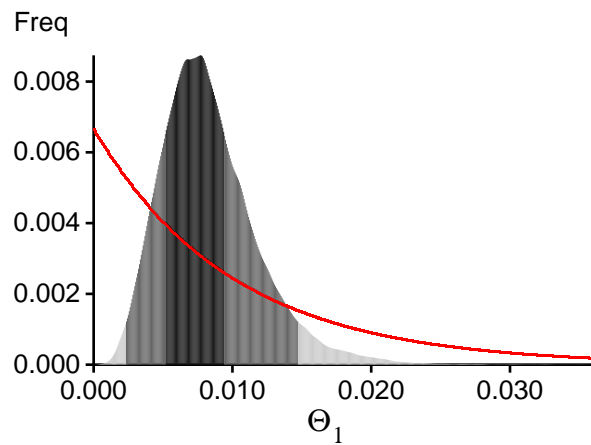


Bayesian Analysis: Posterior distribution for locus 8

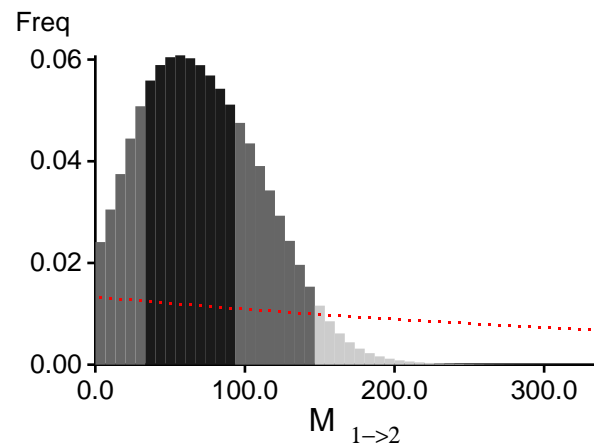
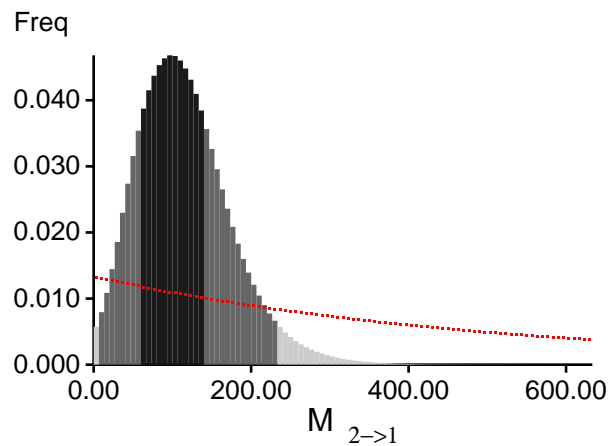
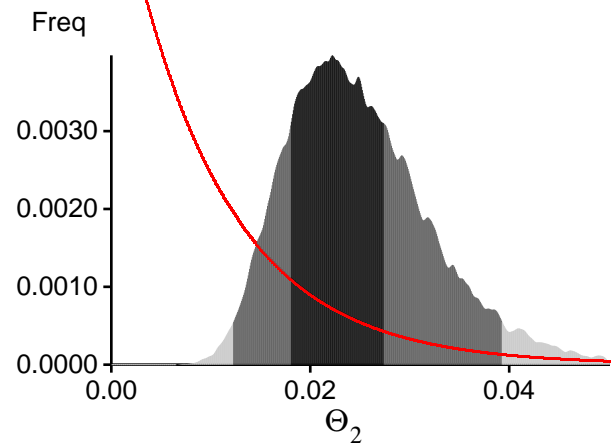
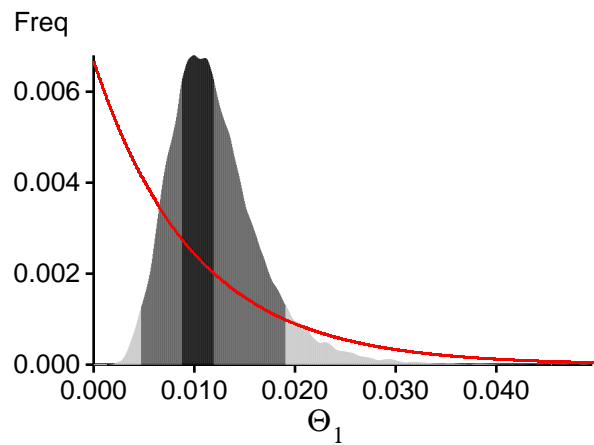


Bayesian Analysis: Posterior distribution for locus 9

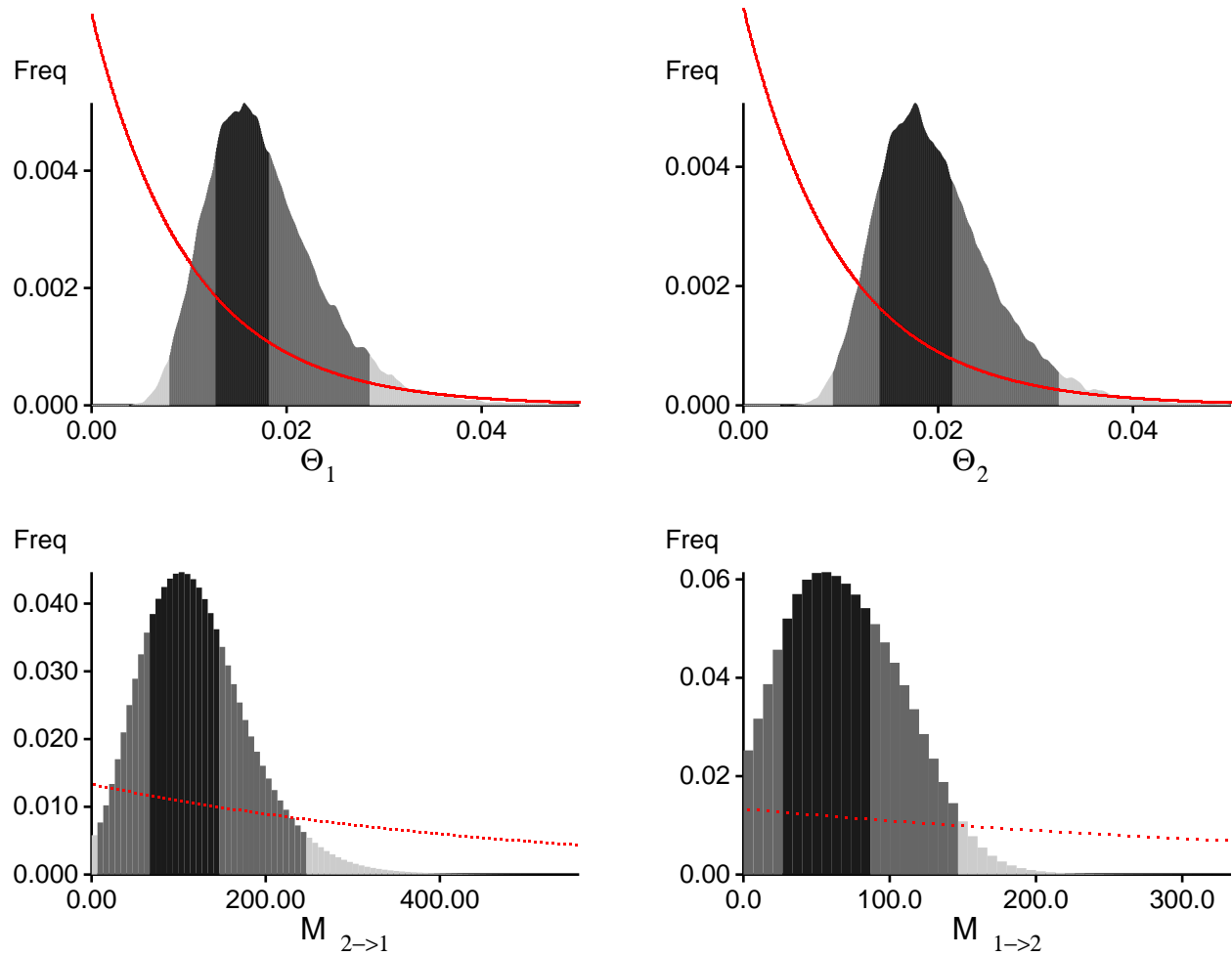
Bayesian Analysis: Posterior distribution for locus 10



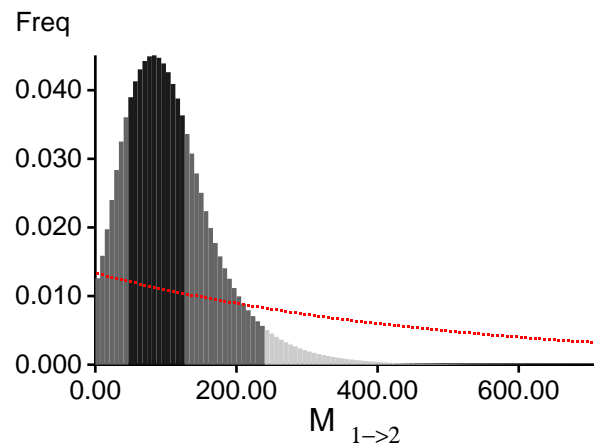
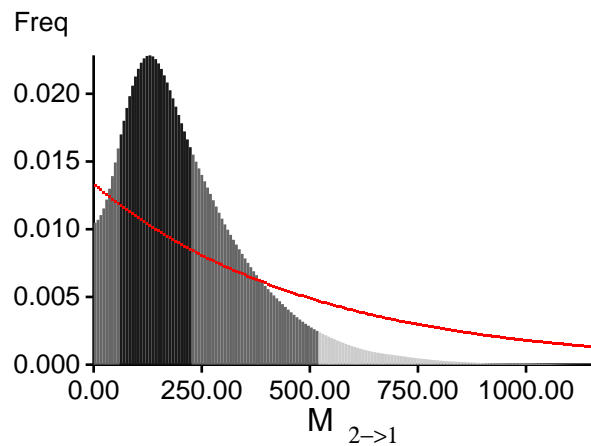
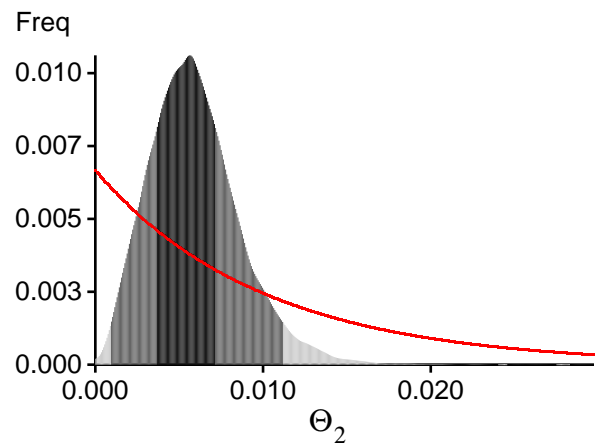
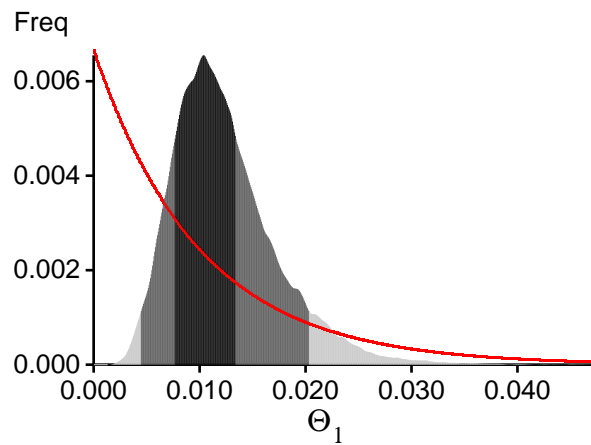
Bayesian Analysis: Posterior distribution for locus 11



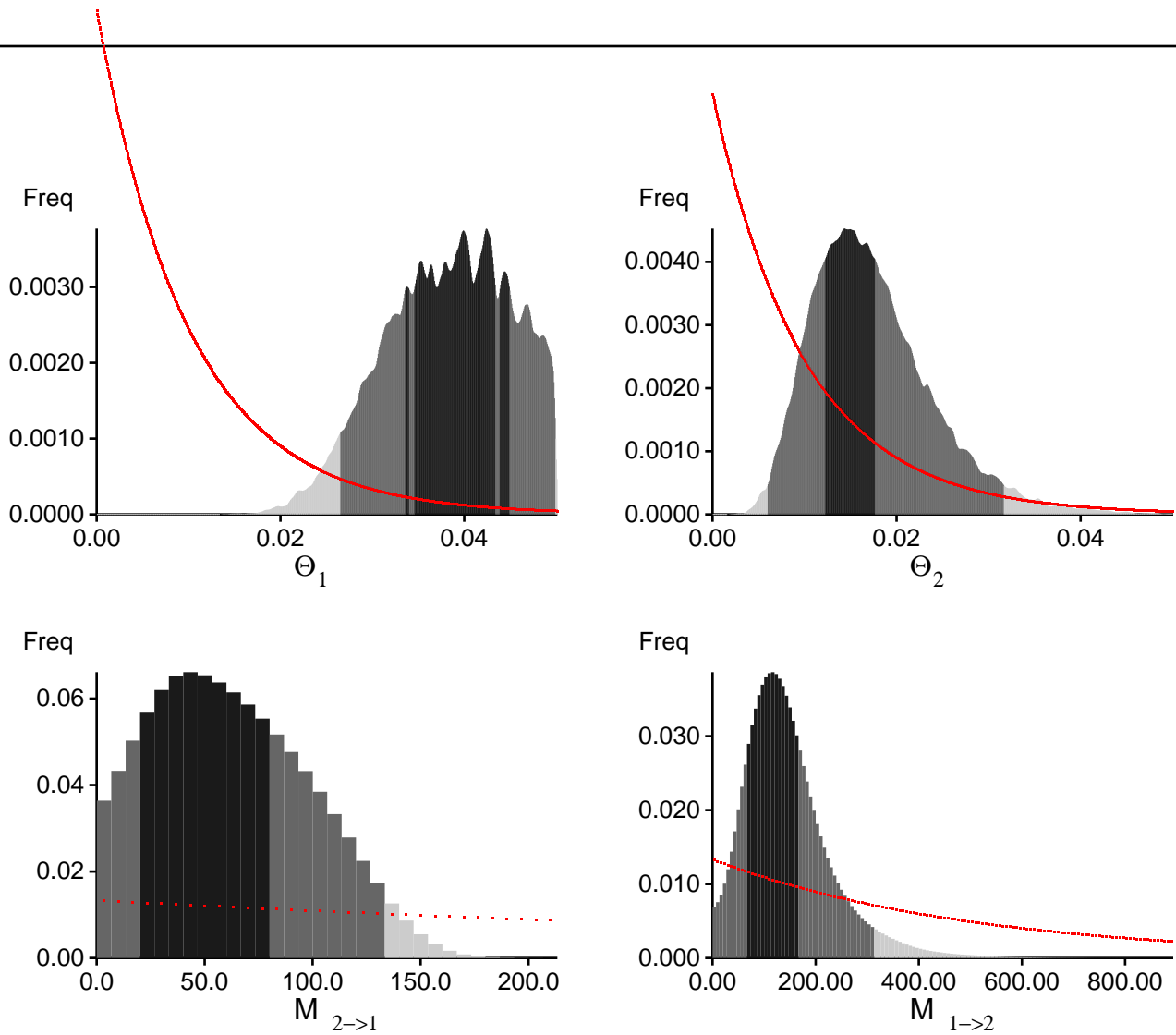
Bayesian Analysis: Posterior distribution for locus 12



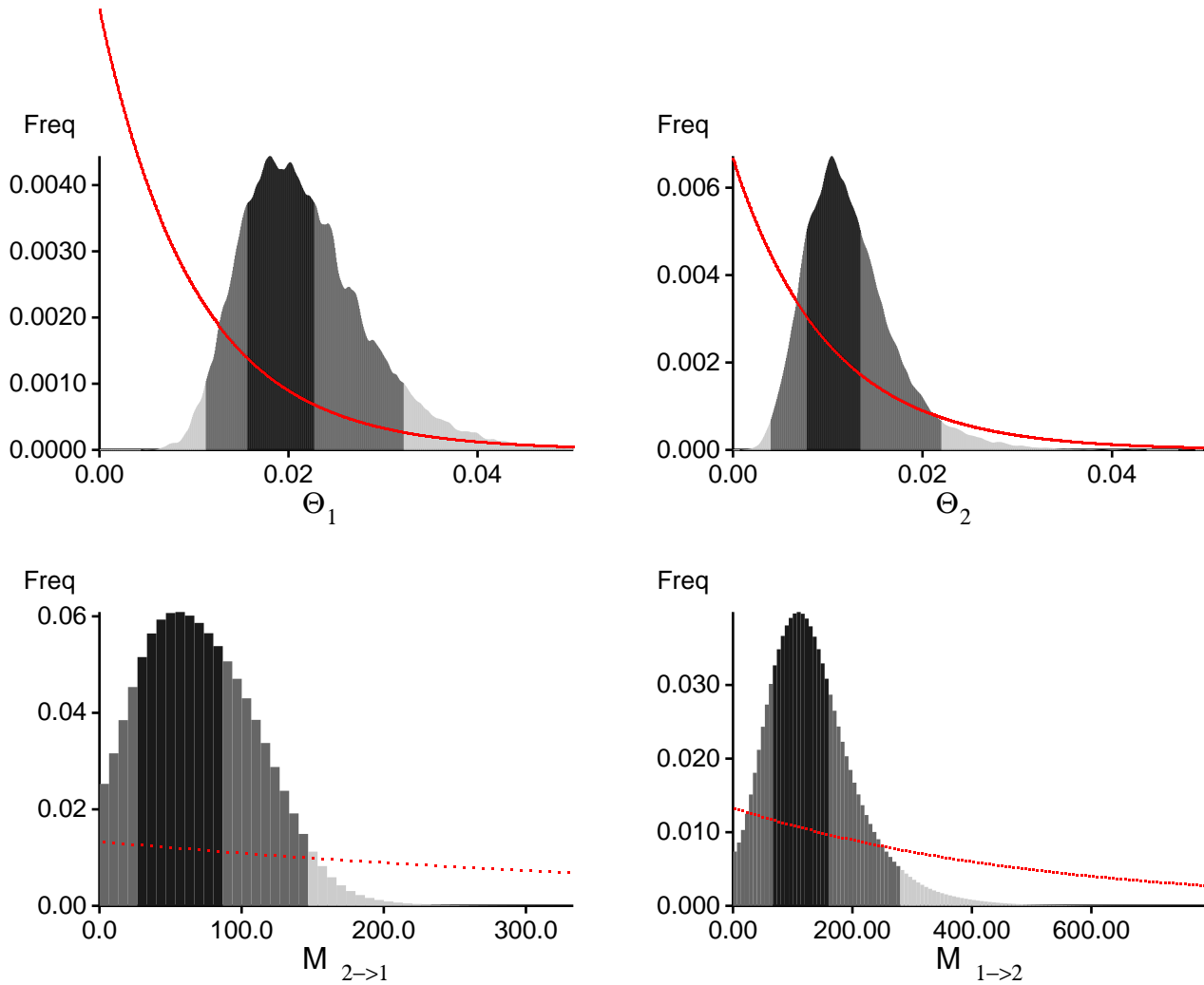
Bayesian Analysis: Posterior distribution for locus 13



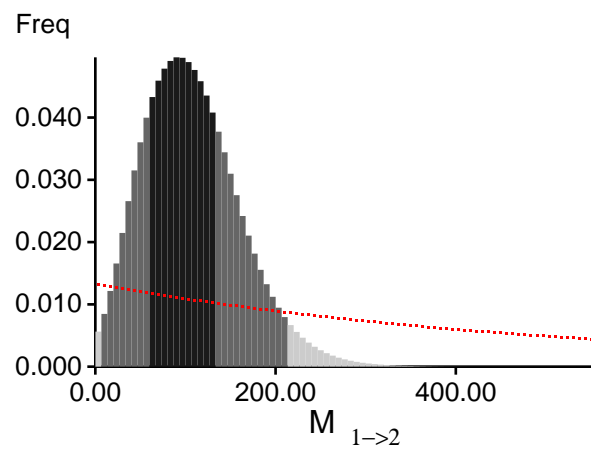
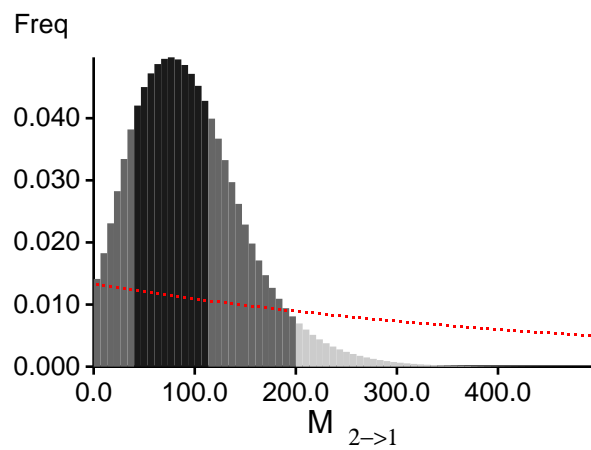
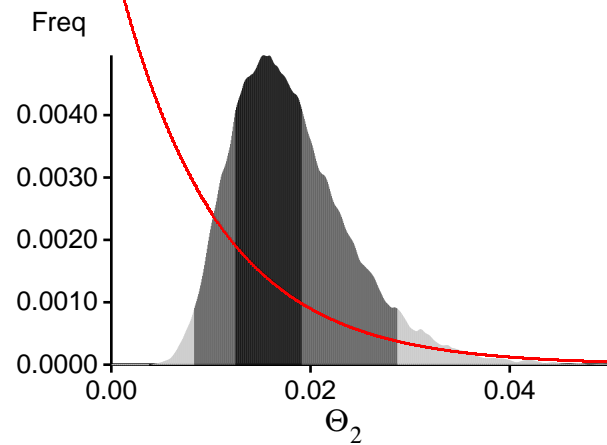
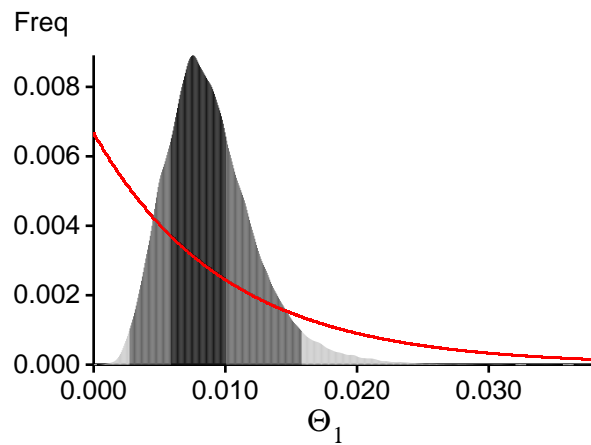
Bayesian Analysis: Posterior distribution for locus 14



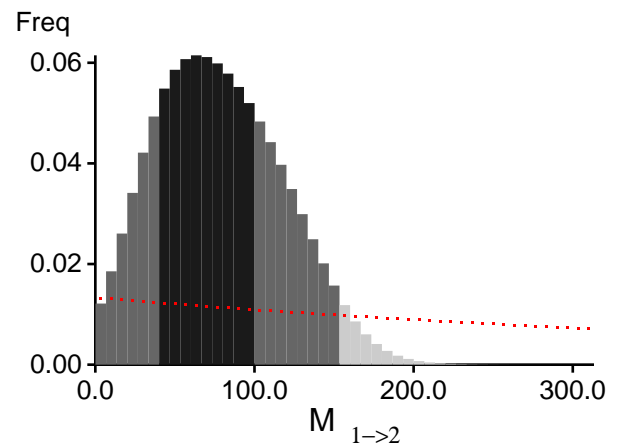
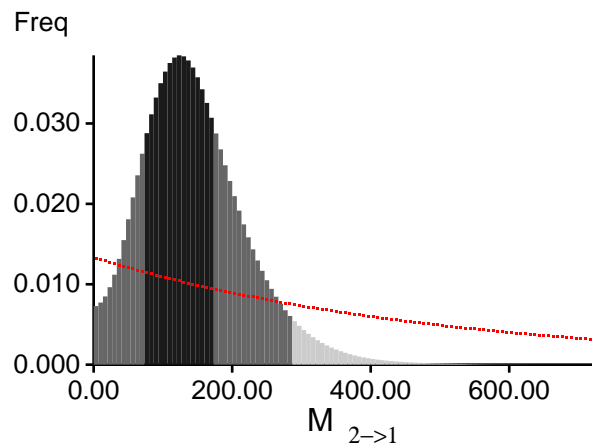
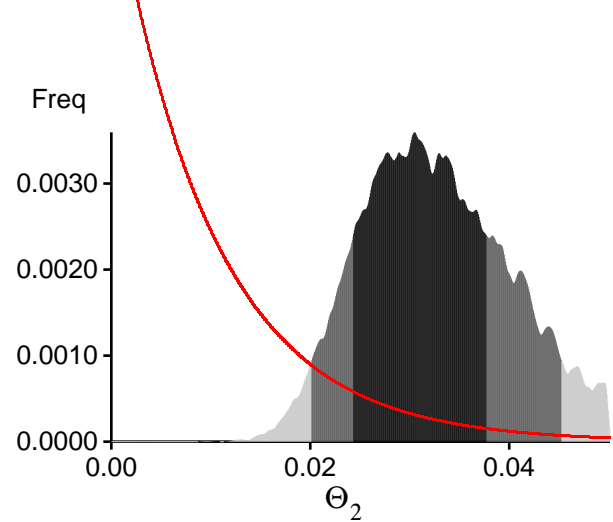
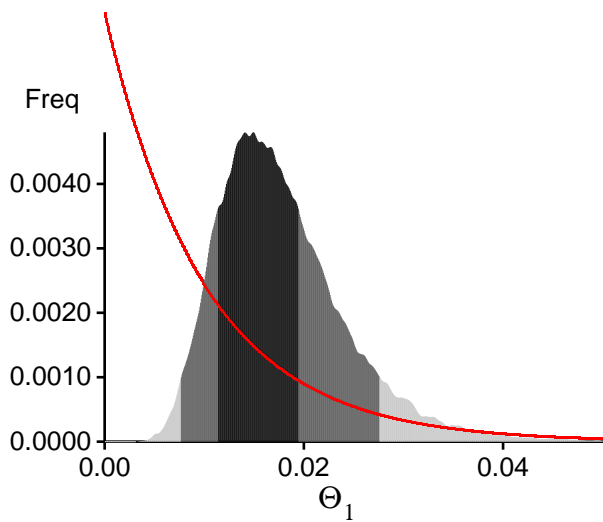
Bayesian Analysis: Posterior distribution for locus 15



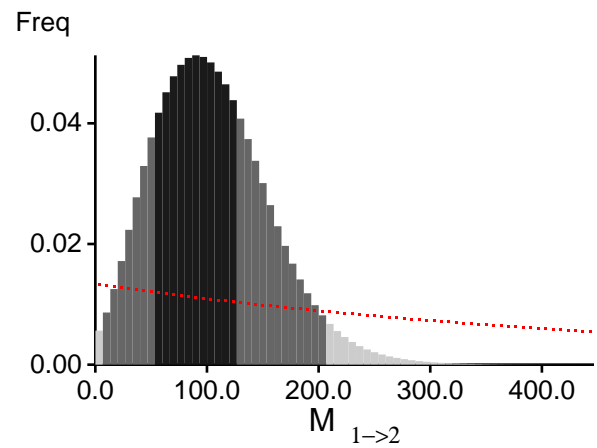
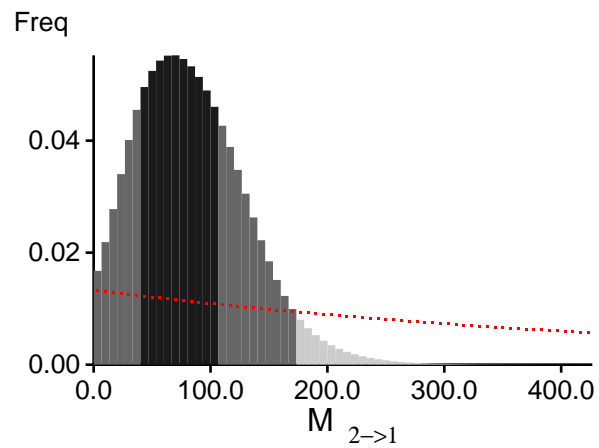
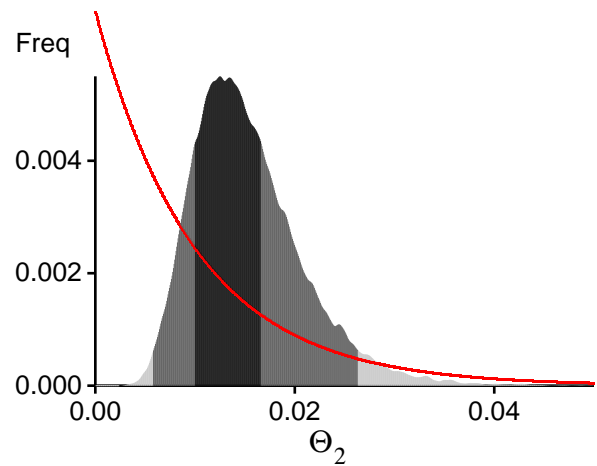
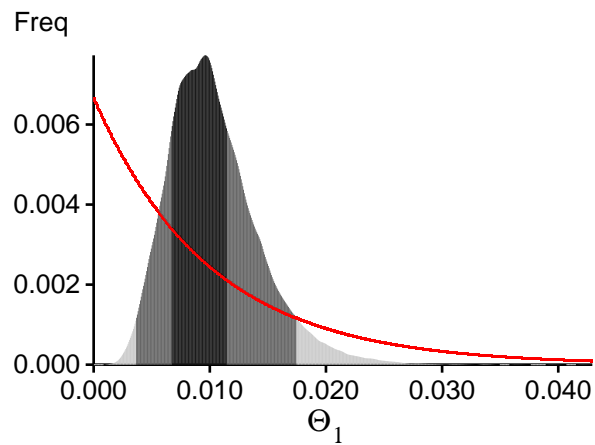
Bayesian Analysis: Posterior distribution for locus 16



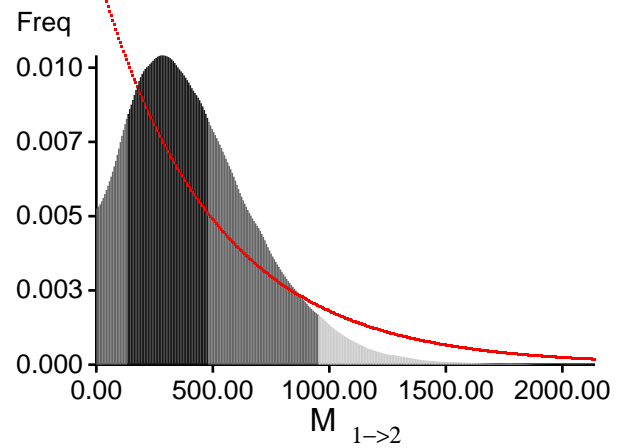
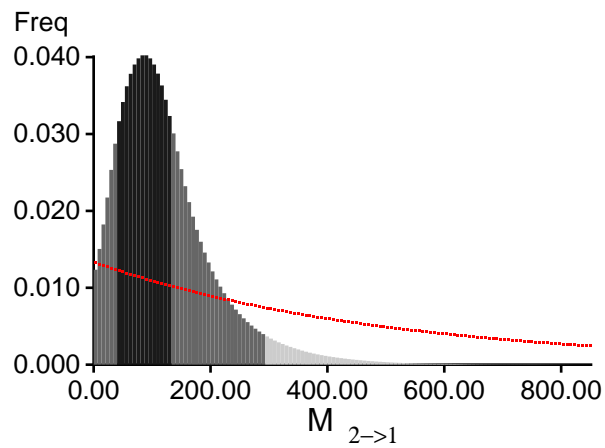
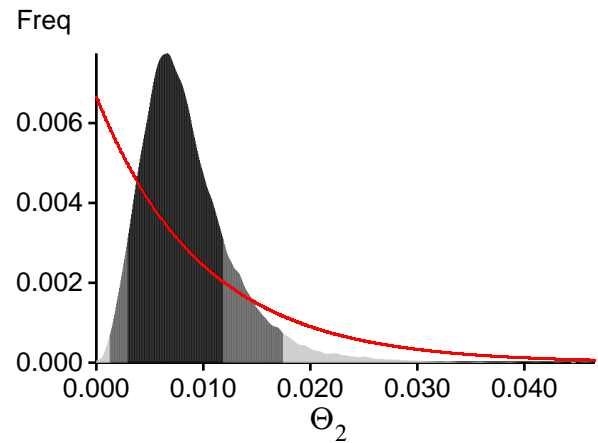
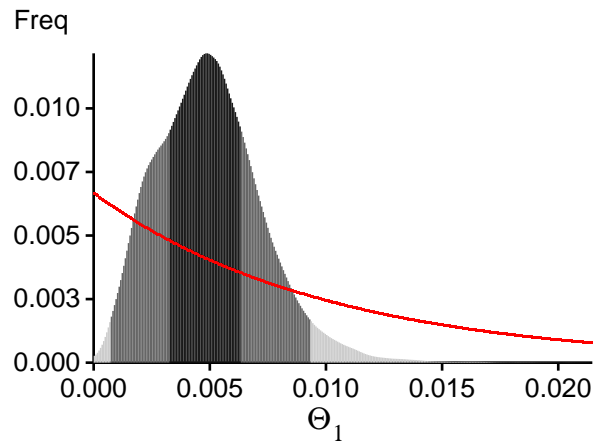
Bayesian Analysis: Posterior distribution for locus 17



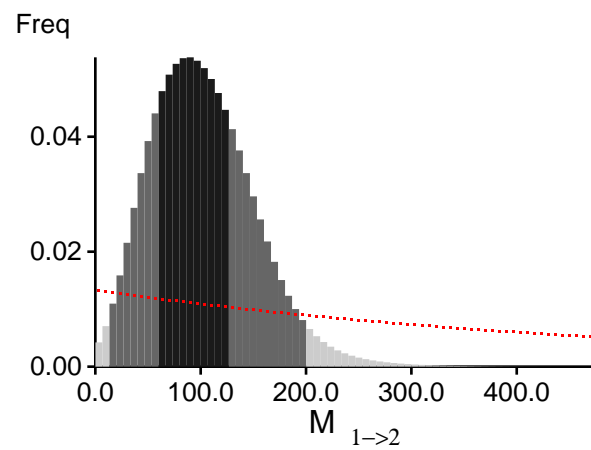
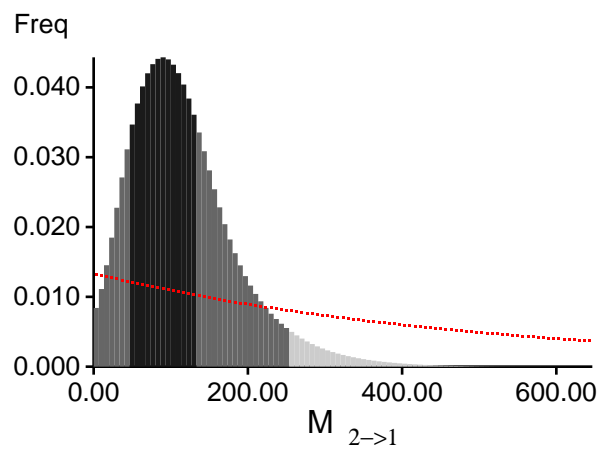
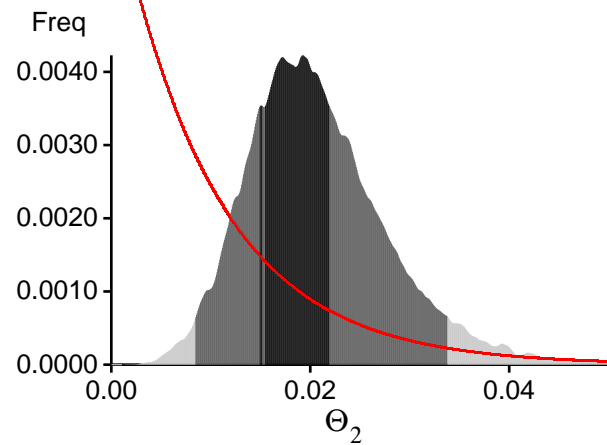
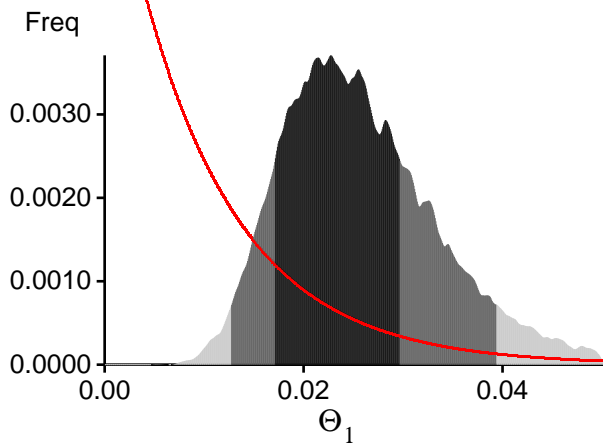
Bayesian Analysis: Posterior distribution for locus 18

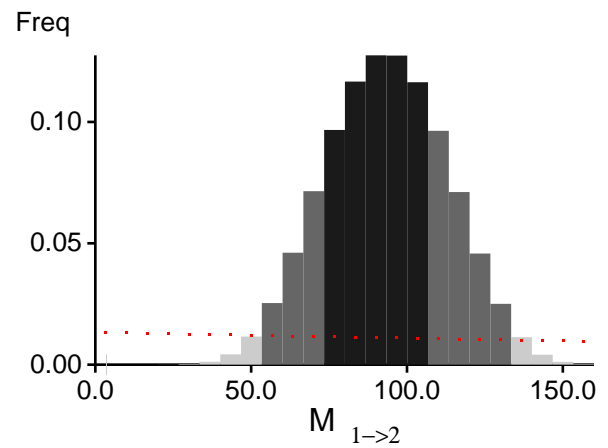
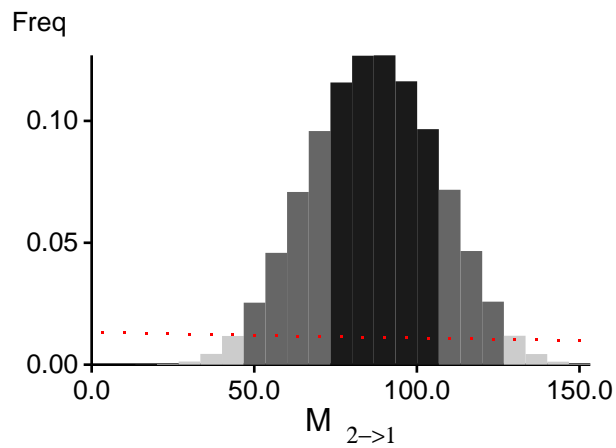
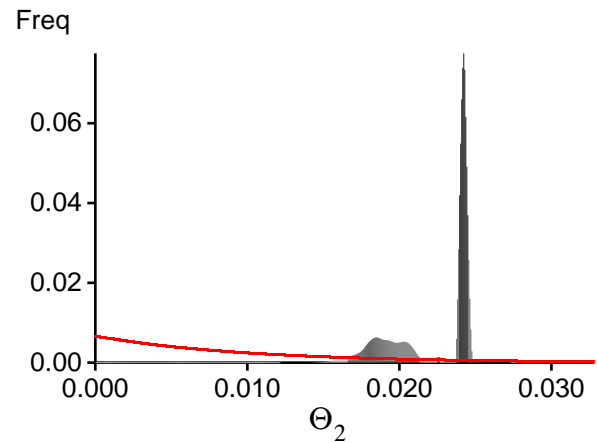
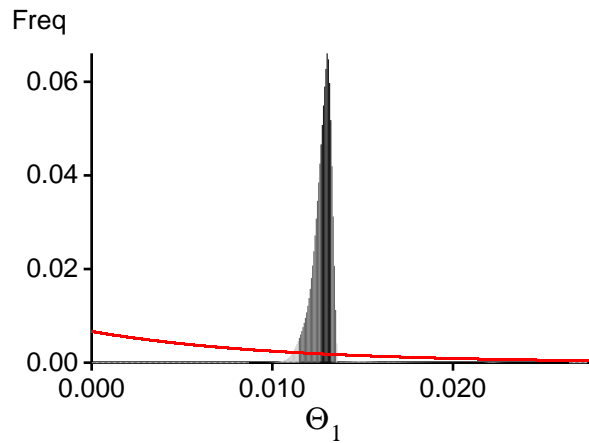


Bayesian Analysis: Posterior distribution for locus 19



Bayesian Analysis: Posterior distribution for locus 20



Bayesian Analysis: Posterior distribution 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	-17177.16	-13019.77	-12355.62
2	-12687.30	-10094.23	-10788.74
3	-12770.97	-10370.45	-10066.35
4	-12688.97	-10537.67	-10353.06
5	-16482.02	-12321.82	-11040.65
6	-14325.84	-11375.17	-10599.94
7	-14119.10	-11436.29	-10824.46
8	-13914.81	-10968.06	-10483.63
9	-16134.70	-13270.16	-12492.25
10	-16353.62	-13362.45	-12974.66
11	-12788.74	-10585.29	-10273.51
12	-14088.24	-10691.28	-10747.17
13	-17140.86	-13874.06	-14767.42
14	-16436.06	-13350.20	-12192.97
15	-13593.61	-10877.76	-10630.86
16	-14618.26	-12066.79	-12122.46
17	-13572.93	-11076.57	-10128.32
18	-15484.58	-12659.27	-11727.87
19	-15382.12	-12421.33	-12910.62
20	-14765.33	-11822.36	-10971.72
All	-294770.45	-236426.20	-228697.51

(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 = -245.217718]

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	690913/2501421	0.27621
Θ_2	643290/2500187	0.25730
$M_{2 \rightarrow 1}$	409000/2499197	0.16365
$M_{1 \rightarrow 2}$	446711/2499728	0.17870
Genealogies	267359/9999467	0.02674

MCMC-Autocorrelation and Effective MCMC Sample Size

Parameter	Autocorrelation	Effective Sample Size
Θ_1	0.14132	403877.31
Θ_2	0.15386	386830.63
$M_{2 \rightarrow 1}$	0.37571	249484.54
$M_{1 \rightarrow 2}$	0.30720	286462.74
Genealogies	0.93291	17998.85

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