

# 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]

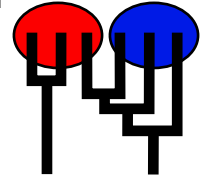
Compiled for PARALLEL computer architectures

One master and 8 compute nodes are available.

Compiled for a SYMMETRIC multiprocessors (Grandcentral)

Program started at Fri Jul 24 17:12:02 2020

Program finished at Fri Jul 24 17:57:06 2020 [Runtime:0000:00:45:04]



## 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) 2681389017

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	*	d
2 Pop2	0	*

Order of parameters:

1	$\Theta_1$	<displayed>
2	$\Theta_2$	<displayed>

3  $\Delta_{2 \rightarrow 1}$  <displayed>

4  $\sigma_{2 \rightarrow 1}$  <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

-Divergence time estimation:

Normal Distribution Shortcut (mean and standard dev.)

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 Splittime mean **	Gamma	0.000000	0.010	0.100	0.010	1500	0.12500
4 Splittime std **	Gamma	0.000000	0.010	0.100	0.010	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	
Total of all populations	11	10	
	12	10	
	13	10	
	14	10	
	15	10	
	16	10	
	17	10	
	18	10	
	19	10	
	20	10	
	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	$\Theta_1$	0.00000	0.00000	0.00117	0.00760	0.03367	0.00763	0.01186
1	$\Theta_2$	0.00000	0.00007	0.00177	0.00747	0.02993	0.00737	0.00636
1	$D_{2 \rightarrow 1}$	0.00000	0.00007	0.00123	0.00747	0.02827	0.00737	0.00367
1	$S_{2 \rightarrow 1}$	0.00000	0.00000	0.00123	0.01213	0.03160	0.00750	0.00285
2	$\Theta_1$	0.00000	0.00007	0.00130	0.00673	0.02093	0.01163	0.02252
2	$\Theta_2$	0.00000	0.00000	0.00130	0.01280	0.03247	0.00817	0.01547
2	$D_{2 \rightarrow 1}$	0.00000	0.00007	0.00130	0.00727	0.03520	0.01037	0.00430
2	$S_{2 \rightarrow 1}$	0.00000	0.00073	0.00123	0.00387	0.03353	0.00970	0.00319
3	$\Theta_1$	0.00000	0.00000	0.00123	0.00747	0.02993	0.00890	0.01591
3	$\Theta_2$	0.00000	0.00000	0.00137	0.00753	0.03187	0.00757	0.00977
3	$D_{2 \rightarrow 1}$	0.00000	0.00000	0.00123	0.01613	0.03267	0.00903	0.00406
3	$S_{2 \rightarrow 1}$	0.00000	0.00020	0.00143	0.00820	0.03207	0.00803	0.00276
4	$\Theta_1$	0.00000	0.00067	0.00130	0.00220	0.02580	0.01010	0.06881
4	$\Theta_2$	0.00000	0.00013	0.00123	0.00647	0.02660	0.00790	0.04146
4	$D_{2 \rightarrow 1}$	0.00000	0.00000	0.00130	0.01120	0.04420	0.02177	0.00948
4	$S_{2 \rightarrow 1}$	0.00073	0.00787	0.01297	0.02500	0.04320	0.02143	0.00693
5	$\Theta_1$	0.00000	0.00000	0.00143	0.00787	0.02987	0.00823	0.03216
5	$\Theta_2$	0.00000	0.00000	0.00130	0.00927	0.02713	0.00737	0.02191
5	$D_{2 \rightarrow 1}$	0.00000	0.00000	0.00117	0.00980	0.03287	0.01010	0.00518
5	$S_{2 \rightarrow 1}$	0.00000	0.00000	0.00177	0.01493	0.03653	0.01070	0.00352
6	$\Theta_1$	0.00000	0.00000	0.00117	0.00753	0.03033	0.00757	0.01837
6	$\Theta_2$	0.00000	0.00000	0.00137	0.00727	0.02760	0.00723	0.00952
6	$D_{2 \rightarrow 1}$	0.00000	0.00000	0.00130	0.00780	0.03307	0.00783	0.00458
6	$S_{2 \rightarrow 1}$	0.00000	0.00000	0.00123	0.00827	0.03140	0.00870	0.00345
7	$\Theta_1$	0.00000	0.00000	0.00150	0.00673	0.02907	0.00730	0.00986
7	$\Theta_2$	0.00000	0.00000	0.00123	0.00733	0.03007	0.00730	0.00504
7	$D_{2 \rightarrow 1}$	0.00000	0.00027	0.00137	0.00540	0.02733	0.00717	0.00328
7	$S_{2 \rightarrow 1}$	0.00000	0.00007	0.00143	0.00727	0.02927	0.00717	0.00250
8	$\Theta_1$	0.00000	0.00000	0.00110	0.00900	0.01760	0.02263	0.03646

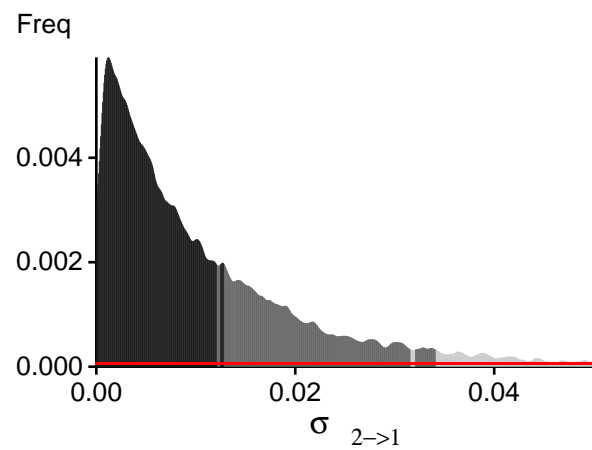
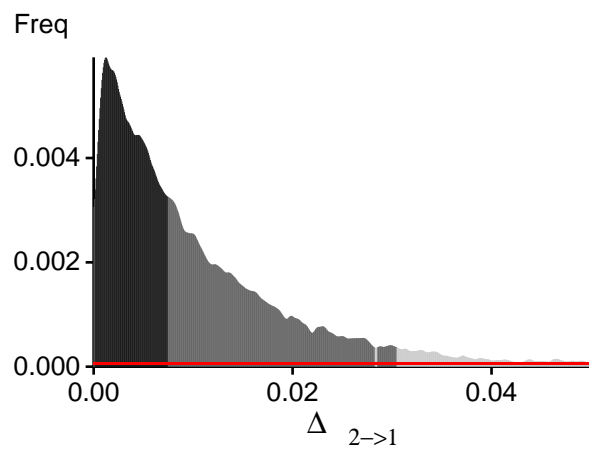
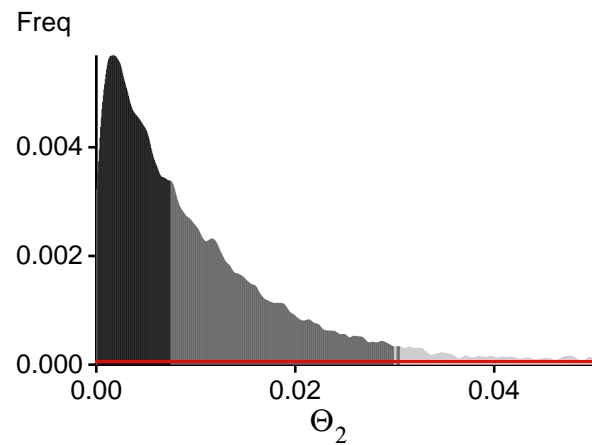
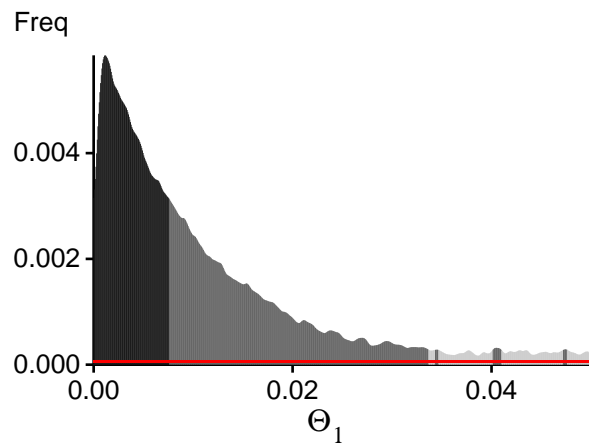
Locus	Parameter	2.5%	25.0%	Mode	75.0%	97.5%	Median	Mean
8	$\Theta_2$	0.00000	0.00067	0.00137	0.00300	0.03033	0.00743	0.03095
8	$D_{2 \rightarrow 1}$	0.00000	0.00007	0.00137	0.00927	0.03553	0.01037	0.00522
8	$S_{2 \rightarrow 1}$	0.00000	0.00000	0.00250	0.00800	0.01540	0.02303	0.00669
9	$\Theta_1$	0.00000	0.00000	0.00137	0.00713	0.02813	0.00717	0.00993
9	$\Theta_2$	0.00000	0.00000	0.00130	0.00747	0.02807	0.00743	0.00506
9	$D_{2 \rightarrow 1}$	0.00000	0.00007	0.00123	0.00727	0.02853	0.00717	0.00333
9	$S_{2 \rightarrow 1}$	0.00000	0.00100	0.00150	0.00200	0.02933	0.00723	0.00248
10	$\Theta_1$	0.00000	0.00013	0.00123	0.00740	0.02973	0.00730	0.01023
10	$\Theta_2$	0.00000	0.00007	0.00117	0.00753	0.03180	0.00743	0.00522
10	$D_{2 \rightarrow 1}$	0.00000	0.00000	0.00137	0.00740	0.02827	0.00737	0.00345
10	$S_{2 \rightarrow 1}$	0.00000	0.00000	0.00117	0.00733	0.03013	0.00730	0.00256
11	$\Theta_1$	0.00000	0.00000	0.00137	0.00787	0.03253	0.00783	0.01231
11	$\Theta_2$	0.00000	0.00027	0.00123	0.00513	0.02753	0.00723	0.00707
11	$D_{2 \rightarrow 1}$	0.00000	0.00000	0.00123	0.01147	0.03060	0.00763	0.00362
11	$S_{2 \rightarrow 1}$	0.00000	0.00000	0.00130	0.00747	0.03093	0.00743	0.00261
12	$\Theta_1$	0.00000	0.00000	0.00123	0.01433	0.03040	0.00737	0.01013
12	$\Theta_2$	0.00000	0.00007	0.00130	0.00707	0.02773	0.00723	0.00502
12	$D_{2 \rightarrow 1}$	0.00000	0.00007	0.00117	0.00740	0.02733	0.00730	0.00333
12	$S_{2 \rightarrow 1}$	0.00000	0.00013	0.00130	0.00620	0.02813	0.00723	0.00250
13	$\Theta_1$	0.00000	0.00000	0.00123	0.02013	0.03013	0.00737	0.01008
13	$\Theta_2$	0.00000	0.00067	0.00123	0.00273	0.02840	0.00730	0.00507
13	$D_{2 \rightarrow 1}$	0.00000	0.00007	0.00123	0.00740	0.02940	0.00730	0.00336
13	$S_{2 \rightarrow 1}$	0.00000	0.00000	0.00130	0.00727	0.02840	0.00723	0.00250
14	$\Theta_1$	0.00000	0.00000	0.00117	0.00733	0.03067	0.00737	0.01032
14	$\Theta_2$	0.00000	0.00000	0.00143	0.00727	0.03000	0.00730	0.00510
14	$D_{2 \rightarrow 1}$	0.00000	0.00007	0.00130	0.00760	0.03107	0.00750	0.00340
14	$S_{2 \rightarrow 1}$	0.00000	0.00000	0.00123	0.00807	0.02867	0.00730	0.00255
15	$\Theta_1$	0.00000	0.00000	0.00130	0.00740	0.02913	0.00737	0.01008
15	$\Theta_2$	0.00000	0.00007	0.00130	0.00733	0.02740	0.00723	0.00496
15	$D_{2 \rightarrow 1}$	0.00000	0.00000	0.00130	0.00727	0.02840	0.00723	0.00332
15	$S_{2 \rightarrow 1}$	0.00000	0.00007	0.00130	0.00760	0.02833	0.00737	0.00252
16	$\Theta_1$	0.00000	0.00000	0.00130	0.01173	0.02867	0.00730	0.01009
16	$\Theta_2$	0.00000	0.00000	0.00130	0.01340	0.02913	0.00717	0.00505

Locus	Parameter	2.5%	25.0%	Mode	75.0%	97.5%	Median	Mean
16	$D_{2 \rightarrow 1}$	0.00000	0.00000	0.00123	0.00700	0.02887	0.00703	0.00328
16	$S_{2 \rightarrow 1}$	0.00000	0.00033	0.00123	0.00460	0.02860	0.00703	0.00246
17	$\Theta_1$	0.02773	0.04500	0.04677	0.04993	0.05027	0.04343	0.05499
17	$\Theta_2$	0.04513	0.04580	0.04637	0.04753	0.05013	0.02337	0.04423
17	$D_{2 \rightarrow 1}$	0.02180	0.04253	0.04677	0.04987	0.05013	0.03623	0.01274
17	$S_{2 \rightarrow 1}$	0.00000	0.00133	0.00570	0.01367	0.03747	0.00943	0.00385
18	$\Theta_1$	0.00000	0.00000	0.00130	0.01527	0.02780	0.00717	0.00987
18	$\Theta_2$	0.00000	0.00000	0.00130	0.00733	0.02860	0.00730	0.00502
18	$D_{2 \rightarrow 1}$	0.00000	0.00000	0.00143	0.00707	0.02667	0.00703	0.00330
18	$S_{2 \rightarrow 1}$	0.00000	0.00000	0.00130	0.00993	0.02707	0.00723	0.00249
19	$\Theta_1$	0.00000	0.00000	0.00130	0.01133	0.03107	0.00757	0.01341
19	$\Theta_2$	0.00000	0.00000	0.00130	0.01167	0.02820	0.00730	0.00733
19	$D_{2 \rightarrow 1}$	0.00000	0.00000	0.00130	0.00747	0.03240	0.00750	0.00389
19	$S_{2 \rightarrow 1}$	0.00000	0.00000	0.00123	0.00780	0.03293	0.00783	0.00301
20	$\Theta_1$	0.03327	0.04427	0.04803	0.04980	0.05013	0.04437	0.06798
20	$\Theta_2$	0.00000	0.00000	0.00003	0.09993	0.09993	0.00003	0.04804
20	$D_{2 \rightarrow 1}$	0.00000	0.00020	0.00123	0.00987	0.03487	0.01250	0.00495
20	$S_{2 \rightarrow 1}$	0.00727	0.01647	0.02083	0.02740	0.04453	0.02423	0.00685
All	$\Theta_1$	0.04733	0.04833	0.04863	0.04933	0.04993	0.04883	0.04869
All	$\Theta_2$	0.04707	0.04767	0.04810	0.04833	0.04907	0.04810	0.04809
All	$D_{2 \rightarrow 1}$	0.04713	0.04780	0.04823	0.04933	0.04993	0.04650	0.04615
All	$S_{2 \rightarrow 1}$	0.04020	0.04820	0.04890	0.04940	0.04987	0.04857	0.04668

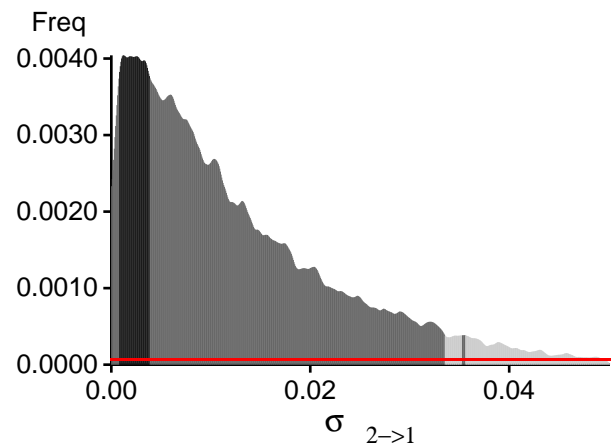
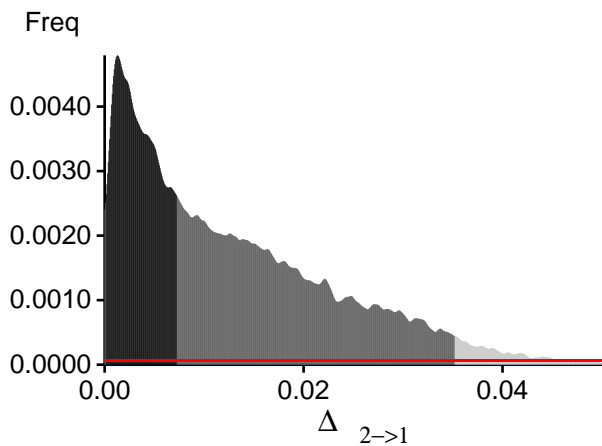
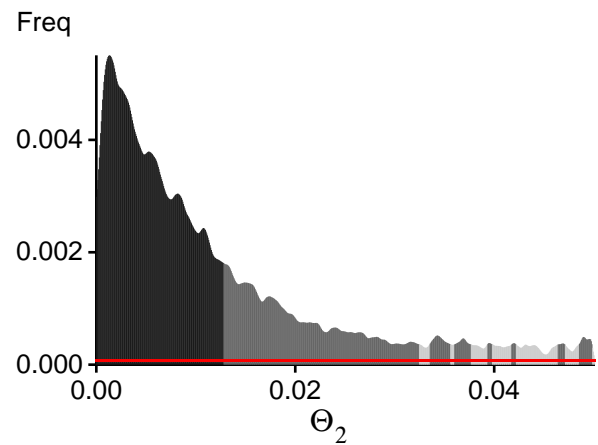
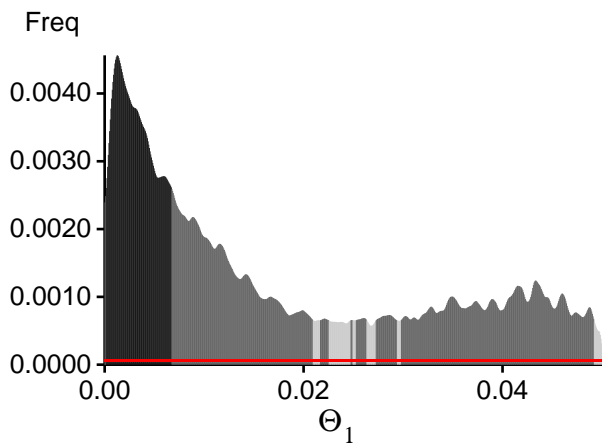
## Citation suggestions:

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.

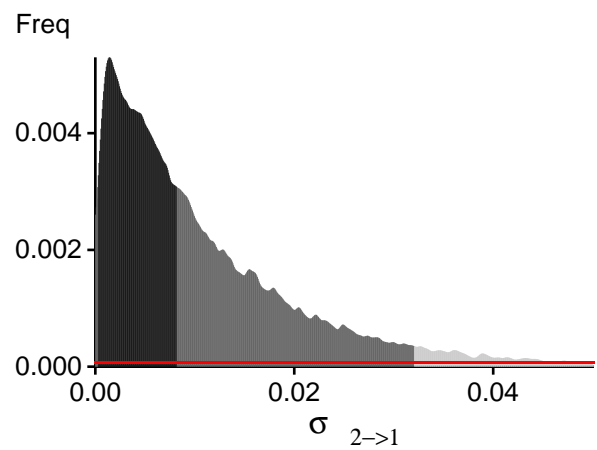
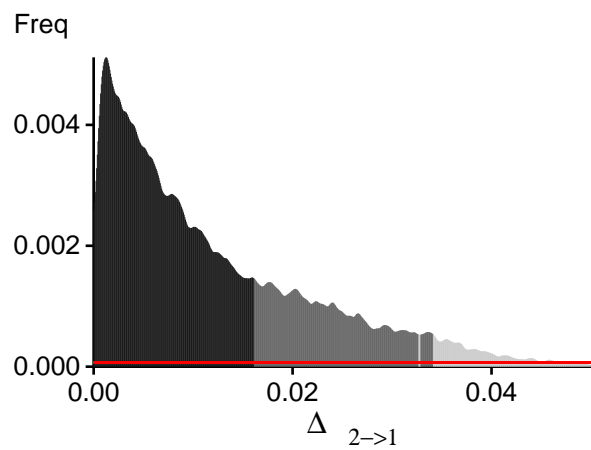
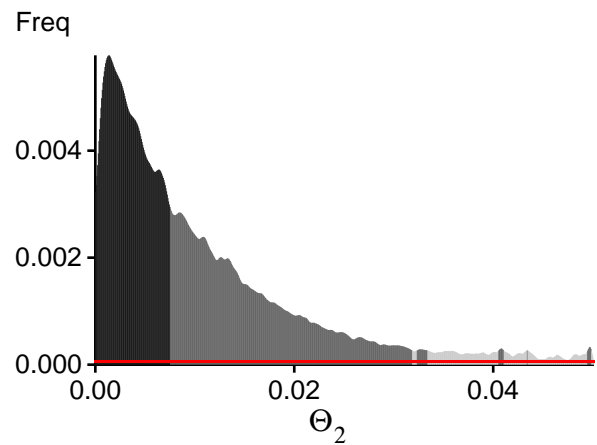
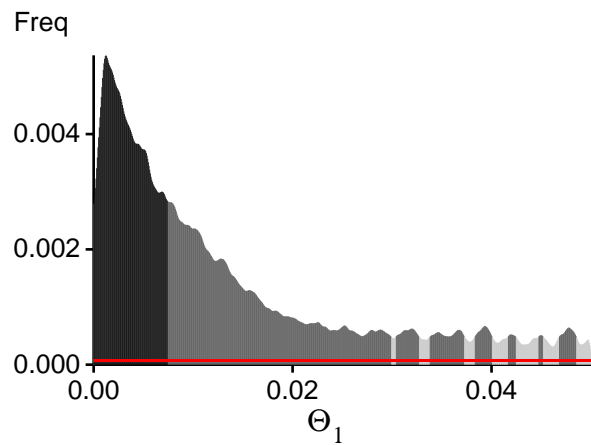
*Bayesian Analysis: Posterior distribution for locus 1*

## *Bayesian Analysis: Posterior distribution for locus 2*

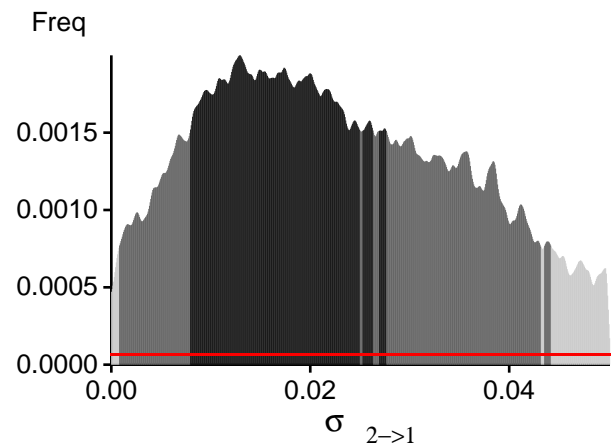
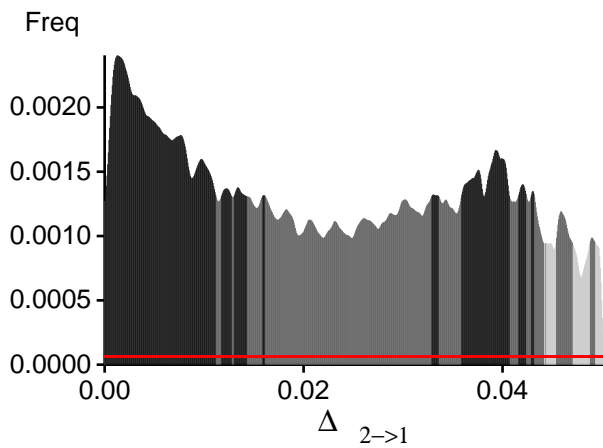
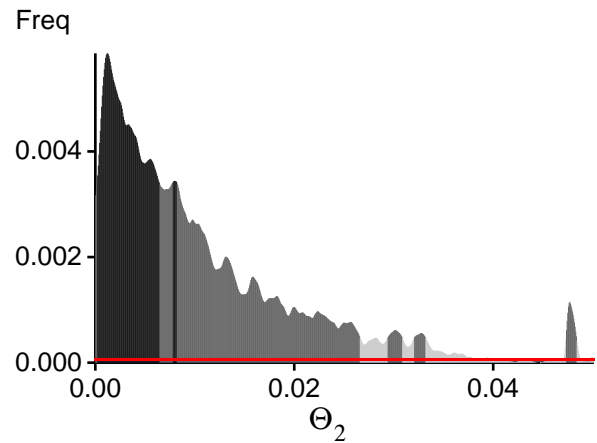
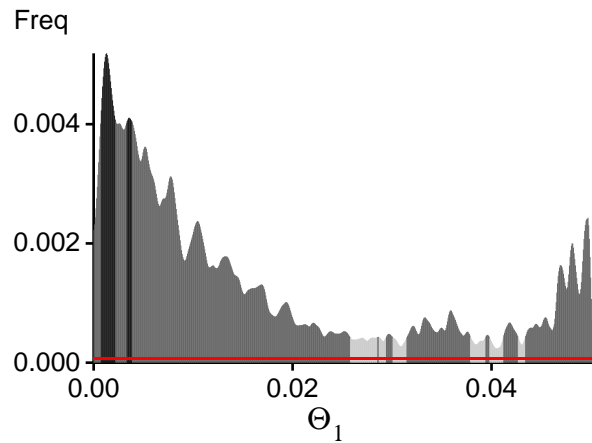




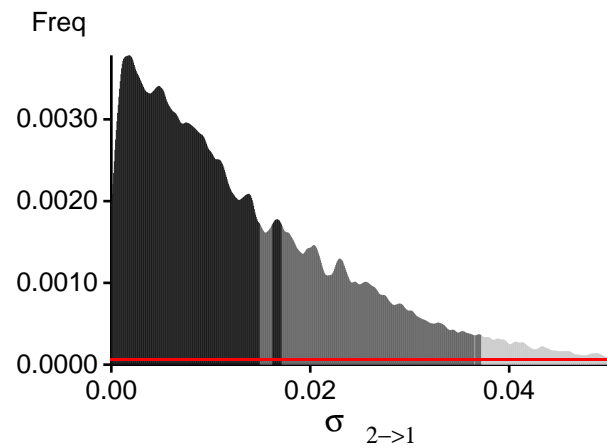
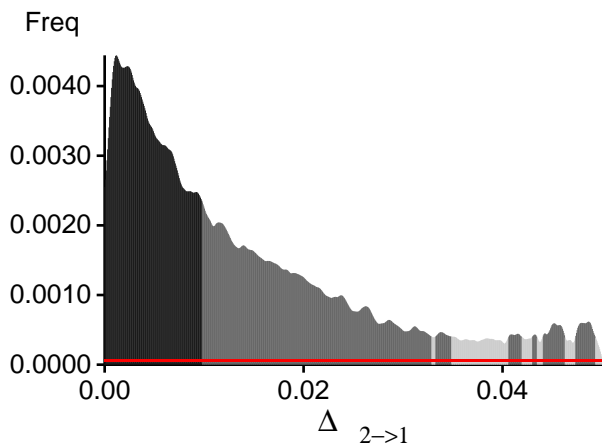
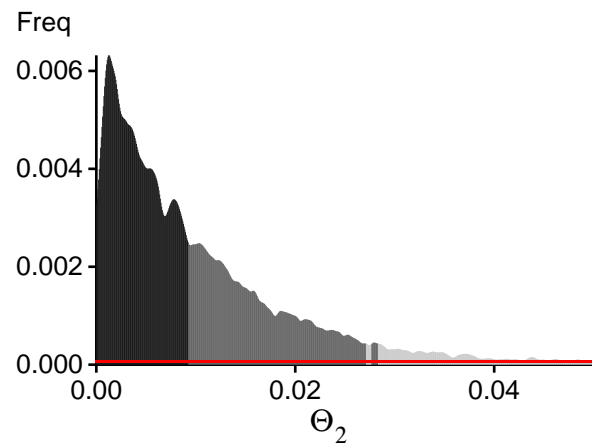
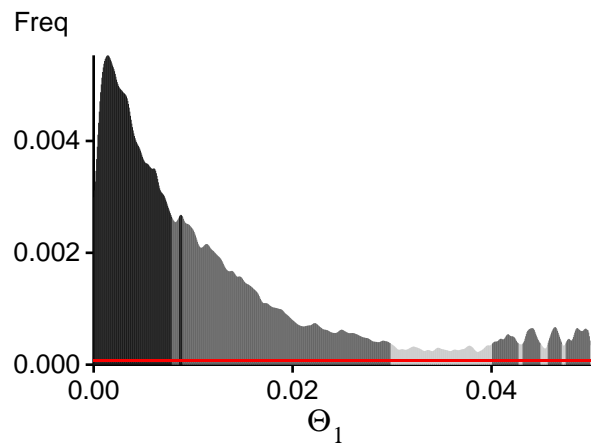
### *Bayesian Analysis: Posterior distribution for locus 3*

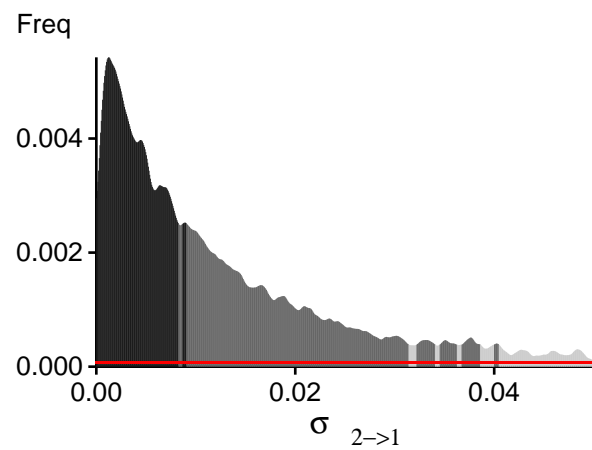
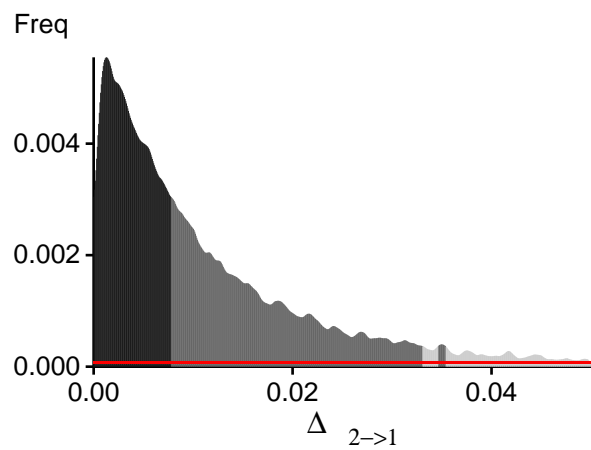
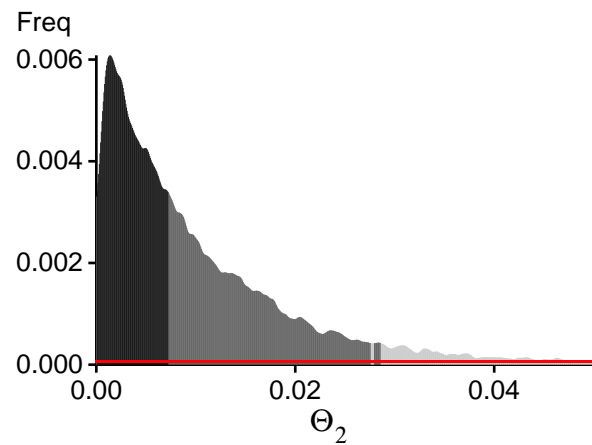
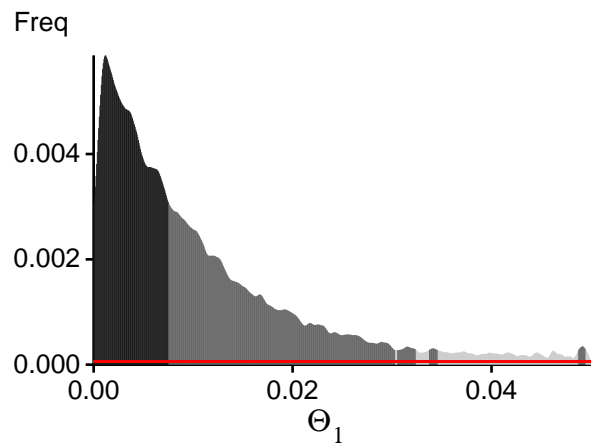


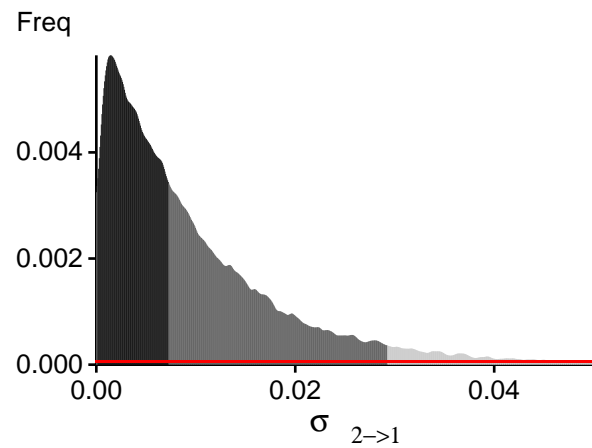
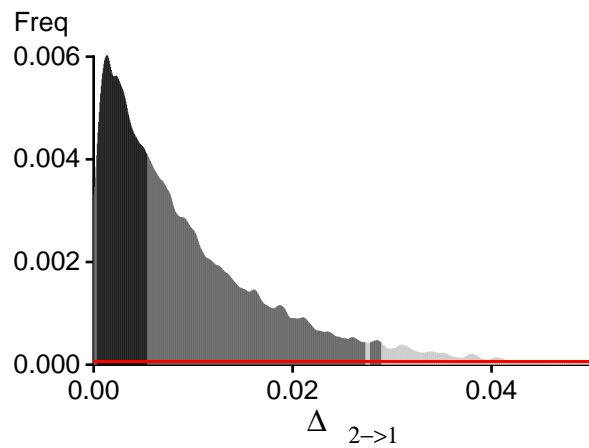
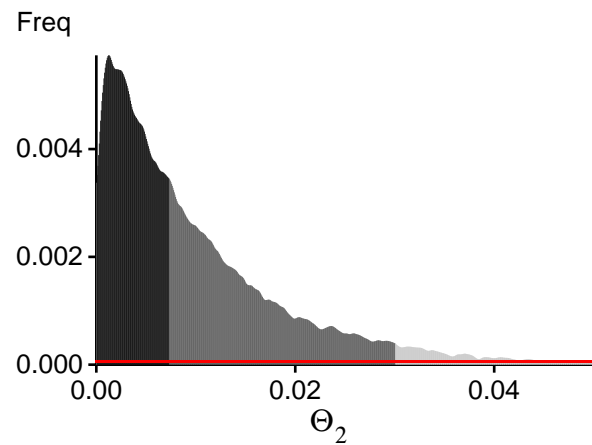
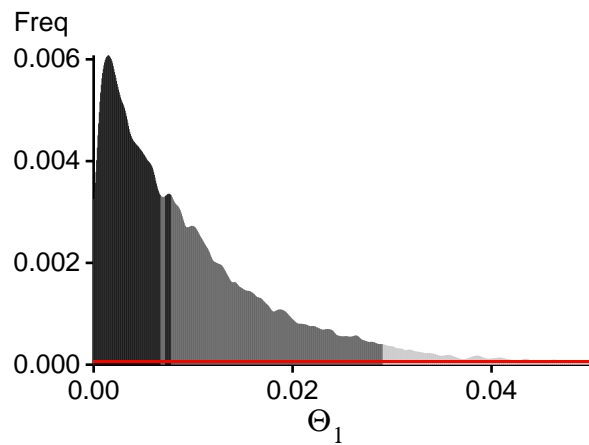
## *Bayesian Analysis: Posterior distribution for locus 4*

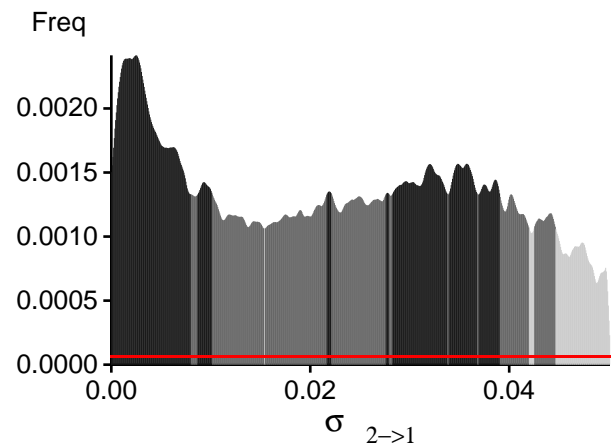
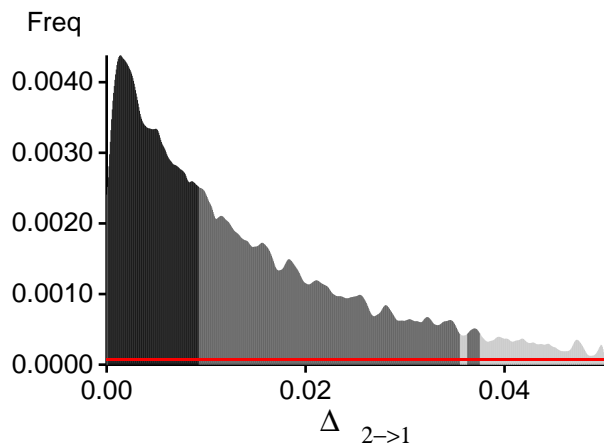
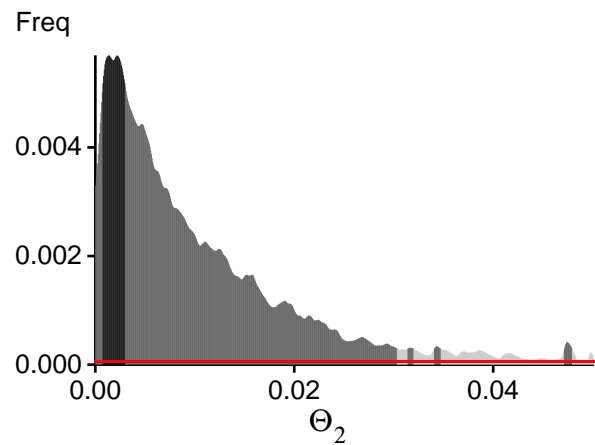
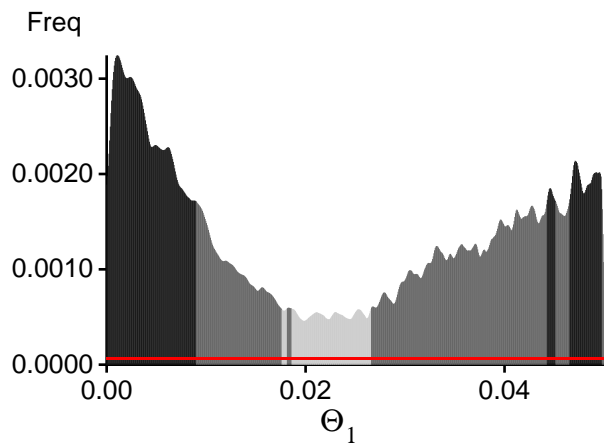


## *Bayesian Analysis: Posterior distribution for locus 5*

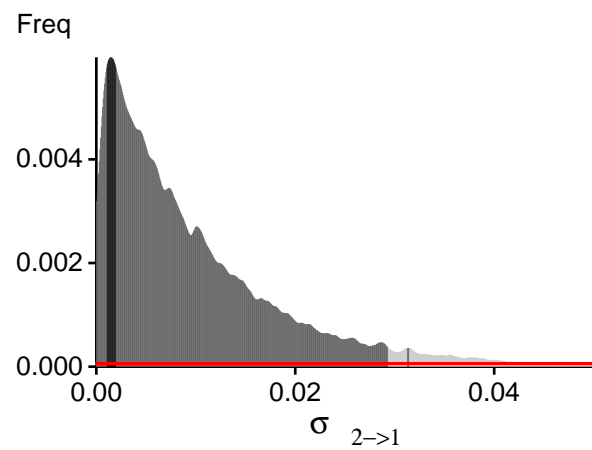
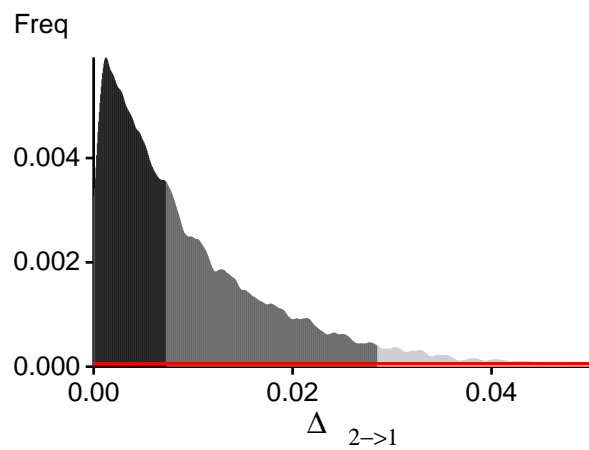
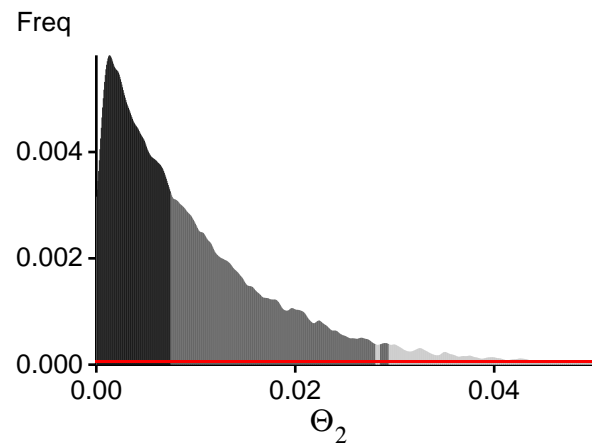
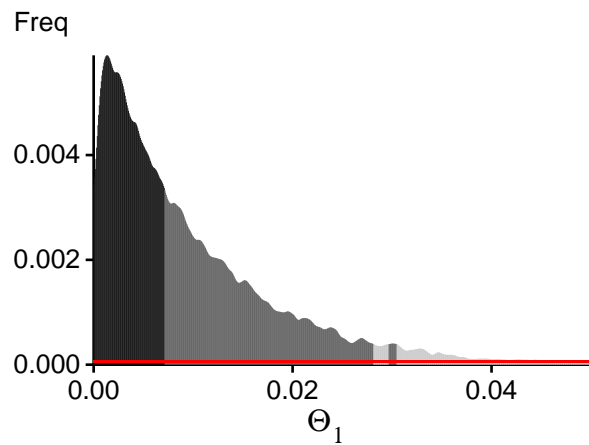


*Bayesian Analysis: Posterior distribution for locus 6*

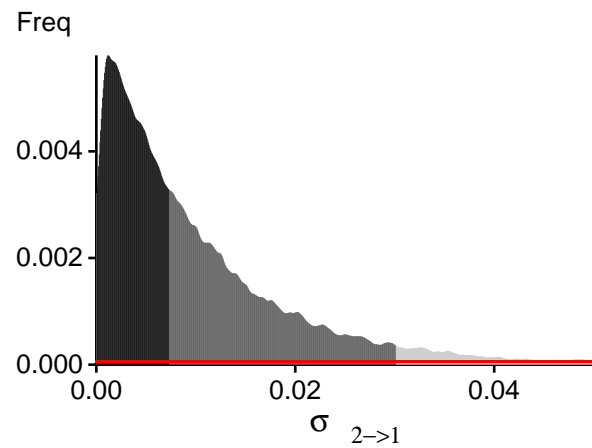
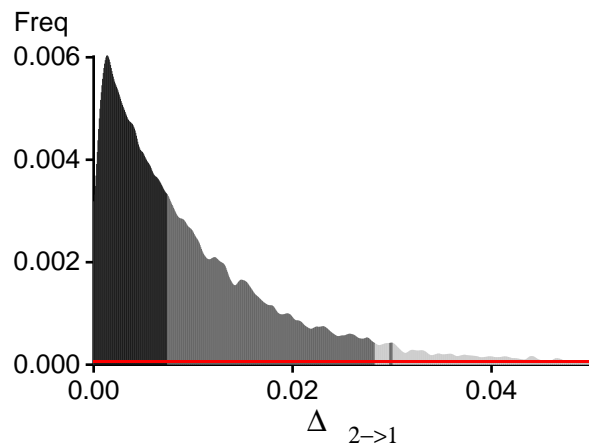
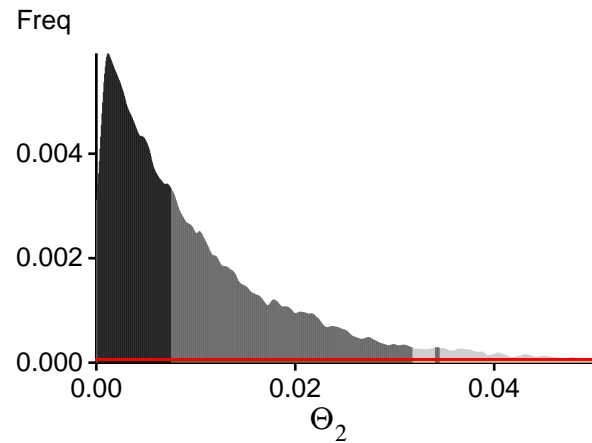
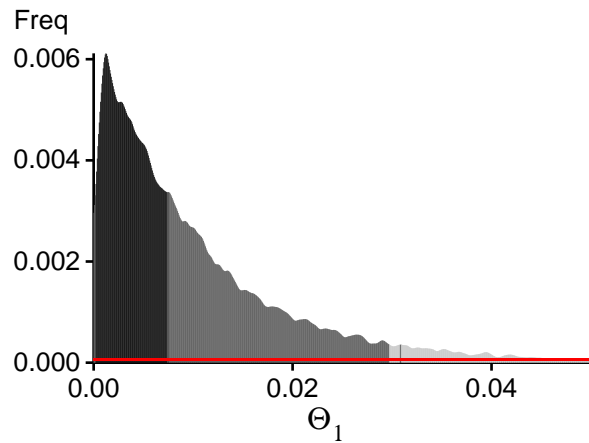
*Bayesian Analysis: Posterior distribution for locus 7*

*Bayesian Analysis: Posterior distribution for locus 8*

## *Bayesian Analysis: Posterior distribution for locus 9*

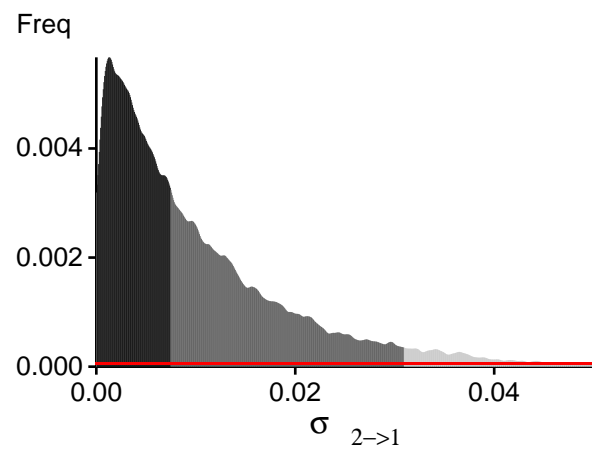
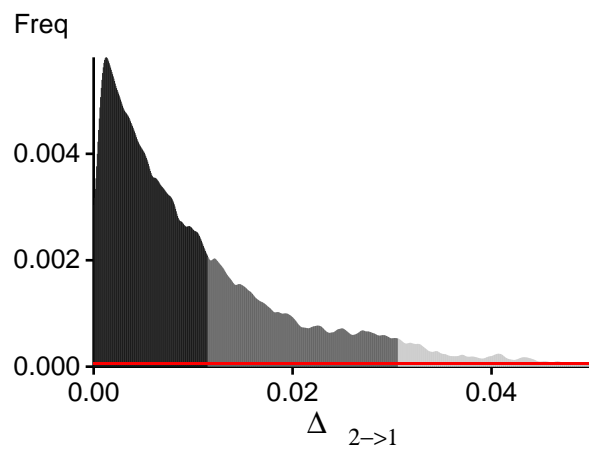
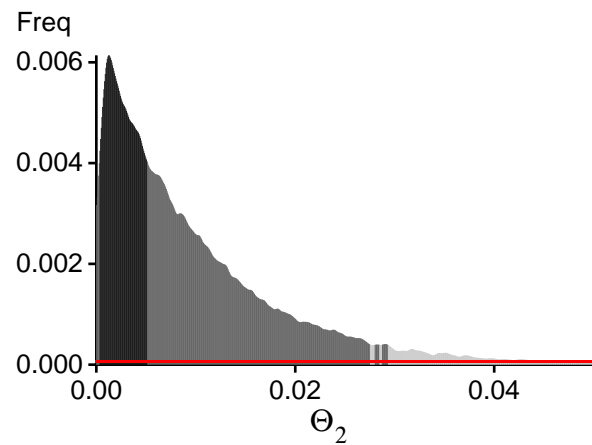
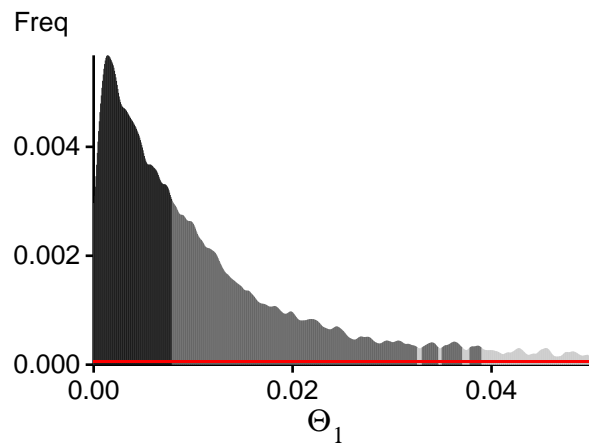


## Bayesian Analysis: Posterior distribution for locus 10

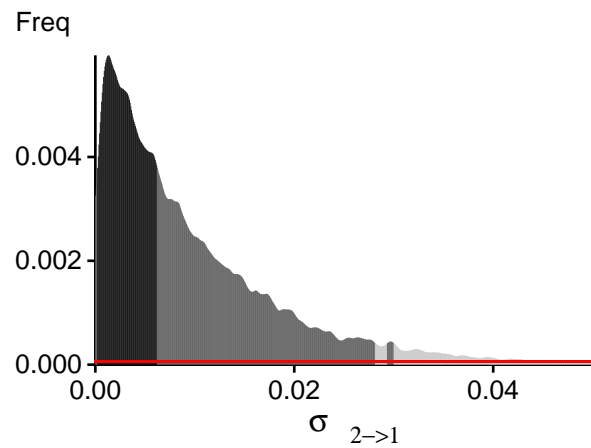
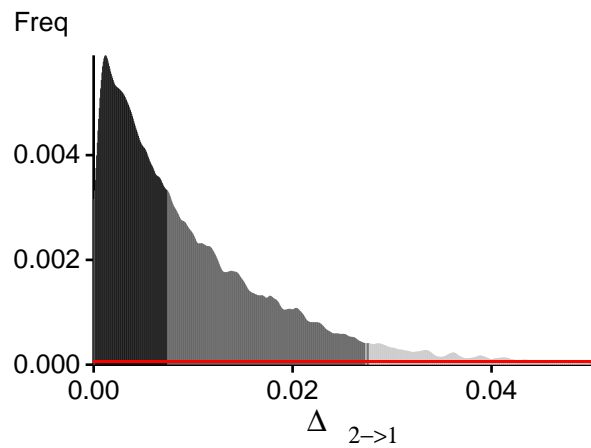
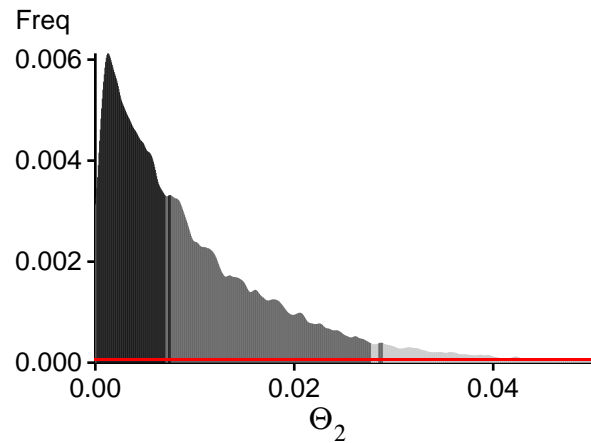
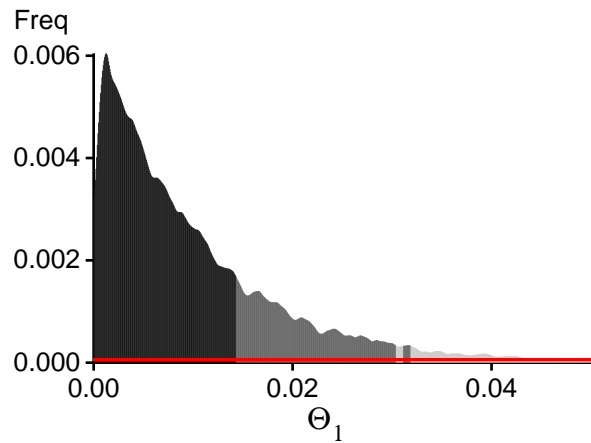




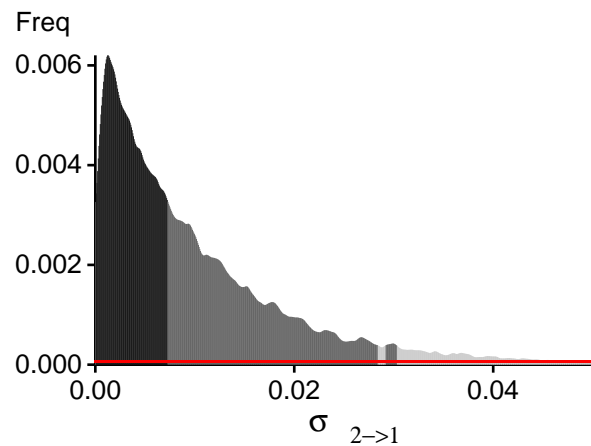
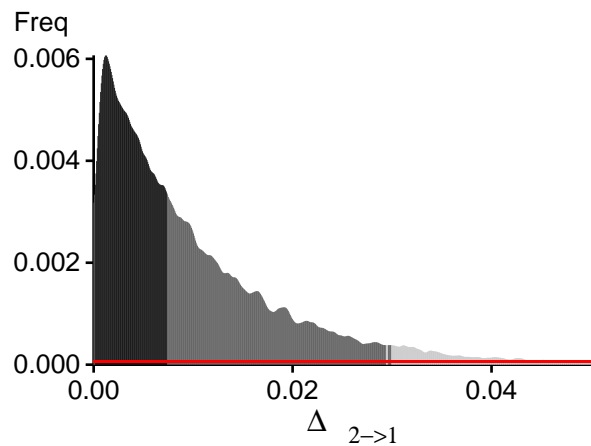
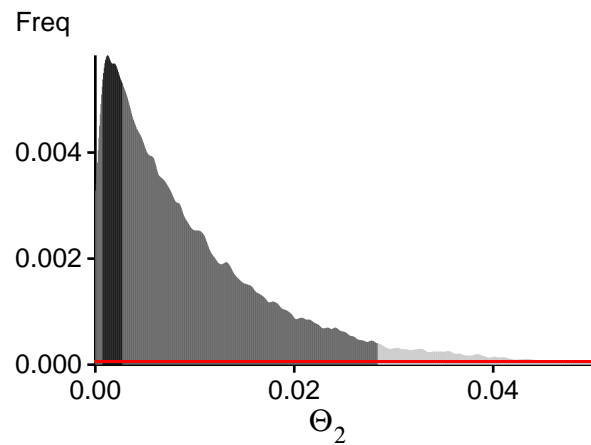
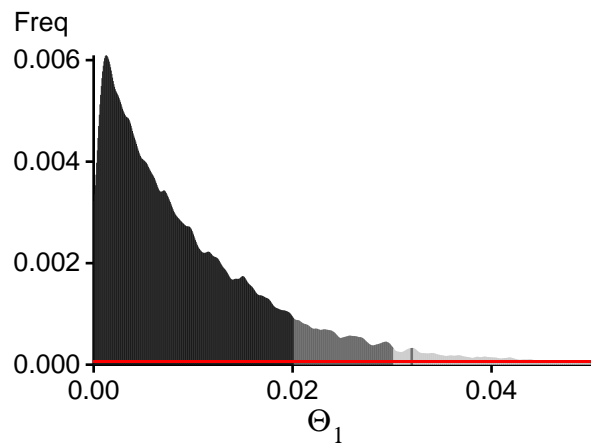
## *Bayesian Analysis: Posterior distribution for locus 11*



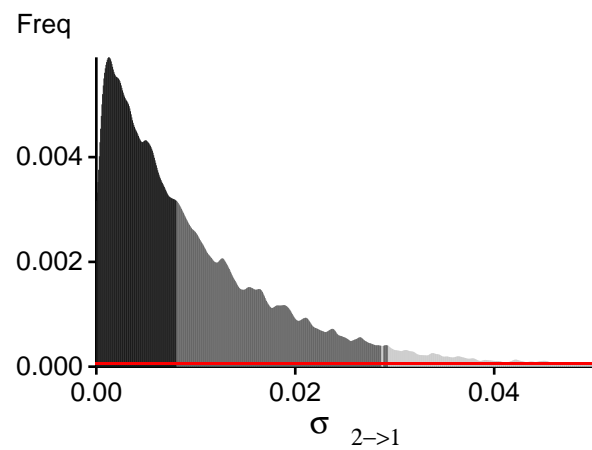
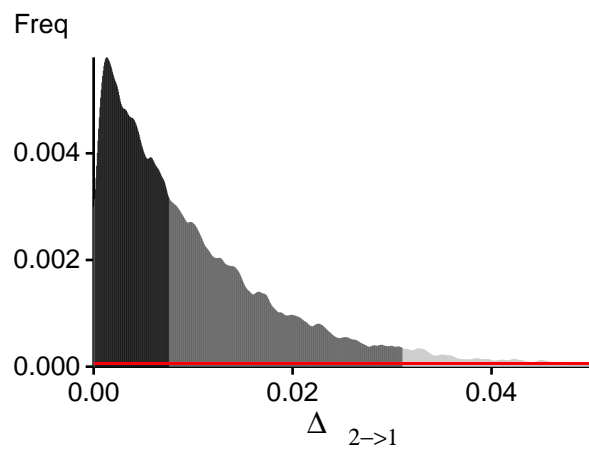
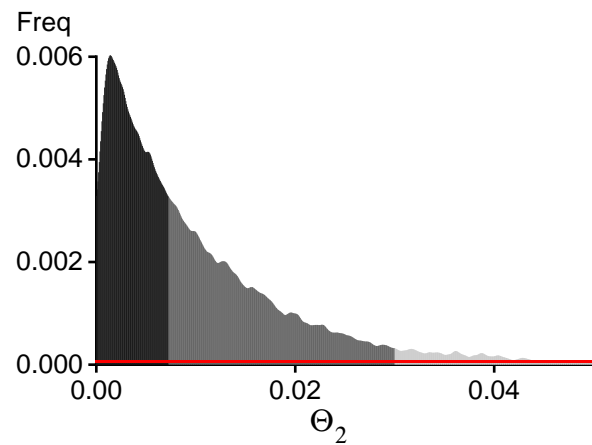
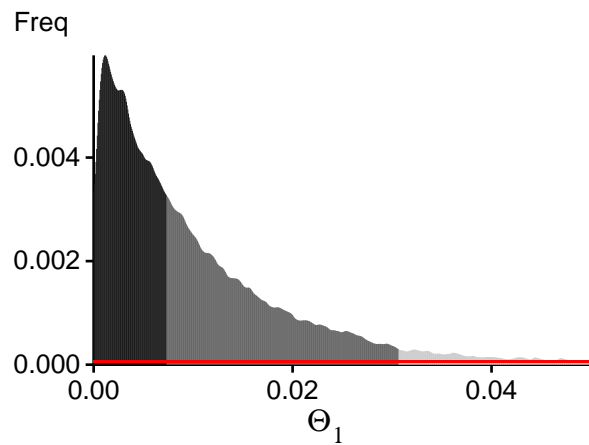
## Bayesian Analysis: Posterior distribution for locus 12



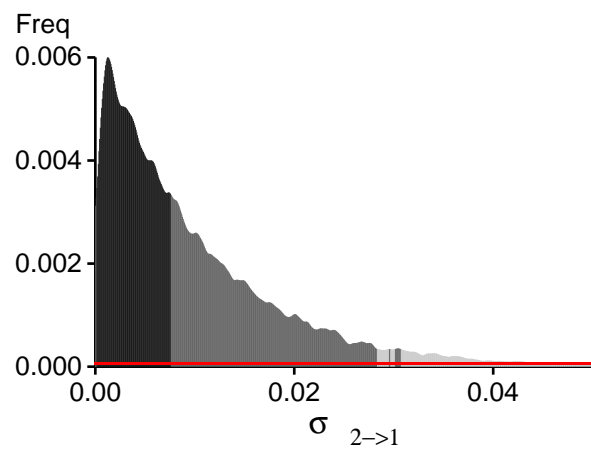
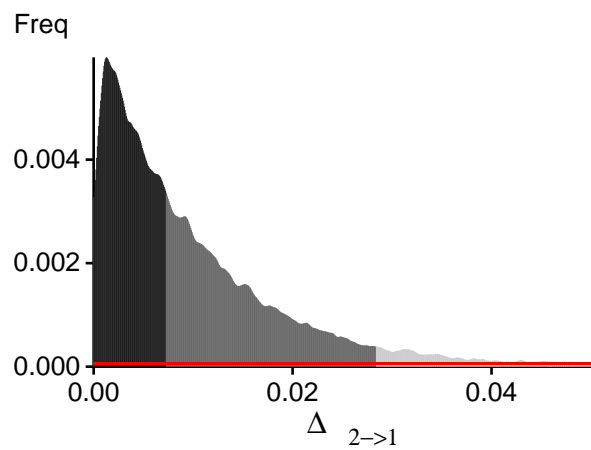
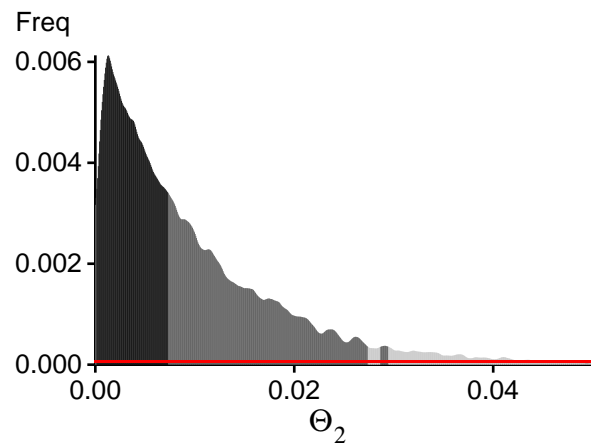
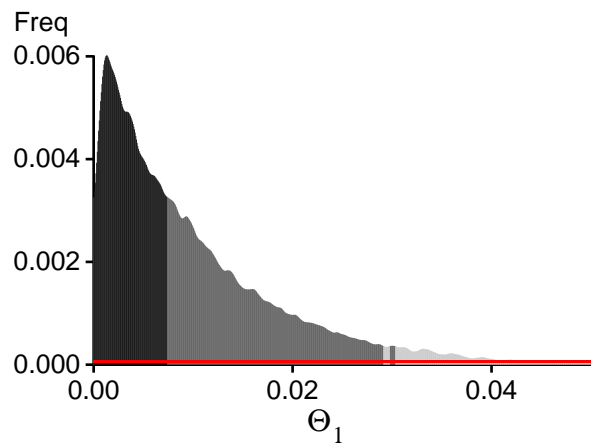
## *Bayesian Analysis: Posterior distribution for locus 13*



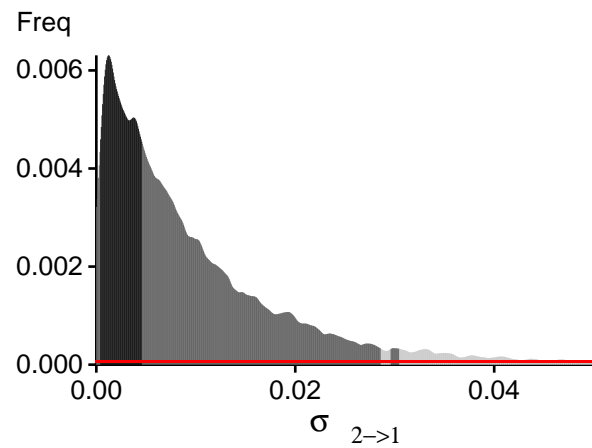
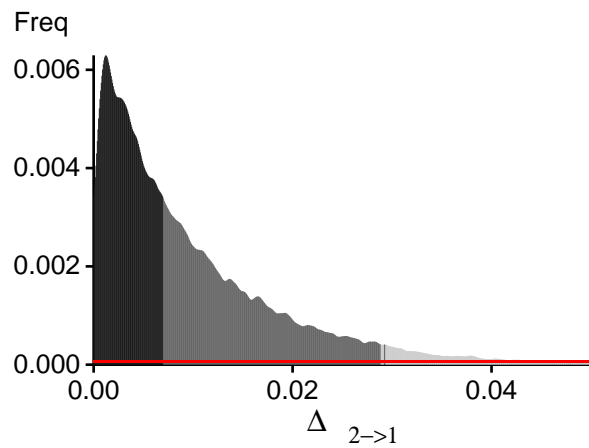
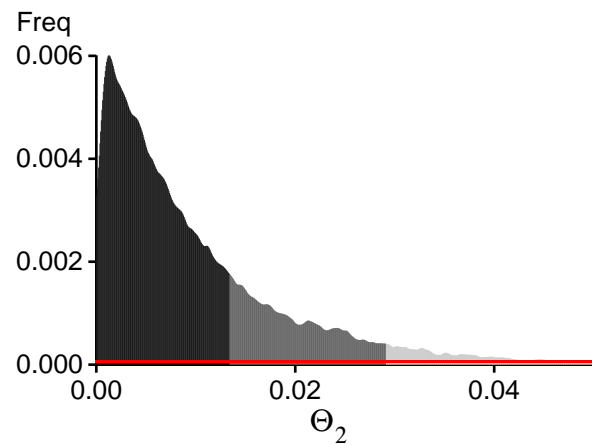
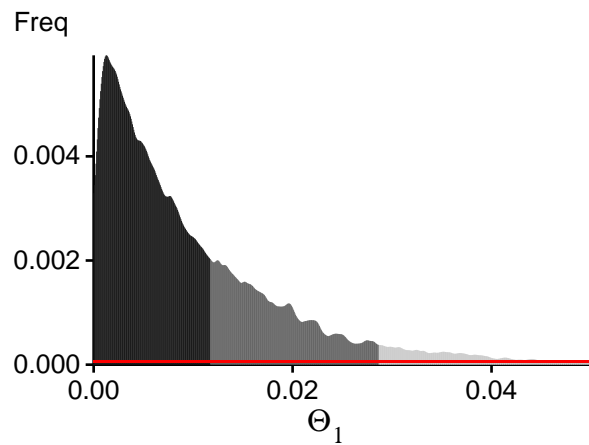
## *Bayesian Analysis: Posterior distribution for locus 14*



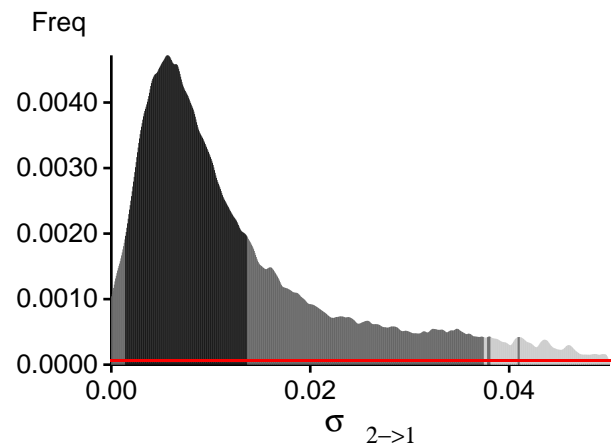
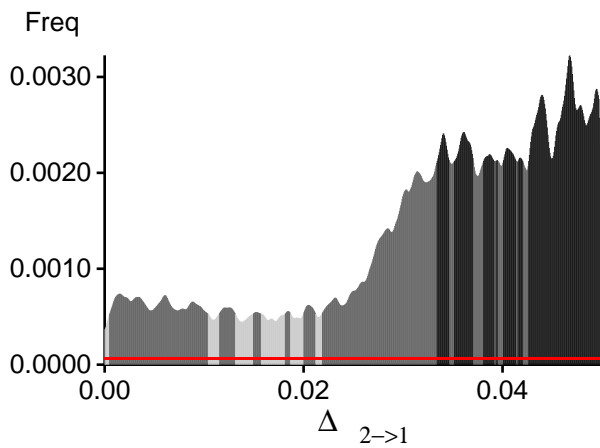
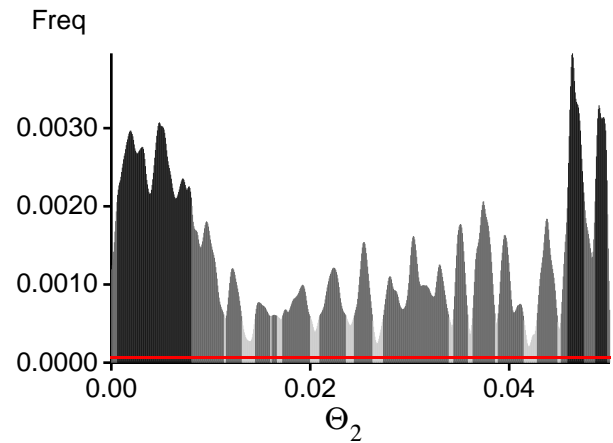
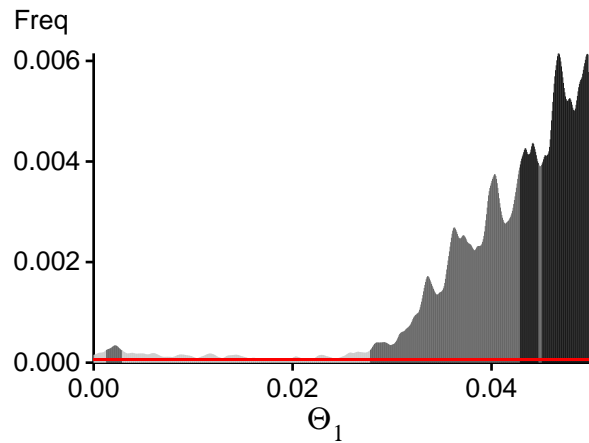
## *Bayesian Analysis: Posterior distribution for locus 15*



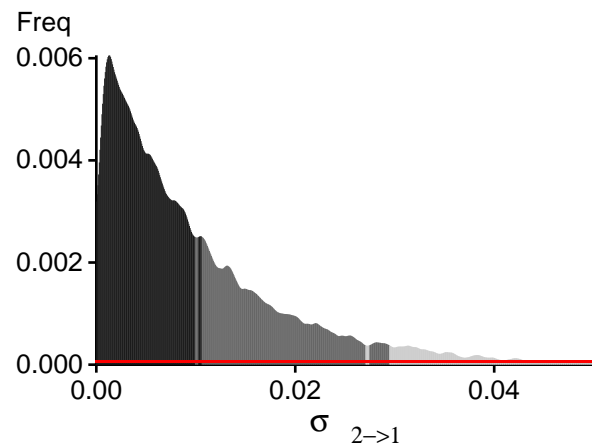
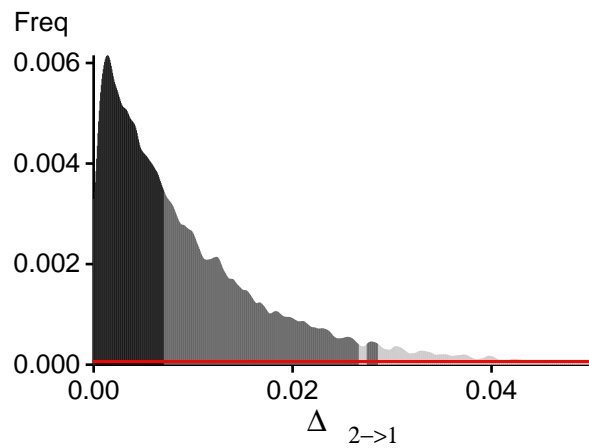
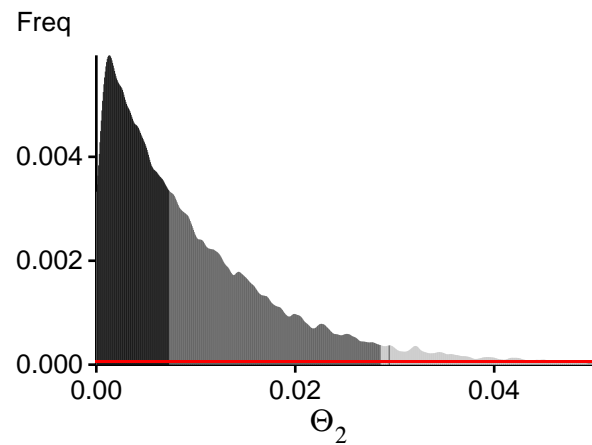
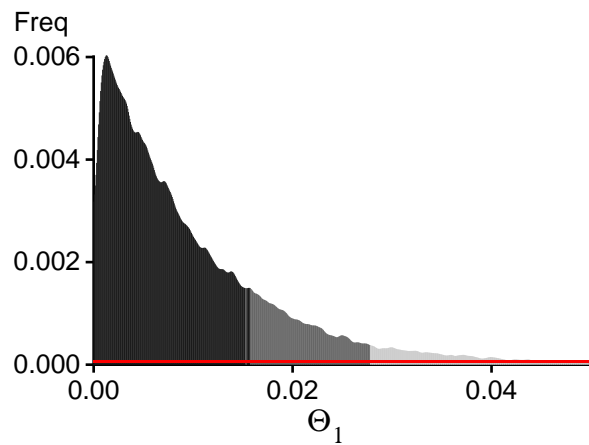
## Bayesian Analysis: Posterior distribution for locus 16



## Bayesian Analysis: Posterior distribution for locus 17

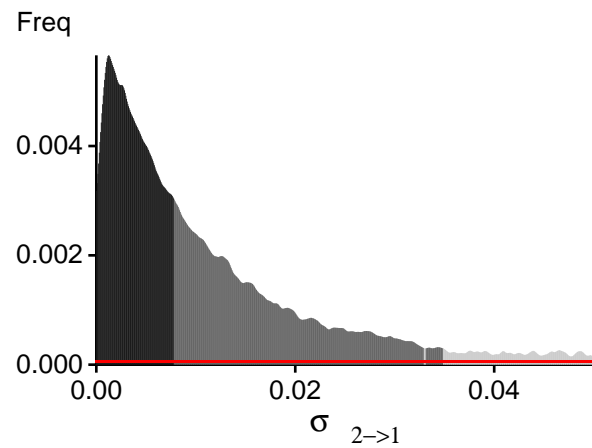
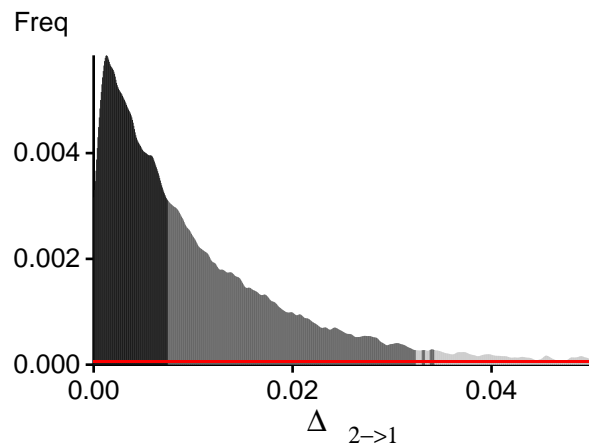
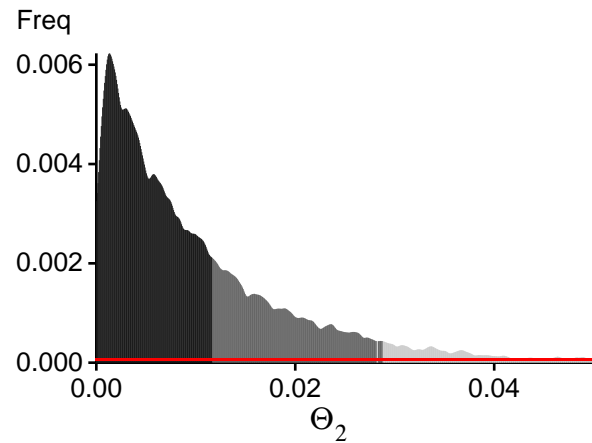
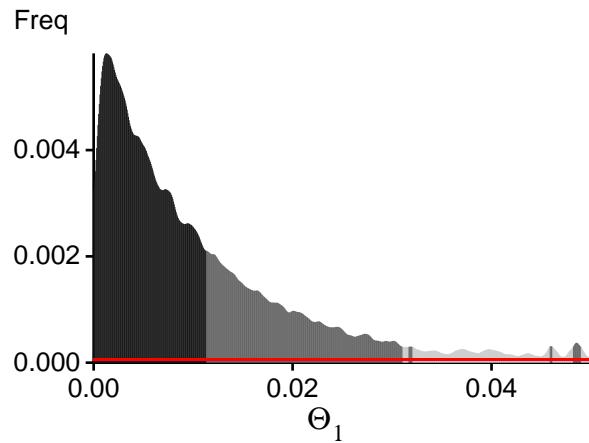


## Bayesian Analysis: Posterior distribution for locus 18

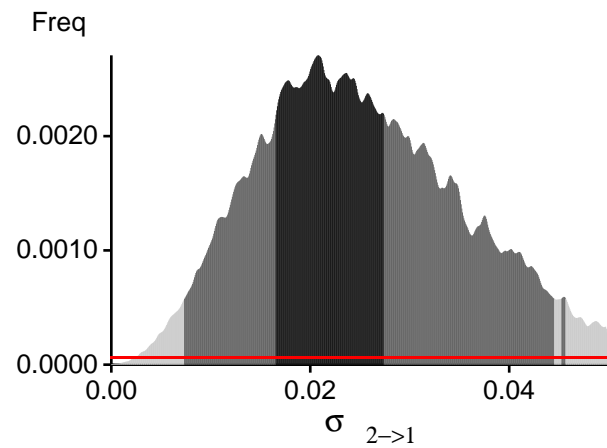
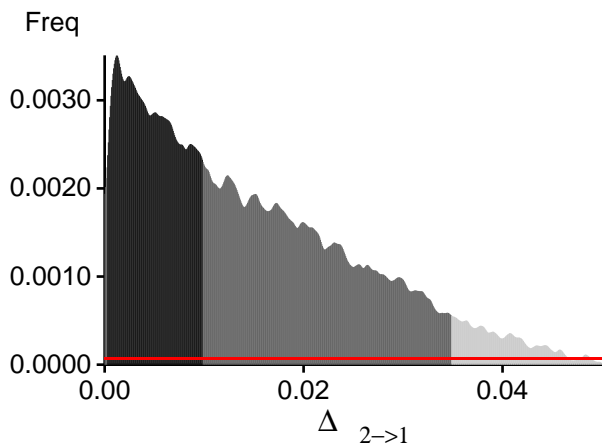
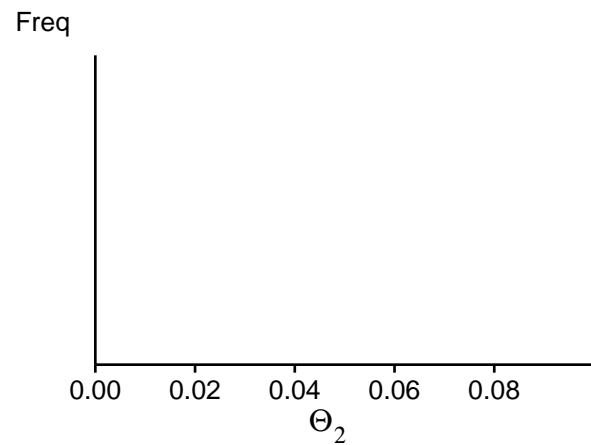
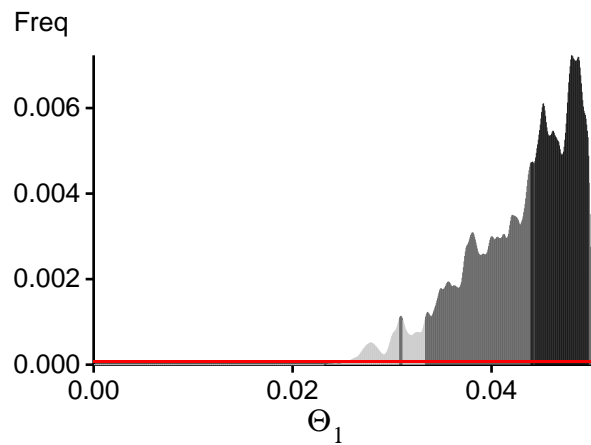


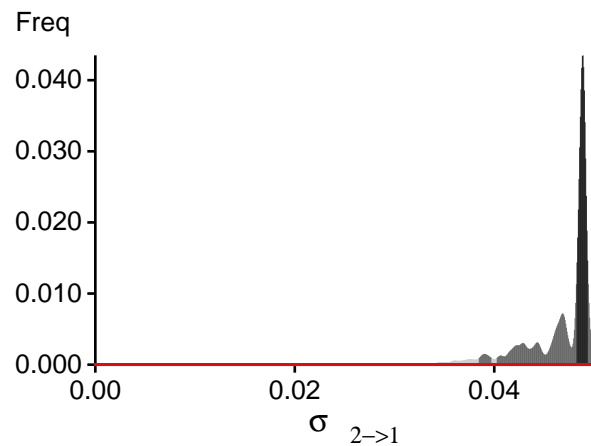
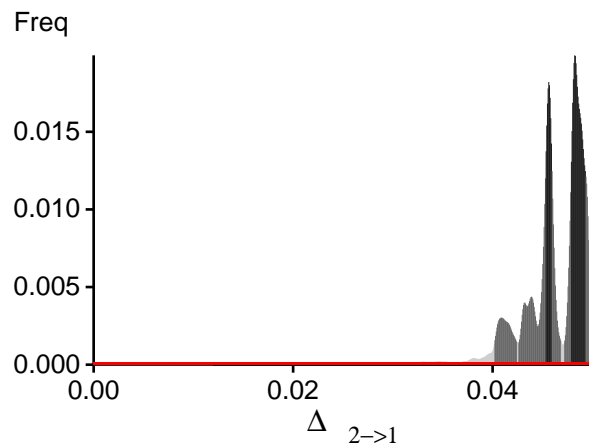
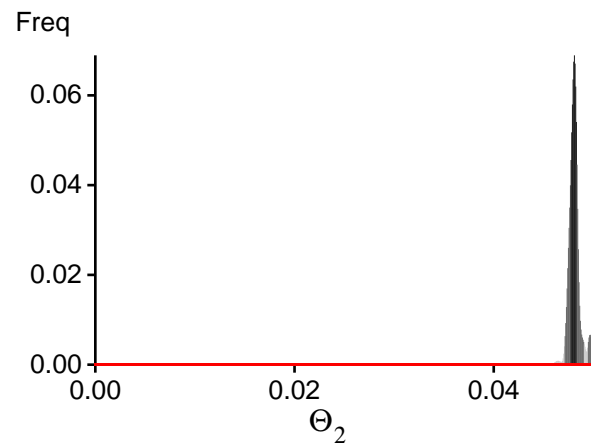
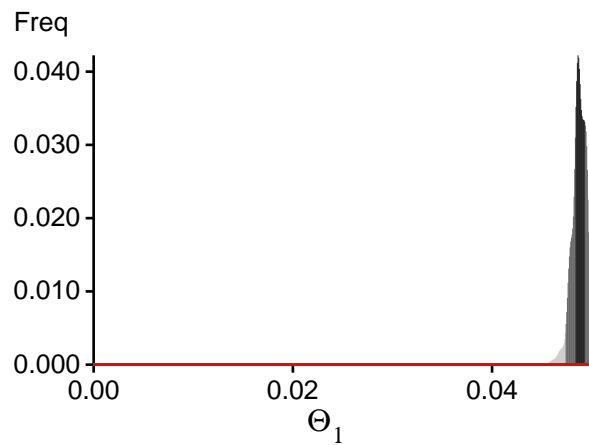


## *Bayesian Analysis: Posterior distribution for locus 19*



## *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	-12297.66	-9094.53	-9120.52
2	-9072.45	-7241.38	-6984.35
3	-9438.17	-7594.24	-7571.29
4	-9494.27	-7694.42	-7366.25
5	-11920.57	-8811.92	-8001.90
6	-10261.49	-7853.67	-7345.22
7	-10354.07	-8216.92	-8072.59
8	-10093.87	-7780.12	-7344.06
9	-11575.81	-9244.04	-9446.35
10	-11670.44	-9026.64	-8932.01
11	-9622.09	-7836.17	-7677.98
12	-10588.83	-8103.27	-8070.37
13	-12362.63	-9665.00	-9965.87
14	-12073.79	-9499.04	-9964.04
15	-9841.86	-7665.14	-8054.50
16	-10542.60	-8453.31	-8573.02
17	-10130.26	-8145.58	-7613.48
18	-10892.17	-8756.77	-8417.51
19	-11015.22	-8376.39	-8462.87
20	-10983.07	-8517.30	-8172.12
All	-214622.43	-167966.92	-165547.38

(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 = -391.075363]

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
$\Theta_1$	1922469/2502196	0.76831
$\Theta_2$	1915073/2501654	0.76552
$\Delta_{2 \rightarrow 1}$	2165458/2497408	0.86708
$\sigma_{2 \rightarrow 1}$	2068240/2502029	0.82663
Genealogies	310114/9996713	0.03102

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

Parameter	Autocorrelation	Effective Sample Size
$\Theta_1$	0.43255	269310.15
$\Theta_2$	0.49101	244474.98
$\Delta_{2 \rightarrow 1}$	0.24620	349013.65
$\sigma_{2 \rightarrow 1}$	0.24174	353689.80
Genealogies	0.24174	353689.80

## *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