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 14:45:30 2020
Program finished at   Fri Jul 24 14:57:46 2020 [Runtime:0000:00:12:16]

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) 1417033491
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	*	0
2 Pop2	d	*

Order of parameters:

1	Θ_1	<displayed>
2	Θ_2	<displayed>

3	$\Delta_{1->2}$	<displayed>
4	$\sigma_{1->2}$	<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
-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
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	

	10	10	
	11	10	
	12	10	
	13	10	
	14	10	
	15	10	
	16	10	
	17	10	
	18	10	
	19	10	
	20	10	
2 Pop2	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	0.00000	0.00013	0.00123	0.00747	0.02700	0.00730	0.01004
1	Θ_2	0.00000	0.00000	0.00123	0.01113	0.02640	0.00717	0.00500
1	$D_{1->2}$	0.00000	0.00000	0.00137	0.01080	0.03160	0.00710	0.00329
1	$S_{1->2}$	0.00000	0.00000	0.00123	0.00713	0.03020	0.00710	0.00248
2	Θ_1	0.00000	0.00000	0.00137	0.01087	0.02813	0.00737	0.03072
2	Θ_2	0.00000	0.00000	0.00150	0.00820	0.03060	0.00823	0.01207
2	$D_{1->2}$	0.00000	0.00000	0.00117	0.01240	0.03207	0.00997	0.00421
2	$S_{1->2}$	0.00000	0.00020	0.00283	0.00733	0.02813	0.00717	0.00261
3	Θ_1	0.00000	0.00040	0.00130	0.00420	0.02820	0.00743	0.01007
3	Θ_2	0.00000	0.00040	0.00137	0.00493	0.02887	0.00717	0.00494
3	$D_{1->2}$	0.00000	0.00053	0.00123	0.00327	0.02873	0.00717	0.00332
3	$S_{1->2}$	0.00000	0.00013	0.00137	0.00633	0.02740	0.00723	0.00249
4	Θ_1	0.00000	0.00000	0.00117	0.00867	0.03040	0.00730	0.06459
4	Θ_2	0.00000	0.00000	0.00123	0.01080	0.02680	0.00863	0.02459
4	$D_{1->2}$	0.00000	0.00000	0.00130	0.00933	0.02113	0.02130	0.01044
4	$S_{1->2}$	0.00000	0.00067	0.00777	0.01207	0.03580	0.01210	0.00448
5	Θ_1	0.00000	0.00000	0.00130	0.00727	0.02840	0.00723	0.00987
5	Θ_2	0.00000	0.00000	0.00137	0.00807	0.03087	0.00723	0.00504
5	$D_{1->2}$	0.00000	0.00007	0.00137	0.00733	0.02833	0.00730	0.00333
5	$S_{1->2}$	0.00000	0.00073	0.00137	0.00293	0.02733	0.00730	0.00250
6	Θ_1	0.00000	0.00000	0.00143	0.00727	0.02860	0.00723	0.01019
6	Θ_2	0.00000	0.00007	0.00123	0.00733	0.02593	0.00723	0.00501
6	$D_{1->2}$	0.00000	0.00000	0.00123	0.00713	0.02787	0.00710	0.00330
6	$S_{1->2}$	0.00000	0.00047	0.00137	0.00367	0.02613	0.00730	0.00254
7	Θ_1	0.00000	0.00000	0.00137	0.00733	0.02833	0.00730	0.00997
7	Θ_2	0.00000	0.00067	0.00130	0.00267	0.03213	0.00730	0.00503
7	$D_{1->2}$	0.00000	0.00000	0.00137	0.01460	0.02773	0.00723	0.00329
7	$S_{1->2}$	0.00000	0.00107	0.00123	0.00133	0.02767	0.00737	0.00251
8	Θ_1	0.00000	0.00000	0.00003	0.09993	0.09993	0.00003	0.09591

Locus	Parameter	2.5%	25.0%	Mode	75.0%	97.5%	Median	Mean
8	Θ_2	0.03560	0.04640	0.04970	0.04993	0.05020	0.04503	0.03363
8	$D_{1->2}$	0.00000	0.00020	0.00137	0.01507	0.04160	0.02170	0.00989
8	$S_{1->2}$	0.00360	0.00887	0.01677	0.02360	0.04513	0.02150	0.00657
9	Θ_1	0.00000	0.00000	0.00003	0.09993	0.09993	0.00003	0.09369
9	Θ_2	0.04747	0.04940	0.04977	0.04993	0.05020	0.04877	0.04179
9	$D_{1->2}$	0.00000	0.00020	0.00157	0.01147	0.02233	0.02357	0.01203
9	$S_{1->2}$	0.00540	0.00847	0.01470	0.02153	0.04567	0.02177	0.00710
10	Θ_1	0.00000	0.00000	0.00130	0.00727	0.02533	0.00723	0.00988
10	Θ_2	0.00000	0.00000	0.00130	0.00740	0.03027	0.00743	0.00511
10	$D_{1->2}$	0.00000	0.00000	0.00150	0.00740	0.02720	0.00737	0.00334
10	$S_{1->2}$	0.00000	0.00007	0.00130	0.00720	0.02820	0.00710	0.00247
11	Θ_1	0.00000	0.00007	0.00130	0.00740	0.02907	0.00730	0.01002
11	Θ_2	0.00000	0.00000	0.00123	0.01327	0.02827	0.00723	0.00498
11	$D_{1->2}$	0.00000	0.00000	0.00130	0.00733	0.02787	0.00730	0.00336
11	$S_{1->2}$	0.00000	0.00027	0.00130	0.00493	0.03080	0.00717	0.00247
12	Θ_1	0.00000	0.00000	0.00123	0.00733	0.02707	0.00730	0.01008
12	Θ_2	0.00000	0.00000	0.00123	0.00727	0.02847	0.00723	0.00506
12	$D_{1->2}$	0.00000	0.00000	0.00123	0.00700	0.02653	0.00703	0.00326
12	$S_{1->2}$	0.00000	0.00000	0.00117	0.00667	0.02853	0.00730	0.00252
13	Θ_1	0.00000	0.00000	0.00123	0.00713	0.02540	0.00717	0.01006
13	Θ_2	0.00000	0.00000	0.00130	0.00720	0.02707	0.00717	0.00495
13	$D_{1->2}$	0.00000	0.00000	0.00130	0.00713	0.02867	0.00710	0.00333
13	$S_{1->2}$	0.00000	0.00000	0.00137	0.00867	0.02873	0.00730	0.00250
14	Θ_1	0.00000	0.00047	0.00130	0.00400	0.02647	0.00743	0.01411
14	Θ_2	0.00000	0.00000	0.00123	0.00760	0.02953	0.00763	0.00588
14	$D_{1->2}$	0.00000	0.00007	0.00123	0.00660	0.02927	0.00750	0.00342
14	$S_{1->2}$	0.00000	0.00000	0.00123	0.00780	0.03380	0.00777	0.00282
15	Θ_1	0.00000	0.00000	0.00123	0.00713	0.02747	0.00717	0.00994
15	Θ_2	0.00000	0.00000	0.00123	0.01313	0.02827	0.00703	0.00498
15	$D_{1->2}$	0.00000	0.00000	0.00177	0.01073	0.03180	0.00730	0.00334
15	$S_{1->2}$	0.00000	0.00007	0.00137	0.00733	0.02787	0.00723	0.00245
16	Θ_1	0.04347	0.04360	0.04403	0.04487	0.04507	0.04130	0.09534
16	Θ_2	0.03673	0.04667	0.04970	0.05000	0.05020	0.04563	0.03943

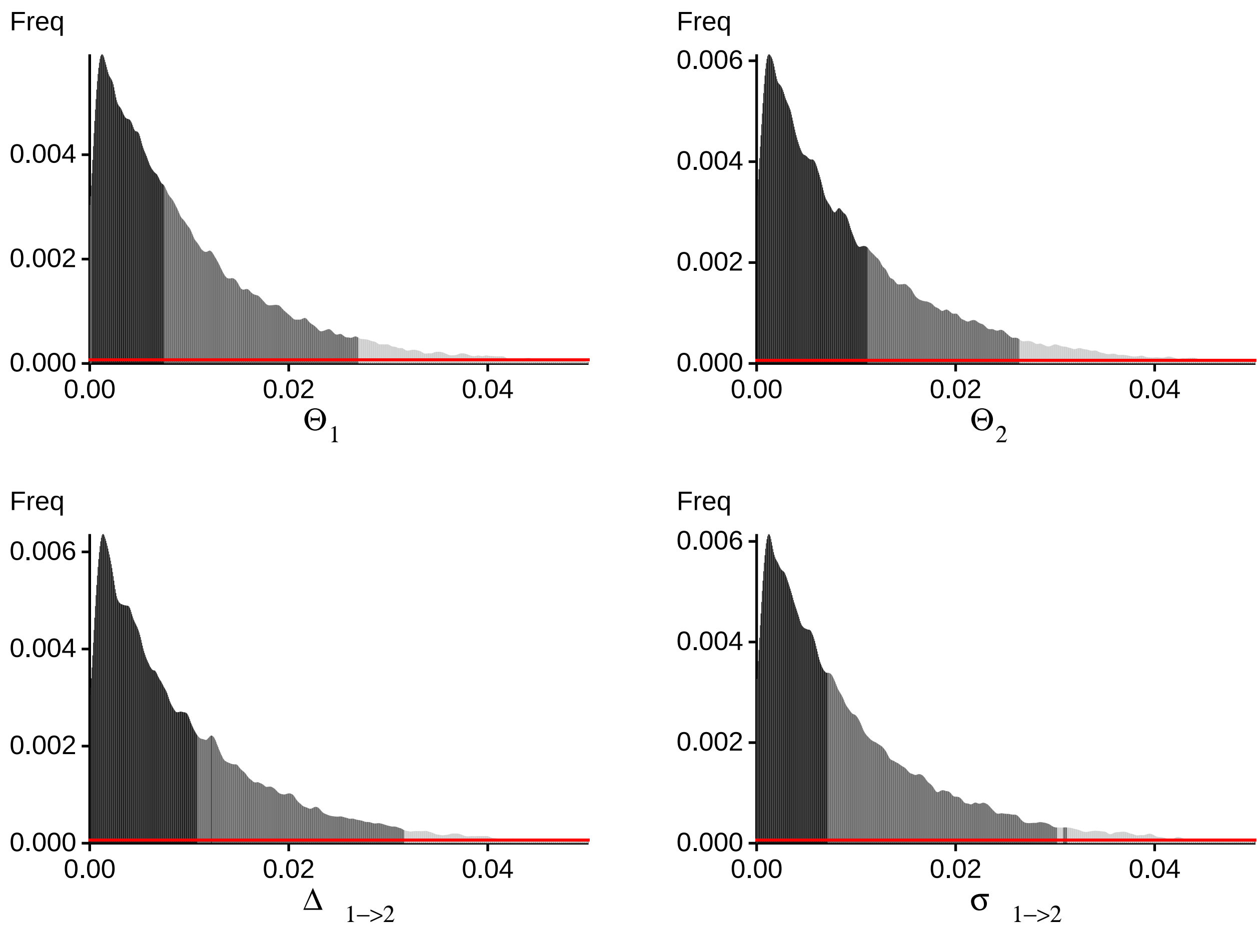
Locus	Parameter	2.5%	25.0%	Mode	75.0%	97.5%	Median	Mean
16	$D_{1->2}$	0.00000	0.00013	0.00143	0.01187	0.03467	0.01490	0.00864
16	$S_{1->2}$	0.00827	0.01433	0.02037	0.02887	0.04507	0.02483	0.00781
17	Θ_1	0.00000	0.00000	0.00003	0.09993	0.09993	0.00003	0.09449
17	Θ_2	0.03200	0.04567	0.04970	0.05000	0.05020	0.04463	0.03360
17	$D_{1->2}$	0.00000	0.00000	0.00123	0.01133	0.02787	0.01243	0.00482
17	$S_{1->2}$	0.00700	0.01813	0.02270	0.02780	0.04400	0.02417	0.00669
18	Θ_1	0.00000	0.00000	0.00137	0.01853	0.02940	0.00717	0.01000
18	Θ_2	0.00000	0.00000	0.00130	0.00733	0.02927	0.00737	0.00515
18	$D_{1->2}$	0.00000	0.00000	0.00117	0.00733	0.02987	0.00730	0.00339
18	$S_{1->2}$	0.00000	0.00000	0.00143	0.00727	0.02840	0.00723	0.00250
19	Θ_1	0.00000	0.00000	0.00163	0.00713	0.02207	0.00710	0.00987
19	Θ_2	0.00000	0.00000	0.00130	0.00720	0.02860	0.00723	0.00507
19	$D_{1->2}$	0.00000	0.00007	0.00130	0.00740	0.02767	0.00737	0.00334
19	$S_{1->2}$	0.00000	0.00000	0.00137	0.00820	0.02933	0.00730	0.00249
20	Θ_1	0.00000	0.00000	0.00130	0.00733	0.02907	0.00730	0.03978
20	Θ_2	0.00000	0.00000	0.00123	0.00853	0.02307	0.01157	0.01218
20	$D_{1->2}$	0.00000	0.00000	0.00190	0.00920	0.03560	0.00923	0.00489
20	$S_{1->2}$	0.00000	0.00000	0.00123	0.01007	0.03940	0.01290	0.00490
All	Θ_1	0.04613	0.04653	0.04710	0.04747	0.04773	0.04697	0.04639
All	Θ_2	0.04893	0.04933	0.04957	0.04980	0.05000	0.04957	0.04930
All	$D_{1->2}$	0.03820	0.04660	0.04710	0.04753	0.05000	0.04490	0.04438
All	$S_{1->2}$	0.03807	0.04740	0.04797	0.04853	0.04987	0.04597	0.04514

Citation suggestions:

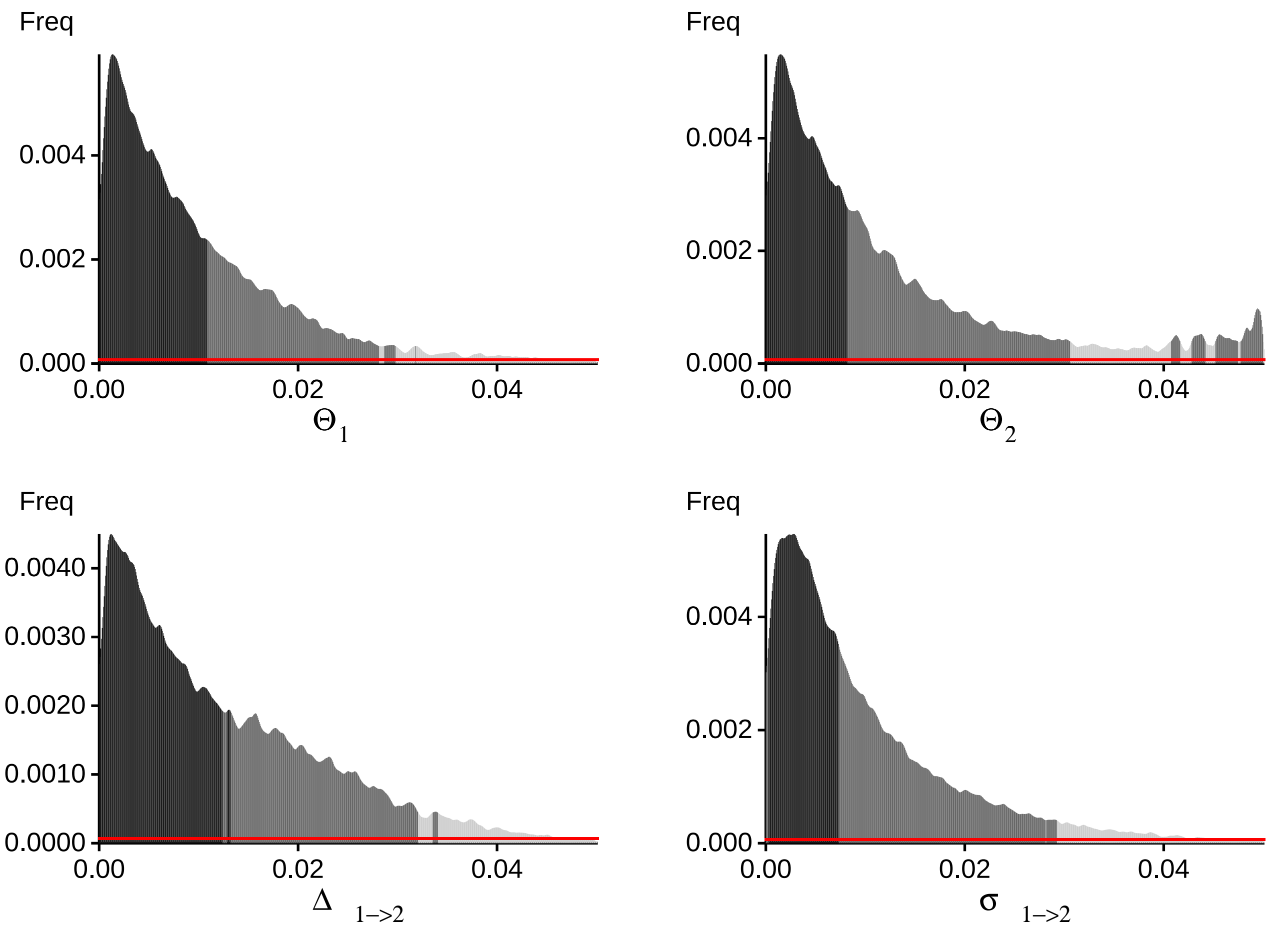
Beerli P., 2006. Comparison of Bayesian and maximum-likelihood inference of population genetic parameters. Bioinformatics 22:341-345

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.

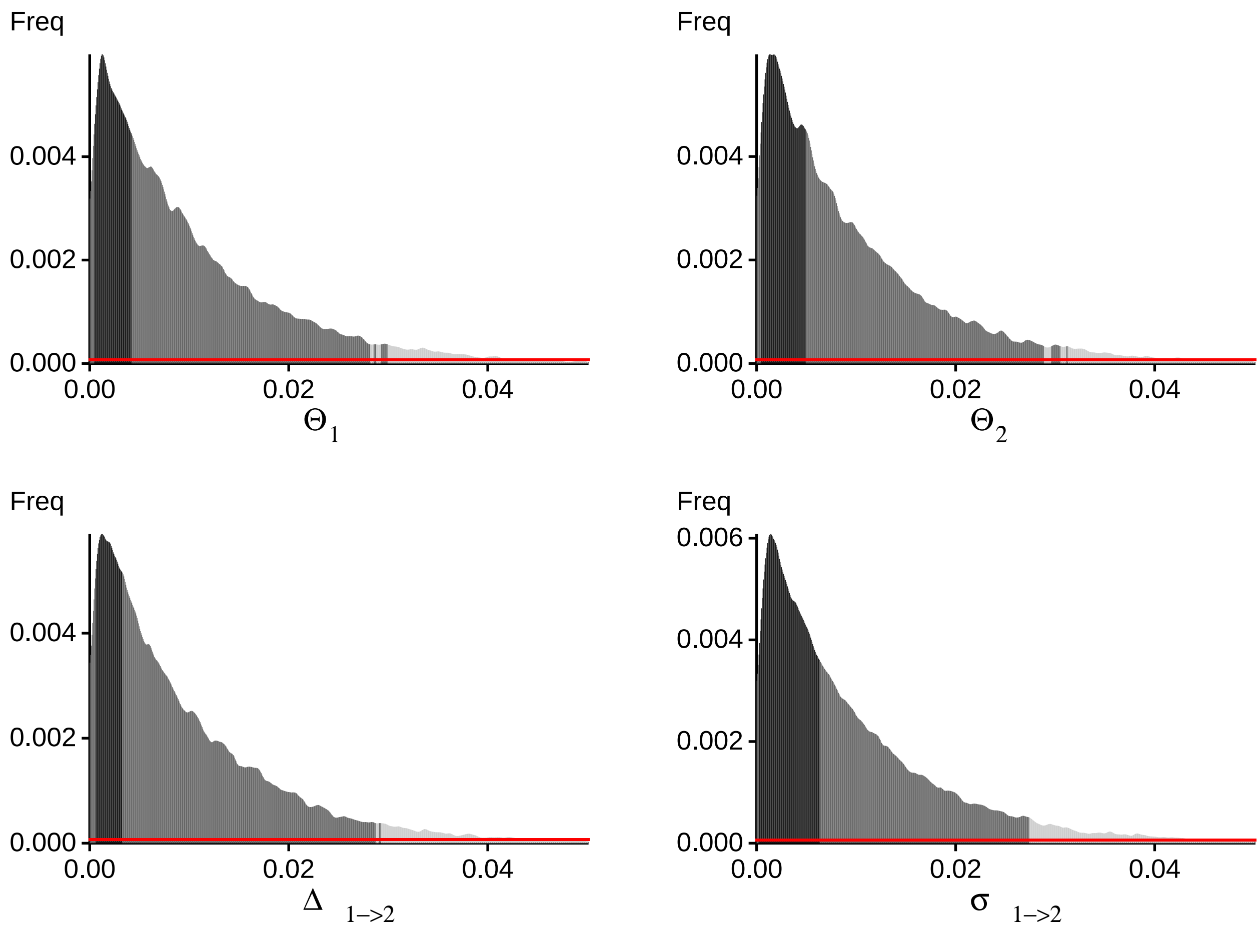
Bayesian Analysis: Posterior distribution for locus 1



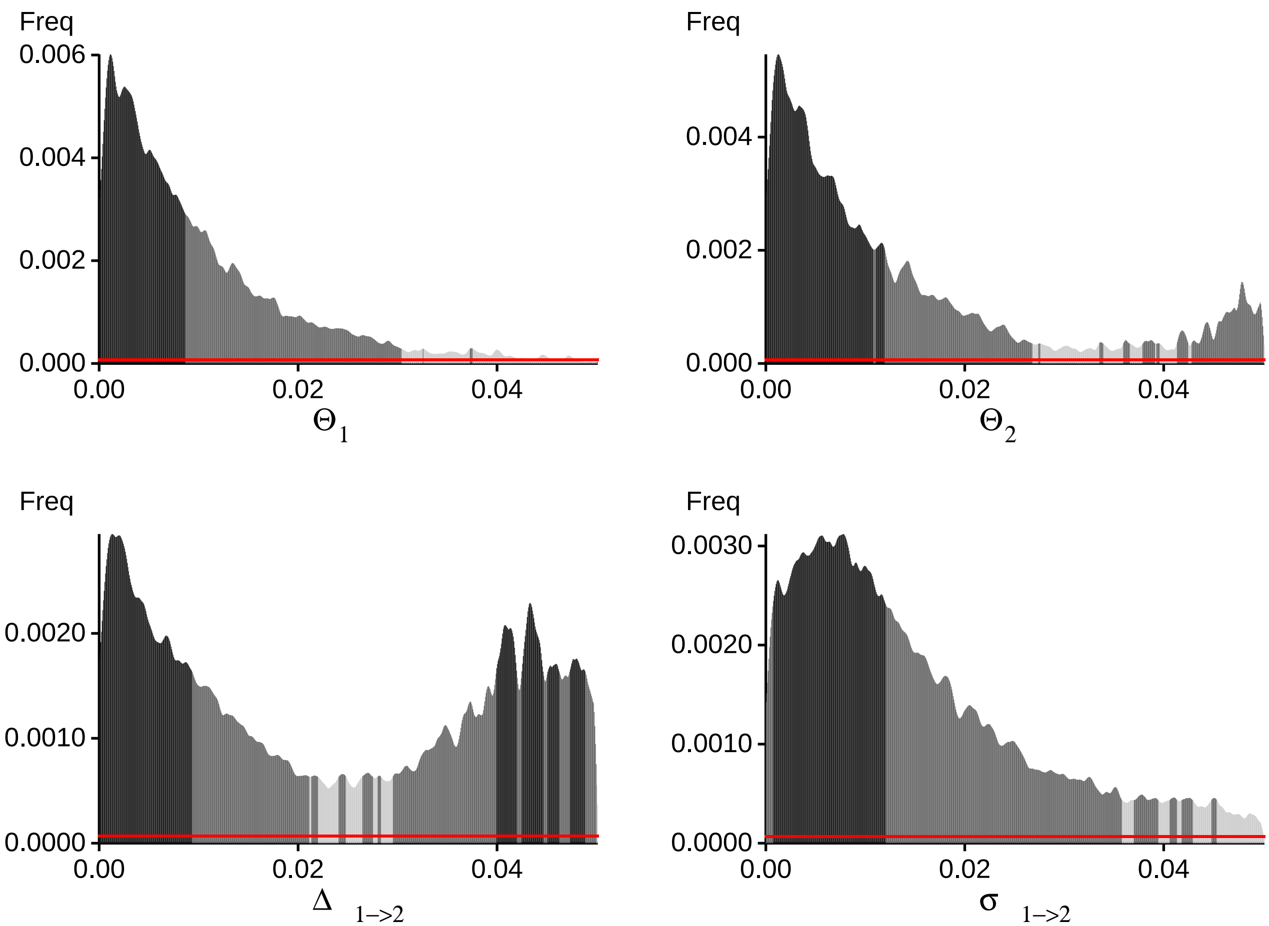
Bayesian Analysis: Posterior distribution for locus 2



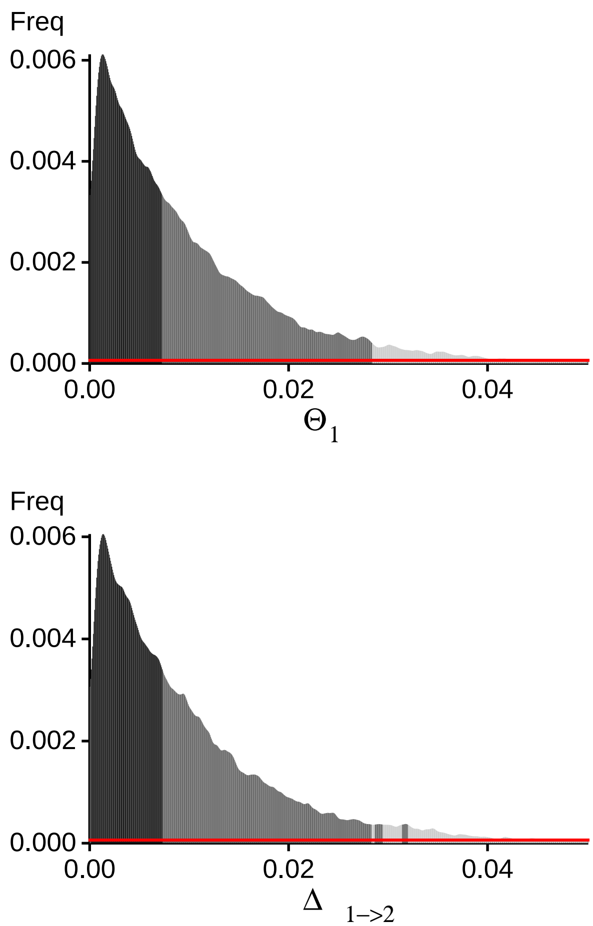
Bayesian Analysis: Posterior distribution for locus 3



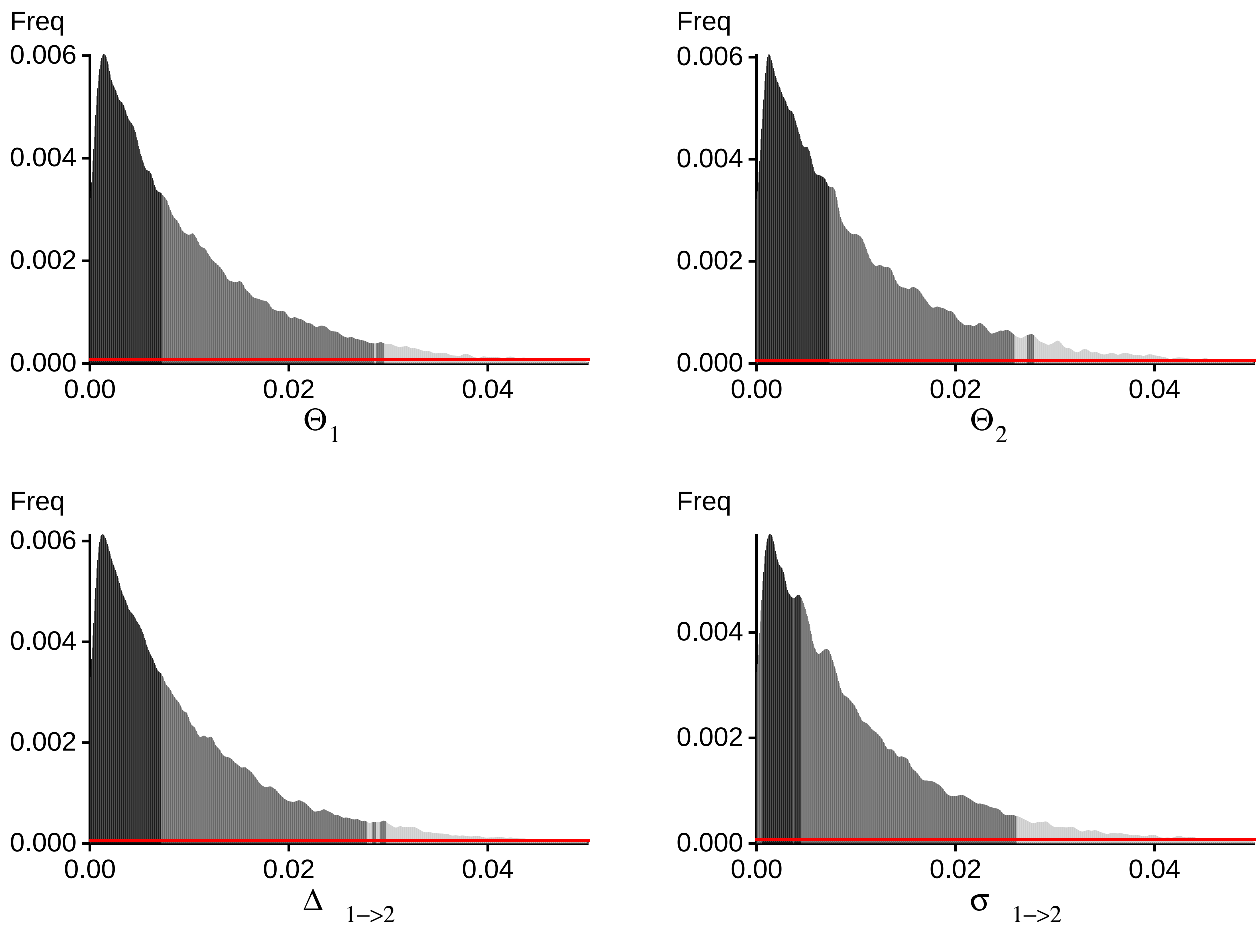
Bayesian Analysis: Posterior distribution for locus 4



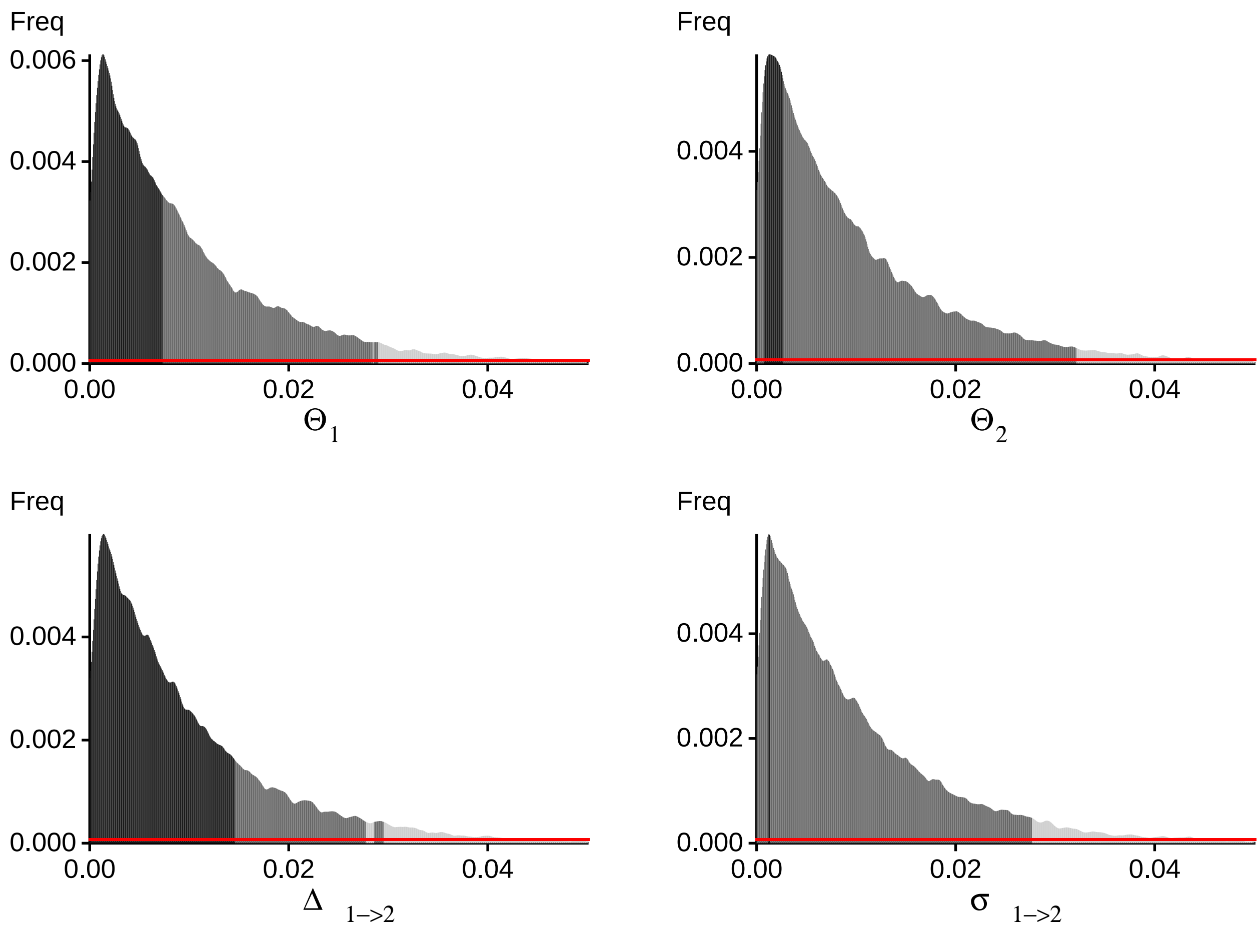
Bayesian Analysis: Posterior distribution for locus 5



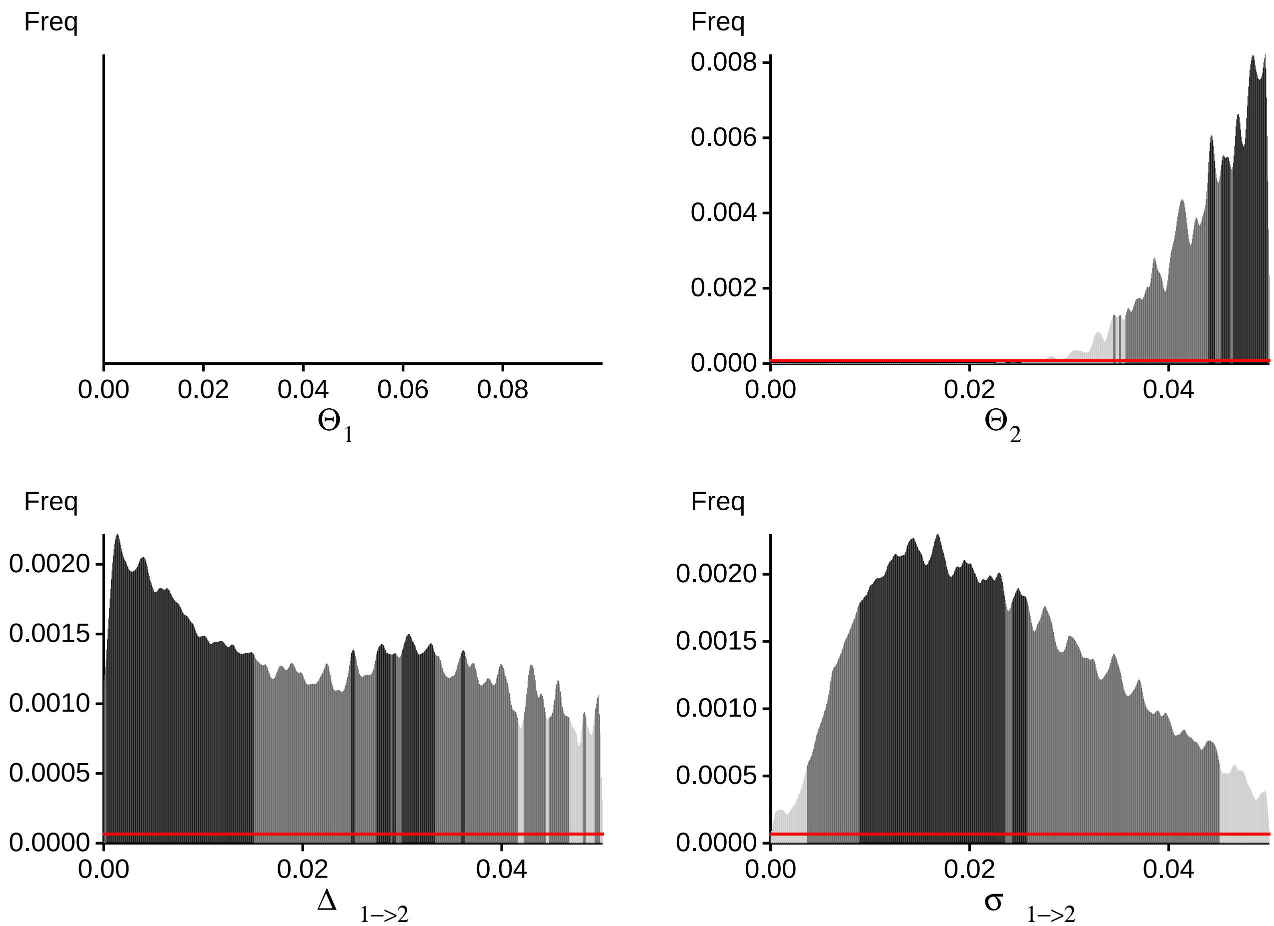
Bayesian Analysis: Posterior distribution for locus 6



Bayesian Analysis: Posterior distribution for locus 7

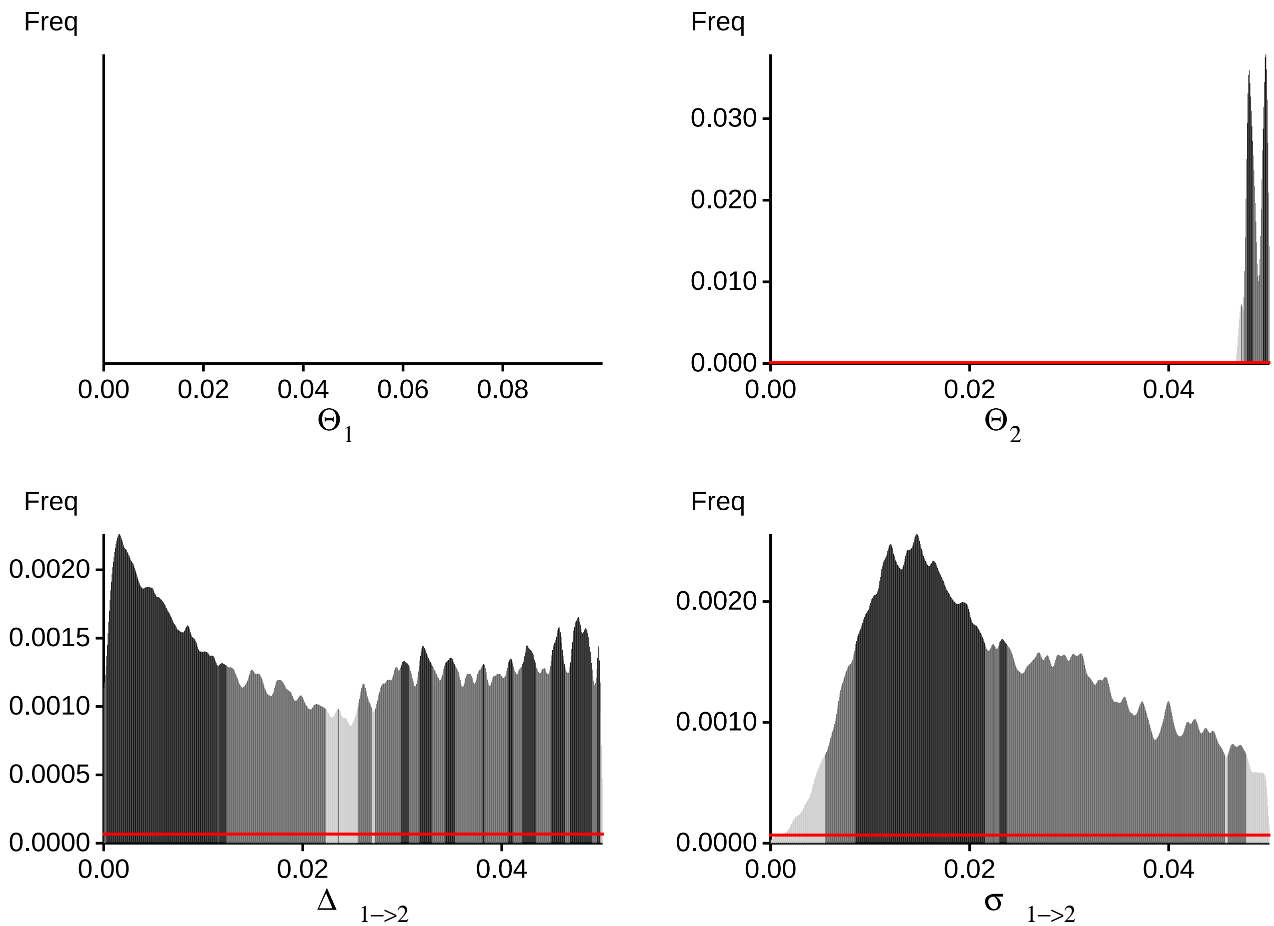


Bayesian Analysis: Posterior distribution for locus 8



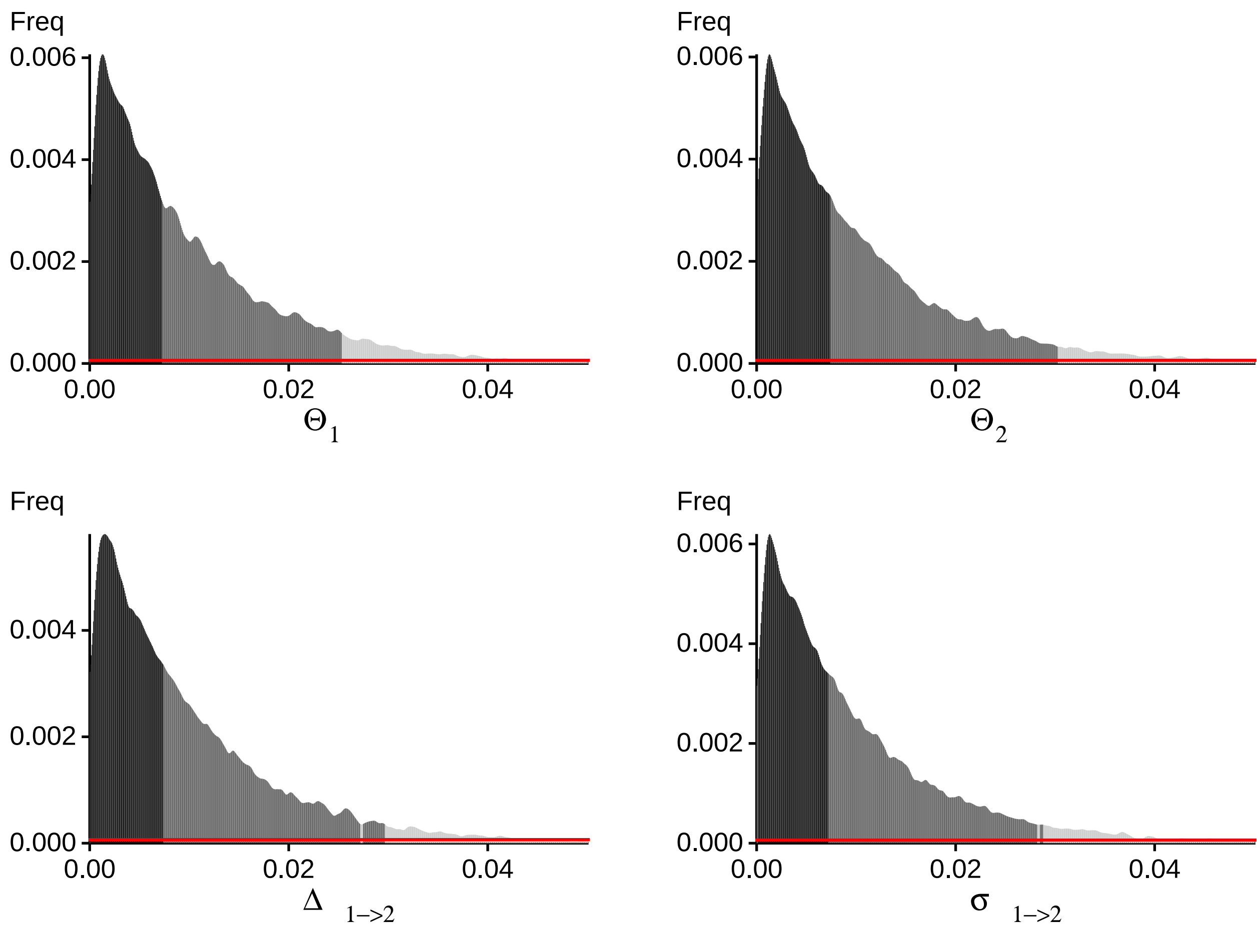
nan

Bayesian Analysis: Posterior distribution for locus 9

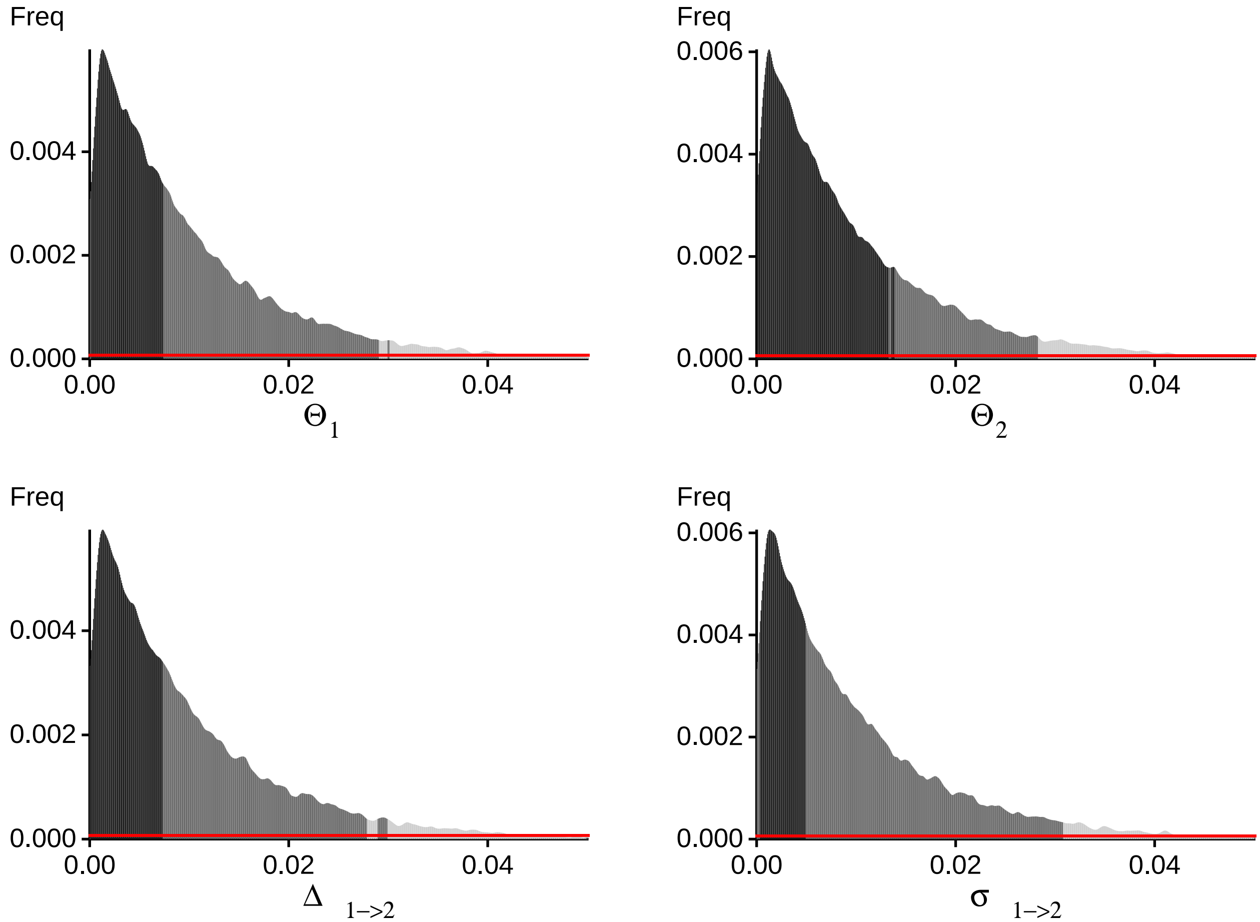


nan

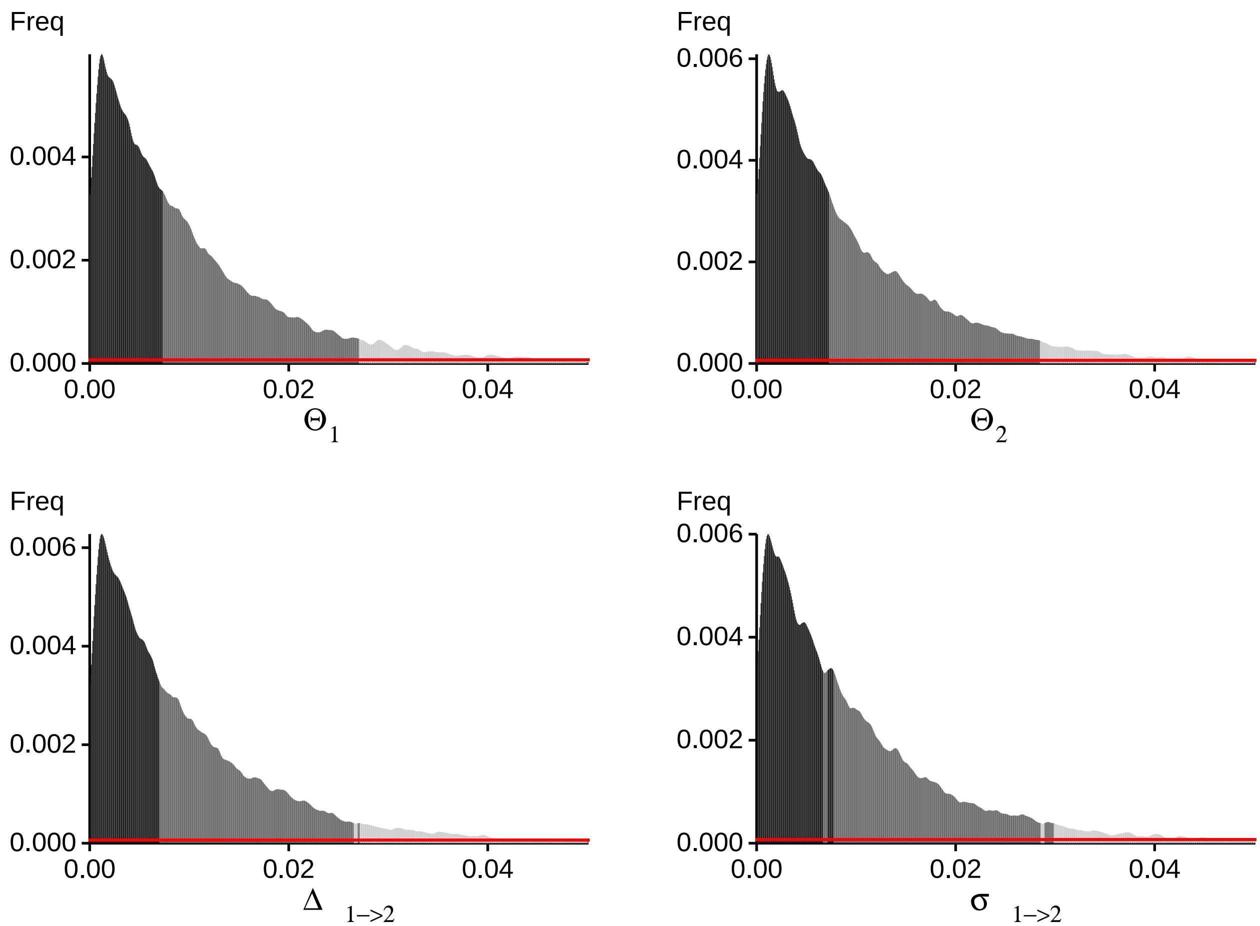
Bayesian Analysis: Posterior distribution for locus 10



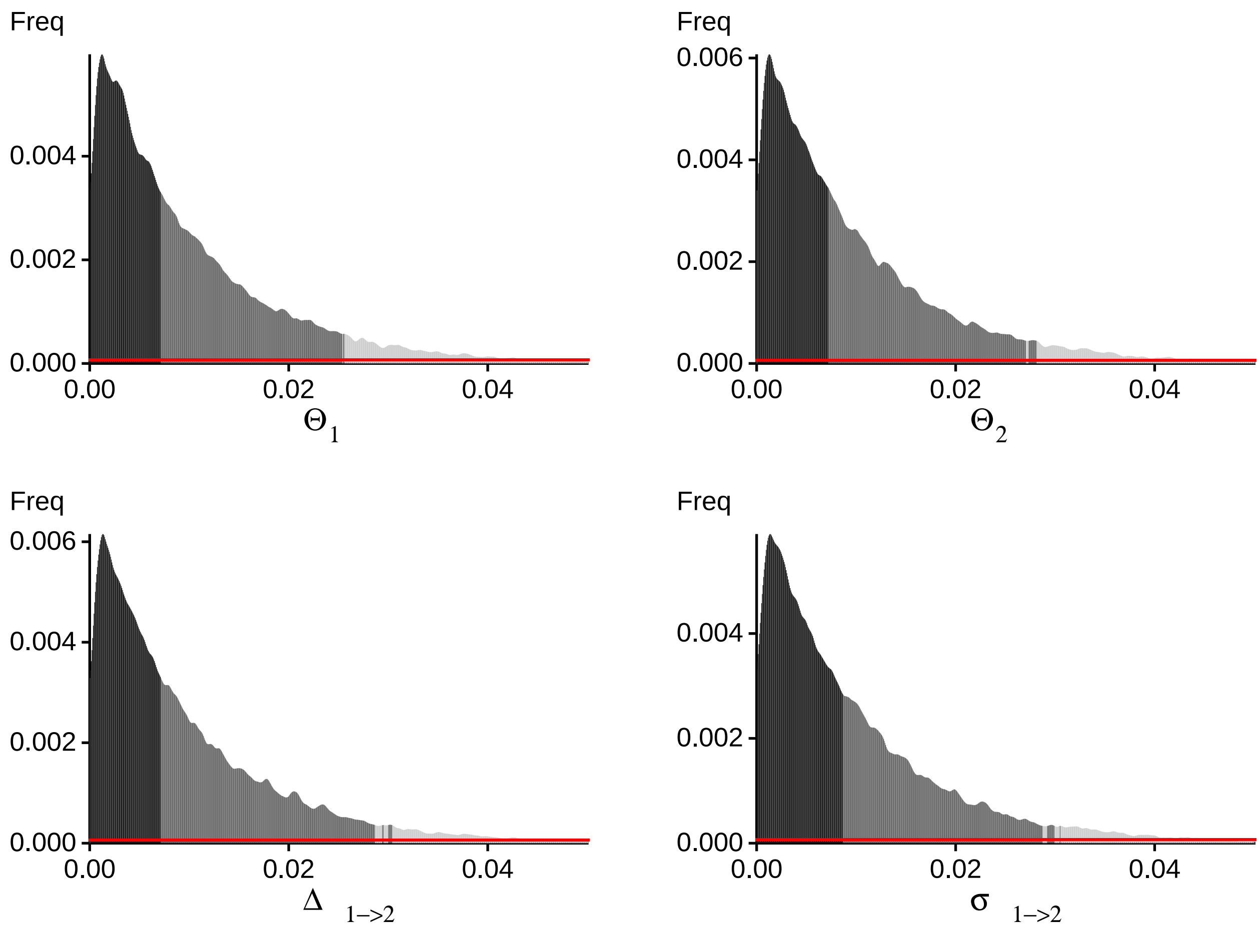
Bayesian Analysis: Posterior distribution for locus 11



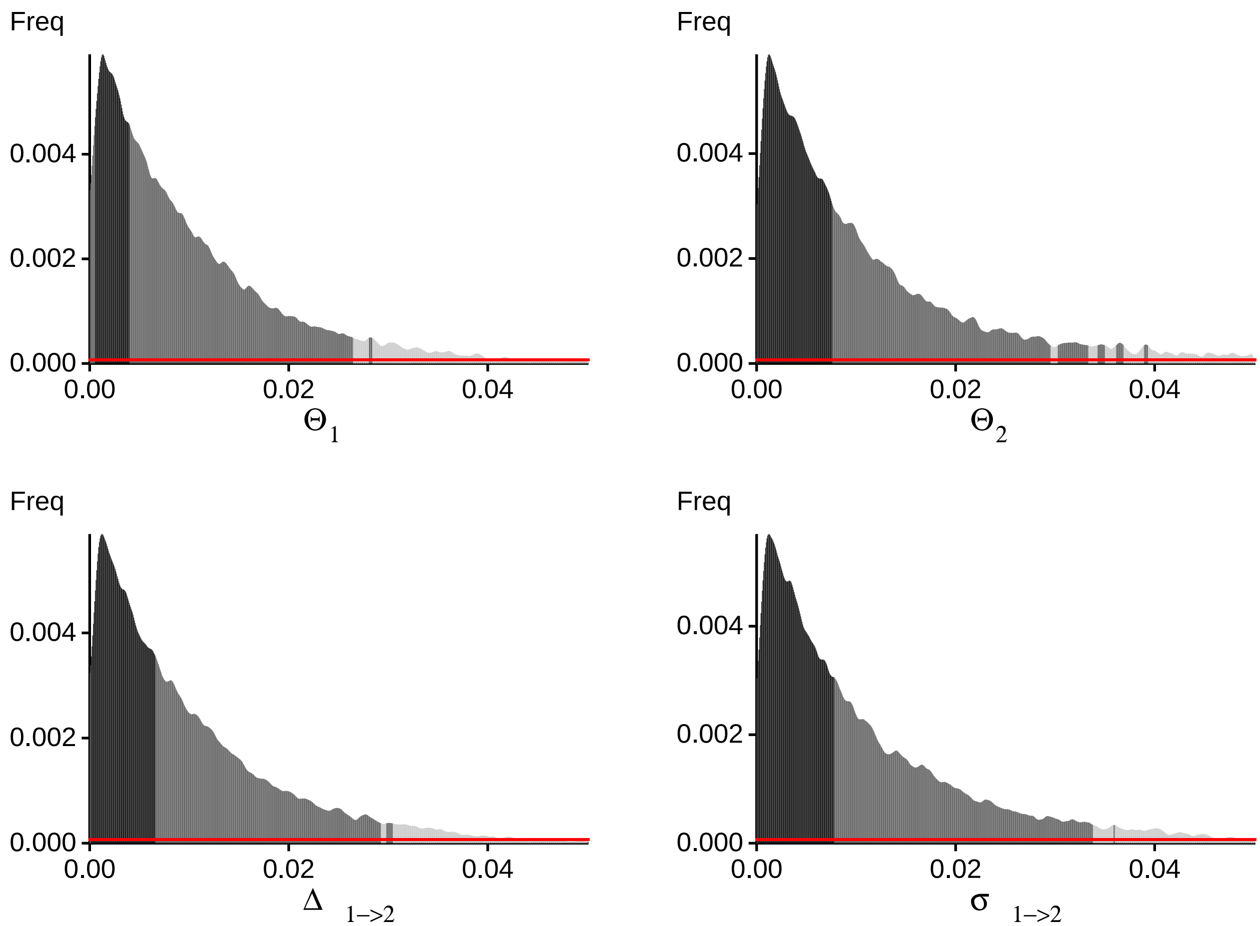
Bayesian Analysis: Posterior distribution for locus 12



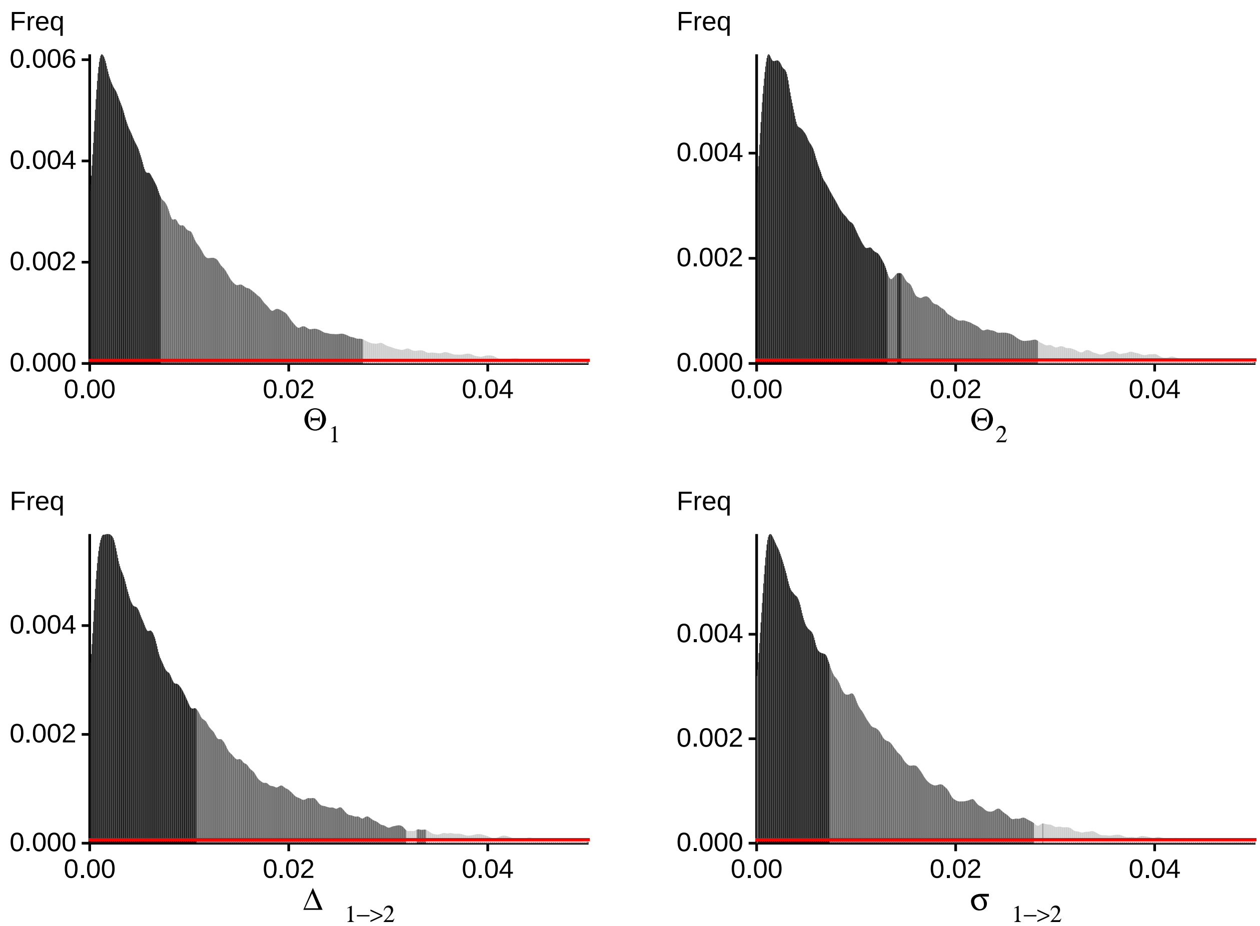
Bayesian Analysis: Posterior distribution for locus 13



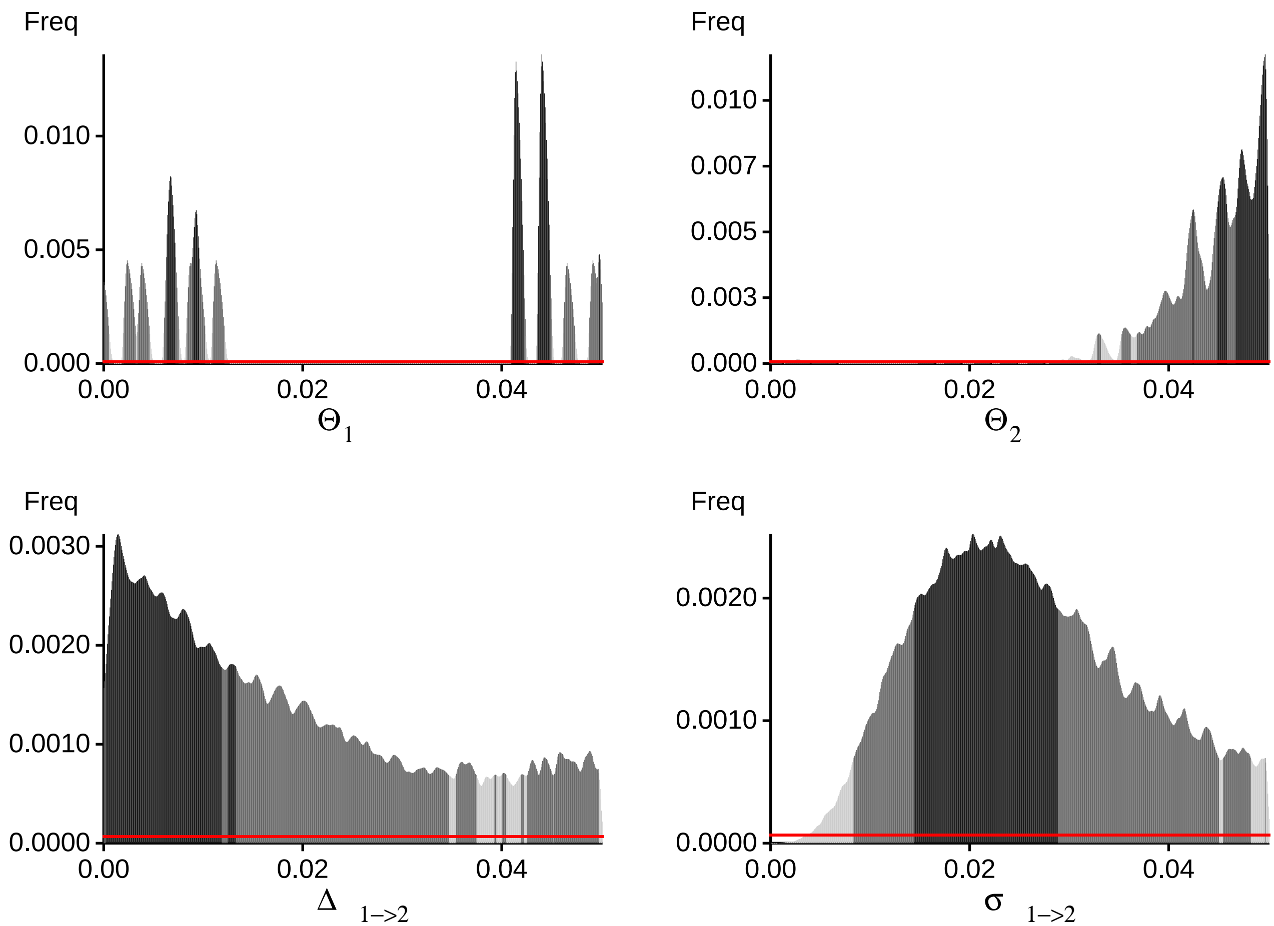
Bayesian Analysis: Posterior distribution for locus 14



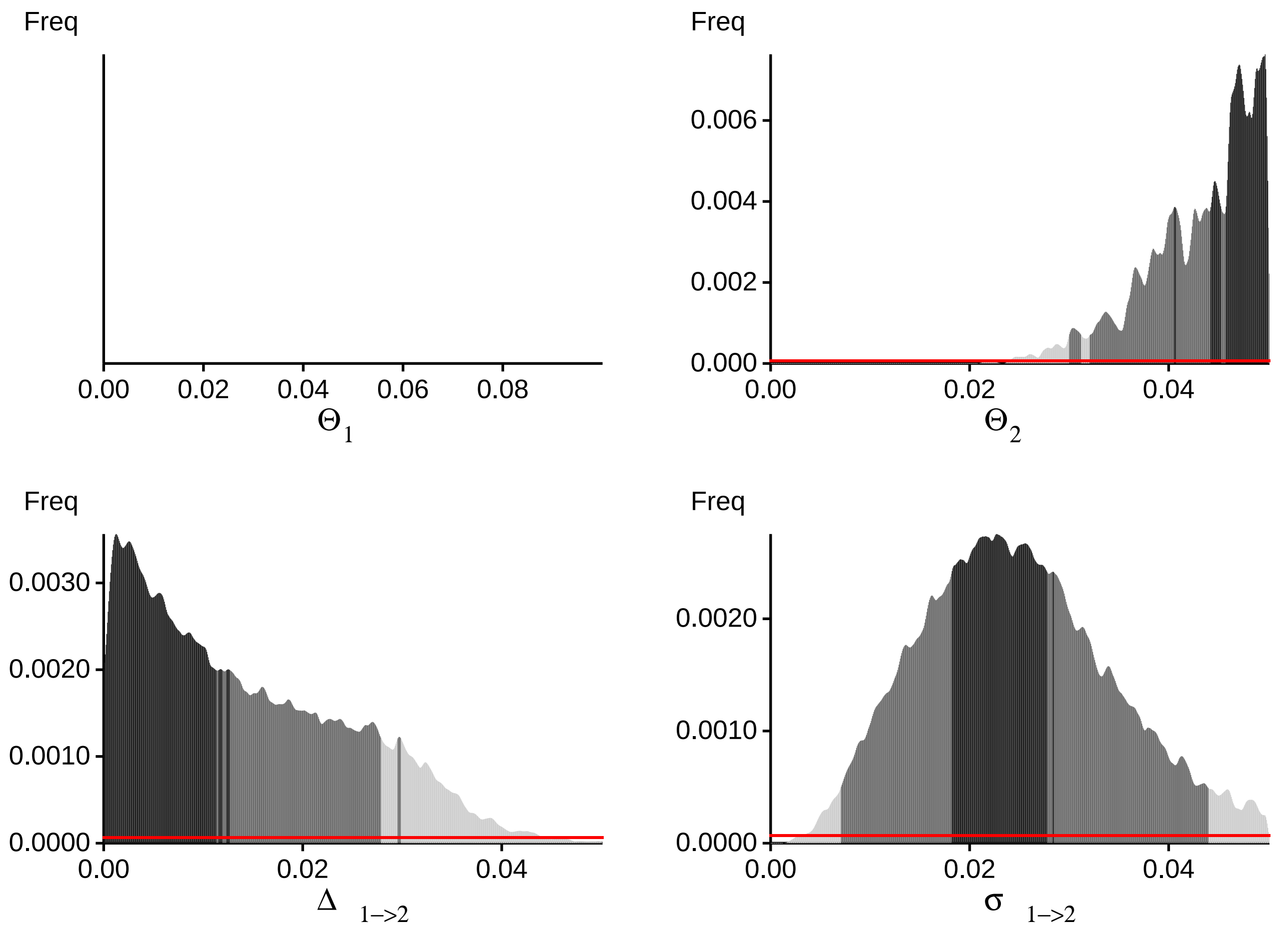
Bayesian Analysis: Posterior distribution for locus 15



Bayesian Analysis: Posterior distribution for locus 16

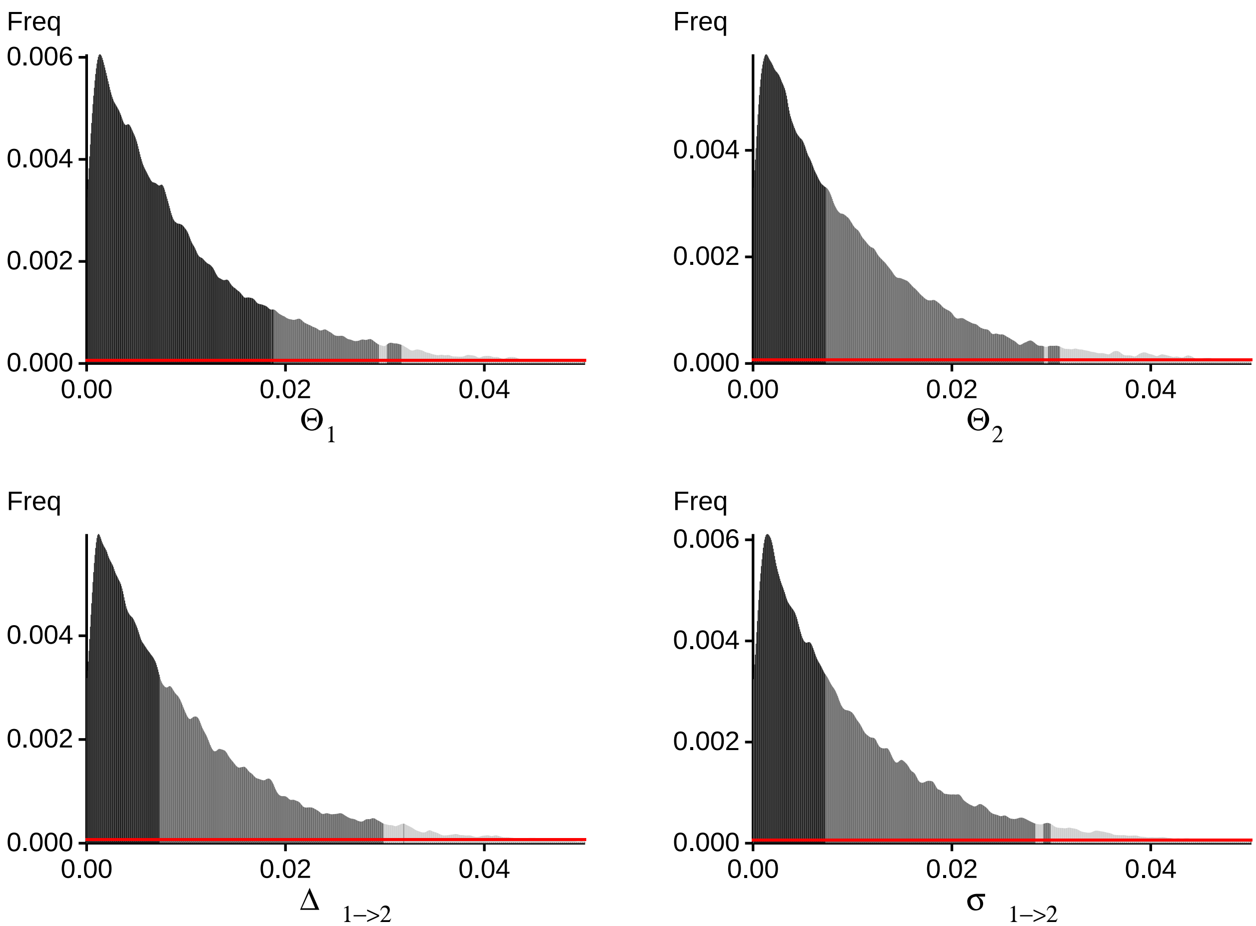


Bayesian Analysis: Posterior distribution for locus 17

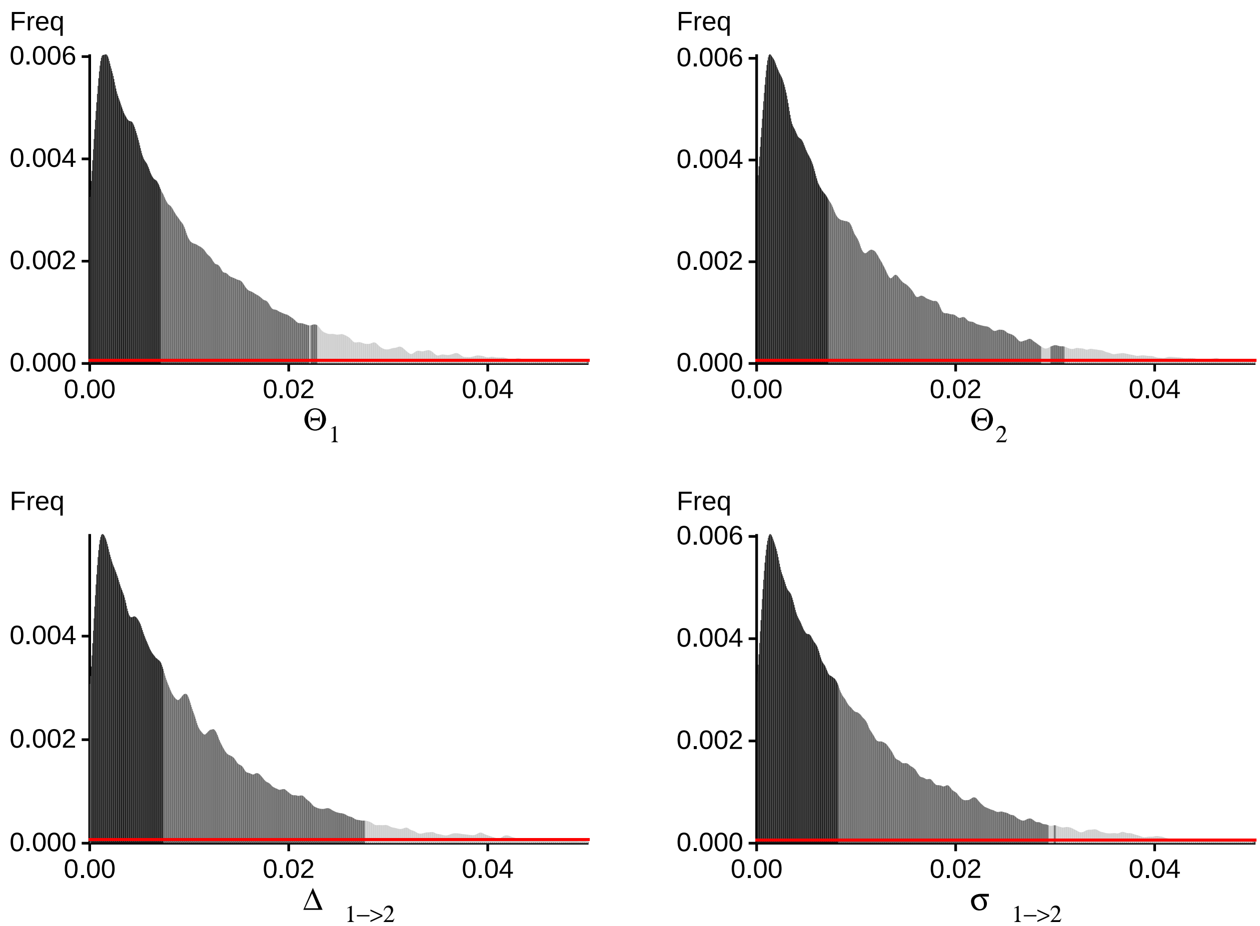


nan

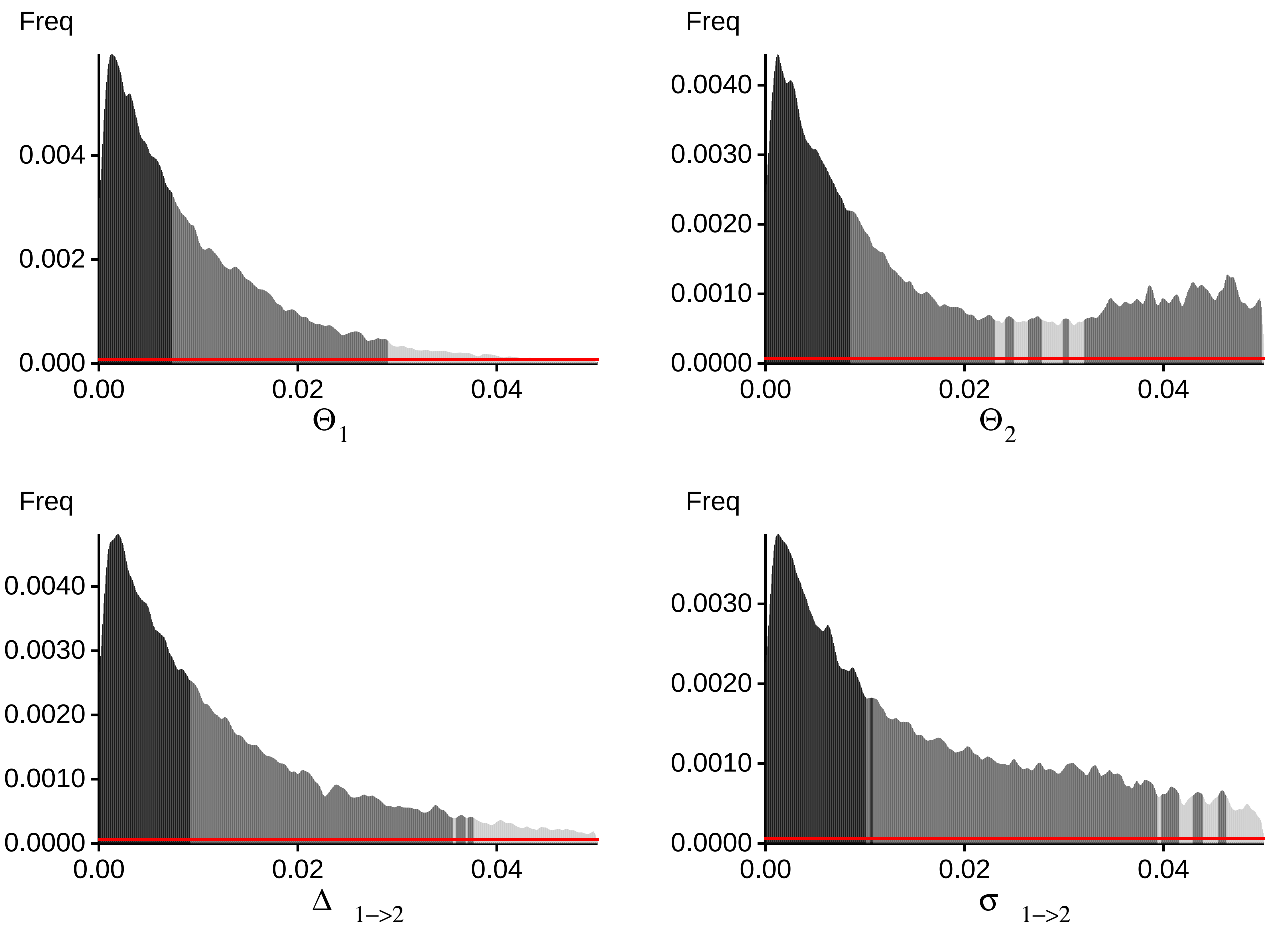
Bayesian Analysis: Posterior distribution for locus 18



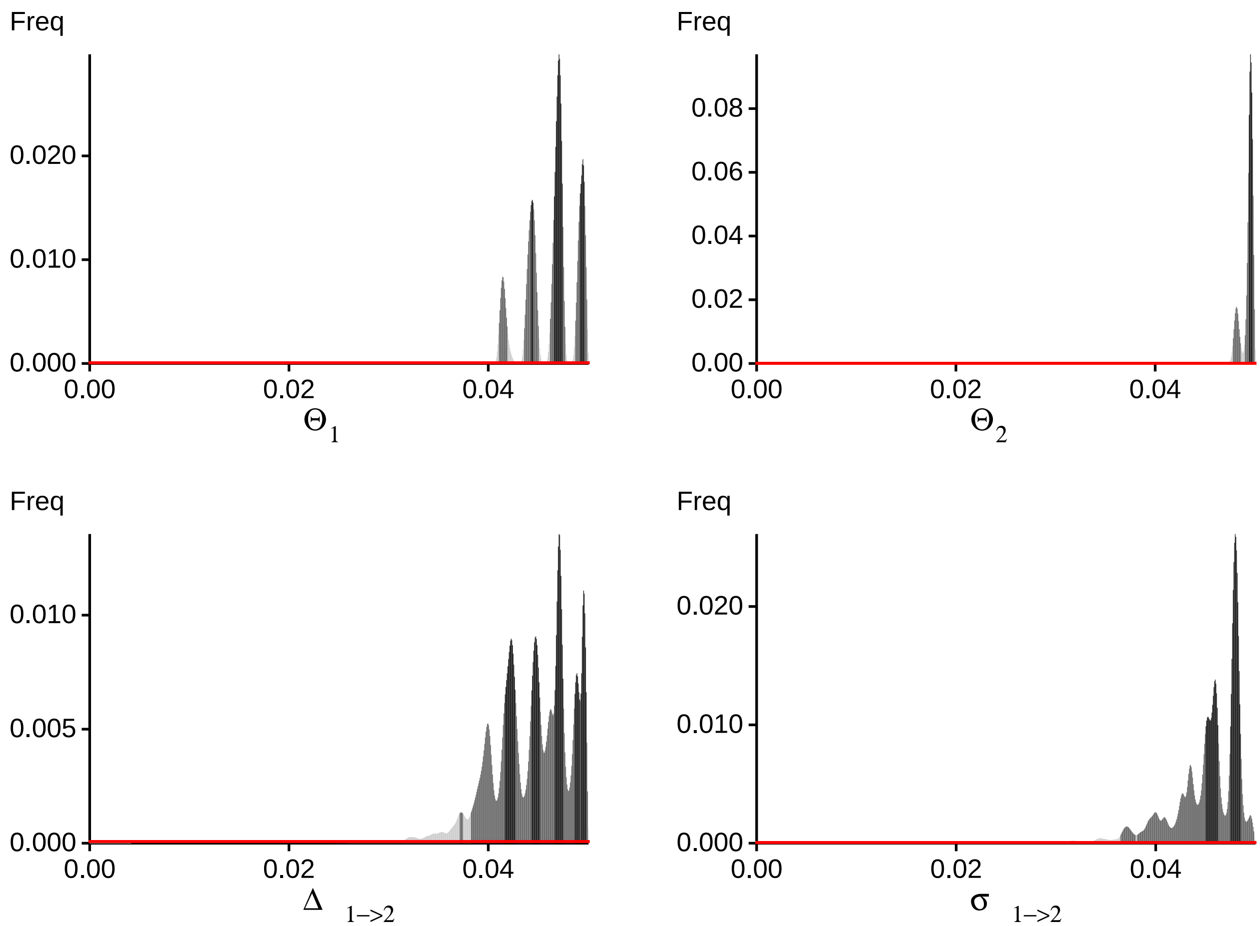
Bayesian Analysis: Posterior distribution for locus 19



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 = 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	-12504.64	-9346.15	-8970.55
2	-9177.75	-7387.33	-6793.46
3	-9281.80	-7355.29	-7382.93
4	-9465.82	-7645.63	-7918.58
5	-12153.63	-9029.74	-8578.15
6	-10531.86	-8163.06	-7932.06
7	-10176.42	-8082.12	-7991.07
8	-10217.44	-7779.00	-7364.64
9	-11301.73	-8994.49	-8943.05
10	-11823.79	-9292.87	-9042.68
11	-9300.47	-7445.38	-7676.73
12	-10636.42	-8183.61	-8101.92
13	-12461.90	-9925.60	-9088.36
14	-11939.34	-9432.85	-8836.92
15	-10250.86	-8126.90	-8066.97
16	-10351.05	-8342.80	-8064.24
17	-9960.07	-7872.54	-7518.76
18	-10542.90	-8306.70	-8617.86
19	-11087.16	-8500.77	-8292.97
20	-10780.00	-8363.00	-8061.41
All	-214413.08	-168043.88	-163711.37

(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 = -468.047812]

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	1834370/2498713	0.73413
Θ_2	1841356/2503656	0.73547
$\Delta_{1->2}$	2118130/2500564	0.84706
$\sigma_{1->2}$	1977665/2496350	0.79222
Genealogies	318790/10000717	0.03188

MCMC-Autocorrelation and Effective MCMC Sample Size

Parameter	Autocorrelation	Effective Sampe Size
Θ_1	0.38475	340682.74
Θ_2	0.35557	347705.44
$\Delta_{1->2}$	0.21963	401328.99
$\sigma_{1->2}$	0.21343	400893.55
Genealogies	0.21343	400893.55

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