Lepidomeda aliciae dataset

POPULATION SIZE, MIGRATION, DIVERGENCE, ASSIGNMENT, HISTORY
Bayesian inference using the structured coalescent
Migrate-n version 4.4.4(git:v4-series-26-ge85c6ff) [June-1-2019]
 Compiled for a SYMMETRIC multiprocessors (Grandcentral)
Program started at   Fri May 21 23:22:56 2021
Program finished at   Sat May 22 04:33:20 2021 [Runtime:0000:05:10:24]

Options

Inheritance scalers in use for Thetas:
0.25 0.25 1.00
                        [The locus with a scaler of 1.0 used as reference]
                        Random number seed: (with internal timer)   3220206820
                        Start parameters:

                        Theta values were generated   RANDOM start value from the prior

                        M values were generated   RANDOM start value from 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 Great_Salt_Lake   *   *
 2 Sevier_Desert   D   *

 Order of parameters:
  1   Θ_1 <displayed>
  2   Θ_2 <displayed>
  3              $M_{2->1}$ <displayed>
  4              $M_{1->2}$ <displayed>

5	$\Delta_{1\to2}$	<displayed>
6	$\sigma_{1\to2}$	<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	**	Uniform	0.000000	0.050	0.100	0.010	1500	0.08333
2	Theta	**	Uniform	0.000000	0.050	0.100	0.010	1500	0.08333
3	M	**	Uniform	0.000000	500.0	1000.	100.0	1500	0.08333
4	M	**	Uniform	0.000000	500.0	1000.	100.0	1500	0.08333
5	Splittime mean	**	Uniform	0.000000	0.250	0.500	0.050	1500	0.08333
6	Splittime std	**	Uniform	0.000000	0.250	0.500	0.050	1500	0.08333

[* * means priors were set globally]

Markov chain settings: Long chain
Number of chains   1
  Recorded steps [a]   10000
  Increment (record every x step [b]   1000
  Number of concurrent chains (replicates) [c]   2
  Visited (sampled) parameter values [a*b*c]   20000000
  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
Haplotyping is turned on:	NO
Output file:	outfile
Log file:	logfile
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: 3

Mutationmodel:

Locus	Sublocus	Mutationmodel	Mutationmodel parameters
1	1	Felsenstein 84	[Bf:0.25 0.29 0.17 0.30, t/t ratio=2.000]
2	1	Felsenstein 84	[Bf:0.31 0.15 0.19 0.35, t/t ratio=2.000]
3	1	Felsenstein 84	[Bf:0.26 0.22 0.20 0.31, t/t ratio=2.000]

Sites per locus

Locus	Sites
1	1109
2	849
3	448

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

Population	Locus	Gene copies data	(missing)
1 Great_Salt_Lake	1	10	
	2	4	
	3	4	
2 Sevier_Desert	1	13	
	2	11	
	3	11	
Total of all populations	1	23	(0)
	2	15	(0)
	3	15	(0)

Bayesian Analysis: Posterior distribution table

| Locus	Parameter	2.5%	25.0%	Mode	75.0%	97.5%	Median	Mean
1	Θ_1	0.00020	0.00040	0.00077	0.00100	0.00193	0.00090	0.00096
1	Θ_2	0.00067	0.00133	0.00243	0.00373	0.01280	0.00377	0.00548
1	$M_{2\to1}$	0.000	0.000	9.667	82.667	332.000	111.000	166.621
1	$M_{1\to2}$	441.333	529.333	530.333	532.000	830.667	540.333	528.982
1	$D_{1\to2}$	0.00900	0.01867	0.02050	0.02067	0.02533	0.24350	0.24686
1	$S_{1\to2}$	0.33233	0.33700	0.33783	0.33833	0.33933	0.25117	0.25073
2	Θ_1	0.00007	0.00027	0.00050	0.00080	0.00193	0.00077	0.00090
2	Θ_2	0.02200	0.02260	0.02483	0.02500	0.02500	0.01677	0.01403
2	$M_{2\to1}$	0.000	0.000	27.000	106.667	450.000	169.667	236.085
2	$M_{1\to2}$	492.667	949.333	961.000	964.000	999.333	772.333	719.735
2	$D_{1\to2}$	0.29033	0.29100	0.29183	0.29200	0.29500	0.25017	0.24887
2	$S_{1\to2}$	0.09167	0.09167	0.09383	0.09400	0.10000	0.25083	0.25012
3	Θ_1	0.04433	0.05320	0.05737	0.06033	0.06907	0.05323	0.04361
3	Θ_2	0.00220	0.00600	0.00777	0.00827	0.01653	0.00837	0.00941
3	$M_{2\to1}$	570.000	928.000	930.333	999.333	999.333	702.333	635.766
3	$M_{1\to2}$	0.000	0.000	35.000	84.000	315.333	151.000	260.444
3	$D_{1\to2}$	0.13867	0.13933	0.13983	0.14000	0.14300	0.25483	0.25292
3	$S_{1\to2}$	0.12700	0.13300	0.13350	0.13433	0.13867	0.24850	0.24813
All	Θ_1	0.00000	0.00100	0.00163	0.00220	0.00287	0.00163	0.00170
All	Θ_2	0.00107	0.00260	0.00363	0.00500	0.01000	0.00437	0.00493
All	$M_{2\to1}$	4.000	4.000	24.333	58.000	58.000	68.333	94.157
All	$M_{1\to2}$	0.000	0.000	61.000	120.667	191.333	215.000	226.941
All	$D_{1\to2}$	0.00700	0.01167	0.02283	0.05000	0.06133	0.12150	0.12173
All	$S_{1\to2}$	0.00000	0.00000	0.00017	0.02567	0.08100	0.12017	0.12095

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 over all loci
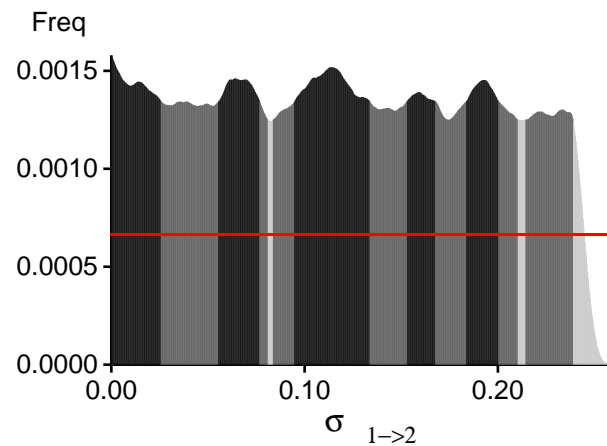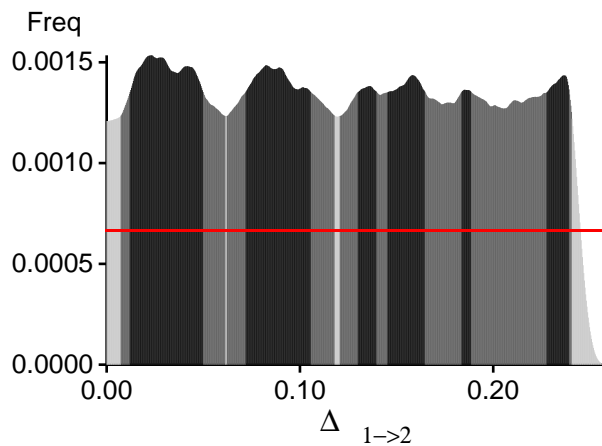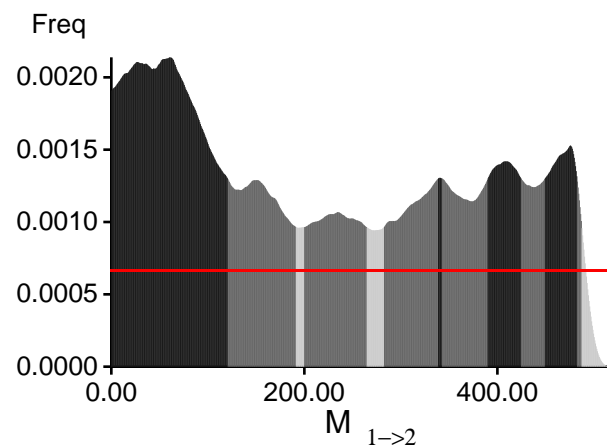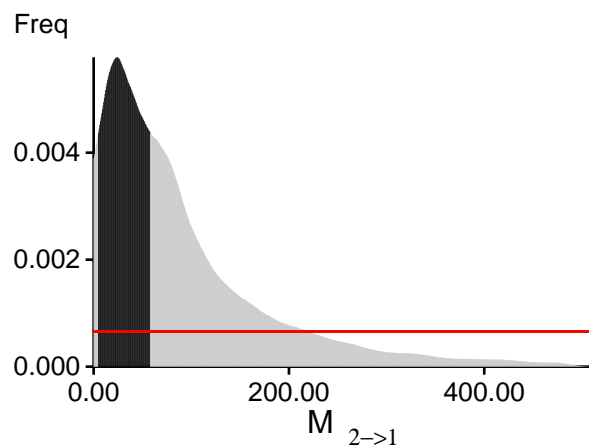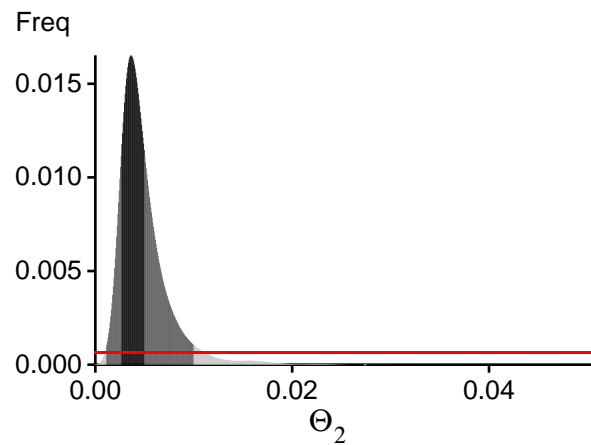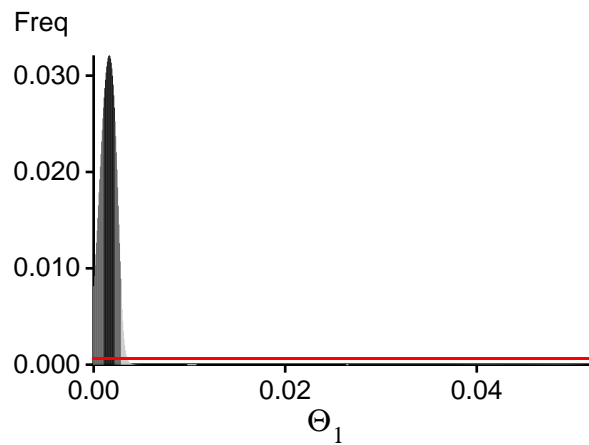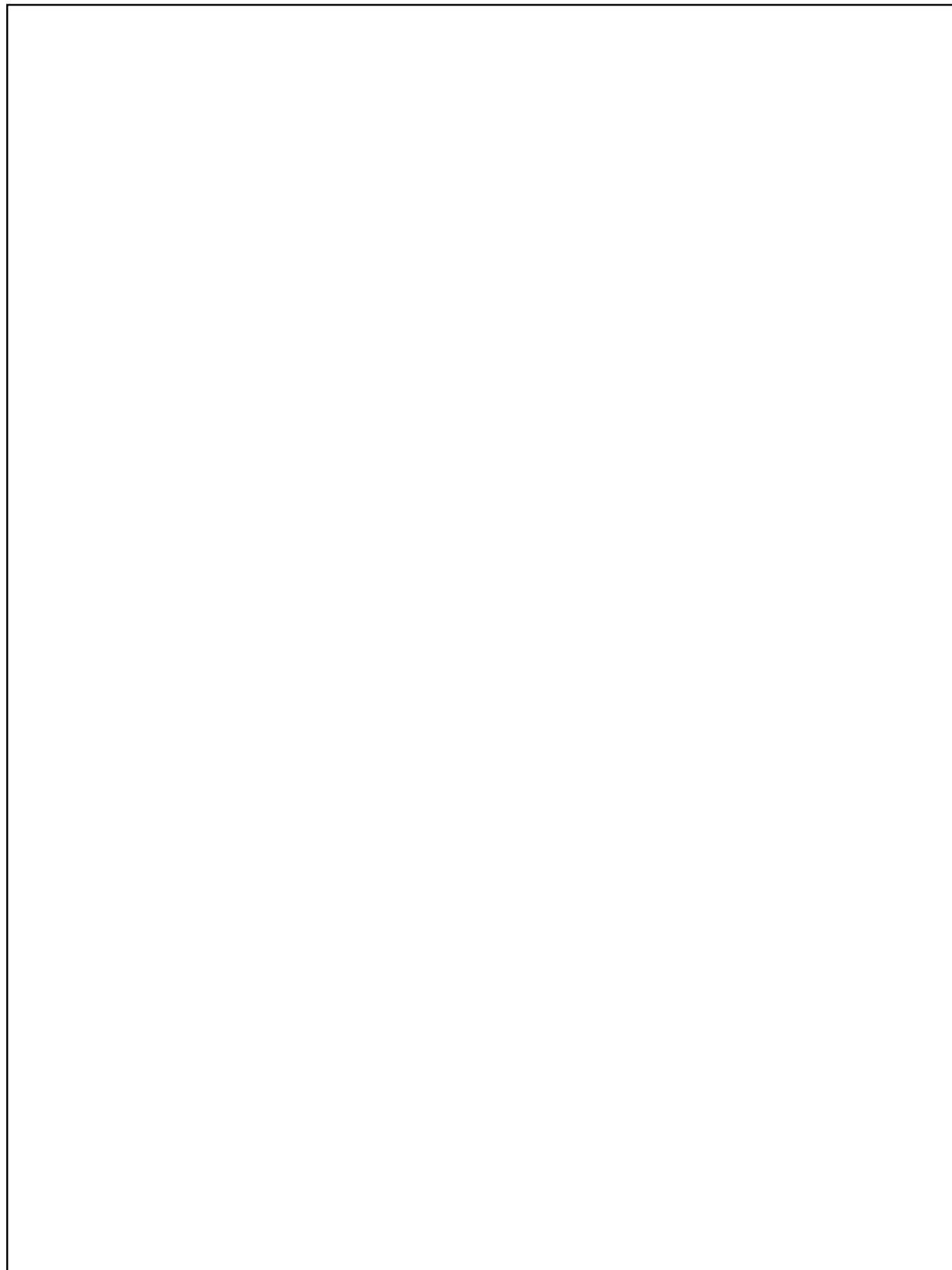
Log-Probability of the data given the model (marginal likelihood)

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	-1819.02	-1730.71	-1725.80
2	-1265.38	-1215.83	-1215.03
3	-683.03	-658.68	-657.46
All	-3777.37	-3615.16	-3608.22

(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 = -9.937915]

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	2876272/4996555	0.57565
Θ_2	2925800/5002008	0.58493
$M_{2\rightarrow1}$	2746919/5001445	0.54923
$M_{1\rightarrow2}$	2785092/4999464	0.55708
$\Delta_{1\rightarrow2}$	4937925/5000746	0.98744
$\sigma_{1\rightarrow2}$	4947323/5000960	0.98927
Genealogies	8265207/29998822	0.27552

MCMC-Autocorrelation and Effective MCMC Sample Size

Parameter	Autocorrelation	Effective Sampe Size
Θ_1	0.50836	23526.74
Θ_2	0.51178	23223.91
$M_{2 \to 1}$	0.25989	36204.27
$M_{1 \to 2}$	0.41935	25602.62
$\Delta_{1 \to 2}$	0.00301	59639.67
$\sigma_{1 \to 2}$	0.00020	59975.29
Genealogies	0.00020	59975.29

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.

Param 4 (Locus 2): Upper prior boundary seems too low!
Param 3 (Locus 3): Upper prior boundary seems too low!