Rhinichthys osculus 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 08:49:46 2021
Program finished at   Fri May 21 15:38:17 2021 [Runtime:0000:06:48:31]

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)   3417689088
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	3
1 Great_Salt_lake	*	D	0
2 Great_Salt_Lake	*	*	D
3 Sevier_Desert	0	*	*

Order of parameters:

1	Θ_1	<displayed>
2	Θ_2	<displayed>
3	Θ_3	<displayed>

4	$M_{2\to1}$		\<displayed\>
5	$M_{1\to2}$		\<displayed\>
6	$M_{3\to2}$		\<displayed\>
7	$M_{2\to3}$		\<displayed\>
8	$\Delta_{2\to1}$		\<displayed\>
9	$\sigma_{2\to1}$		\<displayed\>
10	$\Delta_{3\to2}$		\<displayed\>
11	$\sigma_{3\to2}$		\<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	0.04545
2	Theta	**	Uniform	0.000000	0.050	0.100	0.010	1500	0.04545
3	Theta	**	Uniform	0.000000	0.050	0.100	0.010	1500	0.04545
4	M	**	Uniform	0.000000	500.0	1000.	100.0	1500	0.04545
5	M	**	Uniform	0.000000	500.0	1000.	100.0	1500	0.04545
6	M	**	Uniform	0.000000	500.0	1000.	100.0	1500	0.04545
7	M	**	Uniform	0.000000	500.0	1000.	100.0	1500	0.04545
8	Splittime mean	**	Uniform	0.000000	0.250	0.500	0.050	1500	0.04545
9	Splittime std	**	Uniform	0.000000	0.250	0.500	0.050	1500	0.04545
10	Splittime mean	**	Uniform	0.000000	0.250	0.500	0.050	1500	0.04545
11	Splittime std	**	Uniform	0.000000	0.250	0.500	0.050	1500	0.04545

[* * 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: 2

Mutationmodel:

Locus	Sublocus	Mutationmodel	Mutationmodel parameters
1	1	Kimura	[Basefreq: =0.25, kappa=4.0900]
2	1	Kimura	[Basefreq: =0.25, kappa=4.0900]

Sites per locus

Locus	Sites
1	1140
2	297

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

Population	Locus	Gene copies data	(missing)
1 Great_Salt_lake	1	10	
	2	1	
2 Great_Salt_Lake_Desert	1	22	
	2	11	
3 Sevier_Desert	1	21	
	2	6	
Total of all populations	1	53	(0)
	2	18	(0)

Bayesian Analysis: Posterior distribution table

| Locus	Parameter	2.5%	25.0%	Mode	75.0%	97.5%	Median	Mean
1	Θ_1	0.00400	0.00760	0.00997	0.01113	0.02193	0.01090	0.01207
1	Θ_2	0.00647	0.00947	0.01143	0.01220	0.01873	0.01197	0.01244
1	Θ_3	0.00960	0.01420	0.01543	0.01733	0.02680	0.01790	0.01830
1	$M_{2->1}$	0.000	20.000	28.333	49.333	180.000	60.333	78.872
1	$M_{1->2}$	1.333	31.333	54.333	66.667	174.000	79.000	87.261
1	$M_{3->2}$	0.000	23.333	49.000	80.667	224.667	83.667	102.171
1	$M_{2->3}$	0.000	0.000	3.000	26.000	125.333	28.333	51.070
1	$D_{2->1}$	0.00000	0.00300	0.00517	0.00633	0.04167	0.22417	0.23221
1	$S_{2->1}$	0.47767	0.47900	0.47950	0.48000	0.49500	0.25783	0.25527
1	$D_{3->2}$	0.00000	0.00600	0.00650	0.00867	0.04833	0.23250	0.23748
1	$S_{3->2}$	0.03467	0.03967	0.04050	0.04133	0.04400	0.25283	0.25121
2	Θ_1	0.00007	0.00507	0.01097	0.01340	0.02240	0.01237	0.02575
2	Θ_2	0.00647	0.01487	0.01657	0.02200	0.04947	0.02310	0.02677
2	Θ_3	0.00787	0.02053	0.02263	0.02367	0.05720	0.02963	0.03460
2	$M_{2->1}$	572.000	602.667	604.333	604.667	608.667	496.333	501.785
2	$M_{1->2}$	0.000	23.333	40.333	74.667	244.000	81.667	121.781
2	$M_{3->2}$	0.000	112.000	118.333	147.333	301.333	125.667	158.077
2	$M_{2->3}$	0.000	2.667	21.667	36.667	162.667	57.667	108.408
2	$D_{2->1}$	0.24733	0.25833	0.25883	0.25933	0.26300	0.24617	0.24756
2	$S_{2->1}$	0.44600	0.45767	0.45917	0.45933	0.46100	0.25217	0.25098
2	$D_{3->2}$	0.00033	0.00033	0.00250	0.00467	0.01233	0.24383	0.24511
2	$S_{3->2}$	0.45067	0.45833	0.45883	0.46033	0.46500	0.25317	0.25234
All	Θ_1	0.00553	0.00787	0.00970	0.01147	0.01373	0.00997	0.01028
All	Θ_2	0.00793	0.01040	0.01243	0.01467	0.01933	0.01323	0.01382
All	Θ_3	0.01173	0.01213	0.01677	0.02540	0.02593	0.01857	0.01889
All	$M_{2->1}$	8.667	8.667	46.333	116.000	116.000	75.000	90.494
All	$M_{1->2}$	6.667	31.333	51.000	76.667	144.000	64.333	70.306
All	$M_{3->2}$	22.667	30.667	58.333	92.000	141.333	80.333	89.936
All	$M_{2->3}$	0.000	0.000	9.000	22.667	88.667	23.000	30.457
All	$D_{2->1}$	0.00000	0.00000	0.01283	0.08967	0.24367	0.11017	0.11407
All	$S_{2->1}$	0.00000	0.18933	0.20150	0.22900	0.24933	0.12583	0.12579
All	$D_{3->2}$	0.00000	0.00000	0.01117	0.07967	0.21233	0.11250	0.11480
All	$S_{3->2}$	0.00000	0.20833	0.22217	0.23900	0.25000	0.12483	0.12444

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

Freq

Θ_1

Freq

Θ_2

Freq

Θ_3

Freq

$M_{2->1}$

Freq

$M_{1->2}$

Freq

$M_{3->2}$
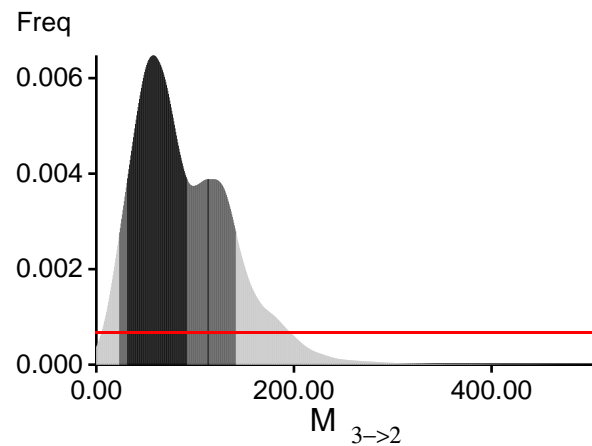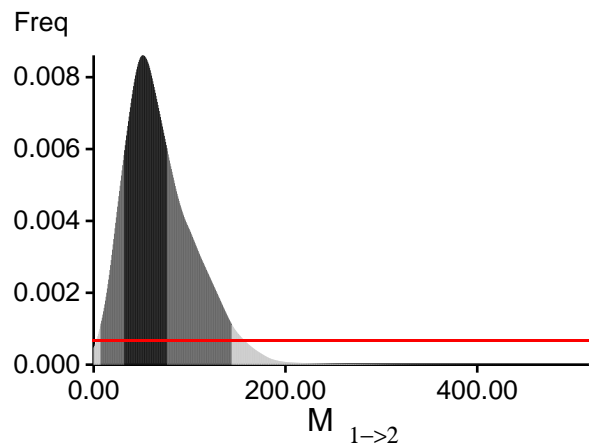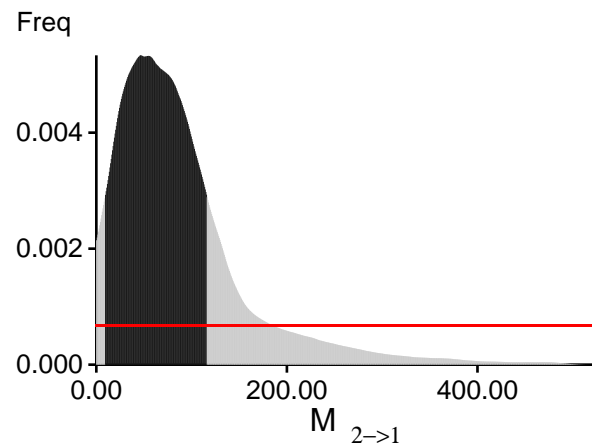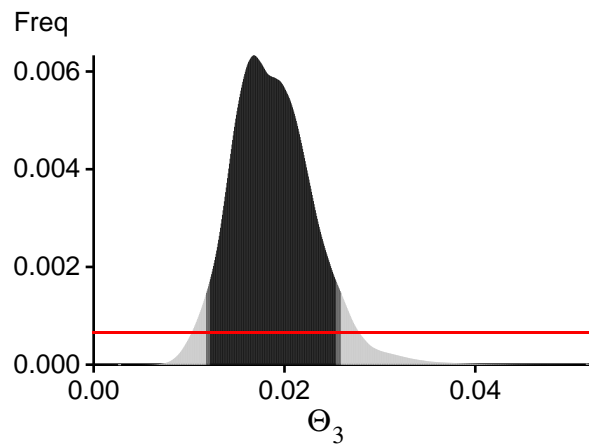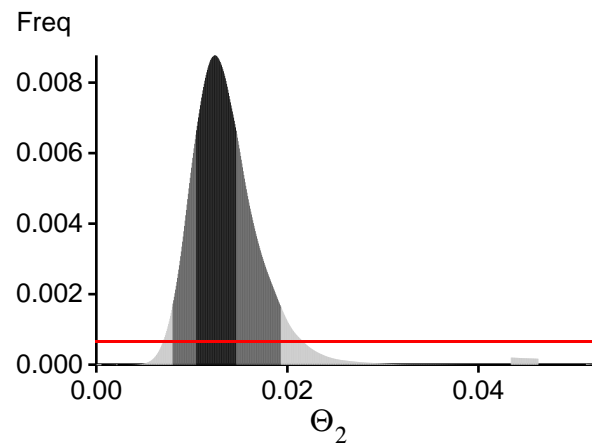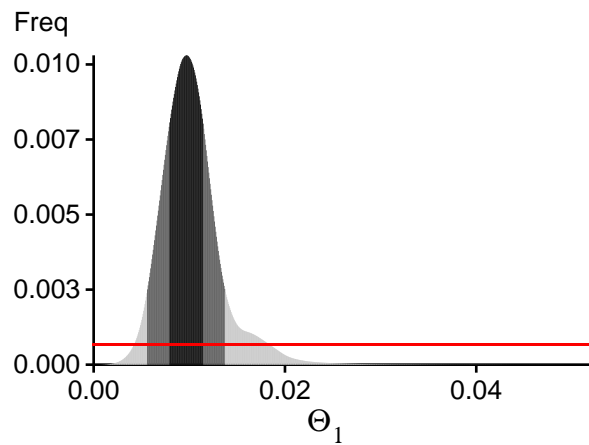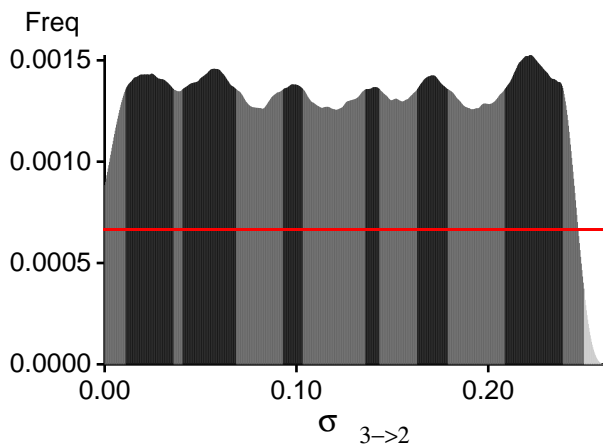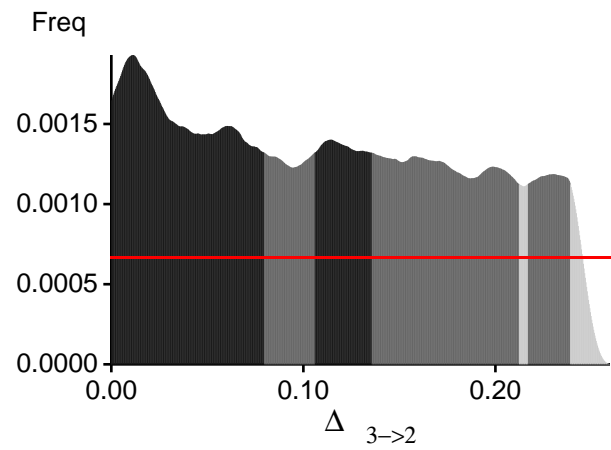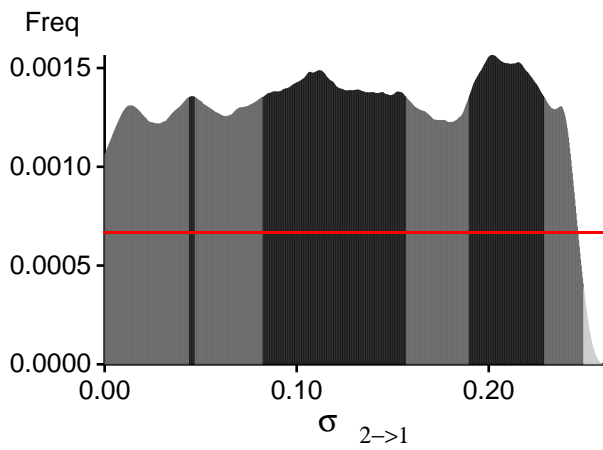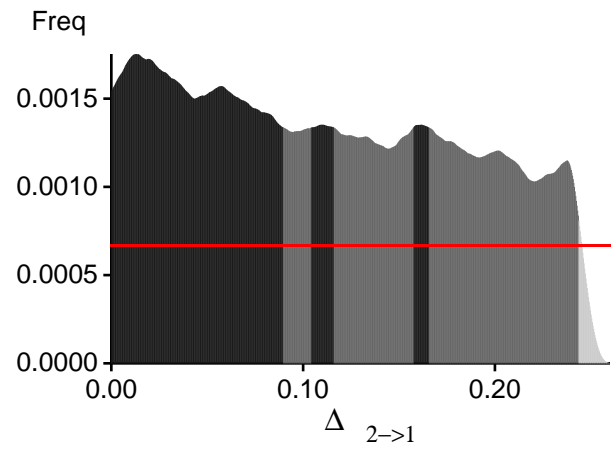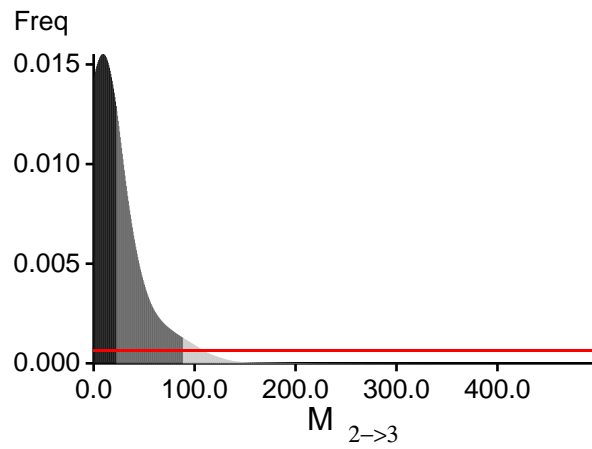
Log-Probability of the data given the model (marginal likelihood)

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	-4689.83	-3535.93	-3322.99
2	-875.92	-757.65	-739.16
All	-5586.92	-4314.75	-4083.33

(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 = -21.176617]

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	1226705/1817273	0.67503
Θ_2	1045508/1817737	0.57517
Θ_3	999471/1817130	0.55003
$M_{2\rightarrow1}$	1175544/1817774	0.64669
$M_{1\rightarrow2}$	1164094/1816959	0.64068
$M_{3\rightarrow2}$	976439/1820245	0.53643
$M_{2\rightarrow3}$	997390/1817676	0.54872
$\Delta_{2\rightarrow1}$	1737342/1819846	0.95466
$\sigma_{2\rightarrow1}$	1750058/1818734	0.96224
$\Delta_{3\rightarrow2}$	1707235/1817418	0.93937
$\sigma_{3\rightarrow2}$	1724692/1815374	0.95005
Genealogies	1936289/20003834	0.09680

MCMC-Autocorrelation and Effective MCMC Sample Size

Parameter	Autocorrelation	Effective Sampe Size
Θ_1	0.41847	19461.86
Θ_2	0.38357	21073.87
Θ_3	0.42505	18673.30
$M_{2\to1}$	0.55137	13013.52
$M_{1\to2}$	0.73695	7153.34
$M_{3\to2}$	0.62245	10141.20
$M_{2\to3}$	0.82011	4124.38
$\Delta_{2\to1}$	0.03183	37551.29
$\sigma_{2\to1}$	-0.00166	40143.59
$\Delta_{3\to2}$	0.04816	36350.70
$\sigma_{3\to2}$	0.01789	38603.75
Genealogies	0.01789	38603.75

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 11 (Locus 1): Upper prior boundary seems too low!
Param 11 (Locus 2): Upper prior boundary seems too low!
Param 13 (Locus 2): Upper prior boundary seems too low!