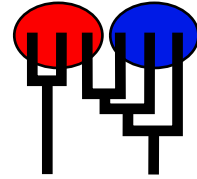


MIGRATION RATE AND POPULATION SIZE ESTIMATION
 using the coalescent and maximum likelihood or Bayesian inference
 Migrate-n version 3.6.11 [June-18-15]
 Program started at Wed Jun 1 08:36:02 2022
 Program finished at Wed Jun 1 11:51:17 2022



Options

Datatype: Microsatellite data [Brownian motion]
 Missing data: not included

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) 1443459182

Start parameters:

Theta values were generated from the FST-calculation

M values were generated from the FST-calculation

Connection type matrix:
 where m = average (average over a group of Thetas or M,
 s = symmetric M, S = symmetric 4Nm, 0 = zero, and not estimated,
 * = free to vary, Thetas are on diagonal

Population	1	2
1 population_num	*	*
2 population_num	*	*

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: Varying ([crudely] estimated from data)
 Rates per locus: 0.83237, 0.52023, 1.24855, 1.14451, 1.45665,
 0.83237, 1.76879, 0.52023, 0.52023, 0.72832, 1.04046,
 0.83237, 0.93642, 1.24855, 1.24855, 0.93642, 1.56069,
 0.62428

Analysis strategy: Bayesian inference

Proposal distributions for parameter

Parameter	Proposal
Theta	Metropolis sampling
M	Metropolis sampling

Prior distribution for parameter

Parameter	Prior	Minimum	Mean*	Maximum	Delta	Bins
Theta	Uniform	0.000000	5000.000000	10000.000000	1500.000000	1500
M	Uniform	0.000000	10000.000000	20000.000000	2000.000000	1500

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:	rift_infile
Output file:	rift_outfile
Posterior distribution raw histogram file:	bayesfile
Print data:	No
Print genealogies [only some for some data type]:	None

Data summary

Datatype: Microsatellite data
[Data was used as repeat-length information]
 Number of loci: 18

Population	Locus	Gene copies data	(missing)	
1 population_number__0	1	62	(0)	
	2	62	(0)	
	3	62	(0)	
	4	62	(0)	
	5	62	(0)	
	6	62	(0)	
	7	62	(0)	
	8	62	(0)	
	9	62	(0)	
	10	62	(0)	
	11	62	(0)	
	12	62	(0)	
	13	62	(0)	
	14	62	(0)	
	15	62	(0)	
	16	62	(0)	
	2 population_number__1	1	128	(0)
		2	128	(0)
3		128	(0)	
4		128	(0)	
5		128	(0)	
6		128	(0)	
7		128	(0)	
8		128	(0)	
9		128	(0)	
10		128	(0)	
11		128	(0)	
12		128	(0)	
13		128	(0)	
14		128	(0)	
15		128	(0)	
16		128	(0)	

	17	128	(0)
	18	128	(0)
Total of all populations	1	190	(0)
	2	190	(0)
	3	190	(0)
	4	190	(0)
	5	190	(0)
	6	190	(0)
	7	190	(0)
	8	190	(0)
	9	190	(0)
	10	190	(0)
	11	190	(0)
	12	190	(0)
	13	190	(0)
	14	190	(0)
	15	190	(0)
	16	190	(0)
	17	190	(0)
	18	190	(0)

Relative mutation rate among loci estimated from the data

Locus	Relative mutation rate	Number of alleles
1	0.83237	8
2	0.52023	5
3	1.24855	12
4	1.14451	11
5	1.45665	14
6	0.83237	8
7	1.76879	17
8	0.52023	5
9	0.52023	5
10	0.72832	7
11	1.04046	10
12	0.83237	8
13	0.93642	9
14	1.24855	12
15	1.24855	12
16	0.93642	9
17	1.56069	15
18	0.62428	6
All	1.00000	9.6

Bayesian Analysis: Posterior distribution table

Locus	Parameter	2.5%	25.0%	Mode	75.0%	97.5%	Median	Mean
1	Θ_1	0.00000	0.00000	3.33333	53.33333	140.00000	56.66667	3.81801
1	Θ_2	0.00000	0.00000	3.33333	53.33333	140.00000	56.66667	0.00146
1	$M_{2 \rightarrow 1}$	0.000	0.000	6.667	106.667	280.000	113.333	2.158
1	$M_{1 \rightarrow 2}$	0.000	0.000	86.667	200.000	586.667	206.667	94.044
2	Θ_1	0.00000	0.00000	3.33333	53.33333	140.00000	56.66667	0.46172
2	Θ_2	0.00000	0.00000	3.33333	53.33333	140.00000	56.66667	0.02815
2	$M_{2 \rightarrow 1}$	0.000	0.000	6.667	106.667	280.000	113.333	5.889
2	$M_{1 \rightarrow 2}$	226.667	480.000	646.667	800.000	1040.000	660.000	642.659
3	Θ_1	0.00000	0.00000	3.33333	53.33333	173.33333	56.66667	68.69088
3	Θ_2	0.00000	0.00000	3.33333	53.33333	140.00000	56.66667	6.83918
3	$M_{2 \rightarrow 1}$	0.000	0.000	33.333	160.000	360.000	166.667	36.010
3	$M_{1 \rightarrow 2}$	0.000	0.000	6.667	106.667	280.000	113.333	4.032
4	Θ_1	0.00000	0.00000	3.33333	273.33334	2500.00000	3376.66675	3724.09546
4	Θ_2	0.00000	0.00000	3.33333	53.33333	140.00000	56.66667	0.00136
4	$M_{2 \rightarrow 1}$	0.000	0.000	6.667	106.667	320.000	113.333	42.630
4	$M_{1 \rightarrow 2}$	1413.333	1613.333	1833.333	2040.000	2226.667	1753.333	1514.657
5	Θ_1	0.00000	0.00000	3.33333	53.33333	140.00000	56.66667	2.50111
5	Θ_2	0.00000	0.00000	3.33333	53.33333	140.00000	56.66667	3.23909
5	$M_{2 \rightarrow 1}$	0.000	0.000	33.333	160.000	360.000	166.667	32.678
5	$M_{1 \rightarrow 2}$	0.000	0.000	6.667	106.667	306.667	113.333	14.005
6	Θ_1	0.00000	0.00000	30.00000	246.66667	720.00000	570.00000	566.90686
6	Θ_2	0.00000	0.00000	3.33333	53.33333	140.00000	56.66667	2.61720
6	$M_{2 \rightarrow 1}$	0.000	0.000	46.667	160.000	373.333	166.667	45.480
6	$M_{1 \rightarrow 2}$	0.000	0.000	6.667	106.667	280.000	113.333	2.701
7	Θ_1	0.00000	0.00000	3.33333	53.33333	160.00000	56.66667	79.94057
7	Θ_2	0.00000	0.00000	3.33333	53.33333	146.66667	56.66667	7.04245
7	$M_{2 \rightarrow 1}$	0.000	0.000	6.667	106.667	280.000	113.333	9.306
7	$M_{1 \rightarrow 2}$	0.000	0.000	6.667	106.667	280.000	113.333	4.010
8	Θ_1	293.33334	880.00000	1223.33337	1506.66663	1880.00000	1143.33337	1090.88025

Locus	Parameter	2.5%	25.0%	Mode	75.0%	97.5%	Median	Mean
8	Θ_2	0.00000	0.00000	3.33333	53.33333	140.00000	56.66667	5.34841
8	$M_{2 \rightarrow 1}$	0.000	0.000	6.667	120.000	333.333	126.667	31.206
8	$M_{1 \rightarrow 2}$	0.000	0.000	6.667	106.667	280.000	113.333	1.732
9	Θ_1	8400.00000	9633.33301	9856.66699	9993.33301	10000.00000	4996.66650	4945.83594
9	Θ_2	0.00000	0.00000	3.33333	53.33333	140.00000	56.66667	2.55457
9	$M_{2 \rightarrow 1}$	0.000	0.000	33.333	160.000	360.000	166.667	30.034
9	$M_{1 \rightarrow 2}$	0.000	0.000	6.667	106.667	280.000	113.333	12.522
10	Θ_1	0.00000	0.00000	3.33333	166.66667	3000.00000	170.00000	4277.82471
10	Θ_2	0.00000	0.00000	3.33333	53.33333	146.66667	56.66667	7.56731
10	$M_{2 \rightarrow 1}$	0.000	0.000	6.667	133.333	346.667	140.000	49.048
10	$M_{1 \rightarrow 2}$	0.000	0.000	6.667	106.667	280.000	113.333	2.124
11	Θ_1	0.00000	0.00000	3.33333	53.33333	140.00000	56.66667	1.58731
11	Θ_2	0.00000	0.00000	3.33333	73.33334	186.66667	76.66666	523.24963
11	$M_{2 \rightarrow 1}$	0.000	0.000	46.667	160.000	360.000	166.667	41.702
11	$M_{1 \rightarrow 2}$	0.000	160.000	313.333	453.333	626.667	340.000	313.414
12	Θ_1	0.00000	0.00000	3.33333	53.33333	140.00000	56.66667	3.84535
12	Θ_2	0.00000	0.00000	3.33333	53.33333	140.00000	56.66667	2.47724
12	$M_{2 \rightarrow 1}$	0.000	0.000	6.667	106.667	280.000	113.333	10.939
12	$M_{1 \rightarrow 2}$	0.000	0.000	6.667	106.667	280.000	113.333	6.506
13	Θ_1	0.00000	0.00000	3.33333	60.00000	200.00000	63.33333	252.30815
13	Θ_2	0.00000	0.00000	3.33333	53.33333	140.00000	56.66667	3.37849
13	$M_{2 \rightarrow 1}$	0.000	0.000	33.333	160.000	360.000	166.667	35.592
13	$M_{1 \rightarrow 2}$	0.000	0.000	6.667	106.667	280.000	113.333	7.476
14	Θ_1	0.00000	0.00000	3.33333	53.33333	140.00000	56.66667	0.00916
14	Θ_2	0.00000	0.00000	3.33333	53.33333	140.00000	56.66667	1.02319
14	$M_{2 \rightarrow 1}$	1786.667	2040.000	2206.667	2360.000	2613.333	2220.000	2195.482
14	$M_{1 \rightarrow 2}$	0.000	66.667	206.667	320.000	506.667	260.000	203.128
15	Θ_1	0.00000	0.00000	3.33333	53.33333	166.66667	56.66667	49.84624
15	Θ_2	0.00000	0.00000	3.33333	53.33333	140.00000	56.66667	5.09162
15	$M_{2 \rightarrow 1}$	0.000	0.000	113.333	213.333	426.667	206.667	114.747
15	$M_{1 \rightarrow 2}$	0.000	0.000	20.000	160.000	346.667	166.667	14.659
16	Θ_1	0.00000	0.00000	3.33333	53.33333	140.00000	56.66667	8.16709
16	Θ_2	0.00000	0.00000	3.33333	53.33333	140.00000	56.66667	4.80604

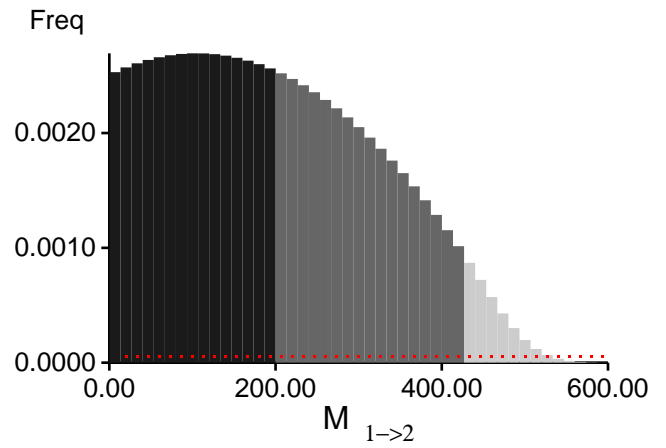
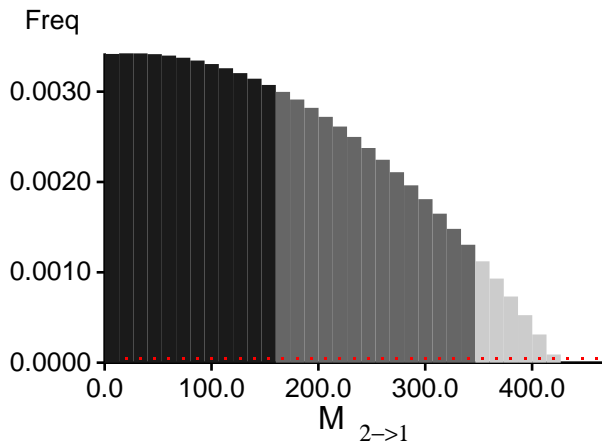
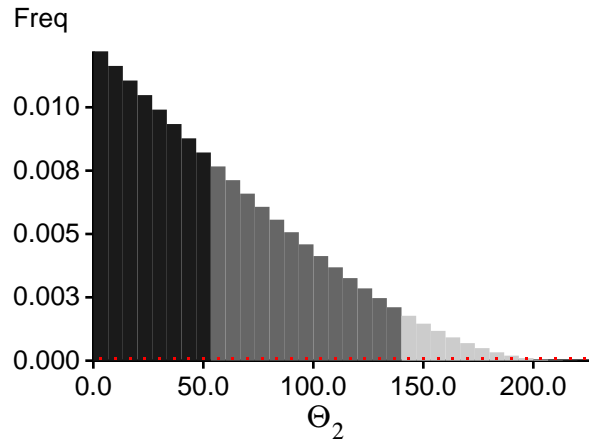
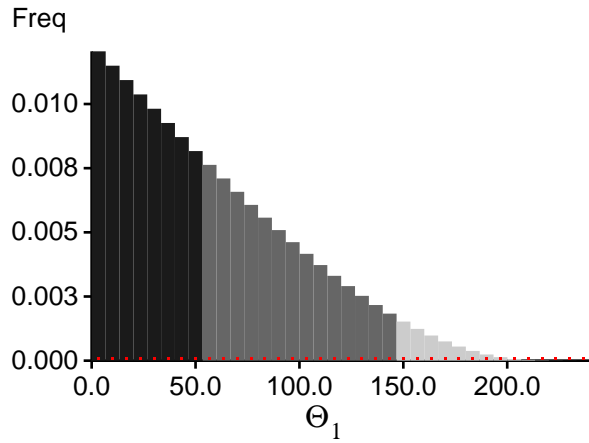
Locus	Parameter	2.5%	25.0%	Mode	75.0%	97.5%	Median	Mean
16	$M_{2 \rightarrow 1}$	0.000	0.000	6.667	106.667	280.000	113.333	3.861
16	$M_{1 \rightarrow 2}$	0.000	0.000	6.667	106.667	280.000	113.333	1.790
17	Θ_1	0.00000	0.00000	3.33333	53.33333	140.00000	56.66667	0.03904
17	Θ_2	0.00000	0.00000	3.33333	53.33333	140.00000	56.66667	2.80105
17	$M_{2 \rightarrow 1}$	586.667	786.667	953.333	1093.333	1293.333	966.667	951.050
17	$M_{1 \rightarrow 2}$	0.000	0.000	46.667	173.333	373.333	180.000	50.987
18	Θ_1	0.00000	0.00000	3.33333	53.33333	140.00000	56.66667	1.11976
18	Θ_2	0.00000	0.00000	3.33333	53.33333	140.00000	56.66667	6.15243
18	$M_{2 \rightarrow 1}$	0.000	0.000	6.667	106.667	280.000	113.333	8.902
18	$M_{1 \rightarrow 2}$	0.000	0.000	6.667	106.667	280.000	113.333	1.894
All	Θ_1	0.00000	0.00000	3.33333	53.33333	146.66667	56.66667	9.46755
All	Θ_2	0.00000	0.00000	3.33333	53.33333	140.00000	56.66667	7.57615
All	$M_{2 \rightarrow 1}$	0.000	0.000	20.000	160.000	346.667	166.667	25.370
All	$M_{1 \rightarrow 2}$	0.000	0.000	100.000	200.000	426.667	206.667	105.189

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:

$$BF = \text{Exp}[\ln(\text{Prob}(D \mid \text{thisModel}) - \ln(\text{Prob}(D \mid \text{otherModel}))]$$

$$\text{or as LBF} = 2 (\ln(\text{Prob}(D \mid \text{thisModel}) - \ln(\text{Prob}(D \mid \text{otherModel})))$$

shows the support for thisModel]

Locus	Raw thermodynamic score(1a)	Bezier approximation score(1b)	Harmonic mean(2)
1	-4178818.41	-673062.36	-5072.15
2	-1558620.05	-857126.88	-11367.44
3	-874658.73	-140835.75	-1221.97
4	-4081398.87	-899849.49	-2562.03
5	-728042.80	-118371.97	-3389.35
6	-458758.29	-75468.75	-1713.20
7	-555523.33	-89194.11	-437.47
8	-11371.79	-1886.96	-28.86
9	-84092.49	-13506.98	-27.84
10	-246336.14	-39807.75	-550.41
11	-2390837.71	-390927.39	-2405.01
12	-129267.75	-20891.57	-43.98
13	-313097.34	-50922.09	-1427.63
14	-1107276.08	-191005.37	-12361.82
15	-584577.67	-94348.30	-1175.49
16	-266847.19	-43155.92	-510.99
17	-606699.24	-99624.68	-2796.79
18	-263108.50	-42206.75	-39.13

All	-18439061.22	-3841921.90	-46860.41
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(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 = 271.165880

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	842013/2250985	0.37406
Θ_2	301059/2248234	0.13391
$M_{2 \rightarrow 1}$	657979/2250232	0.29240
$M_{1 \rightarrow 2}$	490043/2249574	0.21784
Genealogies	2552298/9000975	0.28356

MCMC-Autocorrelation and Effective MCMC Sample Size

Parameter	Autocorrelation	Effective Sampe Size
Θ_1	0.82066	23071.30
Θ_2	0.93157	6578.78
$M_{2 \rightarrow 1}$	0.91259	10547.53
$M_{1 \rightarrow 2}$	0.91635	8546.27
$\text{Ln}[\text{Prob}(D G)]$	0.96132	3807.67

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.

Param 1 (Locus 9): Upper prior boundary seems too low!