Preliminary migrate analysis of M. californianus

MIGRATION RATE AND POPULATION SIZE ESTIMATION
using the coalescent and maximum likelihood or Bayesian inference
Migrate-n version 3.7.2 [April-12-18]
Program started at Wed Jun 2 17:54:48 2021
Program finished at Wed Jun 2 22:05:32 2021

Options

Datatype: DNA sequence data

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) 1012207441
Start parameters:

Theta values were generated from guessed values
Theta = 0.01000
M values were generated from guessed values
M-matrix:
100000.00 [all are the same]
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	3	4	5	6	7	8	9	10	11	12
1 ElfinCo	*	*	0	0	0	0	0	0	0	0	0	0
2 Bamfiel	*	*	*	0	0	0	0	0	0	0	0	0
3 PortRen	0	*	*	*	0	0	0	0	0	0	0	0
4 WalkOnB	0	0	*	*	*	0	0	0	0	0	0	0
5 BodegaH	0	0	0	*	*	*	0	0	0	0	0	0
6 Davenpo	0	0	0	0	*	*	*	0	0	0	0	0
7 VistaDe	0	0	0	0	0	*	*	*	0	0	0	0
8 HazardR	0	0	0	0	0	0	*	*	*	0	0	0
9 Refugio	0	0	0	0	0	0	0	*	*	*	0	0
10 Carpint	0	0	0	0	0	0	0	0	*	*	*	0

11 WhitePo	0	0	0	0	0	0	0	0	0	*	*	*
12 LaJolla	0	0	0	0	0	0	0	0	0	0	*	*

Order of parameters:

1	Θ_1	<displayed>
2	Θ_2	<displayed>
3	Θ_3	<displayed>
4	Θ_4	<displayed>
5	Θ_5	<displayed>
6	Θ_6	<displayed>
7	Θ_7	<displayed>
8	Θ_8	<displayed>
9	Θ_9	<displayed>
10	Θ_{10}	<displayed>
11	Θ_{11}	<displayed>
12	Θ_{12}	<displayed>
13	$M_{2\to1}$	<displayed>
24	$M_{1\to2}$	<displayed>
25	$M_{3\to2}$	<displayed>
36	$M_{2\to3}$	<displayed>
37	$M_{4\to3}$	<displayed>
48	$M_{3\to4}$	<displayed>
49	$M_{5\to4}$	<displayed>
60	$M_{4\to5}$	<displayed>
61	$M_{6\to5}$	<displayed>
72	$M_{5\to6}$	<displayed>
73	$M_{7\to6}$	<displayed>
84	$M_{6\to7}$	<displayed>
85	$M_{8\to7}$	<displayed>
96	$M_{7\to8}$	<displayed>
97	$M_{9\to8}$	<displayed>
108	$M_{8\to9}$	<displayed>
109	$M_{10\to9}$	<displayed>
120	$M_{9\to10}$	<displayed>
121	$M_{11\to10}$	<displayed>
132	$M_{10\to11}$	<displayed>
133	$M_{12\to11}$	<displayed>
144	$M_{11\to12}$	<displayed>

Mutation rate among loci:	Mutation rate is constant
Analysis strategy:	Bayesian inference

Proposal distributions for parameter

Parameter	Proposal
Theta	Metropolis sampling
M	Slice sampling

Prior distribution for parameter

Parameter	Prior	Minimum	Mean*	Maximum	Delta	Bins
Theta	Exp window	0.000010	0.010000	10.000000	1.000000	500
M	Exp window	0.000100	100000.000000	1000000.000000	100000.000000	500

Markov chain settings:	Long chain
Number of chains	1
Recorded steps [a]	1000
Increment (record every x step [b]	100
Number of concurrent chains (replicates) [c]	3
Visited (sampled) parameter values [a*b*c]	300000
Number of discard trees per chain (burn-in)	1000

Multiple Markov chains:

Static heating scheme — 4 chains with temperatures

100000.00 3.00 1.50 1.00

Swapping interval is 1

Print options:	
Data file:	../../mcalifornianus_210528.mig
Output file:	outfile.txt
Posterior distribution raw histogram file:	bayesfile
Print data:	No
Print genealogies [only some for some data type]:	None

Data summary

Datatype:	Sequence data
Number of loci:	1

Population	Locus	Gene copies
1 ElfinCo	1	19
2 Bamfiel	1	23
3 PortRen	1	15
4 WalkOnB	1	16
5 BodegaH	1	7
6 Davenpo	1	17
7 VistaDe	1	19
8 HazardR	1	23
9 Refugio	1	16
10 Carpint	1	19
11 WhitePo	1	11
12 LaJolla	1	8
Total of all populations	1	193

Bayesian Analysis: Posterior distribution table

Locus	Parameter	2.5%	25.0%	Mode	75.0%	97.5%	Median	Mean
1	Θ_{1}	0.00001	0.00001	0.01001	0.06001	0.18001	0.07001	0.02780
1	Θ_{2}	0.00001	0.00001	0.01001	0.06001	0.16001	0.07001	0.02288
1	Θ_{3}	0.00001	0.00001	0.01001	0.06001	0.18001	0.07001	0.02827
1	Θ_{4}	0.00001	0.00001	0.01001	0.06001	0.18001	0.07001	0.02187
1	Θ_{5}	0.00001	0.00001	0.01001	0.06001	0.16001	0.07001	0.01133
1	Θ_{6}	0.00001	0.00001	0.01001	0.08001	0.18001	0.09001	0.03074
1	Θ_{7}	0.00001	0.00001	0.01001	0.06001	0.16001	0.07001	0.02147
1	Θ_{8}	0.00001	0.00001	0.01001	0.06001	0.16001	0.07001	0.02130
1	Θ_{9}	0.00001	0.00001	0.01001	0.06001	0.16001	0.07001	0.01293
1	Θ_{10}	0.00001	0.00001	0.01001	0.06001	0.16001	0.07001	0.01472
1	Θ_{11}	0.00001	0.00001	0.01001	0.06001	0.16001	0.07001	0.01430
1	Θ_{12}	0.00001	0.00001	0.01001	0.06001	0.16001	0.07001	0.00533
1	$M_{2->1}$	38000.0	74000.0	87000.0	100000.0	108000.0	69000.0	52288.5
1	$M_{1->2}$	0.0	0.0	1000.0	12000.0	20000.0	69000.0	53237.3
1	$M_{3->2}$	0.0	0.0	9000.0	20000.0	30000.0	21000.0	23804.4
1	$M_{2->3}$	0.0	8000.0	21000.0	32000.0	62000.0	27000.0	28526.5
1	$M_{4->3}$	0.0	0.0	9000.0	20000.0	28000.0	21000.0	32056.0
1	$M_{3->4}$	2000.0	34000.0	49000.0	62000.0	68000.0	45000.0	38555.8
1	$M_{5->4}$	8000.0	22000.0	31000.0	42000.0	54000.0	33000.0	31719.1
1	$M_{4->5}$	48000.0	54000.0	75000.0	94000.0	100000.0	175000.0	195771.1
1	$M_{6->5}$	16000.0	76000.0	99000.0	116000.0	124000.0	89000.0	78199.2
1	$M_{5->6}$	0.0	0.0	9000.0	20000.0	28000.0	21000.0	23913.8
1	$M_{7->6}$	0.0	30000.0	47000.0	58000.0	66000.0	41000.0	36571.9
1	$M_{6->7}$	56000.0	68000.0	83000.0	98000.0	106000.0	77000.0	67562.1
1	$M_{8->7}$	34000.0	52000.0	63000.0	74000.0	90000.0	65000.0	63689.8
1	$M_{7->8}$	40000.0	54000.0	69000.0	80000.0	104000.0	73000.0	71365.5
1	$M_{9->8}$	0.0	0.0	1000.0	18000.0	30000.0	19000.0	52053.5
1	$M_{8->9}$	44000.0	54000.0	71000.0	84000.0	118000.0	67000.0	60156.4
1	$M_{10->9}$	2000.0	10000.0	25000.0	36000.0	46000.0	33000.0	43657.7
1	$M_{9->10}$	26000.0	38000.0	57000.0	74000.0	96000.0	71000.0	118156.4
1	$M_{11->10}$	26000.0	50000.0	69000.0	84000.0	150000.0	79000.0	85223.6
1	$M_{10->11}$	58000.0	72000.0	87000.0	100000.0	118000.0	81000.0	62364.3
1	$M_{12->11}$	34000.0	44000.0	61000.0	78000.0	130000.0	73000.0	78486.8
1	$M_{11->12}$	0.0	0.0	1000.0	20000.0	26000.0	117000.0	164114.0

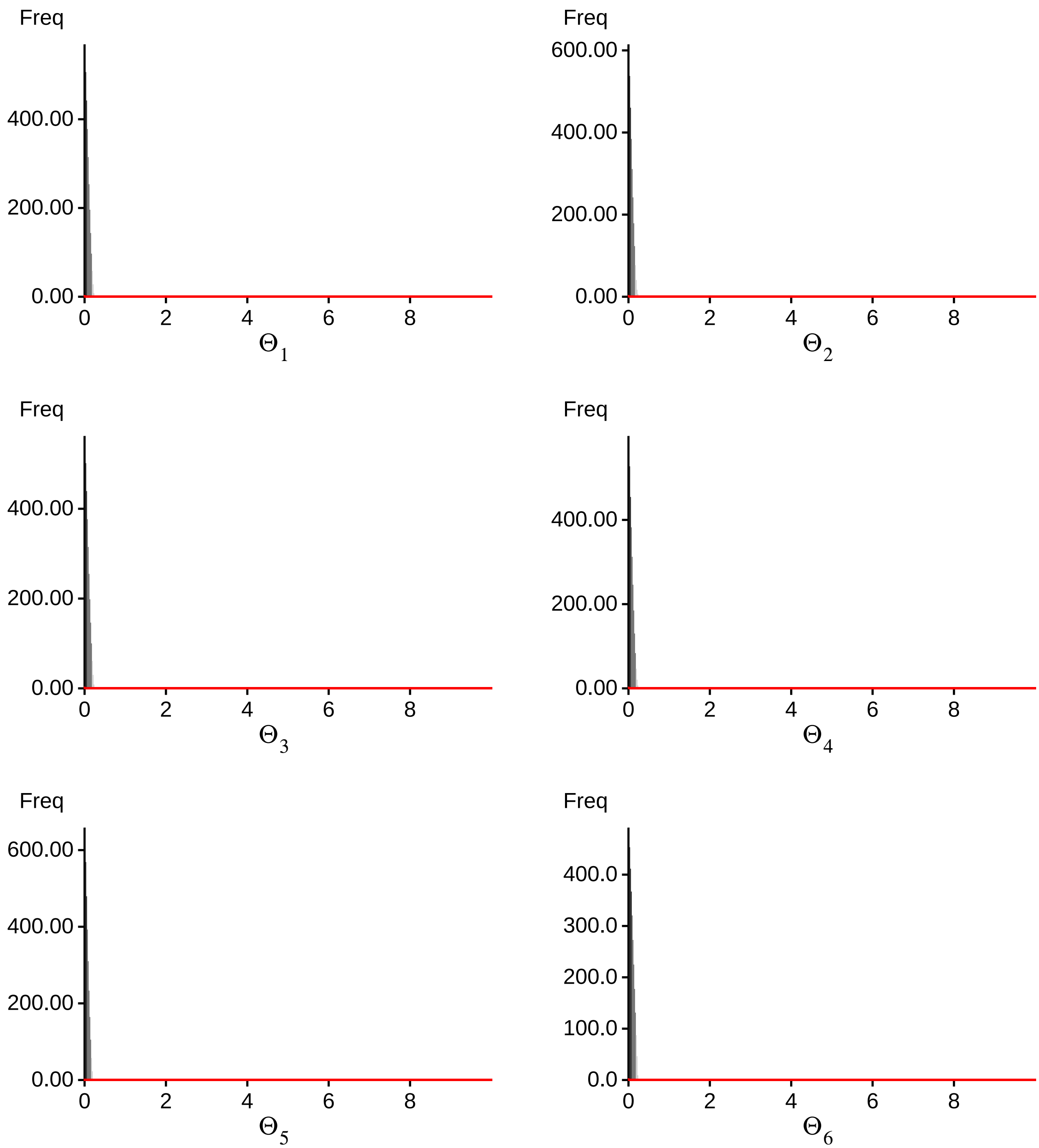
Citation suggestions:

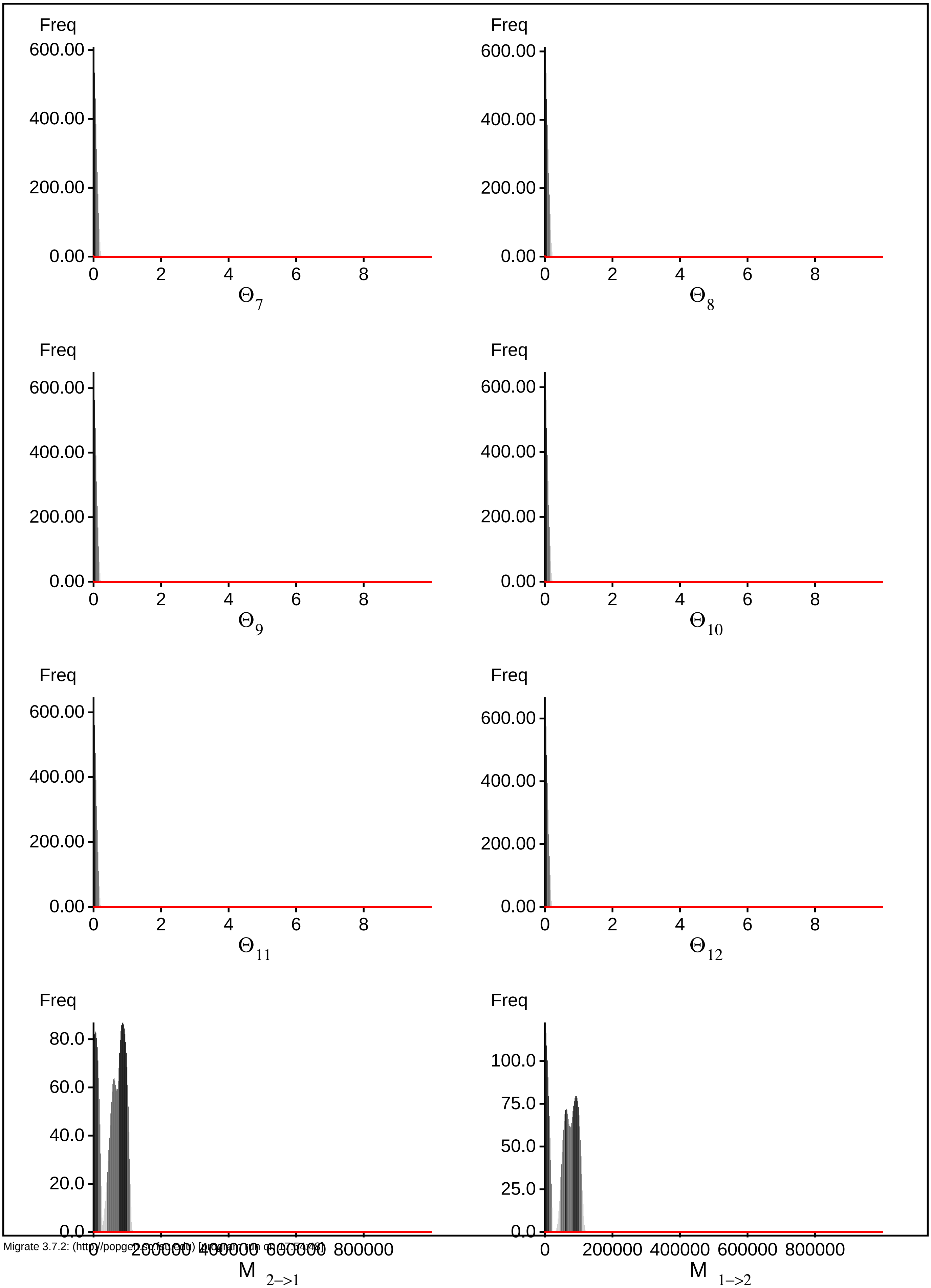
Beerli P., 2006. Comparison of Bayesian and maximum-likelihood inference of population genetic parameters. Bioinformatics 22:341-345

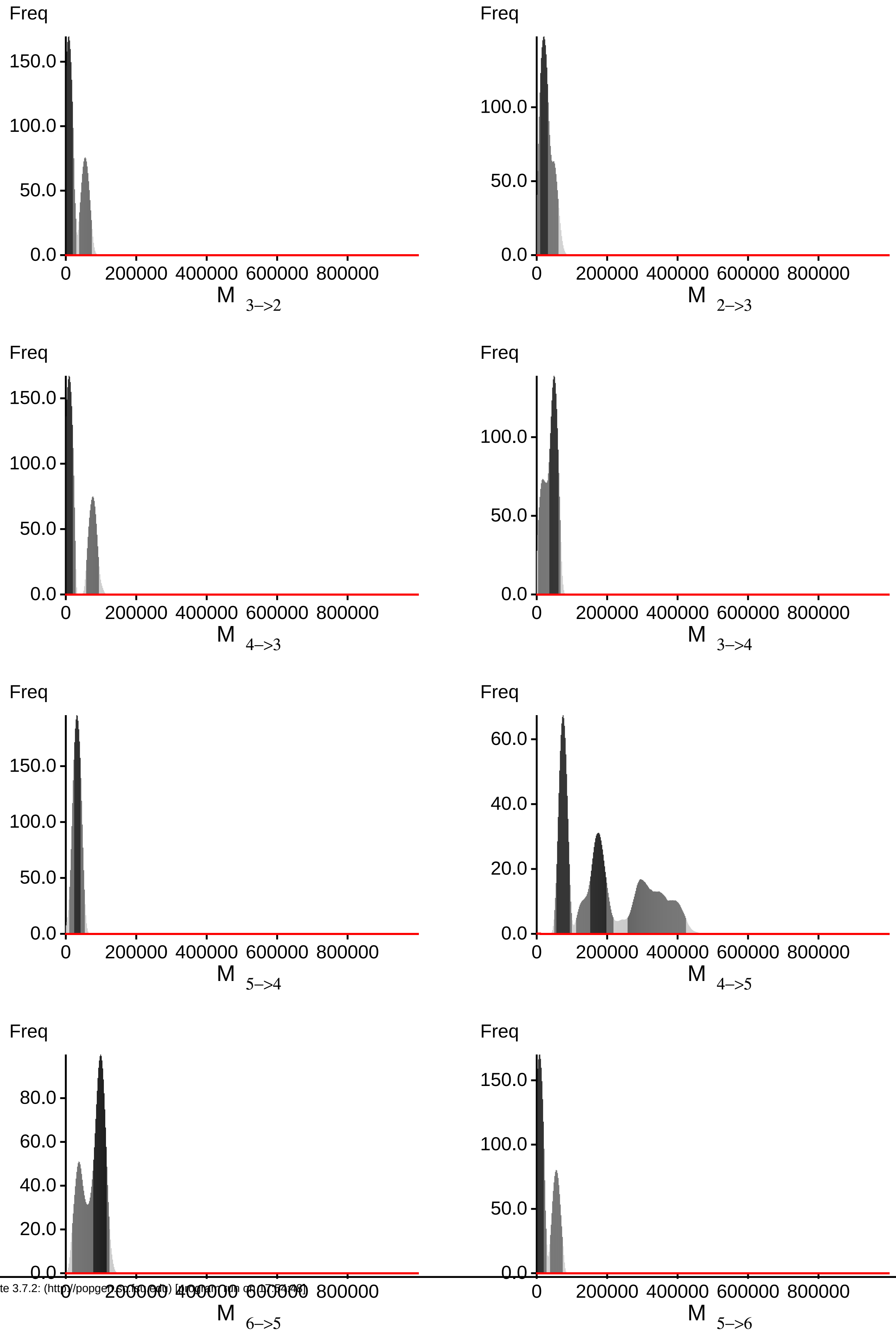
Beerli P., 2007. Estimation of the population scaled mutation rate from microsatellite data, Genetics, 177:1967-1968.

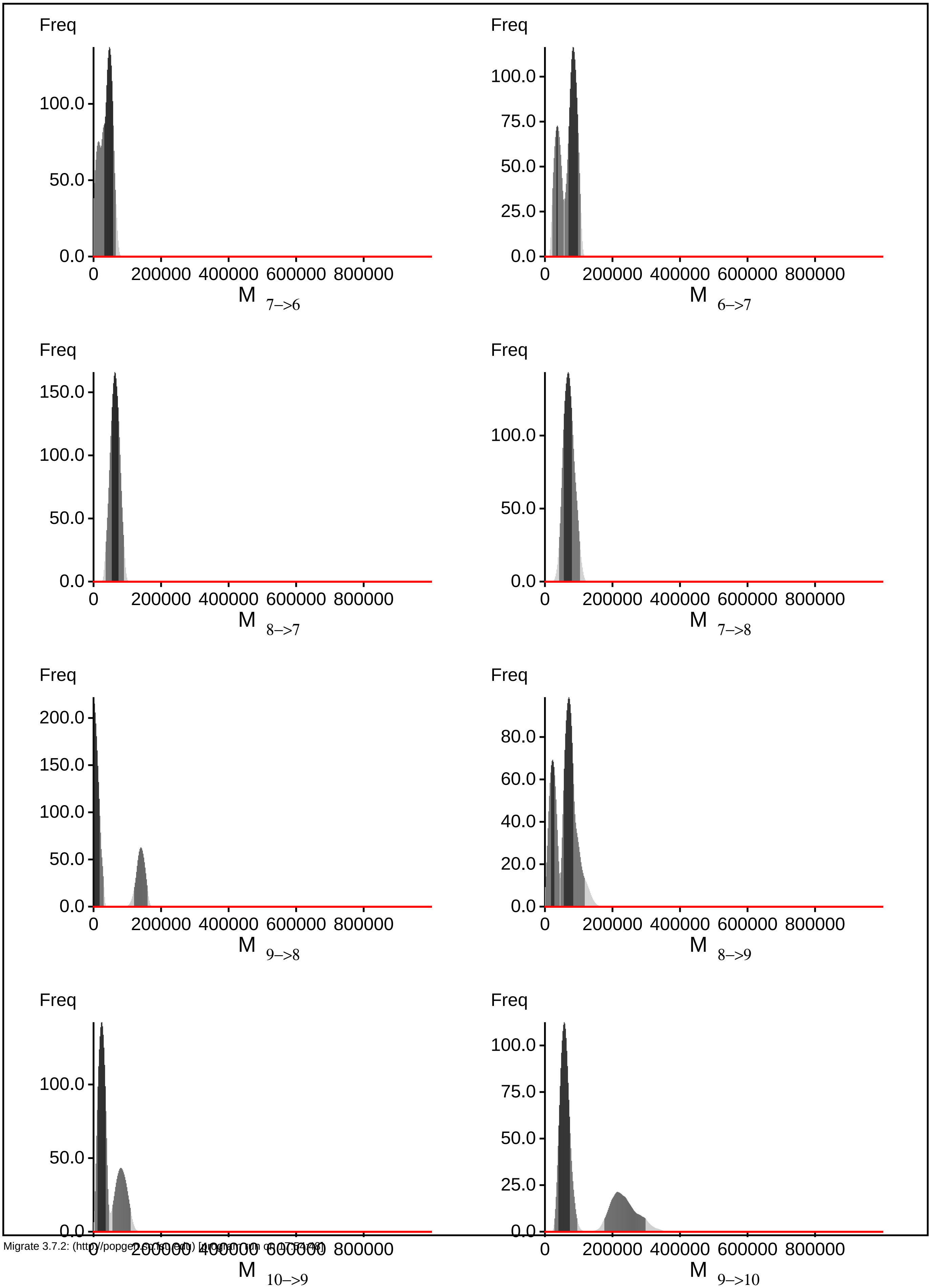
Beerli P., 2009. How to use MIGRATE or why are Markov chain Monte Carlo programs difficult to use? In Population Genetics for Animal Conservation, G. Bertorelle, M. W. Bruford, H. C. Hauffe, A. Rizzoli, and C. Vernesi, eds., vol. 17 of Conservation Biology, Cambridge University Press, Cambridge UK, pp. 42-79.

Bayesian Analysis: Posterior distribution over all loci




Freq
600.00
400.00
200.00
0.00
0
2
4
6
8
Θ7
Freq
Θ8
Θ9
Θ10
Θ11
Θ12
80.0
60.0
40.0
20.0
0.0
200000
400000
600000
800000
M 2->1
100.0
75.0
50.0
25.0
M 1->2


Freq
150.0
100.0
50.0
0.0
0 200000 400000 600000 800000
M 3–>2
Freq
100.0
50.0
0.0
0 200000 400000 600000 800000
M 2–>3
Freq
150.0
100.0
50.0
0.0
0 200000 400000 600000 800000
M 4–>3
Freq
100.0
50.0
0.0
0 200000 400000 600000 800000
M 3–>4
Freq
150.0
100.0
50.0
0.0
0 200000 400000 600000 800000
M 5–>4
Freq
60.0
40.0
20.0
0.0
0 200000 400000 600000 800000
M 4–>5
Freq
80.0
60.0
40.0
20.0
0.0
0 200000 400000 600000 800000
M 6–>5
Freq
150.0
100.0
50.0
0.0
0 200000 400000 600000 800000
M 5–>6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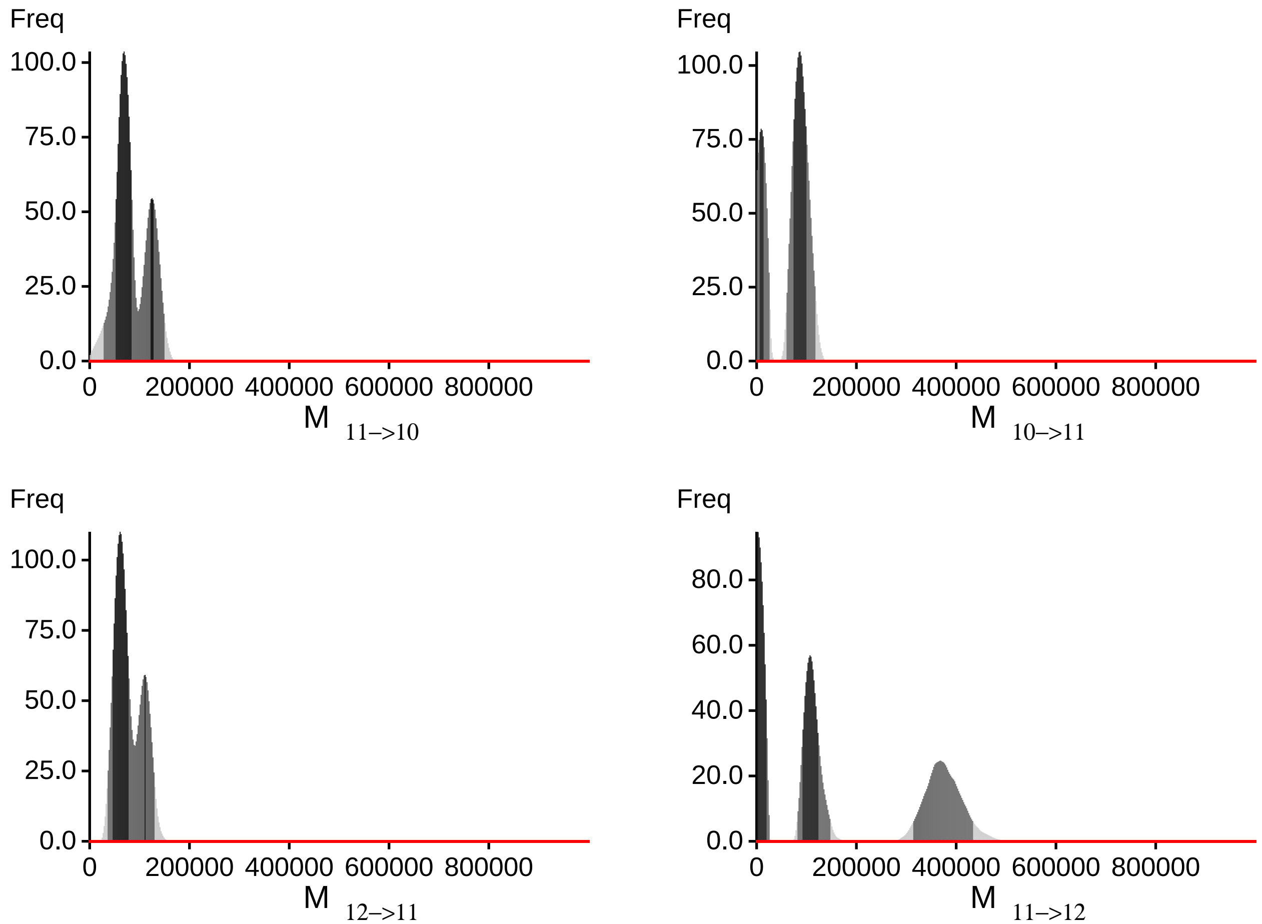
100.0
50.0
0.0
0 200000 400000 600000 800000
M 7–>6
Freq
100.0
75.0
50.0
25.0
0.0
0 200000 400000 600000 800000
M 6–>7
Freq
150.0
100.0
50.0
0.0
0 200000 400000 600000 800000
M 8–>7
Freq
100.0
50.0
0.0
0 200000 400000 600000 800000
M 7–>8
Freq
200.0
150.0
100.0
50.0
0.0
0 200000 400000 600000 800000
M 9–>8
Freq
80.0
60.0
40.0
20.0
0.0
0 200000 400000 600000 800000
M 8–>9
Freq
100.0
50.0
0.0
0 200000 400000 600000 800000
M 10–>9
Freq
100.0
75.0
50.0
25.0
0.0
0 200000 400000 600000 800000
M 9–>10


Freq
100.0
75.0
50.0
25.0
0.0
0
200000
400000
600000
800000
M 11–>10
Freq
100.0
75.0
50.0
25.0
0.0
0
200000
400000
600000
800000
M 10–>11
Freq
100.0
75.0
50.0
25.0
0.0
0
200000
400000
600000
800000
M 12–>11
Freq
80.0
60.0
40.0
20.0
0.0
0
200000
400000
600000
800000
M 11–>12

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]

Method	ln(Prob(D|Model))	Notes
Thermodynamic integration	-2211.451887	(1a)
	-2133.707585	(1b)
Harmonic mean	-1897.261405	(2)

(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

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	887/4348	0.20400
Θ_2	925/4482	0.20638
Θ_3	1091/4408	0.24750
Θ_4	469/4471	0.10490
Θ_5	3076/4454	0.69062
Θ_6	597/4280	0.13949
Θ_7	1247/4510	0.27650
Θ_8	1270/4479	0.28355
Θ_9	1419/4510	0.31463
Θ_{10}	2606/4386	0.59416
Θ_{11}	1880/4312	0.43599
Θ_{12}	1427/4301	0.33178
$M_{2\to1}$	4358/4358	1.00000
$M_{1\to2}$	4383/4383	1.00000
$M_{3\to2}$	4381/4381	1.00000
$M_{2\to3}$	4525/4525	1.00000
$M_{4\to3}$	4417/4417	1.00000
$M_{3\to4}$	4445/4445	1.00000
$M_{5\to4}$	4434/4434	1.00000
$M_{4\to5}$	4425/4425	1.00000
$M_{6\to5}$	4425/4425	1.00000
$M_{5\to6}$	4380/4380	1.00000
$M_{7\to6}$	4324/4324	1.00000
$M_{6\to7}$	4323/4323	1.00000
$M_{8\to7}$	4416/4416	1.00000
$M_{7\to8}$	4459/4459	1.00000
$M_{9\to8}$	4485/4485	1.00000
$M_{8\to9}$	4443/4443	1.00000
$M_{10\to9}$	4385/4385	1.00000
$M_{9\to10}$	4498/4498	1.00000
$M_{11\to10}$	4406/4406	1.00000
$M_{10\to11}$	4454/4454	1.00000
$M_{12\to11}$	4459/4459	1.00000
$M_{11\to12}$	4361/4361	1.00000
Genealogies	43290/149873	0.28884

MCMC-Autocorrelation and Effective MCMC Sample Size

Parameter	Autocorrelation	Effective Sampe Size
Θ_1	0.85462	262.54
Θ_2	0.87724	214.47
Θ_3	0.82021	318.78
Θ_4	0.93814	97.49
Θ_5	0.48628	1074.60
Θ_6	0.91816	131.45
Θ_7	0.79758	343.23
Θ_8	0.83566	268.70
Θ_9	0.74973	449.86
Θ_{10}	0.51004	1049.68
Θ_{11}	0.66148	614.15
Θ_{12}	0.66519	673.63
$M_{2\to1}$	0.85902	228.19
$M_{1\to2}$	0.80618	323.88
$M_{3\to2}$	0.81198	318.05
$M_{2\to3}$	0.83000	287.69
$M_{4\to3}$	0.81890	301.68
$M_{3\to4}$	0.83660	267.81
$M_{5\to4}$	0.90448	151.40
$M_{4\to5}$	0.84439	257.26
$M_{6\to5}$	0.77551	384.11
$M_{5\to6}$	0.87584	198.46
$M_{7\to6}$	0.77066	388.65
$M_{6\to7}$	0.81231	310.86
$M_{8\to7}$	0.87391	204.24
$M_{7\to8}$	0.81056	316.12
$M_{9\to8}$	0.74817	438.99
$M_{8\to9}$	0.81274	311.36
$M_{10\to9}$	0.77213	387.65
$M_{9\to10}$	0.75486	418.89
$M_{11\to10}$	0.72208	485.99
$M_{10\to11}$	0.80497	328.10
$M_{12\to11}$	0.77006	395.62
$M_{11\to12}$	0.81341	319.71
Ln[Prob(D|G)]	0.98508	22.55

Potential Problems

This section reports potential problems with your run, but such reporting is often not very accurate. Whith many parameters in a multilocus 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 wether 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