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 Fri May 28 11:32:32 2021
Program finished at Fri May 28 19:41:14 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) 2030783339
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	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	$M_{2->1}$	<displayed>
24	$M_{1->2}$	<displayed>
25	$M_{3->2}$	<displayed>
36	$M_{2->3}$	<displayed>
37	$M_{4->3}$	<displayed>
48	$M_{3->4}$	<displayed>
49	$M_{5->4}$	<displayed>
60	$M_{4->5}$	<displayed>
61	$M_{6->5}$	<displayed>
72	$M_{5->6}$	<displayed>
73	$M_{7->6}$	<displayed>
84	$M_{6->7}$	<displayed>
85	$M_{8->7}$	<displayed>
96	$M_{7->8}$	<displayed>
97	$M_{9->8}$	<displayed>
108	$M_{8->9}$	<displayed>
109	$M_{10->9}$	<displayed>
120	$M_{9->10}$	<displayed>
121	$M_{11->10}$	<displayed>
132	$M_{10->11}$	<displayed>
133	$M_{12->11}$	<displayed>
144	$M_{11->12}$	<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	10
12	1	0
Total of all populations	1	184

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	0.16001	0.07001	0.01841
1	Θ_2	0.00001	0.00001	0.01001	0.06001	0.16001	0.07001	0.01950
1	Θ_3	0.00001	0.00001	0.01001	0.08001	0.20001	0.09001	0.03665
1	Θ_4	0.00001	0.00001	0.01001	0.06001	0.18001	0.07001	0.02648
1	Θ_5	0.00001	0.00001	0.01001	0.06001	0.16001	0.07001	0.01654
1	Θ_6	0.00001	0.00001	0.01001	0.06001	0.16001	0.07001	0.01827
1	Θ_7	0.00001	0.00001	0.01001	0.06001	0.16001	0.07001	0.01632
1	Θ_8	0.00001	0.00001	0.01001	0.06001	0.16001	0.07001	0.01246
1	Θ_9	0.00001	0.00001	0.01001	0.06001	0.16001	0.07001	0.01303
1	Θ_{10}	0.00001	0.00001	0.01001	0.06001	0.16001	0.07001	0.01840
1	Θ_{11}	0.00001	0.00001	0.01001	0.06001	0.16001	0.07001	0.01420
1	Θ_{12}	0.00001	0.00001	0.01001	0.06001	0.16001	0.07001	0.01283
1	$M_{2->1}$	20000.0	32000.0	51000.0	68000.0	80000.0	63000.0	80441.5
1	$M_{1->2}$	62000.0	82000.0	99000.0	112000.0	122000.0	87000.0	75797.8
1	$M_{3->2}$	2000.0	38000.0	53000.0	64000.0	70000.0	47000.0	40915.8
1	$M_{2->3}$	0.0	0.0	1000.0	16000.0	42000.0	17000.0	19152.6
1	$M_{4->3}$	38000.0	82000.0	95000.0	110000.0	126000.0	87000.0	84146.6
1	$M_{3->4}$	24000.0	34000.0	43000.0	50000.0	60000.0	87000.0	80696.6
1	$M_{5->4}$	68000.0	78000.0	93000.0	106000.0	118000.0	89000.0	67257.2
1	$M_{4->5}$	84000.0	96000.0	107000.0	116000.0	128000.0	109000.0	113937.9
1	$M_{6->5}$	56000.0	70000.0	81000.0	90000.0	104000.0	85000.0	82026.7
1	$M_{5->6}$	4000.0	14000.0	35000.0	54000.0	68000.0	49000.0	61880.4
1	$M_{7->6}$	0.0	0.0	13000.0	24000.0	32000.0	91000.0	91766.6
1	$M_{6->7}$	10000.0	24000.0	33000.0	42000.0	54000.0	35000.0	33363.6
1	$M_{8->7}$	24000.0	50000.0	73000.0	84000.0	106000.0	67000.0	65672.8
1	$M_{7->8}$	2000.0	10000.0	19000.0	26000.0	98000.0	55000.0	52355.6
1	$M_{9->8}$	8000.0	28000.0	51000.0	56000.0	74000.0	45000.0	42178.9
1	$M_{8->9}$	20000.0	36000.0	59000.0	74000.0	90000.0	71000.0	91192.8
1	$M_{10->9}$	38000.0	54000.0	67000.0	76000.0	92000.0	69000.0	65946.5
1	$M_{9->10}$	4000.0	10000.0	25000.0	36000.0	72000.0	33000.0	35696.5
1	$M_{11->10}$	0.0	0.0	1000.0	10000.0	18000.0	49000.0	40686.7
1	$M_{10->11}$	18000.0	26000.0	43000.0	60000.0	84000.0	59000.0	81459.2
1	$M_{12->11}$	0.0	0.0	17000.0	32000.0	36000.0	89000.0	98322.1
1	$M_{11->12}$	36000.0	52000.0	67000.0	84000.0	140000.0	107000.0	267877.1

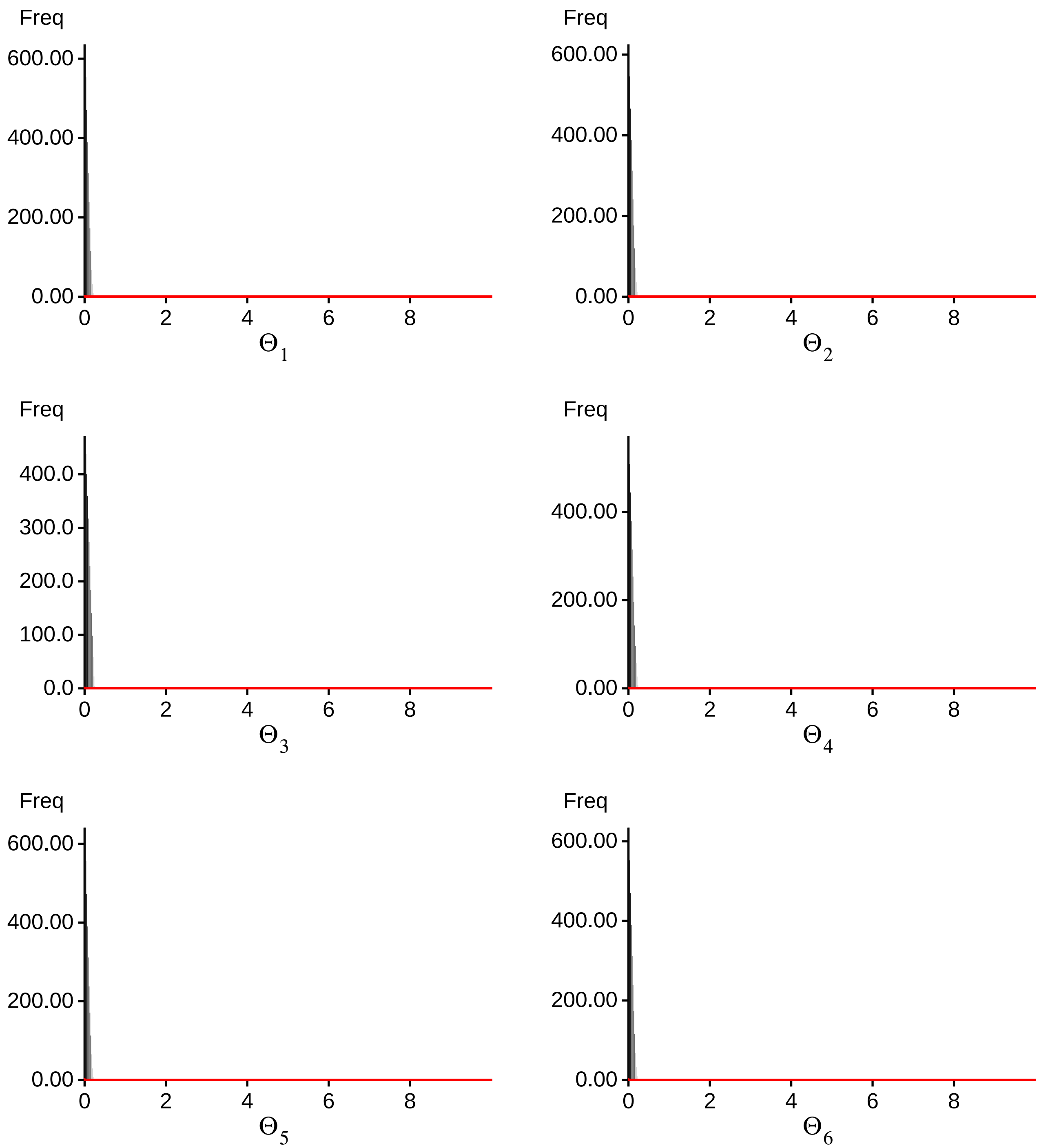
Citation suggestions:

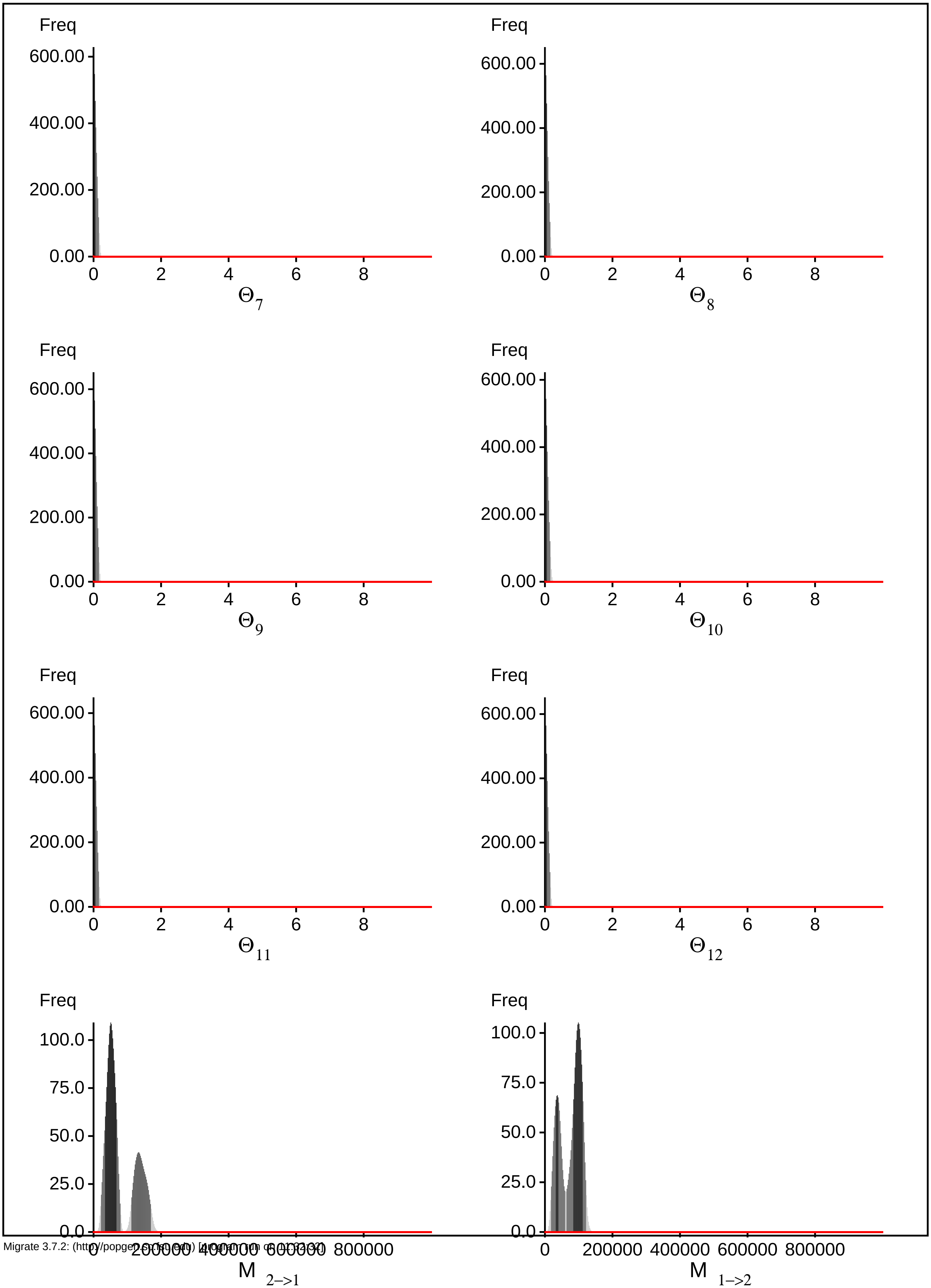
Beerli P., 2006. Comparison of Bayesian and maximum-likelihood inference of population genetic parameters. Bioinformatics 22:341-345

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

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400.00
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2
4
6
8
Θ7
Freq
600.00
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Θ8
Freq
Θ9
Freq
Θ10
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Θ11
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Θ12
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100.0
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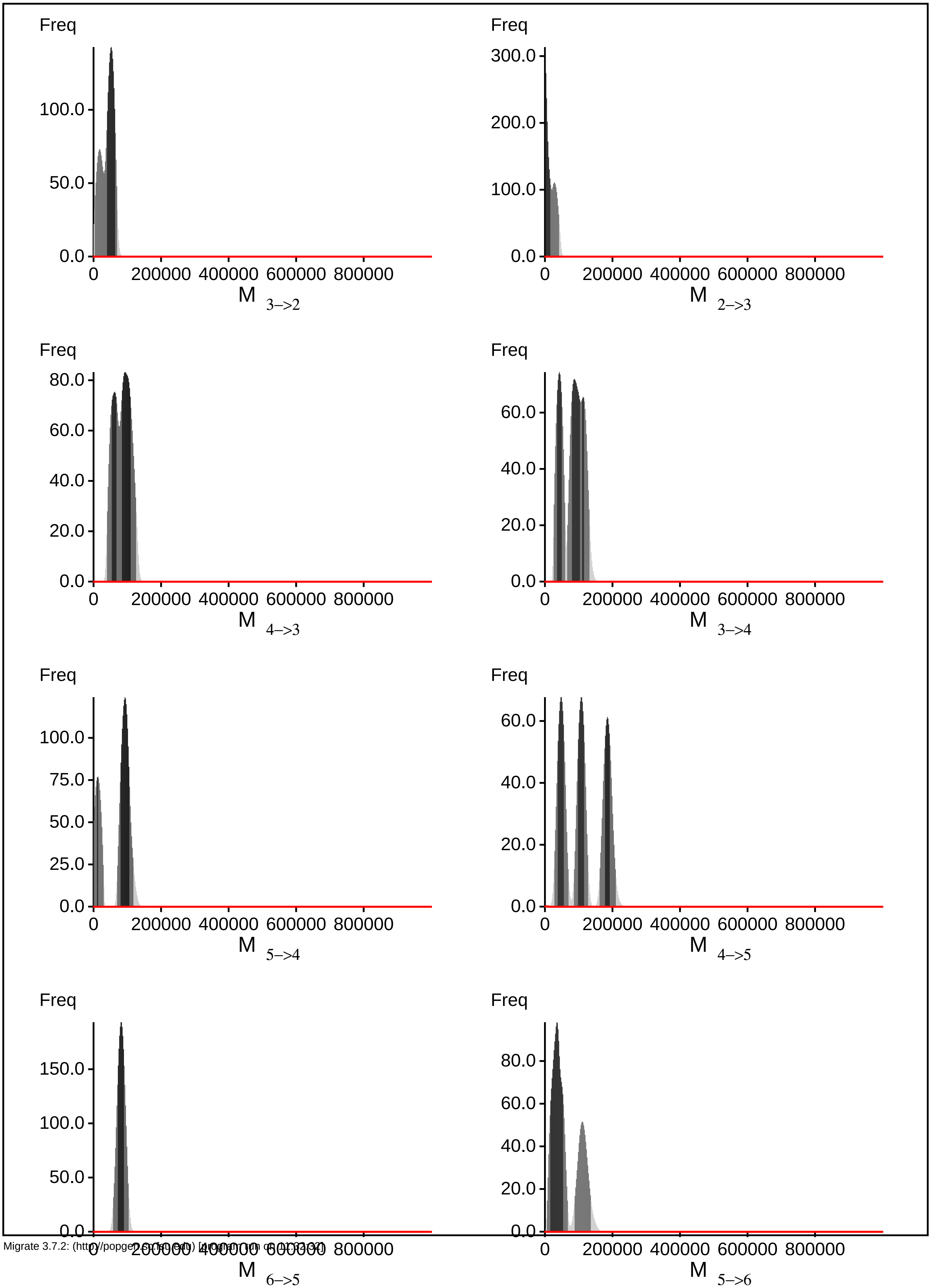
M 2->1
Freq
M 1->2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M 3–>2
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M 2–>3
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M 4–>3
Freq
M 3–>4
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M 5–>4
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Freq
M 6–>5
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M 5–>6
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600000
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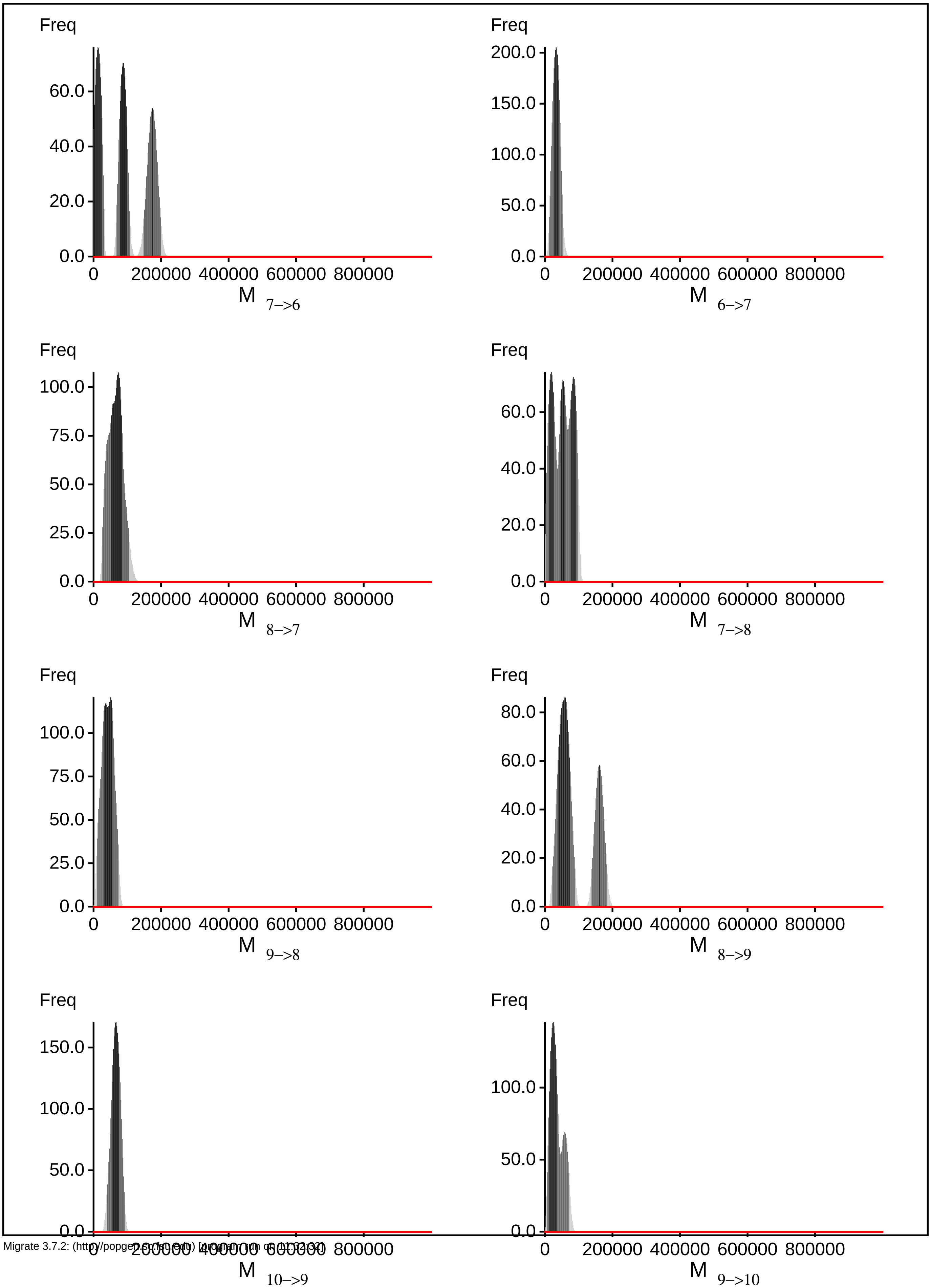
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200000
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600000
800000
M 7–>6
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0.0
50.0
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150.0
200.0
M 6–>7
Freq
0.0
25.0
50.0
75.0
100.0
M 8–>7
Freq
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20.0
40.0
60.0
M 7–>8
Freq
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25.0
50.0
75.0
100.0
M 9–>8
Freq
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60.0
80.0
M 8–>9
Freq
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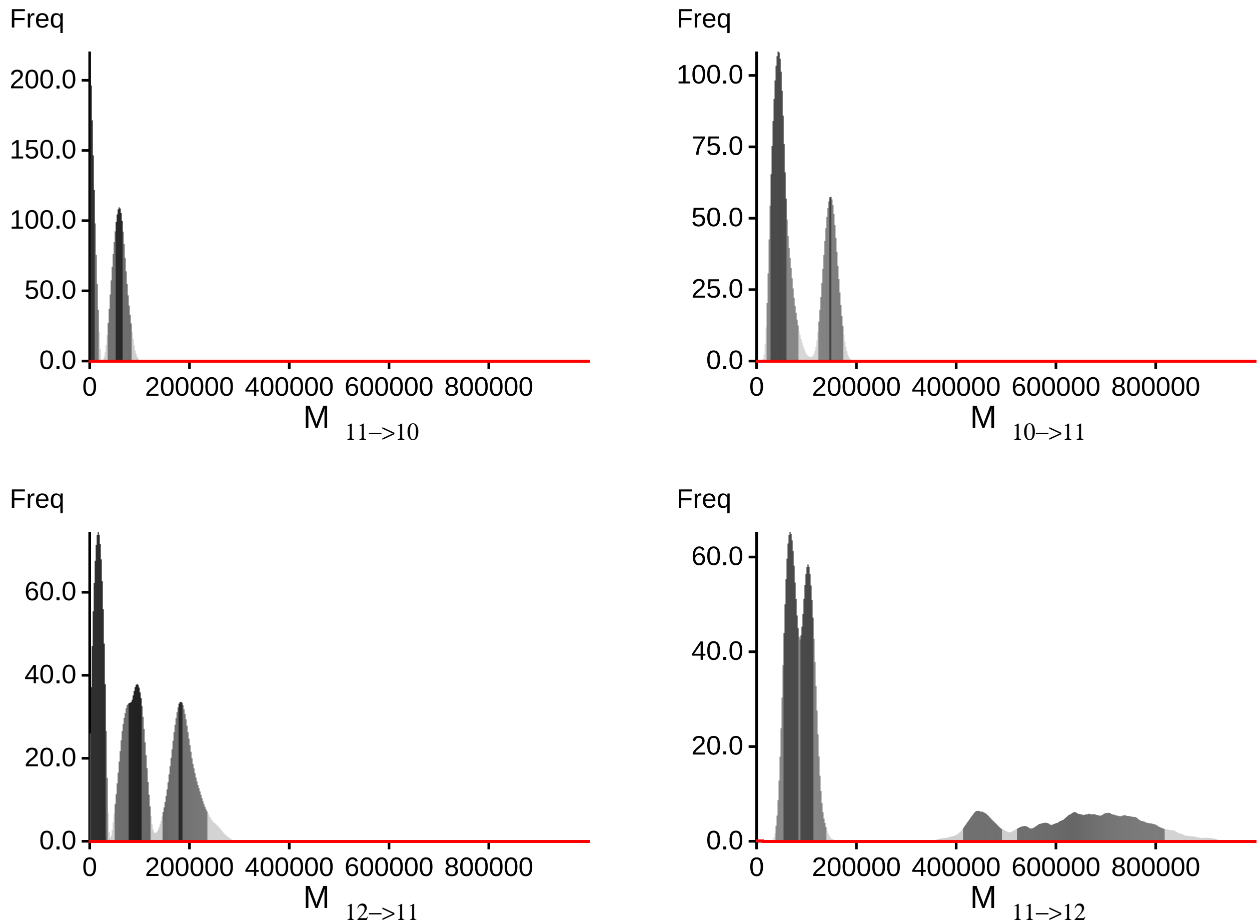
100.0
150.0
M 10–>9
Freq
0.0
50.0
100.0
M 9–>10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150.0
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0 200000 400000 600000 800000
M 11–>10
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0 200000 400000 600000 800000
M 10–>11
Freq
60.0
40.0
20.0
0.0
0 200000 400000 600000 800000
M 12–>11
Freq
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	-2143.738989	(1a)
	-2062.890290	(1b)
Harmonic mean	-1831.468406	(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	1559/4424	0.35240
Θ_2	1548/4441	0.34857
Θ_3	551/4472	0.12321
Θ_4	943/4363	0.21614
Θ_5	2125/4568	0.46519
Θ_6	1703/4234	0.40222
Θ_7	1019/4398	0.23170
Θ_8	784/4374	0.17924
Θ_9	1995/4525	0.44088
Θ_{10}	850/4481	0.18969
Θ_{11}	2375/4491	0.52884
Θ_{12}	3121/4436	0.70356
$M_{2\to1}$	4374/4374	1.00000
$M_{1\to2}$	4344/4344	1.00000
$M_{3\to2}$	4343/4343	1.00000
$M_{2\to3}$	4293/4293	1.00000
$M_{4\to3}$	4434/4434	1.00000
$M_{3\to4}$	4457/4457	1.00000
$M_{5\to4}$	4420/4420	1.00000
$M_{4\to5}$	4315/4315	1.00000
$M_{6\to5}$	4421/4421	1.00000
$M_{5\to6}$	4401/4401	1.00000
$M_{7\to6}$	4368/4368	1.00000
$M_{6\to7}$	4408/4408	1.00000
$M_{8\to7}$	4521/4521	1.00000
$M_{7\to8}$	4430/4430	1.00000
$M_{9\to8}$	4340/4340	1.00000
$M_{8\to9}$	4423/4423	1.00000
$M_{10\to9}$	4407/4407	1.00000
$M_{9\to10}$	4359/4359	1.00000
$M_{11\to10}$	4367/4367	1.00000
$M_{10\to11}$	4406/4406	1.00000
$M_{12\to11}$	4438/4438	1.00000
$M_{11\to12}$	4367/4367	1.00000
Genealogies	33621/150157	0.22391

MCMC-Autocorrelation and Effective MCMC Sample Size

Parameter	Autocorrelation	Effective Sampe Size
Θ_1	0.78754	361.13
Θ_2	0.71849	493.32
Θ_3	0.92668	114.31
Θ_4	0.82658	292.72
Θ_5	0.66382	608.43
Θ_6	0.67921	611.71
Θ_7	0.83735	290.15
Θ_8	0.89615	175.38
Θ_9	0.70889	515.93
Θ_{10}	0.85297	257.86
Θ_{11}	0.58833	840.63
Θ_{12}	0.51959	971.21
$M_{2\to1}$	0.84699	250.91
$M_{1\to2}$	0.83475	280.74
$M_{3\to2}$	0.66903	594.85
$M_{2\to3}$	0.85600	232.78
$M_{4\to3}$	0.84717	249.34
$M_{3\to4}$	0.73665	458.26
$M_{5\to4}$	0.78253	370.39
$M_{4\to5}$	0.69423	556.99
$M_{6\to5}$	0.75286	422.92
$M_{5\to6}$	0.82969	279.05
$M_{7\to6}$	0.75592	420.90
$M_{6\to7}$	0.82314	291.22
$M_{8\to7}$	0.82064	296.90
$M_{7\to8}$	0.76144	406.09
$M_{9\to8}$	0.78919	355.50
$M_{8\to9}$	0.83149	283.83
$M_{10\to9}$	0.78916	358.87
$M_{9\to10}$	0.79597	342.34
$M_{11\to10}$	0.82540	287.53
$M_{10\to11}$	0.75653	418.39
$M_{12\to11}$	0.84350	260.46
$M_{11\to12}$	0.78569	374.47
Ln[Prob(D|G)]	0.97345	40.39

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