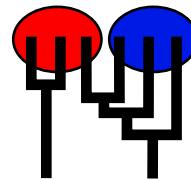


Preliminary migrate analysis of M. californianus

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 Mon May 31 15:26:49 2021
 Program finished at Mon May 31 16:09:37 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) 1384053781

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	*	s	0	0	0	0	0	0	0	0	s	*
2 Bamfiel	s	0	0	0	0	0	0	0	0	s	*	s
3 PortRen	0	0	0	0	0	0	0	0	s	*	s	0
4 WalkOnB	0	0	0	0	0	0	0	s	*	s	0	0
5 BodegaH	0	0	0	0	0	0	s	*	s	0	0	0
6 Davenpo	0	0	0	0	0	s	*	s	0	0	0	0
7 VistaDe	0	0	0	0	s	*	s	0	0	0	0	0
8 HazardR	0	0	0	s	*	s	0	0	0	0	0	0
9 Refugio	0	0	s	*	0	0	0	0	0	0	0	0
10 Carpint	0	s	0	0	0	0	0	0	0	0	0	0

Preliminary migrate analysis of *M. californianus* CO1 haplotypes for Evolution 2 -- 2

Order of parameters:

1	Θ_1			<displayed>
6	Θ_6	=	Θ_6	[s] <displayed>
7	Θ_7	=	Θ_6	[s]
11	Θ_{11}			<displayed>
12	Θ_{12}			<displayed>
13	$M_{2 \rightarrow 1}$	=	$M_{2 \rightarrow 1}$	[s] <displayed>
22	$M_{11 \rightarrow 1}$	=	$M_{11 \rightarrow 1}$	[s] <displayed>
23	$M_{12 \rightarrow 1}$			<displayed>
24	$M_{1 \rightarrow 2}$	=	$M_{2 \rightarrow 1}$	[s]
32	$M_{10 \rightarrow 2}$	=	$M_{10 \rightarrow 2}$	[s] <displayed>
33	$M_{11 \rightarrow 2}$			<displayed>
34	$M_{12 \rightarrow 2}$	=	$M_{12 \rightarrow 2}$	[s] <displayed>
42	$M_{9 \rightarrow 3}$	=	$M_{9 \rightarrow 3}$	[s] <displayed>
43	$M_{10 \rightarrow 3}$			<displayed>
44	$M_{11 \rightarrow 3}$	=	$M_{11 \rightarrow 3}$	[s] <displayed>
52	$M_{8 \rightarrow 4}$	=	$M_{8 \rightarrow 4}$	[s] <displayed>
53	$M_{9 \rightarrow 4}$			<displayed>
54	$M_{10 \rightarrow 4}$	=	$M_{10 \rightarrow 4}$	[s] <displayed>
62	$M_{7 \rightarrow 5}$	=	$M_{7 \rightarrow 5}$	[s] <displayed>
63	$M_{8 \rightarrow 5}$			<displayed>
64	$M_{9 \rightarrow 5}$	=	$M_{9 \rightarrow 5}$	[s] <displayed>
73	$M_{7 \rightarrow 6}$			<displayed>
74	$M_{8 \rightarrow 6}$	=	$M_{8 \rightarrow 6}$	[s] <displayed>
83	$M_{5 \rightarrow 7}$	=	$M_{7 \rightarrow 5}$	[s]
84	$M_{6 \rightarrow 7}$			<displayed>
93	$M_{4 \rightarrow 8}$	=	$M_{8 \rightarrow 4}$	[s]
94	$M_{5 \rightarrow 8}$			<displayed>
95	$M_{6 \rightarrow 8}$	=	$M_{8 \rightarrow 6}$	[s]
103	$M_{3 \rightarrow 9}$	=	$M_{9 \rightarrow 3}$	[s]
104	$M_{4 \rightarrow 9}$			<displayed>
113	$M_{2 \rightarrow 10}$	=	$M_{10 \rightarrow 2}$	[s]
123	$M_{1 \rightarrow 11}$			<displayed>
124	$M_{2 \rightarrow 11}$			<displayed>
125	$M_{3 \rightarrow 11}$			<displayed>
126	$M_{4 \rightarrow 11}$			<displayed>
127	$M_{5 \rightarrow 11}$			<displayed>
128	$M_{6 \rightarrow 11}$			<displayed>
129	$M_{7 \rightarrow 11}$			<displayed>
130	$M_{8 \rightarrow 11}$			<displayed>
131	$M_{9 \rightarrow 11}$			<displayed>

Preliminary migrate analysis of *M. californianus* CO1 haplotypes for Evolution 2 -- 3

132	M	10->11	<displayed>				
133	M	12->11	<displayed>				
134	M	1->12	<displayed>				
135	M	2->12	<displayed>				
136	M	3->12	<displayed>				
137	M	4->12	<displayed>				
138	M	5->12	<displayed>				
139	M	6->12	<displayed>				
140	M	7->12	<displayed>				
141	M	8->12	<displayed>				
142	M	9->12	<displayed>				
143	M	10->12	<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:				4 chains with temperatures			
Static heating scheme				100000.00	3.00	1.50	1.00
				Swapping interval is 1			
Print options:				.../mcalifornianus_210528.mig			
Data file:							

Preliminary migrate analysis of *M. californianus* CO1 haplotypes for Evolution 2 -- 4

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	0.16001	0.07001	0.01000
1	Θ_6	0.00001	0.00001	0.01001	0.06001	0.16001	0.07001	0.01000
1	Θ_7	0.00001	0.00001	0.01001	0.06001	0.16001	0.07001	0.01000
1	Θ_{11}	0.00001	0.00001	0.01001	0.06001	0.16001	0.07001	0.01000
1	Θ_{12}	0.00001	0.00001	0.01001	0.06001	0.16001	0.07001	0.01000
1	$M_{2->1}$	0.0	0.0	1000.0	260000.0	756000.0	357000.0	427161.3
1	$M_{11->1}$	0.0	0.0	1000.0	16000.0	18000.0	517000.0	561104.5
1	$M_{12->1}$	0.0	0.0	1000.0	18000.0	618000.0	297000.0	424863.4
1	$M_{1->2}$	0.0	0.0	1000.0	260000.0	756000.0	357000.0	427161.3
1	$M_{10->2}$	0.0	0.0	1000.0	78000.0	754000.0	251000.0	338974.5
1	$M_{11->2}$	0.0	0.0	1000.0	28000.0	802000.0	273000.0	374554.6
1	$M_{12->2}$	0.0	0.0	1000.0	16000.0	20000.0	651000.0	598813.6
1	$M_{9->3}$	0.0	0.0	1000.0	90000.0	356000.0	381000.0	477204.5
1	$M_{10->3}$	0.0	0.0	1000.0	20000.0	54000.0	471000.0	520654.5
1	$M_{11->3}$	0.0	0.0	1000.0	182000.0	538000.0	309000.0	444829.1
1	$M_{8->4}$	0.0	0.0	1000.0	20000.0	318000.0	497000.0	510470.9
1	$M_{9->4}$	0.0	0.0	1000.0	20000.0	114000.0	445000.0	487110.2
1	$M_{10->4}$	0.0	0.0	1000.0	18000.0	34000.0	575000.0	614729.2
1	$M_{7->5}$	0.0	0.0	1000.0	20000.0	678000.0	335000.0	471057.6
1	$M_{8->5}$	0.0	0.0	1000.0	20000.0	338000.0	463000.0	545268.2
1	$M_{9->5}$	0.0	0.0	1000.0	20000.0	560000.0	359000.0	473593.1
1	$M_{7->6}$	0.0	0.0	1000.0	14000.0	18000.0	675000.0	700875.5
1	$M_{8->6}$	0.0	0.0	1000.0	140000.0	610000.0	321000.0	461771.9
1	$M_{5->7}$	0.0	0.0	1000.0	20000.0	678000.0	335000.0	471057.6
1	$M_{6->7}$	0.0	0.0	1000.0	40000.0	190000.0	391000.0	434711.2
1	$M_{4->8}$	0.0	0.0	1000.0	20000.0	318000.0	497000.0	510470.9
1	$M_{5->8}$	0.0	0.0	1000.0	64000.0	780000.0	375000.0	421405.2
1	$M_{6->8}$	0.0	0.0	1000.0	140000.0	610000.0	321000.0	461771.9
1	$M_{3->9}$	0.0	0.0	1000.0	90000.0	356000.0	381000.0	477204.5
1	$M_{4->9}$	0.0	0.0	1000.0	16000.0	20000.0	553000.0	573712.0
1	$M_{2->10}$	0.0	0.0	1000.0	78000.0	754000.0	251000.0	338974.5
1	$M_{1->11}$	0.0	0.0	1000.0	18000.0	20000.0	457000.0	558847.6
1	$M_{2->11}$	0.0	0.0	1000.0	20000.0	28000.0	397000.0	466956.7
1	$M_{3->11}$	0.0	0.0	1000.0	20000.0	542000.0	329000.0	445776.2
1	$M_{4->11}$	0.0	0.0	1000.0	16000.0	20000.0	619000.0	635586.4
1	$M_{5->11}$	0.0	0.0	1000.0	20000.0	550000.0	367000.0	480620.6

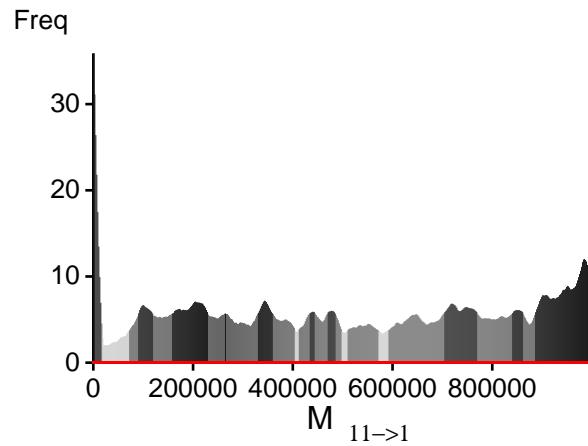
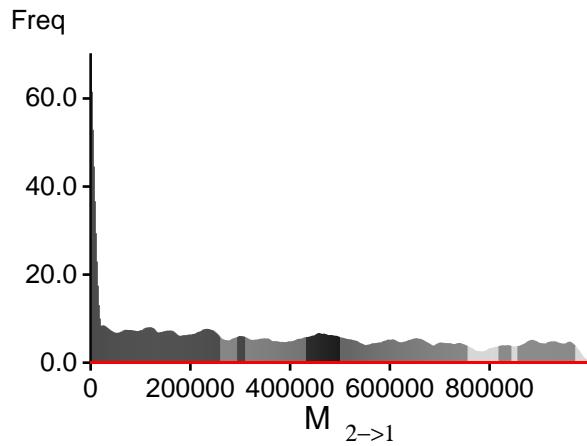
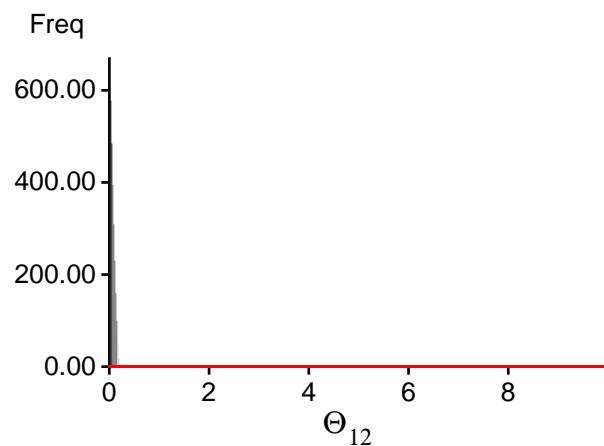
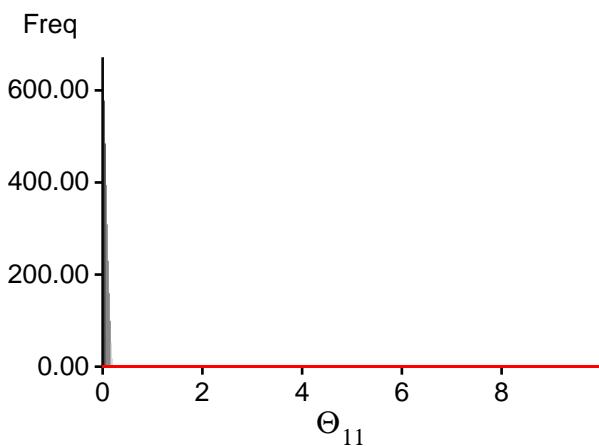
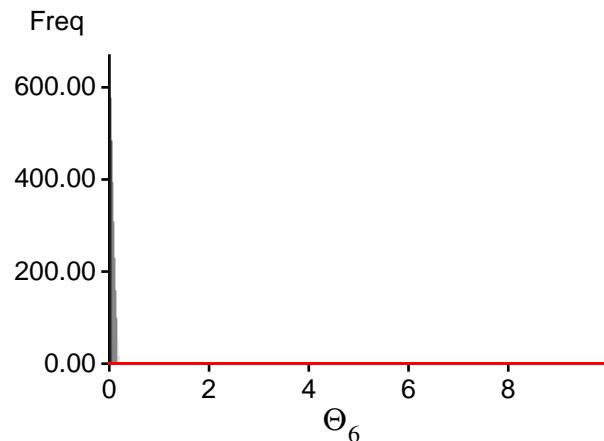
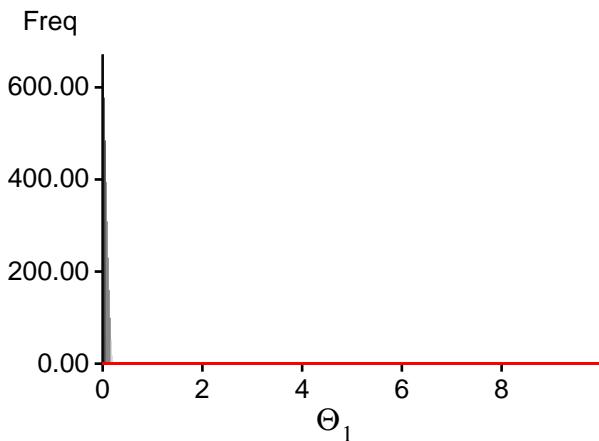
Locus	Parameter	2.5%	25.0%	Mode	75.0%	97.5%	Median	Mean
1	$M_{6 \rightarrow 11}$	0.0	0.0	1000.0	18000.0	168000.0	609000.0	585135.8
1	$M_{7 \rightarrow 11}$	0.0	0.0	1000.0	18000.0	20000.0	613000.0	639845.7
1	$M_{8 \rightarrow 11}$	0.0	0.0	1000.0	20000.0	224000.0	439000.0	516299.8
1	$M_{9 \rightarrow 11}$	0.0	0.0	1000.0	18000.0	20000.0	555000.0	598567.6
1	$M_{10 \rightarrow 11}$	0.0	0.0	1000.0	20000.0	704000.0	379000.0	458090.9
1	$M_{12 \rightarrow 11}$	0.0	0.0	1000.0	18000.0	628000.0	363000.0	470893.7
1	$M_{1 \rightarrow 12}$	0.0	0.0	1000.0	20000.0	370000.0	473000.0	531046.6
1	$M_{2 \rightarrow 12}$	0.0	0.0	1000.0	18000.0	20000.0	605000.0	597359.8
1	$M_{3 \rightarrow 12}$	0.0	0.0	1000.0	20000.0	324000.0	299000.0	442935.5
1	$M_{4 \rightarrow 12}$	0.0	0.0	1000.0	12000.0	18000.0	605000.0	612956.1
1	$M_{5 \rightarrow 12}$	0.0	0.0	1000.0	18000.0	22000.0	575000.0	564847.5
1	$M_{6 \rightarrow 12}$	0.0	0.0	1000.0	18000.0	20000.0	495000.0	533203.7
1	$M_{7 \rightarrow 12}$	0.0	0.0	1000.0	20000.0	300000.0	501000.0	526238.4
1	$M_{8 \rightarrow 12}$	0.0	0.0	1000.0	18000.0	216000.0	623000.0	641185.4
1	$M_{9 \rightarrow 12}$	0.0	0.0	1000.0	20000.0	136000.0	403000.0	505540.6
1	$M_{10 \rightarrow 12}$	0.0	0.0	1000.0	18000.0	20000.0	547000.0	592066.9
1	$M_{11 \rightarrow 12}$	0.0	0.0	1000.0	16000.0	20000.0	655000.0	643273.7

Citation suggestions:

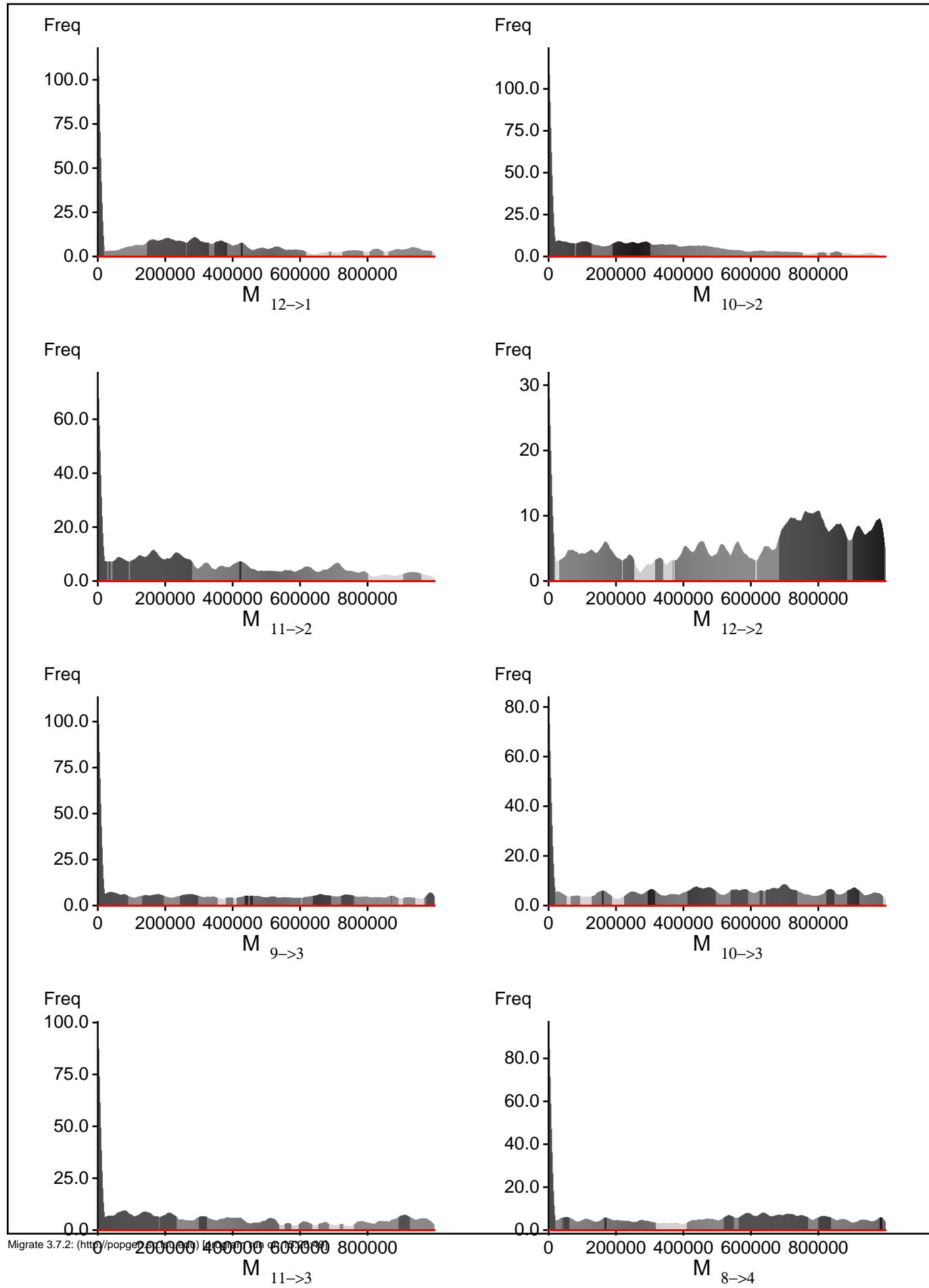
Beerli P., 2006. Comparison of Bayesian and maximum-likelihood inference of population genetic parameters. *Bioinformatics* 22:341-345

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

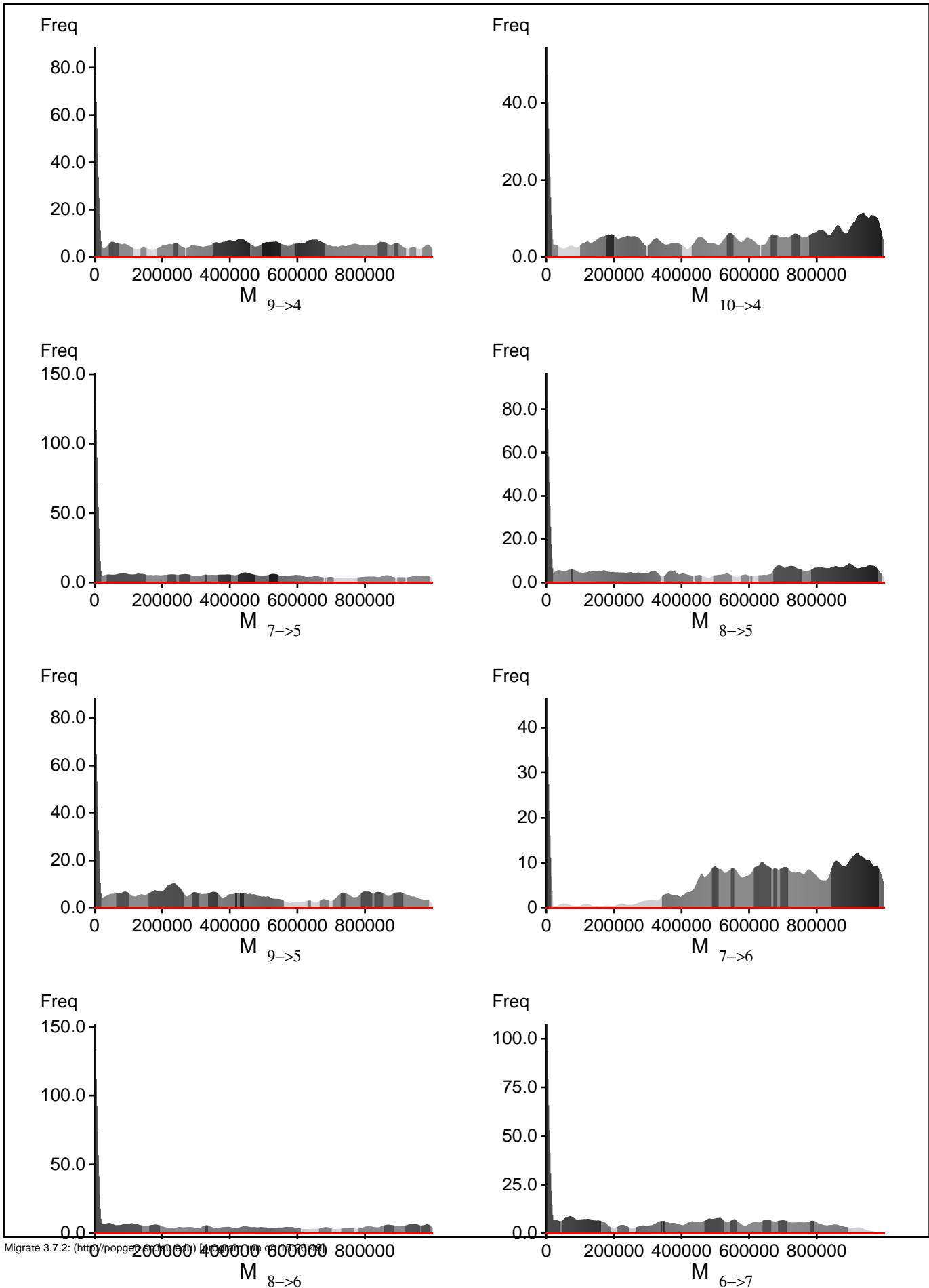
Beerli P., 2009. How to use MIGRATE or why are Markov chain Monte Carlo programs difficult to use? In Population Genetics for Animal Conservation, G. Bertorelle, M. W. Bruford, H. C. Hauffe, A. Rizzoli, and C. Vernesi, eds., vol. 17 of Conservation Biology, Cambridge University Press, Cambridge UK, pp.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

Bayesian Analysis: Posterior distribution over all loci

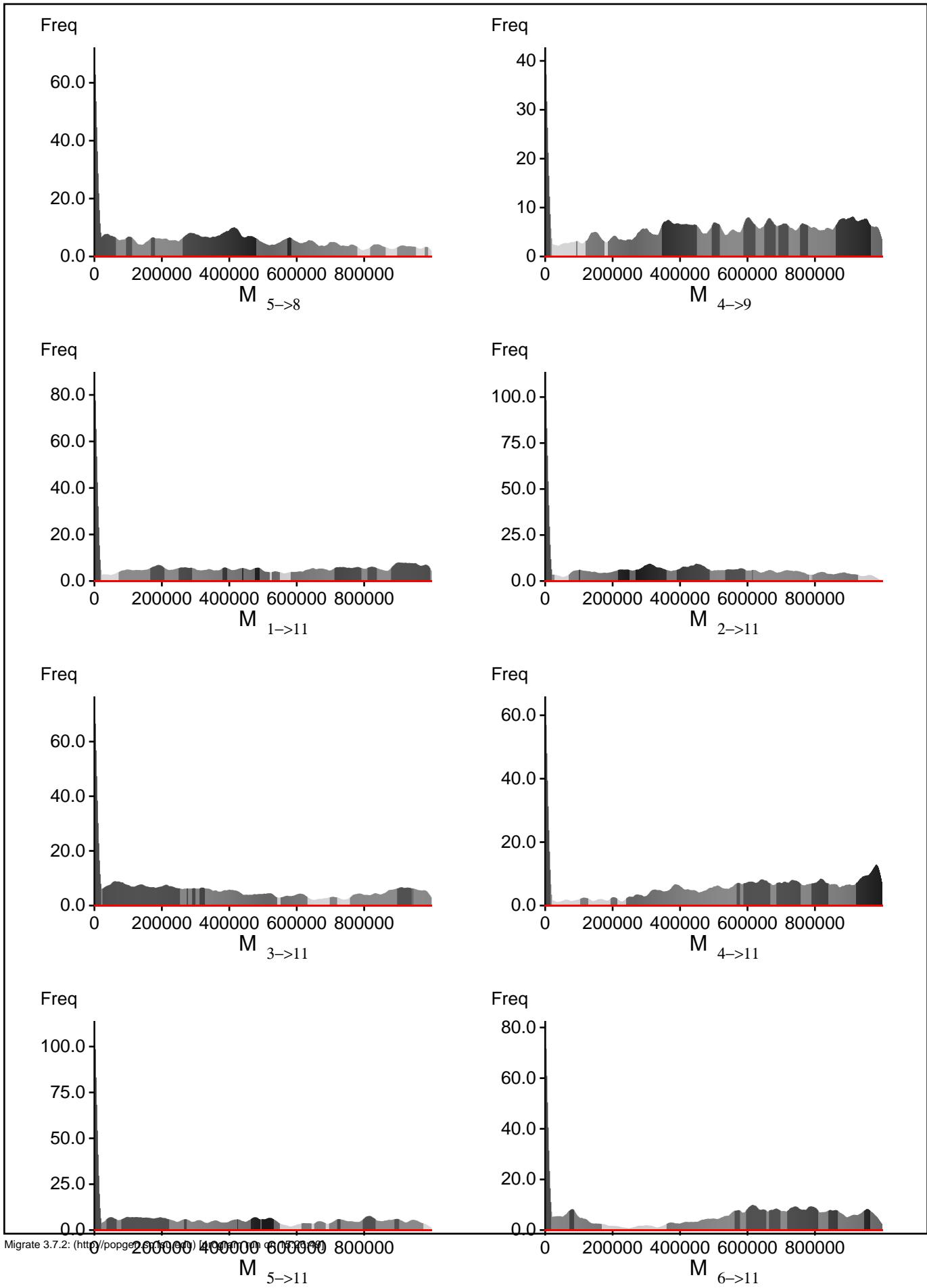
Preliminary migrate analysis of *M. californianus* CO1 haplotypes for Evolution 2 -- 9



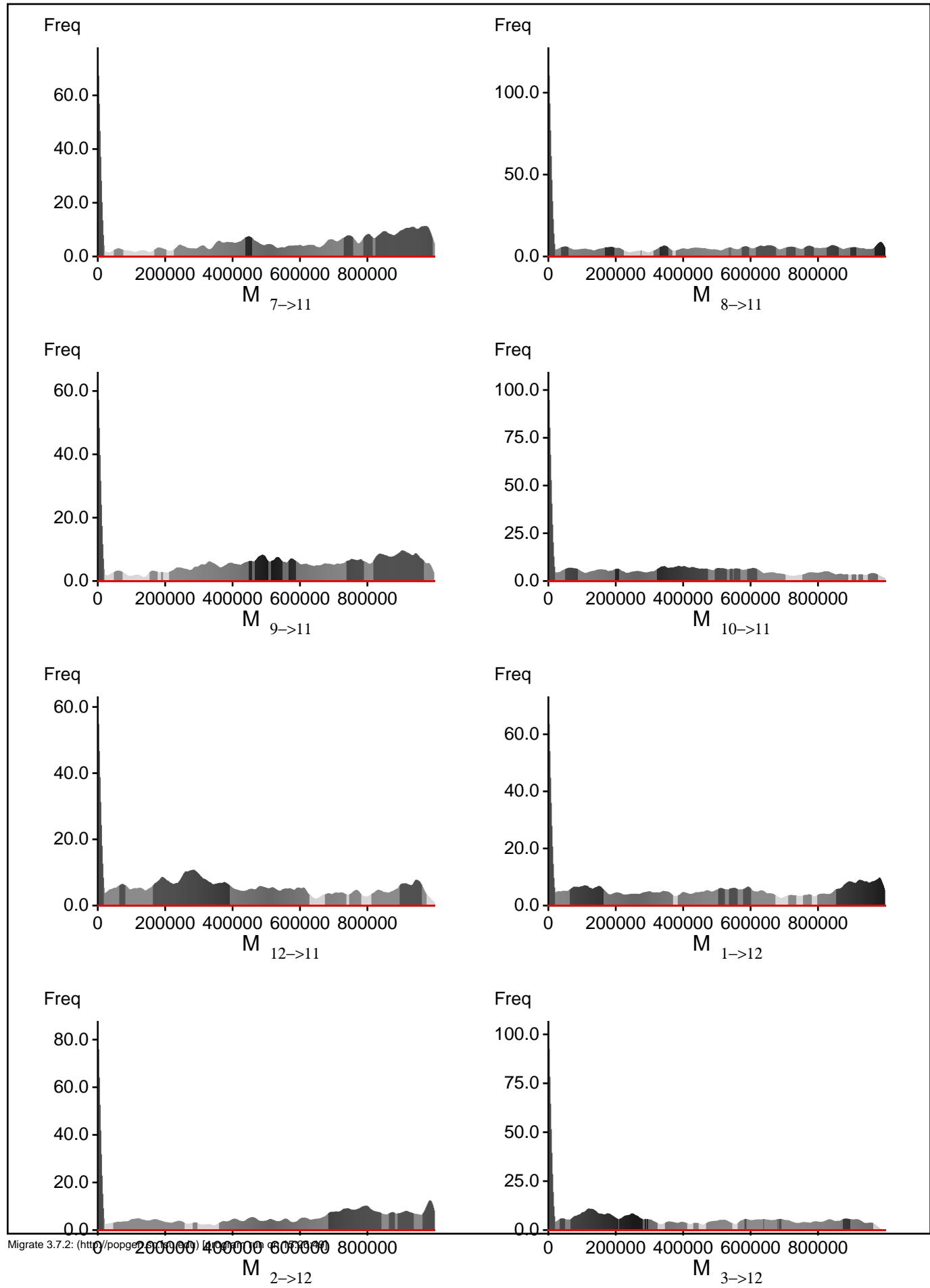
Preliminary migrate analysis of *M. californianus* CO1 haplotypes for Evolution 2 -- 10



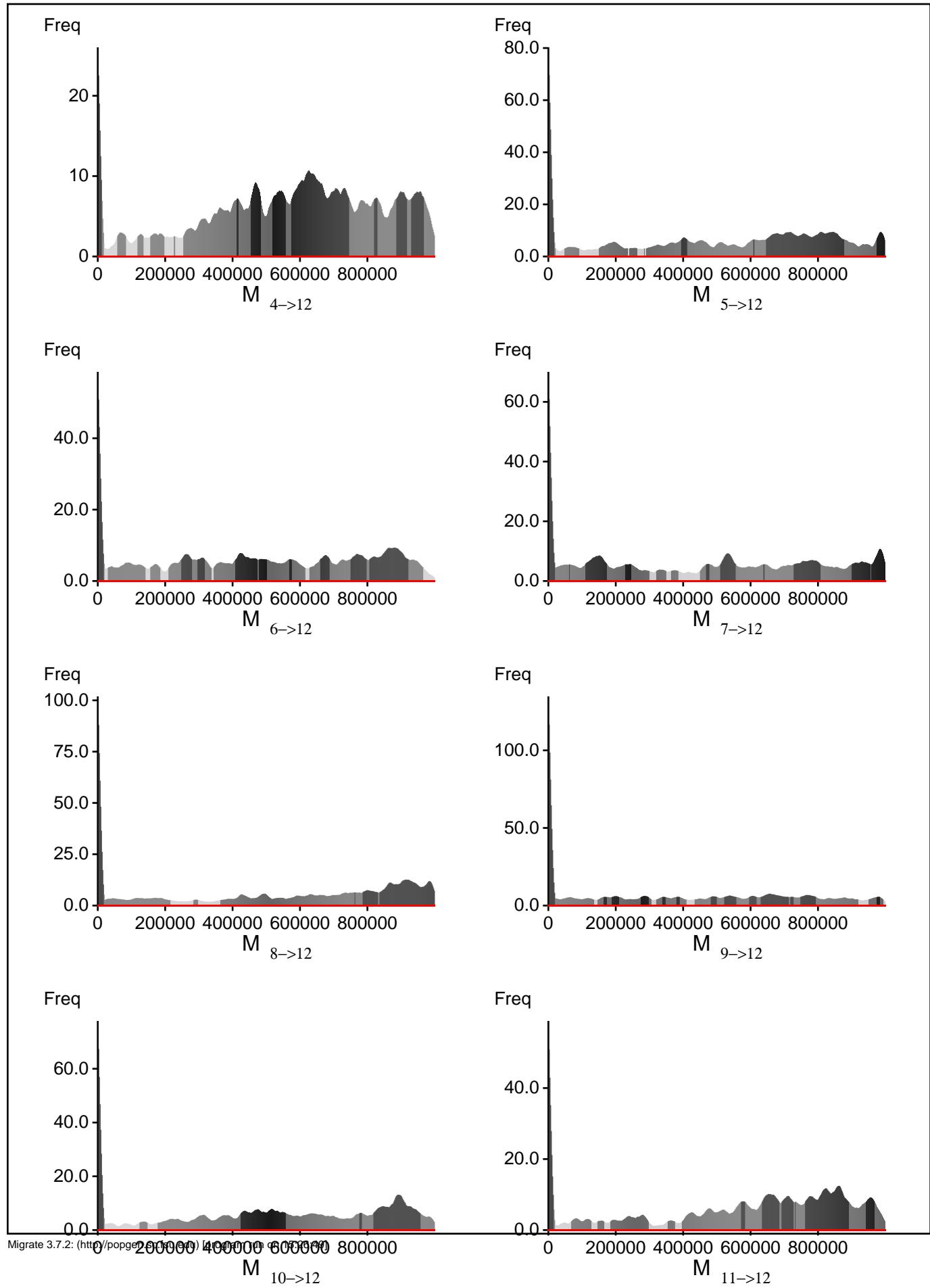
Preliminary migrate analysis of *M. californianus* CO1 haplotypes for Evolution 2 -- 11



Preliminary migrate analysis of *M. californianus* CO1 haplotypes for Evolution 2 -- 12



Preliminary migrate analysis of *M. californianus* CO1 haplotypes for Evolution 2 -- 13



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

Use this value for Bayes factor calculations:

$BF = \text{Exp}[\ln(\text{Prob}(D | \text{thisModel})) - \ln(\text{Prob}(D | \text{otherModel}))]$
 or as $LBF = 2(\ln(\text{Prob}(D | \text{thisModel})) - \ln(\text{Prob}(D | \text{otherModel})))$
 shows the support for thisModel]

Method	$\ln(\text{Prob}(D \text{Model}))$	Notes
Thermodynamic integration	0.000000 0.000000	(1a) (1b)
Harmonic mean	inf	(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	0/2842	0.00000
Θ_6	0/2859	0.00000
Θ_7	0/2859	0.00000
Θ_{11}	0/2911	0.00000
Θ_{12}	0/2853	0.00000
$M_{2 \rightarrow 1}$	2840/2840	1.00000
$M_{11 \rightarrow 1}$	2756/2756	1.00000
$M_{12 \rightarrow 1}$	2706/2706	1.00000
$M_{1 \rightarrow 2}$	2840/2840	1.00000
$M_{10 \rightarrow 2}$	2924/2924	1.00000
$M_{11 \rightarrow 2}$	2793/2793	1.00000
$M_{12 \rightarrow 2}$	2851/2851	1.00000
$M_{9 \rightarrow 3}$	2888/2888	1.00000
$M_{10 \rightarrow 3}$	2800/2800	1.00000
$M_{11 \rightarrow 3}$	2778/2778	1.00000
$M_{8 \rightarrow 4}$	2811/2811	1.00000
$M_{9 \rightarrow 4}$	2850/2850	1.00000
$M_{10 \rightarrow 4}$	2799/2799	1.00000
$M_{7 \rightarrow 5}$	2857/2857	1.00000
$M_{8 \rightarrow 5}$	2762/2762	1.00000
$M_{9 \rightarrow 5}$	2848/2848	1.00000
$M_{7 \rightarrow 6}$	2963/2963	1.00000
$M_{8 \rightarrow 6}$	2821/2821	1.00000
$M_{5 \rightarrow 7}$	2857/2857	1.00000
$M_{6 \rightarrow 7}$	2884/2884	1.00000
$M_{4 \rightarrow 8}$	2811/2811	1.00000
$M_{5 \rightarrow 8}$	2776/2776	1.00000
$M_{6 \rightarrow 8}$	2821/2821	1.00000
$M_{3 \rightarrow 9}$	2888/2888	1.00000
$M_{4 \rightarrow 9}$	2806/2806	1.00000
$M_{2 \rightarrow 10}$	2924/2924	1.00000
$M_{1 \rightarrow 11}$	2823/2823	1.00000
$M_{2 \rightarrow 11}$	2786/2786	1.00000
$M_{3 \rightarrow 11}$	2799/2799	1.00000
$M_{4 \rightarrow 11}$	2916/2916	1.00000
$M_{5 \rightarrow 11}$	2780/2780	1.00000
$M_{6 \rightarrow 11}$	2825/2825	1.00000

Preliminary migrate analysis of *M. californianus* CO1 haplotypes for Evolution 2 -- 17

M	7->11	2771/2771	1.00000
M	8->11	2833/2833	1.00000
M	9->11	2847/2847	1.00000
M	10->11	2935/2935	1.00000
M	12->11	2789/2789	1.00000
M	1->12	2874/2874	1.00000
M	2->12	2800/2800	1.00000
M	3->12	2868/2868	1.00000
M	4->12	2863/2863	1.00000
M	5->12	2808/2808	1.00000
M	6->12	2792/2792	1.00000
M	7->12	2862/2862	1.00000
M	8->12	2822/2822	1.00000
M	9->12	2896/2896	1.00000
M	10->12	2798/2798	1.00000
M	11->12	2816/2816	1.00000
Genealogies		0/149881	0.00000

MCMC-Autocorrelation and Effective MCMC Sample Size

Parameter	Autocorrelation	Effective Sample Size
Θ_1	1.00000	0.00
Θ_2	0.00000	0.00
Θ_3	0.00000	0.00
Θ_4	0.00000	0.00
Θ_5	0.00000	0.00
Θ_6	1.00000	0.00
Θ_7	1.00000	0.00
Θ_8	0.00000	0.00
Θ_9	0.00000	0.00
Θ_{10}	0.00000	0.00
Θ_{11}	1.00000	0.00
Θ_{12}	1.00000	0.00
$M_{2 \rightarrow 1}$	0.98873	16.99
$M_{11 \rightarrow 1}$	0.99025	14.69
$M_{12 \rightarrow 1}$	0.98829	17.66
$M_{1 \rightarrow 2}$	0.98873	16.99
$M_{10 \rightarrow 2}$	0.98600	21.13
$M_{11 \rightarrow 2}$	0.98714	19.41
$M_{12 \rightarrow 2}$	0.98437	23.63
$M_{9 \rightarrow 3}$	0.98918	16.30
$M_{10 \rightarrow 3}$	0.98957	15.71
$M_{11 \rightarrow 3}$	0.98691	19.76
$M_{8 \rightarrow 4}$	0.98874	16.96
$M_{9 \rightarrow 4}$	0.98997	15.11
$M_{10 \rightarrow 4}$	0.98960	15.67
$M_{7 \rightarrow 5}$	0.98925	16.20
$M_{8 \rightarrow 5}$	0.99149	12.80
$M_{9 \rightarrow 5}$	0.98911	16.42
$M_{7 \rightarrow 6}$	0.98233	26.72
$M_{8 \rightarrow 6}$	0.98961	15.66
$M_{5 \rightarrow 7}$	0.98925	16.20
$M_{6 \rightarrow 7}$	0.98058	29.44
$M_{4 \rightarrow 8}$	0.98874	16.96
$M_{5 \rightarrow 8}$	0.98857	17.23
$M_{6 \rightarrow 8}$	0.98961	15.66
$M_{3 \rightarrow 9}$	0.98918	16.30
$M_{4 \rightarrow 9}$	0.98789	18.27

Preliminary migrate analysis of *M. californianus* CO1 haplotypes for Evolution 2 -- 19

M	2->10	0.98600	21.13
M	1->11	0.97797	33.39
M	2->11	0.98690	19.76
M	3->11	0.97216	42.45
M	4->11	0.98529	22.24
M	5->11	0.98979	15.39
M	6->11	0.98550	21.90
M	7->11	0.98691	19.75
M	8->11	0.98979	15.38
M	9->11	0.98551	21.90
M	10->11	0.98950	15.82
M	12->11	0.98596	21.22
M	1->12	0.99063	14.11
M	2->12	0.96954	46.49
M	3->12	0.99120	13.25
M	4->12	0.98478	22.99
M	5->12	0.98737	19.06
M	6->12	0.98605	21.06
M	7->12	0.98681	19.93
M	8->12	0.98803	18.06
M	9->12	0.98663	20.22
M	10->12	0.98594	21.22
M	11->12	0.98218	26.99
	Ln[Prob(D G)]	1.00000	0.00

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: Effective sample size of run seems too short!
Param 6: Effective sample size of run seems too short!
Param 6: Effective sample size of run seems too short!
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Param 74: Effective sample size of run seems too short!
Param 62: Effective sample size of run seems too short!
Param 52: Effective sample size of run seems too short!
Param 94: Effective sample size of run seems too short!
Param 74: Effective sample size of run seems too short!
Param 42: Effective sample size of run seems too short!
Param 104: Effective sample size of run seems too short!
Param 124: Effective sample size of run seems too short!

Param 127: Effective sample size of run seems too short!
Param 129: Effective sample size of run seems too short!
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Param 132: Effective sample size of run seems too short!
Param 134: Effective sample size of run seems too short!
Param 136: Effective sample size of run seems too short!
Param 138: Effective sample size of run seems too short!
Param 140: Effective sample size of run seems too short!
Param 141: Effective sample size of run seems too short!