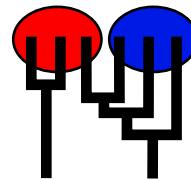


Preliminary migrate analysis of M. californianus

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 15:26:50 2021
 Program finished at Mon May 31 16:06:12 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) 3267260526

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

11 WhitePo * * * * * * * * * *

12 LaJolla * * * * * * * * * *

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:						
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				

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	16000.0	18000.0	487000.0	526467.4
1	$M_{11->1}$	0.0	0.0	1000.0	18000.0	18000.0	549000.0	574634.5
1	$M_{12->1}$	0.0	0.0	1000.0	18000.0	20000.0	431000.0	497848.7
1	$M_{1->2}$	0.0	0.0	1000.0	16000.0	18000.0	487000.0	526467.4
1	$M_{10->2}$	0.0	0.0	1000.0	16000.0	20000.0	681000.0	649679.1
1	$M_{11->2}$	0.0	0.0	1000.0	20000.0	28000.0	361000.0	466869.8
1	$M_{12->2}$	0.0	0.0	1000.0	20000.0	700000.0	273000.0	366261.5
1	$M_{9->3}$	0.0	0.0	1000.0	20000.0	66000.0	535000.0	547098.8
1	$M_{10->3}$	0.0	0.0	1000.0	18000.0	20000.0	471000.0	551596.4
1	$M_{11->3}$	0.0	0.0	1000.0	20000.0	680000.0	257000.0	382695.8
1	$M_{8->4}$	0.0	0.0	1000.0	16000.0	20000.0	631000.0	633789.4
1	$M_{9->4}$	0.0	0.0	1000.0	134000.0	758000.0	229000.0	342564.4
1	$M_{10->4}$	0.0	0.0	1000.0	294000.0	640000.0	297000.0	396640.4
1	$M_{7->5}$	0.0	0.0	1000.0	14000.0	18000.0	543000.0	563870.8
1	$M_{8->5}$	0.0	0.0	1000.0	16000.0	20000.0	653000.0	627009.3
1	$M_{9->5}$	0.0	0.0	1000.0	20000.0	236000.0	567000.0	601201.8
1	$M_{7->6}$	0.0	0.0	1000.0	20000.0	174000.0	525000.0	547198.7
1	$M_{8->6}$	0.0	0.0	1000.0	20000.0	72000.0	449000.0	519613.2
1	$M_{5->7}$	0.0	0.0	1000.0	14000.0	18000.0	543000.0	563870.8
1	$M_{6->7}$	0.0	0.0	1000.0	18000.0	22000.0	389000.0	482725.9
1	$M_{4->8}$	0.0	0.0	1000.0	16000.0	20000.0	631000.0	633789.4
1	$M_{5->8}$	0.0	0.0	1000.0	20000.0	686000.0	403000.0	476063.1
1	$M_{6->8}$	0.0	0.0	1000.0	20000.0	72000.0	449000.0	519613.2
1	$M_{3->9}$	0.0	0.0	1000.0	20000.0	66000.0	535000.0	547098.8
1	$M_{4->9}$	0.0	0.0	1000.0	138000.0	366000.0	377000.0	454239.2
1	$M_{2->10}$	0.0	0.0	1000.0	16000.0	20000.0	681000.0	649679.1
1	$M_{1->11}$	0.0	0.0	1000.0	16000.0	20000.0	565000.0	575380.5
1	$M_{2->11}$	0.0	0.0	1000.0	18000.0	772000.0	367000.0	432663.8
1	$M_{3->11}$	0.0	0.0	1000.0	20000.0	698000.0	293000.0	383706.1
1	$M_{4->11}$	0.0	0.0	1000.0	18000.0	20000.0	575000.0	570512.3
1	$M_{5->11}$	0.0	0.0	1000.0	20000.0	126000.0	457000.0	511009.5

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	20000.0	457000.0	522721.7
1	$M_{7 \rightarrow 11}$	0.0	0.0	1000.0	18000.0	512000.0	325000.0	426967.6
1	$M_{8 \rightarrow 11}$	0.0	0.0	1000.0	120000.0	758000.0	271000.0	367748.9
1	$M_{9 \rightarrow 11}$	0.0	0.0	1000.0	20000.0	46000.0	475000.0	505785.3
1	$M_{10 \rightarrow 11}$	0.0	0.0	1000.0	14000.0	20000.0	733000.0	704086.2
1	$M_{12 \rightarrow 11}$	0.0	0.0	1000.0	18000.0	20000.0	497000.0	574059.9
1	$M_{1 \rightarrow 12}$	0.0	0.0	1000.0	18000.0	110000.0	489000.0	545600.6
1	$M_{2 \rightarrow 12}$	0.0	0.0	1000.0	20000.0	722000.0	265000.0	366396.6
1	$M_{3 \rightarrow 12}$	0.0	0.0	1000.0	12000.0	64000.0	763000.0	690281.1
1	$M_{4 \rightarrow 12}$	0.0	0.0	1000.0	18000.0	20000.0	437000.0	480148.1
1	$M_{5 \rightarrow 12}$	0.0	0.0	1000.0	166000.0	372000.0	279000.0	397780.8
1	$M_{6 \rightarrow 12}$	0.0	0.0	1000.0	18000.0	20000.0	495000.0	511552.1
1	$M_{7 \rightarrow 12}$	0.0	0.0	1000.0	16000.0	18000.0	525000.0	583799.5
1	$M_{8 \rightarrow 12}$	0.0	0.0	1000.0	20000.0	484000.0	413000.0	506620.2
1	$M_{9 \rightarrow 12}$	0.0	0.0	1000.0	16000.0	18000.0	669000.0	674536.7
1	$M_{10 \rightarrow 12}$	0.0	0.0	1000.0	18000.0	20000.0	559000.0	576938.0
1	$M_{11 \rightarrow 12}$	0.0	0.0	1000.0	20000.0	850000.0	379000.0	448058.7

Citation suggestions:

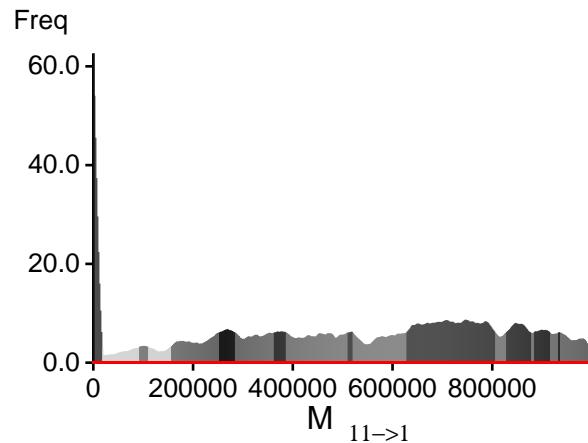
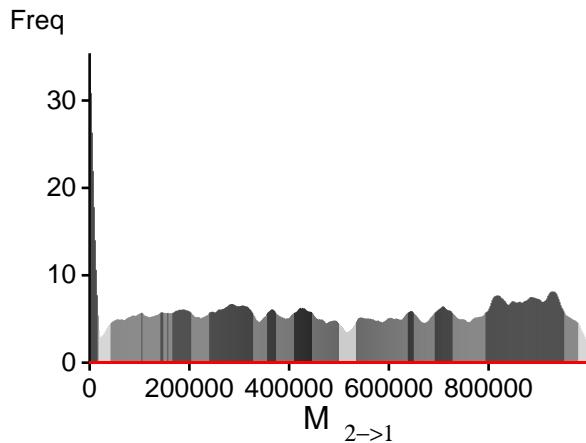
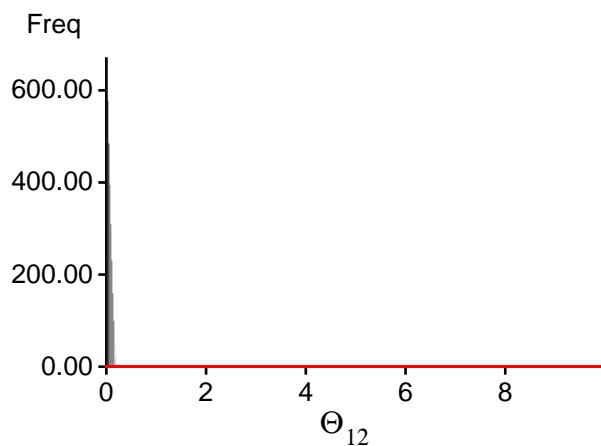
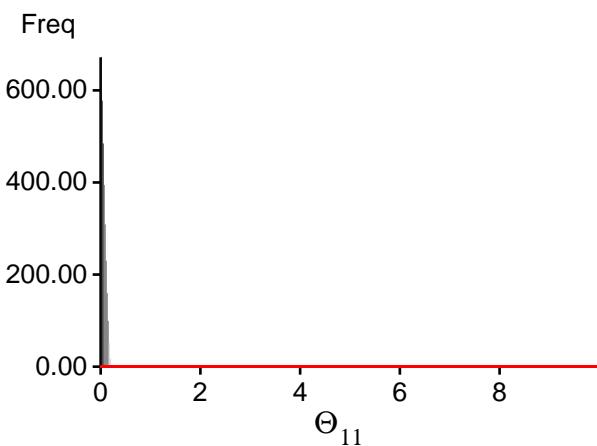
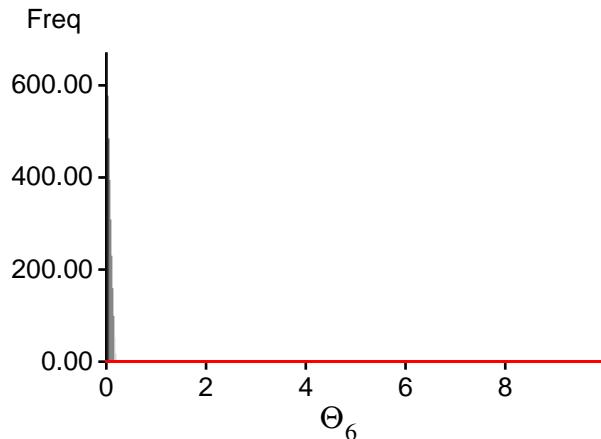
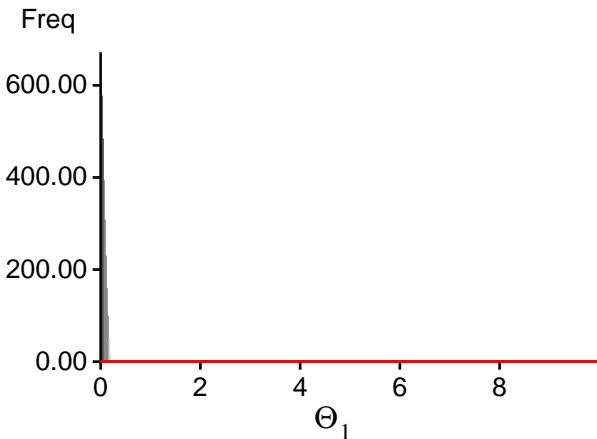
Beerli P., 2006. Comparison of Bayesian and maximum-likelihood inference of population genetic parameters.

Bioinformatics 22:341-345

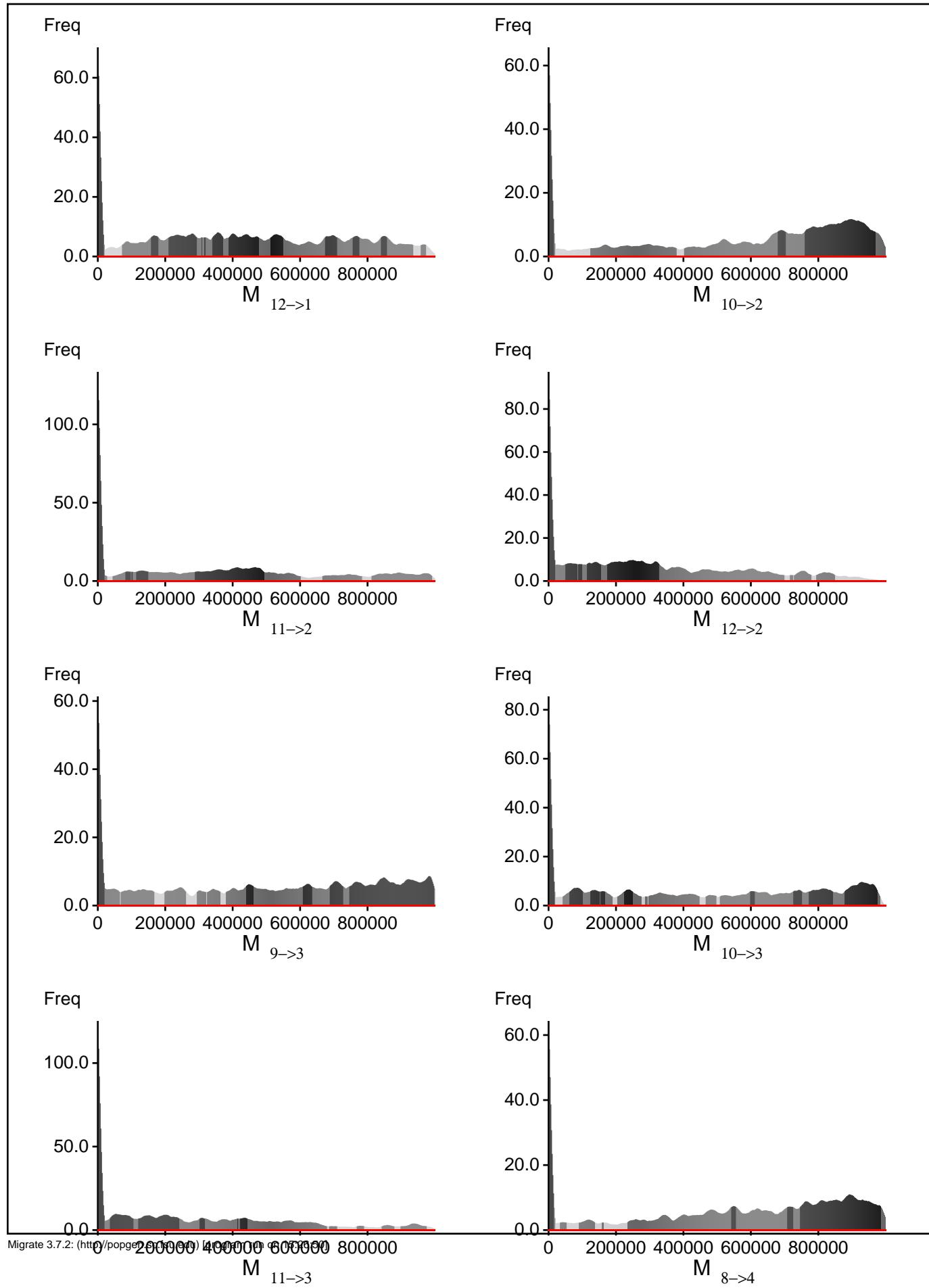
Beerli P., 2007. Estimation of the population scaled mutation rate from microsatellite data,
Genetics, 177:1967-1968.

Beerli P., 2009. How to use MIGRATE or why are Markov chain Monte Carlo programs difficult to use?

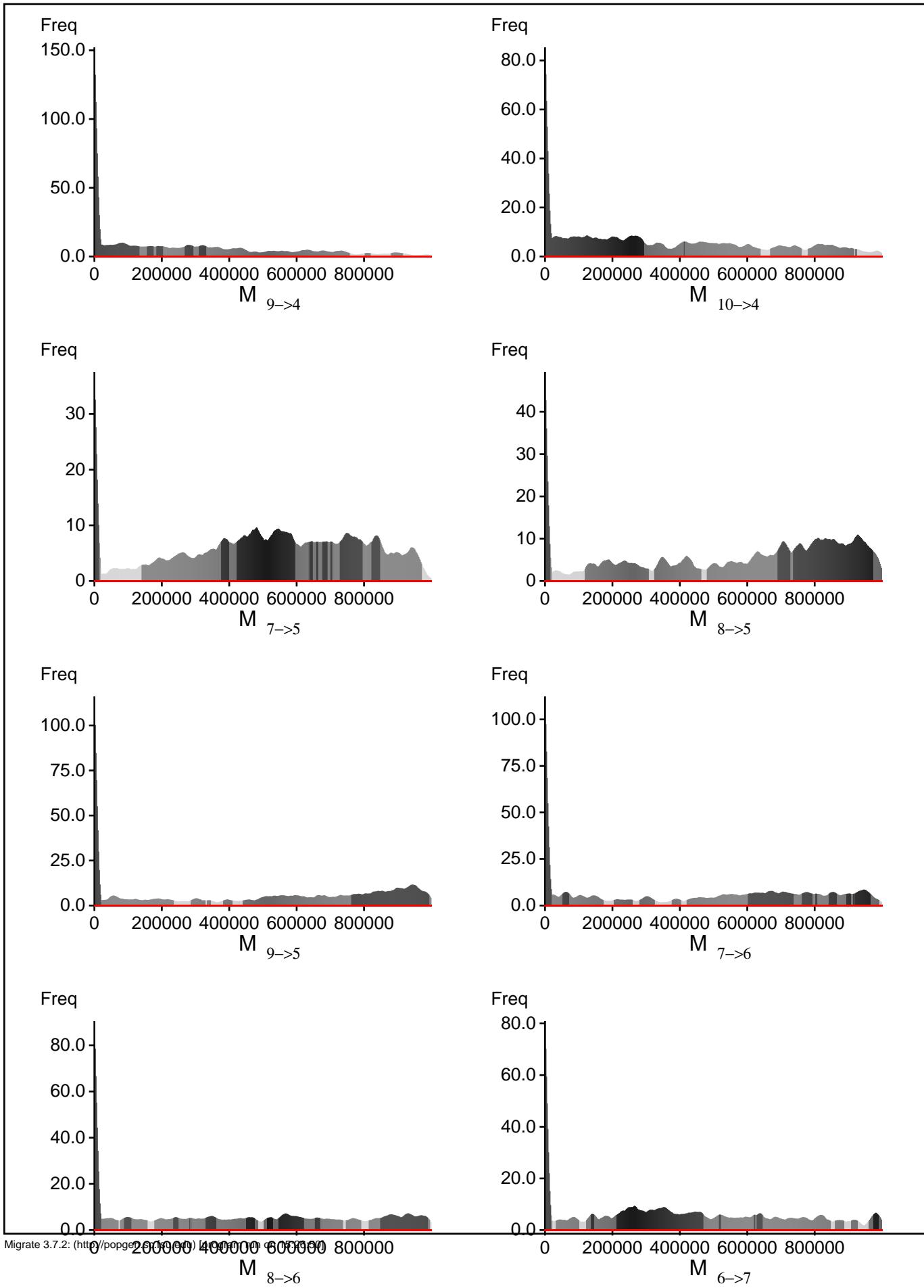
In Population Genetics for Animal Conservation, G. Bertorelle, M. W. Bruford, H. C. Hauffe, A. Rizzoli,
and C. Vernesi, eds., vol. 17 of Conservation Biology, Cambridge University Press, Cambridge UK, pp. 42-79.

Bayesian Analysis: Posterior distribution over all loci

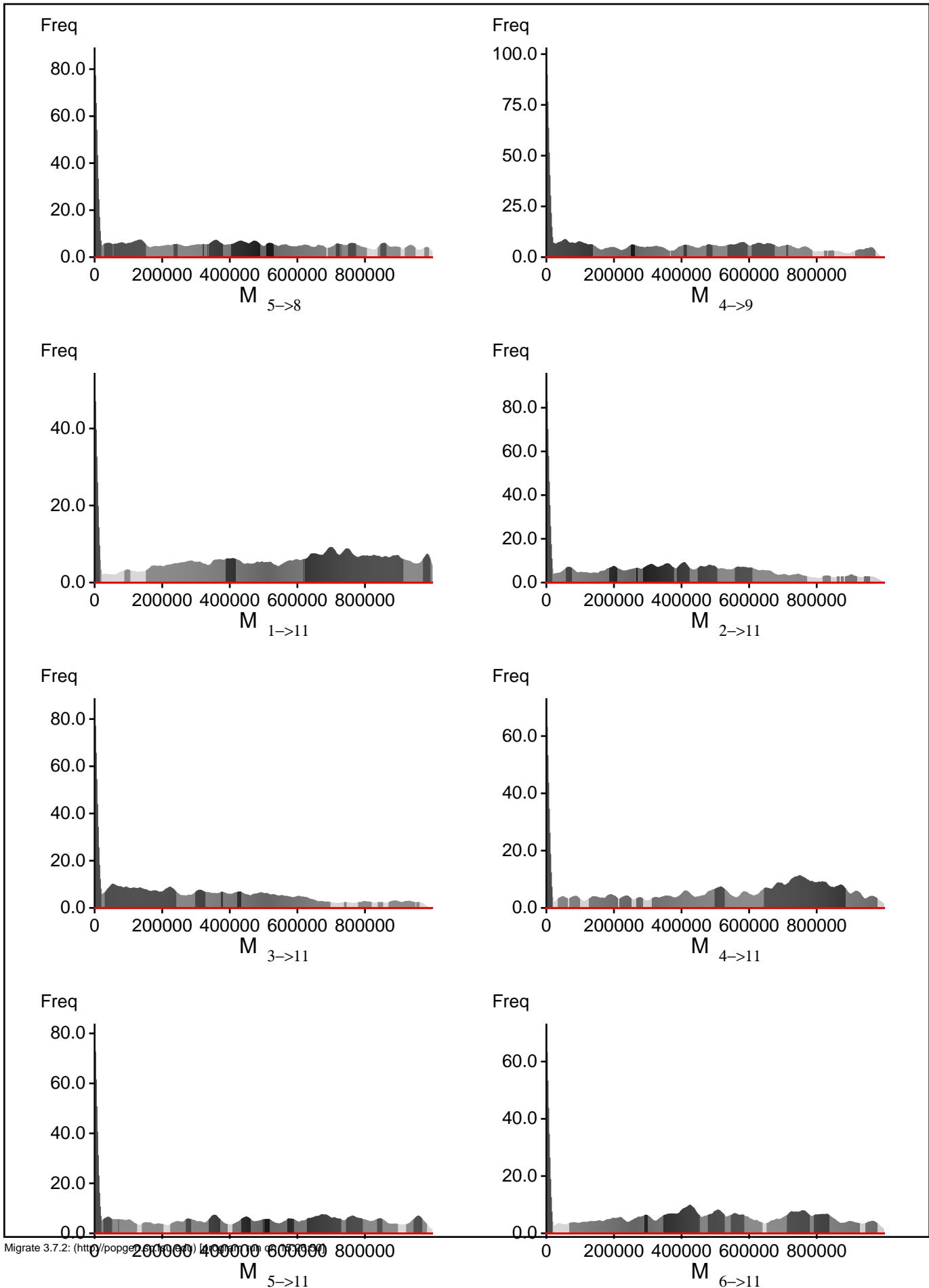
Preliminary migrate analysis of *M. californianus* CO1 haplotypes for Evolution 2 -- 9



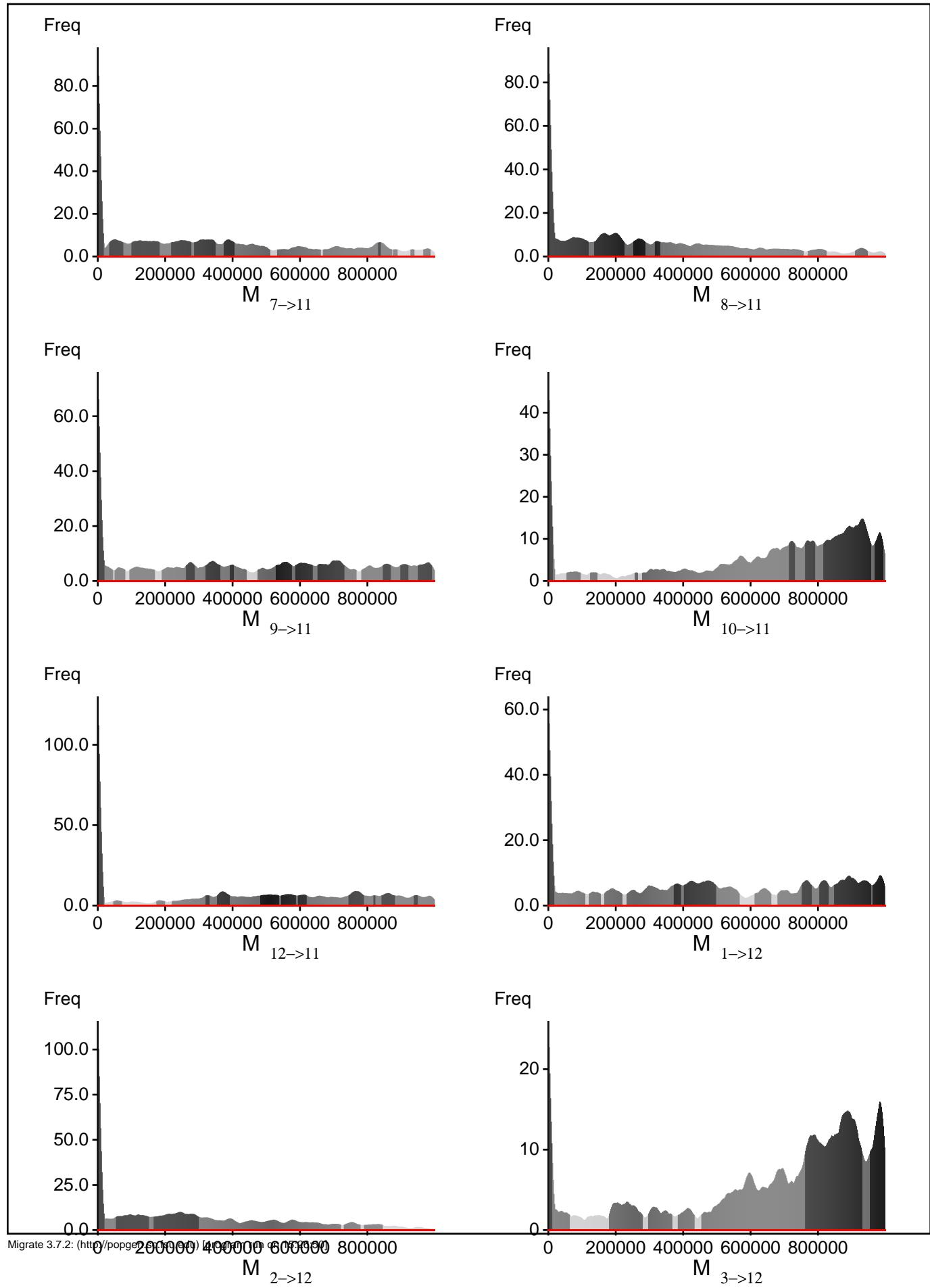
Preliminary migrate analysis of *M. californianus* CO1 haplotypes for Evolution 2 -- 10



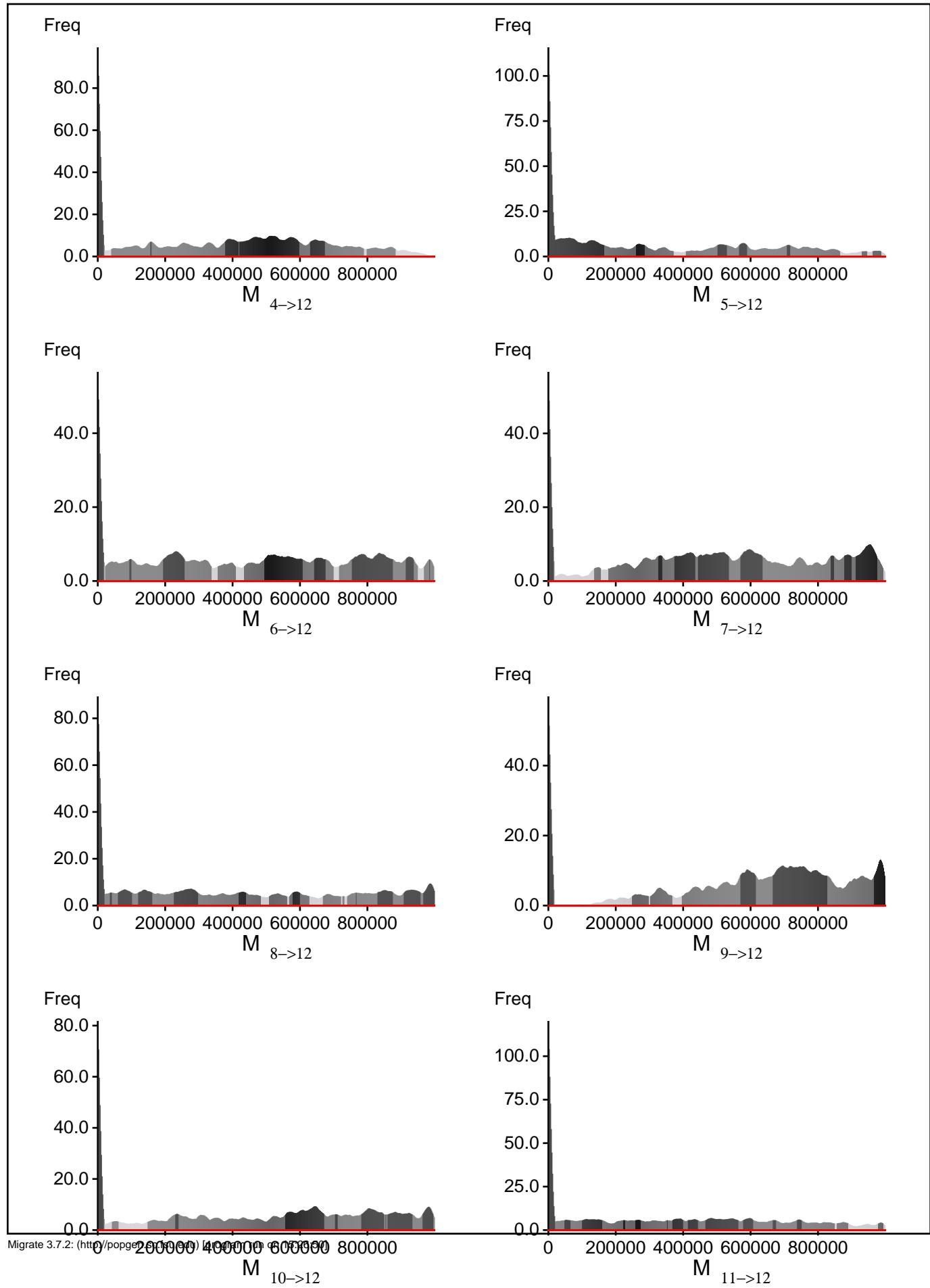
Preliminary migrate analysis of *M. californianus* CO1 haplotypes for Evolution 2 -- 11



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	0/2837	0.00000
Θ_6	0/2812	0.00000
Θ_7	0/2812	0.00000
Θ_{11}	0/2856	0.00000
Θ_{12}	0/2857	0.00000
$M_{2 \rightarrow 1}$	2900/2900	1.00000
$M_{11 \rightarrow 1}$	2969/2969	1.00000
$M_{12 \rightarrow 1}$	2861/2861	1.00000
$M_{1 \rightarrow 2}$	2900/2900	1.00000
$M_{10 \rightarrow 2}$	2793/2793	1.00000
$M_{11 \rightarrow 2}$	2835/2835	1.00000
$M_{12 \rightarrow 2}$	2858/2858	1.00000
$M_{9 \rightarrow 3}$	2910/2910	1.00000
$M_{10 \rightarrow 3}$	2836/2836	1.00000
$M_{11 \rightarrow 3}$	2845/2845	1.00000
$M_{8 \rightarrow 4}$	2846/2846	1.00000
$M_{9 \rightarrow 4}$	2843/2843	1.00000
$M_{10 \rightarrow 4}$	2789/2789	1.00000
$M_{7 \rightarrow 5}$	2885/2885	1.00000
$M_{8 \rightarrow 5}$	2827/2827	1.00000
$M_{9 \rightarrow 5}$	2753/2753	1.00000
$M_{7 \rightarrow 6}$	2867/2867	1.00000
$M_{8 \rightarrow 6}$	2819/2819	1.00000
$M_{5 \rightarrow 7}$	2885/2885	1.00000
$M_{6 \rightarrow 7}$	2880/2880	1.00000
$M_{4 \rightarrow 8}$	2846/2846	1.00000
$M_{5 \rightarrow 8}$	2843/2843	1.00000
$M_{6 \rightarrow 8}$	2819/2819	1.00000
$M_{3 \rightarrow 9}$	2910/2910	1.00000
$M_{4 \rightarrow 9}$	2843/2843	1.00000
$M_{2 \rightarrow 10}$	2793/2793	1.00000
$M_{1 \rightarrow 11}$	2885/2885	1.00000
$M_{2 \rightarrow 11}$	2871/2871	1.00000
$M_{3 \rightarrow 11}$	2713/2713	1.00000
$M_{4 \rightarrow 11}$	2849/2849	1.00000
$M_{5 \rightarrow 11}$	2778/2778	1.00000
$M_{6 \rightarrow 11}$	2841/2841	1.00000

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

M	7->11	2800/2800	1.00000
M	8->11	2837/2837	1.00000
M	9->11	2893/2893	1.00000
M	10->11	2823/2823	1.00000
M	12->11	2897/2897	1.00000
M	1->12	2820/2820	1.00000
M	2->12	2890/2890	1.00000
M	3->12	2911/2911	1.00000
M	4->12	2863/2863	1.00000
M	5->12	2799/2799	1.00000
M	6->12	2877/2877	1.00000
M	7->12	2912/2912	1.00000
M	8->12	2768/2768	1.00000
M	9->12	2780/2780	1.00000
M	10->12	2756/2756	1.00000
M	11->12	2855/2855	1.00000
Genealogies		0/149511	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
$M_{2 \rightarrow 1}$	0.98918	16.31
$M_{11 \rightarrow 1}$	0.98518	22.38
$M_{12 \rightarrow 1}$	0.98931	16.11
$M_{1 \rightarrow 2}$	0.98918	16.31
$M_{10 \rightarrow 2}$	0.98343	25.10
$M_{11 \rightarrow 2}$	0.98142	28.16
$M_{12 \rightarrow 2}$	0.98709	19.48
$M_{9 \rightarrow 3}$	0.99025	14.68
$M_{10 \rightarrow 3}$	0.99041	14.44
$M_{11 \rightarrow 3}$	0.98374	24.61
$M_{8 \rightarrow 4}$	0.98576	21.50
$M_{9 \rightarrow 4}$	0.98632	20.65
$M_{10 \rightarrow 4}$	0.98244	26.62
$M_{7 \rightarrow 5}$	0.98347	24.98
$M_{8 \rightarrow 5}$	0.98959	15.68
$M_{9 \rightarrow 5}$	0.98042	29.63
$M_{7 \rightarrow 6}$	0.99094	13.64
$M_{8 \rightarrow 6}$	0.99051	14.29
$M_{5 \rightarrow 7}$	0.98347	24.98
$M_{6 \rightarrow 7}$	0.98869	17.05
$M_{4 \rightarrow 8}$	0.98576	21.50
$M_{5 \rightarrow 8}$	0.98950	15.83
$M_{6 \rightarrow 8}$	0.99051	14.29
$M_{3 \rightarrow 9}$	0.99025	14.68
$M_{4 \rightarrow 9}$	0.98986	15.27

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

M	2->10	0.98343	25.10
M	1->11	0.96987	45.86
M	2->11	0.98712	19.43
M	3->11	0.96777	49.28
M	4->11	0.98836	17.55
M	5->11	0.98915	16.35
M	6->11	0.98708	19.49
M	7->11	0.99013	14.86
M	8->11	0.98931	16.11
M	9->11	0.98953	15.78
M	10->11	0.98356	24.89
M	12->11	0.98568	21.63
M	1->12	0.98795	18.18
M	2->12	0.97313	40.83
M	3->12	0.97550	37.34
M	4->12	0.98500	22.65
M	5->12	0.99103	13.51
M	6->12	0.98664	20.15
M	7->12	0.98461	23.26
M	8->12	0.99021	14.74
M	9->12	0.98217	26.97
M	10->12	0.98524	22.29
M	11->12	0.98777	18.45
	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!
Param 11: Effective sample size of run seems too short!
Param 12: Effective sample size of run seems too short!
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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 126: Effective sample size of run seems too short!
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Param 130: Effective sample size of run seems too short!
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Param 134: Effective sample size of run seems too short!

Param 138: Effective sample size of run seems too short!
Param 141: Effective sample size of run seems too short!
Param 144: Effective sample size of run seems too short!
Param 145: Effective sample size of run seems too short!