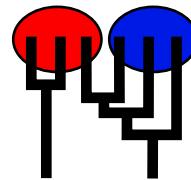


# Preliminary migrate analysis of M. californianus

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 16:04:58 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) 2649589931

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	$\Theta_1$		<displayed>
6	$\Theta_6$	=	$\Theta_6$ [s] <displayed>
7	$\Theta_7$	=	$\Theta_6$ [s]
11	$\Theta_{11}$		<displayed>
12	$\Theta_{12}$		<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	$\Theta_1$	0.00001	0.00001	0.01001	0.06001	0.16001	0.07001	0.01000
1	$\Theta_6$	0.00001	0.00001	0.01001	0.06001	0.16001	0.07001	0.01000
1	$\Theta_7$	0.00001	0.00001	0.01001	0.06001	0.16001	0.07001	0.01000
1	$\Theta_{11}$	0.00001	0.00001	0.01001	0.06001	0.16001	0.07001	0.01000
1	$\Theta_{12}$	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	20000.0	525000.0	550953.0
1	$M_{11->1}$	0.0	0.0	1000.0	182000.0	354000.0	185000.0	403712.8
1	$M_{12->1}$	0.0	0.0	1000.0	20000.0	782000.0	363000.0	436594.9
1	$M_{1->2}$	0.0	0.0	1000.0	16000.0	20000.0	525000.0	550953.0
1	$M_{10->2}$	0.0	0.0	1000.0	20000.0	528000.0	381000.0	452056.8
1	$M_{11->2}$	0.0	0.0	1000.0	18000.0	20000.0	507000.0	551540.9
1	$M_{12->2}$	0.0	0.0	1000.0	20000.0	44000.0	487000.0	530470.2
1	$M_{9->3}$	0.0	0.0	1000.0	20000.0	172000.0	575000.0	565890.8
1	$M_{10->3}$	0.0	0.0	1000.0	18000.0	20000.0	547000.0	572285.6
1	$M_{11->3}$	0.0	0.0	1000.0	20000.0	798000.0	319000.0	430674.0
1	$M_{8->4}$	0.0	0.0	1000.0	20000.0	54000.0	519000.0	561049.9
1	$M_{9->4}$	0.0	0.0	1000.0	18000.0	20000.0	447000.0	522040.8
1	$M_{10->4}$	0.0	0.0	1000.0	18000.0	20000.0	525000.0	544801.1
1	$M_{7->5}$	0.0	0.0	1000.0	84000.0	786000.0	351000.0	440983.2
1	$M_{8->5}$	0.0	0.0	1000.0	20000.0	404000.0	419000.0	490422.4
1	$M_{9->5}$	0.0	0.0	1000.0	20000.0	630000.0	251000.0	361926.5
1	$M_{7->6}$	0.0	0.0	1000.0	18000.0	20000.0	565000.0	560540.9
1	$M_{8->6}$	0.0	0.0	1000.0	20000.0	776000.0	419000.0	465590.6
1	$M_{5->7}$	0.0	0.0	1000.0	84000.0	786000.0	351000.0	440983.2
1	$M_{6->7}$	0.0	0.0	1000.0	20000.0	190000.0	483000.0	530287.4
1	$M_{4->8}$	0.0	0.0	1000.0	20000.0	54000.0	519000.0	561049.9
1	$M_{5->8}$	0.0	0.0	1000.0	20000.0	112000.0	445000.0	541368.2
1	$M_{6->8}$	0.0	0.0	1000.0	20000.0	776000.0	419000.0	465590.6
1	$M_{3->9}$	0.0	0.0	1000.0	20000.0	172000.0	575000.0	565890.8
1	$M_{4->9}$	0.0	0.0	1000.0	18000.0	20000.0	633000.0	633818.4
1	$M_{2->10}$	0.0	0.0	1000.0	20000.0	528000.0	381000.0	452056.8
1	$M_{1->11}$	0.0	0.0	1000.0	188000.0	378000.0	199000.0	406299.1
1	$M_{2->11}$	0.0	0.0	1000.0	18000.0	20000.0	383000.0	475029.2
1	$M_{3->11}$	0.0	0.0	1000.0	20000.0	834000.0	365000.0	431416.8
1	$M_{4->11}$	0.0	0.0	1000.0	16000.0	20000.0	639000.0	627780.1
1	$M_{5->11}$	0.0	0.0	1000.0	18000.0	442000.0	361000.0	489995.8

Locus	Parameter	2.5%	25.0%	Mode	75.0%	97.5%	Median	Mean
1	$M_{6 \rightarrow 11}$	0.0	0.0	1000.0	14000.0	18000.0	713000.0	662145.0
1	$M_{7 \rightarrow 11}$	0.0	0.0	1000.0	18000.0	18000.0	511000.0	558492.7
1	$M_{8 \rightarrow 11}$	0.0	0.0	1000.0	20000.0	818000.0	311000.0	394591.1
1	$M_{9 \rightarrow 11}$	0.0	0.0	1000.0	18000.0	178000.0	487000.0	531042.8
1	$M_{10 \rightarrow 11}$	0.0	0.0	1000.0	16000.0	18000.0	709000.0	721110.2
1	$M_{12 \rightarrow 11}$	0.0	0.0	1000.0	20000.0	20000.0	411000.0	500902.3
1	$M_{1 \rightarrow 12}$	0.0	0.0	1000.0	18000.0	20000.0	553000.0	571135.9
1	$M_{2 \rightarrow 12}$	0.0	0.0	1000.0	18000.0	20000.0	489000.0	530211.1
1	$M_{3 \rightarrow 12}$	0.0	0.0	1000.0	20000.0	672000.0	379000.0	462579.2
1	$M_{4 \rightarrow 12}$	0.0	0.0	1000.0	18000.0	46000.0	623000.0	600442.7
1	$M_{5 \rightarrow 12}$	0.0	0.0	1000.0	218000.0	576000.0	231000.0	391195.4
1	$M_{6 \rightarrow 12}$	0.0	0.0	1000.0	16000.0	18000.0	567000.0	583300.8
1	$M_{7 \rightarrow 12}$	0.0	0.0	1000.0	208000.0	468000.0	283000.0	445163.4
1	$M_{8 \rightarrow 12}$	0.0	0.0	1000.0	112000.0	426000.0	303000.0	444675.6
1	$M_{9 \rightarrow 12}$	0.0	0.0	1000.0	18000.0	58000.0	527000.0	549460.6
1	$M_{10 \rightarrow 12}$	0.0	0.0	1000.0	20000.0	608000.0	285000.0	402260.8
1	$M_{11 \rightarrow 12}$	0.0	0.0	1000.0	20000.0	102000.0	435000.0	512082.8

## Citation suggestions:

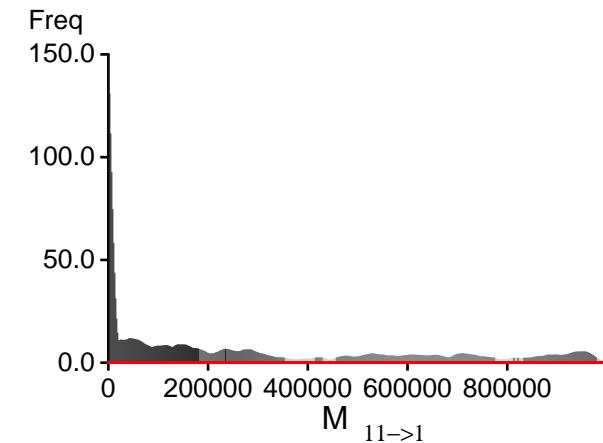
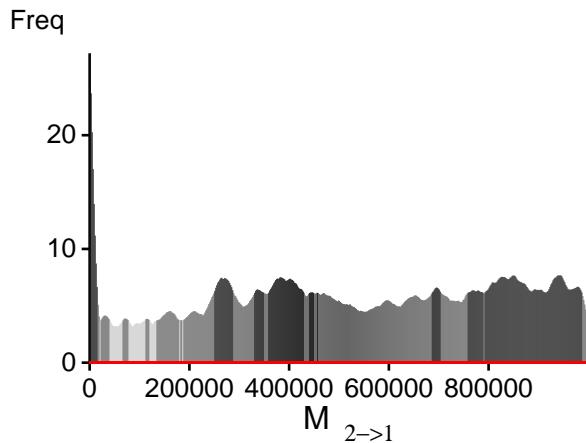
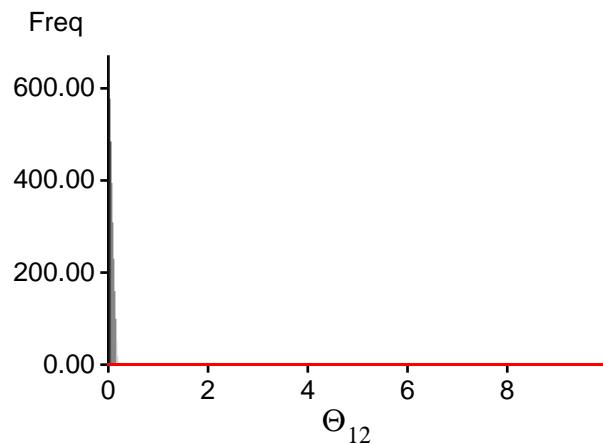
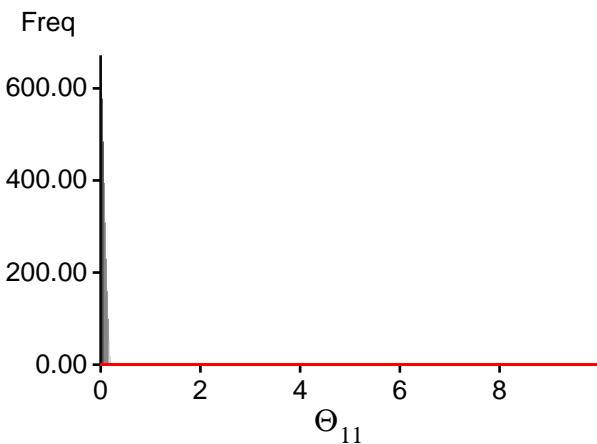
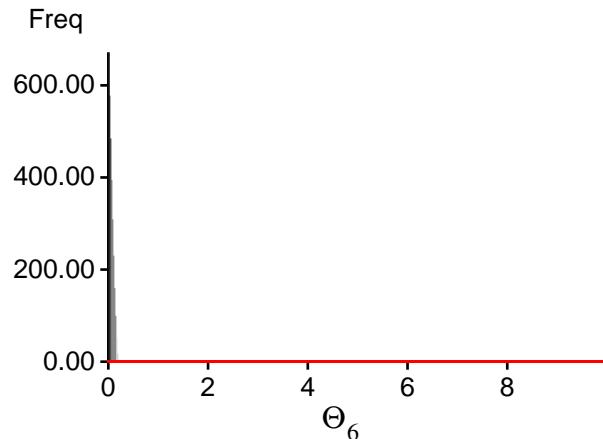
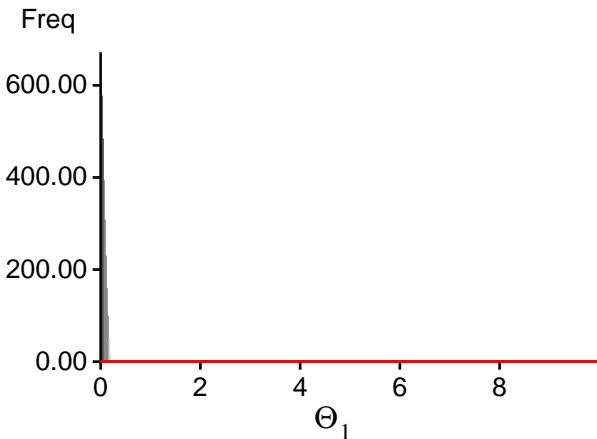
Beerli P., 2006. Comparison of Bayesian and maximum-likelihood inference of population genetic parameters.

Bioinformatics 22:341-345

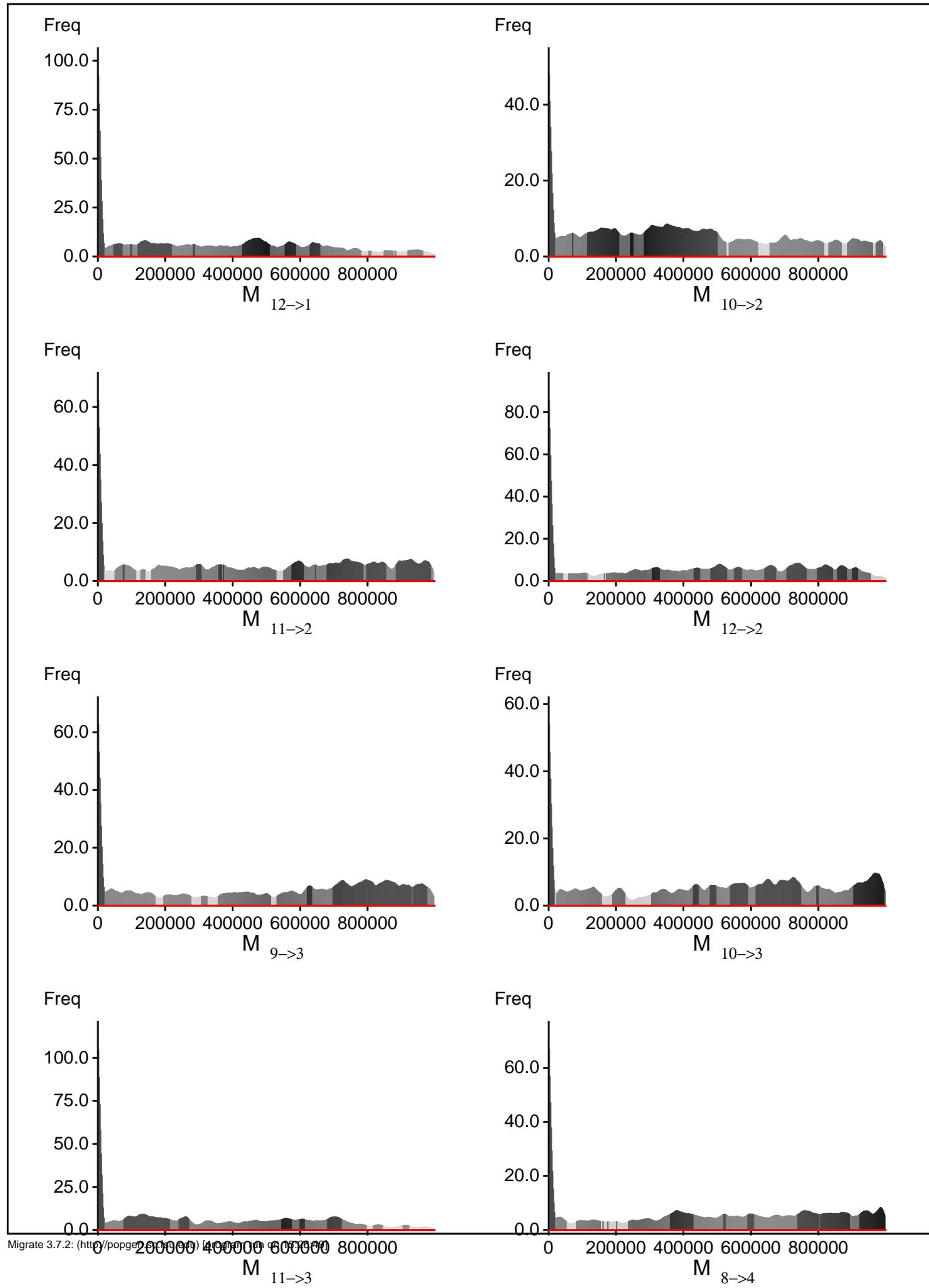
Beerli P., 2007. Estimation of the population scaled mutation rate from microsatellite data,  
Genetics, 177:1967-1968.

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

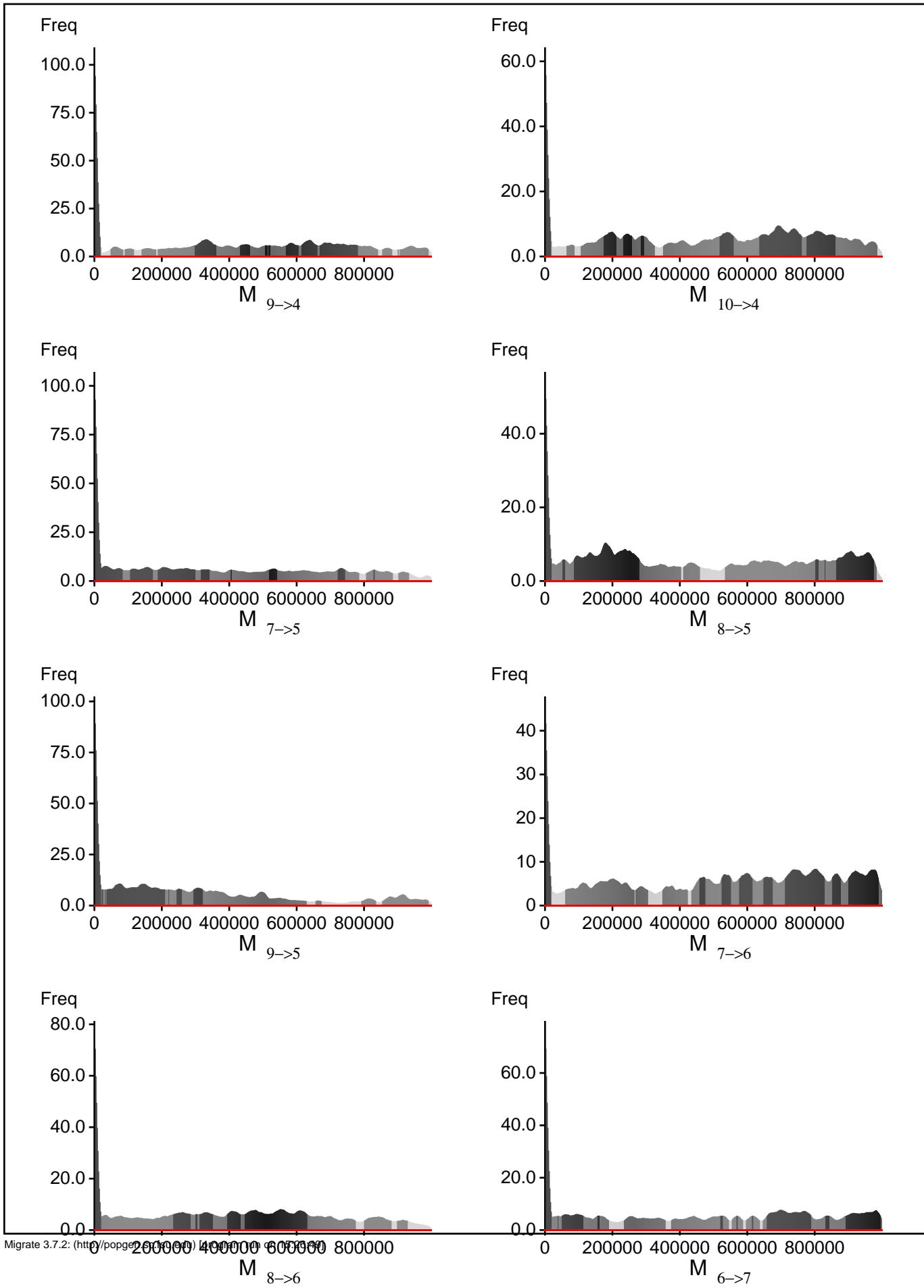
In Population Genetics for Animal Conservation, G. Bertorelle, M. W. Bruford, H. C. Hauffe, A. Rizzoli,  
and C. Vernesi, eds., vol. 17 of Conservation Biology, Cambridge University Press, Cambridge UK, pp. 42-79.

***Bayesian Analysis: Posterior distribution over all loci***

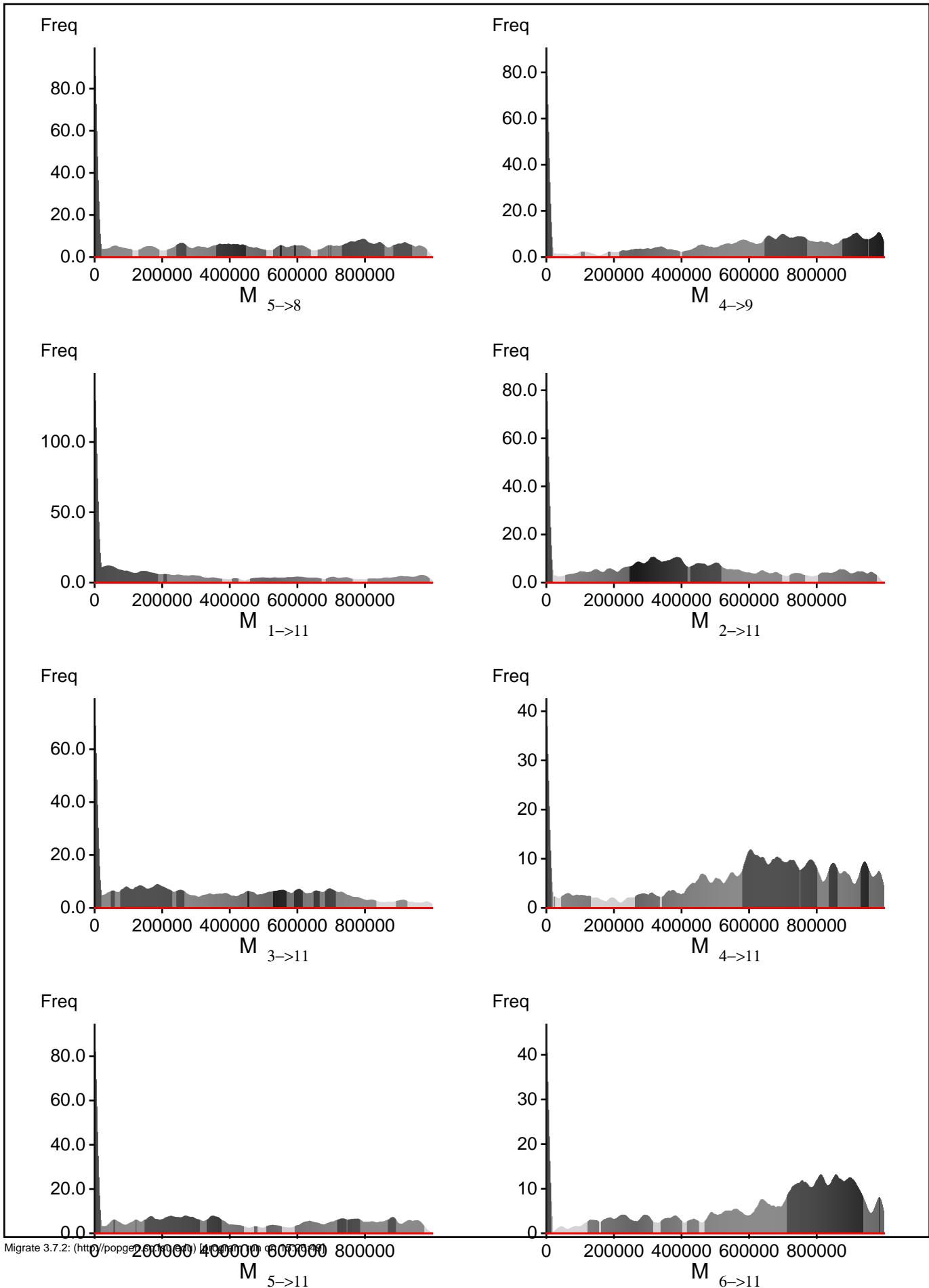
Preliminary migrate analysis of *M. californianus* CO1 haplotypes for Evolution 2 -- 9



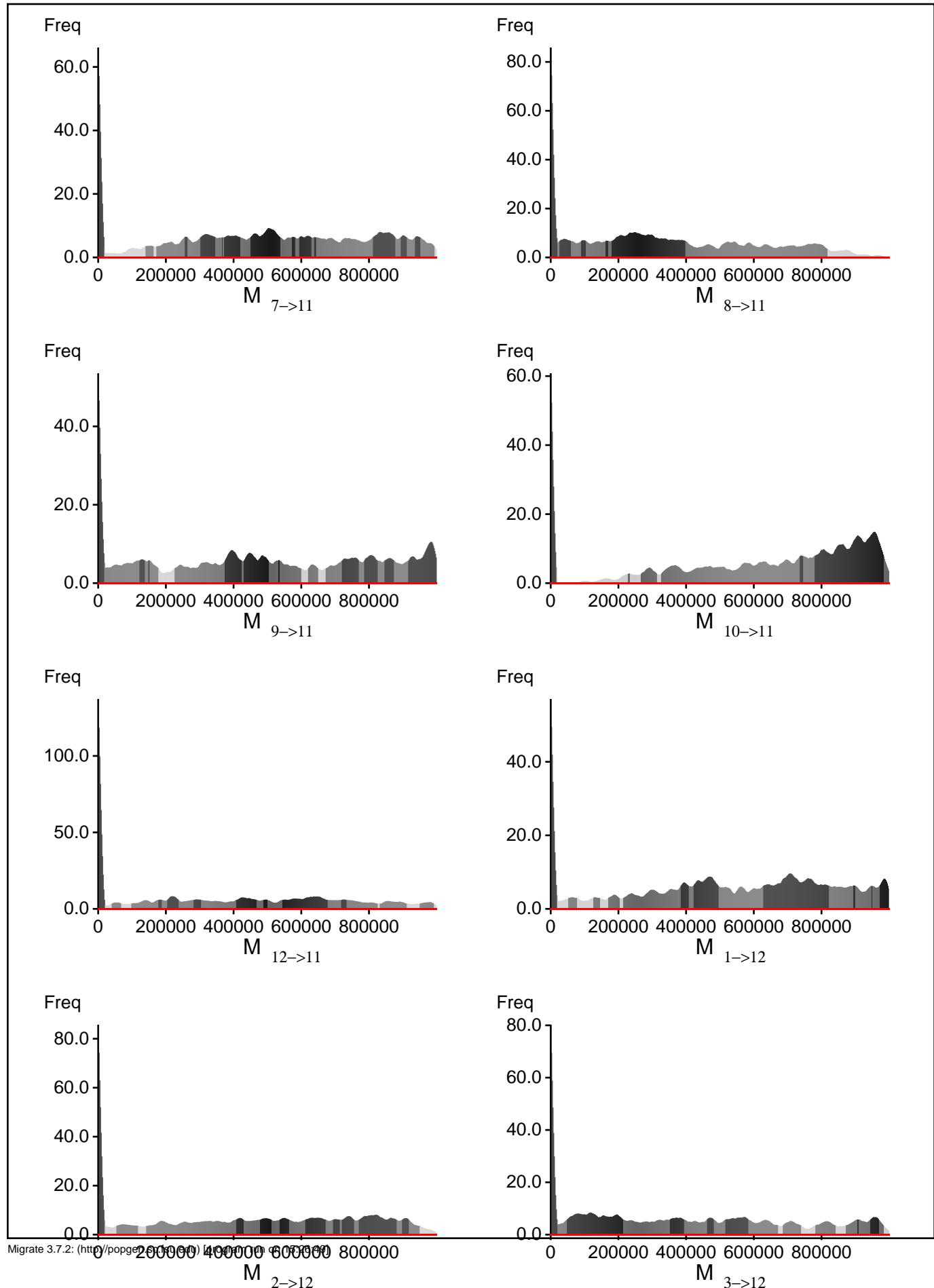
Preliminary migrate analysis of *M. californianus* CO1 haplotypes for Evolution 2 -- 10



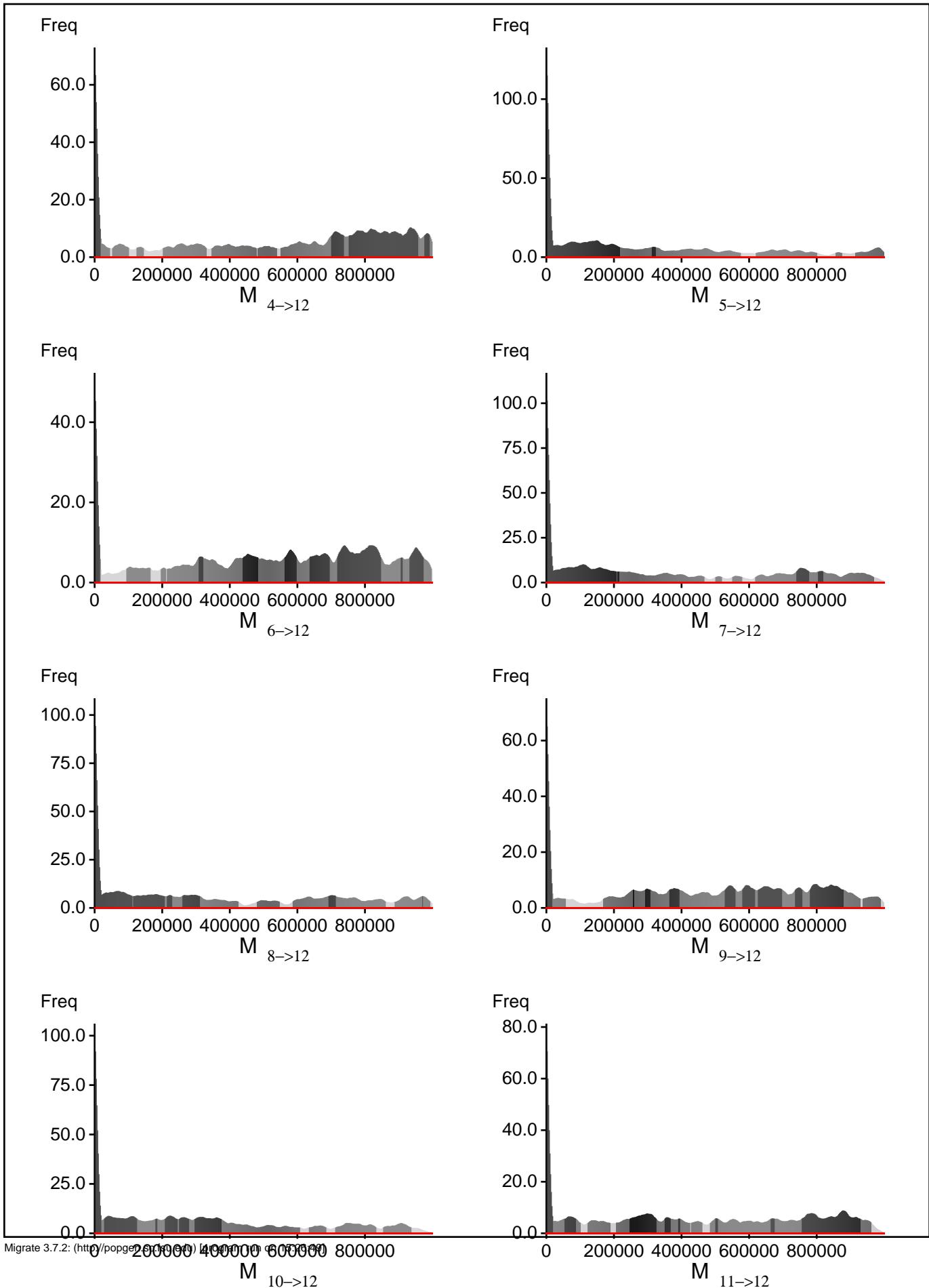
Preliminary migrate analysis of *M. californianus* CO1 haplotypes for Evolution 2 -- 11



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
$\Theta_1$	0/2767	0.00000
$\Theta_6$	0/2839	0.00000
$\Theta_7$	0/2839	0.00000
$\Theta_{11}$	0/2823	0.00000
$\Theta_{12}$	0/2778	0.00000
$M_{2 \rightarrow 1}$	2846/2846	1.00000
$M_{11 \rightarrow 1}$	2784/2784	1.00000
$M_{12 \rightarrow 1}$	2780/2780	1.00000
$M_{1 \rightarrow 2}$	2846/2846	1.00000
$M_{10 \rightarrow 2}$	2842/2842	1.00000
$M_{11 \rightarrow 2}$	2793/2793	1.00000
$M_{12 \rightarrow 2}$	2842/2842	1.00000
$M_{9 \rightarrow 3}$	2838/2838	1.00000
$M_{10 \rightarrow 3}$	2834/2834	1.00000
$M_{11 \rightarrow 3}$	2764/2764	1.00000
$M_{8 \rightarrow 4}$	2852/2852	1.00000
$M_{9 \rightarrow 4}$	2766/2766	1.00000
$M_{10 \rightarrow 4}$	2848/2848	1.00000
$M_{7 \rightarrow 5}$	2767/2767	1.00000
$M_{8 \rightarrow 5}$	2960/2960	1.00000
$M_{9 \rightarrow 5}$	2856/2856	1.00000
$M_{7 \rightarrow 6}$	2790/2790	1.00000
$M_{8 \rightarrow 6}$	2781/2781	1.00000
$M_{5 \rightarrow 7}$	2767/2767	1.00000
$M_{6 \rightarrow 7}$	3000/3000	1.00000
$M_{4 \rightarrow 8}$	2852/2852	1.00000
$M_{5 \rightarrow 8}$	2818/2818	1.00000
$M_{6 \rightarrow 8}$	2781/2781	1.00000
$M_{3 \rightarrow 9}$	2838/2838	1.00000
$M_{4 \rightarrow 9}$	2814/2814	1.00000
$M_{2 \rightarrow 10}$	2842/2842	1.00000
$M_{1 \rightarrow 11}$	2778/2778	1.00000
$M_{2 \rightarrow 11}$	2870/2870	1.00000
$M_{3 \rightarrow 11}$	2671/2671	1.00000
$M_{4 \rightarrow 11}$	2907/2907	1.00000
$M_{5 \rightarrow 11}$	2855/2855	1.00000
$M_{6 \rightarrow 11}$	2746/2746	1.00000

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

M	7->11	2811/2811	1.00000
M	8->11	2829/2829	1.00000
M	9->11	2844/2844	1.00000
M	10->11	2748/2748	1.00000
M	12->11	2867/2867	1.00000
M	1->12	2811/2811	1.00000
M	2->12	2813/2813	1.00000
M	3->12	2880/2880	1.00000
M	4->12	2801/2801	1.00000
M	5->12	2804/2804	1.00000
M	6->12	2778/2778	1.00000
M	7->12	2805/2805	1.00000
M	8->12	2855/2855	1.00000
M	9->12	2852/2852	1.00000
M	10->12	2841/2841	1.00000
M	11->12	2875/2875	1.00000
Genealogies		0/150343	0.00000

## MCMC-Autocorrelation and Effective MCMC Sample Size

Parameter	Autocorrelation	Effective Sample Size
$\Theta_1$	1.00000	0.00
$\Theta_2$	0.00000	0.00
$\Theta_3$	0.00000	0.00
$\Theta_4$	0.00000	0.00
$\Theta_5$	0.00000	0.00
$\Theta_6$	1.00000	0.00
$\Theta_7$	1.00000	0.00
$\Theta_8$	0.00000	0.00
$\Theta_9$	0.00000	0.00
$\Theta_{10}$	0.00000	0.00
$\Theta_{11}$	1.00000	0.00
$\Theta_{12}$	1.00000	0.00
$M_{2 \rightarrow 1}$	0.98941	15.95
$M_{11 \rightarrow 1}$	0.99151	12.78
$M_{12 \rightarrow 1}$	0.98381	24.47
$M_{1 \rightarrow 2}$	0.98941	15.95
$M_{10 \rightarrow 2}$	0.98636	20.59
$M_{11 \rightarrow 2}$	0.99073	13.96
$M_{12 \rightarrow 2}$	0.98883	16.84
$M_{9 \rightarrow 3}$	0.98700	19.61
$M_{10 \rightarrow 3}$	0.98885	16.81
$M_{11 \rightarrow 3}$	0.98694	19.73
$M_{8 \rightarrow 4}$	0.98725	19.24
$M_{9 \rightarrow 4}$	0.98969	15.54
$M_{10 \rightarrow 4}$	0.98796	18.16
$M_{7 \rightarrow 5}$	0.98970	15.51
$M_{8 \rightarrow 5}$	0.98954	15.75
$M_{9 \rightarrow 5}$	0.98326	25.34
$M_{7 \rightarrow 6}$	0.98835	17.56
$M_{8 \rightarrow 6}$	0.98785	18.32
$M_{5 \rightarrow 7}$	0.98970	15.51
$M_{6 \rightarrow 7}$	0.98034	29.85
$M_{4 \rightarrow 8}$	0.98725	19.24
$M_{5 \rightarrow 8}$	0.99131	13.08
$M_{6 \rightarrow 8}$	0.98785	18.32
$M_{3 \rightarrow 9}$	0.98700	19.61
$M_{4 \rightarrow 9}$	0.98652	20.35

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

M	2->10	0.98636	20.59
M	1->11	0.98266	26.24
M	2->11	0.98130	28.34
M	3->11	0.97281	41.36
M	4->11	0.98147	28.06
M	5->11	0.98737	19.09
M	6->11	0.97170	43.28
M	7->11	0.98588	21.33
M	8->11	0.98429	23.75
M	9->11	0.98955	15.74
M	10->11	0.98720	19.31
M	12->11	0.98828	17.68
M	1->12	0.98596	21.21
M	2->12	0.97541	37.32
M	3->12	0.98392	24.31
M	4->12	0.98626	20.79
M	5->12	0.98894	16.68
M	6->12	0.98467	23.17
M	7->12	0.96832	48.72
M	8->12	0.98995	15.14
M	9->12	0.98146	28.05
M	10->12	0.97843	32.69
M	11->12	0.98493	22.76
	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 127: Effective sample size of run seems too short!  
Param 131: Effective sample size of run seems too short!

Param 132: Effective sample size of run seems too short!  
Param 133: 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!