

Preliminary migrate analysis of *M. californianus*

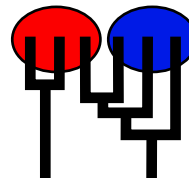
MIGRATION RATE AND POPULATION SIZE ESTIMATION

using the coalescent and maximum likelihood or Bayesian inference

Migrate-n version 3.7.2 [April-12-18]

Program started at Tue Jun 1 10:52:05 2021

Program finished at Tue Jun 1 18:24:26 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)

251481462

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

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

Order of parameters:

1	Θ_1	=	Θ_1	[m]	<displayed>
2	Θ_2	=	Θ_1	[m]	
3	Θ_3	=	Θ_1	[m]	
4	Θ_4	=	Θ_1	[m]	
5	Θ_5	=	Θ_1	[m]	
6	Θ_6	=	Θ_1	[m]	
7	Θ_7	=	Θ_1	[m]	
8	Θ_8	=	Θ_1	[m]	
9	Θ_9	=	Θ_1	[m]	
10	Θ_{10}	=	Θ_1	[m]	
11	Θ_{11}				<displayed>
12	Θ_{12}				<displayed>
13	$M_{2 \rightarrow 1}$	=	$M_{2 \rightarrow 1}$	[m]	<displayed>
14	$M_{3 \rightarrow 1}$	=	$M_{2 \rightarrow 1}$	[m]	
15	$M_{4 \rightarrow 1}$	=	$M_{2 \rightarrow 1}$	[m]	
16	$M_{5 \rightarrow 1}$	=	$M_{2 \rightarrow 1}$	[m]	
17	$M_{6 \rightarrow 1}$	=	$M_{2 \rightarrow 1}$	[m]	
18	$M_{7 \rightarrow 1}$	=	$M_{2 \rightarrow 1}$	[m]	
19	$M_{8 \rightarrow 1}$	=	$M_{2 \rightarrow 1}$	[m]	
20	$M_{9 \rightarrow 1}$	=	$M_{2 \rightarrow 1}$	[m]	
21	$M_{10 \rightarrow 1}$	=	$M_{2 \rightarrow 1}$	[m]	
22	$M_{11 \rightarrow 1}$	=	$M_{2 \rightarrow 1}$	[m]	
23	$M_{12 \rightarrow 1}$	=	$M_{2 \rightarrow 1}$	[m]	
24	$M_{1 \rightarrow 2}$	=	$M_{2 \rightarrow 1}$	[m]	
25	$M_{3 \rightarrow 2}$	=	$M_{2 \rightarrow 1}$	[m]	
26	$M_{4 \rightarrow 2}$	=	$M_{2 \rightarrow 1}$	[m]	
27	$M_{5 \rightarrow 2}$	=	$M_{2 \rightarrow 1}$	[m]	
28	$M_{6 \rightarrow 2}$	=	$M_{2 \rightarrow 1}$	[m]	
29	$M_{7 \rightarrow 2}$	=	$M_{2 \rightarrow 1}$	[m]	
30	$M_{8 \rightarrow 2}$	=	$M_{2 \rightarrow 1}$	[m]	
31	$M_{9 \rightarrow 2}$	=	$M_{2 \rightarrow 1}$	[m]	
32	$M_{10 \rightarrow 2}$	=	$M_{2 \rightarrow 1}$	[m]	
33	$M_{11 \rightarrow 2}$	=	$M_{2 \rightarrow 1}$	[m]	
34	$M_{12 \rightarrow 2}$	=	$M_{2 \rightarrow 1}$	[m]	
35	$M_{1 \rightarrow 3}$	=	$M_{2 \rightarrow 1}$	[m]	
36	$M_{2 \rightarrow 3}$	=	$M_{2 \rightarrow 1}$	[m]	
37	$M_{4 \rightarrow 3}$	=	$M_{2 \rightarrow 1}$	[m]	
38	$M_{5 \rightarrow 3}$	=	$M_{2 \rightarrow 1}$	[m]	
39	$M_{6 \rightarrow 3}$	=	$M_{2 \rightarrow 1}$	[m]	
40	$M_{7 \rightarrow 3}$	=	$M_{2 \rightarrow 1}$	[m]	

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

41	M	8->3 =	M	2->1 [m]
42	M	9->3 =	M	2->1 [m]
43	M	10->3 =	M	2->1 [m]
44	M	11->3 =	M	2->1 [m]
45	M	12->3 =	M	2->1 [m]
46	M	1->4 =	M	2->1 [m]
47	M	2->4 =	M	2->1 [m]
48	M	3->4 =	M	2->1 [m]
49	M	5->4 =	M	2->1 [m]
50	M	6->4 =	M	2->1 [m]
51	M	7->4 =	M	2->1 [m]
52	M	8->4 =	M	2->1 [m]
53	M	9->4 =	M	2->1 [m]
54	M	10->4 =	M	2->1 [m]
55	M	11->4 =	M	2->1 [m]
56	M	12->4 =	M	2->1 [m]
57	M	1->5 =	M	2->1 [m]
58	M	2->5 =	M	2->1 [m]
59	M	3->5 =	M	2->1 [m]
60	M	4->5 =	M	2->1 [m]
61	M	6->5 =	M	2->1 [m]
62	M	7->5 =	M	2->1 [m]
63	M	8->5 =	M	2->1 [m]
64	M	9->5 =	M	2->1 [m]
65	M	10->5 =	M	2->1 [m]
66	M	11->5 =	M	2->1 [m]
67	M	12->5 =	M	2->1 [m]
68	M	1->6 =	M	2->1 [m]
69	M	2->6 =	M	2->1 [m]
70	M	3->6 =	M	2->1 [m]
71	M	4->6 =	M	2->1 [m]
72	M	5->6 =	M	2->1 [m]
73	M	7->6 =	M	2->1 [m]
74	M	8->6 =	M	2->1 [m]
75	M	9->6 =	M	2->1 [m]
76	M	10->6 =	M	2->1 [m]
77	M	11->6 =	M	2->1 [m]
78	M	12->6 =	M	2->1 [m]
79	M	1->7 =	M	2->1 [m]
80	M	2->7 =	M	2->1 [m]
81	M	3->7 =	M	2->1 [m]
82	M	4->7 =	M	2->1 [m]
83	M	5->7 =	M	2->1 [m]
84	M	6->7 =	M	2->1 [m]
85	M	8->7 =	M	2->1 [m]

86	M	9->7 =	M	2->1 [m]	
87	M	10->7 =	M	2->1 [m]	
88	M	11->7 =	M	2->1 [m]	
89	M	12->7 =	M	2->1 [m]	
90	M	1->8 =	M	2->1 [m]	
91	M	2->8 =	M	2->1 [m]	
92	M	3->8 =	M	2->1 [m]	
93	M	4->8 =	M	2->1 [m]	
94	M	5->8 =	M	2->1 [m]	
95	M	6->8 =	M	2->1 [m]	
96	M	7->8 =	M	2->1 [m]	
97	M	9->8 =	M	2->1 [m]	
98	M	10->8 =	M	2->1 [m]	
99	M	11->8 =	M	2->1 [m]	
100	M	12->8 =	M	2->1 [m]	
101	M	1->9 =	M	2->1 [m]	
102	M	2->9 =	M	2->1 [m]	
103	M	3->9 =	M	2->1 [m]	
104	M	4->9 =	M	2->1 [m]	
105	M	5->9 =	M	2->1 [m]	
106	M	6->9 =	M	2->1 [m]	
107	M	7->9 =	M	2->1 [m]	
108	M	8->9 =	M	2->1 [m]	
109	M	10->9 =	M	2->1 [m]	
110	M	11->9 =	M	2->1 [m]	
111	M	12->9 =	M	2->1 [m]	
112	M	1->10 =	M	2->1 [m]	
113	M	2->10 =	M	2->1 [m]	
114	M	3->10 =	M	2->1 [m]	
115	M	4->10 =	M	2->1 [m]	
116	M	5->10 =	M	2->1 [m]	
117	M	6->10 =	M	2->1 [m]	
118	M	7->10 =	M	2->1 [m]	
119	M	8->10 =	M	2->1 [m]	
120	M	9->10 =	M	2->1 [m]	
121	M	11->10 =	M	2->1 [m]	
122	M	12->10 =	M	2->1 [m]	
123	M	1->11		<displayed>	
124	M	2->11		<displayed>	
125	M	3->11		<displayed>	
126	M	4->11		<displayed>	
127	M	5->11		<displayed>	
128	M	6->11		<displayed>	
129	M	7->11		<displayed>	
130	M	8->11		<displayed>	

131	M	9->11	<displayed>
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
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	0.00060
1	Θ_2	0.00001	0.00001	0.01001	0.06001	0.16001	0.07001	0.00060
1	Θ_3	0.00001	0.00001	0.01001	0.06001	0.16001	0.07001	0.00060
1	Θ_4	0.00001	0.00001	0.01001	0.06001	0.16001	0.07001	0.00060
1	Θ_5	0.00001	0.00001	0.01001	0.06001	0.16001	0.07001	0.00060
1	Θ_6	0.00001	0.00001	0.01001	0.06001	0.16001	0.07001	0.00060
1	Θ_7	0.00001	0.00001	0.01001	0.06001	0.16001	0.07001	0.00060
1	Θ_8	0.00001	0.00001	0.01001	0.06001	0.16001	0.07001	0.00060
1	Θ_9	0.00001	0.00001	0.01001	0.06001	0.16001	0.07001	0.00060
1	Θ_{10}	0.00001	0.00001	0.01001	0.06001	0.16001	0.07001	0.00060
1	Θ_{11}	0.00001	0.00001	0.01001	0.06001	0.16001	0.07001	0.01198
1	Θ_{12}	0.00001	0.00001	0.01001	0.06001	0.16001	0.07001	0.01085
1	$M_{2 \rightarrow 1}$	34000.0	46000.0	61000.0	68000.0	86000.0	61000.0	60432.2
1	$M_{3 \rightarrow 1}$	34000.0	46000.0	61000.0	68000.0	86000.0	61000.0	60432.2
1	$M_{4 \rightarrow 1}$	34000.0	46000.0	61000.0	68000.0	86000.0	61000.0	60432.2
1	$M_{5 \rightarrow 1}$	34000.0	46000.0	61000.0	68000.0	86000.0	61000.0	60432.2
1	$M_{6 \rightarrow 1}$	34000.0	46000.0	61000.0	68000.0	86000.0	61000.0	60432.2
1	$M_{7 \rightarrow 1}$	34000.0	46000.0	61000.0	68000.0	86000.0	61000.0	60432.2
1	$M_{8 \rightarrow 1}$	34000.0	46000.0	61000.0	68000.0	86000.0	61000.0	60432.2
1	$M_{9 \rightarrow 1}$	34000.0	46000.0	61000.0	68000.0	86000.0	61000.0	60432.2
1	$M_{10 \rightarrow 1}$	34000.0	46000.0	61000.0	68000.0	86000.0	61000.0	60432.2
1	$M_{11 \rightarrow 1}$	34000.0	46000.0	61000.0	68000.0	86000.0	61000.0	60432.2
1	$M_{12 \rightarrow 1}$	34000.0	46000.0	61000.0	68000.0	86000.0	61000.0	60432.2
1	$M_{1 \rightarrow 2}$	34000.0	46000.0	61000.0	68000.0	86000.0	61000.0	60432.2
1	$M_{3 \rightarrow 2}$	34000.0	46000.0	61000.0	68000.0	86000.0	61000.0	60432.2
1	$M_{4 \rightarrow 2}$	34000.0	46000.0	61000.0	68000.0	86000.0	61000.0	60432.2
1	$M_{5 \rightarrow 2}$	34000.0	46000.0	61000.0	68000.0	86000.0	61000.0	60432.2
1	$M_{6 \rightarrow 2}$	34000.0	46000.0	61000.0	68000.0	86000.0	61000.0	60432.2
1	$M_{7 \rightarrow 2}$	34000.0	46000.0	61000.0	68000.0	86000.0	61000.0	60432.2
1	$M_{8 \rightarrow 2}$	34000.0	46000.0	61000.0	68000.0	86000.0	61000.0	60432.2
1	$M_{9 \rightarrow 2}$	34000.0	46000.0	61000.0	68000.0	86000.0	61000.0	60432.2
1	$M_{10 \rightarrow 2}$	34000.0	46000.0	61000.0	68000.0	86000.0	61000.0	60432.2
1	$M_{11 \rightarrow 2}$	34000.0	46000.0	61000.0	68000.0	86000.0	61000.0	60432.2
1	$M_{12 \rightarrow 2}$	34000.0	46000.0	61000.0	68000.0	86000.0	61000.0	60432.2
1	$M_{1 \rightarrow 3}$	34000.0	46000.0	61000.0	68000.0	86000.0	61000.0	60432.2
1	$M_{2 \rightarrow 3}$	34000.0	46000.0	61000.0	68000.0	86000.0	61000.0	60432.2

Locus	Parameter	2.5%	25.0%	Mode	75.0%	97.5%	Median	Mean
1	M _{4->3}	34000.0	46000.0	61000.0	68000.0	86000.0	61000.0	60432.2
1	M _{5->3}	34000.0	46000.0	61000.0	68000.0	86000.0	61000.0	60432.2
1	M _{6->3}	34000.0	46000.0	61000.0	68000.0	86000.0	61000.0	60432.2
1	M _{7->3}	34000.0	46000.0	61000.0	68000.0	86000.0	61000.0	60432.2
1	M _{8->3}	34000.0	46000.0	61000.0	68000.0	86000.0	61000.0	60432.2
1	M _{9->3}	34000.0	46000.0	61000.0	68000.0	86000.0	61000.0	60432.2
1	M _{10->3}	34000.0	46000.0	61000.0	68000.0	86000.0	61000.0	60432.2
1	M _{11->3}	34000.0	46000.0	61000.0	68000.0	86000.0	61000.0	60432.2
1	M _{12->3}	34000.0	46000.0	61000.0	68000.0	86000.0	61000.0	60432.2
1	M _{1->4}	34000.0	46000.0	61000.0	68000.0	86000.0	61000.0	60432.2
1	M _{2->4}	34000.0	46000.0	61000.0	68000.0	86000.0	61000.0	60432.2
1	M _{3->4}	34000.0	46000.0	61000.0	68000.0	86000.0	61000.0	60432.2
1	M _{5->4}	34000.0	46000.0	61000.0	68000.0	86000.0	61000.0	60432.2
1	M _{6->4}	34000.0	46000.0	61000.0	68000.0	86000.0	61000.0	60432.2
1	M _{7->4}	34000.0	46000.0	61000.0	68000.0	86000.0	61000.0	60432.2
1	M _{8->4}	34000.0	46000.0	61000.0	68000.0	86000.0	61000.0	60432.2
1	M _{9->4}	34000.0	46000.0	61000.0	68000.0	86000.0	61000.0	60432.2
1	M _{10->4}	34000.0	46000.0	61000.0	68000.0	86000.0	61000.0	60432.2
1	M _{11->4}	34000.0	46000.0	61000.0	68000.0	86000.0	61000.0	60432.2
1	M _{12->4}	34000.0	46000.0	61000.0	68000.0	86000.0	61000.0	60432.2
1	M _{1->5}	34000.0	46000.0	61000.0	68000.0	86000.0	61000.0	60432.2
1	M _{2->5}	34000.0	46000.0	61000.0	68000.0	86000.0	61000.0	60432.2
1	M _{3->5}	34000.0	46000.0	61000.0	68000.0	86000.0	61000.0	60432.2
1	M _{4->5}	34000.0	46000.0	61000.0	68000.0	86000.0	61000.0	60432.2
1	M _{6->5}	34000.0	46000.0	61000.0	68000.0	86000.0	61000.0	60432.2
1	M _{7->5}	34000.0	46000.0	61000.0	68000.0	86000.0	61000.0	60432.2
1	M _{8->5}	34000.0	46000.0	61000.0	68000.0	86000.0	61000.0	60432.2
1	M _{9->5}	34000.0	46000.0	61000.0	68000.0	86000.0	61000.0	60432.2
1	M _{10->5}	34000.0	46000.0	61000.0	68000.0	86000.0	61000.0	60432.2
1	M _{11->5}	34000.0	46000.0	61000.0	68000.0	86000.0	61000.0	60432.2
1	M _{12->5}	34000.0	46000.0	61000.0	68000.0	86000.0	61000.0	60432.2
1	M _{1->6}	34000.0	46000.0	61000.0	68000.0	86000.0	61000.0	60432.2
1	M _{2->6}	34000.0	46000.0	61000.0	68000.0	86000.0	61000.0	60432.2
1	M _{3->6}	34000.0	46000.0	61000.0	68000.0	86000.0	61000.0	60432.2
1	M _{4->6}	34000.0	46000.0	61000.0	68000.0	86000.0	61000.0	60432.2
1	M _{5->6}	34000.0	46000.0	61000.0	68000.0	86000.0	61000.0	60432.2
1	M _{7->6}	34000.0	46000.0	61000.0	68000.0	86000.0	61000.0	60432.2
1	M _{8->6}	34000.0	46000.0	61000.0	68000.0	86000.0	61000.0	60432.2
1	M _{9->6}	34000.0	46000.0	61000.0	68000.0	86000.0	61000.0	60432.2
1	M _{10->6}	34000.0	46000.0	61000.0	68000.0	86000.0	61000.0	60432.2
1	M _{11->6}	34000.0	46000.0	61000.0	68000.0	86000.0	61000.0	60432.2

Locus	Parameter	2.5%	25.0%	Mode	75.0%	97.5%	Median	Mean
1	M _{12->6}	34000.0	46000.0	61000.0	68000.0	86000.0	61000.0	60432.2
1	M _{1->7}	34000.0	46000.0	61000.0	68000.0	86000.0	61000.0	60432.2
1	M _{2->7}	34000.0	46000.0	61000.0	68000.0	86000.0	61000.0	60432.2
1	M _{3->7}	34000.0	46000.0	61000.0	68000.0	86000.0	61000.0	60432.2
1	M _{4->7}	34000.0	46000.0	61000.0	68000.0	86000.0	61000.0	60432.2
1	M _{5->7}	34000.0	46000.0	61000.0	68000.0	86000.0	61000.0	60432.2
1	M _{6->7}	34000.0	46000.0	61000.0	68000.0	86000.0	61000.0	60432.2
1	M _{8->7}	34000.0	46000.0	61000.0	68000.0	86000.0	61000.0	60432.2
1	M _{9->7}	34000.0	46000.0	61000.0	68000.0	86000.0	61000.0	60432.2
1	M _{10->7}	34000.0	46000.0	61000.0	68000.0	86000.0	61000.0	60432.2
1	M _{11->7}	34000.0	46000.0	61000.0	68000.0	86000.0	61000.0	60432.2
1	M _{12->7}	34000.0	46000.0	61000.0	68000.0	86000.0	61000.0	60432.2
1	M _{1->8}	34000.0	46000.0	61000.0	68000.0	86000.0	61000.0	60432.2
1	M _{2->8}	34000.0	46000.0	61000.0	68000.0	86000.0	61000.0	60432.2
1	M _{3->8}	34000.0	46000.0	61000.0	68000.0	86000.0	61000.0	60432.2
1	M _{4->8}	34000.0	46000.0	61000.0	68000.0	86000.0	61000.0	60432.2
1	M _{5->8}	34000.0	46000.0	61000.0	68000.0	86000.0	61000.0	60432.2
1	M _{6->8}	34000.0	46000.0	61000.0	68000.0	86000.0	61000.0	60432.2
1	M _{7->8}	34000.0	46000.0	61000.0	68000.0	86000.0	61000.0	60432.2
1	M _{9->8}	34000.0	46000.0	61000.0	68000.0	86000.0	61000.0	60432.2
1	M _{10->8}	34000.0	46000.0	61000.0	68000.0	86000.0	61000.0	60432.2
1	M _{11->8}	34000.0	46000.0	61000.0	68000.0	86000.0	61000.0	60432.2
1	M _{12->8}	34000.0	46000.0	61000.0	68000.0	86000.0	61000.0	60432.2
1	M _{1->9}	34000.0	46000.0	61000.0	68000.0	86000.0	61000.0	60432.2
1	M _{2->9}	34000.0	46000.0	61000.0	68000.0	86000.0	61000.0	60432.2
1	M _{3->9}	34000.0	46000.0	61000.0	68000.0	86000.0	61000.0	60432.2
1	M _{4->9}	34000.0	46000.0	61000.0	68000.0	86000.0	61000.0	60432.2
1	M _{5->9}	34000.0	46000.0	61000.0	68000.0	86000.0	61000.0	60432.2
1	M _{6->9}	34000.0	46000.0	61000.0	68000.0	86000.0	61000.0	60432.2
1	M _{7->9}	34000.0	46000.0	61000.0	68000.0	86000.0	61000.0	60432.2
1	M _{8->9}	34000.0	46000.0	61000.0	68000.0	86000.0	61000.0	60432.2
1	M _{10->9}	34000.0	46000.0	61000.0	68000.0	86000.0	61000.0	60432.2
1	M _{11->9}	34000.0	46000.0	61000.0	68000.0	86000.0	61000.0	60432.2
1	M _{12->9}	34000.0	46000.0	61000.0	68000.0	86000.0	61000.0	60432.2
1	M _{1->10}	34000.0	46000.0	61000.0	68000.0	86000.0	61000.0	60432.2
1	M _{2->10}	34000.0	46000.0	61000.0	68000.0	86000.0	61000.0	60432.2
1	M _{3->10}	34000.0	46000.0	61000.0	68000.0	86000.0	61000.0	60432.2
1	M _{4->10}	34000.0	46000.0	61000.0	68000.0	86000.0	61000.0	60432.2
1	M _{5->10}	34000.0	46000.0	61000.0	68000.0	86000.0	61000.0	60432.2
1	M _{6->10}	34000.0	46000.0	61000.0	68000.0	86000.0	61000.0	60432.2
1	M _{7->10}	34000.0	46000.0	61000.0	68000.0	86000.0	61000.0	60432.2

Locus	Parameter	2.5%	25.0%	Mode	75.0%	97.5%	Median	Mean
1	M _{8->10}	34000.0	46000.0	61000.0	68000.0	86000.0	61000.0	60432.2
1	M _{9->10}	34000.0	46000.0	61000.0	68000.0	86000.0	61000.0	60432.2
1	M _{11->10}	34000.0	46000.0	61000.0	68000.0	86000.0	61000.0	60432.2
1	M _{12->10}	34000.0	46000.0	61000.0	68000.0	86000.0	61000.0	60432.2
1	M _{1->11}	6000.0	22000.0	39000.0	62000.0	104000.0	53000.0	53677.4
1	M _{2->11}	32000.0	56000.0	73000.0	86000.0	114000.0	75000.0	73574.2
1	M _{3->11}	26000.0	50000.0	67000.0	94000.0	140000.0	81000.0	81071.6
1	M _{4->11}	60000.0	148000.0	179000.0	212000.0	236000.0	169000.0	156546.7
1	M _{5->11}	18000.0	80000.0	99000.0	118000.0	174000.0	97000.0	94566.0
1	M _{6->11}	42000.0	66000.0	89000.0	110000.0	180000.0	97000.0	101891.6
1	M _{7->11}	118000.0	154000.0	175000.0	196000.0	230000.0	177000.0	175685.8
1	M _{8->11}	36000.0	92000.0	117000.0	134000.0	160000.0	105000.0	100375.6
1	M _{9->11}	46000.0	80000.0	105000.0	130000.0	186000.0	113000.0	114153.9
1	M _{10->11}	78000.0	158000.0	203000.0	224000.0	272000.0	185000.0	177194.3
1	M _{12->11}	24000.0	70000.0	91000.0	108000.0	142000.0	89000.0	86217.9
1	M _{1->12}	0.0	76000.0	115000.0	130000.0	154000.0	85000.0	79427.7
1	M _{2->12}	20000.0	42000.0	61000.0	84000.0	152000.0	73000.0	76597.9
1	M _{3->12}	70000.0	80000.0	109000.0	134000.0	244000.0	133000.0	147980.1
1	M _{4->12}	0.0	4000.0	27000.0	54000.0	64000.0	247000.0	231639.8
1	M _{5->12}	36000.0	50000.0	73000.0	96000.0	130000.0	91000.0	121564.4
1	M _{6->12}	0.0	14000.0	43000.0	66000.0	86000.0	59000.0	93817.6
1	M _{7->12}	44000.0	58000.0	73000.0	88000.0	184000.0	115000.0	113375.6
1	M _{8->12}	64000.0	86000.0	115000.0	156000.0	182000.0	145000.0	198629.1
1	M _{9->12}	66000.0	130000.0	153000.0	192000.0	232000.0	155000.0	151045.1
1	M _{10->12}	88000.0	114000.0	135000.0	164000.0	216000.0	149000.0	150416.8
1	M _{11->12}	14000.0	56000.0	93000.0	110000.0	136000.0	79000.0	77125.7

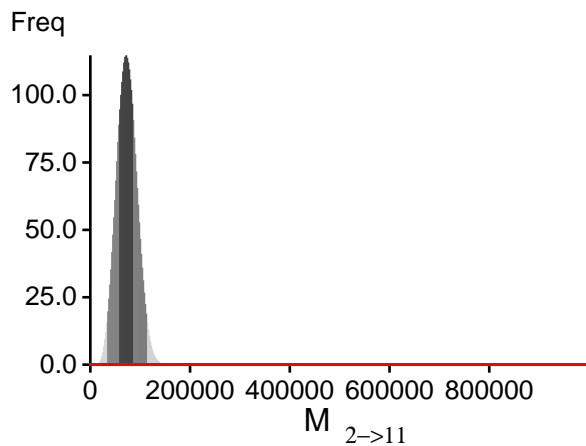
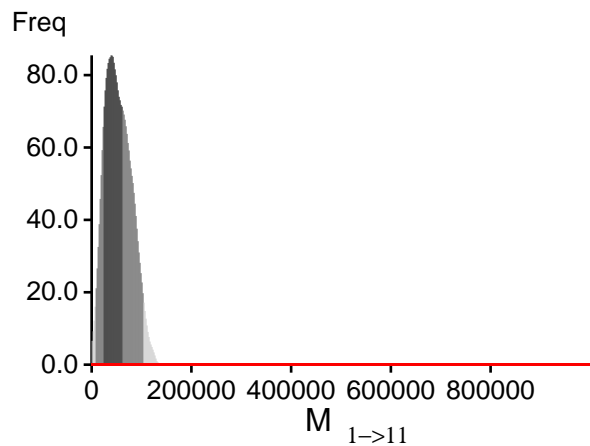
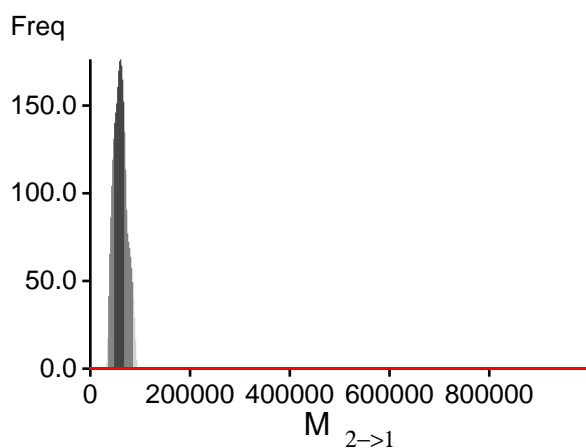
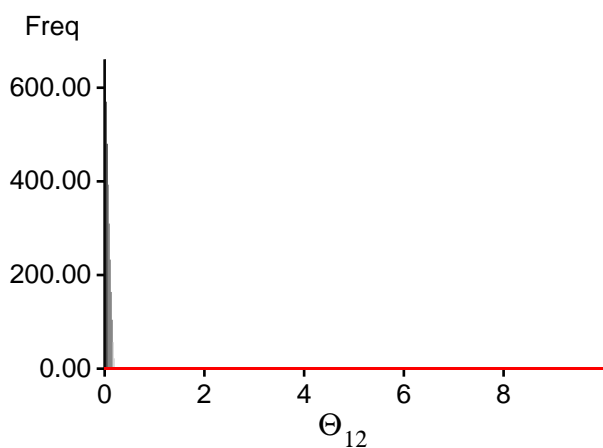
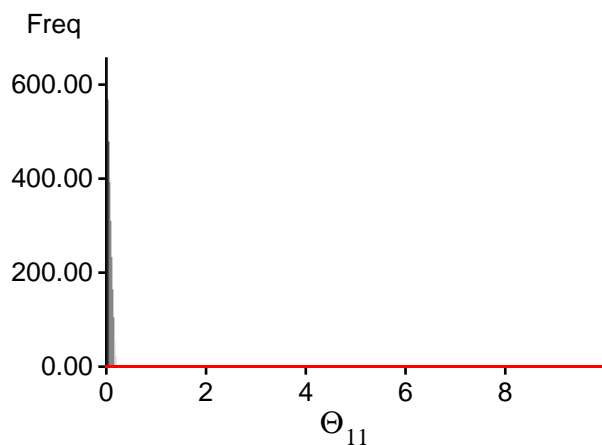
Citation suggestions:

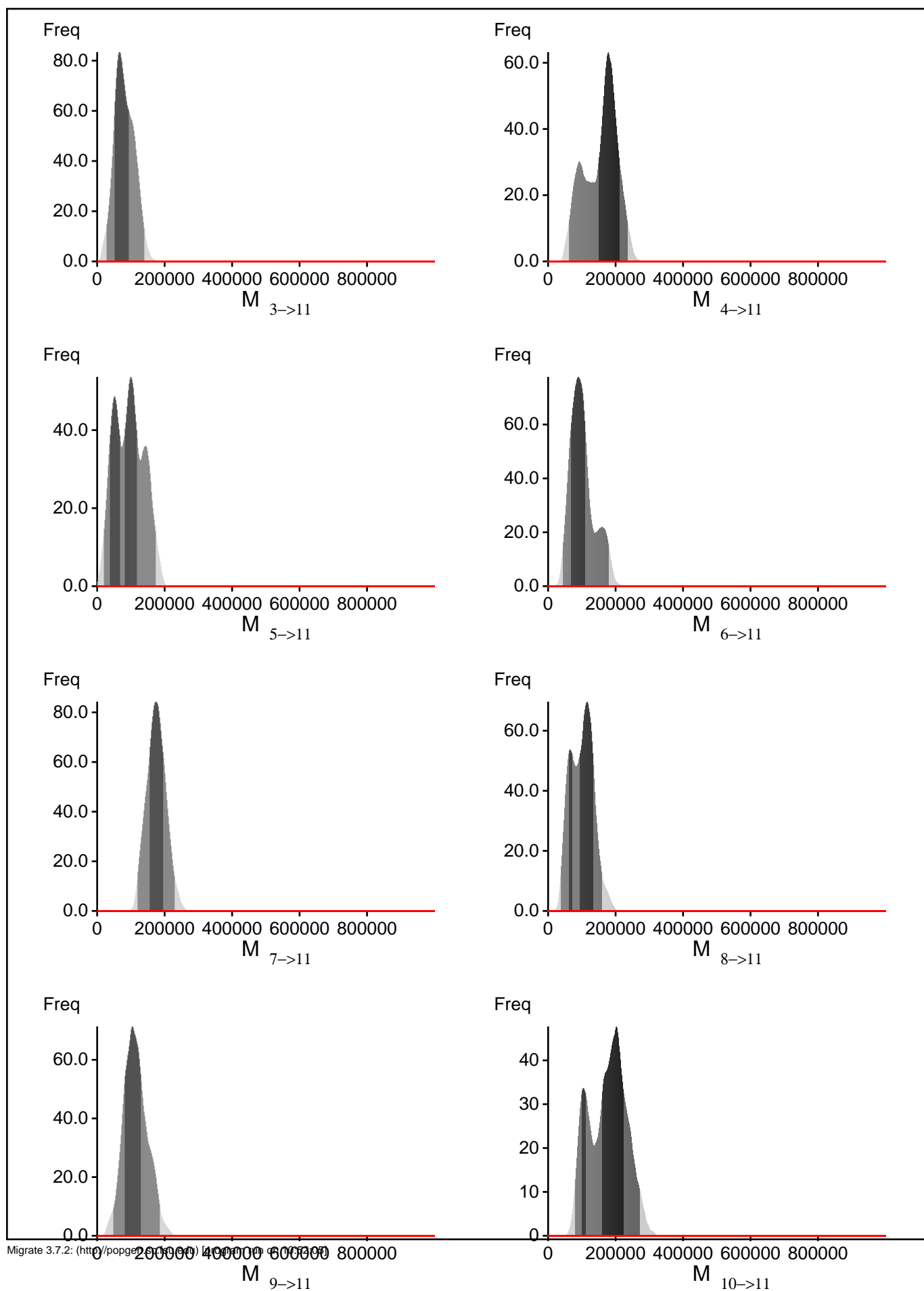
Beerli P., 2006. Comparison of Bayesian and maximum-likelihood inference of population genetic parameters.
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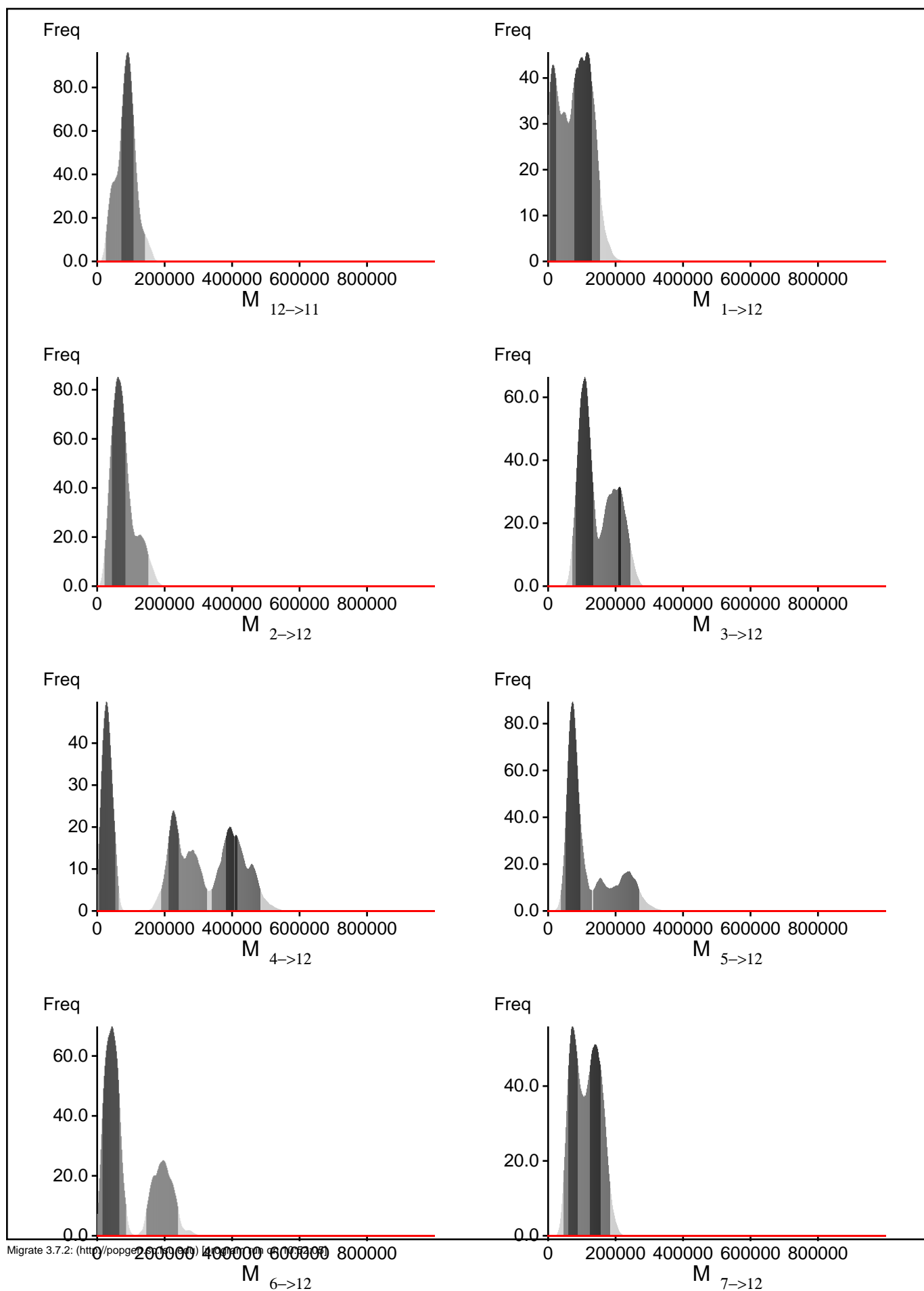
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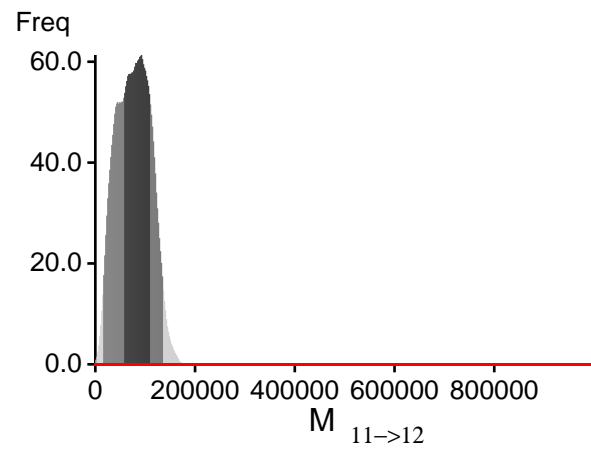
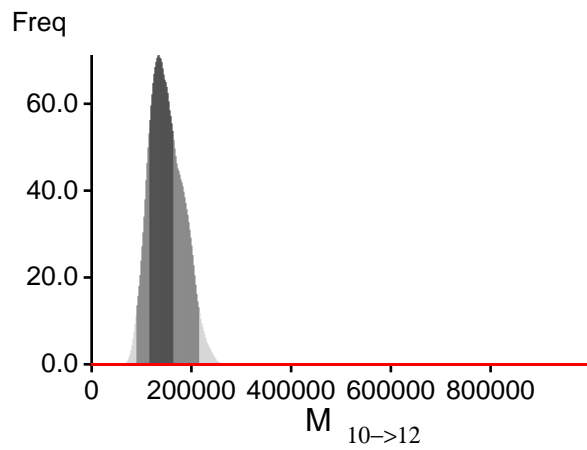
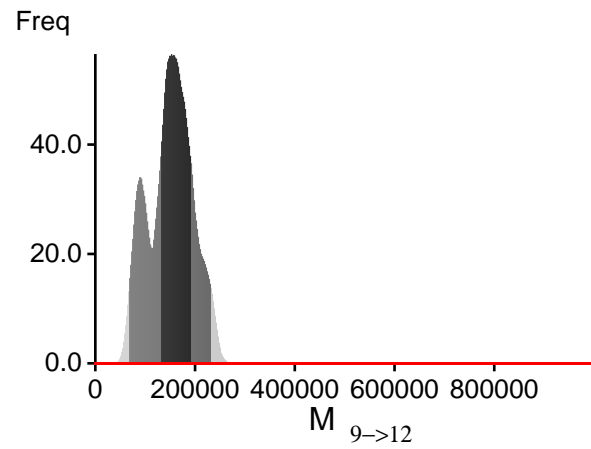
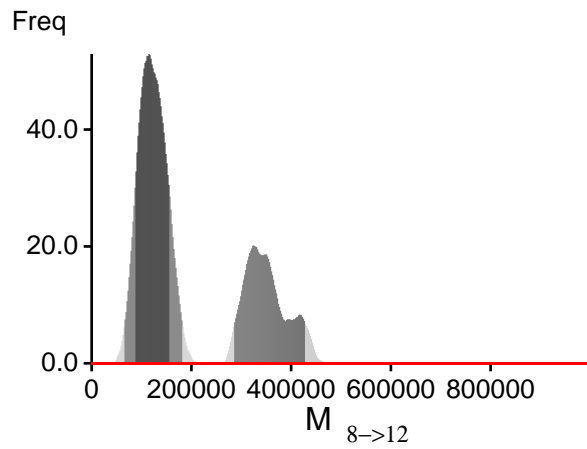
Beerli P., 2009. How to use MIGRATE or why are Markov chain Monte Carlo programs difficult to use?
 In Population Genetics for Animal Conservation, G. Bertorelle, M. W. Bruford, H. C. Hauffe, A. Rizzoli,
 and C. Vernesi, eds., vol. 17 of Conservation Biology, Cambridge University Press, Cambridge UK, pp. 42-79.

Bayesian Analysis: Posterior distribution over all loci









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

Use this value for Bayes factor calculations:

$BF = \text{Exp}[\ln(\text{Prob}(D \mid \text{thisModel}) - \ln(\text{Prob}(D \mid \text{otherModel}))]$

or as $LBF = 2 (\ln(\text{Prob}(D \mid \text{thisModel}) - \ln(\text{Prob}(D \mid \text{otherModel})))$

shows the support for thisModel]

Method	$\ln(\text{Prob}(D \mid \text{Model}))$	Notes
Thermodynamic integration	-2378.728296	(1a)
	-2261.629025	(1b)
Harmonic mean	-1965.908118	(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	11/1018	0.01081
Θ_2	11/1018	0.01081
Θ_3	11/1018	0.01081
Θ_4	11/1018	0.01081
Θ_5	11/1018	0.01081
Θ_6	11/1018	0.01081
Θ_7	11/1018	0.01081
Θ_8	11/1018	0.01081
Θ_9	11/1018	0.01081
Θ_{10}	11/1018	0.01081
Θ_{11}	673/1005	0.66965
Θ_{12}	661/982	0.67312
$M_{2 \rightarrow 1}$	1036/1036	1.00000
$M_{3 \rightarrow 1}$	1036/1036	1.00000
$M_{4 \rightarrow 1}$	1036/1036	1.00000
$M_{5 \rightarrow 1}$	1036/1036	1.00000
$M_{6 \rightarrow 1}$	1036/1036	1.00000
$M_{7 \rightarrow 1}$	1036/1036	1.00000
$M_{8 \rightarrow 1}$	1036/1036	1.00000
$M_{9 \rightarrow 1}$	1036/1036	1.00000
$M_{10 \rightarrow 1}$	1036/1036	1.00000
$M_{11 \rightarrow 1}$	1036/1036	1.00000
$M_{12 \rightarrow 1}$	1036/1036	1.00000
$M_{1 \rightarrow 2}$	1036/1036	1.00000
$M_{3 \rightarrow 2}$	1036/1036	1.00000
$M_{4 \rightarrow 2}$	1036/1036	1.00000
$M_{5 \rightarrow 2}$	1036/1036	1.00000
$M_{6 \rightarrow 2}$	1036/1036	1.00000
$M_{7 \rightarrow 2}$	1036/1036	1.00000
$M_{8 \rightarrow 2}$	1036/1036	1.00000
$M_{9 \rightarrow 2}$	1036/1036	1.00000
$M_{10 \rightarrow 2}$	1036/1036	1.00000
$M_{11 \rightarrow 2}$	1036/1036	1.00000
$M_{12 \rightarrow 2}$	1036/1036	1.00000
$M_{1 \rightarrow 3}$	1036/1036	1.00000
$M_{2 \rightarrow 3}$	1036/1036	1.00000
$M_{4 \rightarrow 3}$	1036/1036	1.00000

M	5->3	1036/1036	1.00000
M	6->3	1036/1036	1.00000
M	7->3	1036/1036	1.00000
M	8->3	1036/1036	1.00000
M	9->3	1036/1036	1.00000
M	10->3	1036/1036	1.00000
M	11->3	1036/1036	1.00000
M	12->3	1036/1036	1.00000
M	1->4	1036/1036	1.00000
M	2->4	1036/1036	1.00000
M	3->4	1036/1036	1.00000
M	5->4	1036/1036	1.00000
M	6->4	1036/1036	1.00000
M	7->4	1036/1036	1.00000
M	8->4	1036/1036	1.00000
M	9->4	1036/1036	1.00000
M	10->4	1036/1036	1.00000
M	11->4	1036/1036	1.00000
M	12->4	1036/1036	1.00000
M	1->5	1036/1036	1.00000
M	2->5	1036/1036	1.00000
M	3->5	1036/1036	1.00000
M	4->5	1036/1036	1.00000
M	6->5	1036/1036	1.00000
M	7->5	1036/1036	1.00000
M	8->5	1036/1036	1.00000
M	9->5	1036/1036	1.00000
M	10->5	1036/1036	1.00000
M	11->5	1036/1036	1.00000
M	12->5	1036/1036	1.00000
M	1->6	1036/1036	1.00000
M	2->6	1036/1036	1.00000
M	3->6	1036/1036	1.00000
M	4->6	1036/1036	1.00000
M	5->6	1036/1036	1.00000
M	7->6	1036/1036	1.00000
M	8->6	1036/1036	1.00000
M	9->6	1036/1036	1.00000
M	10->6	1036/1036	1.00000
M	11->6	1036/1036	1.00000
M	12->6	1036/1036	1.00000
M	1->7	1036/1036	1.00000
M	2->7	1036/1036	1.00000
M	3->7	1036/1036	1.00000
M	4->7	1036/1036	1.00000

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

M	5->7	1036/1036	1.00000
M	6->7	1036/1036	1.00000
M	8->7	1036/1036	1.00000
M	9->7	1036/1036	1.00000
M	10->7	1036/1036	1.00000
M	11->7	1036/1036	1.00000
M	12->7	1036/1036	1.00000
M	1->8	1036/1036	1.00000
M	2->8	1036/1036	1.00000
M	3->8	1036/1036	1.00000
M	4->8	1036/1036	1.00000
M	5->8	1036/1036	1.00000
M	6->8	1036/1036	1.00000
M	7->8	1036/1036	1.00000
M	9->8	1036/1036	1.00000
M	10->8	1036/1036	1.00000
M	11->8	1036/1036	1.00000
M	12->8	1036/1036	1.00000
M	1->9	1036/1036	1.00000
M	2->9	1036/1036	1.00000
M	3->9	1036/1036	1.00000
M	4->9	1036/1036	1.00000
M	5->9	1036/1036	1.00000
M	6->9	1036/1036	1.00000
M	7->9	1036/1036	1.00000
M	8->9	1036/1036	1.00000
M	10->9	1036/1036	1.00000
M	11->9	1036/1036	1.00000
M	12->9	1036/1036	1.00000
M	1->10	1036/1036	1.00000
M	2->10	1036/1036	1.00000
M	3->10	1036/1036	1.00000
M	4->10	1036/1036	1.00000
M	5->10	1036/1036	1.00000
M	6->10	1036/1036	1.00000
M	7->10	1036/1036	1.00000
M	8->10	1036/1036	1.00000
M	9->10	1036/1036	1.00000
M	11->10	1036/1036	1.00000
M	12->10	1036/1036	1.00000
M	1->11	1081/1081	1.00000
M	2->11	1066/1066	1.00000
M	3->11	1083/1083	1.00000
M	4->11	1013/1013	1.00000
M	5->11	1031/1031	1.00000

M	6->11	1022/1022	1.00000
M	7->11	1017/1017	1.00000
M	8->11	998/998	1.00000
M	9->11	1014/1014	1.00000
M	10->11	1086/1086	1.00000
M	12->11	1045/1045	1.00000
M	1->12	1024/1024	1.00000
M	2->12	1016/1016	1.00000
M	3->12	1060/1060	1.00000
M	4->12	1035/1035	1.00000
M	5->12	955/955	1.00000
M	6->12	1093/1093	1.00000
M	7->12	1071/1071	1.00000
M	8->12	1032/1032	1.00000
M	9->12	1046/1046	1.00000
M	10->12	1085/1085	1.00000
M	11->12	1026/1026	1.00000
Genealogies		22821/150514	0.15162

MCMC-Autocorrelation and Effective MCMC Sample Size

Parameter	Autocorrelation	Effective Sample Size
Θ_1	0.99206	11.95
Θ_2	0.99206	11.95
Θ_3	0.99206	11.95
Θ_4	0.99206	11.95
Θ_5	0.99206	11.95
Θ_6	0.99206	11.95
Θ_7	0.99206	11.95
Θ_8	0.99206	11.95
Θ_9	0.99206	11.95
Θ_{10}	0.99206	11.95
Θ_{11}	0.86242	222.05
Θ_{12}	0.82324	291.35
$M_{2 \rightarrow 1}$	0.99009	14.93
$M_{3 \rightarrow 1}$	0.99009	14.93
$M_{4 \rightarrow 1}$	0.99009	14.93
$M_{5 \rightarrow 1}$	0.99009	14.93
$M_{6 \rightarrow 1}$	0.99009	14.93
$M_{7 \rightarrow 1}$	0.99009	14.93
$M_{8 \rightarrow 1}$	0.99009	14.93
$M_{9 \rightarrow 1}$	0.99009	14.93
$M_{10 \rightarrow 1}$	0.99009	14.93
$M_{11 \rightarrow 1}$	0.99009	14.93
$M_{12 \rightarrow 1}$	0.99009	14.93
$M_{1 \rightarrow 2}$	0.99009	14.93
$M_{3 \rightarrow 2}$	0.99009	14.93
$M_{4 \rightarrow 2}$	0.99009	14.93
$M_{5 \rightarrow 2}$	0.99009	14.93
$M_{6 \rightarrow 2}$	0.99009	14.93
$M_{7 \rightarrow 2}$	0.99009	14.93
$M_{8 \rightarrow 2}$	0.99009	14.93
$M_{9 \rightarrow 2}$	0.99009	14.93
$M_{10 \rightarrow 2}$	0.99009	14.93
$M_{11 \rightarrow 2}$	0.99009	14.93
$M_{12 \rightarrow 2}$	0.99009	14.93
$M_{1 \rightarrow 3}$	0.99009	14.93
$M_{2 \rightarrow 3}$	0.99009	14.93
$M_{4 \rightarrow 3}$	0.99009	14.93

M	5->3	0.99009	14.93
M	6->3	0.99009	14.93
M	7->3	0.99009	14.93
M	8->3	0.99009	14.93
M	9->3	0.99009	14.93
M	10->3	0.99009	14.93
M	11->3	0.99009	14.93
M	12->3	0.99009	14.93
M	1->4	0.99009	14.93
M	2->4	0.99009	14.93
M	3->4	0.99009	14.93
M	5->4	0.99009	14.93
M	6->4	0.99009	14.93
M	7->4	0.99009	14.93
M	8->4	0.99009	14.93
M	9->4	0.99009	14.93
M	10->4	0.99009	14.93
M	11->4	0.99009	14.93
M	12->4	0.99009	14.93
M	1->5	0.99009	14.93
M	2->5	0.99009	14.93
M	3->5	0.99009	14.93
M	4->5	0.99009	14.93
M	6->5	0.99009	14.93
M	7->5	0.99009	14.93
M	8->5	0.99009	14.93
M	9->5	0.99009	14.93
M	10->5	0.99009	14.93
M	11->5	0.99009	14.93
M	12->5	0.99009	14.93
M	1->6	0.99009	14.93
M	2->6	0.99009	14.93
M	3->6	0.99009	14.93
M	4->6	0.99009	14.93
M	5->6	0.99009	14.93
M	7->6	0.99009	14.93
M	8->6	0.99009	14.93
M	9->6	0.99009	14.93
M	10->6	0.99009	14.93
M	11->6	0.99009	14.93
M	12->6	0.99009	14.93
M	1->7	0.99009	14.93
M	2->7	0.99009	14.93
M	3->7	0.99009	14.93
M	4->7	0.99009	14.93

Preliminary migrate analysis of *M. californianus* CO1 haplotypes for Evolution 2 -- 23

M	5->7	0.99009	14.93
M	6->7	0.99009	14.93
M	8->7	0.99009	14.93
M	9->7	0.99009	14.93
M	10->7	0.99009	14.93
M	11->7	0.99009	14.93
M	12->7	0.99009	14.93
M	1->8	0.99009	14.93
M	2->8	0.99009	14.93
M	3->8	0.99009	14.93
M	4->8	0.99009	14.93
M	5->8	0.99009	14.93
M	6->8	0.99009	14.93
M	7->8	0.99009	14.93
M	9->8	0.99009	14.93
M	10->8	0.99009	14.93
M	11->8	0.99009	14.93
M	12->8	0.99009	14.93
M	1->9	0.99009	14.93
M	2->9	0.99009	14.93
M	3->9	0.99009	14.93
M	4->9	0.99009	14.93
M	5->9	0.99009	14.93
M	6->9	0.99009	14.93
M	7->9	0.99009	14.93
M	8->9	0.99009	14.93
M	10->9	0.99009	14.93
M	11->9	0.99009	14.93
M	12->9	0.99009	14.93
M	1->10	0.99009	14.93
M	2->10	0.99009	14.93
M	3->10	0.99009	14.93
M	4->10	0.99009	14.93
M	5->10	0.99009	14.93
M	6->10	0.99009	14.93
M	7->10	0.99009	14.93
M	8->10	0.99009	14.93
M	9->10	0.99009	14.93
M	11->10	0.99009	14.93
M	12->10	0.99009	14.93
M	1->11	0.92860	111.36
M	2->11	0.87552	199.95
M	3->11	0.88277	187.91
M	4->11	0.86589	219.54
M	5->11	0.89010	174.70

M	6->11	0.88272	189.25
M	7->11	0.88661	180.23
M	8->11	0.87899	194.14
M	9->11	0.91572	131.90
M	10->11	0.90554	149.27
M	12->11	0.90667	149.70
M	1->12	0.95441	69.94
M	2->12	0.89372	169.38
M	3->12	0.91485	134.64
M	4->12	0.91882	127.13
M	5->12	0.92170	122.68
M	6->12	0.89190	171.44
M	7->12	0.88200	188.48
M	8->12	0.87822	195.07
M	9->12	0.91911	127.01
M	10->12	0.92418	118.72
M	11->12	0.87603	198.86
Ln[Prob(D G)]		0.98435	23.66

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!
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Param 13: Effective sample size of run seems too short!

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