

panpen_CI

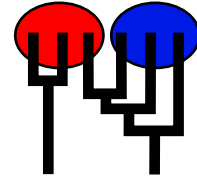
MIGRATION RATE AND POPULATION SIZE ESTIMATION

using the coalescent and maximum likelihood or Bayesian inference

Migrate-n version 3.6.11 [June-18-15]

Program started at Sat Dec 26 06:11:13 2015

Program finished at Mon Dec 28 08:12:42 2015



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)

351035819

Start parameters:

Theta values were generated

from guessed values

Theta = 0.01000

M values were generated

from guessed values

M-matrix:

1000.00 [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
1 Hawa	*	*	0	0	0	0	0	0
2 Maui	*	*	*	0	0	0	0	0
3 Kaua	0	*	*	*	0	0	0	0
4 Neck	0	0	*	*	*	0	0	0
5 Fren	0	0	0	*	*	*	0	0
6 Maro	0	0	0	0	*	*	*	0
7 Lisi	0	0	0	0	0	*	*	*
8 Pear	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	M _{2→1}	<displayed>
16	M _{1→2}	<displayed>
17	M _{3→2}	<displayed>
24	M _{2→3}	<displayed>
25	M _{4→3}	<displayed>
32	M _{3→4}	<displayed>
33	M _{5→4}	<displayed>
40	M _{4→5}	<displayed>
41	M _{6→5}	<displayed>
48	M _{5→6}	<displayed>
49	M _{7→6}	<displayed>
56	M _{6→7}	<displayed>
57	M _{8→7}	<displayed>
64	M _{7→8}	<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	0.000000	0.010000	0.100000	0.010000	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]	50000
Increment (record every x step [b])	100
Number of concurrent chains (replicates) [c]	3

Visited (sampled) parameter values [a*b*c]	15000000
Number of discard trees per chain (burn-in)	20000

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:	../../../../Migrate_datafiles_noghost/panpen_CI_lacchei.mig
Output file:	panpen_CI_lacchei_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 Hawa	1	47
2 Maui	1	69
3 Kaua	1	52
4 Neck	1	5
5 Fren	1	42
6 Maro	1	5
7 Lisi	1	18
8 Pear	1	30
Total of all populations	1	268

Bayesian Analysis: Posterior distribution table

Locus	Parameter	2.5%	25.0%	Mode	75.0%	97.5%	Median	Mean
1	Θ_1	0.00900	0.01740	0.02230	0.03260	0.05620	0.02890	0.03086
1	Θ_2	0.00820	0.01160	0.01370	0.01600	0.02080	0.01450	0.01446
1	Θ_3	0.01600	0.02820	0.04350	0.05240	0.07640	0.04410	0.04524
1	Θ_4	0.00000	0.00000	0.00190	0.01320	0.04160	0.01330	0.01578
1	Θ_5	0.00100	0.01360	0.02250	0.03300	0.06080	0.02670	0.02904
1	Θ_6	0.00000	0.00060	0.00330	0.01180	0.03920	0.01130	0.01429
1	Θ_7	0.00000	0.00140	0.00550	0.01220	0.03580	0.01130	0.01373
1	Θ_8	0.00000	0.00340	0.00910	0.01460	0.03540	0.01270	0.01485
1	$M_{2 \rightarrow 1}$	0.0	0.0	3000.0	10000.0	22000.0	11000.0	4830.0
1	$M_{1 \rightarrow 2}$	0.0	0.0	1000.0	6000.0	16000.0	7000.0	769.3
1	$M_{3 \rightarrow 2}$	0.0	0.0	1000.0	6000.0	16000.0	7000.0	932.7
1	$M_{2 \rightarrow 3}$	0.0	0.0	5000.0	10000.0	22000.0	11000.0	5611.5
1	$M_{4 \rightarrow 3}$	0.0	0.0	1000.0	6000.0	16000.0	7000.0	1780.6
1	$M_{3 \rightarrow 4}$	0.0	0.0	13000.0	52000.0	270000.0	63000.0	140908.5
1	$M_{5 \rightarrow 4}$	0.0	0.0	1000.0	16000.0	204000.0	17000.0	83299.6
1	$M_{4 \rightarrow 5}$	0.0	2000.0	13000.0	22000.0	118000.0	19000.0	27296.6
1	$M_{6 \rightarrow 5}$	0.0	0.0	1000.0	8000.0	24000.0	9000.0	6248.7
1	$M_{5 \rightarrow 6}$	0.0	0.0	11000.0	30000.0	304000.0	143000.0	214310.9
1	$M_{7 \rightarrow 6}$	0.0	0.0	1000.0	24000.0	222000.0	27000.0	65941.8
1	$M_{6 \rightarrow 7}$	0.0	10000.0	31000.0	74000.0	686000.0	69000.0	176572.1
1	$M_{8 \rightarrow 7}$	0.0	0.0	1000.0	20000.0	192000.0	21000.0	63548.1
1	$M_{7 \rightarrow 8}$	0.0	0.0	7000.0	20000.0	126000.0	21000.0	29013.0

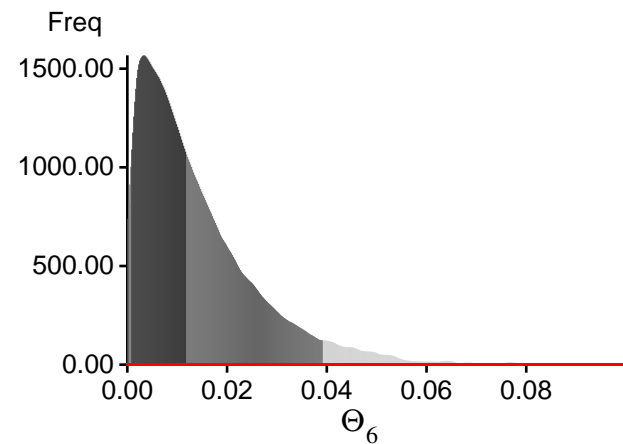
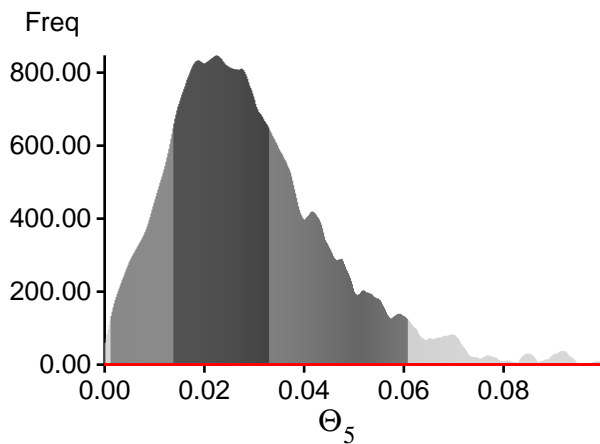
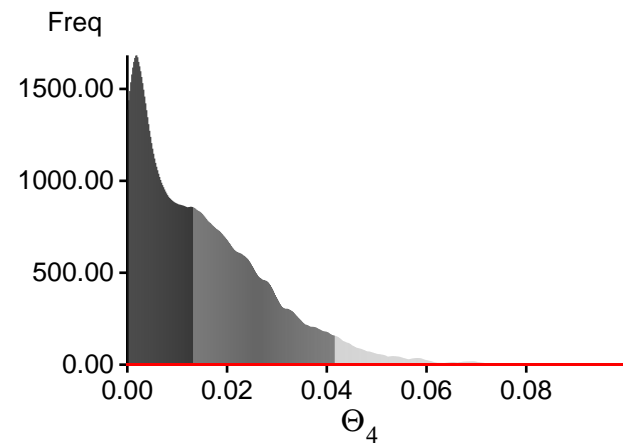
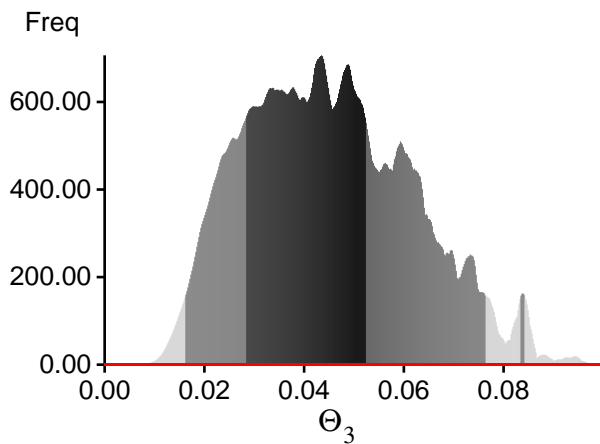
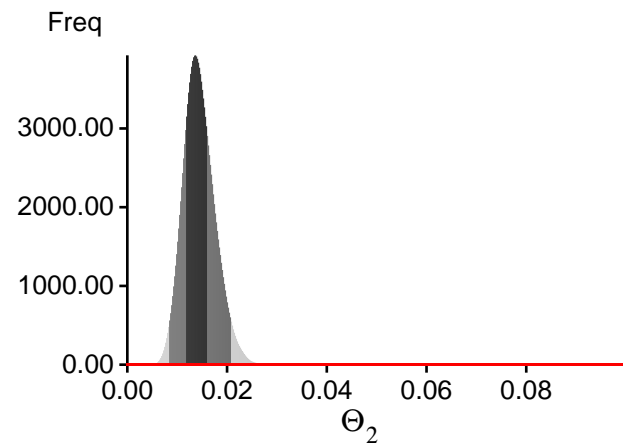
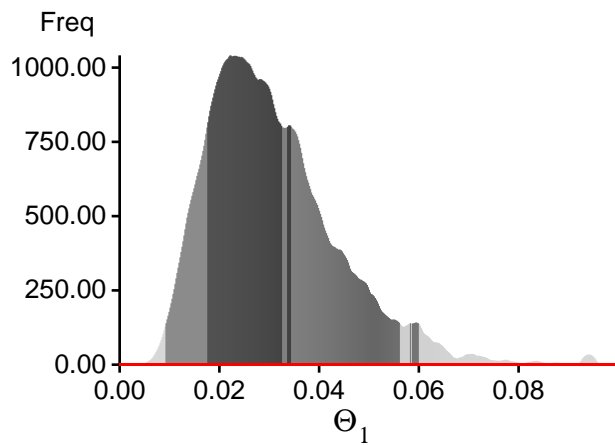
Citation suggestions:

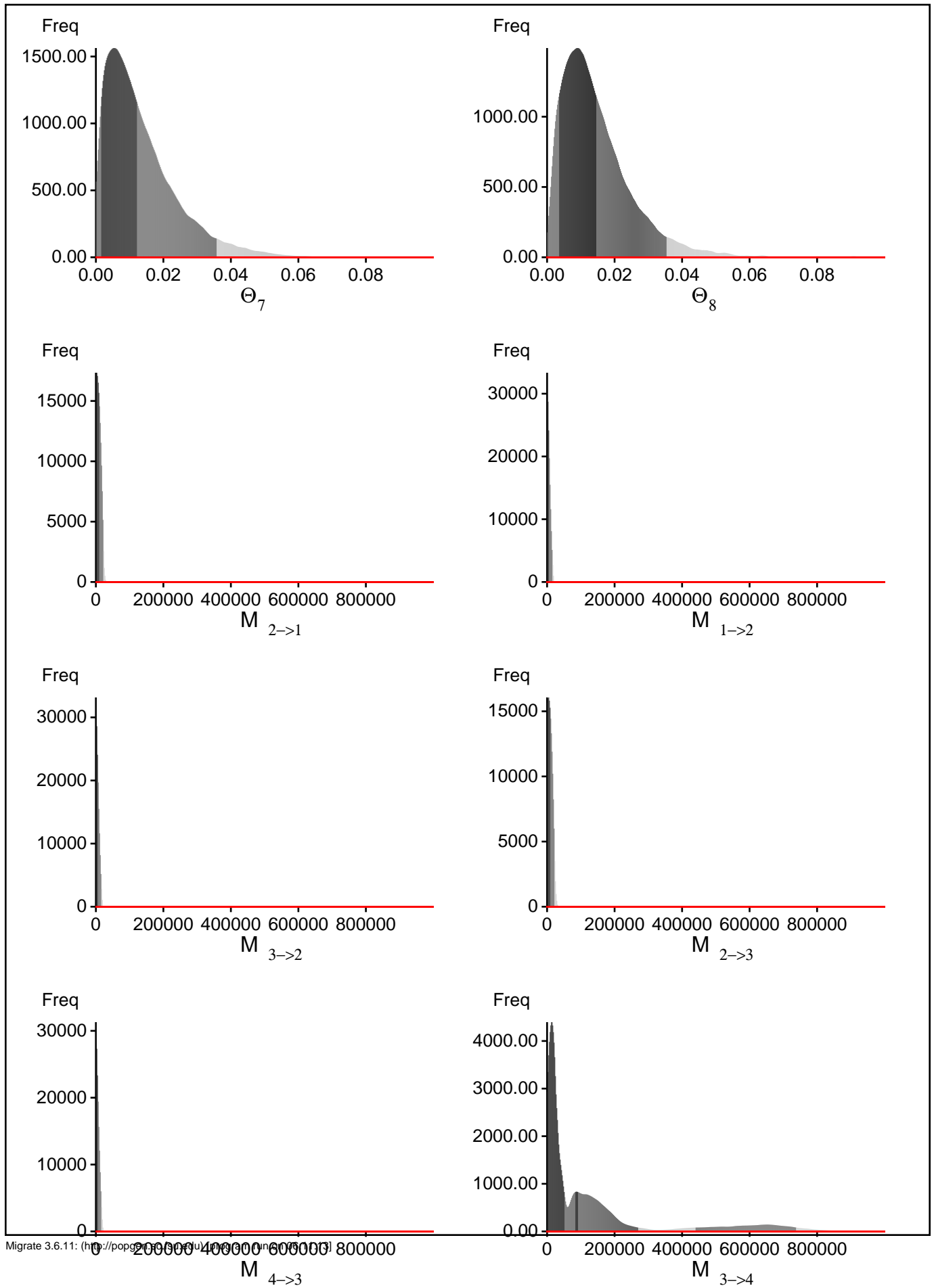
Beerli P., 2006. Comparison of Bayesian and maximum-likelihood inference of population genetic parameters. *Bioinformatics* 22:341-345

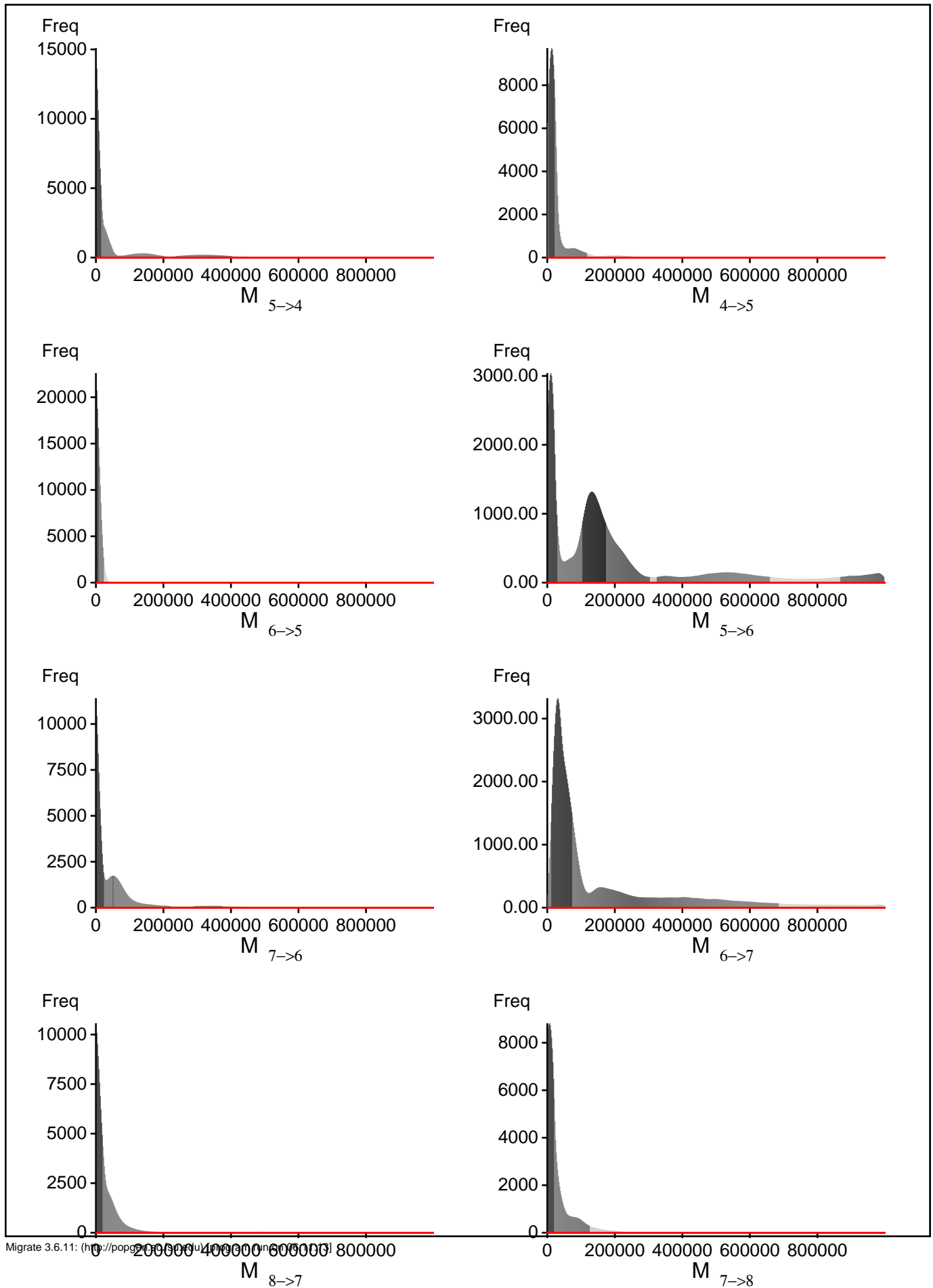
Beerli P., 2007. Estimation of the population scaled mutation rate from microsatellite data, *Genetics*, 177:1967-1968.

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







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	-2205.532355	(1a)
	-1997.304616	(1b)
Harmonic mean	-1509.103602	(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	42617/341230	0.12489
Θ_2	24924/341148	0.07306
Θ_3	15556/341006	0.04562
Θ_4	163136/340637	0.47891
Θ_5	66159/341892	0.19351
Θ_6	220791/340635	0.64817
Θ_7	217487/341254	0.63732
Θ_8	128718/339137	0.37955
M _{2→1}	341101/341101	1.00000
M _{1→2}	340092/340092	1.00000
M _{3→2}	340136/340136	1.00000
M _{2→3}	341494/341494	1.00000
M _{4→3}	339855/339855	1.00000
M _{3→4}	341892/341892	1.00000
M _{5→4}	340605/340605	1.00000
M _{4→5}	340602/340602	1.00000
M _{6→5}	340662/340662	1.00000
M _{5→6}	340945/340945	1.00000
M _{7→6}	341362/341362	1.00000
M _{6→7}	341984/341984	1.00000
M _{8→7}	340582/340582	1.00000
M _{7→8}	341347/341347	1.00000
Genealogies	1247394/7500402	0.16631

MCMC-Autocorrelation and Effective MCMC Sample Size

Parameter	Autocorrelation	Effective Sampe Size
Θ_1	0.92661	5715.70
Θ_2	0.97738	1715.88
Θ_3	0.98068	1465.54
Θ_4	0.61359	42086.82
Θ_5	0.89203	8713.55
Θ_6	0.42387	67108.90
Θ_7	0.43768	61436.25
Θ_8	0.73765	23118.41
$M_{2 \rightarrow 1}$	0.88868	9003.64
$M_{1 \rightarrow 2}$	0.96766	2485.91
$M_{3 \rightarrow 2}$	0.96323	2814.84
$M_{2 \rightarrow 3}$	0.94763	4034.05
$M_{4 \rightarrow 3}$	0.94076	4618.93
$M_{3 \rightarrow 4}$	0.97676	1764.64
$M_{5 \rightarrow 4}$	0.94511	4256.21
$M_{4 \rightarrow 5}$	0.94356	4394.36
$M_{6 \rightarrow 5}$	0.92959	5507.05
$M_{5 \rightarrow 6}$	0.95113	3799.41
$M_{7 \rightarrow 6}$	0.92197	6155.86
$M_{6 \rightarrow 7}$	0.95682	3331.13
$M_{8 \rightarrow 7}$	0.92703	5767.90
$M_{7 \rightarrow 8}$	0.93443	5109.45
$\text{Ln}[\text{Prob}(\mathbf{D} \mathbf{G})]$	0.99089	686.17

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.

No warning was recorded during the run