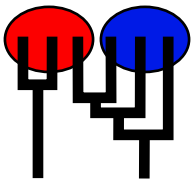
POPULATION SIZE, MIGRATION, DIVERGENCE, ASSIGNMENT, HISTORY
Bayesian inference using the structured coalescent
Migrate-n version 4.2.14 [April-16-2017]
Using Intel AVX (Advanced Vector Extensions)
Program started at Thu Apr 26 16:57:47 2018
Program finished at Thu Apr 26 21:19:57 2018 [Runtime:0000:04:22:10]



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) 1969903762
Start parameters:

Theta values were generated Using a percent value of the prior

M values were generated Using a percent value of the prior

Connection matrix:
m = average (average over a group of Thetas or M,
s = symmetric migration M, S = symmetric 4Nm,
0 = zero, and not estimated,
* = migration free to vary, Thetas are on diagonal
d = row population split off column population, D = split and then migration

Population	1	2	3	4	5
1 Romanshorn_0	*	0	0	0	c
2 Arbon_1	*	*	0	0	0
3 Kreuzlingen_2	0	*	*	*	0
4 Frauenfeld_3	0	0	0	*	*
5 Guendelhart_4	c	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	$M_{1->2}$	<displayed>
7	$M_{2->3}$	<displayed>
8	$M_{4->3}$	<displayed>
9	$M_{5->4}$	<displayed>

Mutation rate among loci: Mutation rate is constant for all loci

Analysis strategy: Bayesian inference
-Population size estimation: Exponential Distribution
-Geneflow estimation: Exponential Distribution

Proposal distributions for parameter

Parameter	Proposal
Theta	Metropolis sampling
M	Metropolis sampling
Divergence	Metropolis sampling
Divergence Spread	Metropolis sampling
Genealogy	Metropolis-Hastings

Prior distribution for parameter

Parameter			Prior	Minimum	Mean	Maximum	Delta	Bins	UpdateFreq
1	Theta	00	Uniform	0.000000	0.010	0.100	0.010	1500	0.05556
2	Theta	11	Uniform	0.000000	0.010	0.100	0.010	1500	0.05556
3	Theta	22	Uniform	0.000000	0.010	0.100	0.010	1500	0.05556
4	Theta	33	Uniform	0.000000	0.010	0.100	0.010	1500	0.05556
5	Theta	44	Uniform	0.000000	0.010	0.100	0.010	1500	0.05556
6	M	30	Uniform	0.000000	500.0	5000.	500.0	1500	0.05556
7	M	12	Uniform	0.000000	500.0	5000.	500.0	1500	0.05556
8	M	31	Uniform	0.000000	500.0	5000.	500.0	1500	0.05556
9	M	23	Uniform	0.000000	500.0	5000.	500.0	1500	0.05556

[-1 -1 means priors were set globally]

Markov chain settings: Long chain

Number of chains	1
Recorded steps [a]	5000
Increment (record every x step [b]	100
Number of concurrent chains (replicates) [c]	1
Visited (sampled) parameter values [a*b*c]	500000
Number of discard trees per chain (burn-in)	500

Multiple Markov chains:

Static heating scheme		4 chains with	temperatures	
	1000000.00	3.00	1.50	1.00
		Swapping interval is 1		

Print options:

Data file:	infile1
Haplotyping is turned on:	NO
Output file:	outfile_d
Posterior distribution raw histogram file:	bayesfile
Raw data from the MCMC run:	bayesallfile.gz
Print data:	No
Print genealogies [only some for some data type]:	None
Histogram of the frequency of migration events	mighistfile_d

Data summary

Data file: infile1
Datatype: Sequence data
Number of loci: 2

Mutationmodel:

Locus	Sublocus	Mutationmodel	Mutationmodel parameters
1	1	Felsenstein 84	[Bf:0.26 0.24 0.26 0.24, t/t ratio=2.000]
2	1	Felsenstein 84	[Bf:0.25 0.26 0.25 0.25, t/t ratio=2.000]

Sites per locus

Locus	Sites
1	1000
2	1000

Site rate variation and probabilities:

Locus	Sublocus	Region type	Rate of change	Probability	Patch size
1	1	1	1.000	1.000	1.000
2	1	1	1.000	1.000	1.000

Population	Locus	Gene copies
1 Romanshorn_0	1	5
	2	5
2 Arbon_1	1	5
	2	5
3 Kreuzlingen_2	1	5
	2	5
4 Frauenfeld_3	1	5
	2	5
5 Guendelhart_4	1	5
	2	5
Total of all populations	1	25
	2	25

Bayesian Analysis: Posterior distribution table

Locus	Parameter	2.5%	25.0%	Mode	75.0%	97.5%	Median	Mean
1	Θ_1	0.00000	0.00000	0.00003	0.09993	0.09993	0.00003	0.09181
1	Θ_2	0.02633	0.04247	0.04477	0.04980	0.05160	0.04123	0.08456
1	Θ_3	0.00287	0.02873	0.03117	0.03353	0.05013	0.02850	0.05388
1	Θ_4	0.00653	0.03380	0.03710	0.04427	0.05013	0.02883	0.05466
1	Θ_5	0.00000	0.00000	0.00003	0.09993	0.09993	0.00003	0.09226
1	$M_{1->2}$	0.0	0.0	15.0	63.3	166.7	65.0	36.9
1	$M_{2->3}$	890.0	1900.0	2391.7	2450.0	2566.7	1931.7	3353.5
1	$M_{4->3}$	0.0	0.0	1.7	553.3	2066.7	555.0	1042.7
1	$M_{5->4}$	580.0	1653.3	1758.3	2130.0	2523.3	1635.0	2516.4
2	Θ_1	0.00000	0.00000	0.00003	0.09993	0.09993	0.00003	0.09180
2	Θ_2	0.00927	0.02967	0.03410	0.03820	0.05053	0.03277	0.05897
2	Θ_3	0.00367	0.02827	0.03097	0.03367	0.04920	0.02643	0.05042
2	Θ_4	0.00807	0.02713	0.03677	0.03920	0.05047	0.03090	0.05670
2	Θ_5	0.00000	0.00000	0.00003	0.09993	0.09993	0.00003	0.09192
2	$M_{1->2}$	100.0	290.0	371.7	470.0	2416.7	741.7	1524.8
2	$M_{2->3}$	0.0	0.0	1.7	120.0	176.7	1218.3	2655.4
2	$M_{4->3}$	0.0	0.0	1.7	560.0	1980.0	838.3	1751.6
2	$M_{5->4}$	0.0	20.0	148.3	426.7	2080.0	865.0	1735.1
All	Θ_1	0.00000	0.00000	0.00003	0.09993	0.09993	0.00003	0.09508
All	Θ_2	0.00860	0.02647	0.03363	0.04313	0.05020	0.03150	0.07334
All	Θ_3	0.00447	0.02840	0.03103	0.03453	0.04920	0.02737	0.05220
All	Θ_4	0.00753	0.04360	0.04777	0.04913	0.05067	0.03097	0.05726
All	Θ_5	0.00000	0.00000	0.00003	0.09993	0.09993	0.00003	0.09522
All	$M_{1->2}$	0.0	0.0	11.7	170.0	1806.7	221.7	800.1
All	$M_{2->3}$	0.0	0.0	1.7	173.3	1583.3	1281.7	3057.2
All	$M_{4->3}$	0.0	0.0	1.7	343.3	1786.7	345.0	931.0
All	$M_{5->4}$	3.3	20.0	141.7	300.0	530.0	1178.3	1916.3

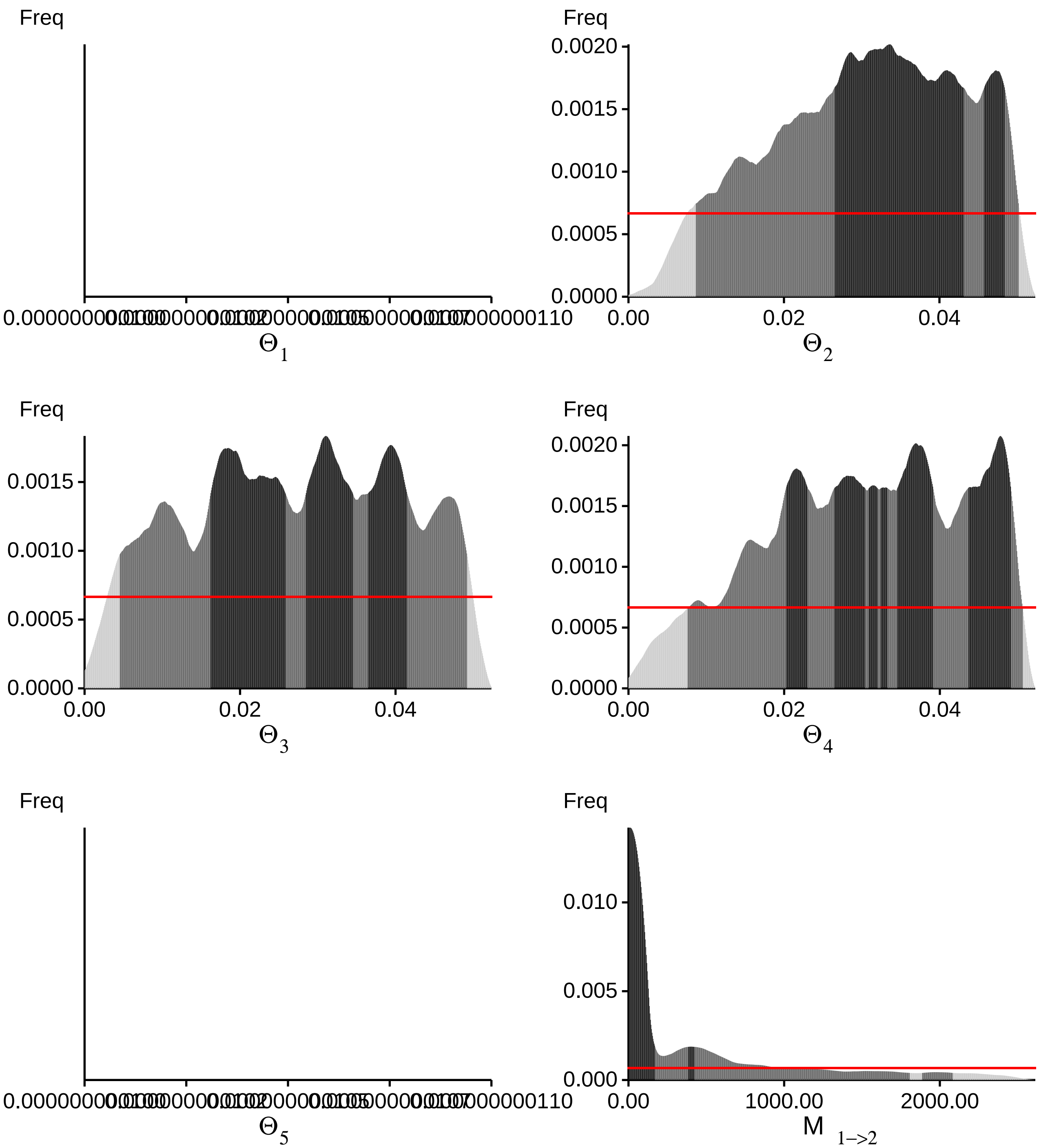
Citation suggestions:

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

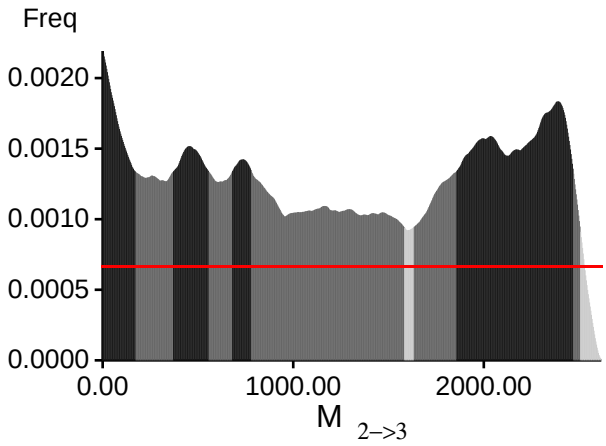
Beerli P., 2007. Estimation of the population scaled mutation rate from microsatellite data, Genetics, 177:1967-1968.

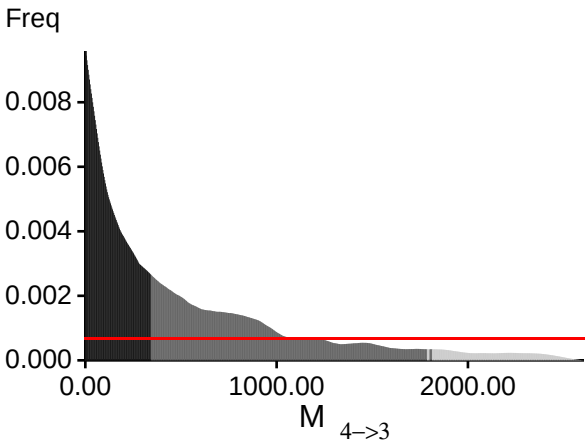
Beerli P., 2009. How to use MIGRATE or why are Markov chain Monte Carlo programs difficult to use? In Population Genetics for Animal Conservation, G. Bertorelle, M. W. Bruford, H. C. Hauffe, A. Rizzoli, and C. Vernesi, eds., vol. 17 of Conservation Biology, Cambridge University Press, Cambridge UK, pp.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

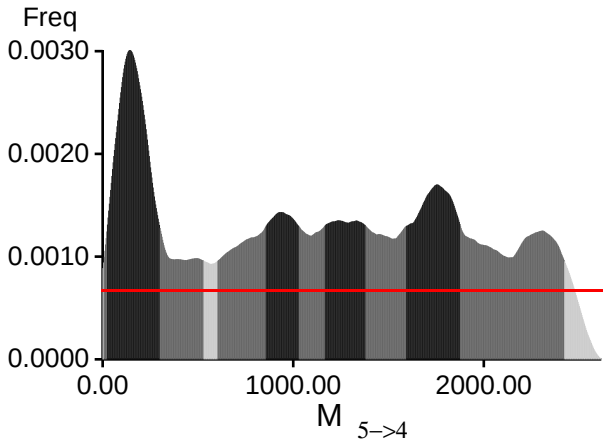
Bayesian Analysis: Posterior distribution over all loci



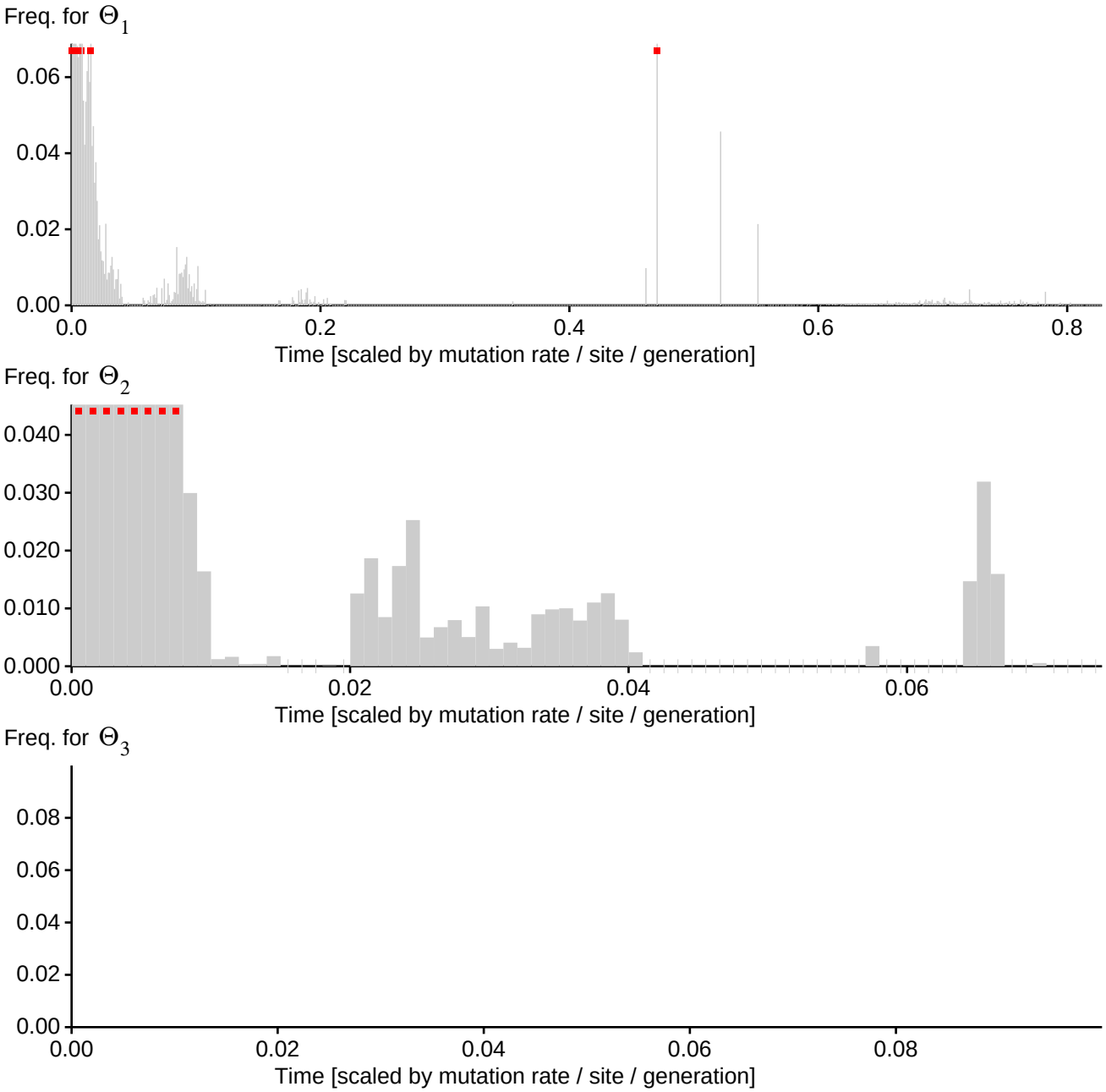
nan

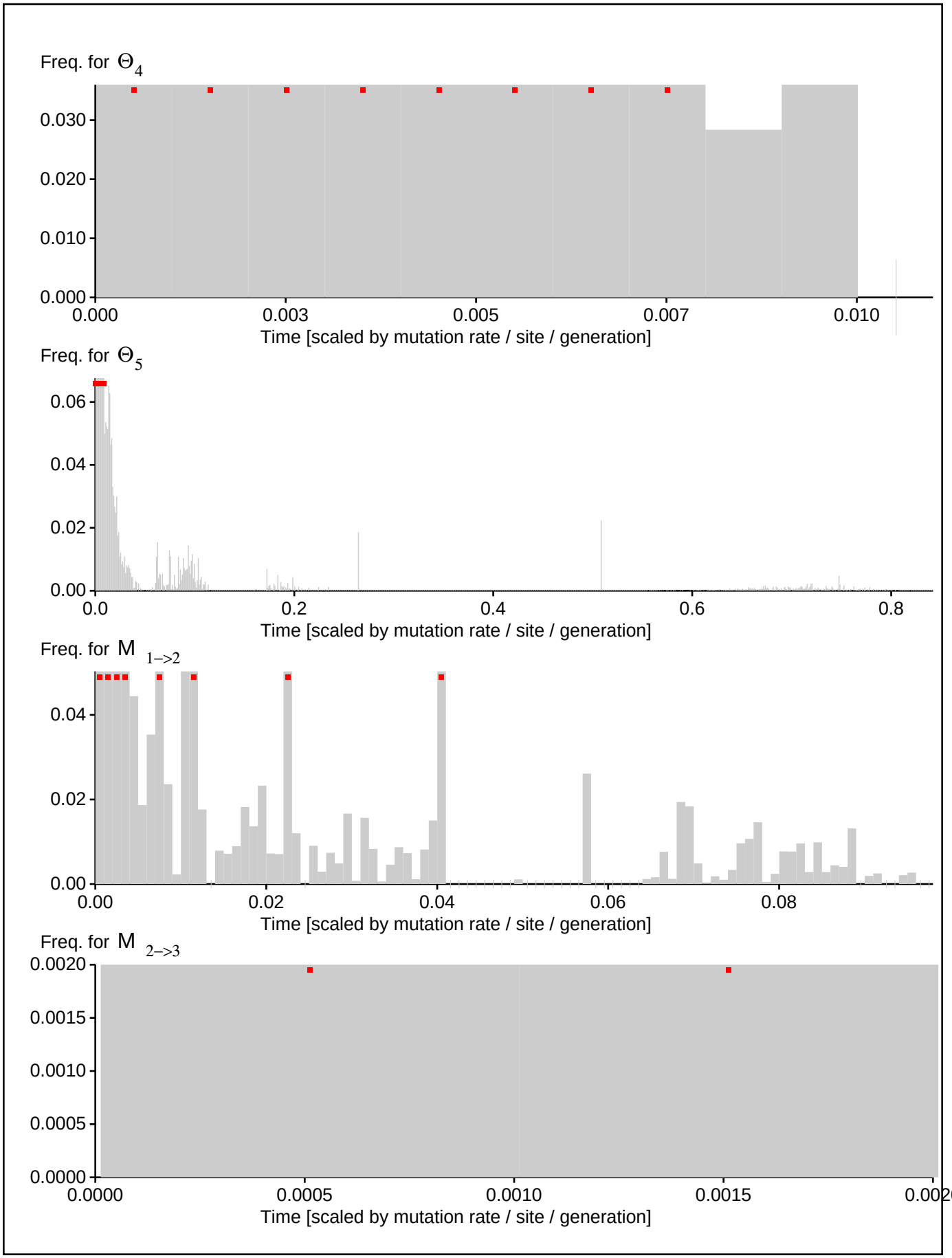

Freq
0.0020
0.0015
0.0010
0.0005
0.0000
0.00
1000.00
2000.00
M 2–>3

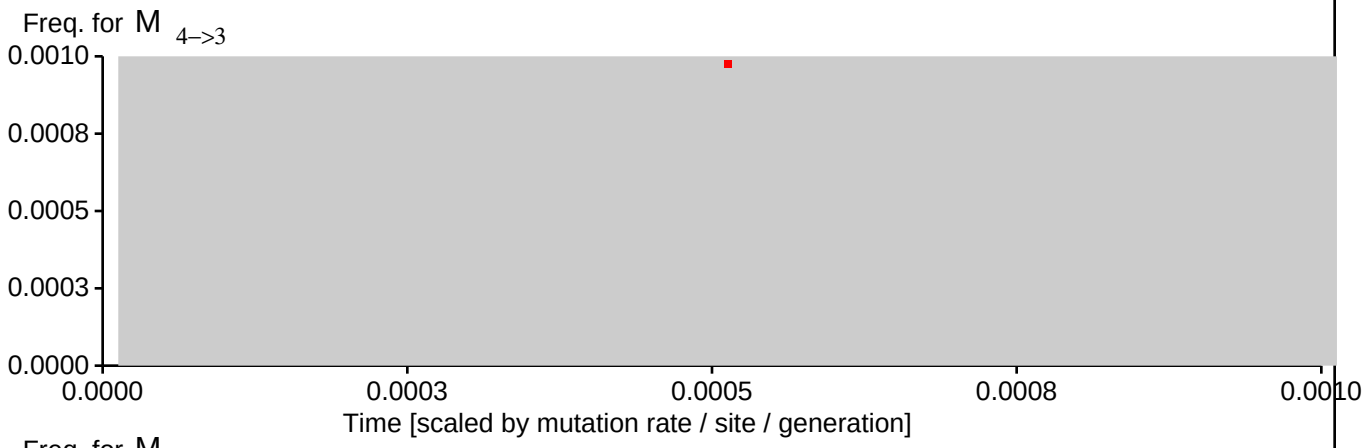

Freq
0.008
0.006
0.004
0.002
0.000
0.00
1000.00
2000.00
M 4–>3

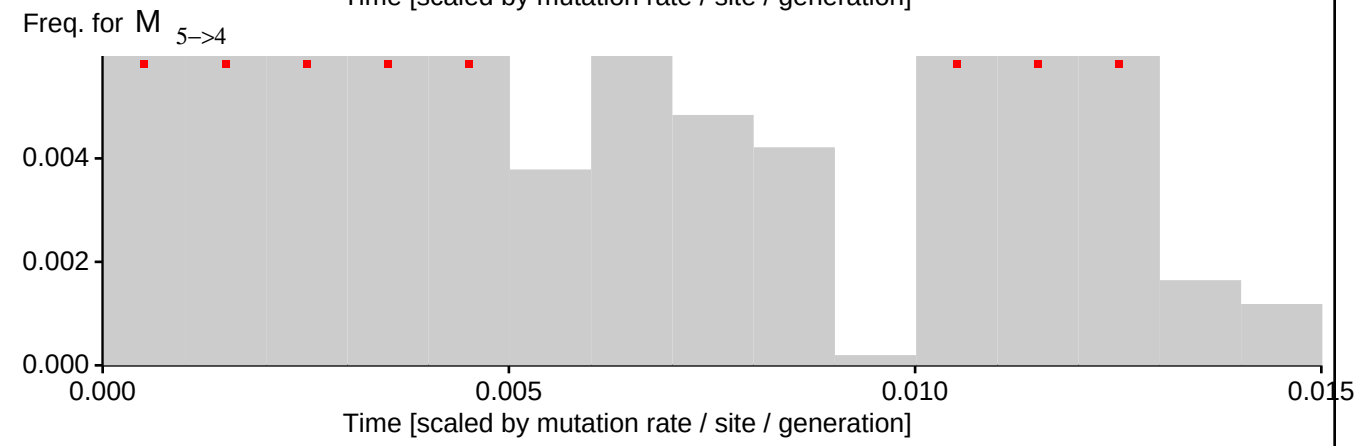

Freq
0.0030
0.0020
0.0010
0.0000
0.00
1000.00
2000.00
M 5–>4

Summary of events through time over all loci




Freq. for Θ4
0.030
0.020
0.010
0.000
0.000
0.003
0.005
0.007
0.010
Time [scaled by mutation rate / site / generation]
Freq. for Θ5
0.06
0.04
0.02
0.00
0.0
0.2
0.4
0.6
0.8
Time [scaled by mutation rate / site / generation]
Freq. for M 1–>2
0.04
0.02
0.00
0.00
0.02
0.04
0.06
0.08
Time [scaled by mutation rate / site / generation]
Freq. for M 2–>3
0.0020
0.0015
0.0010
0.0005
0.0000
0.0000
0.0005
0.0010
0.0015
0.0020
Time [scaled by mutation rate / site / generation]


Freq. for M 4–>3
0.0010
0.0008
0.0005
0.0003
0.0000
0.0000
0.0003
0.0005
0.0008
0.0010
Time [scaled by mutation rate / site / generation]


Freq. for M 5–>4
0.004
0.002
0.000
0.000
0.005
0.010
0.015
Time [scaled by mutation rate / site / generation]

Summary statistics of events through time

Locus 1

Population		Time			Frequency
From	To	Average	Median	Std	
1	1	0.101400	0.018500	0.192010	0.001604
2	2	0.016981	0.006500	0.021188	0.000956
5	5	0.078252	0.016500	0.175236	0.001695
1	2	0.028643	0.019500	0.025890	0.000777
2	3	0.000526	0.000000	0.000194	0.000846
4	3	0.000500	0.000000	0.000000	0.000040
5	4	0.000673	0.000000	0.000619	0.000927

Locus 2

Population		Time			Frequency
From	To	Average	Median	Std	
1	1	0.082374	0.009500	0.182736	0.002044
2	2	0.001546	0.001500	0.000903	0.000061
3	3	0.000860	0.000000	0.000480	0.000021
4	4	0.004413	0.003500	0.002441	0.000069
5	5	0.055772	0.008500	0.145058	0.001980
1	2	0.001453	0.000000	0.001886	0.001402
2	3	0.000571	0.000000	0.000361	0.000593
4	3	0.000608	0.000000	0.000325	0.000256
5	4	0.001518	0.000000	0.002204	0.001057

All loci

Population		Time			Frequency
From	To	Average	Median	Std	
1	1	0.091887	0.028000	0.187430	0.001824
2	2	0.009264	0.008000	0.014996	0.000508
3	3	0.000430	0.001500	0.000339	0.000011
4	4	0.002207	0.005000	0.001726	0.000034
5	5	0.067012	0.025000	0.160856	0.001837
1	2	0.015048	0.019500	0.018356	0.001089
2	3	0.000548	0.000000	0.000290	0.000719
4	3	0.000554	0.000000	0.000230	0.000148

5	4	0.001096	0.000000	0.001619	0.000992

Time and probability of location of most recent common ancestor

Locus 1

Population	Time			Frequency
	Average	Median	Std	
1	0.722224	0.718500	0.035442	0.462492
5	0.722671	0.719500	0.034449	0.537508

Locus 2

Population	Time			Frequency
	Average	Median	Std	
1	0.678552	0.671500	0.049131	0.490298
5	0.677346	0.671500	0.046806	0.509702

All loci

Population	Time			Frequency
	Average	Median	Std	
1	0.700388	1.390000	0.042837	0.476395
5	0.700009	1.391000	0.041094	0.523605

Legend for Skyline and Event plots

Skyline plots:

Skyline plots visualize the changes of population sizes and migration rates through time (today is on the left side and time is measured into the past. The time scale is in units of expected mutations per generation. To calculate the absolute time scale you must supply an mutation rate per year and the duration of a generation in years in the data option. You can calculate the absolute time by multiplying the scale by generation time times mutation rate per year (per site for DNA; per locus for all other datatypes).

With estimated mutation rate only the combined rate modifier is plotted. [this will change to mutation rate plot].

The gray bars cover 1.96 * approximate standard error (std in file skylinefile/number of observations in the bin) up and down from the expected value. The bar with different shades of gray on top of each plot indicates the number of values that were used to to calculate the expected value, white means there were very few and black means that there were many thousands of samples per bin.

On some plots one can see red squares below the grayscale bar, these suggest that either the upper quantile and/or the main value was higher than the visible part of the axis.

Event histograms:

All accepted events (migration events, coalescent events) are recorded and their frequency are shown as histograms over time with recent time on the left side. The frequency plots of populations with constant size and constant immigration rates show histograms that are similar to exponential distribution, if the populations come from a divergence model without migration then the frequency of migration events can show a peak in the past.

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

Use this value for Bayes factor calculations:
BF = Exp[ln(Prob(D | thisModel) - ln(Prob(D | otherModel)
or as LBF = 2 (ln(Prob(D | thisModel) - ln(Prob(D | otherModel))
shows the support for thisModel]

Locus	Raw thermodynamic score(1a)	Bezier approximation score(1b)	Harmonic mean(2)
1	-15669.21	-9372.59	-8211.61
2	-15637.42	-8728.07	-7433.97
All	-31329.32	-18123.36	-15668.27

(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
[Scaling factor = -22.698060]
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	29155/55488	0.52543
Θ_2	47115/55756	0.84502
Θ_3	52994/55507	0.95473
Θ_4	51399/55580	0.92478
Θ_5	28993/55712	0.52041
$M_{1->2}$	24833/55785	0.44516
$M_{2->3}$	43437/55616	0.78102
$M_{4->3}$	40286/55311	0.72835
$M_{5->4}$	36048/55522	0.64926
Genealogies	10912/499723	0.02184

MCMC-Autocorrelation and Effective MCMC Sample Size

Parameter	Autocorrelation	Effective Sampe Size
Θ_1	0.24065	6130.09
Θ_2	0.43759	4096.54
Θ_3	0.51676	3636.68
Θ_4	0.52708	3514.71
Θ_5	0.23432	6202.29
$M_{1->2}$	0.91512	454.57
$M_{2->3}$	0.70672	1723.69
$M_{4->3}$	0.71689	1672.83
$M_{5->4}$	0.81041	1047.45
Genealogies	0.97990	102.32

Potential Problems

This section reports potential problems with your run, but such reporting is often not very accurate. Whith many parameters in a multilocus analysi s, it is very common that some parameters for some loci will not be very informative, triggering suggestions (for example to increase the prior ran ge) that are not sensible. This suggestion tool will improve with time, therefore do not blindly follow its suggestions. If some parameters are fla gged, inspect the tables carefully and judge wether an action is required. For example, if you run a Bayesian inference with sequence data, for mac roscopic 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 rou tes 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