POPULATION SIZE, MIGRATION, DIVERGENCE, ASSIGNMENT, HISTORY
Bayesian inference using the structured coalescent
Migrate-n version 4.4.4(git:v4-series-30-gb190f74) [June-1-2019]
Compiled for a SYMMETRIC multiprocessors (Grandcentral)
Program started at Mon Nov 18 14:22:56 2019
Program finished at Mon Nov 18 14:32:37 2019 [Runtime:0000:00:09:41]

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)	1662225684
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
2 Arbon_1	*	*	*	0	0
3 Kreuzlingen_2	0	*	*	*	0
4 Frauenfeld_3	0	0	*	*	*
5 Guendelhart_4	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	$M_{2\to1}$	<displayed>
7	$M_{1\to2}$	<displayed>
8	$M_{3\to2}$	<displayed>
9	$M_{2\to3}$	<displayed>
10	$M_{4\to3}$	<displayed>
11	$M_{3\to4}$	<displayed>
12	$M_{5\to4}$	<displayed>
13	$M_{4\to5}$	<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	0.03846
2	Theta	11	Uniform	0.000000	0.010	0.100	0.010	1500	0.03846
3	Theta	22	Uniform	0.000000	0.010	0.100	0.010	1500	0.03846
4	Theta	33	Uniform	0.000000	0.010	0.100	0.010	1500	0.03846
5	Theta	44	Uniform	0.000000	0.010	0.100	0.010	1500	0.03846
6	M	10	Uniform	0.000000	100.0	1000.	100.0	1500	0.03846
7	M	30	Uniform	0.000000	100.0	1000.	100.0	1500	0.03846
8	M	03	Uniform	0.000000	100.0	1000.	100.0	1500	0.03846
9	M	12	Uniform	0.000000	100.0	1000.	100.0	1500	0.03846
10	M	31	Uniform	0.000000	100.0	1000.	100.0	1500	0.03846
11	M	32	Uniform	0.000000	100.0	1000.	100.0	1500	0.03846
12	M	23	Uniform	0.000000	100.0	1000.	100.0	1500	0.03846
13	M	34	Uniform	0.000000	100.0	1000.	100.0	1500	0.03846

[* * 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_c
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

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	0.09753	0.09887	0.09903	0.09907	0.09913	0.06903	0.06660
1	Θ_2	0.04300	0.05147	0.05183	0.05187	0.05827	0.05650	0.05788
1	Θ_3	0.05300	0.05307	0.05343	0.05347	0.05387	0.06317	0.06235
1	Θ_4	0.08287	0.08507	0.08517	0.08520	0.08713	0.07123	0.06957
1	Θ_5	0.03120	0.03127	0.03143	0.03207	0.03507	0.04297	0.04647
1	$M_{2->1}$	58.0	83.3	91.0	95.3	225.3	141.7	154.9
1	$M_{1->2}$	0.0	80.7	83.0	86.7	121.3	66.3	64.6
1	$M_{3->2}$	50.0	91.3	92.3	94.0	155.3	108.3	113.3
1	$M_{2->3}$	64.7	134.0	137.0	137.3	288.0	171.0	192.0
1	$M_{4->3}$	0.0	0.0	1.0	5.3	24.0	5.7	8.4
1	$M_{3->4}$	0.0	0.0	5.0	16.7	25.3	9.0	10.2
1	$M_{5->4}$	0.0	0.0	5.0	19.3	46.0	13.0	22.6
1	$M_{4->5}$	0.0	3.3	21.0	57.3	86.7	280.3	302.8
2	Θ_1	0.04173	0.04173	0.04183	0.04193	0.04267	0.04737	0.05048
2	Θ_2	0.02647	0.02733	0.02743	0.02747	0.02893	0.05237	0.05356
2	Θ_3	0.01533	0.02140	0.02190	0.02200	0.02467	0.02990	0.03379
2	Θ_4	0.02827	0.02873	0.02897	0.02907	0.03200	0.05010	0.05202
2	Θ_5	0.00653	0.01333	0.01350	0.01360	0.03800	0.02950	0.03526
2	$M_{2->1}$	40.0	60.0	63.0	64.0	155.3	101.0	108.7
2	$M_{1->2}$	69.3	88.7	89.7	90.7	286.7	187.0	196.4
2	$M_{3->2}$	50.7	86.0	89.0	99.3	258.7	158.3	184.1
2	$M_{2->3}$	18.0	34.0	35.7	36.7	110.7	59.0	64.1
2	$M_{4->3}$	0.0	0.0	1.0	2.7	139.3	74.3	76.5
2	$M_{3->4}$	77.3	124.7	125.7	128.0	240.7	159.7	162.5
2	$M_{5->4}$	36.0	100.7	106.3	112.7	211.3	169.7	197.8
2	$M_{4->5}$	103.3	138.7	143.0	147.3	270.0	222.3	270.1
All	Θ_1	0.02267	0.03800	0.04743	0.04833	0.04993	0.03890	0.03760
All	Θ_2	0.02360	0.03933	0.04063	0.04380	0.05007	0.03957	0.03803
All	Θ_3	0.01787	0.02433	0.03043	0.03927	0.04893	0.03290	0.03293
All	Θ_4	0.02393	0.04053	0.04783	0.04887	0.05060	0.04117	0.03943
All	Θ_5	0.00967	0.01727	0.02077	0.02687	0.04560	0.02583	0.02662
All	$M_{2->1}$	56.0	72.0	89.7	122.0	152.7	106.3	111.4
All	$M_{1->2}$	23.3	74.7	89.7	104.7	172.0	98.3	121.4
All	$M_{3->2}$	46.7	75.3	97.0	122.0	196.0	109.0	118.1

Locus	Parameter	2.5%	25.0%	Mode	75.0%	97.5%	Median	Mean
All	$M_{2\text{->}3}$	23.3	52.7	69.0	100.7	174.0	88.3	108.1
All	$M_{4\text{->}3}$	0.0	0.0	0.3	9.3	32.0	9.7	12.1
All	$M_{3\text{->}4}$	0.0	8.0	23.7	38.0	48.0	137.7	130.3
All	$M_{5\text{->}4}$	0.0	23.3	61.7	83.3	115.3	73.0	132.9
All	$M_{4\text{->}5}$	15.3	22.7	45.7	81.3	427.3	201.0	207.3

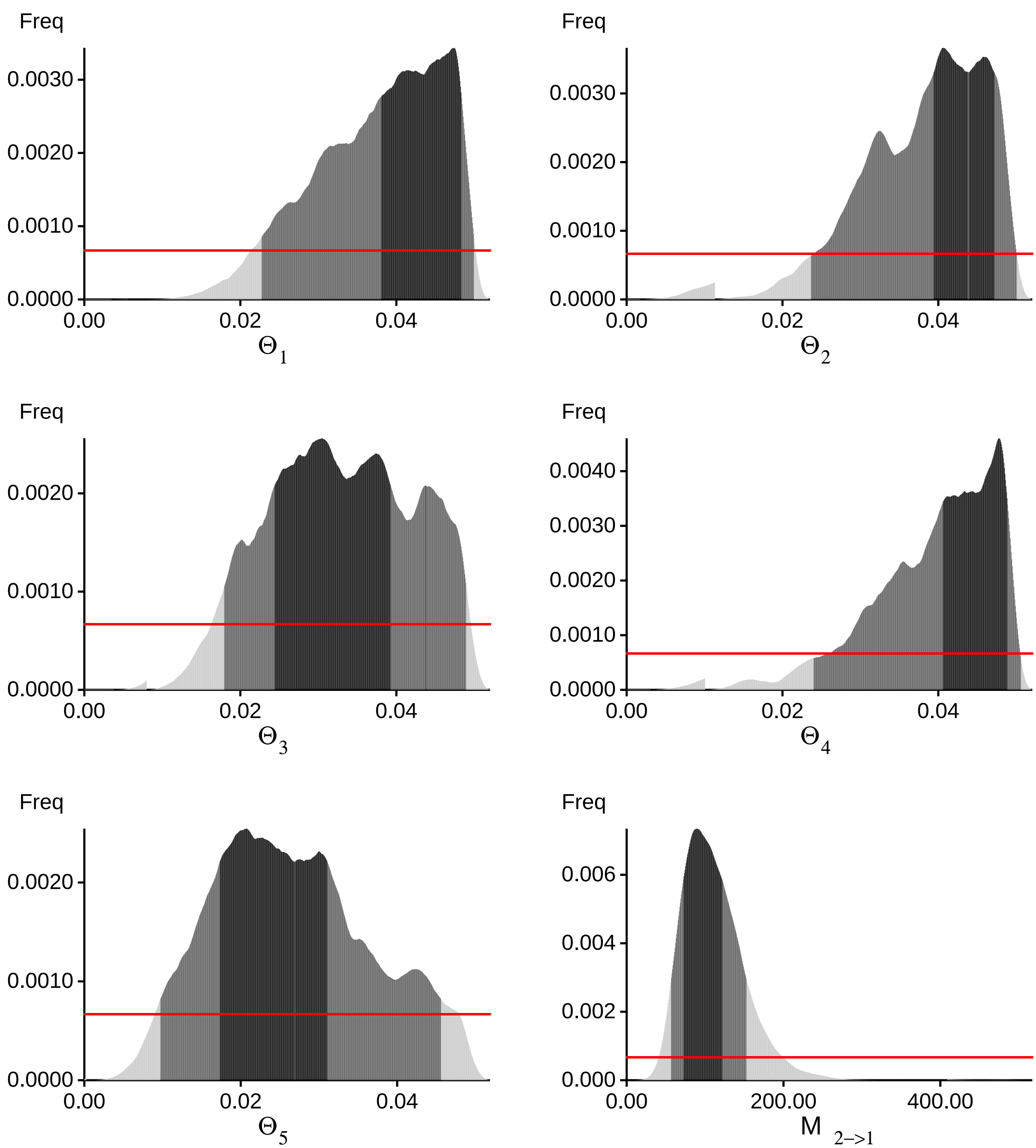
Citation suggestions:

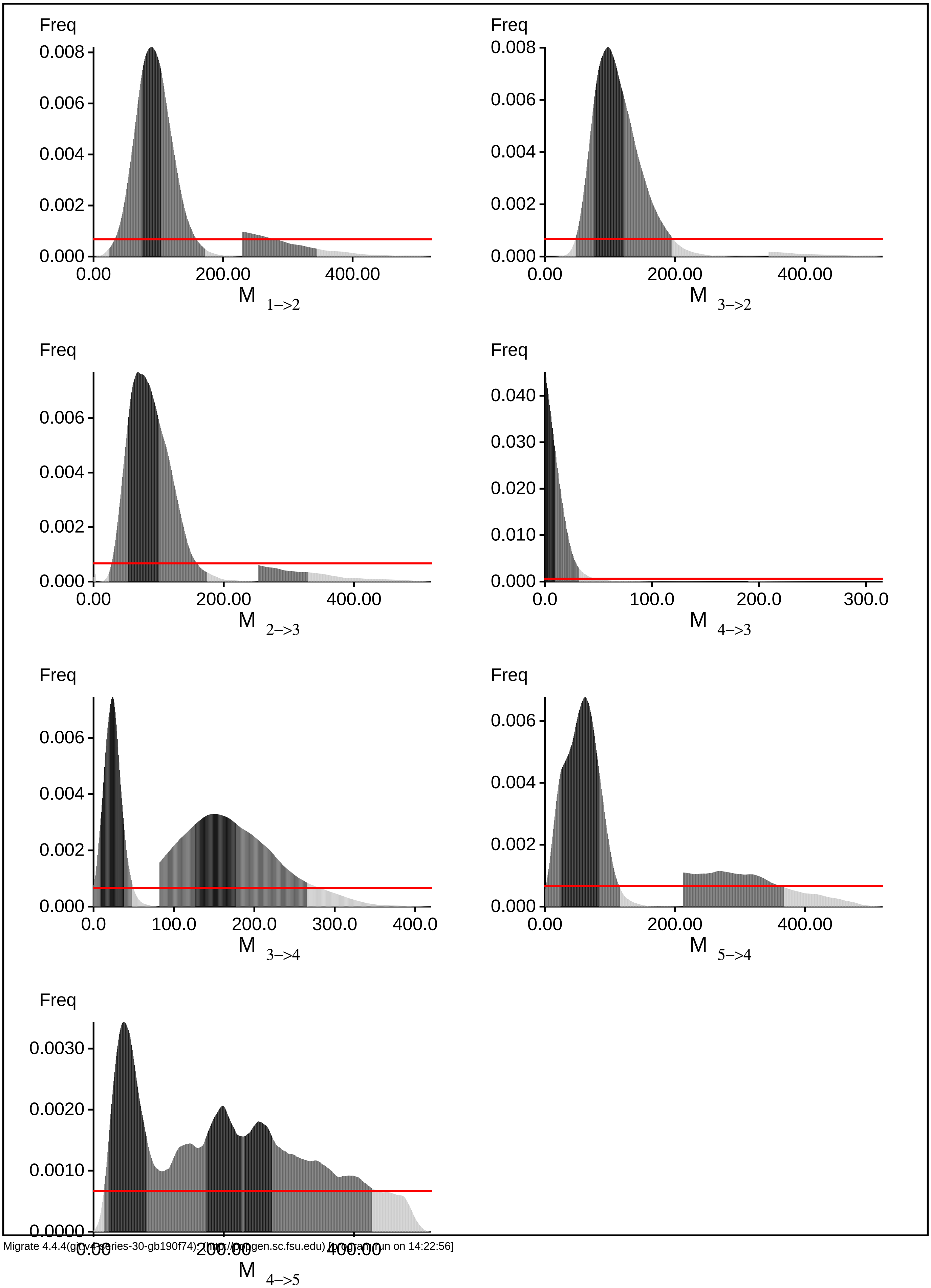
Beerli P., 2006. Comparison of Bayesian and maximum-likelihood inference of population genetic parameters. Bioinformatics 22:341-345

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




Freq
0.008
0.006
0.004
0.002
0.000
0.00
200.00
400.00
M 1->2
Freq
0.008
0.006
0.004
0.002
0.000
0.00
200.00
400.00
M 3->2
Freq
0.006
0.004
0.002
0.000
0.00
200.00
400.00
M 2->3
Freq
0.040
0.030
0.020
0.010
0.000
0.0
100.0
200.0
300.0
M 4->3
Freq
0.006
0.004
0.002
0.000
0.0
100.0
200.0
300.0
400.0
M 3->4
Freq
0.006
0.004
0.002
0.000
0.00
200.00
400.00
M 5->4
Freq
0.0030
0.0020
0.0010
0.0000
0.00
200.00
400.00
M 4->5

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	-14674.94	-10281.08	-9162.43
2	-16177.28	-10610.54	-8518.03
All	-30891.41	-20930.81	-17719.66

(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 = -39.196628]
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	33340/38910	0.85685
Θ_2	33787/38469	0.87829
Θ_3	29203/38246	0.76356
Θ_4	33881/38613	0.87745
Θ_5	31009/38410	0.80732
$M_{2\rightarrow 1}$	15453/38242	0.40408
$M_{1\rightarrow 2}$	23527/38588	0.60970
$M_{3\rightarrow 2}$	21183/38436	0.55112
$M_{2\rightarrow 3}$	14424/38390	0.37572
$M_{4\rightarrow 3}$	19190/38461	0.49895
$M_{3\rightarrow 4}$	24629/38101	0.64641
$M_{5\rightarrow 4}$	18615/38601	0.48224
$M_{4\rightarrow 5}$	22731/38480	0.59072
Genealogies	16826/500053	0.03365

MCMC-Autocorrelation and Effective MCMC Sample Size

Parameter	Autocorrelation	Effective Sampe Size
Θ_1	0.76834	1344.70
Θ_2	0.78294	1236.49
Θ_3	0.81793	1018.70
Θ_4	0.78250	1233.53
Θ_5	0.81420	1051.19
$M_{2\rightarrow1}$	0.74371	1470.50
$M_{1\rightarrow2}$	0.87880	653.96
$M_{3\rightarrow2}$	0.82695	975.23
$M_{2\rightarrow3}$	0.77906	1292.38
$M_{4\rightarrow3}$	0.74768	1476.20
$M_{3\rightarrow4}$	0.64324	2590.47
$M_{5\rightarrow4}$	0.90454	504.11
$M_{4\rightarrow5}$	0.91819	429.67
Genealogies	0.95240	243.80

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