Current protocols example dataset

POPULATION SIZE, MIGRATION, DIVERGENCE, ASSIGNMENT, HISTORY
Bayesian inference using the structured coalescent
Migrate-n version 4.4.3(git:) [March-21-2019]
  Using Intel AVX (Advanced Vector Extensions)
  Compiled for PARALLEL computer architectures
  One master and 8 compute nodes are available.
  Compiled for a SYMMETRIC multiprocessors (Grandcentral)
Program started at   Sat Jun 1 23:31:36 2019
Program finished at   Sun Jun 2 00:01:40 2019 [Runtime:0000:00:30:04]

Options

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)   3913099567
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
1 Arbon_1	*	*	*
2 Berg_2	*	*	*
3 Chur_3	*	*	*

 Order of parameters:

1	Θ_1	<displayed>
2	Θ_2	<displayed>
3	Θ_3	<displayed>
4	$M_{2\to1}$	<displayed>
5	$M_{3\to1}$	<displayed>
6	$M_{1\to2}$	<displayed>
7	$M_{3\to2}$	<displayed>
8	$M_{1\to3}$	<displayed>
9	$M_{2\to3}$	<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	**	Uniform	0.000000	0.050	0.100	0.010	1500	0.05556
2	Theta	**	Uniform	0.000000	0.050	0.100	0.010	1500	0.05556
3	Theta	**	Uniform	0.000000	0.050	0.100	0.010	1500	0.05556
4	M	**	Uniform	0.000000	2500.	5000.	500.0	1500	0.05556
5	M	**	Uniform	0.000000	2500.	5000.	500.0	1500	0.05556
6	M	**	Uniform	0.000000	2500.	5000.	500.0	1500	0.05556
7	M	**	Uniform	0.000000	2500.	5000.	500.0	1500	0.05556
8	M	**	Uniform	0.000000	2500.	5000.	500.0	1500	0.05556
9	M	**	Uniform	0.000000	2500.	5000.	500.0	1500	0.05556

[* * 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)   5000

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: infile
   Haplotyping is turned on: NO
   Output file: outfile_short
   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: infile
Datatype: Haplotype data
Number of loci: 10

Mutationmodel:

Locus	Sublocus	Mutationmodel	Mutationmodel parameters
1	1	Jukes-Cantor	[Basefreq: =0.25]
2	1	Jukes-Cantor	[Basefreq: =0.25]
3	1	Jukes-Cantor	[Basefreq: =0.25]
4	1	Jukes-Cantor	[Basefreq: =0.25]
5	1	Jukes-Cantor	[Basefreq: =0.25]
6	1	Jukes-Cantor	[Basefreq: =0.25]
7	1	Jukes-Cantor	[Basefreq: =0.25]
8	1	Jukes-Cantor	[Basefreq: =0.25]
9	1	Jukes-Cantor	[Basefreq: =0.25]
10	1	Jukes-Cantor	[Basefreq: =0.25]

Sites per locus

Locus	Sites
1	1000
2	1000
3	1000
4	1000
5	1000
6	1000
7	1000
8	1000
9	1000
10	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
3	1	1	1.000	1.000	1.000
4	1	1	1.000	1.000	1.000
5	1	1	1.000	1.000	1.000
6	1	1	1.000	1.000	1.000

7	1	1	1.000	1.000	1.000
8	1	1	1.000	1.000	1.000
9	1	1	1.000	1.000	1.000
10	1	1	1.000	1.000	1.000

Population	Locus	Gene copies	
		data	(missing)
1 Arbon_1	1	10	
	2	10	
	3	10	
	4	10	
	5	10	
	6	10	
	7	10	
	8	10	
	9	10	
	10	10	
2 Berg_2	1	10	
	2	10	
	3	10	
	4	10	
	5	10	
	6	10	
	7	10	
	8	10	
	9	10	
	10	10	
3 Chur_3	1	10	
	2	10	
	3	10	
	4	10	
	5	10	
	6	10	
	7	10	
	8	10	
	9	10	
	10	10	
Total of all populations	1	30	(0)
	2	30	(0)
	3	30	(0)
	4	30	(0)
	5	30	(0)
	6	30	(0)
	7	30	(0)
	8	30	(0)
	9	30	(0)

10   30   (0)

Bayesian Analysis: Posterior distribution table

Locus	Parameter	2.5%	25.0%	Mode	75.0%	97.5%	Median	Mean
1	Θ_1	0.00147	0.00300	0.00310	0.00360	0.01553	0.00877	0.01845
1	Θ_2	0.00093	0.00253	0.00270	0.00400	0.00787	0.00397	0.00436
1	Θ_3	0.00347	0.00660	0.00710	0.00840	0.01940	0.01123	0.01518
1	$M_{2->1}$	0.000	0.000	1.667	6.667	583.333	258.333	305.031
1	$M_{3->1}$	590.000	930.000	951.667	960.000	1663.333	1168.333	1214.622
1	$M_{1->2}$	23.333	153.333	171.667	173.333	300.000	161.667	179.972
1	$M_{3->2}$	0.000	30.000	58.333	106.667	320.000	125.000	142.079
1	$M_{1->3}$	280.000	596.667	648.333	656.667	1010.000	631.667	651.761
1	$M_{2->3}$	96.667	350.000	358.333	370.000	610.000	338.333	361.873
2	Θ_1	0.00060	0.00140	0.00170	0.00273	0.00687	0.00277	0.00329
2	Θ_2	0.00047	0.00173	0.00197	0.00347	0.00773	0.00317	0.00367
2	Θ_3	0.00153	0.00260	0.00330	0.00420	0.00860	0.00437	0.00473
2	$M_{2->1}$	106.667	413.333	421.667	433.333	840.000	475.000	525.792
2	$M_{3->1}$	163.333	416.667	421.667	486.667	1036.667	561.667	620.030
2	$M_{1->2}$	53.333	210.000	215.000	376.667	1046.667	518.333	646.068
2	$M_{3->2}$	63.333	236.667	251.667	293.333	563.333	378.333	447.607
2	$M_{1->3}$	36.667	143.333	148.333	186.667	426.667	228.333	246.535
2	$M_{2->3}$	50.000	116.667	208.333	220.000	446.667	225.000	241.192
3	Θ_1	0.00093	0.00207	0.00217	0.00380	0.00667	0.00337	0.00367
3	Θ_2	0.00113	0.00240	0.00470	0.00767	0.01680	0.01017	0.02589
3	Θ_3	0.00340	0.00547	0.00577	0.00760	0.02027	0.01077	0.01393
3	$M_{2->1}$	136.667	443.333	451.667	473.333	690.000	461.667	489.907
3	$M_{3->1}$	96.667	270.000	285.000	310.000	643.333	371.667	402.881
3	$M_{1->2}$	680.000	1000.000	1028.333	1043.333	1720.000	1161.667	1186.044
3	$M_{3->2}$	0.000	0.000	1.667	46.667	210.000	55.000	77.437
3	$M_{1->3}$	0.000	40.000	101.667	160.000	383.333	148.333	174.079
3	$M_{2->3}$	93.333	196.667	205.000	233.333	573.333	371.667	414.189
4	Θ_1	0.00067	0.00140	0.00210	0.00293	0.00560	0.00283	0.00315
4	Θ_2	0.00087	0.00200	0.00303	0.00400	0.00793	0.00390	0.00443
4	Θ_3	0.00113	0.00260	0.00437	0.00487	0.00900	0.00470	0.00536
4	$M_{2->1}$	273.333	533.333	538.333	543.333	1316.667	821.667	865.503
4	$M_{3->1}$	3.333	40.000	68.333	120.000	406.667	151.667	181.657
4	$M_{1->2}$	163.333	416.667	428.333	573.333	953.333	525.000	584.903

Locus	Parameter	2.5%	25.0%	Mode	75.0%	97.5%	Median	Mean
4	$M_{3->2}$	16.667	100.000	108.333	133.333	473.333	225.000	257.138
4	$M_{1->3}$	86.667	380.000	408.333	433.333	816.667	445.000	524.060
4	$M_{2->3}$	0.000	0.000	15.000	93.333	376.667	115.000	168.241
5	Θ_1	0.00133	0.00133	0.00143	0.00153	0.00153	0.03337	0.03946
5	Θ_2	0.00147	0.00253	0.00357	0.00413	0.00667	0.00383	0.00406
5	Θ_3	0.00293	0.00593	0.00777	0.00820	0.01887	0.00970	0.01116
5	$M_{2->1}$	996.667	1853.333	1865.000	1870.000	2363.333	1748.333	1799.072
5	$M_{3->1}$	0.000	26.667	111.667	173.333	510.000	198.333	253.307
5	$M_{1->2}$	26.667	156.667	168.333	170.000	550.000	268.333	304.124
5	$M_{3->2}$	20.000	106.667	151.667	183.333	406.667	191.667	211.774
5	$M_{1->3}$	16.667	130.000	178.333	266.667	530.000	268.333	301.529
5	$M_{2->3}$	0.000	0.000	1.667	73.333	270.000	75.000	97.413
6	Θ_1	0.00100	0.00213	0.00270	0.00387	0.00687	0.00350	0.00387
6	Θ_2	0.00067	0.00127	0.00283	0.00713	0.01780	0.00830	0.01857
6	Θ_3	0.00627	0.01067	0.01083	0.01087	0.02487	0.01590	0.01765
6	$M_{2->1}$	0.000	0.000	15.000	93.333	593.333	218.333	466.837
6	$M_{3->1}$	0.000	0.000	15.000	50.000	333.333	101.667	134.614
6	$M_{1->2}$	1156.667	1180.000	1201.667	1216.667	1216.667	1998.333	2236.587
6	$M_{3->2}$	0.000	0.000	11.667	136.667	650.000	165.000	255.691
6	$M_{1->3}$	0.000	0.000	1.667	36.667	143.333	38.333	50.541
6	$M_{2->3}$	0.000	0.000	5.000	36.667	160.000	38.333	53.580
7	Θ_1	0.00193	0.00367	0.00430	0.00480	0.00880	0.00503	0.00533
7	Θ_2	0.00233	0.00320	0.00343	0.00347	0.02047	0.02963	0.03658
7	Θ_3	0.00507	0.01307	0.01357	0.01380	0.03193	0.01797	0.02215
7	$M_{2->1}$	0.000	36.667	68.333	110.000	276.667	111.667	125.635
7	$M_{3->1}$	163.333	400.000	421.667	480.000	776.667	461.667	481.794
7	$M_{1->2}$	933.333	1426.667	1431.667	1443.333	2230.000	1605.000	1683.723
7	$M_{3->2}$	70.000	320.000	351.667	356.667	946.667	465.000	535.994
7	$M_{1->3}$	116.667	303.333	325.000	353.333	610.000	361.667	376.467
7	$M_{2->3}$	40.000	140.000	178.333	186.667	523.333	265.000	294.328
8	Θ_1	0.00200	0.00353	0.00490	0.00587	0.01100	0.00563	0.00607
8	Θ_2	0.00087	0.00227	0.00397	0.00500	0.01507	0.00590	0.01157
8	Θ_3	0.00333	0.00667	0.00783	0.00813	0.01953	0.00903	0.01058
8	$M_{2->1}$	126.667	286.667	315.000	383.333	553.333	331.667	340.659
8	$M_{3->1}$	73.333	150.000	205.000	226.667	413.333	228.333	241.692
8	$M_{1->2}$	100.000	326.667	365.000	376.667	770.000	441.667	482.029
8	$M_{3->2}$	583.333	1256.667	1261.667	1263.333	1736.667	1158.333	1227.185

| Locus	Parameter	2.5%	25.0%	Mode	75.0%	97.5%	Median	Mean
8	$M_{1->3}$	286.667	446.667	468.333	470.000	740.000	525.000	538.567
8	$M_{2->3}$	53.333	133.333	151.667	240.000	390.000	211.667	221.208
9	Θ_1	0.00300	0.00753	0.00763	0.00800	0.01793	0.00957	0.01199
9	Θ_2	0.00067	0.00187	0.00283	0.00293	0.00720	0.00343	0.00377
9	Θ_3	0.00267	0.00673	0.00810	0.00813	0.01747	0.01303	0.02003
9	$M_{2->1}$	80.000	173.333	185.000	193.333	453.333	268.333	290.738
9	$M_{3->1}$	196.667	373.333	401.667	420.000	583.333	378.333	385.825
9	$M_{1->2}$	140.000	350.000	385.000	423.333	823.333	465.000	493.417
9	$M_{3->2}$	13.333	103.333	171.667	186.667	386.667	201.667	224.347
9	$M_{1->3}$	446.667	700.000	718.333	733.333	1206.667	805.000	831.165
9	$M_{2->3}$	0.000	0.000	5.000	36.667	140.000	38.333	52.911
10	Θ_1	0.00093	0.00180	0.00297	0.00353	0.00560	0.00310	0.00325
10	Θ_2	0.00020	0.00087	0.00157	0.00300	0.01387	0.00357	0.00820
10	Θ_3	0.01073	0.01387	0.01403	0.01427	0.03293	0.02077	0.02477
10	$M_{2->1}$	0.000	0.000	18.333	50.000	316.667	105.000	136.217
10	$M_{3->1}$	203.333	646.667	658.333	660.000	1076.667	701.667	781.322
10	$M_{1->2}$	10.000	546.667	571.667	583.333	1666.667	1211.667	1443.884
10	$M_{3->2}$	523.333	1233.333	1261.667	1266.667	1550.000	1768.333	1946.770
10	$M_{1->3}$	213.333	396.667	485.000	530.000	866.667	528.333	596.930
10	$M_{2->3}$	0.000	93.333	101.667	103.333	353.333	155.000	172.118
All	Θ_1	0.00260	0.00333	0.00383	0.00427	0.00520	0.00397	0.00391
All	Θ_2	0.00220	0.00300	0.00350	0.00400	0.00493	0.00363	0.00360
All	Θ_3	0.00580	0.00707	0.00797	0.00880	0.01087	0.00823	0.00827
All	$M_{2->1}$	86.667	106.667	131.667	133.333	133.333	261.667	243.125
All	$M_{3->1}$	220.000	313.333	361.667	396.667	466.667	355.000	349.973
All	$M_{1->2}$	100.000	123.333	138.333	140.000	140.000	458.333	437.542
All	$M_{3->2}$	56.667	110.000	131.667	133.333	133.333	118.333	114.981
All	$M_{1->3}$	213.333	270.000	311.667	353.333	423.333	328.333	346.754
All	$M_{2->3}$	50.000	86.667	115.000	140.000	196.667	121.667	121.233

Citation suggestions:

Beerli P., 2006. Comparison of Bayesian and maximum-likelihood inference of population genetic parameters.
  Bioinformatics 22:341-345
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
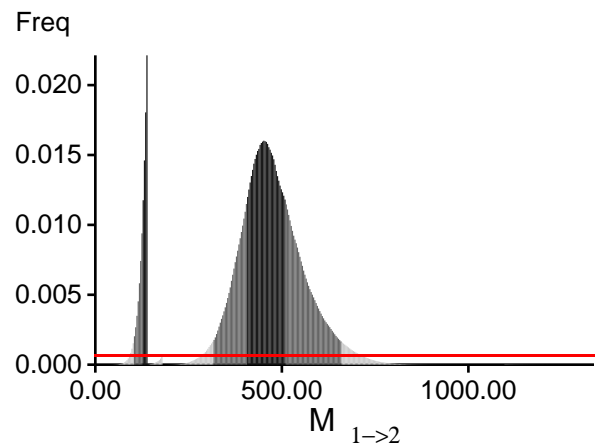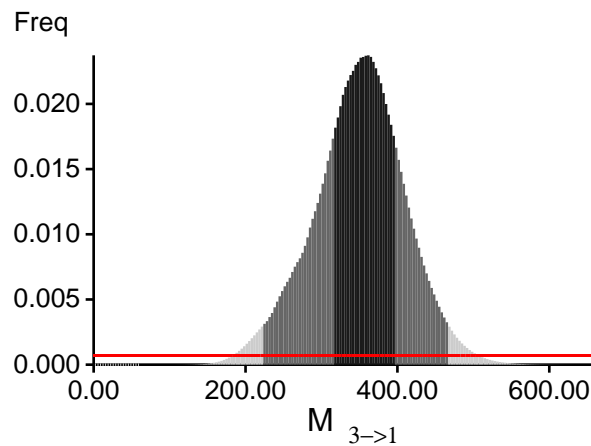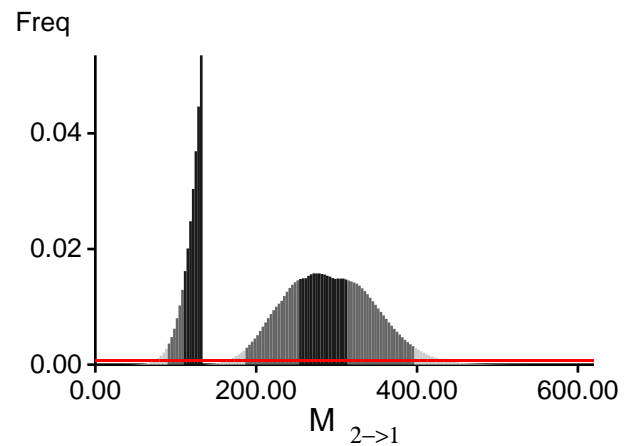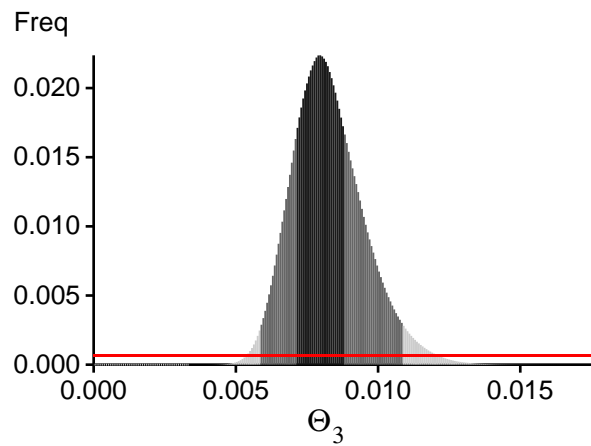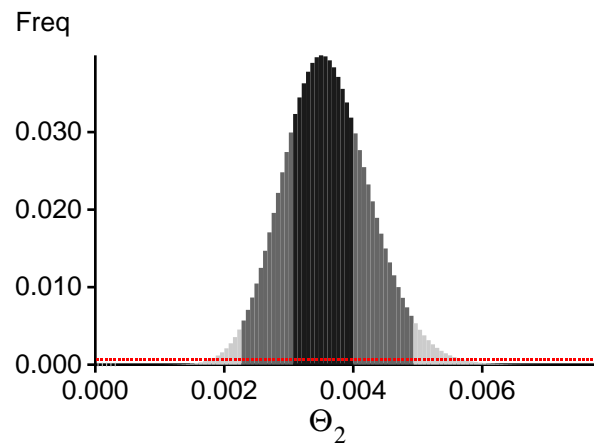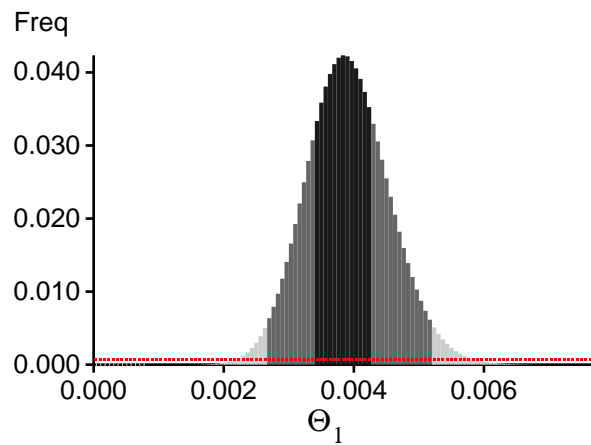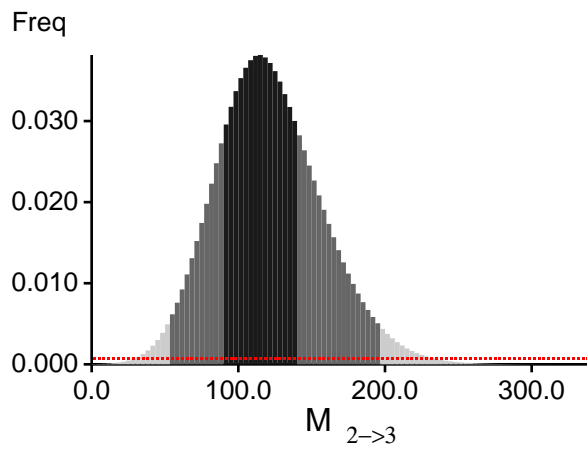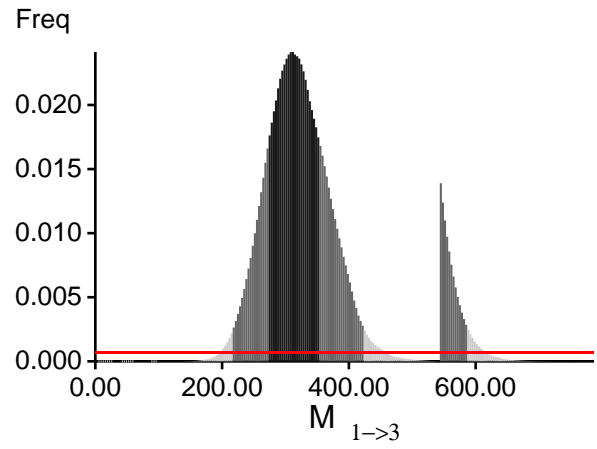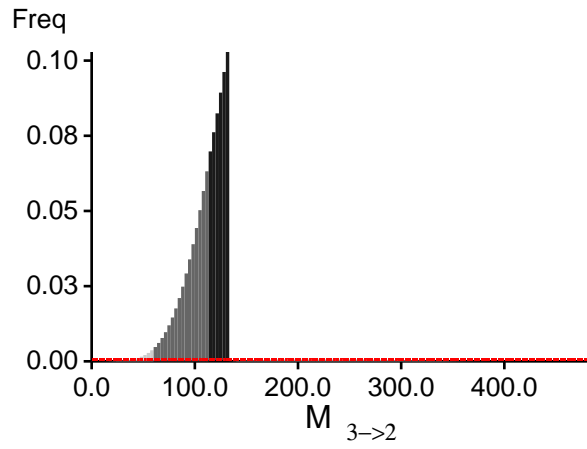
Log-Probability of the data given the model (marginal likelihood)

Use this value for Bayes factor calculations:
BF = 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	-3133.03	-2505.52	-2320.00
2	-2702.27	-2129.53	-1985.86
3	-2878.71	-2284.30	-2123.76
4	-3398.68	-2505.39	-2314.32
5	-3120.24	-2378.22	-2205.87
6	-3190.50	-2601.90	-2363.43
7	-3052.12	-2394.88	-2203.73
8	-3196.54	-2429.39	-2230.30
9	-3323.72	-2483.81	-2288.96
10	-3029.65	-2341.08	-2174.63
All	-30919.14	-23947.72	-22104.54

(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 = 106.313878]
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	118575/277202	0.42776
Θ_2	158582/277353	0.57177
Θ_3	129609/277517	0.46703
$M_{2 \to 1}$	110262/278218	0.39632
$M_{3 \to 1}$	130893/277886	0.47103
$M_{1 \to 2}$	149383/278007	0.53734
$M_{3 \to 2}$	132335/277673	0.47659
$M_{1 \to 3}$	120997/278675	0.43419
$M_{2 \to 3}$	123827/278301	0.44494
Genealogies	328604/2499168	0.13149

MCMC-Autocorrelation and Effective MCMC Sample Size

Parameter	Autocorrelation	Effective Sampe Size
Θ_1	0.69000	12978.81
Θ_2	0.81105	8028.75
Θ_3	0.61217	16714.90
$M_{2\to1}$	0.66474	15079.01
$M_{3\to1}$	0.56890	19618.08
$M_{1\to2}$	0.71043	12470.83
$M_{3\to2}$	0.61739	17647.60
$M_{1\to3}$	0.64674	15468.84
$M_{2\to3}$	0.60904	18156.16
Genealogies	0.85437	6201.40

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