Two fake Swiss 'towns'

POPULATION SIZE, MIGRATION, DIVERGENCE, ASSIGNMENT, HISTORY
Bayesian inference using the structured coalescent
Migrate-n version 4.2.7 [April-1-2016]
 Using Intel AVX (Advanced Vector Extensions)
  Compiled for PARALLEL computer architectures
  One master and 4 compute nodes are available.
  Compiled for a SYMMETRIC multiprocessors (Grandcentral)
Program started at   Wed Jul 6 11:36:04 2016
Program finished at   Wed Jul 6 12:12:30 2016
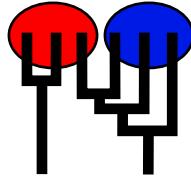
Options

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)   3924661789

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
 1 Ascona   *   0
 2 Brissago   *   *

 Order of parameters:
  1   Θ_1 <displayed>

2	Θ_2	\<displayed\>
3	$M_{1\to2}$	\<displayed\>

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

Analysis strategy: Bayesian inference

Proposal distributions for parameter

Parameter	Proposal
Theta	Metropolis sampling
M	Metropolis sampling

Prior distribution for parameter

Parameter	Prior	Minimum	Mean*	Maximum	Delta	Bins
Theta	Gamma	0.000000	0.010000	0.100000	0.010000	1500
Theta	Gamma	0.000000	0.010000	0.100000	0.010000	1500
M	Gamma	0.000000	500.000000	5000.000000	500.000000	1500
M	Gamma	0.000000	500.000000	5000.000000	500.000000	1500

Markov chain settings:	Long chain
Number of chains	1
Recorded steps [a]	5000
Increment (record every x step [b]	200
Number of concurrent chains (replicates) [c]	10
Visited (sampled) parameter values [a*b*c]	10000000
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_x0xx
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:		5

Mutationmodel:

Locus	Sublocus	Mutationmodel	Mutationmodel parameters
1	1	Felsenstein 84	[Bf:0.24 0.26 0.27 0.22, t/t ratio=2.000]
2	1	Felsenstein 84	[Bf:0.25 0.24 0.26 0.25, t/t ratio=2.000]
3	1	Felsenstein 84	[Bf:0.25 0.24 0.25 0.26, t/t ratio=2.000]
4	1	Felsenstein 84	[Bf:0.26 0.24 0.23 0.27, t/t ratio=2.000]
5	1	Felsenstein 84	[Bf:0.25 0.24 0.27 0.24, t/t ratio=2.000]

Sites per locus

Locus	Sites
1	1000
2	1000
3	1000
4	1000
5	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

Population	Locus	Gene copies data	(missing)
1 Ascona	1	10	
	2	10	
	3	10	
	4	10	
	5	10	
2 Brissago	1	10	
	2	10	
	3	10	
	4	10	

	5	10	
Total of all populations	1	20	(0)
	2	20	(0)
	3	20	(0)
	4	20	(0)
	5	20	(0)

Bayesian Analysis: Posterior distribution table

Locus	Parameter	2.5%	25.0%	Mode	75.0%	97.5%	Median	Mean
1	Θ_1	0.00300	0.00493	0.00717	0.00973	0.01280	0.00797	0.00843
1	Θ_2	0.00007	0.00287	0.00470	0.00653	0.01100	0.00523	0.00549
1	$M_{1->2}$	0.000	0.000	51.667	113.333	306.667	115.000	100.887
2	Θ_1	0.00113	0.00440	0.00657	0.00893	0.01533	0.00737	0.00782
2	Θ_2	0.00020	0.00333	0.00537	0.00760	0.01333	0.00617	0.00655
2	$M_{1->2}$	0.000	33.333	111.667	180.000	396.667	151.667	149.241
3	Θ_1	0.00233	0.00493	0.00610	0.00733	0.01093	0.00683	0.00715
3	Θ_2	0.00547	0.00953	0.01137	0.01347	0.02100	0.01310	0.01410
3	$M_{1->2}$	0.000	60.000	141.667	223.333	446.667	178.333	182.509
4	Θ_1	0.00153	0.00233	0.00523	0.00947	0.01107	0.00670	0.00730
4	Θ_2	0.00380	0.01007	0.01203	0.01413	0.02627	0.01350	0.01429
4	$M_{1->2}$	0.000	0.000	1.667	80.000	213.333	81.667	53.220
5	Θ_1	0.00427	0.00667	0.00897	0.01140	0.01520	0.00977	0.01023
5	Θ_2	0.00000	0.00287	0.00690	0.01273	0.02960	0.00817	0.00893
5	$M_{1->2}$	60.000	63.333	231.667	500.000	503.333	325.000	367.853
All	Θ_1	0.00400	0.00627	0.00763	0.00900	0.01167	0.00783	0.00784
All	Θ_2	0.00433	0.00680	0.00830	0.00987	0.01327	0.00863	0.00874
All	$M_{1->2}$	0.000	60.000	115.000	160.000	230.000	121.667	113.978

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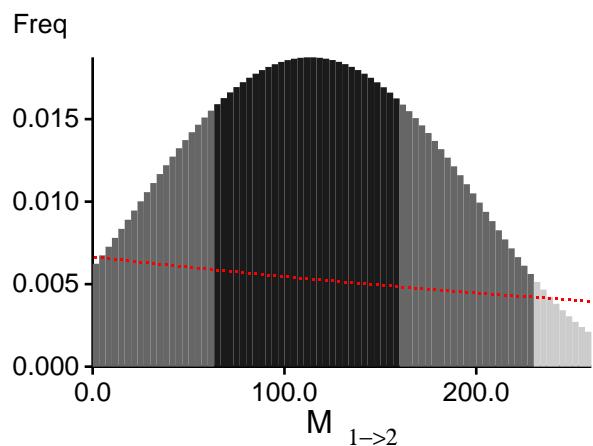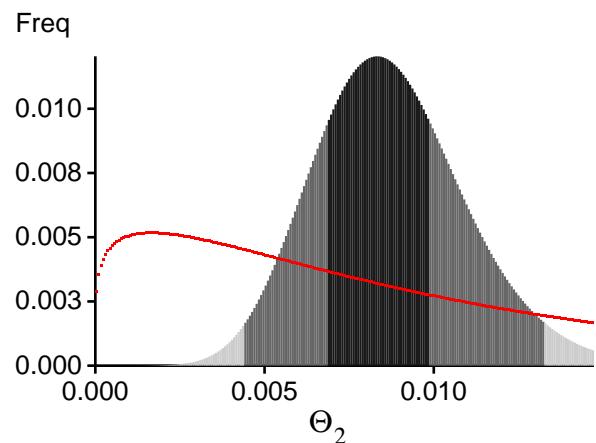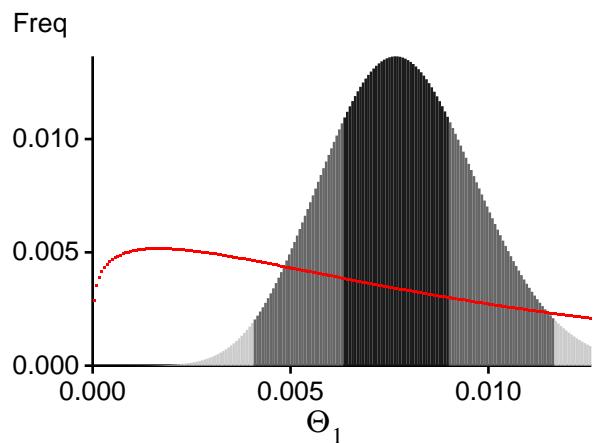
Log-Probability of the data given the model (marginal likelihood)

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	-1959.03	-1811.48	-1801.41
2	-1930.93	-1802.86	-1795.32
3	-2086.81	-1910.81	-1895.91
4	-2598.02	-2199.97	-2147.00
5	-2131.00	-1910.55	-1887.29
All	-10718.98	-9648.88	-9540.14

(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 = -13.207137]

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	2913532/8339437	0.34937
Θ_2	3301611/8335693	0.39608
$M_{1->2}$	2647218/8332093	0.31771
Genealogies	3914647/24992777	0.15663

MCMC-Autocorrelation and Effective MCMC Sample Size

Parameter	Autocorrelation	Effective Sampe Size
Θ_1	0.24258	222859.62
Θ_2	0.14504	263598.69
$M_{1->2}$	0.22707	227602.16
Ln[Prob(D|G)]	0.32671	177755.38

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