two (fake) Swiss towns

POPULATION SIZE, MIGRATION, DIVERGENCE, ASSIGNMENT, HISTORY
Bayesian inference using the structured coalescent
Migrate-n version 5.0.2(git:v5.0.2-1-g8ac0205) [December-1-2021]
Program started at   Wed Feb 9 16:07:03 2022
Program finished at   Wed Feb 9 16:08:23 2022 [Runtime:0000:00:01:20]

Options

Inheritance multipliers in use for Thetas:
All loci use an inheritance multiplier of 1.0

Random number seed:	(with internal timer)	3051728584
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 Aadorf	*	*
2 Bern	*	*

Order of parameters:

1	Θ_1	<displayed>
2	Θ_2	<displayed>
3	$M_{2->1}$	<displayed>
4	$M_{1->2}$	<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	**Exponent.	0.000000	0.010	0.100	-	1500	0.10417
2	Theta	**Exponent.	0.000000	0.010	0.100	-	1500	0.10417
3	M	** Gamma	0.000000	100.0	10000	1000.	2000	0.10417
4	M	** Gamma	0.000000	100.0	10000	1000.	2000	0.10417

[* * means priors were set globally]

Markov chain settings:	Long chain
Number of chains	1
Recorded steps [a]	10000
Increment (record every x step [b]	50
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:

Adaptive_standard heating scheme — 4 chains with start values temperatures

1000000.00 3.00 1.50 1.00

Swapping interval is 1

Print options:	
Data file:	twoswisstowns
	parmfile.twoswisstowns-assignfreq
Haplotyping is turned on:	NO
Output file:	outfile-twoswisstowns-af
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]:	Yes, only the best

Data summary

Data file:	twoswisstowns
Datatype:	Haplotype data
Number of loci:	3

Mutationmodel:

Locus	Sublocus	Mutationmodel	Mutationmodel parameters
1	1	Tamura-Nei	[Bf:0.30 0.25 0.24 0.22, k1=1.300, k2=0.800]
1	2	Felsenstein 84	[Bf:0.24 0.28 0.22 0.27, t/t ratio=2.000]
2	1	Tamura-Nei	[Bf:0.27 0.23 0.24 0.26, k1=1.300, k2=2.000]
3	1	Jukes-Cantor	[Basefreq: =0.25]

Sites per locus

Locus	Sites	
1	200	800
2	500	
3	500	

Site rate variation and probabilities:

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

Population	Locus	Gene copies data	(missing)
1 Aadorf	1	10	
	2	10	
	3	10	
2 Bern	1	10	
	2	10	
	3	10	
Total of all populations	1	20	(0)
	2	20	(0)
	3	20	(0)

Bayesian Analysis: Posterior distribution table

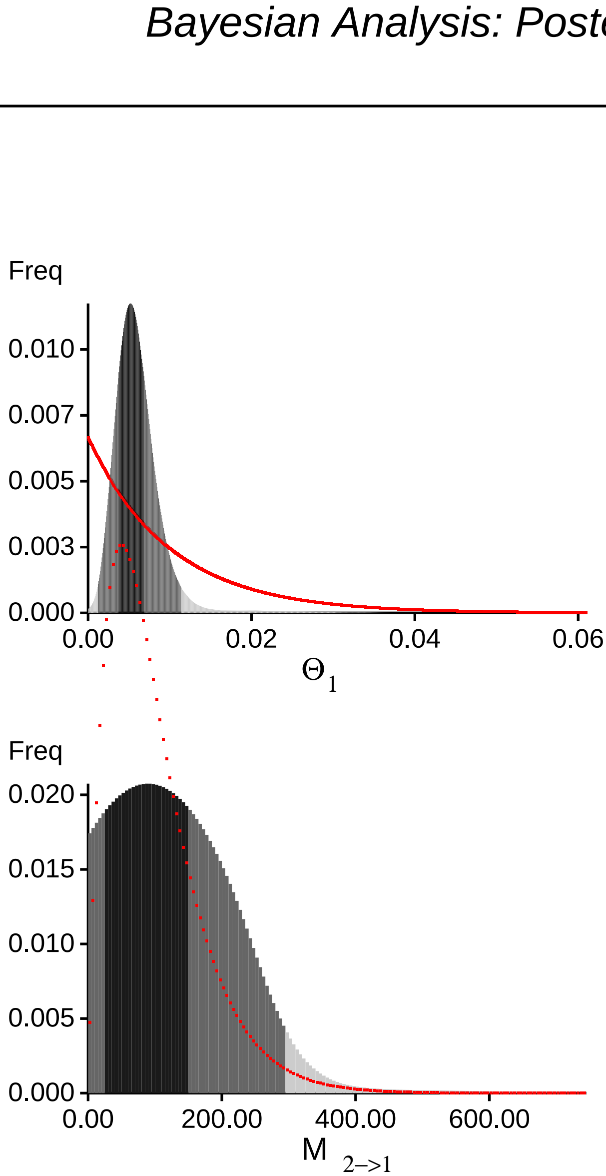
Locus	Parameter	2.5%	25.0%	Mode	75.0%	97.5%	Median	Mean
1	Θ_1	0.00000	0.00167	0.00337	0.00587	0.01380	0.00490	0.00570
1	Θ_2	0.00687	0.01440	0.01850	0.02593	0.04193	0.02190	0.02322
1	$M_{2->1}$	0.000	20.000	87.500	150.000	295.000	132.500	90.056
1	$M_{1->2}$	0.000	5.000	67.500	125.000	260.000	117.500	67.181
2	Θ_1	0.00027	0.00240	0.00410	0.00600	0.01220	0.00503	0.00560
2	Θ_2	0.00467	0.01167	0.01757	0.02313	0.04180	0.01970	0.02140
2	$M_{2->1}$	0.000	25.000	97.500	165.000	320.000	137.500	101.585
2	$M_{1->2}$	0.000	55.000	132.500	205.000	340.000	162.500	135.733
3	Θ_1	0.00147	0.00447	0.00677	0.01013	0.01940	0.00863	0.00945
3	Θ_2	0.01213	0.02127	0.02803	0.03607	0.05860	0.03157	0.03328
3	$M_{2->1}$	0.000	25.000	92.500	155.000	295.000	132.500	93.384
3	$M_{1->2}$	0.000	25.000	97.500	160.000	290.000	132.500	97.255
All	Θ_1	0.00113	0.00367	0.00517	0.00687	0.01140	0.00570	0.00614
All	Θ_2	0.01613	0.02400	0.02697	0.03553	0.04907	0.03103	0.03200
All	$M_{2->1}$	0.000	20.000	87.500	150.000	295.000	132.500	93.717
All	$M_{1->2}$	0.000	30.000	97.500	165.000	290.000	137.500	101.890

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	TI(1a)	BTI(1b)	HS(3)
1	-2408.63	-2271.01	-2245.49
2	-1294.03	-1225.02	-1199.16
3	-1409.63	-1314.83	-1280.66
All	-5125.06	-4823.63	-4738.09

(1a) TI: Thermodynamic integration: log(Prob(D|Model)): Good approximation with many temperatures
(1b) BTI: Bezier-approximated Thermodynamic integration: when using few temperatures USE THIS!
(2) SS: Steppingstone Sampling (Xie et al 2011)
(3) HS: Harmonic mean approximation: Overestimates the marginal likelihood, poor variance
Adaptive heating was ON, therefore the values of (1) may be incorrect),
[Scaling factor = -12.773236]
Citation suggestions:

Beerli P. and M. Palczewski, 2010. Unified framework to evaluate panmixia and migration direction among multiple sampling locations, Genetics, 185: 313-326.

Palczewski M. and P. Beerli, 2014. Population model comparison using multi-locus datasets. In M.-H. Chen, L. Kuo, and P. O. Lewis, editors, Bayesian Phylogenetics: Methods, Algorithms, and Applications, pages 187-200. CRC Press, 2014.

Xie W., P. O. Lewis, Y. Fan, L. Kuo, and M.-H. Chen. 2011. Improving marginal likelihood estimation for Bayesian phylogenetic model selection. Systematic Biology, 60(2):150â 160, 2011.

Acceptance ratios for all parameters and the genealogies

Parameter	Accepted changes	Ratio
Θ_1	42256/156369	0.27023
Θ_2	31550/156289	0.20187
$M_{2\rightarrow1}$	84003/155611	0.53983
$M_{1\rightarrow2}$	72718/156322	0.46518
Genealogies	89412/875409	0.10214

MCMC-Autocorrelation and Effective MCMC Sample Size

Parameter	Autocorrelation	Effective Sampe Size
Θ_1	0.68019	5713.55
Θ_2	0.62752	6954.74
$M_{2->1}$	0.56611	8365.85
$M_{1->2}$	0.58557	7883.50
Genealogies	0.68019	5713.55

Average temperatures during the run

Chain	Temperatures
1	1.00000
2	1.43875
3	3.56820
4	20006.11346

Adaptive heating often fails, if the average temperatures are very close together try to rerun using static heating! If you want to compare models using marginal likelihoods then you MUST use static heating

Potential Problems

This section reports potential problems with your run, but such reporting is often not very accurate. Whith 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 wether 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

Summary Assignment of Individuals to Populations

Individual	Population 1	Population 2
?BAH0	0.999	0.001
?BAF0	0.981	0.019
?BAG1	0.009	0.991
?BAJ1	0.014	0.986
?BAH1	0.058	0.942
?BAI1	0.057	0.943
?BAF1	0.009	0.991

Detailed Assignment of Individuals to Populations

Individual	Locus	Population 1	2
?BAH0	1	0.976	0.024
?BAH0	2	0.802	0.198
?BAH0	3	0.828	0.172
?BAH0	All	0.999	0.001
?BAF0	1	0.828	0.172
?BAF0	2	0.770	0.230
?BAF0	3	0.759	0.241
?BAF0	All	0.981	0.019
?BAG1	1	0.152	0.848
?BAG1	2	0.186	0.814
?BAG1	3	0.178	0.822
?BAG1	All	0.009	0.991
?BAJ1	1	0.221	0.779
?BAJ1	2	0.180	0.820
?BAJ1	3	0.189	0.811
?BAJ1	All	0.014	0.986
?BAH1	1	0.309	0.691
?BAH1	2	0.166	0.834
?BAH1	3	0.407	0.593
?BAH1	All	0.058	0.942
?BAI1	1	0.291	0.709
?BAI1	2	0.161	0.839
?BAI1	3	0.435	0.565
?BAI1	All	0.057	0.943
?BAF1	1	0.199	0.801
?BAF1	2	0.129	0.871
?BAF1	3	0.191	0.809
?BAF1	All	0.009	0.991