

two (fake) Swiss towns

POPULATION SIZE, MIGRATION, DIVERGENCE, ASSIGNMENT, HISTORY

Bayesian inference using the structured coalescent

Migrate-n version 4.1.3a [Feb-22-2015]

Using Intel AVX (Advanced Vector Extensions)

Program started at Sun Feb 22 14:16:11 2015

Program finished at Sun Feb 22 14:16:56 2015



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)

784408000

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	$M_{2 \rightarrow 1}$	<displayed>
4	$M_{1 \rightarrow 2}$	<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	Uniform	0.000000	0.050000	0.100000	0.010000	1500
Theta	Uniform	0.000000	0.050000	0.100000	0.010000	1500
M	Uniform	0.000000	500.000000	1000.000000	100.000000	1500
M	Uniform	0.000000	500.000000	1000.000000	100.000000	1500

Markov chain settings:

Long chain

Number of chains	1
Recorded steps [a]	5000
Increment (record every x step [b])	5
Number of concurrent chains (replicates) [c]	4
Visited (sampled) parameter values [a*b*c]	100000
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:	twoswisstowns
Haplotyping is turned on:	NO
Output file:	outfile-twoswisstowns
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:	twoswisstowns
Datatype:	Haplotype data
Number of loci:	3

Mutationmodel:

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

Sites per locus

Locus	Sites
1	500 500
2	300
3	700

Site rate variation and probabilities:

Locus	Sublocus	Region type	Rate of change	Probability	Patch size
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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

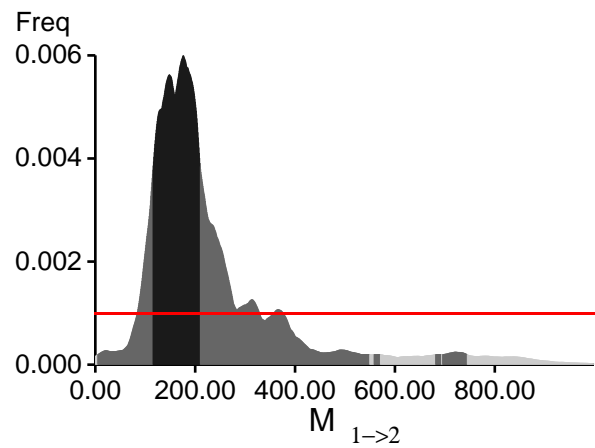
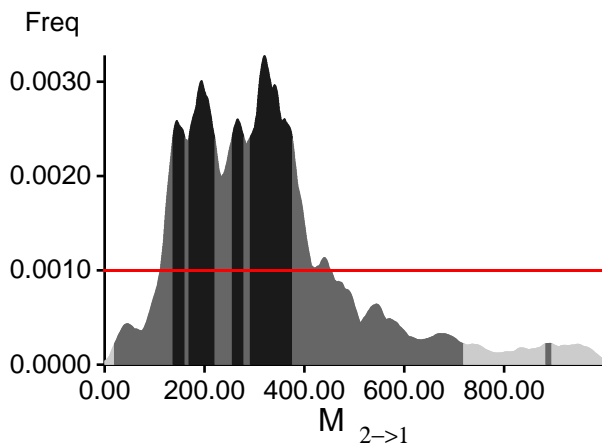
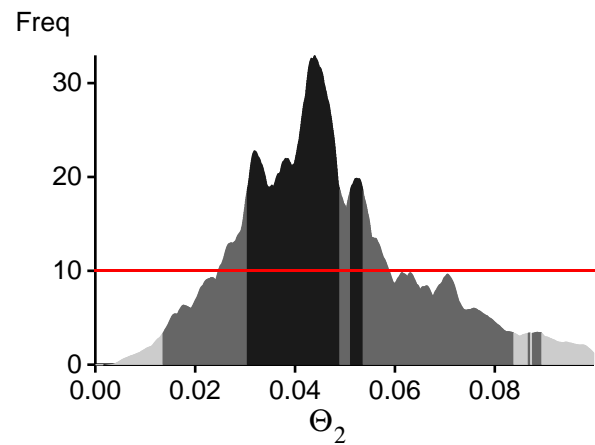
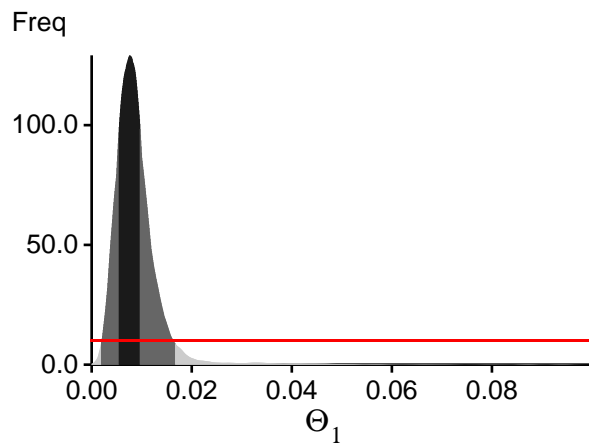
Locus	Parameter	2.5%	25.0%	Mode	75.0%	97.5%	Median	Mean
1	Θ_1	0.00093	0.00400	0.00643	0.00980	0.01860	0.00817	0.00900
1	Θ_2	0.01267	0.02360	0.03330	0.04700	0.08433	0.04090	0.04470
1	$M_{2 \rightarrow 1}$	21.333	86.667	173.667	274.667	678.667	301.000	323.787
1	$M_{1 \rightarrow 2}$	0.000	93.333	148.333	228.667	418.667	190.333	214.738
2	Θ_1	0.00240	0.00767	0.01797	0.02440	0.05327	0.02163	0.02459
2	Θ_2	0.01253	0.01767	0.03237	0.05307	0.09453	0.04743	0.05062
2	$M_{2 \rightarrow 1}$	92.667	108.000	142.333	412.667	496.667	405.000	470.641
2	$M_{1 \rightarrow 2}$	126.000	310.000	379.000	588.000	854.000	444.333	467.873
3	Θ_1	0.00067	0.00353	0.00603	0.01067	0.02547	0.00923	0.01089
3	Θ_2	0.03327	0.04087	0.05477	0.05947	0.09940	0.06277	0.06337
3	$M_{2 \rightarrow 1}$	30.000	167.333	294.333	433.333	774.667	367.000	410.136
3	$M_{1 \rightarrow 2}$	46.667	92.667	127.000	227.333	528.667	205.667	250.139
All	Θ_1	0.00187	0.00540	0.00763	0.00967	0.01673	0.00823	0.00911
All	Θ_2	0.01347	0.03033	0.04397	0.04893	0.08380	0.04463	0.04691
All	$M_{2 \rightarrow 1}$	18.667	290.667	319.667	376.000	718.667	301.000	328.061
All	$M_{1 \rightarrow 2}$	4.000	114.667	176.333	210.000	549.333	190.333	239.422

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:

$BF = \text{Exp}[\ln(\text{Prob}(D \mid \text{thisModel}) - \ln(\text{Prob}(D \mid \text{otherModel}))]$

or as $LBF = 2 (\ln(\text{Prob}(D \mid \text{thisModel}) - \ln(\text{Prob}(D \mid \text{otherModel})))$

shows the support for thisModel]

Locus	Raw thermodynamic score(1a)	Bezier approximation score(1b)	Harmonic mean(2)
1	-2560.54	-2281.92	-2255.51
2	-868.26	-770.13	-752.01
3	-2012.94	-1759.60	-1730.50
All	-5436.69	-4806.58	-4732.96

(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 = 5.059894

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	15813/31271	0.50568
Θ_2	18627/31214	0.59675
$M_{2 \rightarrow 1}$	17099/31359	0.54527
$M_{1 \rightarrow 2}$	17387/31394	0.55383
Genealogies	14727/174762	0.08427

MCMC-Autocorrelation and Effective MCMC Sample Size

Parameter	Autocorrelation	Effective Sample Size
Θ_1	0.94276	1804.09
Θ_2	0.84499	5060.31
$M_{2 \rightarrow 1}$	0.95019	1564.45
$M_{1 \rightarrow 2}$	0.95191	1504.83
$\text{Ln}[\text{Prob}(D G)]$	0.80422	6535.03

Potential Problems

This section reports potential problems with your run, but such reporting is often not very accurate. With 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 whether 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	2
?BAG	0.092	0.908
?BAJ	0.100	0.900
?BAH	0.362	0.638
?BAI	0.304	0.696
?BAF	0.121	0.879

Detailed Assignment of Individuals to Populations

Individual	Locus	Population	
		1	2
?BAG	1	0.298	0.702
?BAG	2	0.365	0.635
?BAG	3	0.294	0.706
?BAG	All	0.092	0.908
?BAJ	1	0.278	0.722
?BAJ	2	0.393	0.607
?BAJ	3	0.308	0.692
?BAJ	All	0.100	0.900
?BAH	1	0.349	0.651
?BAH	2	0.501	0.499
?BAH	3	0.515	0.485
?BAH	All	0.362	0.638
?BAI	1	0.337	0.663
?BAI	2	0.438	0.562
?BAI	3	0.524	0.476
?BAI	All	0.304	0.696
?BAF	1	0.349	0.651
?BAF	2	0.407	0.593
?BAF	3	0.272	0.728
?BAF	All	0.121	0.879