

Japan

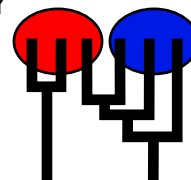
POPULATION SIZE, MIGRATION, DIVERGENCE, ASSIGNMENT, HISTORY

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 16 08:37:32 2022

Program finished at Wed Feb 16 08:44:04 2022 [Runtime:0000:00:06:32]



Options

Datatype: Single nucleotide polymorphism data(Hapmap formatting)

Inheritance multipliers in use for Thetas:

All loci use an inheritance multiplier of 1.0

Random number seed: (with internal timer) 1468988548

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

1 Japan *

Order of parameters:

1 Θ_1 <displayed>

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

Analysis strategy: Bayesian inference

-Population size 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	0.50000

[* * means priors were set globally]

Markov chain settings:

Long chain

Number of chains	1
Recorded steps [a]	10000
Increment (record every x step [b])	100
Number of concurrent chains (replicates) [c]	1
Visited (sampled) parameter values [a*b*c]	1000000
Number of discard trees per chain (burn-in)	1000

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.hapmap
	parmfile.hapmap
Haplotyping is turned on:	NO
Output file:	outfile_hapmap
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.hapmap
 Datatype: SNP data (Hapmap data)
 Number of loci: 9

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]

Sites per locus

Locus	Sites
1	1
2	1
3	1
4	1
5	1
6	1
7	1
8	1
9	1

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	
Population			Locus		Gene copies	
1 Japan			1	72		
			2	90		
			3	88		
			4	90		
			5	90		
			6	88		
			7	90		
			8	90		
			9	90		
Total of all populations			1	72		
			2	90		
			3	88		
			4	90		
			5	90		
			6	88		
			7	90		
			8	90		
			9	90		

Allele frequency spectra

Locus 1

Allele	Pop1	All
G	0.542	0.542
C	0.458	0.458
	-	0.000
	-	0.000
Alleles	0.497	0.497
Samplesize	72	72
H_{exp}		

Locus 2

Allele	Pop1	All
G	1.000	1.000
A	-	0.000
	-	0.000
	-	0.000
Alleles	0.000	0.000
Samplesize	72	72
H_{exp}		

Locus 3

Allele	Pop1	All
C	1.000	1.000
A	-	0.000
	-	0.000
	-	0.000
Alleles	0.000	0.000
Samplesize	72	72
H_{exp}		

Locus 4

Allele	Pop1	All
G	0.125	0.125
A	0.875	0.875
	-	0.000
	-	0.000

Allele	Pop1	All
Alleles	0.219	0.219
Samplesize	72	72
H_{exp}		
Locus 5		
Allele	Pop1	All
T	1.000	1.000
C	-	0.000
	-	0.000
	-	0.000
Alleles	0.000	0.000
Samplesize	72	72
H_{exp}		
Locus 6		
Allele	Pop1	All
C	1.000	1.000
T	-	0.000
	-	0.000
	-	0.000
Alleles	0.000	0.000
Samplesize	72	72
H_{exp}		
Locus 7		
Allele	Pop1	All
C	1.000	1.000
	-	0.000
	-	0.000
	0.000	0.000
Alleles	1	4
Samplesize	72	72
H_{exp}		
Locus 8		
Allele	Pop1	All
G	1.000	1.000
T	-	0.000
	-	0.000

Allele	Pop1	All
	-	0.000
Alleles	0.000	0.000
Samplesize	72	72
H_{exp}		
Locus 9		
Allele	Pop1	All
A	1.000	1.000
G	-	0.000
	-	0.000
	-	0.000
Alleles	0.000	0.000
Samplesize	72	72
H_{exp}		
Average expected heterozygosity		
	Pop1	All
H_{exp}	0.079	0.079

Bayesian Analysis: Posterior distribution table

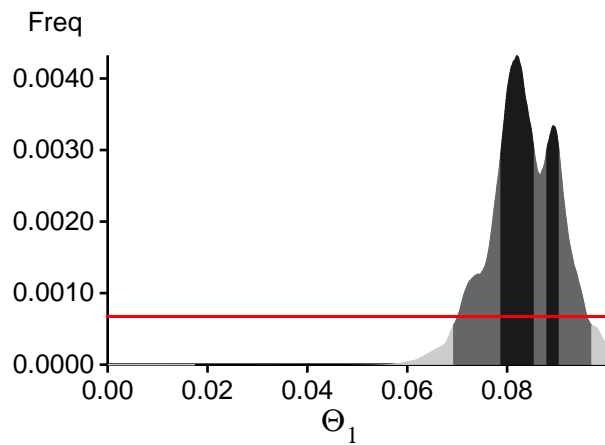
Locus	Parameter	2.5%	25.0%	Mode	75.0%	97.5%	Median	Mean
1	Θ_1	0.04447	0.06500	0.07723	0.08920	0.09993	0.07397	0.07290
2	Θ_1	0.04267	0.05553	0.05997	0.07080	0.08580	0.06410	0.06555
3	Θ_1	0.04947	0.07220	0.08470	0.09340	0.09993	0.07790	0.07643
4	Θ_1	0.06280	0.08620	0.09770	0.09907	0.09993	0.08710	0.08382
5	Θ_1	0.05080	0.07187	0.08123	0.09053	0.09993	0.07783	0.07662
6	Θ_1	0.04960	0.07973	0.08883	0.09547	0.09980	0.08277	0.07848
8	Θ_1	0.05187	0.07727	0.08510	0.09680	0.09993	0.07997	0.07828
9	Θ_1	0.05973	0.06747	0.07217	0.08373	0.09967	0.07670	0.07642
All	Θ_1	0.06920	0.07867	0.08197	0.08540	0.09693	0.08337	0.08345

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	TI(1a)	BTI(1b)	HS(3)
1	-61.69	-40.11	-14.43
2	-8.18	-8.03	-8.20
3	-43.81	-36.41	-18.74
4	-33.81	-30.75	-19.29
5	-16.59	-16.25	-13.59
6	-16.40	-16.04	-15.21
8	-25.13	-24.04	-14.29
9	-28.92	-27.03	-16.35
All	-239.37	-203.50	-124.95

(1a) TI: Thermodynamic integration: $\log(\text{Prob}(D|\text{Model}))$: 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

[Scaling factor = -4.847882]

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	2713125/3999315	0.67840
Genealogies	3344284/4000685	0.83593

MCMC-Autocorrelation and Effective MCMC Sample Size

Parameter	Autocorrelation	Effective Sample Size
Θ_1	0.80973	9375.36
Genealogies	0.80973	9375.36

Average temperatures during the run

Chain	Temperatures
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1	1.00000
2	1.50000
3	3.00000
4	1000000.00000

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. 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