AUTO

POPULATION SIZE, MIGRATION, DIVERGENCE, ASSIGNMENT, HISTORY
Bayesian inference using the structured coalescent
Migrate-n version 5.0.0a [May-20-2017]
  Using Intel AVX (Advanced Vector Extensions)
  Compiled for PARALLEL computer architectures
  One master and 20 compute nodes are available.
Program started at   Wed Oct 25 12:54:34 2017
Program finished at   Wed Oct 25 15:54:08 2017 [Runtime:0000:02:59:34]

Options

Datatype: DNA sequence data

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) 396354647
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
1 Romanshorn_0	*	*
1 Arbon_1	*	*

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	-1 1	Uniform	0.000000	0.050	0.100	0.010	1500	0.20000

[-1 -1 means priors were set globally]

Markov chain settings: Long chain
Number of chains 1
Recorded steps [a] 50000
Increment (record every x step [b] 200
Number of concurrent chains (replicates) [c] 2
Visited (sampled) parameter values [a*b*c] 20000000
Number of discard trees per chain (burn-in) 10000

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.0.7
Haplotyping is turned on: NO
Output file: outfile_0.7_0.4
Posterior distribution raw histogram file: bayesfile
Raw data from the MCMC run: bayesallfile_0.7_0.4
Print data: No
Print genealogies [only some for some data type]: None

Data summary

Data file:	infile.0.7
Datatype:	Sequence 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	10000
2	10000
3	10000
4	10000
5	10000
6	10000
7	10000
8	10000
9	10000
10	10000

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
1 Romanshorn_0	1	10
	2	10
	3	10
	4	10
	5	10
	6	10
	7	10
	8	10
	9	10
	10	10
1 Arbon_1	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	20
	2	20
	3	20
	4	20
	5	20
	6	20
	7	20
	8	20
	9	20
	10	20

Bayesian Analysis: Posterior distribution table

Locus	Parameter	2.5%	25.0%	Mode	75.0%	97.5%	Median	Mean
1	Θ_1	0.00000	0.00000	0.00003	0.09993	0.09993	0.00003	0.09460
2	Θ_1	0.00000	0.00000	0.00003	0.09993	0.09993	0.00003	0.09478
3	Θ_1	0.00000	0.00000	0.00003	0.09993	0.09993	0.00003	0.09463
4	Θ_1	0.00000	0.00000	0.00003	0.09993	0.09993	0.00003	0.09460
5	Θ_1	0.00000	0.00000	0.00003	0.09993	0.09993	0.00003	0.09464
6	Θ_1	0.04487	0.04633	0.04810	0.04980	0.05127	0.04697	0.09417
7	Θ_1	0.00000	0.00000	0.00003	0.09993	0.09993	0.00003	0.09473
8	Θ_1	0.04633	0.04740	0.04843	0.04940	0.05047	0.04850	0.09466
9	Θ_1	0.04420	0.04527	0.04630	0.04727	0.04833	0.04637	0.09466
10	Θ_1	0.00000	0.00000	0.00003	0.09993	0.09993	0.00003	0.09472
All	Θ_1	0.04440	0.04587	0.04777	0.04947	0.05107	0.04723	0.09941

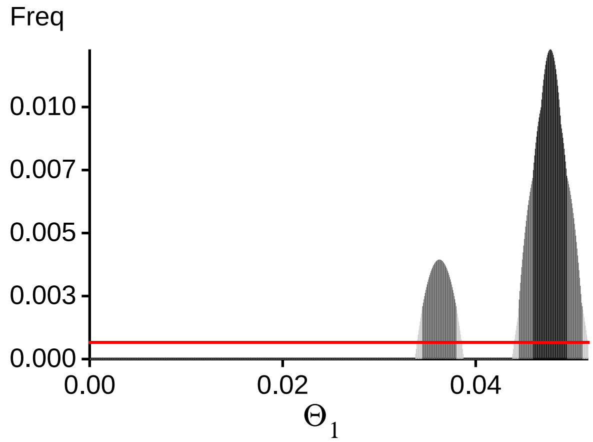
Citation suggestions:

Beerli P., 2006. Comparison of Bayesian and maximum-likelihood inference of population genetic parameters. Bioinformatics 22:341-345

Beerli P., 2007. Estimation of the population scaled mutation rate from microsatellite data, Genetics, 177:1967-1968.

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)	SS(2)	HS(3)
1	-28189.56	-22089.28	-20944.08	-21199.73
2	-31210.13	-22721.17	-nan	-21309.35
3	-78383.36	-40659.55	-nan	-33059.32
4	-33667.97	-28128.83	-nan	-27354.43
5	-27727.41	-21324.24	-nan	-20294.49
6	-22822.33	-19815.63	-nan	-19367.27
7	-48557.31	-35559.76	-nan	-33569.27
8	-26169.61	-20612.60	-nan	-19749.99
9	-23333.55	-19100.88	-nan	-18482.34
10	-36917.30	-27068.57	-nan	-25560.70
All	-356964.62	-257066.61	-nan	-239932.96

(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
[Scaling factor = 13.916173]
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	32320427/39988124	0.80825
Genealogies	1897802/160011876	0.01186

MCMC-Autocorrelation and Effective MCMC Sample Size

Parameter	Autocorrelation	Effective Sampe Size
Θ_1	0.08771	841726.79
Genealogies	0.98686	4818.86

Average temperatures during the run

Chain	Temperatures
1	0.00000
2	0.00000
3	0.00000
4	0.00000

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. 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