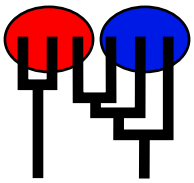
Simulated microsats

POPULATION SIZE, MIGRATION, DIVERGENCE, ASSIGNMENT, HISTORY
Bayesian inference using the structured coalescent
Migrate-n version 4.1.1a []
Compiled for PARALLEL computer architectures
One master and 8 compute nodes are available.
Program started at Thu Jan 29 20:05:28 2015
Program finished at Thu Jan 29 20:17:39 2015



Options

Datatype: Microsatellite data [Brownian motion]
Missing data: not included

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) 578438383
Start parameters:

Theta values were generated RANDOM start value from the prior

M values were generated RANDOM start value from 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 First_populatio *

Order of parameters:
1 Θ_1 <displayed>

Mutation rate among loci: Varying ([crudely] estimated from data)

Rates per locus: 1.08475, 1.22034, 0.94915, 0.81356, 0.81356, 0.94915, 1.22034, 0.94915

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	15.000000	30.000000	3.000000	1500

Markov chain settings: Long chain

Number of chains	1
Recorded steps [a]	5000
Increment (record every x step [b]	100
Number of concurrent chains (replicates) [c]	10
Visited (sampled) parameter values [a*b*c]	5000000
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 5

Print options:

Data file:	infile
Haplotyping is turned on:	NO
Output file:	outfile
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: Microsatellite data [Brownian]
[Data was used as repeat-length information]
Number of loci: 8

Mutationmodel:

Locus	Sublocus	Mutationmodel	Mutationmodel parameters
1	1	Brownian Motion	[none]
2	1	Brownian Motion	[none]
3	1	Brownian Motion	[none]
4	1	Brownian Motion	[none]
5	1	Brownian Motion	[none]
6	1	Brownian Motion	[none]
7	1	Brownian Motion	[none]
8	1	Brownian Motion	[none]

Population	Locus	Gene copies data	(missing)
1 First_population	1	40	(0)
	2	40	(0)
	3	40	(0)
	4	40	(0)
	5	40	(0)
	6	40	(0)
	7	40	(0)
	8	40	(0)
Total of all populations	1	40	(0)
	2	40	(0)
	3	40	(0)
	4	40	(0)
	5	40	(0)
	6	40	(0)
	7	40	(0)
	8	40	(0)

Relative mutation rate among loci estimated from the data

Locus	Relative mutation rate	Number of alleles
1	1.08475	8
2	1.22034	9
3	0.94915	7
4	0.81356	6
5	0.81356	6
6	0.94915	7
7	1.22034	9
8	0.94915	7
All	1.00000	7.4

Allele frequency spectra

Locus 1

Allele	Pop1	All
82	0.175	0.175
87	0.175	0.175
86	0.350	0.350
90	0.075	0.075
85	0.050	0.050
84	0.050	0.050
88	0.125	0.125
Alleles	7	7
Samplesize	40	40
H_{exp}	0.790	0.790

Locus 2

Allele	Pop1	All
82	0.600	0.600
80	0.025	0.025
81	0.250	0.250
78	0.025	0.025
79	0.025	0.025
85	0.025	0.025
84	0.025	0.025
83	0.025	0.025
Alleles	8	8
Samplesize	40	40
H_{exp}	0.574	0.574

Locus 3

Allele	Pop1	All
79	0.125	0.125
80	0.450	0.450
81	0.275	0.275
83	0.025	0.025
78	0.025	0.025
82	0.100	0.100
Alleles	6	6
Samplesize	40	40

Allele	Pop1	All
H_{exp}	0.695	0.695

Locus 4

Allele	Pop1	All
77	0.300	0.300
78	0.475	0.475
79	0.175	0.175
81	0.025	0.025
80	0.025	0.025
Alleles	5	5
Samplesize	40	40
H_{exp}	0.652	0.652

Locus 5

Allele	Pop1	All
83	0.675	0.675
84	0.125	0.125
77	0.125	0.125
80	0.050	0.050
81	0.025	0.025
Alleles	5	5
Samplesize	40	40
H_{exp}	0.510	0.510

Locus 6

Allele	Pop1	All
82	0.325	0.325
81	0.275	0.275
80	0.100	0.100
79	0.125	0.125
74	0.150	0.150
73	0.025	0.025
Alleles	6	6
Samplesize	40	40
H_{exp}	0.770	0.770

Locus 7

Allele	Pop1	All
81	0.175	0.175

Allele	Pop1	All
84	0.150	0.150
86	0.025	0.025
85	0.050	0.050
83	0.175	0.175
82	0.150	0.150
80	0.250	0.250
79	0.025	0.025
Alleles	8	8
Samplesize	40	40
H_{exp}	0.827	0.828

Locus 8

Allele	Pop1	All
82	0.125	0.125
81	0.175	0.175
79	0.425	0.425
80	0.175	0.175
77	0.025	0.025
78	0.075	0.075
Alleles	6	6
Samplesize	40	40
H_{exp}	0.736	0.736

Average expected heterozygosity

	Pop1	All
H_{exp}	0.000	0.000

Bayesian Analysis: Posterior distribution table

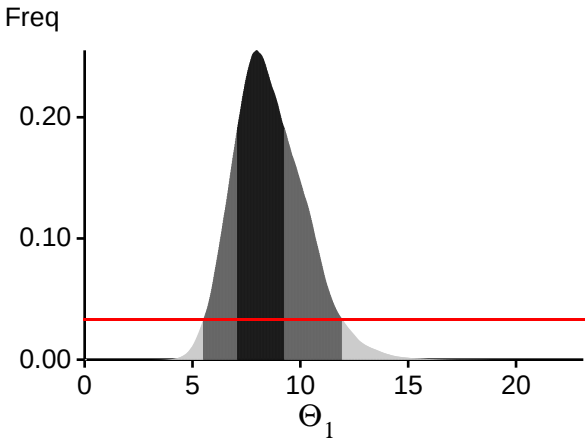
Locus	Parameter	2.5%	25.0%	Mode	75.0%	97.5%	Median	Mean
1	Θ_1	3.84000	6.60000	9.91000	14.42000	26.18000	12.65000	13.70712
2	Θ_1	2.90000	5.48000	7.67000	10.92000	20.14000	9.55000	10.44241
3	Θ_1	3.62000	6.96000	10.49000	14.54000	25.04000	12.51000	13.37036
4	Θ_1	2.14000	4.76000	7.31000	11.48000	21.94000	9.89000	10.87091
5	Θ_1	1.88000	3.58000	5.05000	7.06000	13.24000	6.19000	6.81524
6	Θ_1	2.86000	5.04000	7.79000	11.24000	22.16000	9.97000	11.07466
7	Θ_1	6.84000	11.50000	15.53000	21.12000	29.38000	17.03000	17.28699
8	Θ_1	3.14000	5.82000	8.29000	13.90000	25.74000	12.13000	13.13588
All	Θ_1	5.48000	7.06000	7.97000	9.26000	11.94000	8.45000	8.61378

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	-1143.22	-239.65	-60.59
2	-519.66	-129.13	-54.14
3	-258.77	-88.19	-55.31
4	-214.05	-76.30	-47.57
5	-707.11	-149.63	-38.92
6	-1618.60	-307.55	-52.13
7	-900.60	-203.08	-66.27
8	-361.78	-107.75	-56.69
All	-5719.89	-1297.37	-427.70

(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 = 3.907682
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	8054429/19997640	0.40277
Genealogies	8338569/20002360	0.41688

MCMC-Autocorrelation and Effective MCMC Sample Size

Parameter	Autocorrelation	Effective Sampe Size
Θ_1	0.77336	51311.49
Ln[Prob(D|G)]	0.85832	30606.99

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