

combined

MIGRATION RATE AND POPULATION SIZE ESTIMATION

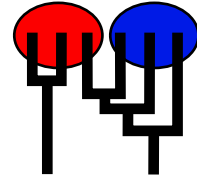
Maximum likelihood or Bayesian inference using the coalescent

Migrate-n version debug 4.0 [x]

Compiled for a SYMMETRIC MULTIPROCESSORS

Program started at Fri Dec 14 16:05:06 2012

Program finished at Fri Dec 14 16:14:39 2012



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) 738709323

Start parameters:

Theta values were generated from the FST-calculation

M values were generated from the FST-calculation

Connection type matrix:

where m = average (average over a group of Thetas or M,

s = symmetric M, S = symmetric 4Nm, 0 = zero, and not estimated,

* = free to vary, Thetas are on diagonal

Population 1

1 urchins *

Order of parameters:

1 Θ_1 <displayed>

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

Analysis strategy: Bayesian inference

Proposal distributions for parameter

Parameter	Proposal
Theta	Slice sampling
M	Slice sampling

Prior distribution for parameter

Parameter	Prior	Minimum	Mean*	Maximum	Delta	Bins
Theta	Uniform	0.000000	0.050000	0.100000	0.010000	1500
M	Uniform	0.000000	2500.000000	5000.000000	500.000000	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]	2
Visited (sampled) parameter values [a*b*c]	1000000
Number of discard trees per chain (burn-in)	10000

Multiple Markov chains:

Static heating scheme	4 chains with temperatures
	100000.00 3.00 1.50 1.00
	Swapping interval is 1

Print options:

Data file:	infile.gap
Haplotyping is turned on:	NO
Output file:	outfile-gap0
Posterior distribution raw histogram file:	bayesfile
Print data:	No
Print genealogies [only some for some data type]:	None

Data summary

Datatype: Unknown data [ERROR]
 [Fragment length is translated to repeats]

Number of loci: 5

Population	Locus	Gene copies data	(missing)
1 urchins	1	24	
	2	24	
	3	24	
	4	24	
	5	24	
Total of all populations	1	24	(0)
	2	24	(0)
	3	24	(0)
	4	24	(0)
	5	24	(0)

Bayesian Analysis: Posterior distribution table

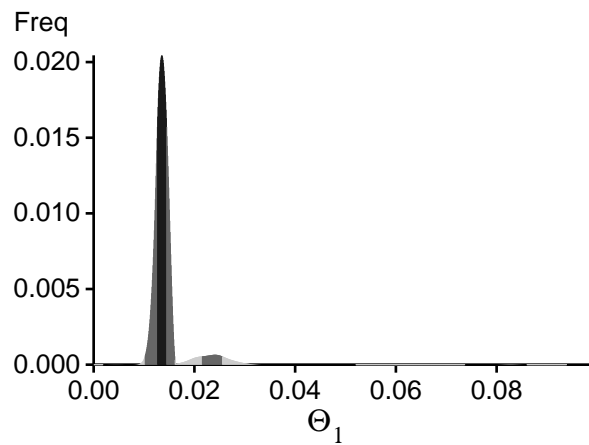
Locus	Parameter	2.5%	25.0%	Mode	75.0%	97.5%	Median	Mean
1	Θ_1	0.00433	0.00827	0.01123	0.01480	0.02547	0.01283	0.01392
2	Θ_1	0.01227	0.01820	0.02223	0.02720	0.04000	0.02417	0.01261
3	Θ_1	0.02453	0.03567	0.04203	0.05267	0.07620	0.04717	0.01631
4	Θ_1	0.00887	0.01373	0.01737	0.02173	0.03400	0.01917	0.00504
5	Θ_1	0.05660	0.07273	0.07997	0.09193	0.10000	0.07950	0.01573
All	Θ_1	0.01014	0.01261	0.01351	0.01448	0.01614	0.01371	0.01433

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	-465.03	-441.64	-427.55
2	-1685.11	-1615.24	-1608.58
3	-1033.13	-964.11	-952.94
4	-907.86	-874.66	-863.25
5	-3000.19	-2485.12	-2414.67
All	-7136.62	-6426.07	-6312.28

(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 = -45.293122

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	2549380/2549380	1.00000
Genealogies	347905/2501493	0.13908

MCMC-Autocorrelation and Effective MCMC Sample Size

Parameter	Autocorrelation	Effective Sampe Size
Θ_1	0.25345	30203.80
$\text{Ln}[\text{Prob}(\text{D} \text{G})]$	0.67238	10471.58

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.

Param 1 (Locus 5): Upper prior boundary seems too low!