Pantosteus platyrhynchus

POPULATION SIZE, MIGRATION, DIVERGENCE, ASSIGNMENT, HISTORY
Bayesian inference using the structured coalescent
Migrate-n version 4.4.4(git:v4-series-26-ge85c6ff) [June-1-2019]
Compiled for a SYMMETRIC multiprocessors (Grandcentral)
Program started at Fri May 21 15:57:31 2021
Program finished at Fri May 21 16:54:17 2021 [Runtime:0000:00:56:46]

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)	3056157581

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	2
1 Great_Salt_lake	*	d
2 Sevier_Desert	0	*

Order of parameters:

1	Θ_1	<displayed>
2	Θ_2	<displayed>
3	$\Delta_{2->1}$	<displayed>

4	$\sigma_{2->1}$	<displayed>

Mutation rate among loci: Mutation rate is constant

Analysis strategy: Bayesian inference
-Population size estimation: Exponential Distribution
-Geneflow estimation: Exponential Distribution
-Divergence time estimation: Normal Distribution Shortcut (mean and standard dev.)

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	0.12500
2	Theta	**	Uniform	0.000000	0.050	0.100	0.010	1500	0.12500
3	Splittime mean	**	Uniform	0.000000	0.250	0.500	0.050	1500	0.12500
4	Splittime std	**	Uniform	0.000000	0.250	0.500	0.050	1500	0.12500

[* * means priors were set globally]

Markov chain settings:	Long chain
Number of chains	1
Recorded steps [a]	10000
Increment (record every x step [b]	1000
Number of concurrent chains (replicates) [c]	2
Visited (sampled) parameter values [a*b*c]	20000000
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
Haplotyping is turned on:	NO
Output file:	outfile
Log file:	logfile

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:	Haplotype data
Number of loci:	1

Mutationmodel:

Locus	Sublocus	Mutationmodel	Mutationmodel parameters
1	1	HKY	[Bf:0.28 0.27 0.16 0.30, kappa=11.220]
1	2	HKY	[Bf:0.28 0.28 0.17 0.27, kappa=11.220]
1	3	HKY	[Bf:0.23 0.28 0.21 0.28, kappa=11.220]
1	4	HKY	[Bf:0.22 0.30 0.20 0.28, kappa=11.220]
1	5	HKY	[Bf:0.26 0.28 0.19 0.28, kappa=11.220]
1	6	HKY	[Bf:0.24 0.28 0.19 0.28, kappa=11.220]

Sites per locus

Locus	Sites					
1	863	2357	975	1047	1673	1140

Site rate variation and probabilities:

Locus	Sublocus	Region type	Rate of change	Probability	Patch size
1	1	1	1.000	1.000	1.000
1	2	1	1.000	1.000	1.000
1	3	1	1.000	1.000	1.000
1	4	1	1.000	1.000	1.000
1	5	1	1.000	1.000	1.000
1	6	1	1.000	1.000	1.000

Population	Locus	Gene copies data	(missing)
1 Great_Salt_lake	1	2	
2 Sevier_Desert	1	3	
Total of all populations	1	5	(0)

Bayesian Analysis: Posterior distribution table

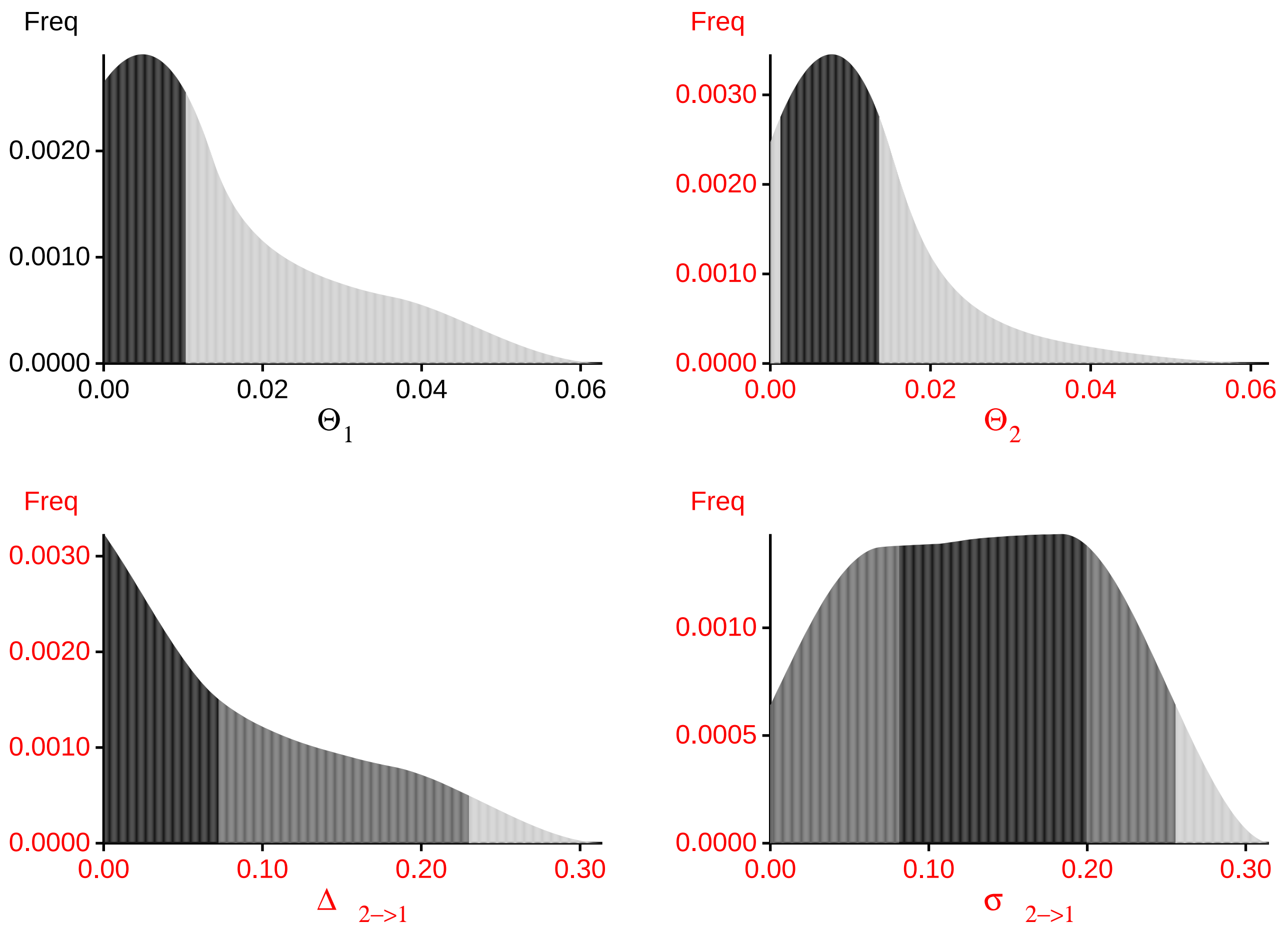
Locus	Parameter	2.5%	25.0%	Mode	75.0%	97.5%	Median	Mean
1	Θ_1	0.00000	0.00000	0.00490	0.01033	0.01033	0.01223	0.02286
1	Θ_2	0.00120	0.00120	0.00763	0.01360	0.01360	0.01050	0.01147
1	$D_{2\text{->}1}$	0.00000	0.00000	0.00017	0.07233	0.23000	0.07250	0.15944
1	$S_{2\text{->}1}$	0.00000	0.08100	0.18383	0.19967	0.25567	0.13483	0.26713

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 for locus 1



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]

Method	ln(Prob(D|Model))	Notes
Thermodynamic integration	-13870.344767	(1a)
	-12816.222729	(1b)
Harmonic mean	-12765.582837	(2)

(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

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	1387875/2497507	0.55570
Θ_2	965919/2500753	0.38625
$\Delta_{2->1}$	1838039/2500606	0.73504
$\sigma_{2->1}$	1972476/2500322	0.78889
Genealogies	733013/10000812	0.07330

MCMC-Autocorrelation and Effective MCMC Sample Size

Parameter	Autocorrelation	Effective Sampe Size
Θ_1	-0.01104	20445.55
Θ_2	0.05393	17961.43
$\Delta_{2->1}$	-0.00814	20328.46
$\sigma_{2->1}$	0.01062	19578.79
Genealogies	0.01062	19578.79

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