

Etelis coruscans

POPULATION SIZE, MIGRATION, DIVERGENCE, ASSIGNMENT, HISTORY

Bayesian inference using the structured coalescent

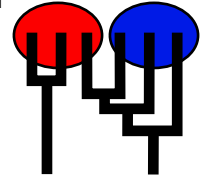
Migrate-n version 5.0.4(git:Distribution-version) [May-09-2022]

Compiled for PARALLEL computer architectures

One master and 119 compute nodes are available.

Program started at Thu Nov 10 12:52:56 2022

Program finished at Thu Nov 10 15:19:39 2022 [Runtime:0000:02:26:43]



Options

Inheritance multipliers in use for Thetas:

All loci use an inheritance multiplier of 1.0

Random number seed: (with internal timer) 58628569

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	2	3	4
1 Pop_Japan	*	*	*	*
2 Pop_Johnston_At	*	*	*	*
3 Pop_MHI	*	*	*	*
4 Pop_NWHI	*	*	*	*

Order of parameters:

1 Θ_1 <displayed>

2 Θ_2 <displayed>

3	Θ_3	<displayed>
4	Θ_4	<displayed>
5	M _{2→1}	<displayed>
6	M _{3→1}	<displayed>
7	M _{4→1}	<displayed>
8	M _{1→2}	<displayed>
9	M _{3→2}	<displayed>
10	M _{4→2}	<displayed>
11	M _{1→3}	<displayed>
12	M _{2→3}	<displayed>
13	M _{4→3}	<displayed>
14	M _{1→4}	<displayed>
15	M _{2→4}	<displayed>
16	M _{3→4}	<displayed>

Mutation rate among loci:

Mutation rate is constant for all loci

Analysis strategy:

Bayesian inference

-Population size estimation:

Exponential Distribution

-Geneflow estimation:

Exponential Distribution

Proposal distributions for parameter

Parameter	Proposal
Theta	Metropolis sampling
M	Slice 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 Exp window	0.000000	0.001	0.100	0.010	2000	0.03125
2	Theta Exp window	0.000000	0.001	0.100	0.010	2000	0.03125
3	Theta Exp window	0.000000	0.001	0.100	0.010	2000	0.03125
4	Theta Exp window	0.000000	0.001	0.100	0.010	2000	0.03125
5	M Exp window	0.010000	10000	10000	10000	2000	0.03125
6	M Exp window	0.010000	10000	10000	10000	2000	0.03125
7	M Exp window	0.010000	10000	10000	10000	2000	0.03125
8	M Exp window	0.010000	10000	10000	10000	2000	0.03125
9	M Exp window	0.010000	10000	10000	10000	2000	0.03125
10	M Exp window	0.010000	10000	10000	10000	2000	0.03125
11	M Exp window	0.010000	10000	10000	10000	2000	0.03125
12	M Exp window	0.010000	10000	10000	10000	2000	0.03125
13	M Exp window	0.010000	10000	10000	10000	2000	0.03125

14	M	Exp window	0.010000	10000	10000	10000	2000	0.03125
15	M	Exp window	0.010000	10000	10000	10000	2000	0.03125
16	M	Exp window	0.010000	10000	10000	10000	2000	0.03125

[* * 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]	3
Visited (sampled) parameter values [a*b*c]	3000000
Number of discard trees per chain (burn-in)	2000

Multiple Markov chains:

Static heating scheme

1000000.00	4 chains with temperatures
3.00	1.50 1.00
	Swapping interval is 1

Print options:

Data file:	../Ecoruscans2.mig
	parmfile
Haplotyping is turned on:	NO
Output file:	outfile.txt
Log file:	logfile.txt
Posterior distribution raw histogram file:	bayesfile
Raw data from the MCMC run:	bayesallfile
Print data:	No
Print genealogies [only some for some data type]:	None

Bayesian Analysis: Posterior distribution over all loci