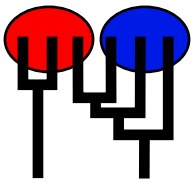
POPULATION SIZE, MIGRATION, DIVERGENCE, ASSIGNMENT, HISTORY
Bayesian inference using the structured coalescent
Migrate-n version 4.4.4(git:) [June-1-2019]
Program started at Sun Oct 24 18:33:59 2021
Program finished at Tue Oct 26 07:35:48 2021 [Runtime:0001:13:01:49]



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]

Data set was subsampled: used a random sample of size:
50 and seed 198235

Random number seed: (with internal timer) 2145934296
Start parameters:

Theta values were generated ERROR

M values were generated ERROR

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
1 POP1	*	0	*
2 POP2	*	*	*
3 POP3	*	*	*

Order of parameters:

1	Θ_1	<displayed>
2	Θ_2	<displayed>
3	Θ_3	<displayed>
4	$M_{3->1}$	<displayed>
5	$M_{1->2}$	<displayed>
6	$M_{3->2}$	<displayed>
7	$M_{1->3}$	<displayed>
8	$M_{2->3}$	<displayed>

Mutation rate among loci: Mutation rate is constant

Analysis strategy: Bayesian inference
-Population size estimation: Exponential Distribution
-Geneflow 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	**	Uniform	0.000000	5.000	10.00	0.010	1500	0.06250
2	Theta	**	Uniform	0.000000	5.000	10.00	0.010	1500	0.06250
3	Theta	**	Uniform	0.000000	5.000	10.00	0.010	1500	0.06250
4	M	**	Uniform	0.000000	500.0	1000.	1.000	1500	0.06250
5	M	**	Uniform	0.000000	500.0	1000.	1.000	1500	0.06250
6	M	**	Uniform	0.000000	500.0	1000.	1.000	1500	0.06250
7	M	**	Uniform	0.000000	500.0	1000.	1.000	1500	0.06250
8	M	**	Uniform	0.000000	500.0	1000.	1.000	1500	0.06250

[* * 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)	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:	Migrate_all.txt
Haplotyping is turned on:	NO
Output file:	outfile_YYfinal_e
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: Migrate_all.txt
Datatype: Sequence data
Number of loci: 1

Mutationmodel:

Locus	Sublocus	Mutationmodel	Mutationmodel parameters
1	1	Felsenstein 84	[Bf:0.25 0.26 0.25 0.25, t/t ratio=2.000]

Data set was subsampled: used a random sample of size: 50

Sites per locus

Locus	Sites
1	13148

Site rate variation and probabilities:

Locus	Sublocus	Region type	Rate of change	Probability	Patch size
1	1	1	1.000	1.000	1.000

Population	Locus	Gene copies
1 POP1	1	160
2 POP2	1	188
3 POP3	1	110
Total of all populations	1	458

Subsampled dataset

Data set was subsampled randomly per population: 50 samples taken

Locus	Population	Individuals
1	POP1	VGNP72.cle VGNP24.cle VGNP86.cle VGNP37.cle VGNP65.cle VGNP13.cle VGNP36.cle VGNP72.cle VGNP27.cle VGNP106.cl VGNP41.cle VGNP10_all VGNP59.cle VGNP1.clea VGNP105.cl VGNP78.cle VGNP9.clea VGNP46.cle VGNP75.cle VGNP34.cle VGNP74.cle VGNP110.cl VGNP21_all VGNP3.clea VGNP66.cle VGNP104.cl VGNP82.cle VGNP4.clea VGNP91.cle VGNP7.clea VGNP13.cle VGNP28.cle VGNP89.cle VGNP35.cle VGNP86.cle VGNP48.cle VGNP22.cle VGNP22.cle VGNP105.cl VGNP70.cle VGNP84.cle VGNP6.clea VGNP96.cle VGNP93.cle VGNP104.cl VGNP63.cle VGNP59.cle VGNP107.cl VGNP63.cle VGNP4.clea
	POP2	VXRM223.cl VXRM204.cl VXRM62.cle VXRM241.cl VXRM209.cl VXRM266.cl VXRM220.cl VXRM176.cl VXRM205.cl VXRM195.cl VXRM214.cl VXRM184.cl VXRM183.cl VXRM243.cl VXRM224.cl VXRM166.cl VXRM201.cl VXRM235.cl VXRM189.cl VXRM247.cl VXRM203.cl VXRM184.cl VXRM252.cl VXRM255.cl VXRM192.cl VXRM206.cl VXRM32.cle VXRM238.cl VXRM264.cl VXRM218.cl VXRM254.cl VXRM178.cl VXRM200.cl VXRM247.cl VXRM232.cl VXRM267.cl VXRM57.cle VXRM236.cl VXRM208.cl VXRM223.cl VXRM248.cl VXRM219.cl VXRM193.cl VXRM188.cl VXRM199.cl VXRM244.cl VXRM174.cl VXRM215.cl VXRM203.cl VXRM251.cl
	POP3	VXRN24.cle VXRN106.cl VXRN52.cle VXRN147.cl VXRN154.cl VXRN121.cl VXRN33.cle VXRN28.cle VXRN150.cl VXRN141.cl VXRN161.cl VXRN28.cle VXRN03.cle VXRN137.cl VXRN130.cl VXRN163.cl VXRN119.cl VXRN30.cle VXRN142.cl VXRN116.cl VXRN136.cl VXRN154.cl VXRN106.cl VXRN147.cl VXRN100.cl VXRN16.cle VXRN143.cl VXRN107.cl VXRN136.cl VXRN155.cl VXRN25.cle VXRN143.cl VXRN52.cle VXRN130.cl VXRN12.cle VXRN65.cle VXRN03.cle VXRN159.cl VXRN128.cl VXRN126.cl VXRN161.cl VXRN146.cl VXRN117.cl VXRN148.cl VXRN162.cl VXRN152.cl VXRN16.cle VXRN135.cl VXRN120.cl VXRN30.cle

Bayesian Analysis: Posterior distribution table

Locus	Parameter	2.5%	25.0%	Mode	75.0%	97.5%	Median	Mean
1	Θ_1	1.00667	1.84667	2.09000	2.32000	3.13333	2.09667	2.08962
1	Θ_2	1.66667	3.10667	3.88333	4.58000	5.60000	3.73667	6.01194
1	Θ_3	1.98667	3.22667	3.78333	4.32000	5.53333	3.77000	4.53445
1	$M_{3->1}$	275.3	378.0	384.3	390.0	496.7	385.0	384.0
1	$M_{1->2}$	304.0	440.0	445.0	448.7	585.3	446.3	466.9
1	$M_{3->2}$	298.7	381.3	420.3	458.0	532.7	420.3	454.8
1	$M_{1->3}$	315.3	381.3	434.3	488.0	556.0	435.7	447.7
1	$M_{2->3}$	320.0	387.3	429.0	469.3	542.0	430.3	428.9

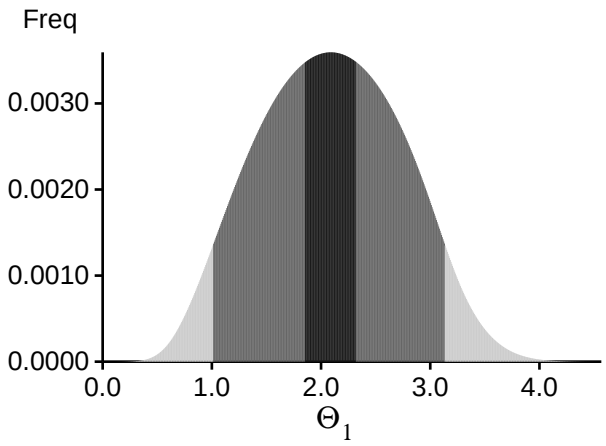
Citation suggestions:

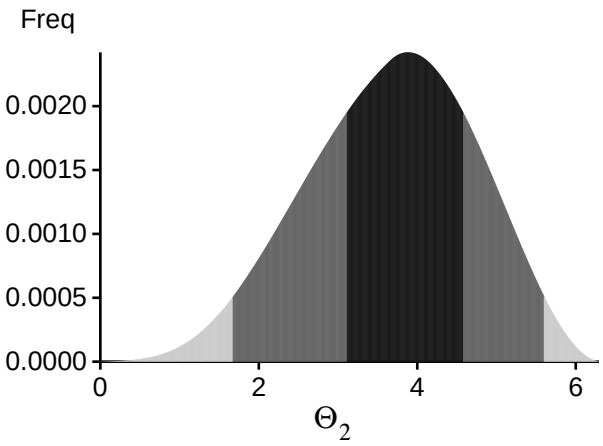
Beerli P., 2006. Comparison of Bayesian and maximum-likelihood inference of population genetic parameters. Bioinformatics 22:341-345

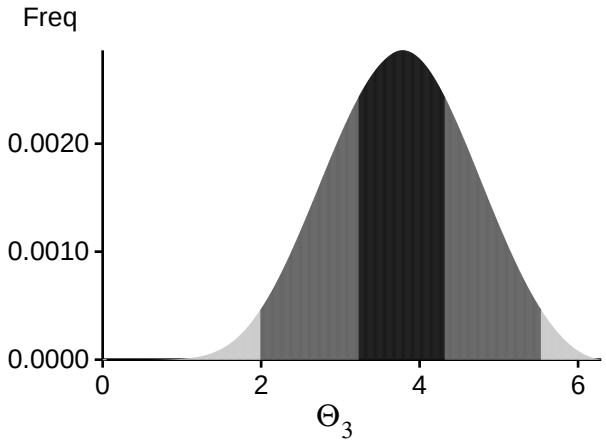
Beerli P., 2007. Estimation of the population scaled mutation rate from microsatellite data, Genetics, 177:1967-1968.

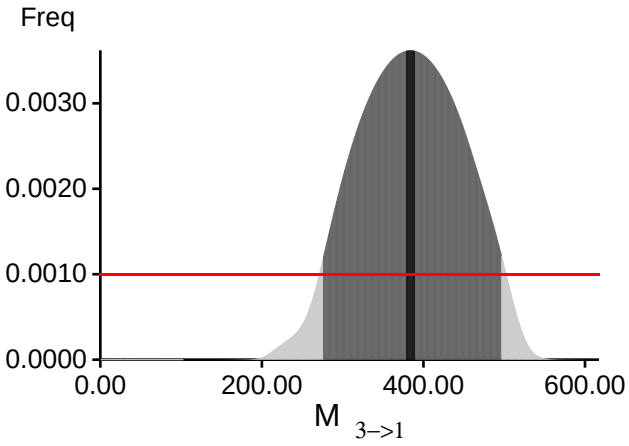
Beerli P., 2009. How to use MIGRATE or why are Markov chain Monte Carlo programs difficult to use? In Population Genetics for Animal Conservation, G. Bertorelle, M. W. Bruford, H. C. Hauffe, A. Rizzoli, and C. Vernesi, eds., vol. 17 of Conservation Biology, Cambridge University Press, Cambridge UK, pp. 42-79.

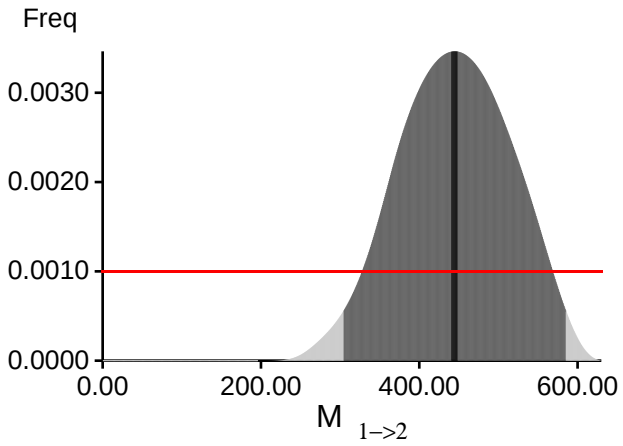
Bayesian Analysis: Posterior distribution for locus 1

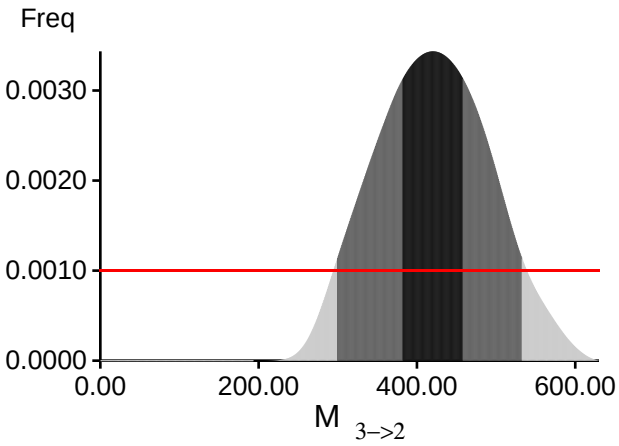


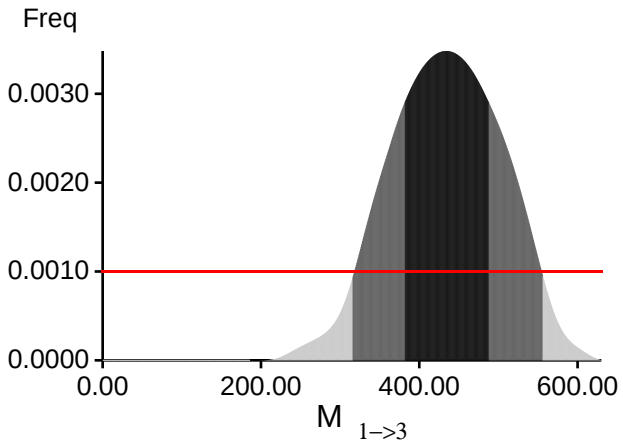








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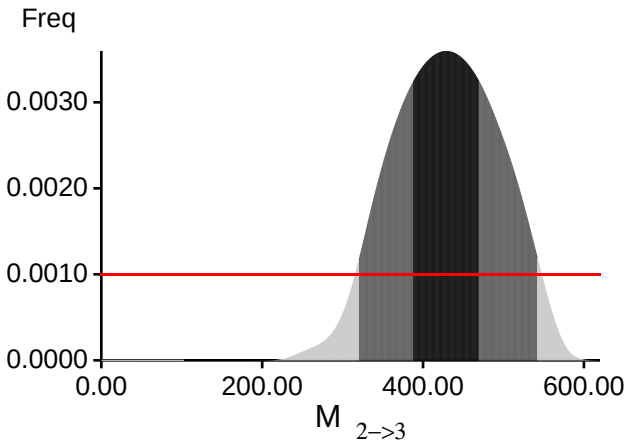
M 1–>3


Freq
0.0030
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0.0010
0.0000
0.00
200.00
400.00
600.00
M 2–>3

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	-834748.117918	(1a)
	-645917.648997	(1b)
Harmonic mean	-617003.083610	(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	110657/186886	0.59211
Θ_2	127853/187136	0.68321
Θ_3	99514/187875	0.52968
$M_{3->1}$	51707/187807	0.27532
$M_{1->2}$	72635/187603	0.38717
$M_{3->2}$	106742/187969	0.56787
$M_{1->3}$	110482/187974	0.58775
$M_{2->3}$	67169/187838	0.35759
Genealogies	883/1498912	0.00059

MCMC-Autocorrelation and Effective MCMC Sample Size

Parameter	Autocorrelation	Effective Sampe Size
Θ_1	0.63834	6749.40
Θ_2	0.18770	20980.25
Θ_3	0.41140	12659.40
$M_{3->1}$	0.66741	6393.21
$M_{1->2}$	0.77753	4297.10
$M_{3->2}$	0.65076	7559.30
$M_{1->3}$	0.64437	8258.86
$M_{2->3}$	0.84215	2665.87
Genealogies	0.99965	5.27

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.

Genealogies 10: Effective sample size of run seems too short!