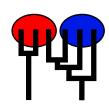
AUTO

MIGRATION RATE AND POPULATION SIZE ESTIMATION using the coalescent and maximum likelihood or Bayesian inference Migrate-n version 3.7.0 [April-06-16]

Program started at Wed Apr 6 23:13:06 2016 Program finished at Wed Apr 6 23:18:28 2016



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]

Random number seed: (from parmfile) 310705631

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	2	3	4
1 Romanshorn0	m	а	b	а
2 Arbon1	а	m	а	b
3 Kreuzlingen2	b	а	m	а
4 Frauenfeld3	а	b	а	m

Order of parameters:

1	Θ_1	=	Θ_1	[m]	<displayed></displayed>
2	Θ_2	=	Θ_1	[m]	
3	Θ_3^-	=	Θ_1	[m]	
4	Θ_4	=	Θ_1	[m]	

5	M ₂₋	_>1 =	M 2->1	[a]	<displayed></displayed>	I.			
6	N /	->1 =	M $_{3->1}^{2}$		<displayed></displayed>				
7	N/I	->1 ->1 =	M $_{4->1}$	[a]	<displayed></displayed>				
8	M 1	=	M $_{1->2}^{4->1}$		<displayed></displayed>				
9	M 2	->2	M $_{3->2}^{1->2}$		<displayed></displayed>				
10	M_{4}^{3}	->2 - 2 =	M $_{4->2}^{3->2}$	[b]	<displayed></displayed>				
11	M ₁	->2 >2 =	$M_{1->3}$		<displayed></displayed>				
12	V //	->3	$M_{2->3}$		<displayed></displayed>				
13	M ₄	->3 = ->3 =			<displayed></displayed>				
14	M ₄ -	->3 =	¬ / /		<displayed></displayed>				
15	M ₂	->4 -	1 / 7	[a] [h]	<displayed></displayed>				
	N / -	_>4 =	M 2->4						
16	M ₃₋	_>4 =	M $_{3->4}$	[a]	<displayed></displayed>				
Mutation rate	among loc	ci:					Muta	tion rate is	constant for all loci
Analysis stra	tegy:							I	Bayesian inference
									-
Proposal dist	ributions fo	r paramete	er						
Parameter		•		Propos	al				
Theta			Slic	e samplir					
M				e samplir	_				
			00	o oampiii	.9				
Prior distribut	tion for nara	ameter							
Parameter	Prior	Minimu	m	Mear	n* Ma	aximum		Delta	Bins
Theta	Uniform	0.00000		0.05000		00000	0.0	10000	500
M	Uniform	0.00000		0.00000			1000.0		
IVI	Offiloffii	0.00000	0 500	0.00000	0 10000.0	00000	1000.0	00000	500
l.,									
Markov chair	•								Long chain
Number of ch									1
Recorded									5000
Increment	(record eve	ery x step [b]						10
Number of	concurrent	chains (re	plicates)	[c]					2
Visited (sa	mpled) para	ameter val	ues [a*b*	c]					100000
Number of	discard tre	es per cha	in (burn-i	n)					5000
Multiple Mark	ov chains:								
Static heat	ing scheme)						4 chains	with temperatures
						100000	0.00	3.00	1.50 1.00
									apping interval is 1
								2	11 9 3
Print options:									
Data file:									infile.4pop
Output file:									outfile-4pop
Output file.	<u> </u>								Juliile-4pop

Posterior distribution raw histogram file: Print data:	bayesfil N
Print genealogies [only some for some data type]:	Noi

Data summary

Datatype: Sequence data Number of loci: 2

Population	Locus	Gene copies
1 Romanshorn0	1	10
	2	10
2 Arbon1	1	10
	2	10
3 Kreuzlingen2	1	10
	2	10
4 Frauenfeld3	1	10
	2	10
Total of all populations	1	40
	2	40

Bayesian Analysis: Posterior distribution table

Locus	Parameter	2.5%	25.0%	Mode	75.0%	97.5%	Median	Mean
1	Θ_1	0.00500	0.00700	0.00850	0.00980	0.01300	0.00890	0.00890
1	Θ_2	0.00500	0.00700	0.00850	0.00980	0.01300	0.00890	0.00890
1	Θ_3	0.00500	0.00700	0.00850	0.00980	0.01300	0.00890	0.00890
1	Θ_4	0.00500	0.00700	0.00850	0.00980	0.01300	0.00890	0.00890
1	M _{2->1}	0.0	60.0	150.0	220.0	320.0	190.0	152.5
1	M _{3->1}	0.0	60.0	150.0	220.0	340.0	190.0	156.3
1	M _{4->1}	0.0	60.0	150.0	220.0	320.0	190.0	152.5
1	M _{1->2}	0.0	60.0	150.0	220.0	320.0	190.0	152.5
1	$M_{3->2}$	0.0	60.0	150.0	220.0	320.0	190.0	152.5
1	M _{4->2}	0.0	60.0	150.0	220.0	340.0	190.0	156.3
1	M _{1->3}	0.0	60.0	150.0	220.0	340.0	190.0	156.3
1	M _{2->3}	0.0	60.0	150.0	220.0	320.0	190.0	152.5
1	M _{4->3}	0.0	60.0	150.0	220.0	320.0	190.0	152.5
1	M _{1->4}	0.0	60.0	150.0	220.0	320.0	190.0	152.5
1	M _{2->4}	0.0	60.0	150.0	220.0	340.0	190.0	156.3
1	$M_{3->4}$	0.0	60.0	150.0	220.0	320.0	190.0	152.5
2	Θ_1	0.01040	0.01340	0.01570	0.01800	0.02340	0.01650	0.01673
2	Θ_2	0.01040	0.01340	0.01570	0.01800	0.02340	0.01650	0.01673
2	Θ_3	0.01040	0.01340	0.01570	0.01800	0.02340	0.01650	0.01673
2	Θ_4	0.01040	0.01340	0.01570	0.01800	0.02340	0.01650	0.01673
2	M _{2->1}	0.0	60.0	150.0	220.0	320.0	170.0	142.9
2	$M_{3->1}$	0.0	20.0	150.0	220.0	400.0	190.0	163.0
2	M _{4->1}	0.0	60.0	150.0	220.0	320.0	170.0	142.9
2	M _{1->2}	0.0	60.0	150.0	220.0	320.0	170.0	142.9
2	$M_{3->2}$	0.0	60.0	150.0	220.0	320.0	170.0	142.9
2	M _{4->2}	0.0	20.0	150.0	220.0	400.0	190.0	163.0
2	M _{1->3}	0.0	20.0	150.0	220.0	400.0	190.0	163.0
2	$M_{2->3}$	0.0	60.0	150.0	220.0	320.0	170.0	142.9
2	$M_{4->3}$	0.0	60.0	150.0	220.0	320.0	170.0	142.9
2	M _{1->4}	0.0	60.0	150.0	220.0	320.0	170.0	142.9
2	M _{2->4}	0.0	20.0	150.0	220.0	400.0	190.0	163.0
2	$M_{3->4}$	0.0	60.0	150.0	220.0	320.0	170.0	142.9
All	Θ_1	0.00460	0.01000	0.01190	0.01360	0.01620	0.01190	0.01146
All	Θ_2	0.00460	0.01000	0.01190	0.01360	0.01620	0.01190	0.01146

Migrate 3.7.0: (http://popgen.sc.fsu.edu) [program run on 23:13:06]

Locus	Parameter	2.5%	25.0%	Mode	75.0%	97.5%	Median	Mean
All	Θ_3	0.00460	0.01000	0.01190	0.01360	0.01620	0.01190	0.01146
All	Θ_4	0.00460	0.01000	0.01190	0.01360	0.01620	0.01190	0.01146
All	M _{2->1}	0.0	60.0	150.0	240.0	360.0	190.0	154.7
All	M _{3->1}	0.0	60.0	170.0	240.0	380.0	190.0	161.5
All	M _{4->1}	0.0	60.0	150.0	240.0	360.0	190.0	154.7
All	M _{1->2}	0.0	60.0	150.0	240.0	360.0	190.0	154.7
All	M _{3->2}	0.0	60.0	150.0	240.0	360.0	190.0	154.7
All	M _{4->2}	0.0	60.0	170.0	240.0	380.0	190.0	161.5
All	M _{1->3}	0.0	60.0	170.0	240.0	380.0	190.0	161.5
All	M _{2->3}	0.0	60.0	150.0	240.0	360.0	190.0	154.7
All	M _{4->3}	0.0	60.0	150.0	240.0	360.0	190.0	154.7
All	M _{1->4}	0.0	60.0	150.0	240.0	360.0	190.0	154.7
All	M _{2->4}	0.0	60.0	170.0	240.0	380.0	190.0	161.5
All	M _{3->4}	0.0	60.0	150.0	240.0	360.0	190.0	154.7

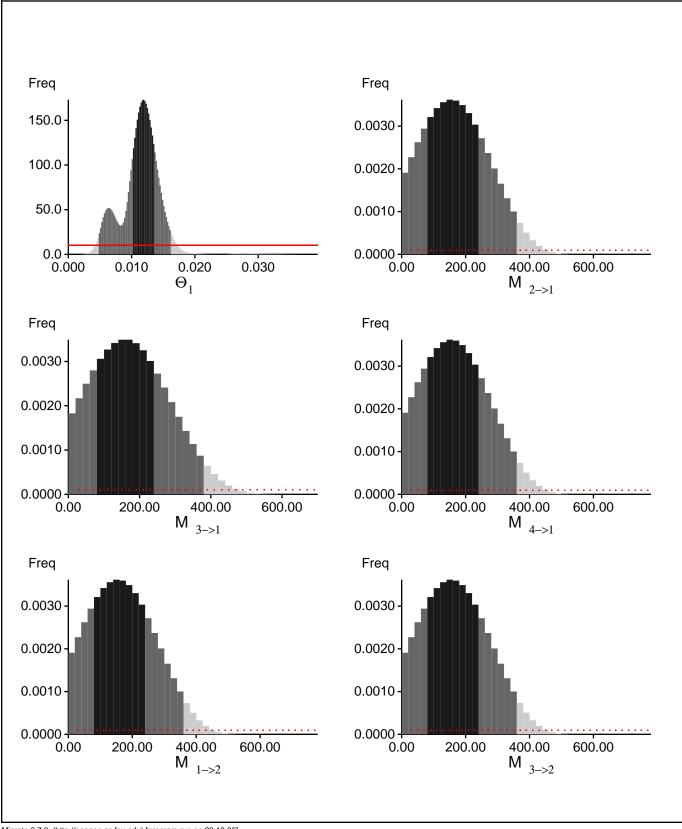
Citation suggestions:

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

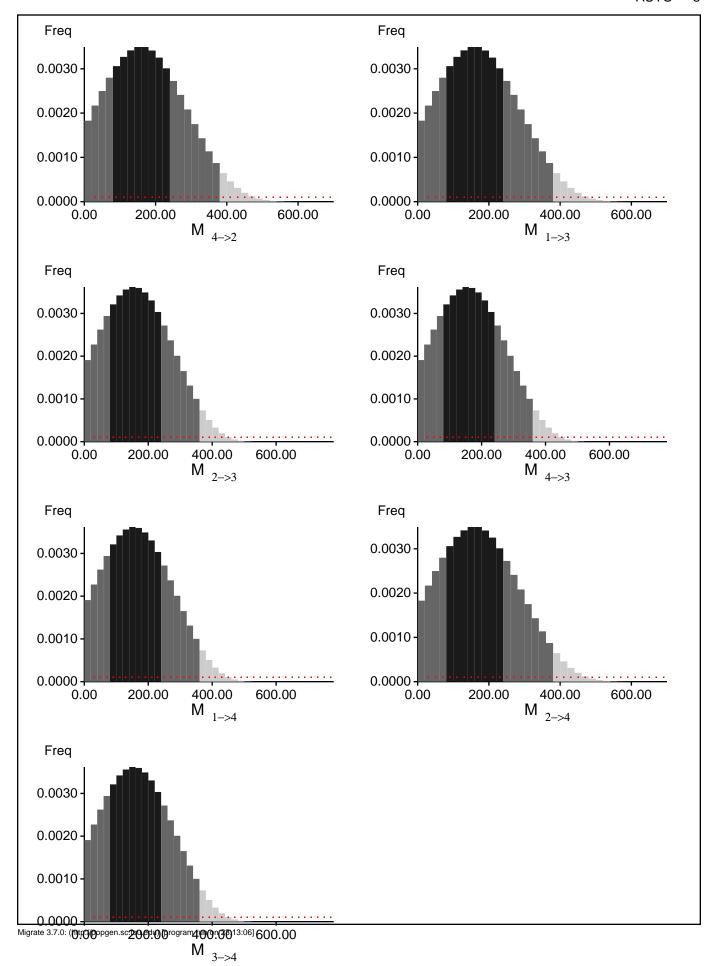
Beerli P., 2007. Estimation of the population scaled mutation rate from microsatellite data, Genetics, 177:1967-1968.

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 over all loci



Migrate 3.7.0: (http://popgen.sc.fsu.edu) [program run on 23:13:06]



Log-Probability of the data given the model (marginal likelihood)

Use this value for Bayes factor calculations: BF = Exp[In(Prob(D | thisModel) - In(Prob(D | otherModel)) or as LBF = 2(In(Prob(D | thisModel) - In(Prob(D | otherModel))) shows the support for thisModel]

Locus	Raw thermodynamic score(1a)	Bezier approximation score(1b)	Harmonic mean(2)
1	-3236.57	-2551.03	-2440.64
2	-3648.64	-2831.27	-2692.21
All	-6844.65	-5341.74	-5092.29

(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 = 40.562384

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	6300/6300	1.00000
Θ_2	6300/6300	1.00000
Θ_3^2	6300/6300	1.00000
Θ_4°	6300/6300	1.00000
$M_{2\rightarrow 1}$	6247/6247	1.00000
$M_{3->1}$	6239/6239	1.00000
$M_{4->1}$	6262/6262	1.00000
$M_{1\rightarrow 2}$	6108/6108	1.00000
$M_{3\rightarrow 2}$	6214/6214	1.00000
$M_{4\rightarrow 2}$	6210/6210	1.00000
$M_{1->3}$	6208/6208	1.00000
$M_{2->3}$	6207/6207	1.00000
$M_{4->3}^{2->3}$	6348/6348	1.00000
M 1->4	6306/6306	1.00000
$M_{2->4}$	6359/6359	1.00000
$M_{3->4}$	6230/6230	1.00000
Genealogies	5754/99941	0.05757

MCMC-Autocorrelation and Effective MCMC Sample Size

Parameter	Autocorrelation	Effective Sampe Size
Θ_1	0.84394	1692.50
Θ_2	0.84394	1692.50
Θ_3^2	0.84394	1692.50
$\Theta_4^{^3}$	0.84394	1692.50
$M_{2->1}$	0.50812	6585.48
$M_{3\rightarrow 1}$	0.64221	4457.40
M $_{4\rightarrow 1}^{3\rightarrow 1}$	0.50812	6585.48
$M_{1->2}$	0.50812	6585.48
$M_{3->2}$	0.50812	6585.48
M $_{4\rightarrow 2}^{3\rightarrow 2}$	0.64221	4457.40
M $_{1->3}^{4->2}$	0.64221	4457.40
$M_{2->3}^{1->3}$	0.50812	6585.48
$M_{4->3}^{2->3}$	0.50812	6585.48
$M_{1->4}^{4->3}$	0.50812	6585.48
M $_{2->4}^{1->4}$	0.64221	4457.40
M $_{3\rightarrow 4}^{2\rightarrow 4}$	0.50812	6585.48
Ln[Prob(D G)]	0.85991	1508.57

Potential Problems

This section reports potential problems with your run, but such reporting is often not very accurate. Whith 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 wether 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.
structions, reducing number of parameters may help in such structions.
No warning was recorded during the run