POPULATION SIZE, MIGRATION, DIVERGENCE, ASSIGNMENT, HISTORY
Bayesian inference using the structured coalescent
Migrate-n version debug 4.2.7 [April-1-2016]
Using Intel AVX (Advanced Vector Extensions)
Compiled for a SYMMETRIC multiprocessors (Grandcentral)
Program started at Mon Apr 11 10:10:19 2016
Program finished at Mon Apr 11 10:54:49 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 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 Romanshorn_0	m	a	b	a
2 Arbon_1	a	m	a	b
3 Kreuzlingen_2	b	a	m	a
4 Frauenfeld_3	a	b	a	m

Order of parameters:

1	Θ_1	=	Θ_1	[m]	<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>
6	$M_{3->1}$	=	$M_{3->1}$	[b]	<displayed>
7	$M_{4->1}$	=	$M_{2->1}$	[a]	
8	$M_{1->2}$	=	$M_{2->1}$	[a]	
9	$M_{3->2}$	=	$M_{2->1}$	[a]	
10	$M_{4->2}$	=	$M_{3->1}$	[b]	
11	$M_{1->3}$	=	$M_{3->1}$	[b]	
12	$M_{2->3}$	=	$M_{2->1}$	[a]	
13	$M_{4->3}$	=	$M_{2->1}$	[a]	
14	$M_{1->4}$	=	$M_{2->1}$	[a]	
15	$M_{2->4}$	=	$M_{3->1}$	[b]	
16	$M_{3->4}$	=	$M_{2->1}$	[a]	

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	500
Theta	Uniform	0.000000	0.050000	0.100000	0.010000	500
Theta	Uniform	0.000000	0.050000	0.100000	0.010000	500
Theta	Uniform	0.000000	0.050000	0.100000	0.010000	500
M	Uniform	0.000000	5000.000000	10000.000000	1000.000000	500
M	Uniform	0.000000	5000.000000	10000.000000	1000.000000	500
M	Uniform	0.000000	5000.000000	10000.000000	1000.000000	500
M	Uniform	0.000000	5000.000000	10000.000000	1000.000000	500
M	Uniform	0.000000	5000.000000	10000.000000	1000.000000	500
M	Uniform	0.000000	5000.000000	10000.000000	1000.000000	500
M	Uniform	0.000000	5000.000000	10000.000000	1000.000000	500
M	Uniform	0.000000	5000.000000	10000.000000	1000.000000	500
M	Uniform	0.000000	5000.000000	10000.000000	1000.000000	500
M	Uniform	0.000000	5000.000000	10000.000000	1000.000000	500
M	Uniform	0.000000	5000.000000	10000.000000	1000.000000	500
M	Uniform	0.000000	5000.000000	10000.000000	1000.000000	500

Markov chain settings:	Long chain
Number of chains	1
Recorded steps [a]	500
Increment (record every x step [b]	10
Number of concurrent chains (replicates) [c]	2
Visited (sampled) parameter values [a*b*c]	10000
Number of discard trees per chain (burn-in)	500

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.xabaaxabbaxaabax
Haplotyping is turned on:	NO
Output file:	outfile-xabaaxabbaxaabax1
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.xabaaxabbaxaabax
Datatype:	Sequence data
Number of loci:	10

Mutationmodel:

Locus	Sublocus	Mutationmodel	Mutationmodel parameters
1	1	Felsenstein 84	[Bf:0.24 0.25 0.25 0.25, t/t ratio=2.000]
2	1	Felsenstein 84	[Bf:0.23 0.26 0.27 0.24, t/t ratio=2.000]
3	1	Felsenstein 84	[Bf:0.25 0.25 0.24 0.26, t/t ratio=2.000]
4	1	Felsenstein 84	[Bf:0.25 0.25 0.23 0.28, t/t ratio=2.000]
5	1	Felsenstein 84	[Bf:0.23 0.27 0.25 0.25, t/t ratio=2.000]
6	1	Felsenstein 84	[Bf:0.27 0.25 0.25 0.24, t/t ratio=2.000]
7	1	Felsenstein 84	[Bf:0.27 0.26 0.23 0.24, t/t ratio=2.000]
8	1	Felsenstein 84	[Bf:0.22 0.24 0.28 0.25, t/t ratio=2.000]
9	1	Felsenstein 84	[Bf:0.26 0.26 0.24 0.24, t/t ratio=2.000]
10	1	Felsenstein 84	[Bf:0.25 0.25 0.24 0.25, t/t ratio=2.000]

Sites per locus

Locus	Sites
1	1000
2	1000
3	1000
4	1000
5	1000
6	1000
7	1000
8	1000
9	1000
10	1000

Site rate variation and probabilities:

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

7	1	1	1.000	1.000	1.000
8	1	1	1.000	1.000	1.000
9	1	1	1.000	1.000	1.000
10	1	1	1.000	1.000	1.000

Population	Locus	Gene copies
1 Romanshorn_0	1	20
	2	20
	3	20
	4	20
	5	20
	6	20
	7	20
	8	20
	9	20
	10	20
2 Arbon_1	1	20
	2	20
	3	20
	4	20
	5	20
	6	20
	7	20
	8	20
	9	20
	10	20
3 Kreuzlingen_2	1	20
	2	20
	3	20
	4	20
	5	20
	6	20
	7	20
	8	20
	9	20
	10	20
4 Frauenfeld_3	1	20
	2	20
	3	20
	4	20
	5	20
	6	20
	7	20
	8	20
	9	20
	10	20

Total of all populations	1	80
	2	80
	3	80
	4	80
	5	80
	6	80
	7	80
	8	80
	9	80
	10	80

Bayesian Analysis: Posterior distribution table

Locus	Parameter	2.5%	25.0%	Mode	75.0%	97.5%	Median	Mean
1	Θ_1	0.00740	0.01000	0.01270	0.01660	0.02560	0.01590	0.01626
1	Θ_2	0.00740	0.01000	0.01270	0.01660	0.02560	0.01590	0.01626
1	Θ_3	0.00740	0.01000	0.01270	0.01660	0.02560	0.01590	0.01626
1	Θ_4	0.00740	0.01000	0.01270	0.01660	0.02560	0.01590	0.01626
1	$M_{2->1}$	620.0	840.0	1030.0	1180.0	1400.0	1050.0	1029.0
1	$M_{3->1}$	600.0	840.0	1030.0	1200.0	1440.0	1050.0	1023.7
1	$M_{4->1}$	620.0	840.0	1030.0	1180.0	1400.0	1050.0	1029.0
1	$M_{1->2}$	620.0	840.0	1030.0	1180.0	1400.0	1050.0	1029.0
1	$M_{3->2}$	620.0	840.0	1030.0	1180.0	1400.0	1050.0	1029.0
1	$M_{4->2}$	600.0	840.0	1030.0	1200.0	1440.0	1050.0	1023.7
1	$M_{1->3}$	600.0	840.0	1030.0	1200.0	1440.0	1050.0	1023.7
1	$M_{2->3}$	620.0	840.0	1030.0	1180.0	1400.0	1050.0	1029.0
1	$M_{4->3}$	620.0	840.0	1030.0	1180.0	1400.0	1050.0	1029.0
1	$M_{1->4}$	620.0	840.0	1030.0	1180.0	1400.0	1050.0	1029.0
1	$M_{2->4}$	600.0	840.0	1030.0	1200.0	1440.0	1050.0	1023.7
1	$M_{3->4}$	620.0	840.0	1030.0	1180.0	1400.0	1050.0	1029.0
2	Θ_1	0.00920	0.01280	0.01550	0.01800	0.02300	0.01610	0.01602
2	Θ_2	0.00920	0.01280	0.01550	0.01800	0.02300	0.01610	0.01602
2	Θ_3	0.00920	0.01280	0.01550	0.01800	0.02300	0.01610	0.01602
2	Θ_4	0.00920	0.01280	0.01550	0.01800	0.02300	0.01610	0.01602
2	$M_{2->1}$	380.0	620.0	810.0	960.0	1200.0	830.0	807.4
2	$M_{3->1}$	460.0	720.0	910.0	1080.0	1320.0	930.0	909.3
2	$M_{4->1}$	380.0	620.0	810.0	960.0	1200.0	830.0	807.4
2	$M_{1->2}$	380.0	620.0	810.0	960.0	1200.0	830.0	807.4
2	$M_{3->2}$	380.0	620.0	810.0	960.0	1200.0	830.0	807.4
2	$M_{4->2}$	460.0	720.0	910.0	1080.0	1320.0	930.0	909.3
2	$M_{1->3}$	460.0	720.0	910.0	1080.0	1320.0	930.0	909.3
2	$M_{2->3}$	380.0	620.0	810.0	960.0	1200.0	830.0	807.4
2	$M_{4->3}$	380.0	620.0	810.0	960.0	1200.0	830.0	807.4
2	$M_{1->4}$	380.0	620.0	810.0	960.0	1200.0	830.0	807.4
2	$M_{2->4}$	460.0	720.0	910.0	1080.0	1320.0	930.0	909.3
2	$M_{3->4}$	380.0	620.0	810.0	960.0	1200.0	830.0	807.4
3	Θ_1	0.01520	0.01920	0.02190	0.02600	0.03340	0.02370	0.02405
3	Θ_2	0.01520	0.01920	0.02190	0.02600	0.03340	0.02370	0.02405

Locus	Parameter	2.5%	25.0%	Mode	75.0%	97.5%	Median	Mean
3	Θ_3	0.01520	0.01920	0.02190	0.02600	0.03340	0.02370	0.02405
3	Θ_4	0.01520	0.01920	0.02190	0.02600	0.03340	0.02370	0.02405
3	$M_{2->1}$	620.0	860.0	1050.0	1220.0	1460.0	1070.0	1049.7
3	$M_{3->1}$	500.0	740.0	930.0	1100.0	1340.0	950.0	923.0
3	$M_{4->1}$	620.0	860.0	1050.0	1220.0	1460.0	1070.0	1049.7
3	$M_{1->2}$	620.0	860.0	1050.0	1220.0	1460.0	1070.0	1049.7
3	$M_{3->2}$	620.0	860.0	1050.0	1220.0	1460.0	1070.0	1049.7
3	$M_{4->2}$	500.0	740.0	930.0	1100.0	1340.0	950.0	923.0
3	$M_{1->3}$	500.0	740.0	930.0	1100.0	1340.0	950.0	923.0
3	$M_{2->3}$	620.0	860.0	1050.0	1220.0	1460.0	1070.0	1049.7
3	$M_{4->3}$	620.0	860.0	1050.0	1220.0	1460.0	1070.0	1049.7
3	$M_{1->4}$	620.0	860.0	1050.0	1220.0	1460.0	1070.0	1049.7
3	$M_{2->4}$	500.0	740.0	930.0	1100.0	1340.0	950.0	923.0
3	$M_{3->4}$	620.0	860.0	1050.0	1220.0	1460.0	1070.0	1049.7
4	Θ_1	0.01080	0.01480	0.01790	0.02120	0.02840	0.01910	0.01932
4	Θ_2	0.01080	0.01480	0.01790	0.02120	0.02840	0.01910	0.01932
4	Θ_3	0.01080	0.01480	0.01790	0.02120	0.02840	0.01910	0.01932
4	Θ_4	0.01080	0.01480	0.01790	0.02120	0.02840	0.01910	0.01932
4	$M_{2->1}$	480.0	760.0	970.0	1140.0	1440.0	990.0	963.0
4	$M_{3->1}$	480.0	740.0	1010.0	1180.0	1620.0	1030.0	1027.3
4	$M_{4->1}$	480.0	760.0	970.0	1140.0	1440.0	990.0	963.0
4	$M_{1->2}$	480.0	760.0	970.0	1140.0	1440.0	990.0	963.0
4	$M_{3->2}$	480.0	760.0	970.0	1140.0	1440.0	990.0	963.0
4	$M_{4->2}$	480.0	740.0	1010.0	1180.0	1620.0	1030.0	1027.3
4	$M_{1->3}$	480.0	740.0	1010.0	1180.0	1620.0	1030.0	1027.3
4	$M_{2->3}$	480.0	760.0	970.0	1140.0	1440.0	990.0	963.0
4	$M_{4->3}$	480.0	760.0	970.0	1140.0	1440.0	990.0	963.0
4	$M_{1->4}$	480.0	760.0	970.0	1140.0	1440.0	990.0	963.0
4	$M_{2->4}$	480.0	740.0	1010.0	1180.0	1620.0	1030.0	1027.3
4	$M_{3->4}$	480.0	760.0	970.0	1140.0	1440.0	990.0	963.0
5	Θ_1	0.01020	0.01420	0.01690	0.02120	0.02840	0.01890	0.01913
5	Θ_2	0.01020	0.01420	0.01690	0.02120	0.02840	0.01890	0.01913
5	Θ_3	0.01020	0.01420	0.01690	0.02120	0.02840	0.01890	0.01913
5	Θ_4	0.01020	0.01420	0.01690	0.02120	0.02840	0.01890	0.01913
5	$M_{2->1}$	520.0	820.0	1030.0	1220.0	1540.0	1050.0	1038.2
5	$M_{3->1}$	540.0	840.0	1050.0	1240.0	1560.0	1070.0	1054.8
5	$M_{4->1}$	520.0	820.0	1030.0	1220.0	1540.0	1050.0	1038.2
5	$M_{1->2}$	520.0	820.0	1030.0	1220.0	1540.0	1050.0	1038.2
5	$M_{3->2}$	520.0	820.0	1030.0	1220.0	1540.0	1050.0	1038.2

Locus	Parameter	2.5%	25.0%	Mode	75.0%	97.5%	Median	Mean
5	$M_{4->2}$	540.0	840.0	1050.0	1240.0	1560.0	1070.0	1054.8
5	$M_{1->3}$	540.0	840.0	1050.0	1240.0	1560.0	1070.0	1054.8
5	$M_{2->3}$	520.0	820.0	1030.0	1220.0	1540.0	1050.0	1038.2
5	$M_{4->3}$	520.0	820.0	1030.0	1220.0	1540.0	1050.0	1038.2
5	$M_{1->4}$	520.0	820.0	1030.0	1220.0	1540.0	1050.0	1038.2
5	$M_{2->4}$	540.0	840.0	1050.0	1240.0	1560.0	1070.0	1054.8
5	$M_{3->4}$	520.0	820.0	1030.0	1220.0	1540.0	1050.0	1038.2
6	Θ_1	0.00880	0.01140	0.01450	0.01800	0.03000	0.01650	0.01773
6	Θ_2	0.00880	0.01140	0.01450	0.01800	0.03000	0.01650	0.01773
6	Θ_3	0.00880	0.01140	0.01450	0.01800	0.03000	0.01650	0.01773
6	Θ_4	0.00880	0.01140	0.01450	0.01800	0.03000	0.01650	0.01773
6	$M_{2->1}$	460.0	680.0	870.0	1020.0	1260.0	890.0	866.3
6	$M_{3->1}$	480.0	760.0	970.0	1140.0	1420.0	990.0	964.7
6	$M_{4->1}$	460.0	680.0	870.0	1020.0	1260.0	890.0	866.3
6	$M_{1->2}$	460.0	680.0	870.0	1020.0	1260.0	890.0	866.3
6	$M_{3->2}$	460.0	680.0	870.0	1020.0	1260.0	890.0	866.3
6	$M_{4->2}$	480.0	760.0	970.0	1140.0	1420.0	990.0	964.7
6	$M_{1->3}$	480.0	760.0	970.0	1140.0	1420.0	990.0	964.7
6	$M_{2->3}$	460.0	680.0	870.0	1020.0	1260.0	890.0	866.3
6	$M_{4->3}$	460.0	680.0	870.0	1020.0	1260.0	890.0	866.3
6	$M_{1->4}$	460.0	680.0	870.0	1020.0	1260.0	890.0	866.3
6	$M_{2->4}$	480.0	760.0	970.0	1140.0	1420.0	990.0	964.7
6	$M_{3->4}$	460.0	680.0	870.0	1020.0	1260.0	890.0	866.3
7	Θ_1	0.00780	0.01280	0.01570	0.01840	0.02280	0.01590	0.01567
7	Θ_2	0.00780	0.01280	0.01570	0.01840	0.02280	0.01590	0.01567
7	Θ_3	0.00780	0.01280	0.01570	0.01840	0.02280	0.01590	0.01567
7	Θ_4	0.00780	0.01280	0.01570	0.01840	0.02280	0.01590	0.01567
7	$M_{2->1}$	400.0	640.0	830.0	980.0	1220.0	850.0	821.2
7	$M_{3->1}$	400.0	700.0	890.0	1080.0	1380.0	910.0	894.6
7	$M_{4->1}$	400.0	640.0	830.0	980.0	1220.0	850.0	821.2
7	$M_{1->2}$	400.0	640.0	830.0	980.0	1220.0	850.0	821.2
7	$M_{3->2}$	400.0	640.0	830.0	980.0	1220.0	850.0	821.2
7	$M_{4->2}$	400.0	700.0	890.0	1080.0	1380.0	910.0	894.6
7	$M_{1->3}$	400.0	700.0	890.0	1080.0	1380.0	910.0	894.6
7	$M_{2->3}$	400.0	640.0	830.0	980.0	1220.0	850.0	821.2
7	$M_{4->3}$	400.0	640.0	830.0	980.0	1220.0	850.0	821.2
7	$M_{1->4}$	400.0	640.0	830.0	980.0	1220.0	850.0	821.2
7	$M_{2->4}$	400.0	700.0	890.0	1080.0	1380.0	910.0	894.6
7	$M_{3->4}$	400.0	640.0	830.0	980.0	1220.0	850.0	821.2

Locus	Parameter	2.5%	25.0%	Mode	75.0%	97.5%	Median	Mean
8	Θ_1	0.00500	0.00820	0.01050	0.01280	0.01820	0.01110	0.01128
8	Θ_2	0.00500	0.00820	0.01050	0.01280	0.01820	0.01110	0.01128
8	Θ_3	0.00500	0.00820	0.01050	0.01280	0.01820	0.01110	0.01128
8	Θ_4	0.00500	0.00820	0.01050	0.01280	0.01820	0.01110	0.01128
8	$M_{2->1}$	400.0	720.0	950.0	1140.0	1460.0	970.0	943.6
8	$M_{3->1}$	400.0	680.0	870.0	1040.0	1300.0	890.0	866.0
8	$M_{4->1}$	400.0	720.0	950.0	1140.0	1460.0	970.0	943.6
8	$M_{1->2}$	400.0	720.0	950.0	1140.0	1460.0	970.0	943.6
8	$M_{3->2}$	400.0	720.0	950.0	1140.0	1460.0	970.0	943.6
8	$M_{4->2}$	400.0	680.0	870.0	1040.0	1300.0	890.0	866.0
8	$M_{1->3}$	400.0	680.0	870.0	1040.0	1300.0	890.0	866.0
8	$M_{2->3}$	400.0	720.0	950.0	1140.0	1460.0	970.0	943.6
8	$M_{4->3}$	400.0	720.0	950.0	1140.0	1460.0	970.0	943.6
8	$M_{1->4}$	400.0	720.0	950.0	1140.0	1460.0	970.0	943.6
8	$M_{2->4}$	400.0	680.0	870.0	1040.0	1300.0	890.0	866.0
8	$M_{3->4}$	400.0	720.0	950.0	1140.0	1460.0	970.0	943.6
9	Θ_1	0.00840	0.01100	0.01410	0.01840	0.02720	0.01670	0.01729
9	Θ_2	0.00840	0.01100	0.01410	0.01840	0.02720	0.01670	0.01729
9	Θ_3	0.00840	0.01100	0.01410	0.01840	0.02720	0.01670	0.01729
9	Θ_4	0.00840	0.01100	0.01410	0.01840	0.02720	0.01670	0.01729
9	$M_{2->1}$	420.0	700.0	890.0	1060.0	1340.0	910.0	888.8
9	$M_{3->1}$	440.0	760.0	950.0	1160.0	1460.0	990.0	957.2
9	$M_{4->1}$	420.0	700.0	890.0	1060.0	1340.0	910.0	888.8
9	$M_{1->2}$	420.0	700.0	890.0	1060.0	1340.0	910.0	888.8
9	$M_{3->2}$	420.0	700.0	890.0	1060.0	1340.0	910.0	888.8
9	$M_{4->2}$	440.0	760.0	950.0	1160.0	1460.0	990.0	957.2
9	$M_{1->3}$	440.0	760.0	950.0	1160.0	1460.0	990.0	957.2
9	$M_{2->3}$	420.0	700.0	890.0	1060.0	1340.0	910.0	888.8
9	$M_{4->3}$	420.0	700.0	890.0	1060.0	1340.0	910.0	888.8
9	$M_{1->4}$	420.0	700.0	890.0	1060.0	1340.0	910.0	888.8
9	$M_{2->4}$	440.0	760.0	950.0	1160.0	1460.0	990.0	957.2
9	$M_{3->4}$	420.0	700.0	890.0	1060.0	1340.0	910.0	888.8
10	Θ_1	0.01100	0.01640	0.01730	0.01840	0.02420	0.01790	0.01800
10	Θ_2	0.01100	0.01640	0.01730	0.01840	0.02420	0.01790	0.01800
10	Θ_3	0.01100	0.01640	0.01730	0.01840	0.02420	0.01790	0.01800
10	Θ_4	0.01100	0.01640	0.01730	0.01840	0.02420	0.01790	0.01800
10	$M_{2->1}$	540.0	820.0	1010.0	1180.0	1460.0	1030.0	1010.7
10	$M_{3->1}$	460.0	720.0	910.0	1080.0	1320.0	930.0	910.1

Locus	Parameter	2.5%	25.0%	Mode	75.0%	97.5%	Median	Mean
10	$M_{4\text{->}1}$	540.0	820.0	1010.0	1180.0	1460.0	1030.0	1010.7
10	$M_{1\text{->}2}$	540.0	820.0	1010.0	1180.0	1460.0	1030.0	1010.7
10	$M_{3\text{->}2}$	540.0	820.0	1010.0	1180.0	1460.0	1030.0	1010.7
10	$M_{4\text{->}2}$	460.0	720.0	910.0	1080.0	1320.0	930.0	910.1
10	$M_{1\text{->}3}$	460.0	720.0	910.0	1080.0	1320.0	930.0	910.1
10	$M_{2\text{->}3}$	540.0	820.0	1010.0	1180.0	1460.0	1030.0	1010.7
10	$M_{4\text{->}3}$	540.0	820.0	1010.0	1180.0	1460.0	1030.0	1010.7
10	$M_{1\text{->}4}$	540.0	820.0	1010.0	1180.0	1460.0	1030.0	1010.7
10	$M_{2\text{->}4}$	460.0	720.0	910.0	1080.0	1320.0	930.0	910.1
10	$M_{3\text{->}4}$	540.0	820.0	1010.0	1180.0	1460.0	1030.0	1010.7
All	Θ_1	0.01000	0.01300	0.01550	0.01720	0.02120	0.01570	0.01553
All	Θ_2	0.01000	0.01300	0.01550	0.01720	0.02120	0.01570	0.01553
All	Θ_3	0.01000	0.01300	0.01550	0.01720	0.02120	0.01570	0.01553
All	Θ_4	0.01000	0.01300	0.01550	0.01720	0.02120	0.01570	0.01553
All	$M_{2\text{->}1}$	520.0	720.0	910.0	1060.0	1260.0	930.0	905.8
All	$M_{3\text{->}1}$	520.0	740.0	930.0	1080.0	1300.0	950.0	921.1
All	$M_{4\text{->}1}$	520.0	720.0	910.0	1060.0	1260.0	930.0	905.8
All	$M_{1\text{->}2}$	520.0	720.0	910.0	1060.0	1260.0	930.0	905.8
All	$M_{3\text{->}2}$	520.0	720.0	910.0	1060.0	1260.0	930.0	905.8
All	$M_{4\text{->}2}$	520.0	740.0	930.0	1080.0	1300.0	950.0	921.1
All	$M_{1\text{->}3}$	520.0	740.0	930.0	1080.0	1300.0	950.0	921.1
All	$M_{2\text{->}3}$	520.0	720.0	910.0	1060.0	1260.0	930.0	905.8
All	$M_{4\text{->}3}$	520.0	720.0	910.0	1060.0	1260.0	930.0	905.8
All	$M_{1\text{->}4}$	520.0	720.0	910.0	1060.0	1260.0	930.0	905.8
All	$M_{2\text{->}4}$	520.0	740.0	930.0	1080.0	1300.0	950.0	921.1
All	$M_{3\text{->}4}$	520.0	720.0	910.0	1060.0	1260.0	930.0	905.8

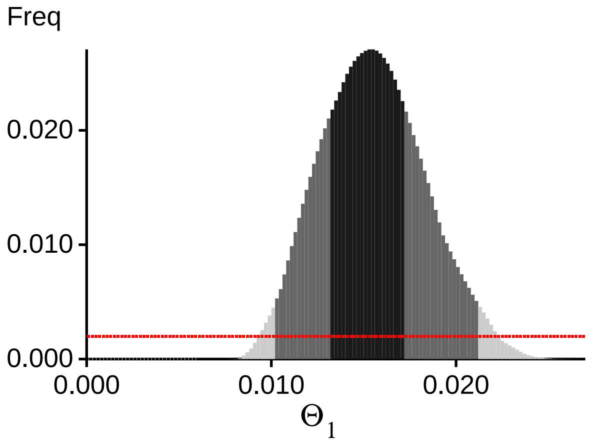
Citation suggestions:

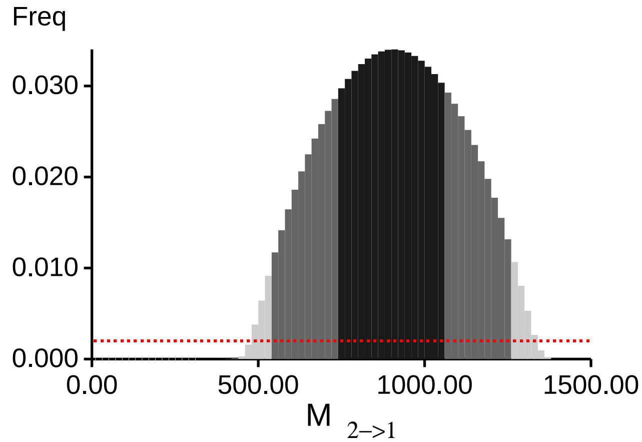
Beerli P., 2006. Comparison of Bayesian and maximum-likelihood inference of population genetic parameters. Bioinformatics 22:341-345

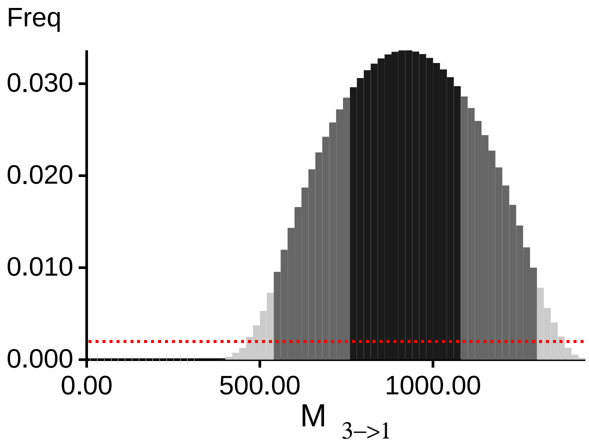
Beerli P., 2007. Estimation of the population scaled mutation rate from microsatellite data, Genetics, 177:1967-1968.

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







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]

Locus	Raw thermodynamic score(1a)	Bezier approximation score(1b)	Harmonic mean(2)
1	-4399.32	-3013.17	-2893.56
2	-5929.42	-3745.10	-3496.08
3	-6722.37	-4068.67	-3787.70
4	-5899.07	-3836.16	-3730.01
5	-6996.16	-3901.59	-3453.86
6	-3991.33	-3036.29	-3002.89
7	-4297.26	-3091.05	-3147.09
8	-4572.08	-3212.24	-3135.26
9	-5911.57	-4157.84	-4147.74
10	-6017.21	-3781.00	-4116.14
All	-54667.21	-35774.55	-34841.74

(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 = 68.581592]
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	3098/3098	1.00000
Θ_2	3098/3098	1.00000
Θ_3	3098/3098	1.00000
Θ_4	3098/3098	1.00000
$M_{2\text{->}1}$	3213/3213	1.00000
$M_{3\text{->}1}$	3141/3141	1.00000
$M_{4\text{->}1}$	3213/3213	1.00000
$M_{1\text{->}2}$	3213/3213	1.00000
$M_{3\text{->}2}$	3213/3213	1.00000
$M_{4\text{->}2}$	3141/3141	1.00000
$M_{1\text{->}3}$	3141/3141	1.00000
$M_{2\text{->}3}$	3213/3213	1.00000
$M_{4\text{->}3}$	3213/3213	1.00000
$M_{1\text{->}4}$	3213/3213	1.00000
$M_{2\text{->}4}$	3141/3141	1.00000
$M_{3\text{->}4}$	3213/3213	1.00000
Genealogies	2677/49995	0.05355

MCMC-Autocorrelation and Effective MCMC Sample Size

Parameter	Autocorrelation	Effective Sampe Size
Θ_1	0.84878	819.62
Θ_2	0.84878	819.62
Θ_3	0.84878	819.62
Θ_4	0.84878	819.62
$M_{2->1}$	0.90624	493.23
$M_{3->1}$	0.85034	818.21
$M_{4->1}$	0.90624	493.23
$M_{1->2}$	0.90624	493.23
$M_{3->2}$	0.90624	493.23
$M_{4->2}$	0.85034	818.21
$M_{1->3}$	0.85034	818.21
$M_{2->3}$	0.90624	493.23
$M_{4->3}$	0.90624	493.23
$M_{1->4}$	0.90624	493.23
$M_{2->4}$	0.85034	818.21
$M_{3->4}$	0.90624	493.23
Ln[Prob(D|G)]	0.98822	60.05

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