xabaaxabbaxaabax

POPULATION SIZE, MIGRATION, DIVERGENCE, ASSIGNMENT, HISTORY
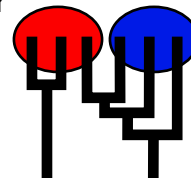Bayesian inference using the structured coalescent
Migrate-n version 4.2.7 [April-1-2016]
 Using Intel AVX (Advanced Vector Extensions)
 Compiled for a SYMMETRIC multiprocessors (Grandcentral)
Program started at   Sun Apr 10 09:12:29 2016
Program finished at   Sun Apr 10 09:12:57 2016

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   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	4
1 Romanshorn_0	*	a	b	a
2 Arbon_1	a	m	a	b
3 Kreuzlingen_2	b	a	m	a
4 Frauenfeld_3	a	b	a	*

 Order of parameters:

1	Θ_1				<displayed>	
2	Θ_2	=	Θ_2	[m]	<displayed>	
3	Θ_3	=	Θ_2	[m]		
4	Θ_4				<displayed>	
5	$M_{2\to1}$	=	$M_{2\to1}$	[a]	<displayed>	
6	$M_{3\to1}$	=	$M_{3\to1}$	[b]	<displayed>	
7	$M_{4\to1}$	=	$M_{2\to1}$	[a]		
8	$M_{1\to2}$	=	$M_{2\to1}$	[a]		
9	$M_{3\to2}$	=	$M_{2\to1}$	[a]		
10	$M_{4\to2}$	=	$M_{3\to1}$	[b]		
11	$M_{1\to3}$	=	$M_{3\to1}$	[b]		
12	$M_{2\to3}$	=	$M_{2\to1}$	[a]		
13	$M_{4\to3}$	=	$M_{2\to1}$	[a]		
14	$M_{1\to4}$	=	$M_{2\to1}$	[a]		
15	$M_{2\to4}$	=	$M_{3\to1}$	[b]		
16	$M_{3\to4}$	=	$M_{2\to1}$	[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]   100
   Increment (record every x step [b]   1
   Number of concurrent chains (replicates) [c]   2
   Visited (sampled) parameter values [a*b*c]   200
   Number of discard trees per chain (burn-in)   100

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	0.04100	0.04360	0.04570	0.04760	0.05020	0.03590	0.05141
1	Θ_2	0.03400	0.04260	0.04530	0.04780	0.04940	0.04410	0.05198
1	Θ_3	0.03400	0.04260	0.04530	0.04780	0.04940	0.04410	0.05198
1	Θ_4	0.03540	0.03760	0.03930	0.04140	0.04880	0.04230	0.04692
1	$M_{2->1}$	4480.0	4700.0	4890.0	5040.0	5280.0	4910.0	4954.9
1	$M_{3->1}$	4360.0	4640.0	4830.0	5020.0	5300.0	4850.0	4915.2
1	$M_{4->1}$	4480.0	4700.0	4890.0	5040.0	5280.0	4910.0	4954.9
1	$M_{1->2}$	4480.0	4700.0	4890.0	5040.0	5280.0	4910.0	4954.9
1	$M_{3->2}$	4480.0	4700.0	4890.0	5040.0	5280.0	4910.0	4954.9
1	$M_{4->2}$	4360.0	4640.0	4830.0	5020.0	5300.0	4850.0	4915.2
1	$M_{1->3}$	4360.0	4640.0	4830.0	5020.0	5300.0	4850.0	4915.2
1	$M_{2->3}$	4480.0	4700.0	4890.0	5040.0	5280.0	4910.0	4954.9
1	$M_{4->3}$	4480.0	4700.0	4890.0	5040.0	5280.0	4910.0	4954.9
1	$M_{1->4}$	4480.0	4700.0	4890.0	5040.0	5280.0	4910.0	4954.9
1	$M_{2->4}$	4360.0	4640.0	4830.0	5020.0	5300.0	4850.0	4915.2
1	$M_{3->4}$	4480.0	4700.0	4890.0	5040.0	5280.0	4910.0	4954.9
2	Θ_1	0.03720	0.04180	0.04430	0.04580	0.04800	0.04370	0.05386
2	Θ_2	0.03060	0.03520	0.03690	0.04000	0.04260	0.03750	0.04904
2	Θ_3	0.03060	0.03520	0.03690	0.04000	0.04260	0.03750	0.04904
2	Θ_4	0.03800	0.04020	0.04190	0.04340	0.04560	0.04210	0.05811
2	$M_{2->1}$	4520.0	4740.0	4910.0	5080.0	5300.0	4930.0	5150.0
2	$M_{3->1}$	4440.0	4680.0	4870.0	5040.0	5280.0	4890.0	4988.6
2	$M_{4->1}$	4520.0	4740.0	4910.0	5080.0	5300.0	4930.0	5150.0
2	$M_{1->2}$	4520.0	4740.0	4910.0	5080.0	5300.0	4930.0	5150.0
2	$M_{3->2}$	4520.0	4740.0	4910.0	5080.0	5300.0	4930.0	5150.0
2	$M_{4->2}$	4440.0	4680.0	4870.0	5040.0	5280.0	4890.0	4988.6
2	$M_{1->3}$	4440.0	4680.0	4870.0	5040.0	5280.0	4890.0	4988.6
2	$M_{2->3}$	4520.0	4740.0	4910.0	5080.0	5300.0	4930.0	5150.0
2	$M_{4->3}$	4520.0	4740.0	4910.0	5080.0	5300.0	4930.0	5150.0
2	$M_{1->4}$	4520.0	4740.0	4910.0	5080.0	5300.0	4930.0	5150.0
2	$M_{2->4}$	4440.0	4680.0	4870.0	5040.0	5280.0	4890.0	4988.6
2	$M_{3->4}$	4520.0	4740.0	4910.0	5080.0	5300.0	4930.0	5150.0
3	Θ_1	0.03140	0.03380	0.03550	0.03700	0.03940	0.03570	0.06105
3	Θ_2	0.03740	0.03960	0.04210	0.04480	0.05260	0.04330	0.05685

Locus	Parameter	2.5%	25.0%	Mode	75.0%	97.5%	Median	Mean
3	Θ_3	0.03740	0.03960	0.04210	0.04480	0.05260	0.04330	0.05685
3	Θ_4	0.04040	0.04460	0.04690	0.04900	0.05140	0.04150	0.04786
3	$M_{2\to1}$	4540.0	4760.0	4930.0	5100.0	5300.0	4950.0	5025.5
3	$M_{3\to1}$	4420.0	4680.0	4870.0	5040.0	5280.0	4890.0	4957.4
3	$M_{4\to1}$	4540.0	4760.0	4930.0	5100.0	5300.0	4950.0	5025.5
3	$M_{1\to2}$	4540.0	4760.0	4930.0	5100.0	5300.0	4950.0	5025.5
3	$M_{3\to2}$	4540.0	4760.0	4930.0	5100.0	5300.0	4950.0	5025.5
3	$M_{4\to2}$	4420.0	4680.0	4870.0	5040.0	5280.0	4890.0	4957.4
3	$M_{1\to3}$	4420.0	4680.0	4870.0	5040.0	5280.0	4890.0	4957.4
3	$M_{2\to3}$	4540.0	4760.0	4930.0	5100.0	5300.0	4950.0	5025.5
3	$M_{4\to3}$	4540.0	4760.0	4930.0	5100.0	5300.0	4950.0	5025.5
3	$M_{1\to4}$	4540.0	4760.0	4930.0	5100.0	5300.0	4950.0	5025.5
3	$M_{2\to4}$	4420.0	4680.0	4870.0	5040.0	5280.0	4890.0	4957.4
3	$M_{3\to4}$	4540.0	4760.0	4930.0	5100.0	5300.0	4950.0	5025.5
4	Θ_1	0.02820	0.03040	0.03230	0.03380	0.03600	0.03250	0.05989
4	Θ_2	0.03740	0.04640	0.04910	0.05100	0.05300	0.04690	0.05124
4	Θ_3	0.03740	0.04640	0.04910	0.05100	0.05300	0.04690	0.05124
4	Θ_4	0.03220	0.04140	0.04430	0.04700	0.04840	0.04250	0.05127
4	$M_{2\to1}$	4520.0	4740.0	4930.0	5080.0	5320.0	4950.0	4995.3
4	$M_{3\to1}$	4440.0	4680.0	4850.0	5020.0	5240.0	4870.0	4993.1
4	$M_{4\to1}$	4520.0	4740.0	4930.0	5080.0	5320.0	4950.0	4995.3
4	$M_{1\to2}$	4520.0	4740.0	4930.0	5080.0	5320.0	4950.0	4995.3
4	$M_{3\to2}$	4520.0	4740.0	4930.0	5080.0	5320.0	4950.0	4995.3
4	$M_{4\to2}$	4440.0	4680.0	4850.0	5020.0	5240.0	4870.0	4993.1
4	$M_{1\to3}$	4440.0	4680.0	4850.0	5020.0	5240.0	4870.0	4993.1
4	$M_{2\to3}$	4520.0	4740.0	4930.0	5080.0	5320.0	4950.0	4995.3
4	$M_{4\to3}$	4520.0	4740.0	4930.0	5080.0	5320.0	4950.0	4995.3
4	$M_{1\to4}$	4520.0	4740.0	4930.0	5080.0	5320.0	4950.0	4995.3
4	$M_{2\to4}$	4440.0	4680.0	4850.0	5020.0	5240.0	4870.0	4993.1
4	$M_{3\to4}$	4520.0	4740.0	4930.0	5080.0	5320.0	4950.0	4995.3
5	Θ_1	0.03580	0.03780	0.04010	0.04220	0.04420	0.03930	0.04980
5	Θ_2	0.04080	0.04280	0.04530	0.04780	0.04960	0.03190	0.04248
5	Θ_3	0.04080	0.04280	0.04530	0.04780	0.04960	0.03190	0.04248
5	Θ_4	0.03240	0.03380	0.03690	0.04020	0.04440	0.03610	0.03468
5	$M_{2\to1}$	4240.0	4520.0	4710.0	4880.0	5160.0	4730.0	4888.6
5	$M_{3\to1}$	4060.0	4360.0	4550.0	4740.0	5040.0	4570.0	4629.5
5	$M_{4\to1}$	4240.0	4520.0	4710.0	4880.0	5160.0	4730.0	4888.6
5	$M_{1\to2}$	4240.0	4520.0	4710.0	4880.0	5160.0	4730.0	4888.6
5	$M_{3\to2}$	4240.0	4520.0	4710.0	4880.0	5160.0	4730.0	4888.6

Locus	Parameter	2.5%	25.0%	Mode	75.0%	97.5%	Median	Mean
5	$M_{4 \to 2}$	4060.0	4360.0	4550.0	4740.0	5040.0	4570.0	4629.5
5	$M_{1 \to 3}$	4060.0	4360.0	4550.0	4740.0	5040.0	4570.0	4629.5
5	$M_{2 \to 3}$	4240.0	4520.0	4710.0	4880.0	5160.0	4730.0	4888.6
5	$M_{4 \to 3}$	4240.0	4520.0	4710.0	4880.0	5160.0	4730.0	4888.6
5	$M_{1 \to 4}$	4240.0	4520.0	4710.0	4880.0	5160.0	4730.0	4888.6
5	$M_{2 \to 4}$	4060.0	4360.0	4550.0	4740.0	5040.0	4570.0	4629.5
5	$M_{3 \to 4}$	4240.0	4520.0	4710.0	4880.0	5160.0	4730.0	4888.6
6	Θ_1	0.02160	0.02840	0.03090	0.03420	0.04220	0.03130	0.04762
6	Θ_2	0.03360	0.03820	0.04050	0.04360	0.04760	0.04090	0.05252
6	Θ_3	0.03360	0.03820	0.04050	0.04360	0.04760	0.04090	0.05252
6	Θ_4	0.03900	0.04200	0.04430	0.04620	0.05060	0.04410	0.05192
6	$M_{2 \to 1}$	4440.0	4660.0	4830.0	5000.0	5220.0	4850.0	5023.1
6	$M_{3 \to 1}$	4560.0	4760.0	4950.0	5100.0	5320.0	4970.0	5217.7
6	$M_{4 \to 1}$	4440.0	4660.0	4830.0	5000.0	5220.0	4850.0	5023.1
6	$M_{1 \to 2}$	4440.0	4660.0	4830.0	5000.0	5220.0	4850.0	5023.1
6	$M_{3 \to 2}$	4440.0	4660.0	4830.0	5000.0	5220.0	4850.0	5023.1
6	$M_{4 \to 2}$	4560.0	4760.0	4950.0	5100.0	5320.0	4970.0	5217.7
6	$M_{1 \to 3}$	4560.0	4760.0	4950.0	5100.0	5320.0	4970.0	5217.7
6	$M_{2 \to 3}$	4440.0	4660.0	4830.0	5000.0	5220.0	4850.0	5023.1
6	$M_{4 \to 3}$	4440.0	4660.0	4830.0	5000.0	5220.0	4850.0	5023.1
6	$M_{1 \to 4}$	4440.0	4660.0	4830.0	5000.0	5220.0	4850.0	5023.1
6	$M_{2 \to 4}$	4560.0	4760.0	4950.0	5100.0	5320.0	4970.0	5217.7
6	$M_{3 \to 4}$	4440.0	4660.0	4830.0	5000.0	5220.0	4850.0	5023.1
7	Θ_1	0.03660	0.03800	0.04070	0.04320	0.04460	0.04250	0.05497
7	Θ_2	0.03240	0.03420	0.03670	0.04000	0.04580	0.03610	0.04984
7	Θ_3	0.03240	0.03420	0.03670	0.04000	0.04580	0.03610	0.04984
7	Θ_4	0.02680	0.02900	0.03070	0.03220	0.03440	0.03090	0.06779
7	$M_{2 \to 1}$	4420.0	4660.0	4830.0	5000.0	5220.0	4850.0	5010.2
7	$M_{3 \to 1}$	4480.0	4720.0	4890.0	5060.0	5280.0	4910.0	4972.8
7	$M_{4 \to 1}$	4420.0	4660.0	4830.0	5000.0	5220.0	4850.0	5010.2
7	$M_{1 \to 2}$	4420.0	4660.0	4830.0	5000.0	5220.0	4850.0	5010.2
7	$M_{3 \to 2}$	4420.0	4660.0	4830.0	5000.0	5220.0	4850.0	5010.2
7	$M_{4 \to 2}$	4480.0	4720.0	4890.0	5060.0	5280.0	4910.0	4972.8
7	$M_{1 \to 3}$	4480.0	4720.0	4890.0	5060.0	5280.0	4910.0	4972.8
7	$M_{2 \to 3}$	4420.0	4660.0	4830.0	5000.0	5220.0	4850.0	5010.2
7	$M_{4 \to 3}$	4420.0	4660.0	4830.0	5000.0	5220.0	4850.0	5010.2
7	$M_{1 \to 4}$	4420.0	4660.0	4830.0	5000.0	5220.0	4850.0	5010.2
7	$M_{2 \to 4}$	4480.0	4720.0	4890.0	5060.0	5280.0	4910.0	4972.8
7	$M_{3 \to 4}$	4420.0	4660.0	4830.0	5000.0	5220.0	4850.0	5010.2

Locus	Parameter	2.5%	25.0%	Mode	75.0%	97.5%	Median	Mean
8	Θ_1	0.03700	0.03900	0.04090	0.04240	0.04460	0.04110	0.04732
8	Θ_2	0.03140	0.03640	0.03910	0.04220	0.04980	0.04010	0.04265
8	Θ_3	0.03140	0.03640	0.03910	0.04220	0.04980	0.04010	0.04265
8	Θ_4	0.03140	0.03280	0.03510	0.03860	0.04440	0.03750	0.05618
8	$M_{2\to1}$	4360.0	4620.0	4810.0	4980.0	5240.0	4830.0	4833.6
8	$M_{3\to1}$	4480.0	4700.0	4870.0	5040.0	5260.0	4890.0	4873.9
8	$M_{4\to1}$	4360.0	4620.0	4810.0	4980.0	5240.0	4830.0	4833.6
8	$M_{1\to2}$	4360.0	4620.0	4810.0	4980.0	5240.0	4830.0	4833.6
8	$M_{3\to2}$	4360.0	4620.0	4810.0	4980.0	5240.0	4830.0	4833.6
8	$M_{4\to2}$	4480.0	4700.0	4870.0	5040.0	5260.0	4890.0	4873.9
8	$M_{1\to3}$	4480.0	4700.0	4870.0	5040.0	5260.0	4890.0	4873.9
8	$M_{2\to3}$	4360.0	4620.0	4810.0	4980.0	5240.0	4830.0	4833.6
8	$M_{4\to3}$	4360.0	4620.0	4810.0	4980.0	5240.0	4830.0	4833.6
8	$M_{1\to4}$	4360.0	4620.0	4810.0	4980.0	5240.0	4830.0	4833.6
8	$M_{2\to4}$	4480.0	4700.0	4870.0	5040.0	5260.0	4890.0	4873.9
8	$M_{3\to4}$	4360.0	4620.0	4810.0	4980.0	5240.0	4830.0	4833.6
9	Θ_1	0.03660	0.03960	0.04170	0.04360	0.04660	0.04190	0.05905
9	Θ_2	0.02560	0.02740	0.02970	0.03200	0.03380	0.03910	0.04302
9	Θ_3	0.02560	0.02740	0.02970	0.03200	0.03380	0.03910	0.04302
9	Θ_4	0.04200	0.04460	0.04650	0.04820	0.05080	0.04670	0.04831
9	$M_{2\to1}$	4500.0	4720.0	4910.0	5060.0	5280.0	4930.0	5076.5
9	$M_{3\to1}$	4540.0	4740.0	4930.0	5080.0	5300.0	4950.0	5117.3
9	$M_{4\to1}$	4500.0	4720.0	4910.0	5060.0	5280.0	4930.0	5076.5
9	$M_{1\to2}$	4500.0	4720.0	4910.0	5060.0	5280.0	4930.0	5076.5
9	$M_{3\to2}$	4500.0	4720.0	4910.0	5060.0	5280.0	4930.0	5076.5
9	$M_{4\to2}$	4540.0	4740.0	4930.0	5080.0	5300.0	4950.0	5117.3
9	$M_{1\to3}$	4540.0	4740.0	4930.0	5080.0	5300.0	4950.0	5117.3
9	$M_{2\to3}$	4500.0	4720.0	4910.0	5060.0	5280.0	4930.0	5076.5
9	$M_{4\to3}$	4500.0	4720.0	4910.0	5060.0	5280.0	4930.0	5076.5
9	$M_{1\to4}$	4500.0	4720.0	4910.0	5060.0	5280.0	4930.0	5076.5
9	$M_{2\to4}$	4540.0	4740.0	4930.0	5080.0	5300.0	4950.0	5117.3
9	$M_{3\to4}$	4500.0	4720.0	4910.0	5060.0	5280.0	4930.0	5076.5
10	Θ_1	0.04160	0.04320	0.04610	0.04880	0.05020	0.04470	0.05852
10	Θ_2	0.03380	0.03720	0.03930	0.04200	0.04660	0.04010	0.05887
10	Θ_3	0.03380	0.03720	0.03930	0.04200	0.04660	0.04010	0.05887
10	Θ_4	0.02880	0.03080	0.03310	0.03520	0.03720	0.03410	0.04838
10	$M_{2\to1}$	4400.0	4640.0	4810.0	4980.0	5220.0	4830.0	4959.6
10	$M_{3\to1}$	4240.0	4540.0	4750.0	4940.0	5240.0	4770.0	4845.3

Locus	Parameter	2.5%	25.0%	Mode	75.0%	97.5%	Median	Mean
10	$M_{4->1}$	4400.0	4640.0	4810.0	4980.0	5220.0	4830.0	4959.6
10	$M_{1->2}$	4400.0	4640.0	4810.0	4980.0	5220.0	4830.0	4959.6
10	$M_{3->2}$	4400.0	4640.0	4810.0	4980.0	5220.0	4830.0	4959.6
10	$M_{4->2}$	4240.0	4540.0	4750.0	4940.0	5240.0	4770.0	4845.3
10	$M_{1->3}$	4240.0	4540.0	4750.0	4940.0	5240.0	4770.0	4845.3
10	$M_{2->3}$	4400.0	4640.0	4810.0	4980.0	5220.0	4830.0	4959.6
10	$M_{4->3}$	4400.0	4640.0	4810.0	4980.0	5220.0	4830.0	4959.6
10	$M_{1->4}$	4400.0	4640.0	4810.0	4980.0	5220.0	4830.0	4959.6
10	$M_{2->4}$	4240.0	4540.0	4750.0	4940.0	5240.0	4770.0	4845.3
10	$M_{3->4}$	4400.0	4640.0	4810.0	4980.0	5220.0	4830.0	4959.6
All	Θ_1	0.03640	0.03840	0.04010	0.04180	0.04380	0.04030	0.04545
All	Θ_2	0.03560	0.04180	0.04450	0.04660	0.05020	0.04430	0.04582
All	Θ_3	0.03560	0.04180	0.04450	0.04660	0.05020	0.04430	0.04582
All	Θ_4	0.03060	0.04340	0.04630	0.04900	0.05140	0.04510	0.05276
All	$M_{2->1}$	4560.0	4780.0	4950.0	5120.0	5320.0	4970.0	5044.0
All	$M_{3->1}$	4580.0	4780.0	4950.0	5120.0	5340.0	4970.0	5051.8
All	$M_{4->1}$	4560.0	4780.0	4950.0	5120.0	5320.0	4970.0	5044.0
All	$M_{1->2}$	4560.0	4780.0	4950.0	5120.0	5320.0	4970.0	5044.0
All	$M_{3->2}$	4560.0	4780.0	4950.0	5120.0	5320.0	4970.0	5044.0
All	$M_{4->2}$	4580.0	4780.0	4950.0	5120.0	5340.0	4970.0	5051.8
All	$M_{1->3}$	4580.0	4780.0	4950.0	5120.0	5340.0	4970.0	5051.8
All	$M_{2->3}$	4560.0	4780.0	4950.0	5120.0	5320.0	4970.0	5044.0
All	$M_{4->3}$	4560.0	4780.0	4950.0	5120.0	5320.0	4970.0	5044.0
All	$M_{1->4}$	4560.0	4780.0	4950.0	5120.0	5320.0	4970.0	5044.0
All	$M_{2->4}$	4580.0	4780.0	4950.0	5120.0	5340.0	4970.0	5051.8
All	$M_{3->4}$	4560.0	4780.0	4950.0	5120.0	5320.0	4970.0	5044.0

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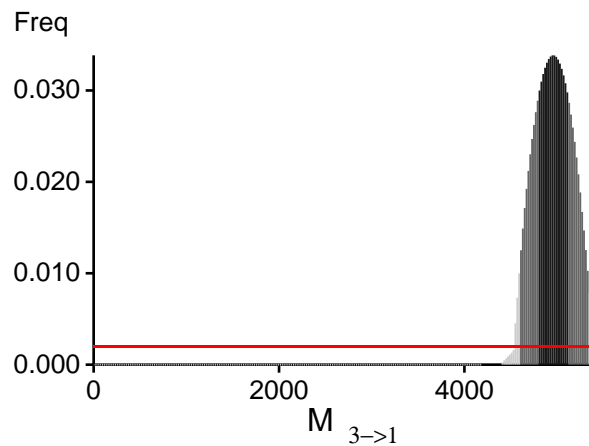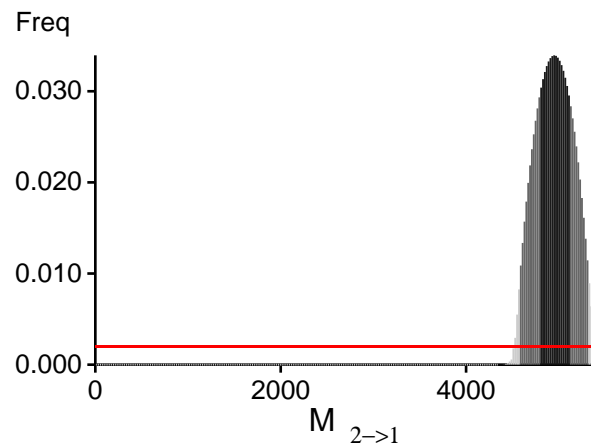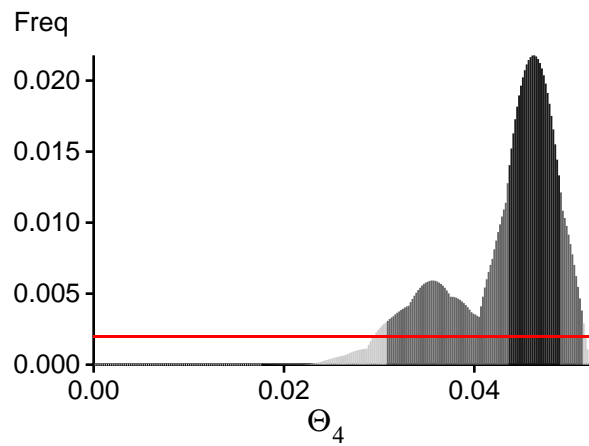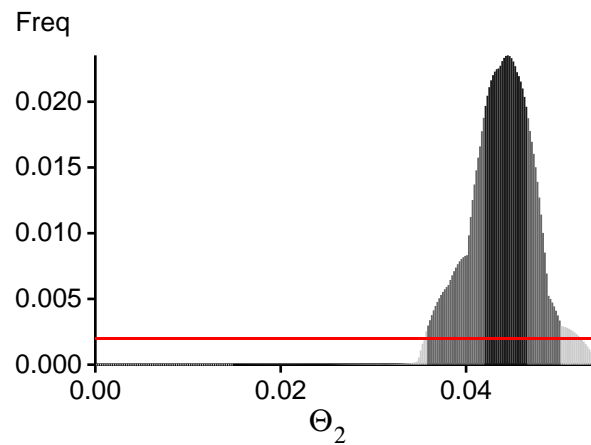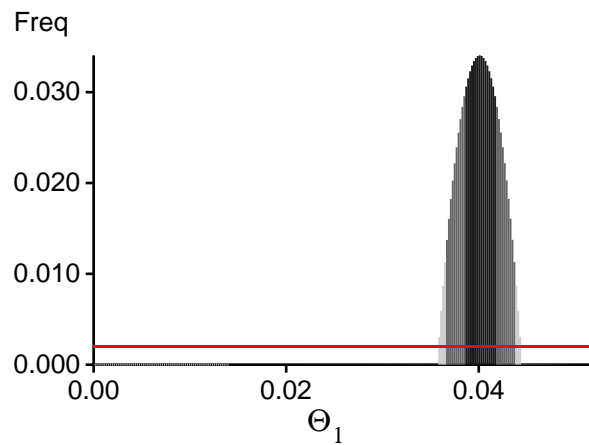
Log-Probability of the data given the model (marginal likelihood)

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	-10134.55	-9728.57	-10705.59
2	-15662.06	-15028.27	-16318.27
3	-17229.42	-16364.75	-17482.77
4	-15770.70	-15081.04	-16377.25
5	-20602.24	-19935.04	-21694.72
6	-8242.62	-8075.92	-8142.25
7	-9651.49	-9393.77	-9913.09
8	-10909.79	-10669.46	-10587.61
9	-13526.48	-13091.39	-13552.49
10	-15379.10	-14670.96	-15688.59
All	-137044.34	-131975.08	-140398.54

(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 = 64.091785]

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	56/56	1.00000
Θ_2	61/61	1.00000
Θ_3	61/61	1.00000
Θ_4	69/69	1.00000
$M_{2\to1}$	63/63	1.00000
$M_{3\to1}$	61/61	1.00000
$M_{4\to1}$	63/63	1.00000
$M_{1\to2}$	63/63	1.00000
$M_{3\to2}$	63/63	1.00000
$M_{4\to2}$	61/61	1.00000
$M_{1\to3}$	61/61	1.00000
$M_{2\to3}$	63/63	1.00000
$M_{4\to3}$	63/63	1.00000
$M_{1\to4}$	63/63	1.00000
$M_{2\to4}$	61/61	1.00000
$M_{3\to4}$	63/63	1.00000
Genealogies	317/984	0.32215

MCMC-Autocorrelation and Effective MCMC Sample Size

Parameter	Autocorrelation	Effective Sampe Size
Θ_1	0.93194	70.98
Θ_2	0.94051	61.19
Θ_3	0.94051	61.19
Θ_4	0.93561	66.63
$M_{2\rightarrow1}$	0.94100	60.40
$M_{3\rightarrow1}$	0.93905	62.45
$M_{4\rightarrow1}$	0.94100	60.40
$M_{1\rightarrow2}$	0.94100	60.40
$M_{3\rightarrow2}$	0.94100	60.40
$M_{4\rightarrow2}$	0.93905	62.45
$M_{1\rightarrow3}$	0.93905	62.45
$M_{2\rightarrow3}$	0.94100	60.40
$M_{4\rightarrow3}$	0.94100	60.40
$M_{1\rightarrow4}$	0.94100	60.40
$M_{2\rightarrow4}$	0.93905	62.45
$M_{3\rightarrow4}$	0.94100	60.40
Ln[Prob(D|G)]	0.94222	59.38

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