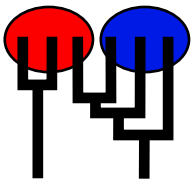
AUTO

MIGRATION RATE AND POPULATION SIZE ESTIMATION
using a Markov chain Monte Carlo approach
Migrate-n version 2.1.8
[EXPERIMENTAL PDF: compare with ASCII outputfile!!]
Compiled for a PARALLEL COMPUTER ARCHITECTURE
Program started at Thu Aug 24 14:39:52 2006
Program finished at Thu Aug 24 14:43:20 2006



Options

Datatype: Microsatellite data [Stepwise mutation]
Missing data: not included
Random number seed: (with internal timer) 1156444793
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	0	1
0 population__num	*	*
1 population__num	*	*

Mutation rate among loci: Mutation rate is constant for all loci

Analysis strategy: Bayesian inference

Used prior distribution for parameter

Parameter	Prior	Minimum	Mean*	Maximum	Delta	Bins
Theta	Exponential	0.000000	1.000000	10.000000	-	200
M	Exponential	0.000000	10.000000	1000.000000	-	200

Markov chain settings: Long chain
Number of chains 1

Recorded genealogies [a]	1600
Increment (record every x genealogy [b]	2
Number of concurrent chains (replicates) [c]	2
Visited (sampled) genealogies [a*b*c]	6400
Number of discard trees per chain (burn-in)	130

Multiple Markov chains:

Static heating scheme 4 chains with temperatures

5.00 3.67 2.33 1.00

Swapping interval is 1

Print options:

Data file:	infile.msat
Output file:	outfile-bayes
Posterior distribution raw histogram file:	bayesfile
Print data:	No
Print genealogies [only some for some data type]:	None

Data summary

Datatype: Microsatellite data
Number of loci: 10

Population	Locus	Gene copies data	(missing)
1 population__number___0	1	50	(0)
	2	50	(0)
	3	50	(0)
	4	50	(0)
	5	50	(0)
	6	50	(0)
	7	50	(0)
	8	50	(0)
	9	50	(0)
	10	50	(0)
2 population__number___1	1	42	(0)
	2	42	(0)
	3	42	(0)
	4	42	(0)
	5	42	(0)
	6	42	(0)
	7	42	(0)
	8	42	(0)
	9	42	(0)
	10	42	(0)
Total of all populations	1	92	(0)
	2	92	(0)
	3	92	(0)
	4	92	(0)
	5	92	(0)
	6	92	(0)
	7	92	(0)
	8	92	(0)
	9	92	(0)
	10	92	(0)

Bayesian Analysis: Posterior distribution table

Locus	Parameter	2.5%	25.0%	Mode	75.0%	97.5%	Median	Mean
1	Θ_1	0.27500	0.42500	0.62500	0.72500	2.57500	1.32500	1.46969
1	Θ_2	0.27500	1.57500	2.02500	2.12500	2.57500	1.82500	1.80411
1	$M_{2->1}$	2.500	2.500	12.500	12.500	12.500	12.500	11.179
1	$M_{1->2}$	2.500	2.500	2.500	2.500	27.500	22.500	13.281
2	Θ_1	0.02500	0.02500	0.02500	0.17500	0.57500	0.22500	0.23212
2	Θ_2	0.02500	0.02500	0.07500	0.32500	0.72500	0.37500	0.57050
2	$M_{2->1}$	72.500	72.500	77.500	77.500	77.500	72.500	68.991
2	$M_{1->2}$	72.500	72.500	77.500	77.500	77.500	77.500	72.775
3	Θ_1	0.02500	0.02500	0.12500	0.47500	1.87500	0.52500	0.69200
3	Θ_2	0.02500	0.02500	0.07500	0.57500	1.57500	0.82500	0.96423
3	$M_{2->1}$	72.500	72.500	77.500	77.500	77.500	52.500	45.283
3	$M_{1->2}$	72.500	72.500	77.500	77.500	77.500	62.500	48.811
4	Θ_1	0.17500	0.22500	0.57500	0.72500	2.07500	0.67500	0.97373
4	Θ_2	0.17500	0.27500	0.47500	0.52500	2.52500	1.57500	1.56576
4	$M_{2->1}$	2.500	17.500	27.500	27.500	32.500	22.500	19.997
4	$M_{1->2}$	2.500	7.500	12.500	17.500	27.500	17.500	15.734
5	Θ_1	0.02500	0.02500	0.12500	0.67500	2.17500	0.87500	1.45356
5	Θ_2	0.02500	0.02500	0.07500	0.67500	2.82500	1.07500	1.35248
5	$M_{2->1}$	72.500	72.500	77.500	77.500	77.500	27.500	31.797
5	$M_{1->2}$	72.500	72.500	77.500	77.500	77.500	32.500	37.939
6	Θ_1	0.17500	0.17500	0.52500	0.72500	2.22500	0.77500	0.99023
6	Θ_2	0.17500	0.17500	0.47500	0.82500	2.22500	0.92500	1.22367
6	$M_{2->1}$	2.500	7.500	22.500	27.500	42.500	27.500	26.669
6	$M_{1->2}$	2.500	2.500	12.500	22.500	47.500	27.500	26.108
7	Θ_1	0.02500	0.02500	0.02500	0.47500	2.12500	0.57500	1.09724
7	Θ_2	0.02500	0.02500	0.07500	0.52500	2.77500	0.57500	1.06576
7	$M_{2->1}$	307.500	307.500	312.500	312.500	312.500	52.500	102.282
7	$M_{1->2}$	307.500	307.500	312.500	312.500	312.500	62.500	106.889
8	Θ_1	0.12500	0.17500	0.52500	0.77500	2.07500	0.77500	0.95144
8	Θ_2	0.17500	0.17500	0.47500	0.87500	2.47500	1.07500	1.27200
8	$M_{2->1}$	2.500	7.500	22.500	27.500	42.500	27.500	26.377
8	$M_{1->2}$	2.500	2.500	17.500	22.500	47.500	27.500	25.387

9	Θ_1	0.02500	0.02500	0.02500	0.67500	2.72500	0.97500	1.33548
9	Θ_2	0.02500	0.02500	0.07500	0.57500	2.77500	1.02500	1.34104
9	$M_{2->1}$	307.500	307.500	312.500	312.500	312.500	27.500	83.922
9	$M_{1->2}$	307.500	307.500	312.500	312.500	312.500	37.500	87.854
10	Θ_1	0.12500	0.12500	0.52500	0.77500	2.07500	0.77500	1.06734
10	Θ_2	0.17500	0.17500	0.42500	0.87500	2.42500	1.07500	1.22003
10	$M_{2->1}$	2.500	7.500	22.500	27.500	47.500	27.500	26.083
10	$M_{1->2}$	2.500	2.500	17.500	22.500	47.500	27.500	26.540
All	Θ_1	0.12500	0.22500	0.37500	0.42500	0.67500	0.42500	0.39593
All	Θ_2	0.17500	0.32500	0.42500	0.47500	0.62500	0.47500	0.41358
All	$M_{2->1}$	2.500	7.500	17.500	17.500	32.500	22.500	17.384
All	$M_{1->2}$	2.500	7.500	12.500	17.500	27.500	22.500	14.930

Acceptance ratios for all parameters and the genealogies

Parameter	Accepted changes	Ratio
Θ_1	4590/42395	0.10827
Θ_2	5895/41320	0.14267
$M_{2->1}$	3150/42605	0.07393
$M_{1->2}$	3280/41810	0.07845
Genealogies	24750/158825	0.15583

Bayesian Analysis: Posterior distribution over all loci