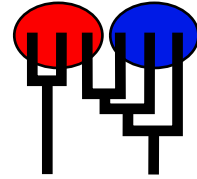


# Example: Microsatellite data set

MIGRATION RATE AND POPULATION SIZE ESTIMATION  
 using the coalescent and maximum likelihood or Bayesian inference  
 Migrate-n version 3.1.4 [1685]  
 Compiled for a PARALLEL COMPUTER ARCHITECTURE  
 One master and 2 compute nodes are available.  
 Program started at Wed May 12 12:21:24 2010  
 Program finished at Wed May 12 12:24:22 2010



## Options

Datatype:	Microsatellite data [Brownian motion]
Missing data:	not included
Random number seed:	(from parmfile) 310705631
Start parameters:	
Theta values were generated	RANDOM start value from U(min,msx)
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 1
1 population__num	* *
1 population__num	* *
Order of parameters:	
1 $\Theta_1$	<displayed>
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	10.000000	20.000000	2.000000	500
M	Uniform	0.000000	10.000000	20.000000	2.000000	500

## Markov chain settings:

Long chain

Number of chains	1
Recorded steps [a]	500
Increment (record every x step [b])	200
Number of concurrent chains (replicates) [c]	2
Visited (sampled) parameter values [a*b*c]	200000
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:	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)
1 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)

*Allele frequency spectra*

## Locus 1

Allele	Pop1	Pop2	All
16	0.196	0.000	0.098
19	0.054	0.000	0.027
18	0.087	0.000	0.043
15	0.130	0.000	0.065
21	0.087	0.000	0.043
23	0.065	0.000	0.033
17	0.196	0.000	0.098
22	0.087	0.000	0.043
25	0.043	0.000	0.022
24	0.011	0.000	0.005
26	0.011	0.000	0.005
27	0.022	0.000	0.011
29	0.011	0.000	0.005

## Locus 2

Allele	Pop1	Pop2	All
16	0.543	0.000	0.272
19	0.022	0.000	0.011
18	0.174	0.000	0.087
17	0.163	0.000	0.082
15	0.011	0.000	0.005
21	0.043	0.000	0.022
20	0.022	0.000	0.011
22	0.022	0.000	0.011

## Locus 3

Allele	Pop1	Pop2	All
19	0.250	0.000	0.125
20	0.370	0.000	0.185
18	0.087	0.000	0.043
21	0.207	0.000	0.103
22	0.087	0.000	0.043

## Locus 4

Allele	Pop1	Pop2	All
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Allele	Pop1	Pop2	All
16	0.076	0.000	0.038
24	0.109	0.000	0.054
15	0.033	0.000	0.016
25	0.163	0.000	0.082
14	0.033	0.000	0.016
19	0.120	0.000	0.060
12	0.033	0.000	0.016
20	0.130	0.000	0.065
23	0.087	0.000	0.043
28	0.011	0.000	0.005
22	0.043	0.000	0.022
21	0.141	0.000	0.071
13	0.011	0.000	0.005
26	0.011	0.000	0.005

## Locus 5

Allele	Pop1	Pop2	All
20	0.457	0.000	0.228
21	0.391	0.000	0.196
19	0.152	0.000	0.076

## Locus 6

Allele	Pop1	Pop2	All
19	0.033	0.000	0.016
20	0.065	0.000	0.033
18	0.261	0.000	0.130
22	0.163	0.000	0.082
21	0.283	0.000	0.141
16	0.033	0.000	0.016
24	0.109	0.000	0.054
17	0.054	0.000	0.027

## Locus 7

Allele	Pop1	Pop2	All
23	0.130	0.000	0.065
20	0.424	0.000	0.212
22	0.185	0.000	0.092
21	0.207	0.000	0.103
19	0.054	0.000	0.027

## Locus 8

Allele	Pop1	Pop2	All
19	0.522	0.000	0.261
17	0.043	0.000	0.022
18	0.087	0.000	0.043
20	0.163	0.000	0.082
16	0.043	0.000	0.022
22	0.076	0.000	0.038
15	0.033	0.000	0.016
23	0.033	0.000	0.016

## Locus 9

Allele	Pop1	Pop2	All
24	0.054	0.000	0.027
19	0.359	0.000	0.179
20	0.239	0.000	0.120
23	0.163	0.000	0.082
22	0.054	0.000	0.027
18	0.043	0.000	0.022
21	0.065	0.000	0.033
25	0.022	0.000	0.011

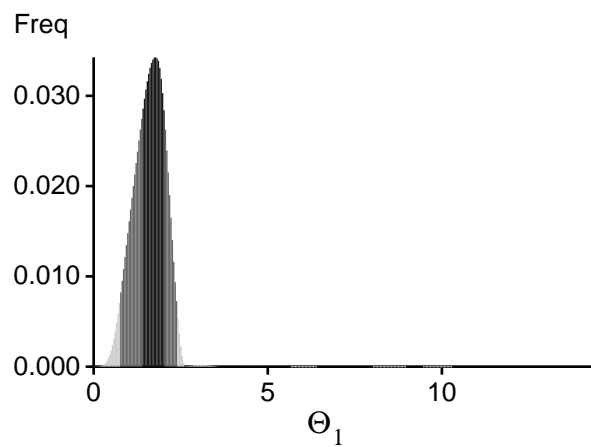
## Locus 10

Allele	Pop1	Pop2	All
22	0.152	0.000	0.076
20	0.337	0.000	0.168
23	0.120	0.000	0.060
24	0.011	0.000	0.005
19	0.163	0.000	0.082
21	0.054	0.000	0.027
18	0.043	0.000	0.022
15	0.043	0.000	0.022
17	0.043	0.000	0.022
25	0.033	0.000	0.016

## *Bayesian Analysis: Posterior distribution table*

Locus	Parameter	2.5%	25.0%	Mode	75.0%	97.5%	Median	Mean
1	$\Theta_1$	11.68000	17.32000	17.86000	19.76000	20.00000	16.82000	16.46171
2	$\Theta_1$	2.84000	3.48000	5.94000	6.92000	13.32000	6.74000	7.60126
3	$\Theta_1$	3.24000	6.36000	8.74000	9.52000	17.16000	9.46000	2.98769
4	$\Theta_1$	10.00000	17.88000	19.70000	20.00000	20.00000	16.58000	4.53204
5	$\Theta_1$	0.52000	1.04000	1.78000	2.48000	5.92000	2.22000	0.48947
6	$\Theta_1$	4.08000	5.16000	6.62000	8.20000	15.44000	8.14000	1.68862
7	$\Theta_1$	0.40000	2.24000	3.54000	4.76000	8.64000	4.02000	0.74389
8	$\Theta_1$	5.88000	7.76000	8.90000	12.12000	19.12000	11.42000	1.56378
9	$\Theta_1$	8.04000	9.12000	10.54000	12.84000	17.12000	12.82000	1.39948
10	$\Theta_1$	7.76000	15.32000	16.70000	18.04000	20.00000	14.54000	1.46853
All	$\Theta_1$	0.72000	1.36000	1.78000	2.04000	2.40000	1.66000	1.60139

## *Bayesian Analysis: Posterior distribution over all loci*





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

Use this value for Bayes factor calculations:

$BF = \text{Exp}[\ln(\text{Prob}(D \mid \text{thisModel}) - \ln(\text{Prob}(D \mid \text{otherModel}))]$

or as  $LBF = 2 (\ln(\text{Prob}(D \mid \text{thisModel}) - \ln(\text{Prob}(D \mid \text{otherModel})))$

shows the support for thisModel]

Locus	Raw thermodynamic score(1a)	Bezier approximation score(1b)	Harmonic mean(2)
1	-14008.11	-2356.43	-102.97
2	-3812.93	-692.52	-76.72
3	-2488.86	-490.27	-86.35
4	-14199.16	-2384.68	-99.66
5	-1159.28	-252.43	-45.47
6	-6549.24	-1141.63	-80.81
7	-1957.51	-397.41	-75.74
8	-4085.64	-746.12	-80.38
9	-6041.32	-1064.32	-86.10
10	-6134.20	-1087.06	-93.27
All	-60530.42	-10707.03	-921.65

(1a, 1b and 2) is an approximation to the marginal likelihood, make sure the program run long enough!

(1a, 1b) and (2) should give a similar result, (2) is considered more

crude than (1), but (1) needs heating with several well-spaced chains,

(1b) is using a Bezier-curve to get better approximations for runs with low number of heated chains

*Acceptance ratios for all parameters and the genealogies*

Parameter	Accepted changes	Ratio
$\Theta_1$	5514235/5514235	1.00000
Genealogies	1447070/5005960	0.28907

## *MCMC-Autocorrelation and Effective MCMC Sample Size*

Parameter	Autocorrelation	Effective Sample Size
$\Theta_1$	0.79080	4481.53
$\ln[\text{Prob}(D G)]$	0.90409	2068.74