

Example: Microsatellite data set

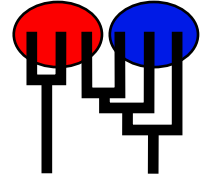
MIGRATION RATE AND POPULATION SIZE ESTIMATION

using the coalescent and maximum likelihood or Bayesian inference

Migrate-n version 2.5.1

Program started at Thu Jul 10 07:52:44 2008

Program finished at Thu Jul 10 07:53:20 2008



Options

Datatype: Microsatellite data [Brownian motion]
 Missing data: not included
 Random number seed: (with internal timer) 1598441029
 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
1 population__num	*	*
2 population__num	*	*

Order of parameters:

1	Θ_1	<displayed>
2	Θ_2	<displayed>
3	$M_{2 \rightarrow 1}$	<displayed>
4	$M_{1 \rightarrow 2}$	<displayed>

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

Analysis strategy: Bayesian inference

Proposal distributions for parameter

Parameter	Proposal
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Theta	Slice sampling					
M	Slice sampling					
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 steps [a]						1600
Increment (record every x step [b])						2
Number of concurrent chains (replicates) [c]						2
Visited (sampled) parameter values [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)

Allele frequency spectra

Locus 1

Allele	Pop1	Pop2	All
16	0.220	0.167	0.193
19	0.040	0.071	0.056
18	0.060	0.119	0.090
15	0.220	0.024	0.122
21	0.020	0.167	0.093
23	0.020	0.119	0.070
17	0.280	0.095	0.188
22	0.060	0.119	0.090
25	0.060	0.024	0.042
24	0.020	0.000	0.010
26	0.000	0.024	0.012
27	0.000	0.048	0.024
29	0.000	0.024	0.012

Locus 2

Allele	Pop1	Pop2	All
16	0.520	0.571	0.546
19	0.040	0.000	0.020
18	0.220	0.119	0.170
17	0.160	0.167	0.163
15	0.020	0.000	0.010
21	0.020	0.071	0.046
20	0.020	0.024	0.022
22	0.000	0.048	0.024

Locus 3

Allele	Pop1	Pop2	All
19	0.240	0.262	0.251
20	0.280	0.476	0.378
18	0.080	0.095	0.088
21	0.280	0.119	0.200
22	0.120	0.048	0.084

Locus 4

Allele	Pop1	Pop2	All
16	0.080	0.071	0.076
24	0.180	0.024	0.102

Allele	Pop1	Pop2	All
15	0.020	0.048	0.034
25	0.160	0.167	0.163
14	0.020	0.048	0.034
19	0.100	0.143	0.121
12	0.060	0.000	0.030
20	0.080	0.190	0.135
23	0.060	0.119	0.090
28	0.020	0.000	0.010
22	0.060	0.024	0.042
21	0.160	0.119	0.140
13	0.000	0.024	0.012
26	0.000	0.024	0.012
Locus 5			
Allele	Pop1	Pop2	All
20	0.400	0.524	0.462
21	0.420	0.357	0.389
19	0.180	0.119	0.150
Locus 6			
Allele	Pop1	Pop2	All
19	0.060	0.000	0.030
20	0.100	0.024	0.062
18	0.300	0.214	0.257
22	0.200	0.119	0.160
21	0.120	0.476	0.298
16	0.060	0.000	0.030
24	0.160	0.048	0.104
17	0.000	0.119	0.060
Locus 7			
Allele	Pop1	Pop2	All
23	0.040	0.238	0.139
20	0.660	0.143	0.401
22	0.180	0.190	0.185
21	0.100	0.333	0.217
19	0.020	0.095	0.058
Locus 8			
Allele	Pop1	Pop2	All
19	0.520	0.524	0.522
17	0.040	0.048	0.044

Allele	Pop1	Pop2	All
18	0.100	0.071	0.086
20	0.140	0.190	0.165
16	0.080	0.000	0.040
22	0.100	0.048	0.074
15	0.020	0.048	0.034
23	0.000	0.071	0.036

Locus 9

Allele	Pop1	Pop2	All
24	0.080	0.024	0.052
19	0.300	0.429	0.364
20	0.300	0.167	0.233
23	0.180	0.143	0.161
22	0.080	0.024	0.052
18	0.020	0.071	0.046
21	0.040	0.095	0.068
25	0.000	0.048	0.024

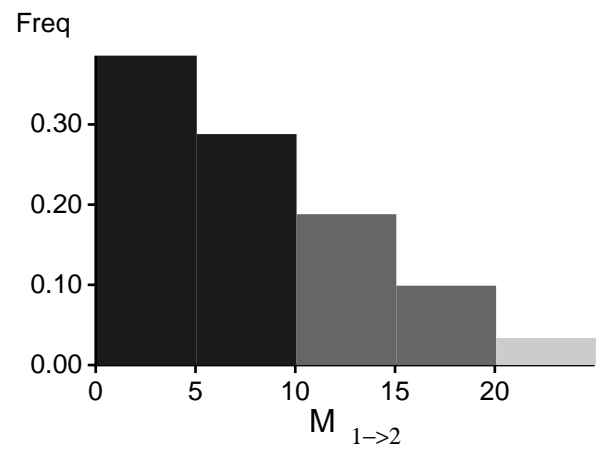
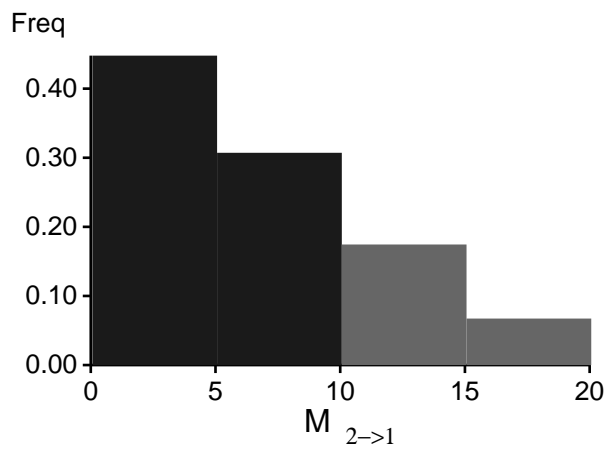
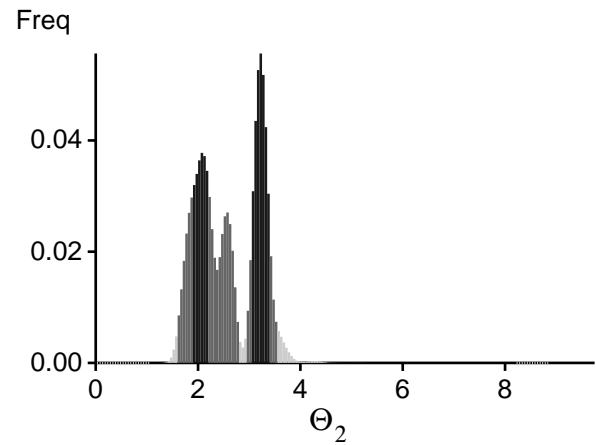
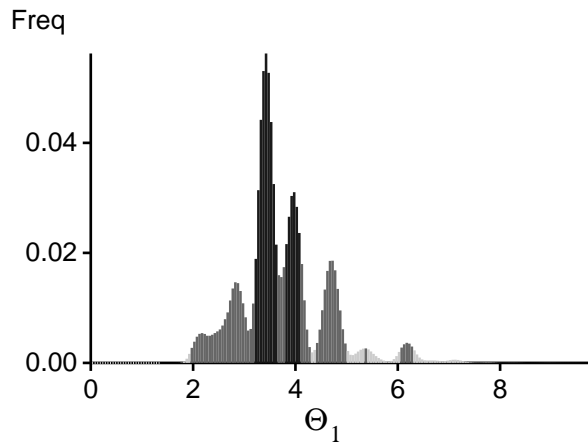
Locus 10

Allele	Pop1	Pop2	All
22	0.100	0.214	0.157
20	0.440	0.214	0.327
23	0.080	0.167	0.123
24	0.020	0.000	0.010
19	0.160	0.167	0.163
21	0.060	0.048	0.054
18	0.080	0.000	0.040
15	0.020	0.071	0.046
17	0.040	0.048	0.044
25	0.000	0.071	0.036

Bayesian Analysis: Posterior distribution table

Locus	Parameter	2.5%	25.0%	Mode	75.0%	97.5%	Median	Mean
1	Θ_1	1.40000	3.35000	4.32500	4.80000	5.05000	4.52500	5.26478
1	Θ_2	7.20000	8.20000	9.77500	10.00000	10.00000	8.27500	7.04778
1	$M_{2 \rightarrow 1}$	0.000	0.000	2.500	10.000	20.000	12.500	4.223
1	$M_{1 \rightarrow 2}$	0.000	0.000	7.500	15.000	25.000	17.500	8.524
2	Θ_1	1.45000	2.80000	3.42500	4.25000	5.80000	3.57500	3.64177
2	Θ_2	1.35000	4.50000	4.87500	5.05000	5.60000	4.32500	5.14776
2	$M_{2 \rightarrow 1}$	0.000	0.000	2.500	10.000	20.000	12.500	4.927
2	$M_{1 \rightarrow 2}$	0.000	0.000	2.500	15.000	25.000	17.500	7.918
3	Θ_1	4.35000	4.45000	4.62500	5.35000	6.65000	5.17500	5.46904
3	Θ_2	1.15000	2.30000	2.62500	3.30000	4.15000	2.82500	2.78699
3	$M_{2 \rightarrow 1}$	0.000	0.000	2.500	10.000	20.000	12.500	4.114
3	$M_{1 \rightarrow 2}$	0.000	0.000	2.500	10.000	25.000	12.500	7.319
4	Θ_1	7.40000	8.45000	9.82500	10.00000	10.00000	8.57500	7.16454
4	Θ_2	4.55000	8.85000	9.07500	9.50000	10.00000	6.47500	6.14968
4	$M_{2 \rightarrow 1}$	0.000	0.000	2.500	10.000	20.000	12.500	4.626
4	$M_{1 \rightarrow 2}$	0.000	0.000	2.500	10.000	25.000	12.500	7.299
5	Θ_1	1.20000	1.45000	1.67500	3.25000	3.65000	3.17500	4.31662
5	Θ_2	1.00000	2.80000	3.17500	3.45000	4.70000	3.02500	3.22268
5	$M_{2 \rightarrow 1}$	0.000	0.000	2.500	10.000	25.000	12.500	5.894
5	$M_{1 \rightarrow 2}$	0.000	0.000	2.500	10.000	25.000	12.500	6.565
6	Θ_1	1.75000	3.70000	4.72500	5.25000	7.50000	4.77500	4.73794
6	Θ_2	1.30000	1.55000	1.97500	3.50000	5.45000	4.22500	5.06340
6	$M_{2 \rightarrow 1}$	0.000	0.000	2.500	10.000	25.000	12.500	5.596
6	$M_{1 \rightarrow 2}$	0.000	0.000	2.500	10.000	25.000	12.500	5.391
7	Θ_1	2.70000	4.90000	5.27500	5.60000	7.95000	5.37500	5.26686
7	Θ_2	0.90000	1.95000	2.57500	3.75000	7.30000	3.92500	4.12347
7	$M_{2 \rightarrow 1}$	0.000	0.000	2.500	10.000	20.000	12.500	3.821
7	$M_{1 \rightarrow 2}$	0.000	0.000	2.500	10.000	25.000	12.500	6.167
8	Θ_1	3.25000	4.40000	5.22500	6.30000	6.40000	5.87500	6.04024
8	Θ_2	0.95000	3.50000	4.52500	5.40000	6.95000	4.37500	4.28143
8	$M_{2 \rightarrow 1}$	0.000	0.000	2.500	10.000	20.000	12.500	3.651
8	$M_{1 \rightarrow 2}$	0.000	0.000	2.500	15.000	25.000	17.500	6.847

9	Θ_1	4.25000	6.75000	7.37500	7.95000	8.95000	6.12500	5.79059
9	Θ_2	1.05000	2.90000	3.87500	4.50000	7.30000	3.97500	4.40128
9	$M_{2 \rightarrow 1}$	0.000	0.000	2.500	10.000	20.000	12.500	3.734
9	$M_{1 \rightarrow 2}$	0.000	0.000	2.500	15.000	25.000	17.500	7.946
10	Θ_1	7.75000	8.35000	9.12500	10.00000	10.00000	7.02500	6.62277
10	Θ_2	7.00000	8.50000	9.67500	10.00000	10.00000	8.17500	6.96102
10	$M_{2 \rightarrow 1}$	0.000	0.000	2.500	10.000	20.000	12.500	4.413
10	$M_{1 \rightarrow 2}$	0.000	0.000	7.500	15.000	30.000	17.500	10.138
All	Θ_1	1.90000	3.15000	3.42500	3.65000	4.30000	3.62500	3.73939
All	Θ_2	2.90000	3.00000	3.22500	3.40000	3.55000	2.62500	2.61171
All	$M_{2 \rightarrow 1}$	0.000	0.000	2.500	10.000	20.000	12.500	2.752
All	$M_{1 \rightarrow 2}$	0.000	0.000	2.500	10.000	20.000	12.500	4.842

Bayesian Analysis: Posterior distribution over all loci

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

Use this value for Bayes factor calculations:

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

Method	$\ln(\text{Prob}(D \mid \text{Model}))$	Notes
Thermodynamic integration	-11105.469570	(1)
Harmonic mean	-171797.952118	(1)

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

(1) and (2) should give a similar result, (2) is considered more crude than (1), but (1) needs heating with several well-spaced chains,

Acceptance ratios for all parameters and the genealogies

Parameter	Accepted changes	Ratio
Θ_1	8245/8245	1.00000
Θ_2	8202/8202	1.00000
$M_{2 \rightarrow 1}$	8219/8219	1.00000
$M_{1 \rightarrow 2}$	8362/8362	1.00000
Genealogies	11457/32296	0.35475

MCMC-Autocorrelation and Effective MCMC Sample Size

Parameter	Autocorrelation	Effective Sample Size
Θ_1	0.96005	656.75
Θ_2	0.94780	865.53
$M_{2 \rightarrow 1}$	0.90610	1583.93
$M_{1 \rightarrow 2}$	0.90364	1653.89
$\text{Ln}[\text{Prob}(D G)]$	0.98468	249.13