Example: Microsatellite data set

MIGRATION RATE AND POPULATION SIZE ESTIMATION
using the coalescent and maximum likelihood or Bayesian inference
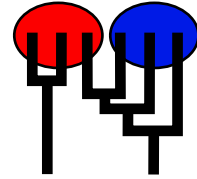Migrate-n version debug 3.0.1
  Compiled for a PARALLEL COMPUTER ARCHITECTURE
  One master and 1 compute nodes are available.
Program started at   Sat Nov 8 12:18:41 2008
Program finished at   Sat Nov 8 12:20:38 2008

Options

Datatype: Microsatellite data [Brownian motion]
Missing data: not included
Random number seed: (with internal timer)   1463564593
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          $M_{2->1}$ <displayed>
  4          $M_{1->2}$ <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	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

Allele	Pop1	Pop2	All
16	0.080	0.071	0.076
24	0.180	0.024	0.102
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
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	0.20000	0.45000	0.92500	1.30000	2.05000	1.22500	1.93988
1	Θ_2	0.25000	0.35000	0.57500	1.50000	1.80000	5.22500	5.02915
1	$M_{2\to1}$	0.000	10.000	22.500	30.000	40.000	27.500	20.097
1	$M_{1\to2}$	0.000	5.000	17.500	30.000	50.000	27.500	22.158
2	Θ_1	0.00000	0.00000	0.02500	0.10000	0.30000	0.12500	0.04229
2	Θ_2	0.00000	0.00000	0.02500	0.20000	0.45000	0.22500	0.13957
2	$M_{2\to1}$	180.000	225.000	272.500	320.000	435.000	352.500	201.392
2	$M_{1\to2}$	70.000	90.000	112.500	155.000	190.000	352.500	158.712
3	Θ_1	0.00000	0.15000	0.27500	0.40000	2.45000	1.42500	0.44706
3	Θ_2	0.05000	1.15000	1.37500	1.55000	1.90000	1.07500	0.33951
3	$M_{2\to1}$	10.000	25.000	42.500	55.000	70.000	47.500	13.701
3	$M_{1\to2}$	0.000	50.000	62.500	70.000	80.000	52.500	15.046
4	Θ_1	0.00000	0.95000	1.52500	2.00000	2.75000	1.57500	0.44434
4	Θ_2	0.00000	0.70000	1.52500	1.90000	4.30000	1.62500	0.50910
4	$M_{2\to1}$	5.000	25.000	42.500	50.000	65.000	42.500	9.433
4	$M_{1\to2}$	0.000	5.000	22.500	35.000	75.000	32.500	7.515
5	Θ_1	0.00000	0.20000	0.32500	0.45000	1.35000	0.72500	0.13597
5	Θ_2	0.00000	0.00000	0.17500	0.30000	2.55000	0.32500	0.19133
5	$M_{2\to1}$	0.000	0.000	12.500	20.000	35.000	17.500	2.847
5	$M_{1\to2}$	0.000	5.000	22.500	30.000	45.000	82.500	13.543
6	Θ_1	0.10000	0.20000	0.47500	0.90000	3.05000	1.77500	0.36392
6	Θ_2	0.05000	0.60000	0.92500	1.20000	2.15000	0.97500	0.16658
6	$M_{2\to1}$	5.000	20.000	37.500	45.000	60.000	42.500	5.859
6	$M_{1\to2}$	35.000	45.000	57.500	70.000	100.000	67.500	10.764
7	Θ_1	0.00000	0.00000	0.02500	0.10000	0.20000	0.12500	0.00258
7	Θ_2	0.00000	0.00000	0.02500	0.15000	0.55000	0.17500	0.02539
7	$M_{2\to1}$	565.000	780.000	847.500	890.000	945.000	787.500	110.675
7	$M_{1\to2}$	200.000	220.000	257.500	290.000	305.000	787.500	92.432
8	Θ_1	0.00000	0.10000	0.27500	0.85000	2.25000	0.82500	0.15735

Locus	Parameter	2.5%	25.0%	Mode	75.0%	97.5%	Median	Mean
8	Θ_2	0.00000	0.20000	0.62500	1.10000	4.55000	1.57500	0.27334
8	$M_{2->1}$	10.000	25.000	42.500	60.000	90.000	52.500	6.307
8	$M_{1->2}$	5.000	15.000	32.500	50.000	85.000	47.500	5.650
9	Θ_1	0.20000	0.50000	0.77500	1.00000	4.30000	1.67500	0.21630
9	Θ_2	0.20000	0.30000	0.57500	0.90000	4.50000	2.47500	0.35446
9	$M_{2->1}$	0.000	10.000	22.500	30.000	40.000	27.500	2.239
9	$M_{1->2}$	0.000	15.000	27.500	40.000	50.000	32.500	3.164
10	Θ_1	0.05000	0.15000	0.32500	0.50000	3.05000	1.37500	0.14823
10	Θ_2	0.00000	0.00000	0.22500	0.95000	3.10000	0.92500	0.11983
10	$M_{2->1}$	0.000	5.000	17.500	30.000	40.000	22.500	1.868
10	$M_{1->2}$	15.000	25.000	42.500	55.000	65.000	57.500	5.974
All	Θ_1	0.10000	0.20000	0.37500	0.45000	0.60000	0.42500	0.37702
All	Θ_2	0.10000	0.20000	0.32500	0.45000	0.60000	0.42500	0.35926
All	$M_{2->1}$	0.000	15.000	27.500	35.000	45.000	32.500	26.835
All	$M_{1->2}$	10.000	25.000	37.500	45.000	55.000	42.500	36.009

Bayesian Analysis: Posterior distribution over all loci
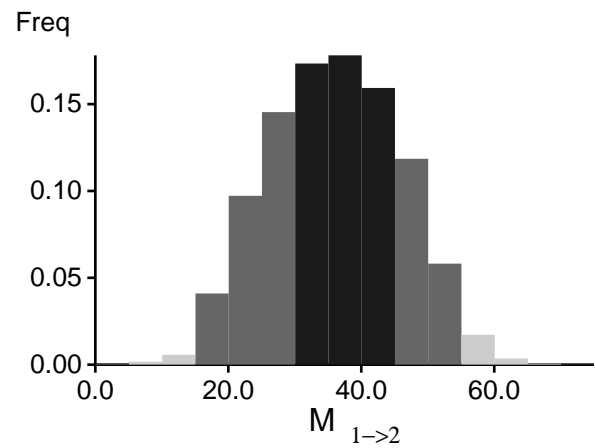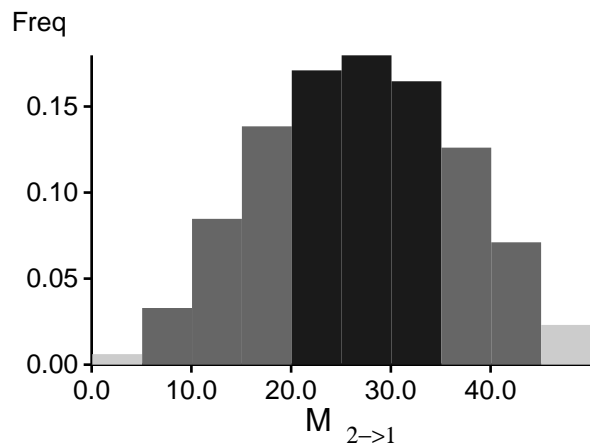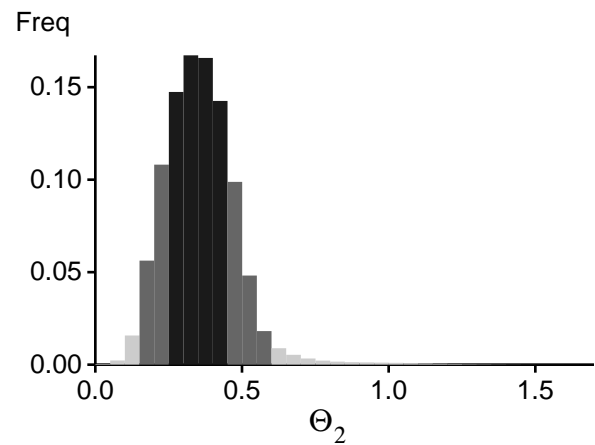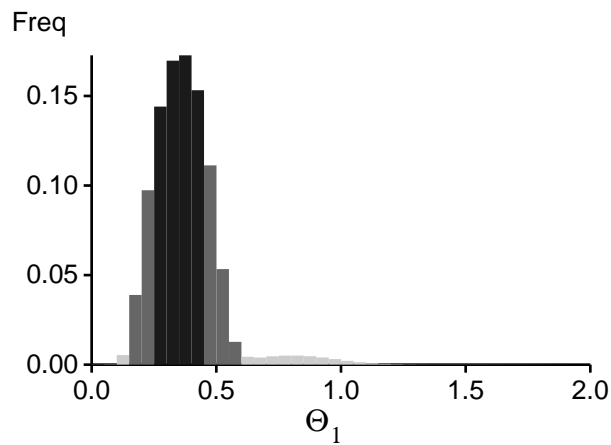
Log-Probability of the data given the model (marginal likelihood)

Use this value for Bayes factor calculations:
BF = Exp[ln(Prob(D | thisModel) - ln(Prob(D | otherModel)
shows the support for thisModel]

Method	ln(Prob(D|Model))	Notes
Thermodynamic integration	-135251.405622	(1)
Harmonic mean	-3323236.294909	(2)

(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	82420/82420	1.00000
Θ_2	83160/83160	1.00000
$M_{2 \to 1}$	82700/82700	1.00000
$M_{1 \to 2}$	83770/83770	1.00000
Genealogies	93400/321330	0.29067

MCMC-Autocorrelation and Effective MCMC Sample Size

Parameter	Autocorrelation	Effective Sampe Size
Θ_1	0.95567	7342.44
Θ_2	0.95584	7321.25
$M_{2->1}$	0.94412	9268.72
$M_{1->2}$	0.93547	10861.71
Ln[Prob(D|G)]	0.98307	2789.41