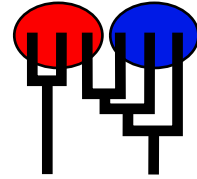


Example: Microsatellite data set

MIGRATION RATE AND POPULATION SIZE ESTIMATION
 using the coalescent and maximum likelihood or Bayesian inference
 Migrate-n version 3.2.8 [1849]
 Compiled for a PARALLEL COMPUTER ARCHITECTURE
 One master and 2 compute nodes are available.
 Compiled for a SYMMETRIC MULTIPROCESSORS
 Program started at Mon Mar 21 16:11:53 2011
 Program finished at Mon Mar 21 16:33:26 2011



Options

Datatype: Microsatellite data [Brownian motion]
 Missing data: not included

Inheritance scalers in use for Thetas: 1.00 1.00
 1.00 1.00 1.00 1.00 1.00
 1.00 1.00 1.00

[Each Theta uses the (true) inheritance scalar of the first locus as a reference]

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 | 2 |
| 1 population_num | * | 0 |
| 2 population_num | * | * |

Order of parameters:
 1 Θ_1 <displayed>

2 Θ_2 <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 |
|-----------|----------------|
| 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] | 5000 |
| Increment (record every x step [b]) | 100 |
| Number of concurrent chains (replicates) [c] | 2 |
| Visited (sampled) parameter values [a*b*c] | 1000000 |
| 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) |
| 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

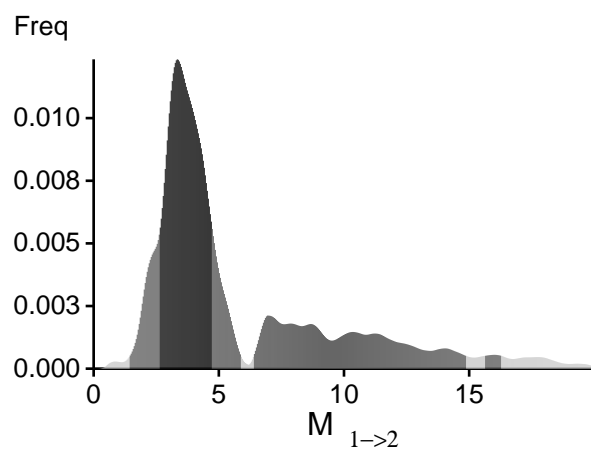
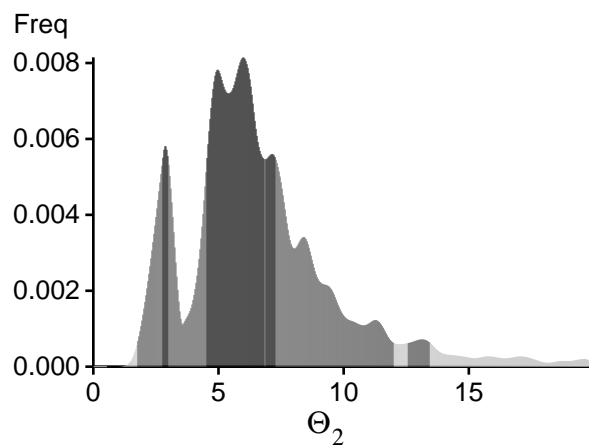
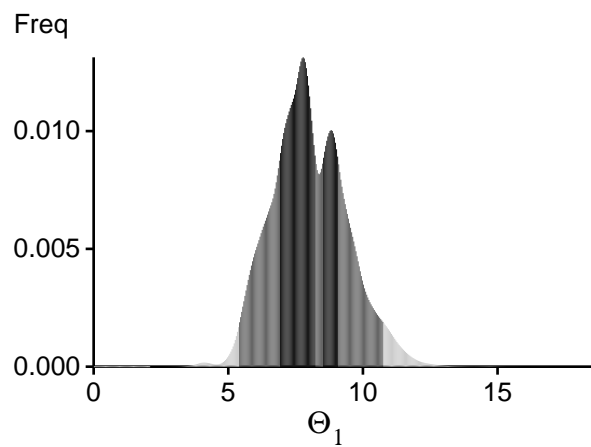
| Allele | Pop1 | Pop2 | All |
|--------|-------|-------|-------|
| 22 | 0.100 | 0.214 | 0.157 |
| 20 | 0.440 | 0.214 | 0.327 |
| 23 | 0.080 | 0.167 | 0.123 |
| 24 | 0.020 | 0.000 | 0.010 |
| 19 | 0.160 | 0.167 | 0.163 |
| 21 | 0.060 | 0.048 | 0.054 |
| 18 | 0.080 | 0.000 | 0.040 |
| 15 | 0.020 | 0.071 | 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 | 9.60000 | 14.80000 | 0.00000 | 18.60000 | 0.00000 | 0.00000 | 15.23731 |
| 1 | Θ_2 | 7.92000 | 15.08000 | 0.00000 | 19.92000 | 0.00000 | 15.22000 | 14.65390 |
| 1 | $M_{1 \rightarrow 2}$ | 0.000 | 0.320 | 0.000 | 1.240 | 0.000 | 1.060 | 1.201 |
| 2 | Θ_1 | 2.44000 | 4.36000 | 0.00000 | 7.92000 | 0.00000 | 0.00000 | 7.36486 |
| 2 | Θ_2 | 0.56000 | 0.84000 | 0.00000 | 6.72000 | 0.00000 | 6.74000 | 8.09118 |
| 2 | $M_{1 \rightarrow 2}$ | 0.000 | 13.560 | 0.000 | 19.880 | 0.000 | 13.500 | 12.603 |
| 3 | Θ_1 | 2.44000 | 5.24000 | 0.00000 | 9.68000 | 0.00000 | 0.00000 | 8.57502 |
| 3 | Θ_2 | 1.20000 | 1.44000 | 0.00000 | 7.84000 | 0.00000 | 8.18000 | 9.06468 |
| 3 | $M_{1 \rightarrow 2}$ | 0.000 | 18.760 | 0.000 | 19.840 | 0.000 | 11.420 | 11.172 |
| 4 | Θ_1 | 11.32000 | 17.44000 | 0.00000 | 19.96000 | 0.00000 | 0.00000 | 16.76846 |
| 4 | Θ_2 | 3.60000 | 12.16000 | 0.00000 | 19.80000 | 0.00000 | 12.38000 | 12.00746 |
| 4 | $M_{1 \rightarrow 2}$ | 0.000 | 1.080 | 0.000 | 8.720 | 0.000 | 8.460 | 9.376 |
| 5 | Θ_1 | 0.32000 | 1.00000 | 0.00000 | 2.76000 | 0.00000 | 0.00000 | 2.83008 |
| 5 | Θ_2 | 0.24000 | 5.36000 | 0.00000 | 8.96000 | 0.00000 | 9.46000 | 9.75400 |
| 5 | $M_{1 \rightarrow 2}$ | 0.000 | 18.920 | 0.000 | 19.680 | 0.000 | 13.540 | 13.254 |
| 6 | Θ_1 | 2.72000 | 4.64000 | 0.00000 | 8.60000 | 0.00000 | 0.00000 | 8.27743 |
| 6 | Θ_2 | 0.00000 | 0.36000 | 0.00000 | 1.88000 | 0.00000 | 1.74000 | 2.93945 |
| 6 | $M_{1 \rightarrow 2}$ | 0.000 | 1.160 | 0.000 | 6.760 | 0.000 | 7.380 | 8.118 |
| 7 | Θ_1 | 0.72000 | 1.56000 | 0.00000 | 4.36000 | 0.00000 | 0.00000 | 4.47605 |
| 7 | Θ_2 | 0.96000 | 1.32000 | 0.00000 | 6.88000 | 0.00000 | 7.06000 | 8.35536 |
| 7 | $M_{1 \rightarrow 2}$ | 0.000 | 0.320 | 0.000 | 2.760 | 0.000 | 2.580 | 3.842 |
| 8 | Θ_1 | 3.84000 | 5.56000 | 0.00000 | 10.00000 | 0.00000 | 0.00000 | 9.54921 |
| 8 | Θ_2 | 1.72000 | 2.12000 | 0.00000 | 9.68000 | 0.00000 | 9.38000 | 9.83750 |
| 8 | $M_{1 \rightarrow 2}$ | 0.000 | 15.000 | 0.000 | 19.840 | 0.000 | 11.900 | 11.693 |
| 9 | Θ_1 | 3.32000 | 6.60000 | 0.00000 | 11.92000 | 0.00000 | 0.00000 | 10.29873 |
| 9 | Θ_2 | 2.80000 | 3.92000 | 0.00000 | 9.36000 | 0.00000 | 9.98000 | 10.34376 |
| 9 | $M_{1 \rightarrow 2}$ | 0.000 | 3.440 | 0.000 | 6.560 | 0.000 | 10.460 | 10.630 |

| | | | | | | | | |
|-----|-----------------------|---------|----------|---------|----------|----------|---------|----------|
| 10 | Θ_1 | 6.68000 | 14.92000 | 0.00000 | 19.92000 | 0.00000 | 0.00000 | 13.68066 |
| 10 | Θ_2 | 1.32000 | 1.96000 | 0.00000 | 8.40000 | 0.00000 | 7.62000 | 8.64818 |
| 10 | $M_{1 \rightarrow 2}$ | 0.000 | 0.360 | 0.000 | 4.920 | 0.000 | 4.780 | 7.003 |
| All | Θ_1 | 5.36000 | 6.88000 | 7.78000 | 8.24000 | 10.76000 | 7.94000 | 8.01937 |
| All | Θ_2 | 1.72000 | 4.48000 | 5.98000 | 6.84000 | 12.00000 | 6.14000 | 6.61349 |
| All | $M_{1 \rightarrow 2}$ | 1.400 | 2.600 | 3.340 | 4.720 | 5.880 | 4.260 | 5.955 |

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 | -7346.97 | -1303.45 | -125.62 |
| 2 | -2168.35 | -438.45 | -82.20 |
| 3 | -1287.70 | -304.25 | -96.24 |
| 4 | -8720.53 | -1525.66 | -122.34 |
| 5 | -739.66 | -191.03 | -70.57 |
| 6 | -3998.99 | -743.70 | -89.18 |
| 7 | -1401.63 | -314.51 | -93.45 |
| 8 | -2320.05 | -471.38 | -94.80 |
| 9 | -2971.22 | -580.34 | -98.67 |
| 10 | -3580.91 | -694.64 | -113.58 |
| All | -34595.62 | -6627.01 | -1046.24 |

(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

[Scaling factor = -59.595907

Acceptance ratios for all parameters and the genealogies

| Parameter | Accepted changes | Ratio |
|-----------------------|------------------|---------|
| Θ_1 | 8501325/8501325 | 1.00000 |
| Θ_2 | 8507800/8507800 | 1.00000 |
| $M_{1 \rightarrow 2}$ | 8506080/8506080 | 1.00000 |
| Genealogies | 7881070/24994790 | 0.31531 |

MCMC-Autocorrelation and Effective MCMC Sample Size

| Parameter | Autocorrelation | Effective Sample Size |
|-------------------------------|-----------------|-----------------------|
| Θ_1 | 0.84612 | 39358.65 |
| Θ_2 | 0.69715 | 84878.68 |
| $M_{1 \rightarrow 2}$ | 0.89913 | 34549.43 |
| $\text{Ln}[\text{Prob}(D G)]$ | 0.95301 | 10194.08 |