# Example: Microsatellite data set

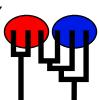POPULATION SIZE, MIGRATION, DIVERGENCE, ASSIGNMENT, HISTORY
Bayesian inference using the structured coalescent
Migrate-n version 4.1.3a [Feb-22-2015]
  Using Intel AVX (Advanced Vector Extensions)
Program started at   Sun Feb 22 12:45:34 2015
Program finished at   Sun Feb 22 12:58:07 2015

# Options

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

Inheritance scalers in use for Thetas:
All loci use an inheritance scaler of 1.0
[The locus with a scaler of 1.0 used as reference]

| | | |
|---|---|---|
| Random number seed: | (from parmfile) | 310705631 |

Start parameters:

Theta values were generated                              Using a percent value of the prior

M values were generated                                  Using a percent value of the prior

Connection matrix:
 m = average (average over a group of Thetas or M,
 s = symmetric migration M, S = symmetric 4Nm,
 0 = zero, and not estimated,
 * = migration free to vary, Thetas are on diagonal
 d = row population split off column population, D = split and then migration

| Population | 1 | 2 |
|---|---|---|
| 1 population_numb | * | 0 |
| 2 population_numb | * | * |

Order of parameters:
| 1 | $\Theta_1$ | <displayed> |
|---|---|---|
| 2 | $\Theta_2$ | <displayed> |

3        M $_{1->2}$                        &lt;displayed&gt;

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 |
| Theta | Uniform | 0.000000 | 10.000000 | 20.000000 | 2.000000 | 500 |
| M | 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] | 50 |
| Number of concurrent chains (replicates) [c] | 2 |
| Visited (sampled) parameter values [a*b*c] | 500000 |
| Number of discard trees per chain (burn-in) | 5000 |

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 |
| Haplotyping is turned on: | NO |
| Output file: | outfile-bayes |
| Posterior distribution raw histogram file: | bayesfile |
| Raw data from the MCMC run: | bayesallfile.gz |
| Print data: | No |
| Print genealogies [only some for some data type]: | None |

# *Data summary*

Data file: infile.msat
Datatype: Microsatellite data [Brownian]
[Data was used as repeat-length information]
Number of loci: 10

Mutationmodel:

| Locus | Sublocus | Mutationmodel | Mutationmodel parameters |
|---|---|---|---|
| 1 | 1 | Brownian Motion | [none] |
| 2 | 1 | Brownian Motion | [none] |
| 3 | 1 | Brownian Motion | [none] |
| 4 | 1 | Brownian Motion | [none] |
| 5 | 1 | Brownian Motion | [none] |
| 6 | 1 | Brownian Motion | [none] |
| 7 | 1 | Brownian Motion | [none] |
| 8 | 1 | Brownian Motion | [none] |
| 9 | 1 | Brownian Motion | [none] |
| 10 | 1 | Brownian Motion | [none] |

| 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 | 0.196 |
| 19 | 0.040 | 0.071 | 0.054 |
| 18 | 0.060 | 0.119 | 0.087 |
| 15 | 0.220 | 0.024 | 0.130 |
| 21 | 0.020 | 0.167 | 0.087 |
| 23 | 0.020 | 0.119 | 0.065 |
| 17 | 0.280 | 0.095 | 0.196 |
| 22 | 0.060 | 0.119 | 0.087 |
| 25 | 0.060 | 0.024 | 0.043 |
| 24 | 0.020 | - | 0.011 |
| 26 | - | 0.024 | 0.011 |
| 27 | - | 0.048 | 0.022 |
| 29 | - | 0.024 | 0.011 |
| Alleles | 10 | 12 | 13 |
| Samplesize | 50 | 42 | 92 |
| $H_{exp}$ | 0.811 | 0.883 | 0.874 |

Locus 2

| Allele | Pop1 | Pop2 | All |
|---|---|---|---|
| 16 | 0.520 | 0.571 | 0.543 |
| 19 | 0.040 | - | 0.022 |
| 18 | 0.220 | 0.119 | 0.174 |
| 17 | 0.160 | 0.167 | 0.163 |
| 15 | 0.020 | - | 0.011 |
| 21 | 0.020 | 0.071 | 0.043 |
| 20 | 0.020 | 0.024 | 0.022 |
| 22 | - | 0.048 | 0.022 |
| Alleles | 7 | 6 | 8 |
| Samplesize | 50 | 42 | 92 |
| $H_{exp}$ | 0.653 | 0.624 | 0.644 |

Locus 3

| Allele | Pop1 | Pop2 | All |
|---|---|---|---|
| 19 | 0.240 | 0.262 | 0.250 |
| 20 | 0.280 | 0.476 | 0.370 |

| Allele | Pop1 | Pop2 | All |
|---|---|---|---|
| 18 | 0.080 | 0.095 | 0.087 |
| 21 | 0.280 | 0.119 | 0.207 |
| 22 | 0.120 | 0.048 | 0.087 |
| Alleles | 5 | 5 | 5 |
| Samplesize | 50 | 42 | 92 |
| $H_{exp}$ | 0.765 | 0.679 | 0.743 |

Locus 4

| Allele | Pop1 | Pop2 | All |
|---|---|---|---|
| 16 | 0.080 | 0.071 | 0.076 |
| 24 | 0.180 | 0.024 | 0.109 |
| 15 | 0.020 | 0.048 | 0.033 |
| 25 | 0.160 | 0.167 | 0.163 |
| 14 | 0.020 | 0.048 | 0.033 |
| 19 | 0.100 | 0.143 | 0.120 |
| 12 | 0.060 | - | 0.033 |
| 20 | 0.080 | 0.190 | 0.130 |
| 23 | 0.060 | 0.119 | 0.087 |
| 28 | 0.020 | - | 0.011 |
| 22 | 0.060 | 0.024 | 0.043 |
| 21 | 0.160 | 0.119 | 0.141 |
| 13 | - | 0.024 | 0.011 |
| 26 | - | 0.024 | 0.011 |
| Alleles | 12 | 12 | 14 |
| Samplesize | 50 | 42 | 92 |
| $H_{exp}$ | 0.882 | 0.875 | 0.892 |

Locus 5

| Allele | Pop1 | Pop2 | All |
|---|---|---|---|
| 20 | 0.400 | 0.524 | 0.457 |
| 21 | 0.420 | 0.357 | 0.391 |
| 19 | 0.180 | 0.119 | 0.152 |
| Alleles | 3 | 3 | 3 |
| Samplesize | 50 | 42 | 92 |
| $H_{exp}$ | 0.631 | 0.584 | 0.615 |

Locus 6

| Allele | Pop1 | Pop2 | All |
|---|---|---|---|
| 19 | 0.060 | - | 0.033 |
| 20 | 0.100 | 0.024 | 0.065 |

| Allele | Pop1 | Pop2 | All |
|---|---|---|---|
| 18 | 0.300 | 0.214 | 0.261 |
| 22 | 0.200 | 0.119 | 0.163 |
| 21 | 0.120 | 0.476 | 0.283 |
| 16 | 0.060 | - | 0.033 |
| 24 | 0.160 | 0.048 | 0.109 |
| 17 | - | 0.119 | 0.054 |
| Alleles | 7 | 6 | 8 |
| Samplesize | 50 | 42 | 92 |
| $H_{exp}$ | 0.813 | 0.696 | 0.804 |

Locus 7

| Allele | Pop1 | Pop2 | All |
|---|---|---|---|
| 23 | 0.040 | 0.238 | 0.130 |
| 20 | 0.660 | 0.143 | 0.424 |
| 22 | 0.180 | 0.190 | 0.185 |
| 21 | 0.100 | 0.333 | 0.207 |
| 19 | 0.020 | 0.095 | 0.054 |
| Alleles | 5 | 5 | 5 |
| Samplesize | 50 | 42 | 92 |
| $H_{exp}$ | 0.520 | 0.766 | 0.724 |

Locus 8

| Allele | Pop1 | Pop2 | All |
|---|---|---|---|
| 19 | 0.520 | 0.524 | 0.522 |
| 17 | 0.040 | 0.048 | 0.043 |
| 18 | 0.100 | 0.071 | 0.087 |
| 20 | 0.140 | 0.190 | 0.163 |
| 16 | 0.080 | - | 0.043 |
| 22 | 0.100 | 0.048 | 0.076 |
| 15 | 0.020 | 0.048 | 0.033 |
| 23 | - | 0.071 | 0.033 |
| Alleles | 7 | 7 | 8 |
| Samplesize | 50 | 42 | 92 |
| $H_{exp}$ | 0.682 | 0.672 | 0.682 |

Locus 9

| Allele | Pop1 | Pop2 | All |
|---|---|---|---|
| 24 | 0.080 | 0.024 | 0.054 |
| 19 | 0.300 | 0.429 | 0.359 |
| 20 | 0.300 | 0.167 | 0.239 |

| Allele | Pop1 | Pop2 | All |
|---|---|---|---|
| 23 | 0.180 | 0.143 | 0.163 |
| 22 | 0.080 | 0.024 | 0.054 |
| 18 | 0.020 | 0.071 | 0.043 |
| 21 | 0.040 | 0.095 | 0.065 |
| 25 | - | 0.048 | 0.022 |
| Alleles | 7 | 8 | 8 |
| Samplesize | 50 | 42 | 92 |
| $H_{exp}$ | 0.773 | 0.751 | 0.775 |

Locus 10

| Allele | Pop1 | Pop2 | All |
|---|---|---|---|
| 22 | 0.100 | 0.214 | 0.152 |
| 20 | 0.440 | 0.214 | 0.337 |
| 23 | 0.080 | 0.167 | 0.120 |
| 24 | 0.020 | - | 0.011 |
| 19 | 0.160 | 0.167 | 0.163 |
| 21 | 0.060 | 0.048 | 0.054 |
| 18 | 0.080 | - | 0.043 |
| 15 | 0.020 | 0.071 | 0.043 |
| 17 | 0.040 | 0.048 | 0.043 |
| 25 | - | 0.071 | 0.033 |
| Alleles | 9 | 8 | 10 |
| Samplesize | 50 | 42 | 92 |
| $H_{exp}$ | 0.752 | 0.838 | 0.813 |

Average expected heterozygosity

| | Pop1 | Pop2 | All |
|---|---|---|---|
| $H_{exp}$ | 0.728 | 0.737 | 0.000 |

# Bayesian Analysis: Posterior distribution table

| Locus | Parameter | 2.5% | 25.0% | Mode | 75.0% | 97.5% | Median | Mean |
|---|---|---|---|---|---|---|---|---|
| 1 | $\Theta_1$ | 8.84000 | 13.60000 | 15.58000 | 18.52000 | 20.00000 | 14.86000 | 14.61700 |
| 1 | $\Theta_2$ | 4.24000 | 14.28000 | 19.14000 | 19.80000 | 20.00000 | 14.54000 | 13.60393 |
| 1 | $M_{1->2}$ | 0.000 | 0.000 | 0.740 | 2.000 | 14.400 | 2.020 | 3.874 |
| 2 | $\Theta_1$ | 2.44000 | 4.56000 | 7.10000 | 8.36000 | 12.56000 | 6.98000 | 7.22636 |
| 2 | $\Theta_2$ | 1.92000 | 2.28000 | 3.58000 | 6.20000 | 19.40000 | 9.98000 | 10.26078 |
| 2 | $M_{1->2}$ | 7.320 | 14.720 | 19.140 | 19.560 | 20.000 | 15.140 | 14.630 |
| 3 | $\Theta_1$ | 2.76000 | 5.28000 | 7.90000 | 10.20000 | 17.04000 | 8.74000 | 9.33329 |
| 3 | $\Theta_2$ | 1.40000 | 1.80000 | 3.90000 | 9.56000 | 15.12000 | 8.82000 | 9.56871 |
| 3 | $M_{1->2}$ | 2.480 | 4.480 | 8.700 | 10.240 | 19.000 | 8.740 | 9.417 |
| 4 | $\Theta_1$ | 12.56000 | 17.12000 | 19.18000 | 19.76000 | 20.00000 | 17.42000 | 17.03526 |
| 4 | $\Theta_2$ | 5.36000 | 8.20000 | 11.66000 | 12.72000 | 19.88000 | 12.50000 | 12.53930 |
| 4 | $M_{1->2}$ | 0.720 | 1.520 | 2.900 | 6.600 | 11.360 | 6.060 | 7.999 |
| 5 | $\Theta_1$ | 0.04000 | 0.88000 | 1.50000 | 2.56000 | 5.20000 | 2.18000 | 2.43874 |
| 5 | $\Theta_2$ | 1.44000 | 3.88000 | 6.06000 | 6.96000 | 19.60000 | 10.42000 | 10.47412 |
| 5 | $M_{1->2}$ | 5.280 | 13.840 | 18.780 | 19.720 | 20.000 | 14.180 | 13.515 |
| 6 | $\Theta_1$ | 2.80000 | 4.76000 | 6.98000 | 9.44000 | 16.28000 | 8.26000 | 8.83058 |
| 6 | $\Theta_2$ | 0.00000 | 0.20000 | 0.82000 | 1.48000 | 5.00000 | 1.34000 | 1.70128 |
| 6 | $M_{1->2}$ | 1.120 | 2.640 | 4.900 | 9.120 | 15.440 | 7.820 | 8.894 |
| 7 | $\Theta_1$ | 0.88000 | 1.80000 | 2.74000 | 4.20000 | 8.84000 | 3.78000 | 4.31644 |
| 7 | $\Theta_2$ | 0.76000 | 1.04000 | 1.74000 | 8.80000 | 18.72000 | 8.58000 | 9.19534 |
| 7 | $M_{1->2}$ | 0.000 | 0.440 | 1.300 | 3.160 | 9.640 | 2.900 | 3.591 |
| 8 | $\Theta_1$ | 3.84000 | 6.08000 | 8.94000 | 10.88000 | 16.92000 | 9.42000 | 9.80119 |
| 8 | $\Theta_2$ | 2.80000 | 5.88000 | 9.38000 | 12.04000 | 19.84000 | 10.98000 | 11.10548 |
| 8 | $M_{1->2}$ | 5.000 | 14.720 | 19.180 | 19.880 | 20.000 | 14.940 | 13.979 |
| 9 | $\Theta_1$ | 4.64000 | 7.20000 | 10.22000 | 12.36000 | 18.04000 | 10.62000 | 10.91378 |
| 9 | $\Theta_2$ | 3.36000 | 5.08000 | 6.14000 | 12.08000 | 19.72000 | 11.14000 | 11.28512 |
| 9 | $M_{1->2}$ | 2.440 | 13.440 | 16.060 | 19.480 | 19.760 | 11.220 | 11.123 |

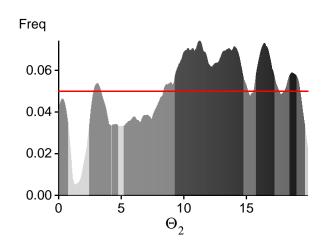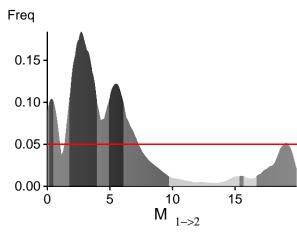| 10 | $\Theta_1$ | 8.60000 | 14.84000 | 18.66000 | 19.44000 | 20.00000 | 15.38000 | 14.97991 |
|---|---|---|---|---|---|---|---|---|
| 10 | $\Theta_2$ | 0.84000 | 1.40000 | 2.94000 | 7.56000 | 17.48000 | 7.06000 | 8.19014 |
| 10 | $M_{1->2}$ | 0.480 | 1.480 | 4.820 | 7.280 | 16.720 | 7.260 | 7.990 |
| All | $\Theta_1$ | 0.04000 | 0.72000 | 1.50000 | 2.36000 | 10.16000 | 4.50000 | 4.96088 |
| All | $\Theta_2$ | 5.16000 | 9.24000 | 11.26000 | 14.76000 | 19.68000 | 11.62000 | 11.04517 |
| All | $M_{1->2}$ | 0.000 | 1.720 | 2.700 | 3.960 | 9.720 | 4.300 | 5.825 |

Citation suggestions:

Beerli P., 2006. Comparison of Bayesian and maximum-likelihood inference of population genetic parameters.
  Bioinformatics 22:341-345
Beerli P., 2009. How to use MIGRATE or why are Markov chain Monte Carlo programs difficult to use?
  In Population Genetics for Animal Conservation, G. Bertorelle, M. W. Bruford, H. C. Hauffe, A. Rizzoli,
  and C. Vernesi, eds., vol. 17 of Conservation Biology, Cambridge University Press, Cambridge UK, pp. 42-79.

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

Freq



$\Theta_1$

Freq



$\Theta_2$

Freq



M $_{1\rightarrow 2}$

# *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)
or as LBF = 2 (ln(Prob(D | thisModel) - ln( Prob( D | otherModel))
shows the support for thisModel]

| Locus | Raw thermodynamic score(1a) | Bezier approximation score(1b) | Harmonic mean(2) |
|---|---|---|---|
| 1 | -11224.80 | -1926.70 | -125.35 |
| 2 | -1394.99 | -315.24 | -91.21 |
| 3 | -2748.49 | -539.43 | -99.85 |
| 4 | -7648.82 | -1358.22 | -117.22 |
| 5 | -1002.82 | -232.57 | -65.48 |
| 6 | -9972.00 | -1702.10 | -75.87 |
| 7 | -751.08 | -211.03 | -85.50 |
| 8 | -2443.76 | -494.06 | -91.75 |
| 9 | -2315.88 | -477.72 | -100.19 |
| 10 | -8335.71 | -1458.77 | -108.78 |
| All | -47839.07 | -8716.57 | -961.94 |

(1a, 1b and 2) are approximations to the marginal likelihood, make sure that the program run long enough!
(1a, 1b) and (2) should give similar results, in principle.
But (2) is overestimating the likelihood, it is presented for historical reasons and should not be used
(1a, 1b) needs heating with chains that span a temperature range of 1.0 to at least 100,000.
(1b) is using a Bezier-curve to get better approximations for runs with low number of heated chains
[Scaling factor = -0.720889
Citation suggestions:

Beerli P. and M. Palczewski, 2010. Unified framework to evaluate panmixia and migration direction among
   multiple sampling locations, Genetics, 185: 313-326.

## *Acceptance ratios for all parameters and the genealogies*

| Parameter | Accepted changes | Ratio |
|---|---|---|
| $\Theta_1$ | 832079/832079 | 1.00000 |
| $\Theta_2$ | 833455/833455 | 1.00000 |
| $M_{1->2}$ | 832531/832531 | 1.00000 |
| Genealogies | 792401/2501935 | 0.31672 |

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

| Parameter | Autocorrelation | Effective Sampe Size |
|---|---|---|
| $\Theta_1$ | 0.84631 | 8652.46 |
| $\Theta_2$ | 0.67816 | 19866.10 |
| $M_{1\rightarrow2}$ | 0.85783 | 7783.23 |
| Ln[Prob(D|G)] | 0.97390 | 1323.03 |

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## *Potential Problems*

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This section reports potential problems with your run, but such reporting is often not very accurate. Whith many parameters in a multilocus analysi    s, it is very common that some parameters for some loci will not be very informative, triggering suggestions (for example to increase the prior ran    ge) that are not sensible. This suggestion tool will improve with time, therefore do not blindly follow its suggestions. If some parameters are fla gged, inspect the tables carefully and judge wether an action is required. For example, if you run a Bayesian inference with sequence data, for mac    roscopic species there is rarely the need to increase the prior for Theta beyond 0.1; but if you use microsatellites it is rather common that your     prior distribution for Theta should have a range from 0.0 to 100 or more. With many populations (>3) it is also very common that some migration rou tes are estimated poorly because the data contains little or no information for that route. Increasing the range will not help in such situations,     reducing number of parameters may help in such situations.

Param 4 (Locus 2): Upper prior boundary seems too low!
Param 4 (Locus 5): Upper prior boundary seems too low!
Param 4 (Locus 8): Upper prior boundary seems too low!
Param 4 (Locus 9): Upper prior boundary seems too low!