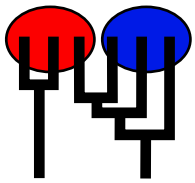
Example: Microsatellite data set

MIGRATION RATE AND POPULATION SIZE ESTIMATION
using the coalescent and maximum likelihood or Bayesian inference
Migrate-n version debug 3.1.4 [x]
Program started at Fri Apr 30 17:53:30 2010
Program finished at Fri Apr 30 17:53:33 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	Θ_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]	160
Increment (record every x step [b]	2
Number of concurrent chains (replicates) [c]	2
Visited (sampled) parameter values [a*b*c]	640

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

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

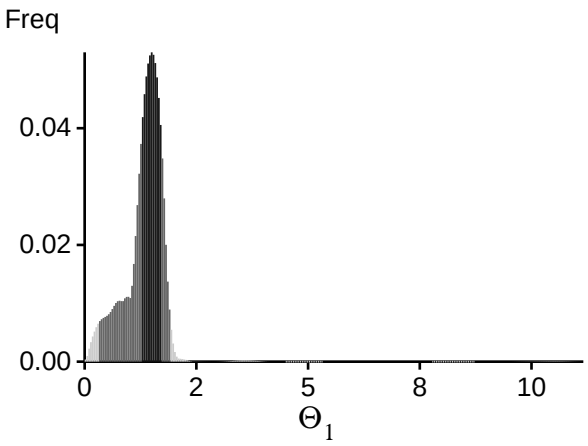
Locus 10

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	Θ_1	0.28000	0.44000	0.78000	1.04000	1.20000	2.70000	2.38701
2	Θ_1	2.56000	2.88000	3.30000	3.72000	4.36000	4.34000	2.29007
3	Θ_1	0.88000	1.24000	1.50000	1.72000	2.12000	1.54000	0.50485
4	Θ_1	0.64000	0.80000	1.18000	1.52000	1.72000	1.94000	0.98973
5	Θ_1	4.36000	4.76000	5.30000	5.84000	8.68000	6.34000	1.29021
6	Θ_1	0.24000	0.36000	0.74000	1.04000	1.16000	1.42000	0.54639
7	Θ_1	2.28000	2.52000	2.94000	3.36000	6.08000	3.74000	0.56294
8	Θ_1	3.40000	3.68000	4.18000	4.96000	5.60000	5.70000	0.73186
9	Θ_1	3.00000	3.44000	3.98000	4.48000	5.08000	5.94000	0.64260
10	Θ_1	4.60000	5.16000	6.06000	6.48000	9.64000	6.82000	0.69561
All	Θ_1	0.28000	1.24000	1.50000	1.72000	1.92000	1.46000	1.34141

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)
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	-2731.95	-531.49	-195.51
2	-591.42	-119.14	-25.82
3	-900.75	-160.76	-15.06
4	-5607.81	-982.46	-156.85
5	-735.65	-149.11	-29.23
6	-1324.78	-253.70	-73.92
7	-554.54	-108.98	-22.18
8	-2512.10	-432.09	-32.75
9	-1235.99	-223.78	-30.74
10	-1679.64	-309.91	-37.18
All	-17970.10	-3366.91	-714.71

(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
Θ_1	3225/3225	1.00000
Genealogies	728/3215	0.22644

MCMC-Autocorrelation and Effective MCMC Sample Size

Parameter	Autocorrelation	Effective Sampe Size
Θ_1	0.22647	1547.04
Ln[Prob(D|G)]	0.94569	54.18