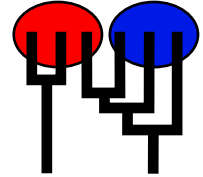# Example: Microsatellite data set

MIGRATION RATE AND POPULATION SIZE ESTIMATION
using the coalescent and maximum likelihood or Bayesian inference
Migrate-n version debug 2.5.1
Program started at   Sat Jul 19 08:39:19 2008
Program finished at   Sat Jul 19 08:39:30 2008

Options

Datatype:	Microsatellite data [Brownian motion]
Missing data:	not included
Random number seed:	(with internal timer) 1466650805
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           $M_{2\rightarrow1}$ <displayed>
  4           $M_{1\rightarrow2}$ <displayed>

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

Analysis strategy is   Maximum likelihood

Markov chain settings:	Short chain	Long chain
Number of chains	10	3

Recorded steps [a]	50	100
Increment (record every x step [b]	2	2
Visited (sampled) genealogies [a*b]	100	200
Number of discard trees per chain (burn-in)	10	10

Multiple Markov chains:
  Averaging over replicates   Over indepedent 2 replicates

Print options:
  Data file: infile.msat
  Output file: outfile-ml
  Print data: No
  Print genealogies [only some for some data type]:   None
  Plot log(likelihood) surface: No
  Profile likelihood: Yes, tables and summary
                                              Percentile method
                                with df=1 and for Theta and M=m/mu

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

Maximum Likelihood estimates

Population [x]	Loc.	Ln(L/L0)	Theta [x Ne mu]	M (m/mu) [+=receiving population 1,+	2,+
1:population	1 1	0.508	4.7274	-	4.022
	1 2	1.698	3.0627	-	2.994
	1 A	3.396	3.0628	-	2.994
	2 1	1.160	2.1466	-	3.407
	2 2	2.883	1.8410	-	1.463
	2 A	5.767	1.8410	-	1.463
	3 1	0.176	3.8444	-	3.239
	3 2	0.261	2.9358	-	4.747
	3 A	0.351	3.8443	-	3.239
	4 1	0.583	2.8384	-	5.290
	4 2	0.335	4.6629	-	2.866
	4 A	1.166	2.8384	-	5.290
	5 1	1.984	1.3496	-	1.557
	5 2	0.802	2.3313	-	4.190
	5 A	3.968	1.3496	-	1.557
	6 1	0.870	3.0187	-	3.047
	6 2	0.471	2.5655	-	5.142
	6 A	1.740	3.0187	-	3.047
	7 1	0.721	1.8829	-	2.276
	7 2	1.053	2.0707	-	5.528
	7 A	1.443	1.8829	-	2.276
	8 1	0.270	2.5908	-	1.361
	8 2	0.792	1.8598	-	1.634
	8 A	1.584	1.8599	-	1.634
	9 1	0.650	2.3084	-	3.824
	9 2	0.556	3.3751	-	3.573
	9 A	1.111	3.3751	-	3.573
	10 1	1.340	3.8366	-	2.134
	10 2	0.561	4.2834	-	3.880
	10 A	1.122	4.2833	-	3.880
	All	-54.428	2.6992	-	3.615
2:population	1 1	0.508	2.6693	5.053	-
	1 2	1.698	4.8153	4.473	-
	1 A	3.396	4.8157	4.473	-
	2 1	1.160	3.5742	8.053	-
	2 2	2.883	1.4351	5.034	-
	2 A	5.767	1.4351	5.034	-
	3 1	0.176	1.4869	4.642	-
	3 2	0.261	2.1489	7.034	-
	3 A	0.351	1.4869	4.642	-

4 1	0.583	5.7859	4.111	-
4 2	0.335	4.1331	3.315	-
4 A	1.166	5.7859	4.111	-
5 1	1.984	2.9201	18.101	-
5 2	0.802	1.5859	9.772	-
5 A	3.968	2.9201	18.101	-
6 1	0.870	1.9341	5.991	-
6 2	0.471	2.1781	4.469	-
6 A	1.740	1.9341	5.991	-
7 1	0.721	2.0223	6.204	-
7 2	1.053	1.5967	1.278	-
7 A	1.443	2.0223	6.204	-
8 1	0.270	1.4046	9.699	-
8 2	0.792	1.8612	6.367	-
8 A	1.584	1.8611	6.368	-
9 1	0.650	2.6599	3.336	-
9 2	0.556	2.9356	6.761	-
9 A	1.111	2.9356	6.761	-
10 1	1.340	4.8551	5.836	-
10 2	0.561	2.7229	5.898	-
10 A	1.122	2.7229	5.898	-
All	-54.428	2.8834	6.080	-

Comments:

The x is 1, 2, or 4 for mtDNA, haploid, or diploid data, respectively

There were 10 short chains (50 used trees out of sampled 100)

and 3 long chains (100 used trees out of sampled 200)

 COMBINATION OF 2 MULTIPLE RUNS

Profile likelihood tables

Profile likelihood table for parameter Q_1

Parameters are evaluated at percentiles using bisection method (slow, but exact).

Per.	Ln(L)	Q_1	Q_1	Q_2	M_21	M_12
0.005	-57.746	2.41609	2.4161	2.8946	3.640	6.077
0.025	-56.349	2.48023	2.4802	2.8915	3.633	6.078
0.050	-55.780	2.51391	2.5139	2.8900	3.630	6.078
0.250	-54.656	2.62103	2.6210	2.8859	3.621	6.080
MLE	-54.428*	2.69921	2.6992	2.8834	3.615	6.080
0.750	-54.656	2.7803	2.7803	2.8810	3.610	6.081
0.950	-55.781	2.90274	2.9027	2.8766	3.606	6.082
0.975	-56.349	2.94412	2.9441	2.8745	3.605	6.082
0.995	-57.745	3.02768	3.0277	2.8682	3.607	6.083

Profile likelihood table for parameter Q_2

Parameters are evaluated at percentiles using bisection method (slow, but exact).

Per.	Ln(L)	Q_2	Q_1	Q_2	M_21	M_12
0.005	-57.745	2.49607	2.7078	2.4961	3.616	6.066
0.025	-56.348	2.58213	2.7049	2.5821	3.614	6.070
0.050	-55.781	2.62759	2.7038	2.6276	3.614	6.071
0.250	-54.656	2.7745	2.7009	2.7745	3.614	6.076
MLE	-54.428*	2.88343	2.6992	2.8834	3.615	6.080
0.750	-54.656	2.99832	2.6974	2.9983	3.616	6.084
0.950	-55.780	3.17463	2.6947	3.1746	3.617	6.090
0.975	-56.348	3.23507	2.6937	3.2351	3.616	6.092
0.995	-57.746	3.35816	2.6916	3.3582	3.613	6.095

Profile likelihood table for parameter M_21

Parameters are evaluated at percentiles using bisection method (slow, but exact).

Per.	Ln(L)	M_21	Q_1	Q_2	M_21	M_12
0.005	-57.745	3.18661	2.7062	2.9142	3.187	6.094
0.025	-56.348	3.29042	2.7074	2.8942	3.290	6.095
0.050	-55.781	3.3426	2.7068	2.8890	3.343	6.093
0.250	-54.656	3.50288	2.7028	2.8832	3.503	6.085
MLE	-54.428*	3.61524	2.6992	2.8834	3.615	6.080
0.750	-54.656	3.72923	2.6955	2.8849	3.729	6.078
0.950	-55.781	3.89583	2.6901	2.8879	3.896	6.076
0.975	-56.349	3.9509	2.6883	2.8889	3.951	6.075

Per.	Ln(L)	M_21	Q_1	Q_2	M_21	M_12
0.995	-57.746	4.06004	2.6847	2.8905	4.060	6.072

Profile likelihood table for parameter M_12
Parameters are evaluated at percentiles using bisection method (slow, but exact).

Per.	Ln(L)	M_12	Q_1	Q_2	M_21	M_12
0.005	-57.746	5.45816	2.6934	2.8712	3.621	5.458
0.025	-56.350	5.6049	2.6971	2.8748	3.619	5.605
0.050	-55.781	5.68011	2.6979	2.8764	3.618	5.680
0.250	-54.655	5.91462	2.6989	2.8807	3.617	5.915
MLE	-54.428*	6.08034	2.6992	2.8834	3.615	6.080
0.750	-54.656	6.24952	2.6996	2.8860	3.612	6.250
0.950	-55.780	6.49881	2.7005	2.8891	3.605	6.499
0.975	-56.348	6.58152	2.7009	2.8901	3.602	6.582
0.995	-57.746	6.74599	2.7017	2.8916	3.594	6.746

Summary of profile likelihood percentiles of all parameters

Parameter	Percentiles								
	0.005	0.025	0.05	0.25	MLE	0.75	0.95	0.975	0.995
Theta_1	2.4161	2.4802	2.5139	2.6210	2.6992	2.7803	2.9027	2.9441	3.0277
Theta_2	2.4961	2.5821	2.6276	2.7745	2.8834	2.9983	3.1746	3.2351	3.3582
M_21	3.1866	3.2904	3.3426	3.5029	3.6152	3.7292	3.8958	3.9509	4.0600
M_12	5.4582	5.6049	5.6801	5.9146	6.0803	6.2495	6.4988	6.5815	6.7460