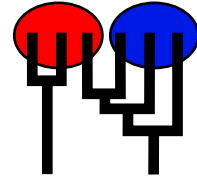# *Example: Microsatellite data set*

MIGRATION RATE AND POPULATION SIZE ESTIMATION
using the coalescent and maximum likelihood or Bayesian inference
Migrate-n version debug 3.1.2 [x]
Program started at   Sun Feb 7 16:01:43 2010
Program finished at   Sun Feb 7 16:10:40 2010

Options

Datatype: Microsatellite data [Brownian motion]
Missing data: not included
Random number seed: (from parmfile)   1407071073
Start parameters:

Theta values were generated   from the FST-calculation

M values were generated   from guessed values
   M-matrix:
     -            1.0,
   1.0,   -

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 is		Maximum likelihood

Markov chain settings:	Short chain	Long chain
Number of chains	10	3
Recorded steps [a]	500	1000
Increment (record every x step [b]	2	2
Visited (sampled) genealogies [a*b]	1000	2000
Number of discard trees per chain (burn-in)	1000	1000

Multiple Markov chains:

Averaging over replicates	Over indepedent 2 replicates
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-ml
Summary of genealogies for further run:	sumfile
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

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

Maximum Likelihood estimates

Population [x]	Loc.	Ln(L/L0)	Theta [x Ne mu]	M (m/mu) [+=receiving population 1,+	2,+
1:population	1 1	42.012	59.84	-	0.010
	1 2	280.611	9.13e+03	-	3.29e-04
	1 A	84.024	59.84	-	0.010
	2 1	171.533	2.97e+04	-	1.23e-04
	2 2	29.732	10.16	-	0.295
	2 A	194.834	3.51e+03	-	4.37e-04
	3 1	10.655	92.23	-	0.019
	3 2	13.014	50.97	-	0.060
	3 A	19.682	42.10	-	0.021
	4 1	29.031	6.48e+02	-	0.002
	4 2	20.250	1.64e+03	-	0.001
	4 A	32.753	6.68e+02	-	3.75e-04
	5 1	13.409	66.27	-	0.018
	5 2	4.049	17.61	-	0.149
	5 A	35.343	35.85	-	0.039
	6 1	245.879	1.15e+02	-	0.029
	6 2	76.918	50.84	-	0.015
	6 A	204.578	13.31	-	0.155
	7 1	6.425	4.3000	-	0.058
	7 2	148.446	4.8777	-	0.409
	7 A	127.738	4.8767	-	0.409
	8 1	10.229	90.57	-	0.024
	8 2	11.678	12.68	-	0.012
	8 A	92.329	32.11	-	0.024
	9 1	62.311	2.40e+02	-	0.009
	9 2	2.944	20.76	-	0.118
	9 A	68.154	55.03	-	0.020
	10 1	151.670	4.49e+02	-	0.005
	10 2	11.105	1.06e+02	-	0.014
	10 A	37.695	90.35	-	0.019
	All	-63.283	1.40e+02	-	0.009
2:population	1 1	42.012	4.57e+02	0.001	-
	1 2	280.611	4.16e+04	1.22e-04	-
	1 A	84.024	4.57e+02	0.001	-
	2 1	171.533	9.35e+03	4.76e-04	-
	2 2	29.732	23.52	0.098	-
	2 A	194.834	2.26e+04	1.02e-04	-

3 1	10.655	77.47	0.015	-
3 2	13.014	27.15	0.113	-
3 A	19.682	25.42	0.086	-
4 1	29.031	1.38e+03	0.001	-
4 2	20.250	1.05e+03	0.003	-
4 A	32.753	3.54e+02	0.002	-
5 1	13.409	29.16	0.032	-
5 2	4.049	9.2883	0.184	-
5 A	35.343	25.53	0.044	-
6 1	245.879	47.38	0.056	-
6 2	76.918	4.68e+02	0.003	-
6 A	204.578	41.78	0.077	-
7 1	6.425	41.27	0.150	-
7 2	148.446	1.66e+02	0.067	-
7 A	127.738	1.66e+02	0.067	-
8 1	10.229	32.65	0.060	-
8 2	11.678	15.84	0.366	-
8 A	92.329	1.74e+02	0.010	-
9 1	62.311	80.62	0.035	-
9 2	2.944	16.85	0.018	-
9 A	68.154	1.01e+02	0.044	-
10 1	151.670	4.34e+02	0.008	-
10 2	11.105	2.52e+02	0.011	-
10 A	37.695	4.39e+02	0.011	-
All	-63.283	1.92e+02	0.009	-

Comments:

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

There were 10 short chains (500 used trees out of sampled 1000)

and 3 long chains (1000 used trees out of sampled 2000)

 COMBINATION OF 2 MULTIPLE RUNS   Static heating with 4 chains was active

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	-66.599	94.1966	94.20	2.90e+02	0.014	0.009
0.025	-65.203	95.5715	95.57	2.90e+02	0.014	0.009
0.050	-64.636	96.172	96.17	2.90e+02	0.014	0.009
0.250	-63.510	97.4554	97.46	2.89e+02	0.014	0.009
MLE	-63.283*	139.888	1.40e+02	1.92e+02	0.009	0.009
0.750	-63.509	251.488	2.51e+02	1.61e+02	0.006	0.014
0.950	-64.635	255.016	2.55e+02	1.62e+02	0.006	0.014
0.975	-65.204	256.756	2.57e+02	1.62e+02	0.006	0.014
0.995	-66.600	261.022	2.61e+02	1.64e+02	0.006	0.014

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	-66.601	102.446	2.13e+02	1.02e+02	0.007	0.018
0.025	-65.203	104.841	2.13e+02	1.05e+02	0.007	0.018
0.050	-64.636	105.974	2.13e+02	1.06e+02	0.007	0.018
0.250	-63.510	108.66	2.14e+02	1.09e+02	0.007	0.018
MLE	-63.283*	191.951	1.40e+02	1.92e+02	0.009	0.009
0.750	-63.510	347.855	1.13e+02	3.48e+02	0.014	0.009
0.950	-64.635	353.894	1.13e+02	3.54e+02	0.014	0.009
0.975	-65.204	356.812	1.13e+02	3.57e+02	0.014	0.009
0.995	-66.601	363.666	1.13e+02	3.64e+02	0.014	0.009

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	-66.601	0.0059751	1.40e+02	2.02e+02	0.006	0.008
0.025	-65.204	0.00652202	1.40e+02	1.99e+02	0.007	0.008
0.050	-64.636	0.00684357	1.40e+02	1.97e+02	0.007	0.009
0.250	-63.510	0.00793046	1.40e+02	1.92e+02	0.008	0.009
MLE	-63.283*	0.00867412	1.40e+02	1.92e+02	0.009	0.009

Per.	Ln(L)	M_21	Q_1	Q_2	M_21	M_12
0.750	-63.511	0.0207628	1.16e+02	2.58e+02	0.021	0.010
0.950	-64.636	0.0212183	1.16e+02	2.57e+02	0.021	0.010
0.975	-65.204	0.021438	1.16e+02	2.57e+02	0.021	0.010
0.995	-66.601	0.0219543	1.16e+02	2.56e+02	0.022	0.010

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	-66.600	0.00677852	1.40e+02	1.99e+02	0.007	0.007
0.025	-65.203	0.00733467	1.40e+02	1.96e+02	0.008	0.007
0.050	-64.636	0.00764734	1.40e+02	1.95e+02	0.008	0.008
0.250	-63.510	0.00864366	1.40e+02	1.92e+02	0.008	0.009
MLE	-63.283*	0.00929288	1.40e+02	1.92e+02	0.009	0.009
0.750	-63.511	0.00993059	1.40e+02	1.92e+02	0.009	0.010
0.950	-64.635	0.0108626	1.40e+02	1.92e+02	0.009	0.011
0.975	-65.203	0.0111751	1.40e+02	1.92e+02	0.009	0.011
0.995	-66.600	0.0132812	1.16e+02	2.54e+02	0.016	0.013

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	94.1966	95.5715	96.1720	97.4554	139.89	251.49	255.02	256.76	261.02
Theta_2	102.45	104.84	105.97	108.66	191.95	347.85	353.89	356.81	363.67
M_21	0.0060	0.0065	0.0068	0.0079	0.0087	0.0208	0.0212	0.0214	0.0220
M_12	0.0068	0.0073	0.0076	0.0086	0.0093	0.0099	0.0109	0.0112	0.0133