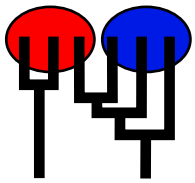
Example: Microsatellite data set

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 SYMMETRIC MULTIPROCESSORS
Program started at Mon Mar 21 14:43:16 2011
Program finished at Mon Mar 21 15:00:14 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) ineritance scalar of the first locus as a reference]
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_numb	*	*
2 population_numb	*	*

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	2
Recorded steps [a]	100	1000
Increment (record every x step [b]	100	100
Visited (sampled) genealogies [a*b]	10000	100000
Number of discard trees per chain (burn-in)	10000	10000

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)	Θ [x Ne mu]	M (m/mu) [+=receiving population 1,+	2,+
1:population	1 1	4.187	1.2355	-	5.423
	1 2	10.352	2.0232	-	4.316
	1 A	20.704	2.0232	-	4.316
	2 1	6.590	1.1976	-	5.403
	2 2	6.301	1.4497	-	7.749
	2 A	13.180	1.1976	-	5.403
	3 1	5.347	1.5975	-	7.579
	3 2	4.784	0.7821	-	32.223
	3 A	11.578	1.4871	-	16.933
	4 1	3.661	3.6127	-	2.422
	4 2	16.309	5.3894	-	2.169
	4 A	16.089	3.0706	-	1.256
	5 1	11.676	0.8307	-	1.812
	5 2	8.233	1.3750	-	9.833
	5 A	23.352	0.8307	-	1.812
	6 1	6.333	1.0407	-	3.980
	6 2	3.767	1.4263	-	4.321
	6 A	7.533	1.4261	-	4.321
	7 1	2.069	1.2106	-	2.799
	7 2	3.084	1.1658	-	2.592
	7 A	5.728	0.6557	-	4.237
	8 1	8.390	1.1852	-	6.794
	8 2	4.603	1.1305	-	6.999
	8 A	13.305	1.2443	-	3.478
	9 1	2.723	1.4310	-	3.786
	9 2	12.457	0.8464	-	8.796
	9 A	24.914	0.8464	-	8.796
	10 1	7.028	1.8761	-	5.907
	10 2	12.135	1.2516	-	3.702
	10 A	18.697	1.3630	-	2.625
	All	103.897	1.1683	-	4.868
2:population	1 1	4.187	2.5071	2.866	-
	1 2	10.352	6.7232	3.444	-
	1 A	20.704	6.7232	3.444	-
	2 1	6.590	1.5002	0.560	-
	2 2	6.301	1.1507	9.299	-
	2 A	13.180	1.5002	0.560	-

3 1	5.347	1.1286	5.136	-
3 2	4.784	1.1561	5.408	-
3 A	11.578	1.4540	10.643	-
4 1	3.661	3.0998	4.415	-
4 2	16.309	2.6532	4.658	-
4 A	16.089	2.3382	6.794	-
5 1	11.676	1.0803	23.111	-
5 2	8.233	0.6357	10.784	-
5 A	23.352	1.0803	23.111	-
6 1	6.333	0.9658	4.620	-
6 2	3.767	1.0095	3.066	-
6 A	7.533	1.0095	3.067	-
7 1	2.069	1.3568	4.147	-
7 2	3.084	0.7502	3.023	-
7 A	5.728	0.8653	3.209	-
8 1	8.390	0.9284	6.239	-
8 2	4.603	1.7235	6.351	-
8 A	13.305	1.2253	6.305	-
9 1	2.723	1.4896	4.568	-
9 2	12.457	1.4293	11.373	-
9 A	24.914	1.4294	11.373	-
10 1	7.028	1.6413	7.930	-
10 2	12.135	0.7908	4.771	-
10 A	18.697	0.9648	4.849	-
All	103.897	1.3345	6.466	-

Comments:

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

There were 10 short chains (100 used trees out of sampled 10000)

and 2 long chains (1000 used trees out of sampled 100000)

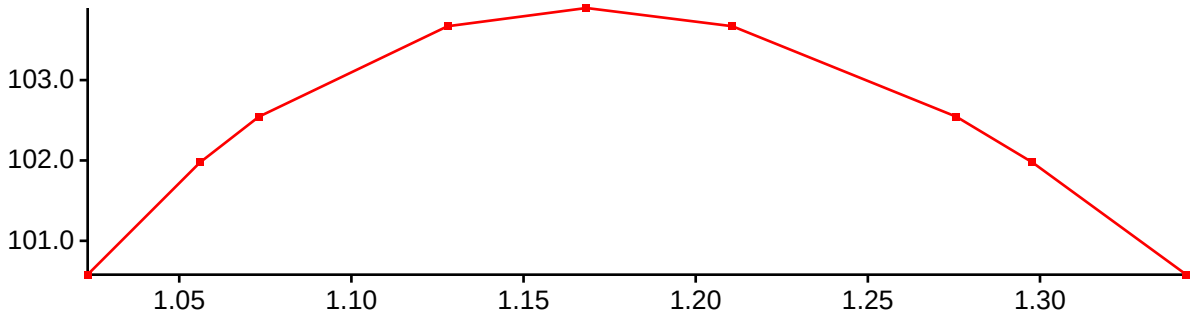
COMBINATION OF 2 MULTIPLE RUNS Static heating with 4 chains was active

Profile likelihood tables and plots

Profile likelihood table and plot for parameter Θ_1

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

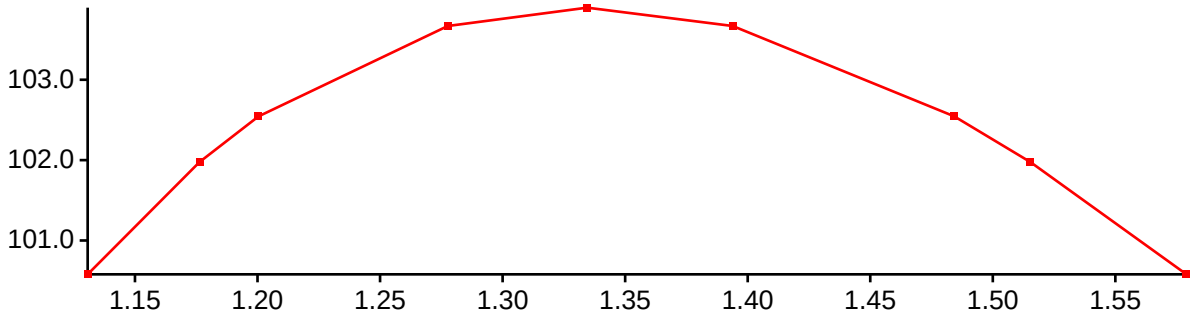
Per.	Ln(L)	Θ_1	Θ_1	Θ_2	$M_{2->1}$	$M_{1->2}$
0.005	100.580	1.0234	1.0234	1.3431	4.973	6.370
0.025	101.975	1.05601	1.0560	1.3441	4.950	6.395
0.050	102.544	1.07311	1.0731	1.3436	4.938	6.407
0.250	103.670	1.12793	1.1279	1.3392	4.898	6.442
MLE	103.897*	1.16826	1.1683	1.3345	4.868	6.466
0.750	103.670	1.21066	1.2107	1.3296	4.839	6.484
0.950	102.544	1.27572	1.2757	1.3244	4.804	6.495
0.975	101.976	1.29779	1.2978	1.3233	4.795	6.494
0.995	100.579	1.3425	1.3425	1.3222	4.779	6.486



Profile likelihood table and plot for parameter Θ_2

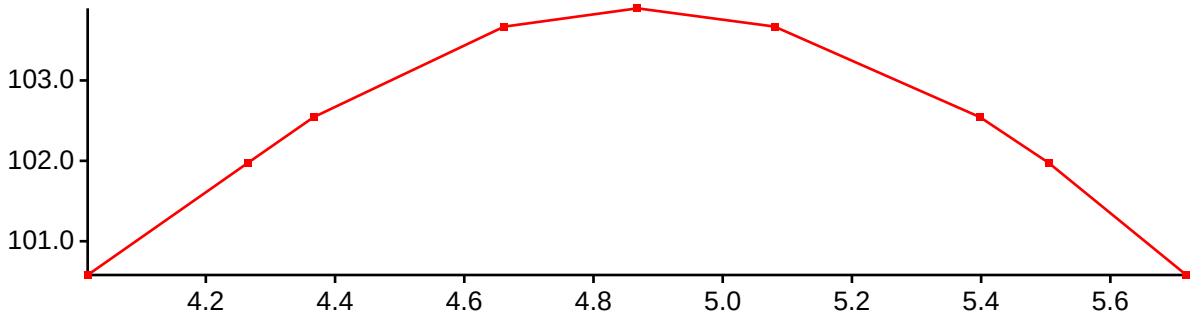
Parameters are evaluated at percentiles using bisection method (slow, but exact).

Per.	Ln(L)	Θ_2	Θ_1	Θ_2	$M_{2->1}$	$M_{1->2}$
0.005	100.579	1.1307	1.1756	1.1307	4.764	6.491
0.025	101.977	1.17637	1.1766	1.1764	4.783	6.501
0.050	102.544	1.20038	1.1762	1.2004	4.794	6.503
0.250	103.669	1.27765	1.1720	1.2777	4.835	6.490
MLE	103.897*	1.33449	1.1683	1.3345	4.868	6.466
0.750	103.669	1.39387	1.1652	1.3939	4.901	6.431
0.950	102.545	1.48425	1.1634	1.4842	4.947	6.368
0.975	101.976	1.51533	1.1635	1.5153	4.962	6.344
0.995	100.580	1.57896	1.1649	1.5790	4.991	6.289



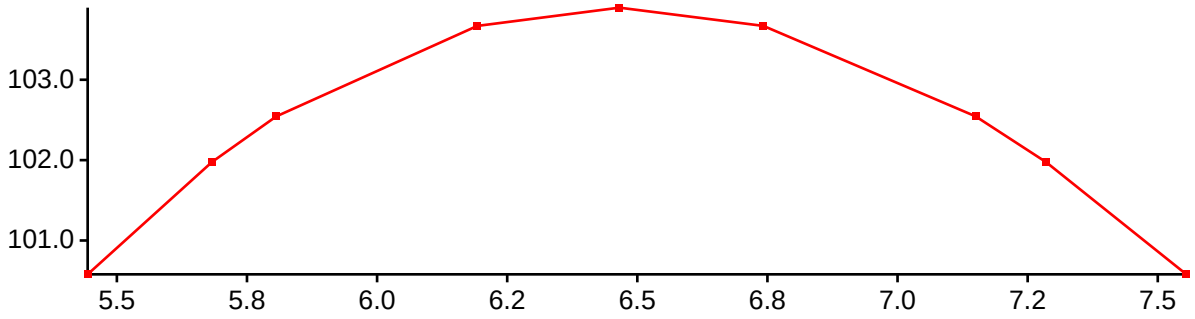
Profile likelihood table and plot for parameter $M_{2->1}$
Parameters are evaluated at percentiles using bisection method (slow, but exact).

Per.	Ln(L)	$M_{2->1}$	Θ_1	Θ_2	$M_{2->1}$	$M_{1->2}$
0.005	100.580	4.01709	1.2199	1.3054	4.017	6.475
0.025	101.975	4.26514	1.1912	1.3131	4.265	6.529
0.050	102.544	4.367	1.1845	1.3159	4.367	6.533
0.250	103.669	4.66156	1.1741	1.3258	4.662	6.504
MLE	103.897*	4.86804	1.1683	1.3345	4.868	6.466
0.750	103.670	5.08027	1.1623	1.3442	5.080	6.419
0.950	102.544	5.3981	1.1545	1.3585	5.398	6.348
0.975	101.976	5.50436	1.1524	1.3630	5.504	6.324
0.995	100.580	5.71758	1.1488	1.3718	5.718	6.276



Profile likelihood table and plot for parameter $M_{1->2}$
Parameters are evaluated at percentiles using bisection method (slow, but exact).

Per.	Ln(L)	$M_{1->2}$	Θ_1	Θ_2	$M_{2->1}$	$M_{1->2}$
0.005	100.579	5.44388	1.1709	1.3657	4.972	5.444
0.025	101.977	5.68284	1.1672	1.3579	4.954	5.683
0.050	102.544	5.80629	1.1660	1.3538	4.942	5.806
0.250	103.670	6.19259	1.1658	1.3417	4.900	6.193
MLE	103.897*	6.46557	1.1683	1.3345	4.868	6.466
0.750	103.670	6.74226	1.1720	1.3290	4.836	6.742
0.950	102.545	7.14994	1.1789	1.3241	4.790	7.150
0.975	101.976	7.28521	1.1816	1.3230	4.776	7.285
0.995	100.579	7.55488	1.1878	1.3213	4.746	7.555


103.0
102.0
101.0
5.5
5.8
6.0
6.2
6.5
6.8
7.0
7.2
7.5

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
Θ_1	1.0234	1.0560	1.0731	1.1279	1.1683	1.2107	1.2757	1.2978	1.3425
Θ_2	1.1307	1.1764	1.2004	1.2777	1.3345	1.3939	1.4842	1.5153	1.5790
M_21	4.0171	4.2651	4.3670	4.6616	4.8680	5.0803	5.3981	5.5044	5.7176
M_12	5.4439	5.6828	5.8063	6.1926	6.4656	6.7423	7.1499	7.2852	7.5549