

# Example: Microsatellite data set

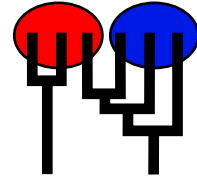
## MIGRATION RATE AND POPULATION SIZE ESTIMATION

using the coalescent and maximum likelihood or Bayesian inference

Migrate-n version 3.0.1

Program started at Wed Oct 22 19:11:17 2008

Program finished at Wed Oct 22 19:12:41 2008



## Options

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

Theta values were generated	from guessed values
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Theta = 1.00000 1.00000

M values were generated	from guessed values
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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	$\Theta_1$	<displayed>
2	$\Theta_2$	<displayed>
3	$M_{2 \rightarrow 1}$	<displayed>
4	$M_{1 \rightarrow 2}$	<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 independent 2 replicates

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
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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	1.352	3.5132	-	2.795
	1 2	3.446	9.3003	-	0.289
	1 A	6.891	9.3003	-	0.289
	2 1	2.159	2.6700	-	1.829
	2 2	0.876	2.9220	-	4.978
	2 A	4.318	2.6700	-	1.829
	3 1	1.200	2.9113	-	5.086
	3 2	0.694	3.4919	-	0.849
	3 A	2.401	2.9113	-	5.086
	4 1	3.277	4.3347	-	2.124
	4 2	0.575	10.88	-	3.757
	4 A	6.554	4.3347	-	2.124
	5 1	0.145	1.1190	-	2.198
	5 2	1.681	1.6876	-	0.338
	5 A	0.290	1.1190	-	2.198
	6 1	3.087	5.4084	-	3.513
	6 2	0.620	4.0594	-	1.597
	6 A	6.174	5.4085	-	3.513
	7 1	0.453	1.2932	-	1.533
	7 2	2.029	3.1201	-	4.36e-09
	7 A	2.568	0.8636	-	1.377
	8 1	2.413	2.5270	-	3.900
	8 2	3.188	2.2475	-	2.644
	8 A	3.838	1.9258	-	2.686
	9 1	2.908	1.8906	-	2.528
	9 2	1.831	5.4039	-	5.276
	9 A	5.816	1.8906	-	2.528
	10 1	2.697	4.5536	-	7.073
	10 2	1.926	3.9960	-	2.360
	10 A	3.851	3.9960	-	2.360
	All	-99.712	3.0817	-	1.953
2:population	1 1	1.352	10.56	2.386	-
	1 2	3.446	5.2835	1.005	-
	1 A	6.891	5.2835	1.005	-
	2 1	2.159	1.4367	1.882	-
	2 2	0.876	5.2719	1.475	-
	2 A	4.318	1.4367	1.882	-

3 1	1.200	2.3245	9.82e-13	-
3 2	0.694	4.4164	4.055	-
3 A	2.401	2.3245	8.16e-12	-
4 1	3.277	5.1162	3.093	-
4 2	0.575	7.0077	3.602	-
4 A	6.554	5.1162	3.093	-
5 1	0.145	1.3979	1.30e-07	-
5 2	1.681	2.2679	12.841	-
5 A	0.290	1.3979	2.13e-12	-
6 1	3.087	1.7392	4.466	-
6 2	0.620	1.3724	2.767	-
6 A	6.174	1.7392	4.466	-
7 1	0.453	2.5539	0.799	-
7 2	2.029	3.0662	3.795	-
7 A	2.568	1.6654	0.482	-
8 1	2.413	5.6085	2.376	-
8 2	3.188	4.5775	2.071	-
8 A	3.838	4.0194	1.927	-
9 1	2.908	3.6574	2.654	-
9 2	1.831	2.1812	5.259	-
9 A	5.816	3.6574	2.654	-
10 1	2.697	4.0183	5.901	-
10 2	1.926	3.0787	4.445	-
10 A	3.851	3.0787	4.445	-
All	-99.712	3.8770	3.240	-

## 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



## *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	-103.028	2.70882	2.7088	3.8998	1.913	3.200
0.025	-101.632	2.79294	2.7929	3.8959	1.918	3.213
0.050	-101.065	2.83722	2.8372	3.8932	1.922	3.219
0.250	-99.939	2.97905	2.9790	3.8836	1.939	3.233
MLE	-99.712*	3.08172	3.0817	3.8770	1.953	3.240
0.750	-99.939	3.18754	3.1875	3.8705	1.966	3.244
0.950	-101.064	3.34474	3.3447	3.8615	1.980	3.244
0.975	-101.632	3.39729	3.3973	3.8585	1.984	3.242
0.995	-103.029	3.5022	3.5022	3.8525	1.990	3.239

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	-103.029	3.33615	3.0934	3.3362	1.954	3.201
0.025	-101.633	3.4571	3.0924	3.4571	1.954	3.214
0.050	-101.064	3.52086	3.0912	3.5209	1.954	3.220
0.250	-99.939	3.72569	3.0860	3.7257	1.954	3.233
MLE	-99.712*	3.87697	3.0817	3.8770	1.953	3.240
0.750	-99.940	4.03683	3.0773	4.0368	1.952	3.247
0.950	-101.065	4.28216	3.0712	4.2822	1.951	3.255
0.975	-101.633	4.36626	3.0693	4.3663	1.950	3.258
0.995	-103.030	4.53752	3.0660	4.5375	1.949	3.263

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	-103.029	1.63063	3.0351	3.8938	1.631	3.198
0.025	-101.632	1.70262	3.0407	3.8874	1.703	3.207
0.050	-101.064	1.74067	3.0447	3.8846	1.741	3.212
0.250	-99.939	1.86397	3.0643	3.8787	1.864	3.229
MLE	-99.712*	1.95323	3.0817	3.8770	1.953	3.240

Per.	Ln(L)	M_21	Q_1	Q_2	M_21	M_12
0.750	-99.939	2.0421	3.0946	3.8761	2.042	3.246
0.950	-101.064	2.16888	3.1020	3.8749	2.169	3.242
0.975	-101.632	2.21016	3.1022	3.8744	2.210	3.238
0.995	-103.029	2.29162	3.0997	3.8732	2.292	3.227

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	-103.030	2.79444	3.0292	3.8297	1.921	2.794
0.025	-101.633	2.90218	3.0501	3.8447	1.926	2.902
0.050	-101.065	2.95665	3.0581	3.8510	1.931	2.957
0.250	-99.940	3.12335	3.0752	3.8672	1.945	3.123
MLE	-99.712*	3.2402	3.0817	3.8770	1.953	3.240
0.750	-99.939	3.35823	3.0849	3.8857	1.959	3.358
0.950	-101.064	3.53144	3.0852	3.8968	1.965	3.531
0.975	-101.632	3.5888	3.0845	3.8999	1.966	3.589
0.995	-103.030	3.70259	3.0823	3.9054	1.968	3.703

## *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	2.7088	2.7929	2.8372	2.9790	3.0817	3.1875	3.3447	3.3973	3.5022
Theta_2	3.3362	3.4571	3.5209	3.7257	3.8770	4.0368	4.2822	4.3663	4.5375
M_21	1.6306	1.7026	1.7407	1.8640	1.9532	2.0421	2.1689	2.2102	2.2916
M_12	2.7944	2.9022	2.9566	3.1233	3.2402	3.3582	3.5314	3.5888	3.7026