

# Example: Microsatellite data set

## MIGRATION RATE AND POPULATION SIZE ESTIMATION

using the coalescent and maximum likelihood or Bayesian inference

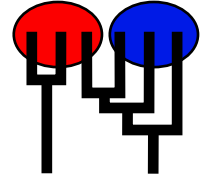
Migrate-n version debug 2.4.2

Compiled for a PARALLEL COMPUTER ARCHITECTURE

One master and 3 compute nodes are available.

Program started at Sun Feb 17 16:45:15 2008

Program finished at Sun Feb 17 16:45:22 2008



## Options

Datatype:	Microsatellite data [Brownian motion]
Missing data:	not included
Random number seed:	(with internal timer) 1881505405
Start parameters:	

Theta values were generated	from the FST-calculation
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M values were generated	from the FST-calculation
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### 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
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Analysis strategy is	Maximum likelihood
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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 independent 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	0.680	0.6953	-	8.763
	1 2	0.080	1.1079	-	10.348
	1 A	0.159	1.1079	-	10.348
	2 1	0.562	0.0426	-	145.11
	2 2	0.732	0.0321	-	260.00
	2 A	1.465	0.0321	-	260.00
	3 1	0.361	0.2622	-	25.256
	3 2	0.826	0.2459	-	63.016
	3 A	1.651	0.2459	-	63.016
	4 1	0.180	0.3960	-	27.457
	4 2	0.086	0.4376	-	32.542
	4 A	0.171	0.4376	-	32.542
	5 1	0.294	1.5217	-	8.802
	5 2	1.831	1.2464	-	2.384
	5 A	3.662	1.2464	-	2.384
	6 1	0.045	0.8237	-	71.770
	6 2	0.083	1.5935	-	56.882
	6 A	0.167	1.5935	-	56.882
	7 1	2.065	0.0040	-	570.97
	7 2	0.916	0.0093	-	687.40
	7 A	1.832	0.0093	-	687.40
	8 1	0.229	0.1917	-	32.858
	8 2	0.745	0.3689	-	33.939
	8 A	1.490	0.3689	-	33.939
	9 1	0.373	1.0292	-	26.424
	9 2	4.613	0.7745	-	16.479
	9 A	9.226	0.7745	-	16.479
	10 1	0.179	2.0499	-	7.178
	10 2	1.039	1.9756	-	2.747
	10 A	2.078	1.9756	-	2.747
	All	-1366.269	0.7019	-	21.813
2:population	1 1	0.680	3.2789	4.102	-
	1 2	0.080	2.4755	11.836	-
	1 A	0.159	2.4755	11.836	-
	2 1	0.562	0.4491	78.174	-
	2 2	0.732	0.6353	64.472	-
	2 A	1.465	0.6353	64.472	-
	3 1	0.361	0.7120	17.079	-
	3 2	0.826	0.6406	16.955	-
	3 A	1.651	0.6406	16.955	-

4 1	0.180	1.2696	25.484	-
4 2	0.086	1.8871	11.088	-
4 A	0.171	1.8871	11.088	-
5 1	0.294	0.0653	24.646	-
5 2	1.831	0.1009	25.773	-
5 A	3.662	0.1009	25.773	-
6 1	0.045	0.3476	56.538	-
6 2	0.083	0.4518	78.347	-
6 A	0.167	0.4518	78.347	-
7 1	2.065	0.1601	250.72	-
7 2	0.916	0.1456	173.43	-
7 A	1.832	0.1456	173.43	-
8 1	0.229	0.8735	44.348	-
8 2	0.745	1.4408	23.964	-
8 A	1.490	1.4408	23.964	-
9 1	0.373	4.3676	19.224	-
9 2	4.613	1.7988	12.967	-
9 A	9.226	1.7988	12.967	-
10 1	0.179	0.1729	83.554	-
10 2	1.039	0.0753	279.82	-
10 A	2.078	0.0753	279.82	-
All	-1366.269	0.8059	26.929	-

## 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