

# Example: Microsatellite data set

## MIGRATION RATE AND POPULATION SIZE ESTIMATION

using the coalescent and maximum likelihood or Bayesian inference

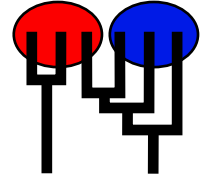
Migrate-n version debug 3.0

Compiled for a PARALLEL COMPUTER ARCHITECTURE

One master and 2 compute nodes are available.

Program started at Wed Oct 15 19:29:22 2008

Program finished at Wed Oct 15 21:01:18 2008



## Options

Datatype:	Microsatellite data [Brownian motion]
Missing data:	not included
Random number seed:	(with internal timer) 1080541521
Start parameters:	

Theta values were generated	from guessed values
Theta = 10.00000 10.00000	

M values were generated	from guessed values
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M-matrix:

-	10.0,
10.0,	-

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	5000
Increment (record every x step [b])	200	200
Visited (sampled) genealogies [a*b]	100000	1000000
Number of discard trees per chain (burn-in)	10000	10000
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: 2

Population	Locus	Gene copies data	(missing)
1 population__number__0	1	50	(0)
	2	50	(0)
2 population__number__1	1	42	(0)
	2	42	(0)
Total of all populations	1	92	(0)
	2	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

## *Maximum Likelihood estimates*

Population [x]	Loc.	Ln(L/L0)	Theta [x Ne mu]	M (m/mu) [+receiving population]	
				1,+	2,+
1:population	1 1	1.870	3.2302	-	11.901
	1 2	0.446	4.8131	-	6.417
	1 A	0.893	4.8131	-	6.417
	2 1	1.217	1.7681	-	14.124
	2 2	0.417	3.40e+08	-	14.572
	2 A	0.833	3.40e+08	-	14.572
	All	3.846	4.3907	-	11.718
2:population	1 1	1.870	37.69	5.376	-
	1 2	0.446	46.86	5.427	-
	1 A	0.893	46.86	5.427	-
	2 1	1.217	15.94	14.731	-
	2 2	0.417	2.2955	5.428	-
	2 A	0.833	2.2955	5.428	-
	All	3.846	68.07	6.336	-

### 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 100000)

and 3 long chains (5000 used trees out of sampled 1000000)

### COMBINATION OF 2 MULTIPLE RUNS

[Last maximization needed 299 cycles of maximal 1000,

Norm(first derivatives)=98.234993 (Normal stopping criteria is < 0.000010)]

## *Profile likelihood tables*

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
****	-21.124	34.0354	2.1190	34.04	11.680	8.238
****	-26.734	51.0531	2.1314	51.05	11.604	8.306
****	-29.353	59.562	2.1480	59.56	11.589	8.369
****	-29.938	63.8164	2.1614	63.82	11.096	7.500
MLE	3.846*	68.0708	4.3907	68.07	11.718	6.336
****	-111.069	42608.1	2.8245	4.26e+04	10.520	8.755
****	-119.391	85148.1	2.8254	8.51e+04	10.529	8.761
****	-127.710	170228	2.8259	1.70e+05	10.533	8.764
****	-136.029	340388	2.8261	3.40e+05	10.535	8.766

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
****	-19.075	2.19536	2.1954	23.14	11.720	8.220
****	-29.637	3.29305	3.2930	22.85	12.477	8.758
****	-36.466	3.84189	3.8419	23.19	12.477	8.723
****	-39.810	4.11631	4.1163	23.39	12.547	8.649
MLE	3.846*	4.39073	4.3907	68.07	11.718	6.336
****	-749.683	2748.32	2.75e+03	15.87	11.564	7.204
****	-831.768	5492.25	5.49e+03	15.78	11.573	7.260
****	-913.781	10980.1	1.10e+04	15.67	11.583	7.321
****	-995.702	21955.8	2.20e+04	15.60	11.590	7.364

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
****	-80.309	5.85875	2.3435	28.32	5.859	7.549
****	-30.996	8.78813	2.3289	24.26	8.788	7.605
****	-22.478	10.2528	2.1255	23.24	10.253	8.179
****	-19.841	10.9852	2.1191	23.21	10.985	8.213
MLE	3.846*	11.7175	4.3907	68.07	11.718	6.336
****	-217971.500	7334.43	2.1491	24.70	7.33e+03	7.352
****	-437931.131	14657.1	2.1491	24.70	1.47e+04	7.352
****	-878098.802	29302.5	2.1491	24.70	2.93e+04	7.352

Per.	Ln(L)	M_21	Q_1	Q_2	M_21	M_12
****	-1758682.768	58593.4	2.1491	24.70	5.86e+04	7.352

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
****	-138.836	3.168	2.2006	22.99	10.590	3.168
****	-56.350	4.75199	2.1540	30.75	11.749	4.752
****	-40.108	5.54399	2.0362	22.83	11.417	5.544
****	-33.380	5.93999	1.9947	22.45	11.580	5.940
MLE	3.846*	6.33599	4.3907	68.07	11.718	6.336
****	-199457.580	3965.94	2.4754	20.78	10.739	3.97e+03
****	-401132.760	7925.54	2.4754	20.78	10.739	7.93e+03
****	-804759.900	15844.7	2.4754	20.78	10.739	1.58e+04
****	-1612291.200	31683.1	2.4754	20.78	10.739	3.17e+04

## *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	2.1954	3.2930	3.8419	4.1163	4.3907	2.75e+03	5.49e+03	1.10e+04	2.20e+04
Theta_2	34.0354	51.0531	59.5620	63.8164	68.0708	4.26e+04	8.51e+04	1.70e+05	3.40e+05
M_21	5.8588	8.7881	10.2528	10.9852	11.7175	7.33e+03	1.47e+04	2.93e+04	5.86e+04
M_12	3.1680	4.7520	5.5440	5.9400	6.3360	3.97e+03	7.93e+03	1.58e+04	3.17e+04