

# Example: Microsatellite data set

## MIGRATION RATE AND POPULATION SIZE ESTIMATION

using the coalescent and maximum likelihood or Bayesian inference

Migrate-n version debug 3.2 [x]

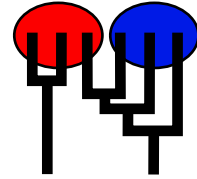
Compiled for a PARALLEL COMPUTER ARCHITECTURE

One master and 2 compute nodes are available.

Compiled for a SYMMETRIC MULTIPROCESSORS

Program started at Fri Oct 8 12:07:59 2010

Program finished at Fri Oct 8 12:09:56 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
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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->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 independent 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
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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)	$\Theta$	M (m/mu) [+receiving population]	
			[x Ne mu]	1,+	2,+
1:population	1 1	2.218	1.8365	-	2.162
	1 2	11.540	1.5217	-	1.699
	1 A	16.676	1.8569	-	1.636
	2 1	2.413	1.0918	-	9.105
	2 2	4.538	1.1812	-	5.203
	2 A	6.815	1.1952	-	5.215
	3 1	11.530	1.2702	-	6.618
	3 2	6.947	0.9388	-	7.372
	3 A	17.295	0.8329	-	5.066
	4 1	4.030	3.1543	-	4.245
	4 2	4.480	1.8320	-	5.126
	4 A	8.938	1.8322	-	5.126
	5 1	2.377	1.1634	-	2.313
	5 2	2.922	1.1520	-	3.958
	5 A	5.841	1.1520	-	3.958
	6 1	1.958	1.8253	-	2.451
	6 2	7.879	1.5483	-	4.493
	6 A	12.978	1.4236	-	4.053
	7 1	0.822	0.9585	-	6.509
	7 2	2.888	1.2192	-	4.887
	7 A	3.823	1.0311	-	4.090
	8 1	8.602	2.4731	-	1.464
	8 2	1.290	1.4362	-	2.687
	8 A	11.717	1.0372	-	1.217
	9 1	4.696	1.4497	-	8.696
	9 2	2.673	1.6409	-	3.052
	9 A	5.338	1.6409	-	3.052
	10 1	15.768	1.9239	-	5.326
	10 2	7.144	1.7962	-	3.496
	10 A	31.526	1.9239	-	5.326
	All	49.771	1.3052	-	3.229
2:population	1 1	2.218	2.4932	1.464	-
	1 2	11.540	1.5896	3.047	-
	1 A	16.676	1.4673	3.901	-
	2 1	2.413	1.9312	6.392	-
	2 2	4.538	1.1874	3.760	-
	2 A	6.815	1.2013	3.715	-

3 1	11.530	0.8836	9.655	-
3 2	6.947	1.2227	8.939	-
3 A	17.295	1.0479	8.255	-
4 1	4.030	2.7963	2.301	-
4 2	4.480	2.6494	3.289	-
4 A	8.938	2.6488	3.289	-
5 1	2.377	1.2803	11.943	-
5 2	2.922	0.7127	3.594	-
5 A	5.841	0.7127	3.594	-
6 1	1.958	0.5894	5.887	-
6 2	7.879	0.8135	3.762	-
6 A	12.978	0.6769	3.105	-
7 1	0.822	1.2549	2.848	-
7 2	2.888	0.8870	2.422	-
7 A	3.823	0.7496	4.005	-
8 1	8.602	1.4290	4.378	-
8 2	1.290	1.4657	5.507	-
8 A	11.717	1.4535	2.053	-
9 1	4.696	1.4774	9.555	-
9 2	2.673	2.1302	2.112	-
9 A	5.338	2.1302	2.112	-
10 1	15.768	2.7885	3.759	-
10 2	7.144	1.8460	3.925	-
10 A	31.526	2.7885	3.759	-
All	49.771	1.2511	3.338	-

## 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



## *Approximate Likelihood Ratio Tests*

Legend for the likelihood ratio tables

Null-Hypothesis: your test model  
is equal to  
full model (the model under which the  
genealogies were sampled)

Migration matrix, migration rates are  
specified as M]

Log(likelihood) of test model  
Log(likelihood) of full model  
Likelihood ratio test value  
Degrees of freedom of test  
[Theta values are on the diagonal of the  
Probability\*  
Probability\*\*  
Akaike's Information Criterion\*\*\*  
Number of parameters used

\*) Probability under the assumption that parameters have range -Inf to Inf

\*\*) Probability under the assumption that parameters have range 0 to Inf

\*\*\*) AIC: the smaller the value the better the model  
[the full model has AIC=-91.542301, num(param)=4]

H0: 1.2781 3.2836 3.2836 1.2781  
= 1.3052 3.2290 3.3382 1.2511  
[ m, m, m, m,]

LnL(test) = 49.583146  
LnL(full) = 49.771150  
LRT = 0.376010  
df = 4  
Prob = 0.984394  
Probc = 0.984394  
AIC = -95.166291  
num(param) = 2

## *Profile likelihood tables and plots*

Profile likelihood table and plot for parameter  $\Theta_1$

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

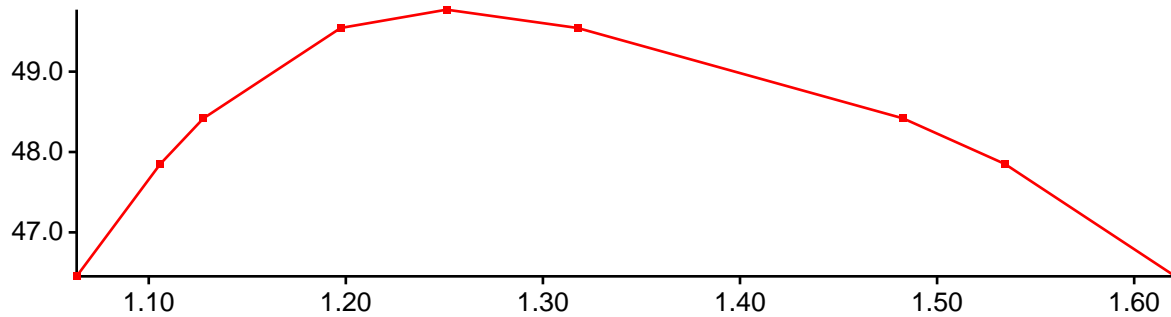
Per.	Ln(L)	$\Theta_1$	$\Theta_1$	$\Theta_2$	$M_{2 \rightarrow 1}$	$M_{1 \rightarrow 2}$
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0.005	46.454	1.14445	1.1444	1.2513	3.205	3.264
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0.025	47.851	1.18062	1.1806	1.2501	3.209	3.281
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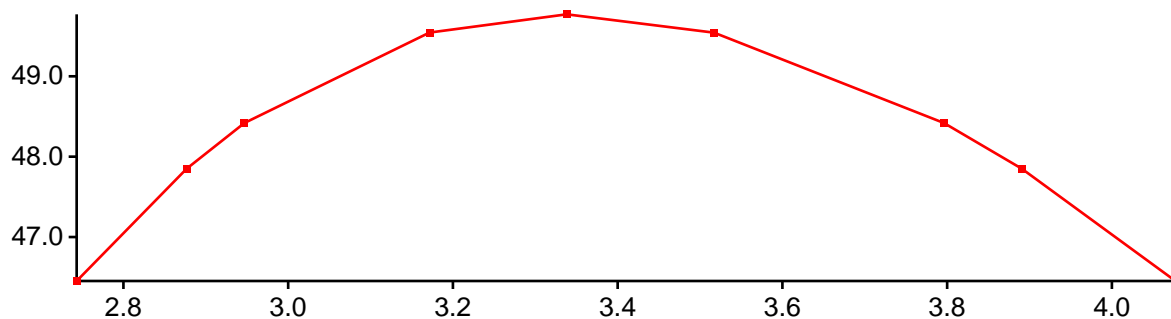
0.050	48.418	1.1996	1.1996	1.2498	3.211	3.290
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0.250	49.544					
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Profile likelihood table and plot for parameter  $M_{1 \rightarrow 2}$ 

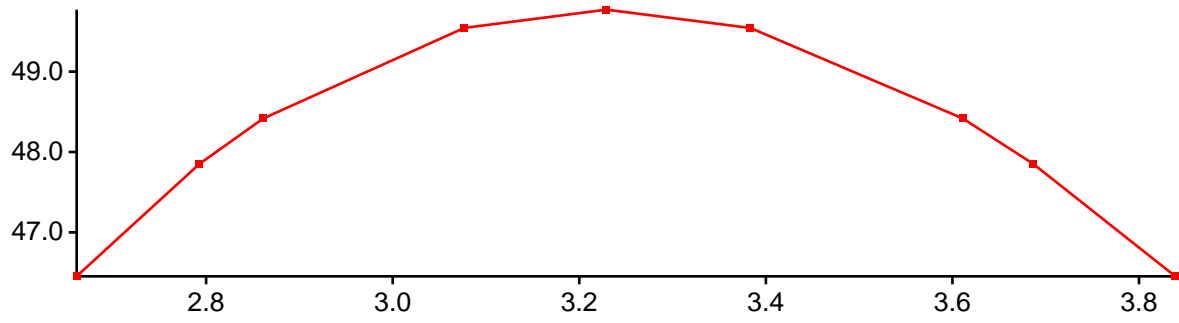
Parameters are evaluated at percentiles using bisection method (slow, but exact).

Per.	Ln(L)	$M_{1 \rightarrow 2}$	$\Theta_1$	$\Theta_2$	$M_{2 \rightarrow 1}$	$M_{1 \rightarrow 2}$
0.005	46.453	2.74323	1.2927	1.2703	3.130	2.743
0.025	47.851	2.87685	1.2947	1.2682	3.155	2.877
0.050	48.419	2.94691	1.2958	1.2665	3.167	2.947
0.250	49.544	3.17157	1.3004	1.2587	3.204	3.172
MLE	49.771*	3.33816	1.3052	1.2511	3.229	3.338
0.750	49.543	3.51704	1.3121	1.2417	3.256	3.517
0.950	48.419	3.7961	1.3239	1.2260	3.297	3.796
0.975	47.851	3.8905	1.3272	1.2214	3.309	3.890
0.995	46.454	4.07701	1.3322	1.2137	3.334	4.077

Profile likelihood table and plot for parameter  $M_{2 \rightarrow 1}$ 

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

Per.	Ln(L)	$M_{2 \rightarrow 1}$	$\Theta_1$	$\Theta_2$	$M_{2 \rightarrow 1}$	$M_{1 \rightarrow 2}$
0.005	46.454	2.66121	1.3038	1.2539	2.661	3.214
0.025	47.851	2.79276	1.3029	1.2575	2.793	3.244
0.050	48.418	2.86135	1.3027	1.2584	2.861	3.260
0.250	49.544	3.07677	1.3032	1.2557	3.077	3.308
MLE	49.771*	3.229	1.3052	1.2511	3.229	3.338
0.750	49.543	3.38343	1.3084	1.2467	3.383	3.365
0.950	48.418	3.61098	1.3153	1.2419	3.611	3.404
0.975	47.851	3.68675	1.3182	1.2407	3.687	3.417
0.995	46.453	3.83893	1.3252	1.2389	3.839	3.446



## *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	1.1444	1.1806	1.1996	1.2605	1.3052	1.3519	1.4234	1.4478	1.5009
Theta_2	1.0634	1.1059	1.1277	1.1974	1.2511	1.3176	1.4827	1.5344	1.6209
M_21	2.6612	2.7928	2.8613	3.0768	3.2290	3.3834	3.6110	3.6867	3.8389
M_12	2.7432	2.8769	2.9469	3.1716	3.3382	3.5170	3.7961	3.8905	4.0770