

Example: Microsatellite data set

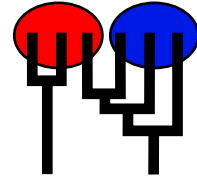
MIGRATION RATE AND POPULATION SIZE ESTIMATION

using the coalescent and maximum likelihood or Bayesian inference

Migrate-n version 3.0.6

Program started at Thu May 14 10:45:25 2009

Program finished at Thu May 14 10:46:29 2009



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	Θ_1	<displayed>
2	Θ_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
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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
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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
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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
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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	4.494	5.7182	-	1.936
	1 2	0.875	2.5130	-	3.636
	1 A	8.989	5.7182	-	1.936
	2 1	1.443	24.86	-	3.327
	2 2	0.261	2.9333	-	2.269
	2 A	2.887	24.86	-	3.327
	3 1	1.756	1.9508	-	1.720
	3 2	1.446	3.2384	-	6.389
	3 A	3.159	1.4841	-	1.787
	4 1	1.166	8.5904	-	2.997
	4 2	1.391	11.36	-	1.291
	4 A	2.782	11.36	-	1.291
	5 1	1.586	1.0024	-	0.629
	5 2	2.804	2.4379	-	11.815
	5 A	3.172	1.0024	-	0.629
	6 1	1.129	4.1326	-	1.735
	6 2	0.322	3.3196	-	0.900
	6 A	2.241	4.1359	-	1.735
	7 1	1.966	1.6283	-	4.241
	7 2	0.463	1.5485	-	3.627
	7 A	3.326	1.7858	-	3.985
	8 1	1.852	1.4162	-	2.838
	8 2	10.768	1.6147	-	3.599
	8 A	5.966	1.7952	-	3.647
	9 1	7.785	3.9014	-	5.616
	9 2	3.697	1.6102	-	3.534
	9 A	15.570	3.9014	-	5.616
	10 1	2.730	6.1811	-	2.955
	10 2	0.163	4.1572	-	1.502
	10 A	0.326	4.1572	-	1.502
	All	-130.117	2.9291	-	2.097
2:population	1 1	4.494	11.37	0.839	-
	1 2	0.875	7.0700	2.264	-
	1 A	8.989	11.37	0.839	-
	2 1	1.443	1.6906	2.016	-
	2 2	0.261	1.2997	1.906	-
	2 A	2.887	1.6906	2.016	-

3 1	1.756	3.6400	3.130	-
3 2	1.446	1.0011	5.877	-
3 A	3.159	2.3637	6.441	-
4 1	1.166	6.8412	0.543	-
4 2	1.391	7.5245	2.205	-
4 A	2.782	7.5245	2.205	-
5 1	1.586	2.3457	3.013	-
5 2	2.804	0.7219	2.88e-12	-
5 A	3.172	2.3457	3.013	-
6 1	1.129	1.9686	1.741	-
6 2	0.322	1.8756	1.865	-
6 A	2.241	1.9686	1.757	-
7 1	1.966	3.1447	0.229	-
7 2	0.463	2.9396	0.773	-
7 A	3.326	3.1944	0.197	-
8 1	1.852	6.0863	3.806	-
8 2	10.768	4.3352	5.295	-
8 A	5.966	2.3949	4.231	-
9 1	7.785	3.3018	4.762	-
9 2	3.697	7.9575	4.879	-
9 A	15.570	3.3018	4.762	-
10 1	2.730	8.1101	4.865	-
10 2	0.163	2.6775	1.914	-
10 A	0.326	2.6775	1.914	-
All	-130.117	3.8034	2.475	-

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	-133.434	2.60227	2.6023	3.7942	2.092	2.478
0.025	-132.038	2.67623	2.6762	3.7973	2.093	2.478
0.050	-131.471	2.715	2.7150	3.7986	2.094	2.477
0.250	-130.346	2.83876	2.8388	3.8019	2.096	2.476
MLE	-130.117*	2.92907	2.9291	3.8034	2.097	2.475
0.750	-130.345	3.02275	3.0227	3.8043	2.099	2.474
0.950	-131.469	3.16417	3.1642	3.8045	2.101	2.474
0.975	-132.038	3.21197	3.2120	3.8043	2.102	2.474
0.995	-133.435	3.30799	3.3080	3.8033	2.104	2.474

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	-133.435	3.28387	2.9231	3.2839	2.116	2.469
0.025	-132.039	3.40183	2.9251	3.4018	2.110	2.471
0.050	-131.470	3.4638	2.9260	3.4638	2.108	2.472
0.250	-130.344	3.6608	2.9281	3.6608	2.101	2.474
MLE	-130.117*	3.80341	2.9291	3.8034	2.097	2.475
0.750	-130.345	3.95137	2.9297	3.9514	2.095	2.476
0.950	-131.470	4.17476	2.9301	4.1748	2.092	2.476
0.975	-132.038	4.25025	2.9301	4.2502	2.091	2.477
0.995	-133.434	4.40212	2.9299	4.4021	2.090	2.477

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	-133.435	1.80946	2.9186	3.8124	1.809	2.481
0.025	-132.038	1.8758	2.9222	3.8124	1.876	2.480
0.050	-131.470	1.9103	2.9237	3.8119	1.910	2.480
0.250	-130.345	2.01913	2.9273	3.8082	2.019	2.477
MLE	-130.117*	2.09729	2.9291	3.8034	2.097	2.475

Per.	Ln(L)	M_21	Q_1	Q_2	M_21	M_12
0.750	-130.346	2.17778	2.9304	3.7965	2.178	2.472
0.950	-131.471	2.29735	2.9316	3.7824	2.297	2.467
0.975	-132.038	2.33732	2.9317	3.7765	2.337	2.465
0.995	-133.434	2.41712	2.9317	3.7630	2.417	2.460

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	-133.435	2.14372	2.9245	3.7680	2.109	2.144
0.025	-132.038	2.22131	2.9273	3.7838	2.106	2.221
0.050	-131.471	2.26121	2.9282	3.7896	2.104	2.261
0.250	-130.345	2.38611	2.9294	3.8006	2.100	2.386
MLE	-130.117*	2.47509	2.9291	3.8034	2.097	2.475
0.750	-130.344	2.5658	2.9279	3.8031	2.095	2.566
0.950	-131.469	2.70055	2.9249	3.7974	2.092	2.701
0.975	-132.038	2.74543	2.9236	3.7942	2.091	2.745
0.995	-133.435	2.83484	2.9209	3.7858	2.090	2.835

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	2.6023	2.6762	2.7150	2.8388	2.9291	3.0227	3.1642	3.2120	3.3080
Theta_2	3.2839	3.4018	3.4638	3.6608	3.8034	3.9514	4.1748	4.2502	4.4021
M_21	1.8095	1.8758	1.9103	2.0191	2.0973	2.1778	2.2974	2.3373	2.4171
M_12	2.1437	2.2213	2.2612	2.3861	2.4751	2.5658	2.7005	2.7454	2.8348