

Example: Microsatellite data set

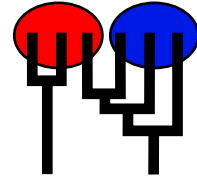
MIGRATION RATE AND POPULATION SIZE ESTIMATION

using the coalescent and maximum likelihood or Bayesian inference

Migrate-n version 3.1.1 [1593]

Program started at Fri Feb 5 19:52:15 2010

Program finished at Fri Feb 5 19:53:50 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

M values were generated from guessed values

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			
Static heating scheme	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 [x Ne mu]	M (m/mu) [+receiving population]	
				1,+	2,+
1:population	1 1	212.211	6.06e+04	-	2.50e-04
	1 2	12.911	9.19e+02	-	8.25e-04
	1 A	46.919	9.59e+02	-	0.002
	2 1	10.879	28.88	-	0.011
	2 2	10.874	23.48	-	0.074
	2 A	21.748	23.48	-	0.074
	3 1	10.657	17.65	-	0.036
	3 2	5.848	20.02	-	0.065
	3 A	18.946	11.36	-	1.53e-13
	4 1	16.821	1.86e+02	-	0.001
	4 2	66.726	2.26e+03	-	0.001
	4 A	33.641	1.86e+02	-	0.001
	5 1	4.060	2.0137	-	1.078
	5 2	7.963	45.38	-	0.025
	5 A	89.384	1.96e+02	-	0.006
	6 1	10.176	1.12e+02	-	0.013
	6 2	7.834	1.55e+02	-	0.014
	6 A	21.491	1.10e+02	-	0.012
	7 1	4.108	10.91	-	0.022
	7 2	31.697	8.0912	-	0.195
	7 A	147.838	65.80	-	0.022
	8 1	26.637	98.80	-	0.021
	8 2	169.204	4.50e+02	-	0.012
	8 A	331.326	4.50e+02	-	0.012
	9 1	4.737	23.05	-	0.010
	9 2	3.608	8.9014	-	0.056
	9 A	10.154	22.72	-	0.029
	10 1	4.855	18.18	-	0.047
	10 2	21.010	7.19e+02	-	0.004
	10 A	16.634	19.58	-	0.044
	All	88.389	2.12e+02	-	0.008
2:population	1 1	212.211	3.10e+04	5.47e-04	-
	1 2	12.911	7.01e+02	0.006	-
	1 A	46.919	2.53e+03	7.96e-04	-
	2 1	10.879	36.79	0.022	-
	2 2	10.874	48.83	0.037	-
	2 A	21.748	48.83	0.037	-

3 1	10.657	19.69	0.026	-
3 2	5.848	37.59	0.114	-
3 A	18.946	13.87	0.008	-
4 1	16.821	2.62e+02	0.003	-
4 2	66.726	2.84e+03	0.001	-
4 A	33.641	2.62e+02	0.003	-
5 1	4.060	7.2952	0.560	-
5 2	7.963	29.79	0.028	-
5 A	89.384	30.67	0.024	-
6 1	10.176	56.13	0.034	-
6 2	7.834	1.55e+02	0.011	-
6 A	21.491	1.51e+02	0.008	-
7 1	4.108	46.91	0.216	-
7 2	31.697	7.3407	0.281	-
7 A	147.838	42.17	0.070	-
8 1	26.637	98.49	0.033	-
8 2	169.204	52.12	0.049	-
8 A	331.326	51.89	0.049	-
9 1	4.737	13.23	0.129	-
9 2	3.608	31.84	0.318	-
9 A	10.154	34.41	0.055	-
10 1	4.855	61.19	0.358	-
10 2	21.010	8.00e+02	0.002	-
10 A	16.634	1.25e+02	0.076	-
All	88.389	1.48e+02	0.025	-

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

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	85.072	189.837	1.90e+02	1.48e+02	0.008	0.025
0.025	86.468	194.967	1.95e+02	1.48e+02	0.008	0.025
0.050	87.035	197.647	1.98e+02	1.48e+02	0.008	0.025
0.250	88.161	206.206	2.06e+02	1.48e+02	0.008	0.025
MLE	88.389*	212.452	2.12e+02	1.48e+02	0.008	0.025
0.750	88.160	219.005	2.19e+02	1.48e+02	0.008	0.025
0.950	87.036	229.313	2.29e+02	1.45e+02	0.008	0.025
0.975	86.469	234.545	2.35e+02	1.37e+02	0.007	0.025
0.995	85.071	246.679	2.47e+02	1.35e+02	0.007	0.025

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	85.071	123.134	2.28e+02	1.23e+02	0.007	0.025
0.025	86.468	130.498	2.26e+02	1.30e+02	0.007	0.025
0.050	87.035	134.456	2.16e+02	1.34e+02	0.007	0.025
0.250	88.162	142.416	2.13e+02	1.42e+02	0.008	0.025
MLE	88.389*	147.818	2.12e+02	1.48e+02	0.008	0.025
0.750	88.162	153.383	2.12e+02	1.53e+02	0.008	0.025
0.950	87.036	161.784	2.12e+02	1.62e+02	0.008	0.025
0.975	86.468	164.623	2.12e+02	1.65e+02	0.008	0.025
0.995	85.071	170.35	2.12e+02	1.70e+02	0.008	0.025

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	85.071	0.00579246	2.12e+02	1.47e+02	0.006	0.024
0.025	86.469	0.00620894	2.12e+02	1.47e+02	0.006	0.025
0.050	87.035	0.00642868	2.12e+02	1.47e+02	0.006	0.025
0.250	88.162	0.00713525	2.12e+02	1.48e+02	0.007	0.025
MLE	88.389*	0.00764673	2.12e+02	1.48e+02	0.008	0.025

Per.	Ln(L)	M_21	Q_1	Q_2	M_21	M_12
0.750	88.162	0.00817461	2.12e+02	1.48e+02	0.008	0.025
0.950	87.036	0.00896515	2.12e+02	1.48e+02	0.009	0.025
0.975	86.467	0.00923038	2.12e+02	1.48e+02	0.009	0.025
0.995	85.071	0.00975964	2.12e+02	1.48e+02	0.010	0.025

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	85.072	0.0195799	2.13e+02	1.46e+02	0.008	0.020
0.025	86.467	0.0207277	2.13e+02	1.46e+02	0.008	0.021
0.050	87.035	0.0213306	2.13e+02	1.47e+02	0.008	0.021
0.250	88.161	0.0232474	2.12e+02	1.47e+02	0.008	0.023
MLE	88.389*	0.024635	2.12e+02	1.48e+02	0.008	0.025
0.750	88.162	0.0260599	2.13e+02	1.48e+02	0.008	0.026
0.950	87.036	0.0281938	2.13e+02	1.48e+02	0.008	0.028
0.975	86.469	0.0289048	2.13e+02	1.48e+02	0.008	0.029
0.995	85.071	0.030328	2.13e+02	1.48e+02	0.008	0.030

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	189.84	194.97	197.65	206.21	212.45	219.01	229.31	234.55	246.68
Theta_2	123.13	130.50	134.46	142.42	147.82	153.38	161.78	164.62	170.35
M_21	0.0058	0.0062	0.0064	0.0071	0.0076	0.0082	0.0090	0.0092	0.0098
M_12	0.0196	0.0207	0.0213	0.0232	0.0246	0.0261	0.0282	0.0289	0.0303