

Example: Microsatellite data set

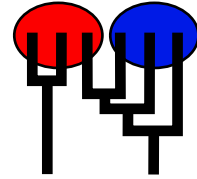
MIGRATION RATE AND POPULATION SIZE ESTIMATION

using the coalescent and maximum likelihood or Bayesian inference

Migrate-n version 3.2.9 []

Program started at Wed Jun 15 16:42:04 2011

Program finished at Wed Jun 15 17:19:10 2011



Options

Datatype: Microsatellite data [Brownian motion]
Missing data: not included

Inheritance scalars in use for Thetas: 1.00 1.00

1.00 1.00 1.00 1.00 1.00

1.00 1.00 1.00

[Each Theta uses the (true) inheritance scalar of the first locus as a reference]

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

2

Recorded steps [a]

100

1000

Increment (record every x step [b])

100

100

Visited (sampled) genealogies [a*b]

10000

100000

Number of discard trees per chain (burn-in)

10000

10000

Multiple Markov chains:

Averaging over replicates

Over independent 2 replicates

Adaptive_standard heating scheme

4 chains with start values 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)	Θ	M (m/mu) [+receiving population]	
			[x Ne mu]	1,+	2,+
1:population	1 1	2.432	2.8078	-	1.737
	1 2	8.388	1.3549	-	3.142
	1 A	15.018	1.2292	-	2.552
	2 1	2.179	2.0557	-	6.758
	2 2	2.543	1.8014	-	6.883
	2 A	4.371	2.0889	-	5.016
	3 1	5.309	1.1489	-	7.682
	3 2	1.331	1.0144	-	9.889
	3 A	10.618	1.1489	-	7.682
	4 1	6.137	5.3389	-	5.585
	4 2	5.337	3.4673	-	3.675
	4 A	15.532	1.3523	-	3.822
	5 1	3.140	0.7467	-	5.422
	5 2	1.144	1.1525	-	12.205
	5 A	5.155	0.9964	-	5.264
	6 1	1.783	1.3860	-	4.548
	6 2	4.701	2.0583	-	2.686
	6 A	9.306	1.8468	-	3.132
	7 1	4.240	1.0686	-	5.715
	7 2	5.225	1.0534	-	3.981
	7 A	9.036	1.2470	-	3.111
	8 1	13.145	1.1269	-	4.904
	8 2	0.681	1.8920	-	7.090
	8 A	12.258	1.1248	-	4.871
	9 1	20.607	0.9851	-	0.243
	9 2	1.233	2.2836	-	4.765
	9 A	37.741	1.0895	-	0.131
	10 1	5.602	2.5572	-	4.674
	10 2	1.276	2.3523	-	3.479
	10 A	15.362	0.7951	-	4.511
	All	80.575	1.2167	-	3.731
2:population	1 1	2.432	5.6497	1.037	-
	1 2	8.388	2.6646	2.091	-
	1 A	15.018	2.0374	0.917	-
	2 1	2.179	1.2375	4.991	-
	2 2	2.543	1.3831	4.059	-
	2 A	4.371	1.1232	3.830	-

3 1	5.309	0.8853	8.883	-
3 2	1.331	2.0040	4.690	-
3 A	10.618	0.8852	8.883	-
4 1	6.137	3.2402	4.172	-
4 2	5.337	3.2459	2.685	-
4 A	15.532	1.1081	3.077	-
5 1	3.140	0.9794	3.873	-
5 2	1.144	1.4847	6.369	-
5 A	5.155	0.5693	8.182	-
6 1	1.783	2.1616	3.190	-
6 2	4.701	1.0930	5.721	-
6 A	9.306	1.4970	5.704	-
7 1	4.240	1.2868	4.035	-
7 2	5.225	0.7950	3.165	-
7 A	9.036	0.9954	1.649	-
8 1	13.145	1.0934	3.167	-
8 2	0.681	2.6670	5.380	-
8 A	12.258	1.0922	3.130	-
9 1	20.607	1.1809	6.314	-
9 2	1.233	1.8669	4.105	-
9 A	37.741	1.0841	6.591	-
10 1	5.602	2.8264	1.984	-
10 2	1.276	1.8759	6.705	-
10 A	15.362	1.1212	1.619	-
All	80.575	1.0633	3.328	-

Comments:

The x is 1, 2, or 4 for mtDNA, haploid, or diploid data, respectively

There were 10 short chains (100 used trees out of sampled 10000)
and 2 long chains (1000 used trees out of sampled 100000)

Adaptive heating with 4 chains was active

Average log-likelihood for average, temperature, 1.064900, 3.134936, 4.729382

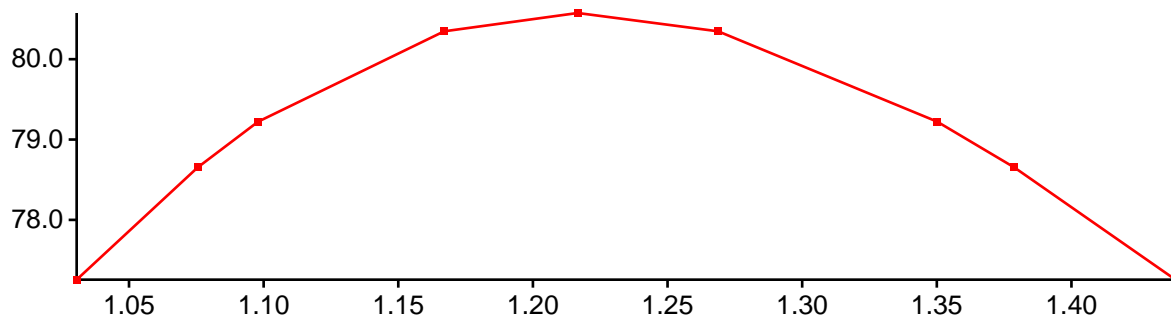
COMBINATION OF 2 MULTIPLE RUNS

Profile likelihood tables and plots

Profile likelihood table and plot for parameter Θ_1

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

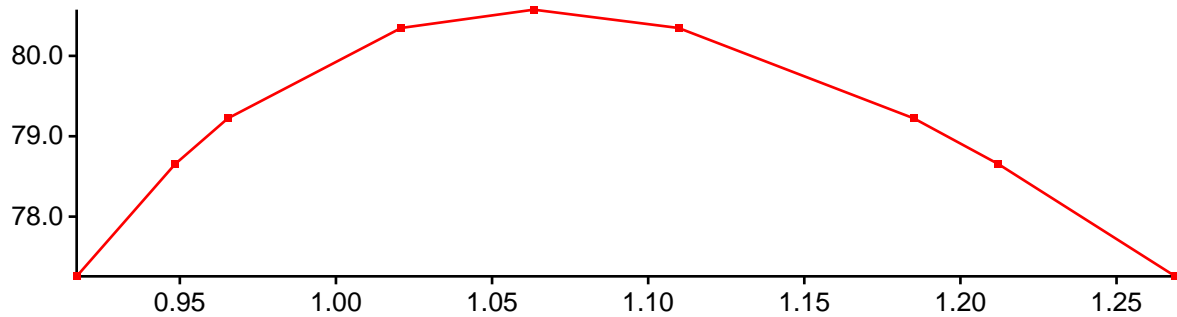
Per.	Ln(L)	Θ_1	Θ_1	Θ_2	$M_{2 \rightarrow 1}$	$M_{1 \rightarrow 2}$
0.005	77.256	1.03056	1.0306	1.0861	3.726	3.221
0.025	78.654	1.07554	1.0755	1.0746	3.741	3.271
0.050	79.222	1.09793	1.0979	1.0710	3.743	3.286
0.250	80.347	1.16703	1.1670	1.0650	3.737	3.315
MLE	80.575*	1.21665	1.2167	1.0633	3.731	3.328
0.750	80.347	1.26879	1.2688	1.0634	3.727	3.341
0.950	79.223	1.35011	1.3501	1.0673	3.724	3.363
0.975	78.653	1.37877	1.3788	1.0701	3.724	3.372
0.995	77.257	1.43858	1.4386	1.0780	3.724	3.391



Profile likelihood table and plot for parameter Θ_2

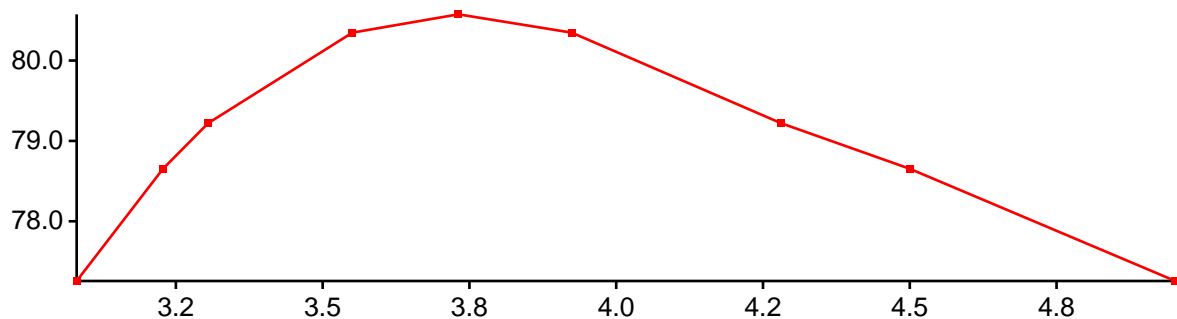
Parameters are evaluated at percentiles using bisection method (slow, but exact).

Per.	Ln(L)	Θ_2	Θ_1	Θ_2	$M_{2 \rightarrow 1}$	$M_{1 \rightarrow 2}$
0.005	77.257	0.916958	1.2178	0.9170	3.762	3.319
0.025	78.653	0.948479	1.2179	0.9485	3.753	3.322
0.050	79.222	0.965361	1.2179	0.9654	3.748	3.324
0.250	80.347	1.02086	1.2174	1.0209	3.737	3.327
MLE	80.575*	1.06334	1.2167	1.0633	3.731	3.328
0.750	80.347	1.10972	1.2155	1.1097	3.726	3.327
0.950	79.222	1.18511	1.2132	1.1851	3.722	3.322
0.975	78.654	1.21214	1.2123	1.2121	3.720	3.320
0.995	77.257	1.26883	1.2105	1.2688	3.718	3.316

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

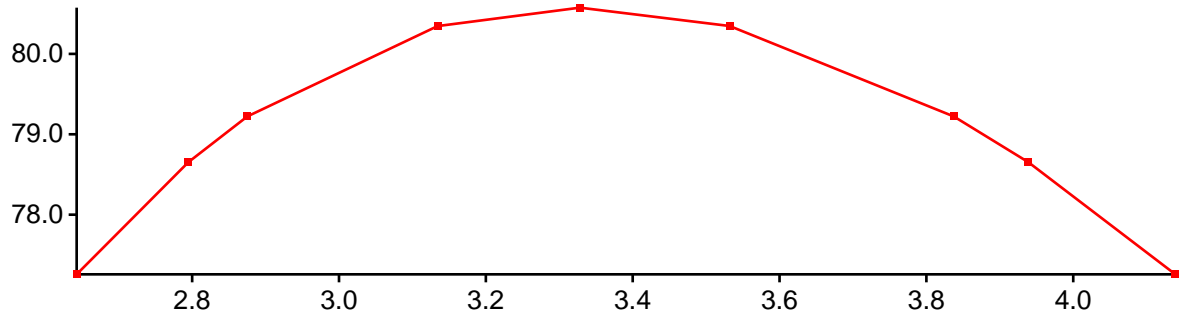
Parameters are evaluated at percentiles using bisection method (slow, but exact).

Per.	Ln(L)	$M_{2 \rightarrow 1}$	Θ_1	Θ_2	$M_{2 \rightarrow 1}$	$M_{1 \rightarrow 2}$
0.005	77.257	3.08102	1.2223	1.0690	3.081	3.310
0.025	78.654	3.22817	1.2216	1.0673	3.228	3.321
0.050	79.221	3.30505	1.2209	1.0666	3.305	3.325
0.250	80.347	3.55059	1.2183	1.0646	3.551	3.330
MLE	80.575*	3.7312	1.2167	1.0633	3.731	3.328
0.750	80.347	3.92435	1.2162	1.0621	3.924	3.320
0.950	79.221	4.28061	1.2315	1.0605	4.281	3.245
0.975	78.654	4.49977	1.2458	1.0632	4.500	3.180
0.995	77.257	4.95232	1.2375	1.0800	4.952	3.127

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)	$M_{1 \rightarrow 2}$	Θ_1	Θ_2	$M_{2 \rightarrow 1}$	$M_{1 \rightarrow 2}$
0.005	77.258	2.6427	1.1922	1.0673	3.743	2.643
0.025	78.654	2.79496	1.2020	1.0644	3.742	2.795
0.050	79.222	2.87514	1.2056	1.0637	3.740	2.875
0.250	80.346	3.13433	1.2132	1.0632	3.734	3.134
MLE	80.575*	3.32805	1.2167	1.0633	3.731	3.328
0.750	80.347	3.53195	1.2199	1.0629	3.726	3.532
0.950	79.222	3.8373	1.2268	1.0607	3.710	3.837
0.975	78.654	3.93868	1.2299	1.0598	3.703	3.939
0.995	77.258	4.13905	1.2370	1.0583	3.688	4.139



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
Θ_1	1.0306	1.0755	1.0979	1.1670	1.2167	1.2688	1.3501	1.3788	1.4386
Θ_2	0.9170	0.9485	0.9654	1.0209	1.0633	1.1097	1.1851	1.2121	1.2688
M_21	3.0810	3.2282	3.3050	3.5506	3.7312	3.9244	4.2806	4.4998	4.9523
M_12	2.6427	2.7950	2.8751	3.1343	3.3281	3.5320	3.8373	3.9387	4.1390

Average temperatures during the run

Chain	Θ_0
1	1.00000
2	1.93190
3	3.13494
4	4.72938

Adaptive heating often fails, if the average temperatures are very close together try to rerun using static heating! If you want to compare models using marginal likelihoods then you MUST use static heating