Example: Microsatellite data set

MIGRATION RATE AND POPULATION SIZE ESTIMATION
using the coalescent and maximum likelihood or Bayesian inference
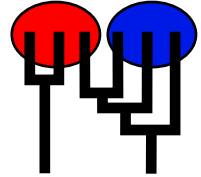Migrate-n version 3.0.1
  Compiled for a PARALLEL COMPUTER ARCHITECTURE
  One master and 2 compute nodes are available.
Program started at   Mon Oct 20 16:55:01 2008
Program finished at   Mon Oct 20 16:57:51 2008

Options

Datatype: Microsatellite data [Brownian motion]
Missing data: not included
Random number seed: (with internal timer)   550844669
Start parameters:

Theta values were generated   from guessed values
   Theta = 1.00000   1.00000
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_numb   *   *
 2 population_numb   *   *

Order of parameters:
   1   Θ_1 <displayed>
   2   Θ_2 <displayed>
   3          $M_{2\to1}$ <displayed>
   4          $M_{1\to2}$ <displayed>

Mutation rate among loci:		Mutation rate is constant
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 indepedent 2 replicates

Print options:

Data file: infile.msat

Output file: outfile-ml

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: 1

Population	Locus	Gene copies data	(missing)
1 population_number_0	1	50	(0)
2 population_number_1	1	42	(0)
Total of all populations	1	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

Maximum Likelihood estimates

Population [x]	Loc.	Ln(L/L0)	Theta [x Ne mu]	M (m/mu) [+=receiving population 1,+	2,+
1:population	1 1	1.951	4.8155	-	1.923
	1 2	4.543	2.7385	-	1.245
	1 A	3.902	4.8155	-	1.923
2:population	1 1	1.951	13.35	2.934	-
	1 2	4.543	9.0544	1.392	-
	1 A	3.902	13.35	2.934	-

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	0.585	3.18307	3.1831	14.54	2.238	3.009
0.025	1.980	3.59116	3.5912	14.46	2.152	3.012
0.050	2.549	3.81474	3.8147	13.89	2.055	2.987
0.250	3.674	4.39719	4.3972	13.28	1.944	2.940
MLE	3.902*	4.81545	4.8155	13.35	1.923	2.934
0.750	3.673	5.27176	5.2718	13.42	1.912	2.933
0.950	2.548	6.01354	6.0135	13.50	1.902	2.933
0.975	1.982	6.28034	6.2803	13.52	1.899	2.933
0.995	0.585	6.84666	6.8467	13.54	1.896	2.932

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	0.585	3.88984	2.6881	3.8898	1.698	1.337
0.025	1.981	4.17956	2.6546	4.1796	1.730	1.330
0.050	2.549	4.32166	2.6352	4.3217	1.748	1.327
0.250	3.674	11.3803	4.7700	11.38	1.927	2.918
MLE	3.902*	13.3454	4.8155	13.35	1.923	2.934
0.750	3.673	15.6624	4.8124	15.66	1.930	2.962
0.950	2.548	19.8994	4.7441	19.90	1.955	2.999
0.975	1.981	21.5801	4.7048	21.58	1.968	3.010
0.995	0.584	25.4391	4.5958	25.44	2.006	3.031

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	0.585	0.458746	2.7829	8.6802	0.459	1.417
0.025	1.980	1.53407	4.8813	13.35	1.534	2.927
0.050	2.549	1.59203	4.8760	13.34	1.592	2.927
0.250	3.674	1.78093	4.8491	13.33	1.781	2.930
MLE	3.902*	1.92326	4.8155	13.35	1.923	2.934
0.750	3.675	2.07674	4.7554	13.42	2.077	2.945
0.950	2.549	2.33903	4.4458	14.23	2.339	2.999
0.975	1.980	2.4615	4.1729	14.88	2.462	3.034

Per.	Ln(L)	M_21	Q_1	Q_2	M_21	M_12
0.995	0.584	2.74712	3.9509	15.20	2.747	3.052

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	0.585	0.651306	2.7571	8.7780	1.207	0.651
0.025	1.981	0.701542	2.7529	8.8410	1.212	0.702
0.050	2.549	0.724097	2.7513	8.8650	1.214	0.724
0.250	3.673	0.773338	2.7482	8.9095	1.219	0.773
MLE	3.902*	2.93442	4.8155	13.35	1.923	2.934
0.750	3.673	3.15175	4.8041	13.60	1.930	3.152
0.950	2.549	3.48801	4.7583	13.95	1.950	3.488
0.975	1.981	3.60489	4.7331	14.06	1.960	3.605
0.995	0.584	3.84558	4.6709	14.29	1.986	3.846

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	3.1831	3.5912	3.8147	4.3972	4.8155	5.2718	6.0135	6.2803	6.8467
Theta_2	3.8898	4.1796	4.3217	11.3803	13.3454	15.6624	19.8994	21.5801	25.4391
M_21	0.4587	1.5341	1.5920	1.7809	1.9233	2.0767	2.3390	2.4615	2.7471
M_12	0.6513	0.7015	0.7241	0.7733	2.9344	3.1517	3.4880	3.6049	3.8456