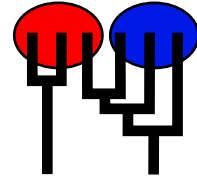# Example: Microsatellite data set

MIGRATION RATE AND POPULATION SIZE ESTIMATION
using the coalescent and maximum likelihood or Bayesian inference
Migrate-n version 3.5.0 [2129]
  Compiled for a PARALLEL COMPUTER ARCHITECTURE
  One master and 8 compute nodes are available.
  Compiled for a SYMMETRIC MULTIPROCESSORS
Program started at   Sun Mar 3 14:20:33 2013
Program finished at   Sun Mar 3 16:11:28 2013

Options

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

Inheritance scalers in use for Thetas:
All loci use an inheritance scaler of 1.0
[The locus with a scaler of 1.0 used as 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_numb   *   *
  2 population_numb   *   *

Order of parameters:

1	Θ_1	<displayed>
2	Θ_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	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	

Multiple Markov chains:

Averaging over replicates   Over indepedent 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

[Data was used as repeat-length information]

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	0.196
19	0.040	0.071	0.054
18	0.060	0.119	0.087
15	0.220	0.024	0.130
21	0.020	0.167	0.087
23	0.020	0.119	0.065
17	0.280	0.095	0.196
22	0.060	0.119	0.087
25	0.060	0.024	0.043
24	0.020	-	0.011
26	-	0.024	0.011
27	-	0.048	0.022
29	-	0.024	0.011
Alleles	10	12	13
Samplesize	50	42	92
H_{exp}	0.811	0.883	0.874

Locus 2

Allele	Pop1	Pop2	All
16	0.520	0.571	0.543
19	0.040	-	0.022
18	0.220	0.119	0.174
17	0.160	0.167	0.163
15	0.020	-	0.011
21	0.020	0.071	0.043
20	0.020	0.024	0.022
22	-	0.048	0.022
Alleles	7	6	8
Samplesize	50	42	92
H_{exp}	0.653	0.624	0.644

Locus 3

Allele	Pop1	Pop2	All
19	0.240	0.262	0.250
20	0.280	0.476	0.370

Allele	Pop1	Pop2	All
18	0.080	0.095	0.087
21	0.280	0.119	0.207
22	0.120	0.048	0.087
Alleles	5	5	5
Samplesize	50	42	92
H_{exp}	0.765	0.679	0.743

Locus 4

Allele	Pop1	Pop2	All
16	0.080	0.071	0.076
24	0.180	0.024	0.109
15	0.020	0.048	0.033
25	0.160	0.167	0.163
14	0.020	0.048	0.033
19	0.100	0.143	0.120
12	0.060	-	0.033
20	0.080	0.190	0.130
23	0.060	0.119	0.087
28	0.020	-	0.011
22	0.060	0.024	0.043
21	0.160	0.119	0.141
13	-	0.024	0.011
26	-	0.024	0.011
Alleles	12	12	14
Samplesize	50	42	92
H_{exp}	0.882	0.875	0.892

Locus 5

Allele	Pop1	Pop2	All
20	0.400	0.524	0.457
21	0.420	0.357	0.391
19	0.180	0.119	0.152
Alleles	3	3	3
Samplesize	50	42	92
H_{exp}	0.631	0.584	0.615

Locus 6

Allele	Pop1	Pop2	All
19	0.060	-	0.033
20	0.100	0.024	0.065

Allele	Pop1	Pop2	All
18	0.300	0.214	0.261
22	0.200	0.119	0.163
21	0.120	0.476	0.283
16	0.060	-	0.033
24	0.160	0.048	0.109
17	-	0.119	0.054
Alleles	7	6	8
Samplesize	50	42	92
H_{exp}	0.813	0.696	0.804

Locus 7

Allele	Pop1	Pop2	All
23	0.040	0.238	0.130
20	0.660	0.143	0.424
22	0.180	0.190	0.185
21	0.100	0.333	0.207
19	0.020	0.095	0.054
Alleles	5	5	5
Samplesize	50	42	92
H_{exp}	0.520	0.766	0.724

Locus 8

Allele	Pop1	Pop2	All
19	0.520	0.524	0.522
17	0.040	0.048	0.043
18	0.100	0.071	0.087
20	0.140	0.190	0.163
16	0.080	-	0.043
22	0.100	0.048	0.076
15	0.020	0.048	0.033
23	-	0.071	0.033
Alleles	7	7	8
Samplesize	50	42	92
H_{exp}	0.682	0.672	0.682

Locus 9

Allele	Pop1	Pop2	All
24	0.080	0.024	0.054
19	0.300	0.429	0.359
20	0.300	0.167	0.239

Allele	Pop1	Pop2	All
23	0.180	0.143	0.163
22	0.080	0.024	0.054
18	0.020	0.071	0.043
21	0.040	0.095	0.065
25	-	0.048	0.022
Alleles	7	8	8
Samplesize	50	42	92
H_{exp}	0.773	0.751	0.775

Locus 10

Allele	Pop1	Pop2	All
22	0.100	0.214	0.152
20	0.440	0.214	0.337
23	0.080	0.167	0.120
24	0.020	-	0.011
19	0.160	0.167	0.163
21	0.060	0.048	0.054
18	0.080	-	0.043
15	0.020	0.071	0.043
17	0.040	0.048	0.043
25	-	0.071	0.033
Alleles	9	8	10
Samplesize	50	42	92
H_{exp}	0.752	0.838	0.813

Average expected heterozygosity

	Pop1	Pop2	All
H_{exp}	0.728	0.737	0.757

Maximum Likelihood estimates

Population [x]	Loc.	Ln(L/L0)	Θ [x Ne mu]	M (m/mu) [+=receiving population 1,+	2,+
1:population	1 1	56.406	0.1799	-	25.803
	1 2	19.348	0.1639	-	23.477
	1 A	49.858	0.1799	-	25.803
	2 1	6.051	0.0070	-	2.09e+03
	2 2	2.639	0.0064	-	3.34e+03
	2 A	6.176	0.0114	-	1.67e+03
	3 1	3.069	0.0787	-	266.81
	3 2	3.033	0.0539	-	344.04
	3 A	5.573	0.0618	-	413.01
	4 1	5.522	0.0945	-	251.37
	4 2	7.199	0.1218	-	178.57
	4 A	14.391	0.1218	-	178.51
	5 1	9.033	0.8613	-	2.39e-09
	5 2	2.446	0.8962	-	1.37e-07
	5 A	4.892	0.8962	-	1.37e-07
	6 1	3.568	1.6381	-	1.05e-13
	6 2	4.590	2.1312	-	1.418
	6 A	9.181	2.1312	-	1.418
	7 1	12.381	0.0050	-	1.54e+03
	7 2	2.832	0.0025	-	1.62e+03
	7 A	14.995	0.0023	-	1.62e+03
	8 1	2.046	0.0643	-	313.19
	8 2	4.239	0.0659	-	165.57
	8 A	8.477	0.0659	-	165.56
	9 1	5.808	0.2953	-	24.308
	9 2	4.746	0.4717	-	79.107
	9 A	9.493	0.4717	-	79.107
	10 1	6.935	2.2070	-	0.449
	10 2	6.734	1.7994	-	2.698
	10 A	13.467	1.7995	-	2.699
	All	-983.026	0.5353	-	9.593
2:population	1 1	56.406	1.3011	1.937	-
	1 2	19.348	1.2313	0.534	-
	1 A	49.858	1.3011	1.937	-
	2 1	6.051	1.1832	6.72e-08	-
	2 2	2.639	1.8196	9.49e-14	-
	2 A	6.176	1.5883	9.49e-14	-

3 1	3.069	0.8242	1.51e-13	-
3 2	3.033	1.1963	2.31e-13	-
3 A	5.573	1.2930	2.31e-13	-
4 1	5.522	4.7183	0.075	-
4 2	7.199	5.6594	2.00e-08	-
4 A	14.391	5.6598	2.00e-08	-
5 1	9.033	0.0236	202.78	-
5 2	2.446	0.0175	517.82	-
5 A	4.892	0.0175	517.70	-
6 1	3.568	0.1845	31.897	-
6 2	4.590	0.2236	17.681	-
6 A	9.181	0.2236	17.681	-
7 1	12.381	1.0136	3.861	-
7 2	2.832	1.0318	0.821	-
7 A	14.995	0.9830	4.582	-
8 1	2.046	1.4320	9.36e-14	-
8 2	4.239	1.8992	0.190	-
8 A	8.477	1.8993	0.190	-
9 1	5.808	1.6140	4.237	-
9 2	4.746	1.4938	5.89e-08	-
9 A	9.493	1.4938	5.89e-08	-
10 1	6.935	0.0214	376.56	-
10 2	6.734	0.0257	463.12	-
10 A	13.467	0.0257	463.15	-
All	-983.026	1.0013	1.371	-

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)

Static heating with 4 chains was active

COMBINATION OF 2 MULTIPLE RUNS

Citation suggestions:

Beerli P., 1998. Estimation of migration rates and population sizes in geographically structured populations.
   In Advances in Molecular Ecology, G. R. Carvalho, ed., vol. 306 of NATO sciences series, Series A: Life sciences,
   ISO Press, Amsterdam, pp. 39-53.

Beerli P. and J. Felsenstein, 1999. Maximum-likelihood estimation of migration rates and effective population
   numbers in two populations using a coalescent approach, Genetics, 152:763-773.

Beerli P. and J. Felsenstein, 2001. Maximum likelihood estimation of a migration matrix and effective
   population sizes in n subpopulations by using a coalescent approach, Proceedings of the National Academy
   of Sciences of the United States of America, 98: p. 4563-4568.

Beerli P., 2007. Estimation of the population scaled mutation rate from microsatellite data,

Genetics, 177:1967-1968.

Beerli P., 2006. Comparison of Bayesian and maximum-likelihood inference of population genetic parameters.
  Bioinformatics 22:341-345
Beerli P., 2009. How to use MIGRATE or why are Markov chain Monte Carlo programs difficult to use?
  In Population Genetics for Animal Conservation, G. Bertorelle, M. W. Bruford, H. C. Hauffe, A. Rizzoli,
  and C. Vernesi, eds., vol. 17 of Conservation Biology, Cambridge University Press, Cambridge UK, pp. 42-79.

Approximate Likelihood Ratio Tests

Legend for the likelihood ratio tables

Null-Hypothesis: your test model	Log(likelihood) of test model
is equal to	Log(likelihood) of full model
full model (the model under which the	Likelihood ratio test value
genealogies were sampled)	Degrees of freedom of test
	[Theta values are on the diagonal of the
	Probability*
Migration matrix, migration rates are	Probability**
specified as M]	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=1974.052527, num(param)=4]

H0: 0.7683 5.4817 5.4817 0.7683	LnL(test)	= -1127.209863
= 0.5353 9.5929 1.3705 1.0013	LnL(full)	= -983.026263
[m, m, m, m,]	LRT	= 288.367199
	df	= 4
	Prob	= 0.000000
	Probc	= 0.000000
	AIC	= 2258.419726
	num(param)	= 2

Profile likelihood tables and plots

Profile likelihood table and plot for parameter Θ_1
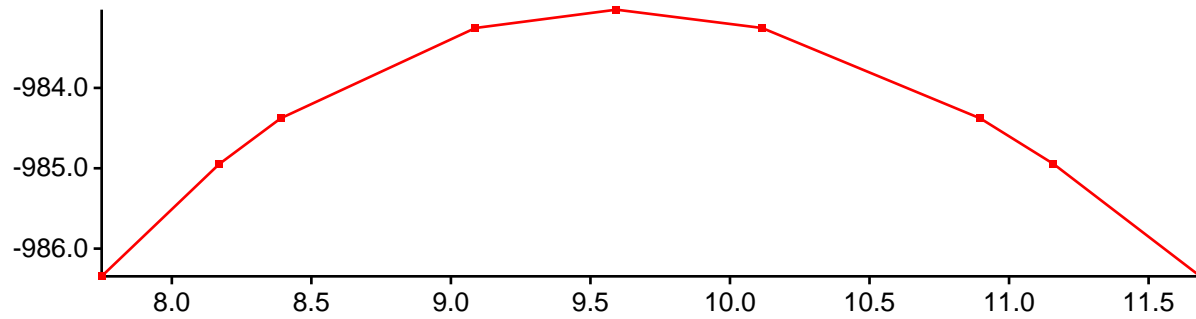Parameters are evaluated at percentiles using bisection method (slow, but exact).

Per.	Ln(L)	Θ_1	Θ_1	Θ_2	$M_{2\to1}$	$M_{1\to2}$
0.005	-986.344	0.468274	0.4683	0.9966	9.549	1.396
0.025	-984.947	0.483288	0.4833	0.9977	9.557	1.388
0.050	-984.378	0.491218	0.4912	0.9983	9.562	1.385
0.250	-983.254	0.516639	0.5166	1.0001	9.579	1.376
MLE	-983.026*	0.535339	0.5353	1.0013	9.593	1.371
0.750	-983.254	0.554912	0.5549	1.0025	9.609	1.367
0.950	-984.379	0.584707	0.5847	1.0041	9.634	1.363
0.975	-984.947	0.594813	0.5948	1.0045	9.642	1.362
0.995	-986.344	0.615262	0.6153	1.0054	9.659	1.361

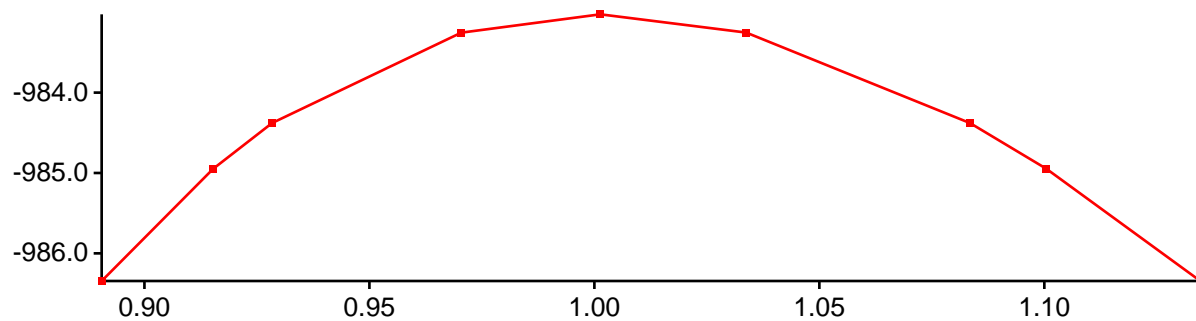

Profile likelihood table and plot for parameter $M_{2\to1}$
Parameters are evaluated at percentiles using bisection method (slow, but exact).

Per.	Ln(L)	$M_{2\to1}$	Θ_1	Θ_2	$M_{2\to1}$	$M_{1\to2}$
0.005	-986.344	7.74857	0.5331	0.9999	7.749	1.409
0.025	-984.947	8.17003	0.5336	0.9997	8.170	1.398
0.050	-984.378	8.39027	0.5339	0.9997	8.390	1.393
0.250	-983.254	9.08789	0.5348	1.0005	9.088	1.379
MLE	-983.026*	9.59291	0.5353	1.0013	9.593	1.371
0.750	-983.254	10.115	0.5359	1.0023	10.115	1.363
0.950	-984.379	10.8969	0.5365	1.0038	10.897	1.354
0.975	-984.946	11.1592	0.5367	1.0042	11.159	1.350
0.995	-986.345	11.6854	0.5370	1.0050	11.685	1.345

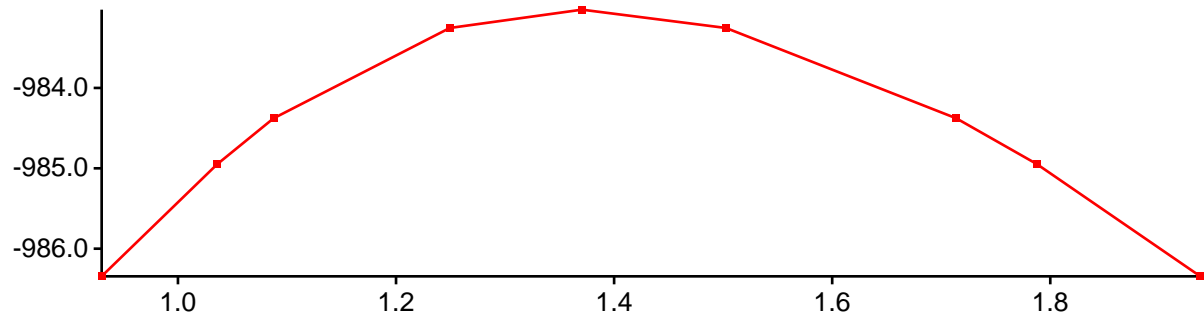Profile likelihood table and plot for parameter Θ_2
Parameters are evaluated at percentiles using bisection method (slow, but exact).

Per.	Ln(L)	Θ_2	Θ_1	Θ_2	$M_{2\rightarrow1}$	$M_{1\rightarrow2}$
0.005	-986.344	0.890495	0.5322	0.8905	9.528	1.396
0.025	-984.948	0.915281	0.5330	0.9153	9.543	1.389
0.050	-984.378	0.92839	0.5334	0.9284	9.551	1.386
0.250	-983.254	0.970416	0.5346	0.9704	9.576	1.377
MLE	-983.026*	1.00133	0.5353	1.0013	9.593	1.371
0.750	-983.253	1.03374	0.5360	1.0337	9.606	1.364
0.950	-984.379	1.08349	0.5367	1.0835	9.616	1.355
0.975	-984.947	1.10043	0.5368	1.1004	9.616	1.353
0.995	-986.344	1.13467	0.5370	1.1347	9.611	1.348

Profile likelihood table and plot for parameter $M_{1\rightarrow2}$
Parameters are evaluated at percentiles using bisection method (slow, but exact).

Per.	Ln(L)	$M_{1\rightarrow2}$	Θ_1	Θ_2	$M_{2\rightarrow1}$	$M_{1\rightarrow2}$
0.005	-986.343	0.930033	0.5377	1.0117	9.390	0.930
0.025	-984.948	1.03607	0.5367	1.0076	9.563	1.036
0.050	-984.378	1.08768	0.5365	1.0061	9.599	1.088
0.250	-983.254	1.24927	0.5359	1.0030	9.616	1.249
MLE	-983.026*	1.37054	0.5353	1.0013	9.593	1.371
0.750	-983.254	1.50263	0.5346	0.9999	9.555	1.503
0.950	-984.378	1.71383	0.5338	0.9987	9.480	1.714
0.975	-984.946	1.78754	0.5338	0.9985	9.452	1.788
0.995	-986.344	1.93762	0.5341	0.9987	9.400	1.938

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	0.4683	0.4833	0.4912	0.5166	0.5353	0.5549	0.5847	0.5948	0.6153
Theta_2	0.8905	0.9153	0.9284	0.9704	1.0013	1.0337	1.0835	1.1004	1.1347
M_21	7.7486	8.1700	8.3903	9.0879	9.5929	10.1150	10.8969	11.1592	11.6854
M_12	0.9300	1.0361	1.0877	1.2493	1.3705	1.5026	1.7138	1.7875	1.9376