

# Example: Microsatellite data set

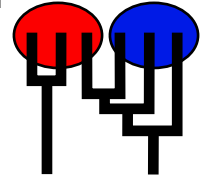
POPULATION SIZE, MIGRATION, DIVERGENCE, ASSIGNMENT, HISTORY

Bayesian inference using the structured coalescent

Migrate-n version 5.0.7 [May-01-2025]

Program started at Sat May 3 12:24:21 2025

Program finished at Sat May 3 12:24:21 2025 [Runtime:0000:00:00:00]



## Options

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

Inheritance multipliers in use for Thetas:  
All loci use an inheritance multiplier of 1.0

Data set was subsampled: used a random sample of size:  
5 and seed 13

Random number seed: (from parmfile) 310705631

Start parameters:

Theta values were generated Using a percent value of the prior

M values were generated Using a percent value of the prior

Connection matrix:

m = average (average over a group of Thetas or M,

s = symmetric migration M, S = symmetric 4Nm,

0 = zero, and not estimated,

\* = migration free to vary, Thetas are on diagonal

d = row population split off column population, D = split and then migration

Population	1	2
1 population_numb	*	0
2 population_numb	D	*

1 population\_numb growing/shrinking

2 population\_num      constant size

Order of parameters:

1	$\Theta_1$	<displayed>
2	$\Theta_2$	<displayed>
3	$M_{1 \rightarrow 2}$	<displayed>
4	$\Delta_{1 \rightarrow 2}$	<displayed>
5	$\sigma_{1 \rightarrow 2}$	<displayed>
6	$g_1$	<displayed>

Mutation rate among loci:

Mutation rate is constant for all loci

Analysis strategy:

Bayesian inference

-Population size estimation:

Exponential Distribution

-Population growth estimation: Growth [Exponential]

-Geneflow estimation:

Exponential Distribution

-Divergence time estimation:

Normal Distribution (mean and standard dev.)

Proposal distributions for parameter

Parameter	Proposal
Theta	Slice sampling
M	Slice sampling
Divergence	Metropolis sampling
Divergence Spread	Metropolis sampling
Growth	Metropolis sampling
Genealogy	Metropolis-Hastings

Prior distribution for parameter

Parameter				Prior	Minimum	Mean*	Maximum	Delta	Bins	UpdateFreq
1	Theta	*	*	Uniform	0.000000	10.00	20.00	2.000000	1500	0.08333
2	Theta	*	*	Uniform	0.000000	10.00	20.00	2.000000	1500	0.08333
3	M	*	*	Uniform	0.000000	10.00	20.00	2.000000	1500	0.08333
4	Splittime mean	*	*	Uniform	0.000000	10.00	20.00	2.000000	1500	0.08333
5	Splittime std	*	*	Uniform	0.000000	10.00	20.00	2.000000	1500	0.08333
6	Growth	*	*	Uniform	-100.000000	0.000	100.0	20.000000	1500	0.08333

[\* \* means priors were set globally]

Posterior distribution:

Parameter values were collected using MCMC, these values

were then used to generate the posterior histograms using KERNEL SMOOTHING (window=41)

and subsequent SAVITZKY-GOLAY SMOOTHING (window=41) for combination over loci

#### Markov chain settings:

Number of chains	Long chain
Recorded steps [a]	1
Increment (record every x step [b]	200
Number of concurrent chains (replicates) [c]	1
Visited (sampled) parameter values [a*b*c]	2
Number of discard trees per replicate (burn-in * b)	400
	50

#### Multiple Markov chains:

Static heating scheme	1000000.00	4 chains with temperatures	3.00	1.50	1.00
		Swapping interval is 1			

#### Print options:

Data file:	infile.msat
	parmfile.msat
Haplotyping is turned on:	NO
Output file:	outfile_msat
Posterior distribution raw histogram file:	bayesfile_msat
Raw data from the MCMC run:	bayesallfile_msat.gz
Print data:	No
Print genealogies [only some for some data type]:	None

## *Data summary*

Data file: infile.msat  
 Datatype: Microsatellite data [Brownian]  
 [Data was used as repeat-length information]  
 Number of loci: 10

### Mutationmodel:

Locus	Sublocus	Mutationmodel	Mutationmodel parameters
1	1	Brownian Motion	[none]
2	1	Brownian Motion	[none]
3	1	Brownian Motion	[none]
4	1	Brownian Motion	[none]
5	1	Brownian Motion	[none]
6	1	Brownian Motion	[none]
7	1	Brownian Motion	[none]
8	1	Brownian Motion	[none]
9	1	Brownian Motion	[none]
10	1	Brownian Motion	[none]

Data set was subsampled: used a random sample of size: 5

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)

Total of all populations	8	42	(0)
	9	42	(0)
	10	42	(0)
	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)

## *Subsampled dataset*

Data set was subsampled randomly per population: 5 samples taken

Locus	Population	Individuals
1	population	0BAC_0BBU 0BBQ_0BBD 0BBO_0BBJ 0BAV_0BAO 0BAX_0BCA
	population	1BBN_1BAX 1BAQ_1BAN 1BAL_1BAV 1BBK_1BAS 1BAP_1BBP
2	population	0BAF_0BBV 0BAL_0BBL 0BAK_0BAD 0BBA_0BAI 0BAC_0BBU
	population	1BAH_1BAT 1BAE_1BAI 1BBF_1BAO 1BBM_1BAM 1BBJ_1BBC
3	population	0BAK_0BAD 0BBK_0BAH 0BBR_0BAW 0BBF_0BAE 0BAN_0BAT
	population	1BBE_1BAJ 1BAL_1BAV 1BAE_1BAI 1BBM_1BAM 1BBD_1BAG
4	population	0BBB_0BBX 0BAU_0BAP 0BAV_0BAO 0BAS_0BBT 0BBF_0BAE
	population	1BAE_1BAI 1BAQ_1BAN 1BBD_1BAG 1BAL_1BAV 1BBF_1BAO
5	population	0BAJ_0BAB 0BAU_0BAP 0BBF_0BAE 0BAC_0BBU 0BAG_0BBI
	population	1BBB_1BBR 1BAC_1BAB 1BAR_1BBA 1BBN_1BAX 1BBK_1BAS
6	population	0BAL_0BBL 0BCB_0BAM 0BAR_0BBW 0BBA_0BAI 0BAJ_0BAB
	population	1BBH_1BBO 1BAR_1BBA 1BBQ_1BBI 1BBL_1BAK 1BBG_1BAU
7	population	0BAU_0BAP 0BAV_0BAO 0BAG_0BBI 0BBF_0BAE 0BBB_0BBX
	population	1BBK_1BAS 1BBQ_1BBI 1BAA_1BAF 1BAE_1BAI 1BBL_1BAK
8	population	0BAF_0BBV 0BBO_0BBJ 0BBP_0BBC 0BCB_0BAM 0BAJ_0BAB
	population	1BBE_1BAJ 1BBH_1BBO 1BAP_1BBP 1BAD_1BAW 1BBL_1BAK
9	population	0BAU_0BAP 0BBR_0BAW 0BBH_0BAA 0BAG_0BBI 0BAS_0BBT
	population	1BAA_1BAF 1BAP_1BBP 1BAC_1BAB 1BBB_1BBR 1BAE_1BAI
10	population	0BBA_0BAI 0BAX_0BCA 0BCB_0BAM 0BAU_0BAP 0BBH_0BAA
	population	1BAP_1BBP 1BAR_1BBA 1BAQ_1BAN 1BBQ_1BBI 1BAD_1BAW

*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 <sub>exp</sub>	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 <sub>exp</sub>	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 <sub>exp</sub>	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 <sub>exp</sub>	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 <sub>exp</sub>	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

## *Bayesian Analysis: Posterior distribution table*

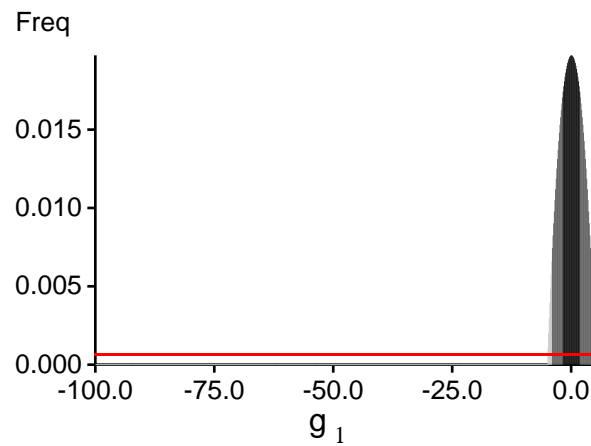
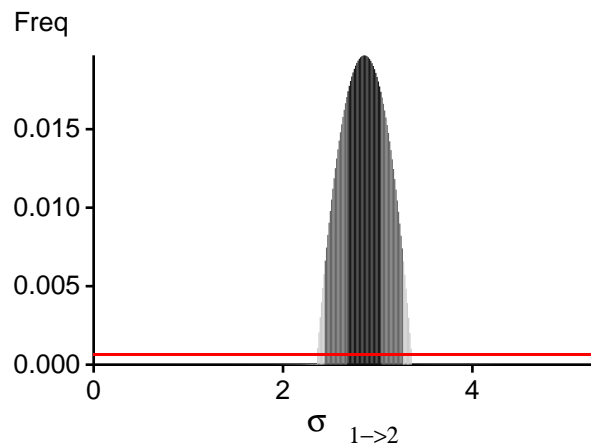
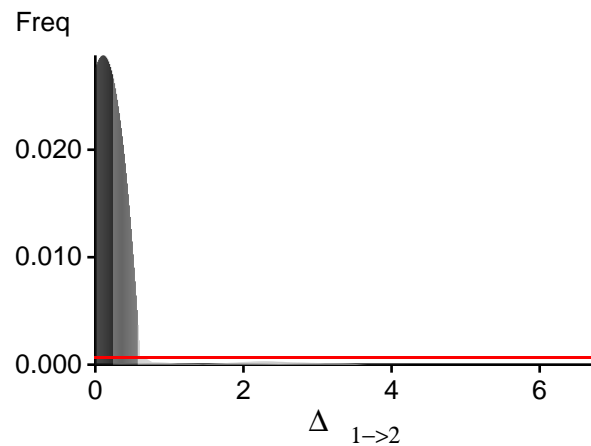
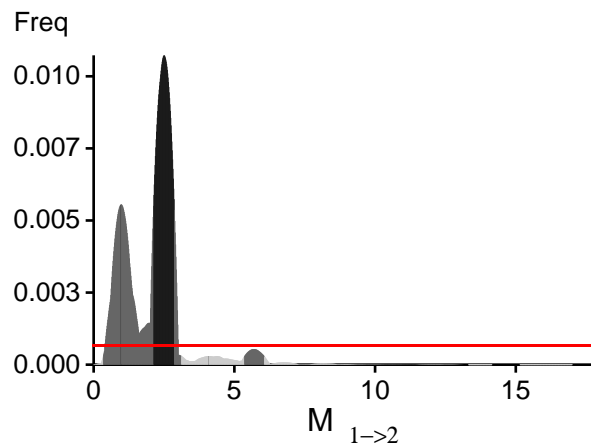
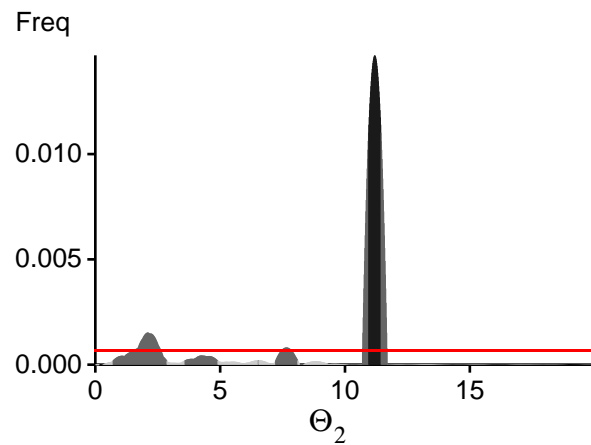
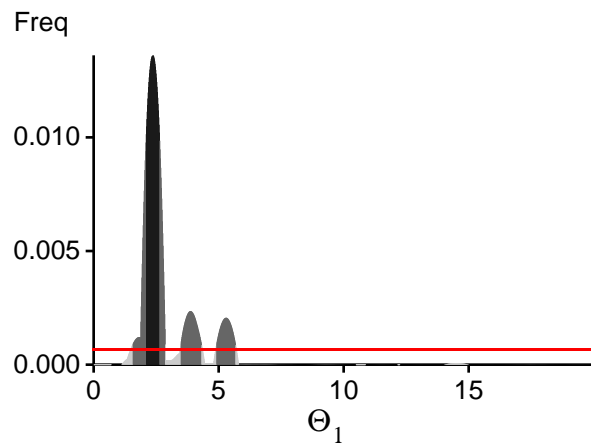
Locus	Parameter	2.5%	25.0%	Mode	75.0%	97.5%	Median	Mean
1	$\Theta_1$	2.06667	2.72000	3.74000	4.21333	4.44000	6.03333	8.37430
1	$\Theta_2$	3.33333	3.52000	3.88667	4.22667	4.44000	3.75333	4.08255
1	$M_{1 \rightarrow 2}$	0.747	5.120	5.553	6.040	6.693	4.633	4.730
1	$D_{1 \rightarrow 2}$	0.00000	0.12000	0.50000	0.98667	2.57333	1.36667	2.04551
1	$S_{1 \rightarrow 2}$	3.14667	3.21333	3.56667	3.89333	3.93333	2.43333	2.19997
1	$g_1$	-3.60000	-1.20000	0.73333	2.53333	4.93333	0.86667	0.67156
2	$\Theta_1$	1.25333	2.01333	2.55333	3.02667	4.05333	2.75333	3.02211
2	$\Theta_2$	1.84000	2.21333	2.78000	3.73333	3.98667	9.95333	9.21780
2	$M_{1 \rightarrow 2}$	7.347	7.573	7.980	9.107	10.240	7.540	7.108
2	$D_{1 \rightarrow 2}$	1.58667	1.88000	2.22000	2.57333	2.84000	2.00667	1.84222
2	$S_{1 \rightarrow 2}$	0.84000	1.38667	1.79333	2.05333	2.66667	1.76667	1.76160
2	$g_1$	-4.53333	-2.00000	-0.06667	1.73333	4.26667	0.06667	-0.08046
3	$\Theta_1$	1.46667	1.66667	2.16667	2.81333	3.66667	3.38000	6.71034
3	$\Theta_2$	0.36000	1.16000	1.86000	2.44000	3.00000	4.26000	5.75152
3	$M_{1 \rightarrow 2}$	0.080	0.453	0.887	1.293	4.347	2.300	2.389
3	$D_{1 \rightarrow 2}$	0.24000	1.06667	1.68667	2.08000	3.38667	1.72667	1.76439
3	$S_{1 \rightarrow 2}$	0.05333	0.20000	0.59333	0.96000	2.25333	0.86000	1.00955
3	$g_1$	-4.00000	-1.60000	0.33333	2.13333	4.53333	0.46667	0.30360
4	$\Theta_1$	2.37333	2.50667	2.98000	4.14667	8.04000	5.86000	7.00615
4	$\Theta_2$	12.70667	12.92000	13.43333	13.93333	14.16000	7.34000	8.04551
4	$M_{1 \rightarrow 2}$	0.133	1.653	2.687	3.053	3.520	2.113	2.083
4	$D_{1 \rightarrow 2}$	0.00000	0.61333	0.98000	1.41333	2.94667	2.24667	2.90958
4	$S_{1 \rightarrow 2}$	2.94667	3.36000	3.90000	4.50667	5.34667	4.19333	4.62447
4	$g_1$	-4.13333	-1.73333	0.06667	1.86667	4.26667	0.20000	0.12602
5	$\Theta_1$	1.24000	1.62667	1.96667	2.57333	3.93333	2.43333	2.64593
5	$\Theta_2$	0.36000	4.04000	4.66000	5.09333	6.14667	4.40667	4.92240
5	$M_{1 \rightarrow 2}$	5.240	5.333	5.793	6.173	7.253	5.460	5.245
5	$D_{1 \rightarrow 2}$	1.26667	2.62667	2.75333	3.05333	5.04000	2.92667	2.86121
5	$S_{1 \rightarrow 2}$	0.50667	1.44000	1.88667	2.40000	3.72000	2.00667	2.06014
5	$g_1$	-4.00000	-1.60000	0.33333	2.13333	4.53333	0.46667	0.25501
6	$\Theta_1$	3.06667	3.98667	4.52667	5.10667	5.81333	5.47333	9.13478

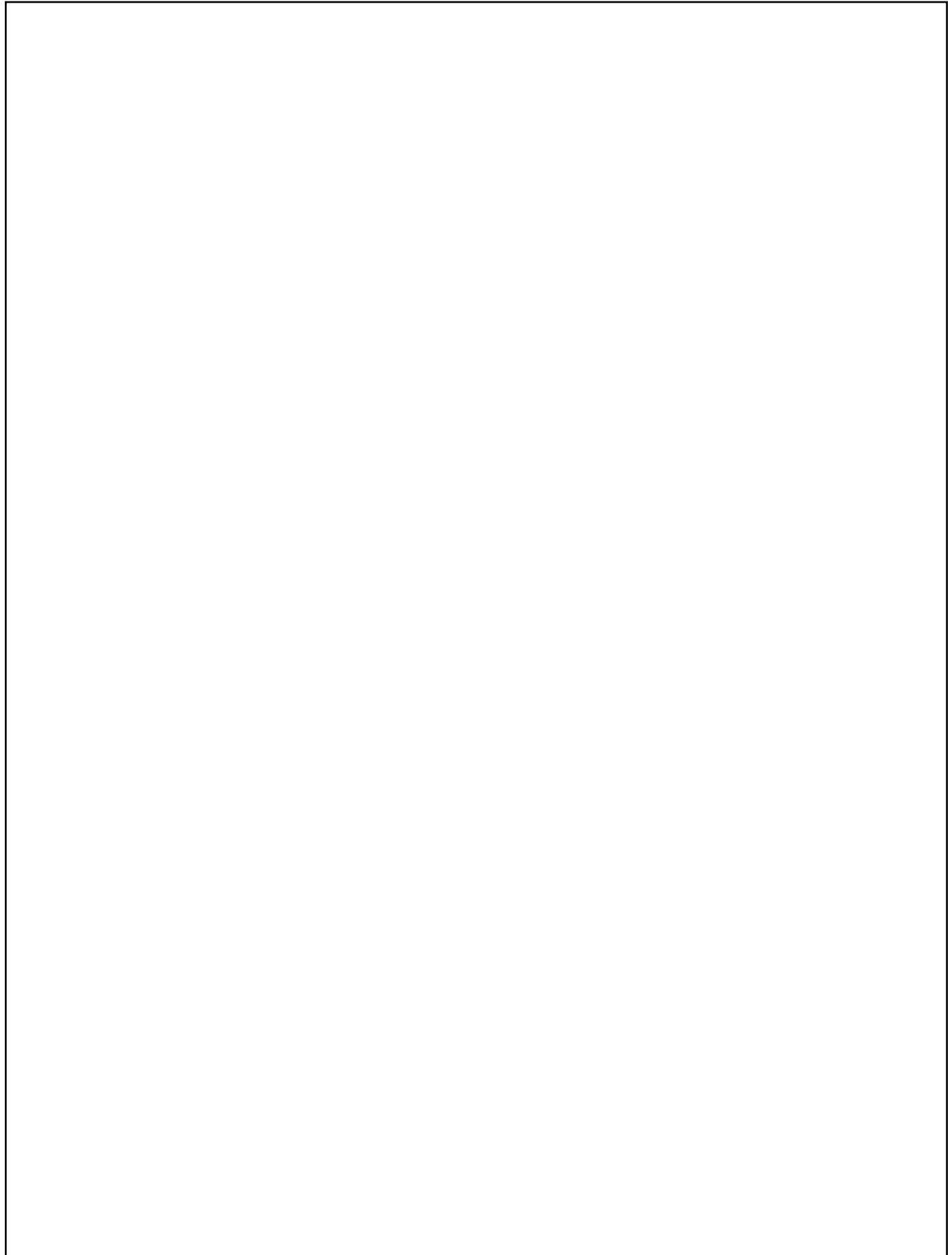
Locus	Parameter	2.5%	25.0%	Mode	75.0%	97.5%	Median	Mean
6	$\Theta_2$	3.34667	4.14667	4.56667	4.90667	5.17333	4.16667	5.36807
6	$M_{1 \rightarrow 2}$	0.000	0.813	1.060	1.507	2.947	1.527	1.540
6	$D_{1 \rightarrow 2}$	0.00000	0.00000	0.31333	0.60000	1.70667	1.63333	1.64083
6	$S_{1 \rightarrow 2}$	1.45333	1.88000	2.06000	2.22667	3.66667	2.59333	2.58037
6	$g_1$	-5.06667	-2.13333	-0.20000	1.86667	4.80000	0.06667	-0.21713
7	$\Theta_1$	1.64000	4.40000	4.94000	5.38667	7.24000	4.98000	5.35538
7	$\Theta_2$	6.22667	6.36000	7.48667	7.94667	8.10667	7.59333	8.93198
7	$M_{1 \rightarrow 2}$	0.267	0.440	0.820	1.173	2.827	3.207	3.462
7	$D_{1 \rightarrow 2}$	0.77333	2.49333	2.96667	3.40000	3.62667	2.55333	2.28157
7	$S_{1 \rightarrow 2}$	1.41333	1.82667	2.40667	2.84000	3.94667	2.56667	2.72622
7	$g_1$	-3.86667	-1.33333	0.60000	2.40000	4.93333	0.73333	0.61233
8	$\Theta_1$	8.73333	8.81333	9.30000	9.72000	9.90667	4.71333	5.62873
8	$\Theta_2$	0.40000	2.10667	4.16667	4.68000	4.94667	4.15333	6.66395
8	$M_{1 \rightarrow 2}$	0.173	0.360	0.780	1.693	2.440	4.100	3.943
8	$D_{1 \rightarrow 2}$	0.00000	0.05333	0.43333	0.78667	2.68000	1.18000	1.31636
8	$S_{1 \rightarrow 2}$	0.65333	0.88000	1.28667	1.64000	4.66667	2.51333	2.57079
8	$g_1$	-4.13333	-1.73333	0.20000	2.00000	4.40000	0.33333	0.23158
9	$\Theta_1$	1.74667	3.32000	3.60667	3.92000	4.89333	3.48667	3.49764
9	$\Theta_2$	0.36000	0.81333	1.39333	1.88000	2.88000	4.76667	6.64425
9	$M_{1 \rightarrow 2}$	0.520	1.733	2.647	3.213	3.320	4.020	5.907
9	$D_{1 \rightarrow 2}$	1.20000	1.70667	2.15333	2.62667	3.48000	2.11333	2.01224
9	$S_{1 \rightarrow 2}$	0.00000	0.13333	0.54000	1.05333	1.73333	2.38000	2.52680
9	$g_1$	-4.26667	-1.86667	0.06667	1.86667	4.13333	0.20000	0.02860
10	$\Theta_1$	1.41333	1.82667	2.30000	2.73333	2.88000	3.64667	3.70170
10	$\Theta_2$	0.30667	1.88000	2.43333	2.96000	4.29333	3.36667	6.92783
10	$M_{1 \rightarrow 2}$	2.440	2.653	3.060	3.853	8.107	5.007	4.969
10	$D_{1 \rightarrow 2}$	0.00000	0.00000	0.19333	0.54667	2.85333	1.04667	1.01289
10	$S_{1 \rightarrow 2}$	1.72000	3.82667	4.23333	4.62667	4.84000	3.76667	3.58304
10	$g_1$	-4.66667	-2.13333	-0.20000	1.60000	4.13333	-0.06667	-0.21024
All	$\Theta_1$	1.56000	2.09333	2.38000	2.64000	2.86667	2.48667	2.90454
All	$\Theta_2$	10.68000	10.93333	11.19333	11.44000	11.69333	11.10000	9.41134
All	$M_{1 \rightarrow 2}$	0.333	2.120	2.500	2.867	3.120	2.327	2.201
All	$D_{1 \rightarrow 2}$	0.00000	0.00000	0.11333	0.24000	0.57333	0.24667	0.15867
All	$S_{1 \rightarrow 2}$	2.42667	2.66667	2.86000	3.04000	3.26667	2.87333	2.85932
All	$g_1$	-4.13333	-1.86667	0.06667	1.86667	4.26667	0.20000	0.06667

Citation suggestions:

- Beerli P., 2006. Comparison of Bayesian and maximum-likelihood inference of population genetic parameters. *Bioinformatics* 22:341-345
- Beerli, P., H. Ashki, S. Mashayekhi, and M. Palczewski, 2022. Population divergence time estimation using individual lineage label switching. *G3 Genes & Genomes & Genetics*, 12(4), 02 2022.
- 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.
- Beerli, P., S. Mashayekhi, M. Sadeghi, M. Khodaei, and K. Shaw, 2019. Population genetic inference with migrate. *Current Protocols in Bioinformatics*, 68(1):e87.

# Bayesian Analysis: Posterior distribution over all loci





## *Log-Probability of the data given the model (marginal likelihood)*

Use this value for Bayes factor calculations:

$BF = \text{Exp}[\ln(\text{Prob}(D \mid \text{thisModel}) - \ln(\text{Prob}(D \mid \text{otherModel}))]$

or as  $LBF = 2 (\ln(\text{Prob}(D \mid \text{thisModel}) - \ln(\text{Prob}(D \mid \text{otherModel})))$

shows the support for thisModel]

Locus	TI(1a)	BTI(1b)	HS(3)
1	-140112.04	-22568.95	-490.85
2	-13782.42	-2248.73	-45.89
3	-319.61	-94.68	-71.19
4	-522.87	-334.77	-1857.85
5	-53.41	-31.80	-26.43
6	-561.49	-189.99	-348.54
7	-1554.27	-279.29	-79.10
8	-234.04	-94.19	-126.01
9	-208.75	-119.91	-247.52
10	-239.78	-85.34	-207.56
All	-157533.48	-25992.47	-3445.74

(1a) TI: Thermodynamic integration:  $\log(\text{Prob}(D \mid \text{Model}))$ : Good approximation with many temperatures

(1b) BTI: Bezier-approximated Thermodynamic integration: when using few temperatures USE THIS!

(3) HS: Harmonic mean approximation: Overestimates the marginal likelihood, poor variance

[Scaling factor = 55.195736]

Citation suggestions:

Beerli P. and M. Palczewski, 2010. Unified framework to evaluate panmixia and migration direction among multiple sampling locations, *Genetics*, 185: 313-326.

Palczewski M. and P. Beerli, 2014. Population model comparison using multi-locus datasets.

In M.-H. Chen, L. Kuo, and P. O. Lewis, editors, *Bayesian Phylogenetics: Methods, Algorithms, and Applications*, pages 187-200. CRC Press, 2014.



*Acceptance ratios for all parameters and the genealogies*

Parameter	Accepted changes	Ratio
$\Theta_1$	351/351	1.00000
$\Theta_2$	330/330	1.00000
$M_{1 \rightarrow 2}$	317/317	1.00000
$\Delta_{1 \rightarrow 2}$	333/353	0.94334
$\sigma_{1 \rightarrow 2}$	304/327	0.92966
$g_1$	25/317	0.07886
Genealogies	943/2005	0.47032

## *MCMC-Autocorrelation and Effective MCMC Sample Size*

Parameter	Autocorrelation	Effective Sample Size
$\Theta_1$	0.93458	136.36
$\Theta_2$	0.92261	161.90
$M_{1 \rightarrow 2}$	0.91389	180.65
$\Delta_{1 \rightarrow 2}$	0.96660	67.96
$\sigma_{1 \rightarrow 2}$	0.95335	95.67
$g_1$	-0.00003	3980.20
Genealogies	0.92028	175.17

*Average temperatures during the run*

Chain	Temperatures
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1	1.00000
2	0.66667
3	0.33333
4	0.00000

## *Potential Problems*

This section reports potential problems with your run, but such reporting is often not very accurate. With many parameters in a multilocus analysis, it is common that some parameters for some loci will not be informative. These parameters then trigger suggestions to increase the prior range that are not sensible. Do not blindly follow the suggestions given. If some parameters are flagged, inspect the tables carefully and judge whether an action is required. Suppose you run a Bayesian inference with sequence data for macroscopic species. In that case, there is rarely the need to increase the prior for Theta beyond 0.1. If you use microsatellites data, it is rather common that your prior distribution for Theta should have a range from 0.0 to 100 or more. With many populations ( $>3$ ), it is also very common that some migration routes are estimated poorly because the data contains little or no information for that route. Increasing the prior range will not help in such situations, but reducing the number of parameters may help.

No warning was recorded during the run