

Example: Microsatellite data set

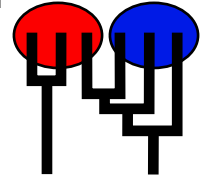
POPULATION SIZE, MIGRATION, DIVERGENCE, ASSIGNMENT, HISTORY

Bayesian inference using the structured coalescent

Migrate-n version 5.0.2(git:v5.0.2-0-gb89fa60-dirty) [December-1-2021]

Program started at Sat Feb 5 10:27:41 2022

Program finished at Sat Feb 5 10:29:38 2022 [Runtime:0000:00:01:57]



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_num	*	0
2 population_num	D	*

1 population_num growing/shrinking

2 population_num growing/shrinking

Order of parameters:

1	Θ_1	<displayed>
2	Θ_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	Slice sampling
Divergence Spread	Slice 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	2.000	1500	0.07143
2 Theta **	Uniform	0.000000	10.00	20.00	2.000	1500	0.07143
3 M **	Uniform	0.000000	10.00	20.00	2.000	1500	0.07143
4 Splittime mean **	Uniform	0.000000	10.00	20.00	2.000	1500	0.07143
5 Splittime std **	Uniform	0.000000	10.00	20.00	2.000	1500	0.07143
6 Growth 00	Uniform	1000.000000	1000.	0.000	100.0	1500	0.07143
7 Growth 00	Uniform	1000.000000	1000.	0.000	100.0	1500	0.07143

[* * means priors were set globally]

Markov chain settings:

Long chain

Number of chains

1

Recorded steps [a]

2000

Increment (record every x step [b])

100

Number of concurrent chains (replicates) [c]	2
Visited (sampled) parameter values [a*b*c]	400000
Number of discard trees per chain (burn-in)	500

Multiple Markov chains:

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
	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 _{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

Bayesian Analysis: Posterior distribution table

Locus	Parameter	2.5%	25.0%	Mode	75.0%	97.5%	Median	Mean
1	Θ_1	7.50667	12.76000	13.26000	13.60000	19.98667	14.00667	13.83287
1	Θ_2	1.60000	5.12000	7.36667	8.01333	14.42667	9.78000	10.07069
1	$M_{1 \rightarrow 2}$	1.520	2.973	5.300	9.653	18.293	9.207	9.760
1	$D_{1 \rightarrow 2}$	18.10667	18.72000	19.24667	19.62667	19.74667	10.04667	10.02460
1	$S_{1 \rightarrow 2}$	0.00000	16.52000	18.22000	18.96000	19.98667	10.10000	10.04018
1	g_1	-22.00000	-10.00000	-0.33333	-0.66667	-0.66667	-8.33333	-15.59372
2	Θ_1	2.28000	4.29333	5.99333	9.40000	15.08000	7.99333	8.60933
2	Θ_2	1.28000	1.92000	3.11333	5.78667	16.17333	9.79333	9.98101
2	$M_{1 \rightarrow 2}$	2.613	6.880	8.313	12.107	19.867	10.540	10.759
2	$D_{1 \rightarrow 2}$	0.38667	2.46667	4.60667	5.81333	8.96000	9.92667	9.91305
2	$S_{1 \rightarrow 2}$	6.68000	18.34667	18.90000	19.49333	19.65333	10.36667	10.18187
2	g_1	-22.00000	-10.00000	-0.33333	-0.66667	-0.66667	-8.33333	-12.01173
3	Θ_1	3.37333	4.34667	7.59333	9.93333	13.68000	8.90000	9.48083
3	Θ_2	0.25333	0.41333	2.22000	6.97333	14.06667	7.38000	8.34118
3	$M_{1 \rightarrow 2}$	0.413	1.400	2.420	4.547	15.120	6.940	8.059
3	$D_{1 \rightarrow 2}$	0.89333	17.24000	17.67333	18.96000	19.74667	10.32667	10.21215
3	$S_{1 \rightarrow 2}$	3.53333	4.04000	4.86000	5.60000	7.64000	10.00667	10.00404
3	g_1	-22.00000	-10.00000	-0.33333	-0.66667	-0.66667	-8.33333	-12.43574
4	Θ_1	8.73333	15.58667	19.38000	19.81333	19.98667	15.74000	15.20864
4	Θ_2	5.16000	6.66667	7.88667	8.50667	12.88000	10.19333	10.42056
4	$M_{1 \rightarrow 2}$	0.000	0.067	0.847	3.560	17.547	3.487	5.332
4	$D_{1 \rightarrow 2}$	0.24000	0.34667	1.75333	2.38667	4.78667	9.82000	9.87331
4	$S_{1 \rightarrow 2}$	10.37333	16.18667	16.99333	18.96000	19.69333	10.26000	10.16822
4	g_1	-22.00000	-10.00000	-0.33333	-0.66667	-0.66667	-8.33333	-17.43387
5	Θ_1	0.22667	1.20000	2.87333	3.93333	10.82667	3.46000	4.20415
5	Θ_2	0.00000	0.06667	0.66000	5.64000	11.37333	5.58000	7.19860
5	$M_{1 \rightarrow 2}$	3.373	12.413	12.913	14.173	19.987	11.393	11.382
5	$D_{1 \rightarrow 2}$	2.65333	3.80000	5.48667	5.94667	6.26667	10.15333	10.06737
5	$S_{1 \rightarrow 2}$	13.72000	18.42667	19.11333	19.64000	19.72000	9.98000	10.04167
5	g_1	-22.00000	-10.00000	-0.33333	-0.66667	-0.66667	-8.33333	-8.02942
6	Θ_1	5.41333	7.48000	12.02000	17.22667	19.76000	12.18000	12.21093

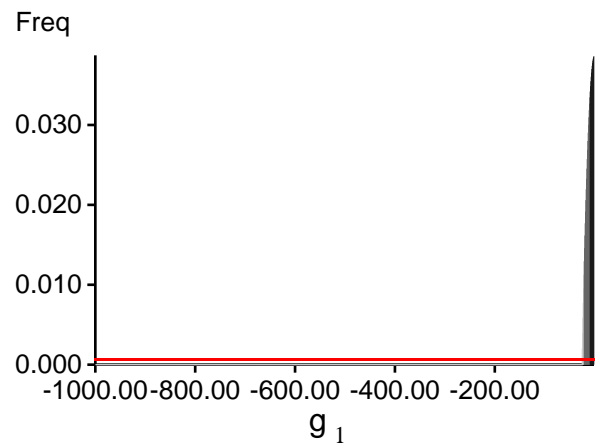
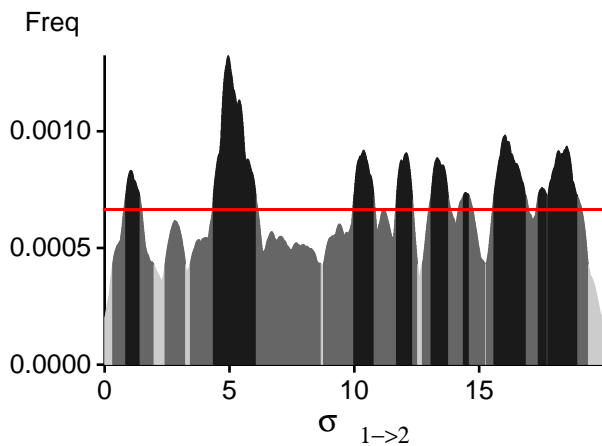
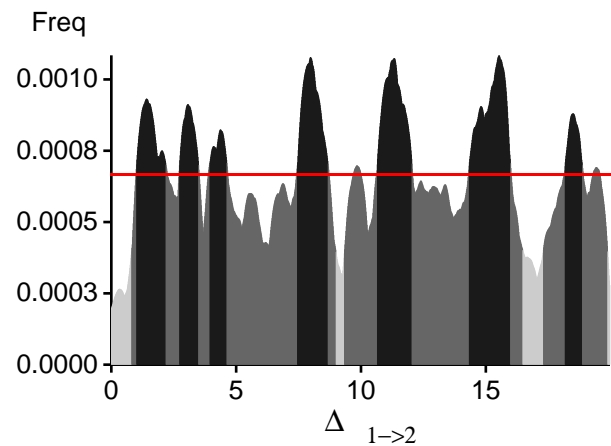
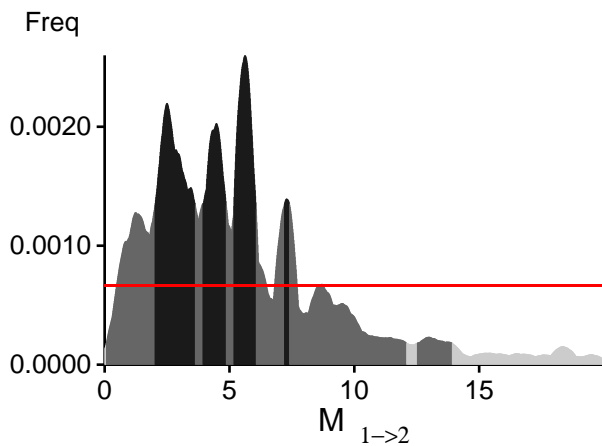
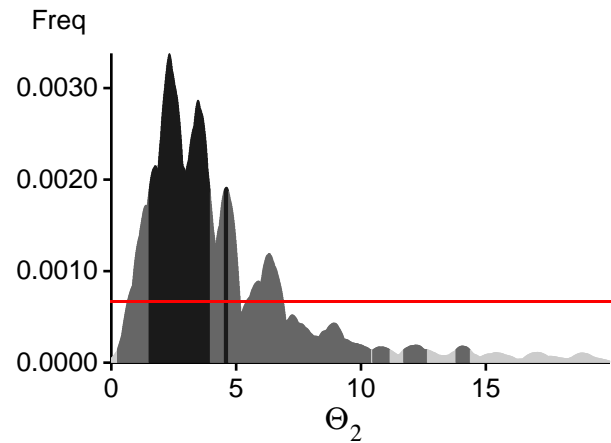
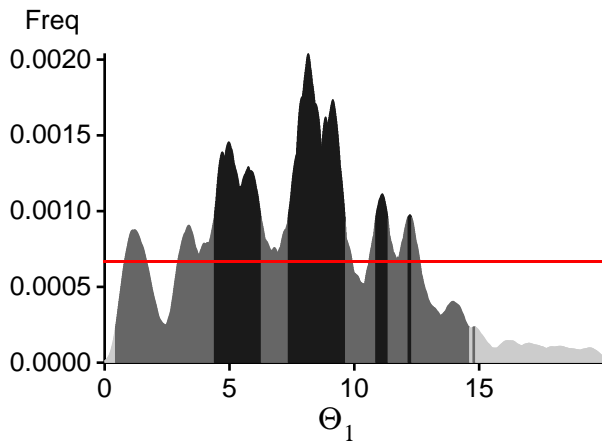
Locus	Parameter	2.5%	25.0%	Mode	75.0%	97.5%	Median	Mean
6	Θ_2	1.65333	2.21333	3.63333	4.32000	18.13333	9.92667	10.10025
6	$M_{1 \rightarrow 2}$	2.493	7.973	9.687	10.867	19.747	10.433	10.625
6	$D_{1 \rightarrow 2}$	17.60000	17.89333	18.44667	19.04000	19.65333	10.11333	10.10107
6	$S_{1 \rightarrow 2}$	0.25333	2.61333	3.06000	3.53333	3.88000	10.20667	10.10235
6	g_1	-22.00000	-10.00000	-0.33333	-0.66667	-0.66667	-8.33333	-14.09214
7	Θ_1	0.00000	0.61333	1.27333	2.77333	8.45333	2.50000	3.33119
7	Θ_2	0.25333	1.12000	2.35333	3.62667	16.86667	6.02000	7.36657
7	$M_{1 \rightarrow 2}$	0.000	0.413	1.127	3.200	13.787	2.967	4.385
7	$D_{1 \rightarrow 2}$	7.88000	11.76000	15.48667	16.06667	16.62667	10.32667	10.18785
7	$S_{1 \rightarrow 2}$	14.04000	14.49333	16.04667	17.17333	18.00000	10.15333	10.08064
7	g_1	-22.00000	-10.00000	-0.33333	-0.66667	-0.66667	-8.33333	-9.09920
8	Θ_1	2.12000	4.38667	7.62000	9.74667	18.28000	8.59333	9.24065
8	Θ_2	0.00000	0.10667	0.84667	6.73333	16.28000	5.94000	7.35921
8	$M_{1 \rightarrow 2}$	1.773	2.080	6.020	7.493	12.667	9.833	10.063
8	$D_{1 \rightarrow 2}$	0.13333	13.45333	15.90000	16.54667	19.72000	10.00667	9.96702
8	$S_{1 \rightarrow 2}$	9.68000	15.33333	16.07333	16.66667	19.66667	10.24667	10.10429
8	g_1	-22.00000	-10.00000	-0.33333	-0.66667	-0.66667	-8.33333	-11.48950
9	Θ_1	3.94667	7.96000	9.14000	11.22667	18.81333	10.70000	11.02888
9	Θ_2	2.14667	18.44000	18.84667	19.28000	19.76000	10.68667	10.72106
9	$M_{1 \rightarrow 2}$	2.573	8.640	9.753	14.053	19.800	10.513	10.605
9	$D_{1 \rightarrow 2}$	2.32000	6.74667	7.52667	8.17333	14.57333	10.11333	10.08344
9	$S_{1 \rightarrow 2}$	14.56000	15.53333	16.18000	16.80000	18.68000	10.00667	10.04206
9	g_1	-22.00000	-10.00000	-0.33333	-0.66667	-0.66667	-8.33333	-13.48132
10	Θ_1	3.34667	5.13333	7.95333	10.33333	12.85333	9.12667	9.63671
10	Θ_2	1.57333	5.62667	6.42000	7.76000	11.33333	9.96667	10.25915
10	$M_{1 \rightarrow 2}$	0.467	0.773	4.180	9.200	18.267	8.500	9.048
10	$D_{1 \rightarrow 2}$	0.00000	12.97333	13.48667	13.89333	19.98667	10.14000	10.01918
10	$S_{1 \rightarrow 2}$	18.05333	18.90667	19.31333	19.61333	19.68000	9.98000	10.01656
10	g_1	-22.00000	-10.00000	-0.33333	-0.66667	-0.66667	-8.33333	-13.01780
All	Θ_1	0.41333	7.33333	8.15333	9.64000	14.61333	7.92667	7.82080
All	Θ_2	0.22667	1.49333	2.32667	3.96000	10.41333	3.56667	4.62305
All	$M_{1 \rightarrow 2}$	0.053	5.160	5.620	6.067	12.093	4.820	5.523
All	$D_{1 \rightarrow 2}$	9.32000	14.32000	15.52667	15.98667	16.48000	10.31333	10.05179
All	$S_{1 \rightarrow 2}$	3.41333	4.33333	4.95333	6.06667	8.66667	10.51333	10.27185
All	g_1	-22.00000	-10.00000	-0.33333	-0.66667	-0.66667	-8.33333	-0.33333

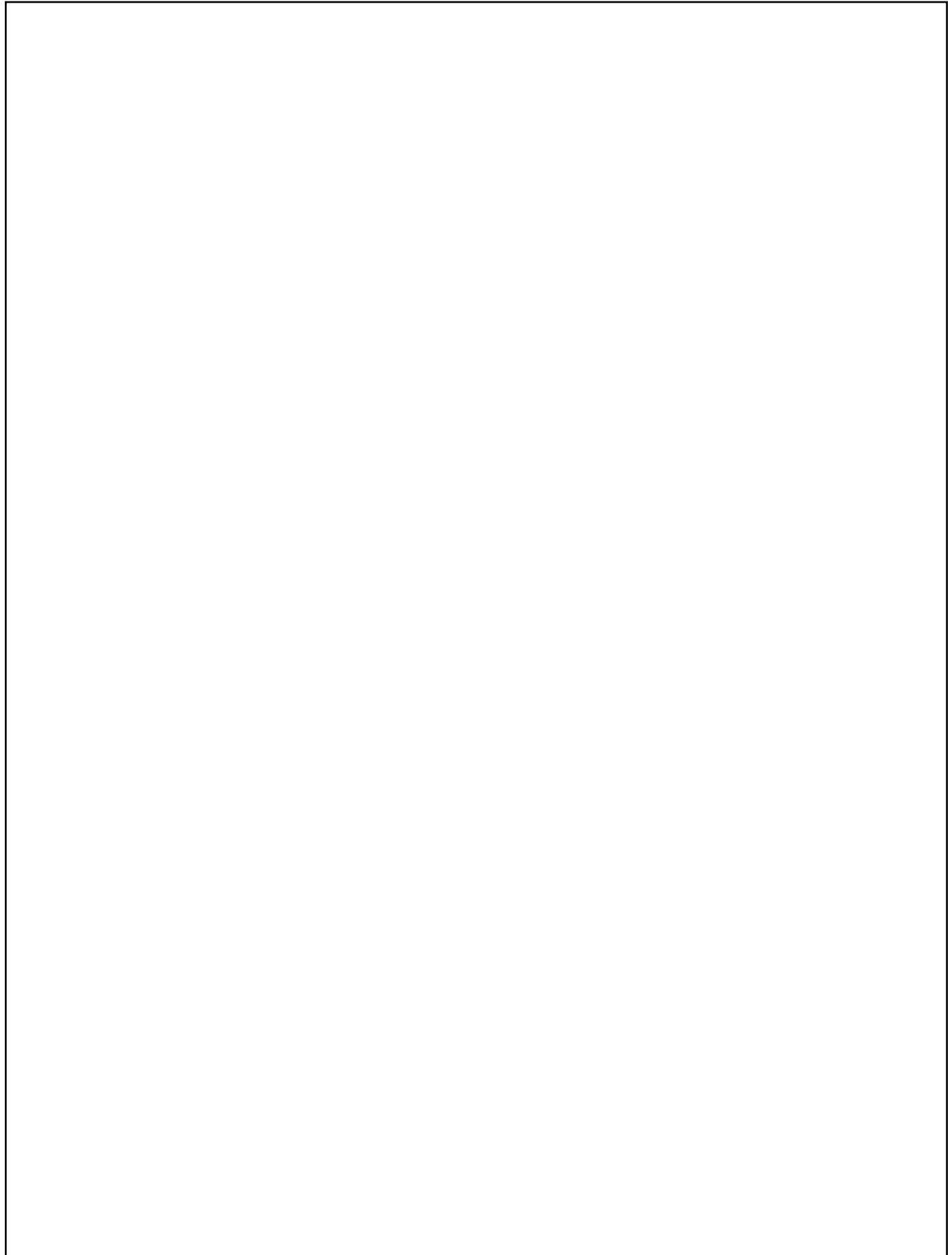
Citation suggestions:

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.

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	-123384.28	-19780.98	-39.01
2	-44840.82	-7201.61	-31.84
3	-54237.26	-8707.47	-32.15
4	-167069.36	-26778.85	-44.21
5	-26886.60	-4322.05	-22.74
6	-119186.45	-19108.31	-36.60
7	-36545.11	-5870.58	-24.81
8	-72804.41	-11679.03	-31.32
9	-83670.73	-13421.69	-35.25
10	-52979.62	-8507.28	-34.11
All	-781555.08	-125328.29	-282.49

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

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

(2) SS: Steppingstone Sampling (Xie et al 2011)

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

[Scaling factor = 49.556466]

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.

Xie W., P. O. Lewis, Y. Fan, L. Kuo, and M.-H. Chen. 2011. Improving marginal likelihood estimation for Bayesian phylogenetic model selection. *Systematic Biology*, 60(2):150â 160, 2011.

Acceptance ratios for all parameters and the genealogies

Parameter	Accepted changes	Ratio
Θ_1	333427/333427	1.00000
Θ_2	333192/333192	1.00000
$M_{1 \rightarrow 2}$	332637/332637	1.00000
$\Delta_{1 \rightarrow 2}$	324150/333625	0.97160
$\sigma_{1 \rightarrow 2}$	325218/333640	0.97476
g_1	38519/333659	0.11544
Genealogies	910024/1999820	0.45505

MCMC-Autocorrelation and Effective MCMC Sample Size

Parameter	Autocorrelation	Effective Sample Size
Θ_1	0.45231	15212.09
Θ_2	0.16071	29089.75
$M_{1 \rightarrow 2}$	0.56490	11306.44
$\Delta_{1 \rightarrow 2}$	0.06214	35332.11
$\sigma_{1 \rightarrow 2}$	0.05246	36036.23
g_1	-0.00000	39980.02
Genealogies	0.51590	12887.11

Average temperatures during the run

Chain	Temperatures
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1	1.00000
2	1.50000
3	3.00000
4	1000000.00000

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

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 very common that some parameters for some loci will not be very informative, triggering suggestions (for example to increase the prior range) that are not sensible. This suggestion tool will improve with time, therefore do not blindly follow its suggestions. If some parameters are flagged, inspect the tables carefully and judge whether an action is required. For example, if you run a Bayesian inference with sequence data, for macroscopic species there is rarely the need to increase the prior for Theta beyond 0.1; but if you use microsatellites 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 range will not help in such situations, reducing number of parameters may help in such situations.

Param 5 (Locus 1): Upper prior boundary seems too low!
 Param 6 (Locus 1): Upper prior boundary seems too low!
 Param 6 (Locus 2): Upper prior boundary seems too low!
 Param 5 (Locus 3): Upper prior boundary seems too low!
 Param 6 (Locus 4): Upper prior boundary seems too low!
 Param 6 (Locus 5): Upper prior boundary seems too low!
 Param 5 (Locus 6): Upper prior boundary seems too low!
 Param 6 (Locus 10): Upper prior boundary seems too low!