taita trush dataset from structure (pritchard et

POPULATION SIZE, MIGRATION, DIVERGENCE, ASSIGNMENT, HISTORY
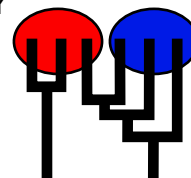Bayesian inference using the structured coalescent
Migrate-n version 5.0.2(git:v5.0.2-0-gb89fa60-dirty) [December-1-2021]
  Compiled for PARALLEL computer architectures
  One master and 7 compute nodes are available.
Program started at   Sat Feb 12 23:41:42 2022
Program finished at   Sat Feb 12 23:43:46 2022 [Runtime:0000:00:02:04]

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

| Random number seed: | (with internal timer) | 919064965 |

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	3	4
1 C	*	0	0	d
2 M	0	*	0	d
3 N	0	0	*	d
4 ancestor	0	0	0	*

Order of parameters:

1	Θ_1	\<displayed\>
2	Θ_2	\<displayed\>
3	Θ_3	\<displayed\>
4	Θ_4	\<displayed\>
5	$\Delta_{4->1}$	\<displayed\>
6	$\sigma_{4->1}$	\<displayed\>
7	$\Delta_{4->2}$	\<displayed\>
8	$\sigma_{4->2}$	\<displayed\>
9	$\Delta_{4->3}$	\<displayed\>
10	$\sigma_{4->3}$	\<displayed\>

Mutation rate among loci: Mutation rate is constant for all loci

Analysis strategy: Bayesian inference
 -Population size estimation: Exponential Distribution
 -Geneflow estimation: Exponential Distribution
 -Divergence time estimation: Normal Distribution (mean and standard dev.)

 Proposal distributions for parameter

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

 Prior distribution for parameter

Parameter			Prior	Minimum	Mean	Maximum	Delta	Bins	UpdateFreq
1	Theta	**	Uniform	0.000000	50.00	100.0	10.00	1500	0.03333
2	Theta	**	Uniform	0.000000	50.00	100.0	10.00	1500	0.03333
3	Theta	**	Uniform	0.000000	50.00	100.0	10.00	1500	0.03333
4	Theta	**	Uniform	0.000000	50.00	100.0	10.00	1500	0.03333
5	Splittime mean	30	Uniform	0.000000	0.010	100.0	10.00	1500	0.03333
6	Splittime std	30	Uniform	0.000000	0.010	100.0	10.00	1500	0.03333
7	Splittime mean	31	Uniform	0.000000	0.010	100.0	10.00	1500	0.03333
8	Splittime std	31	Uniform	0.000000	0.010	100.0	10.00	1500	0.03333
9	Splittime mean	32	Uniform	0.000000	0.010	100.0	10.00	1500	0.03333
10	Splittime std	32	Uniform	0.000000	0.010	100.0	10.00	1500	0.03333

[* * means priors were set globally]

Markov chain settings: Long chain
Number of chains   1
   Recorded steps [a]   10000
   Increment (record every x step [b]   100
   Number of concurrent chains (replicates) [c]   2
   Visited (sampled) parameter values [a*b*c]   2000000
   Number of discard trees per chain (burn-in)   1000

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.assign
      parmfile.taita.assign
   Haplotyping is turned on: NO
   Output file: outfile-assign
   Posterior distribution raw histogram file: bayesfile
   Raw data from the MCMC run: bayesallfile.gz
   Print data: No
   Print genealogies [only some for some data type]:   None

Data summary

Data file: infile.assign
Datatype: Microsatellite data [Brownian]
                                                           [Data was used as repeat-length information]
Number of loci: 7

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]

Population	Locus	Gene copies data	(missing)
1 C	1	12	(0)
	2	12	(0)
	3	12	(0)
	4	12	(0)
	5	9	(3)
	6	12	(0)
	7	12	(0)
2 M	1	10	(2)
	2	12	(0)
	3	12	(0)
	4	12	(0)
	5	11	(1)
	6	12	(0)
	7	12	(0)
3 N	1	12	(0)
	2	12	(0)
	3	12	(0)
	4	12	(0)
	5	7	(5)
	6	12	(0)
	7	12	(0)
4 ancestor	1	0	(0)

2	0	(0)
3	0	(0)
4	0	(0)
5	0	(0)
6	0	(0)
7	0	(0)

Total of all populations

1	34	(2)
2	36	(0)
3	36	(0)
4	36	(0)
5	27	(9)
6	36	(0)
7	36	(0)

Allele frequency spectra

Locus 1

Allele	Pop1	Pop2	Pop3	Pop4	All
3	0.083	-	-	-	0.029
18	0.083	-	-	-	0.029
4	0.500	0.500	0.250	-	0.412
7	0.083	0.100	0.167	-	0.118
12	0.083	0.100	0.167	-	0.118
2	0.083	-	0.083	-	0.059
15	0.083	-	-	-	0.029
1	-	0.100	-	-	0.029
13	-	0.200	-	-	0.059
11	-	-	0.250	-	0.088
19	-	-	0.083	-	0.029
Alleles	7	5	6	0	11
Samplesize	12	10	12	0	34
H_{exp}	0.708	0.680	0.806	nan	0.784

Locus 2

Allele	Pop1	Pop2	Pop3	Pop4	All
4	0.083	-	-	-	0.028
5	0.083	0.083	0.167	-	0.111
3	0.583	0.500	0.167	-	0.417
1	0.167	0.167	0.167	-	0.167
2	0.083	0.250	0.500	-	0.278
Alleles	5	4	4	0	5
Samplesize	12	12	12	0	36
H_{exp}	0.611	0.653	0.667	nan	0.708

Locus 3

Allele	Pop1	Pop2	Pop3	Pop4	All
3	0.083	-	0.250	-	0.111
5	0.083	-	0.083	-	0.056
6	0.750	0.667	0.333	-	0.583
1	0.083	0.250	0.250	-	0.194
4	-	0.083	0.083	-	0.056
Alleles	4	3	5	0	5
Samplesize	12	12	12	0	36

Allele	Pop1	Pop2	Pop3	Pop4	All
H_{exp}	0.417	0.486	0.750	nan	0.603

Locus 4

Allele	Pop1	Pop2	Pop3	Pop4	All
1	0.583	0.667	0.750	-	0.667
3	0.167	0.167	0.167	-	0.167
2	0.250	0.167	0.083	-	0.167
Alleles	3	3	3	0	3
Samplesize	12	12	12	0	36
H_{exp}	0.569	0.500	0.403	nan	0.500

Locus 5

Allele	Pop1	Pop2	Pop3	Pop4	All
2	0.889	0.909	0.714	-	0.852
3	0.111	0.091	0.143	-	0.111
1	-	-	0.143	-	0.037
Alleles	2	2	3	0	3
Samplesize	9	11	7	0	27
H_{exp}	0.198	0.165	0.449	nan	0.261

Locus 6

Allele	Pop1	Pop2	Pop3	Pop4	All
6	0.083	-	0.083	-	0.056
10	0.167	0.083	-	-	0.083
2	0.583	0.667	0.250	-	0.500
3	0.083	0.083	0.250	-	0.139
4	0.083	0.083	0.083	-	0.083
1	-	0.083	0.083	-	0.056
7	-	-	0.083	-	0.028
9	-	-	0.083	-	0.028
8	-	-	0.083	-	0.028
Alleles	5	5	8	0	9
Samplesize	12	12	12	0	36
H_{exp}	0.611	0.528	0.833	nan	0.708

Locus 7

Allele	Pop1	Pop2	Pop3	Pop4	All
2	0.083	-	0.167	-	0.083
6	0.250	0.083	0.250	-	0.194

Allele	Pop1	Pop2	Pop3	Pop4	All
5	0.583	0.500	0.167	-	0.417
1	0.083	0.167	0.167	-	0.139
8	-	0.083	0.083	-	0.056
4	-	0.167	0.167	-	0.111
Alleles	4	5	6	0	6
Samplesize	12	12	12	0	36
H_{exp}	0.583	0.681	0.819	nan	0.747

Average expected heterozygosity

	Pop1	Pop2	Pop3	Pop4	All
H_{exp}	0.528	0.528	0.675	nan	0.616

Bayesian Analysis: Posterior distribution table

Locus	Parameter	2.5%	25.0%	Mode	75.0%	97.5%	Median	Mean
1	Θ_1	27.40000	61.33333	75.63333	80.13333	99.66667	64.50000	63.80167
1	Θ_2	12.06667	22.73333	42.30000	57.40000	94.73333	47.96667	50.39098
1	Θ_3	24.73333	50.93333	65.23333	86.00000	99.66667	63.10000	62.40712
1	Θ_4	6.53333	16.80000	30.16667	54.53333	93.06667	45.16667	47.70649
1	$D_{4->1}$	1.00000	2.13333	13.90000	39.40000	89.06667	44.23333	46.12454
1	$S_{4->1}$	13.26667	75.06667	81.56667	89.06667	99.33333	56.96667	56.56086
1	$D_{4->2}$	1.40000	14.93333	20.30000	51.40000	94.20000	45.43333	47.05286
1	$S_{4->2}$	9.86667	62.66667	75.50000	97.66667	99.13333	55.36667	54.66321
1	$D_{4->3}$	0.66667	2.00000	19.23333	41.40000	92.53333	41.63333	44.39694
1	$S_{4->3}$	13.33333	75.86667	81.50000	96.93333	99.46667	58.03333	57.29692
2	Θ_1	0.00000	2.40000	6.63333	14.60000	51.66667	13.23333	18.11288
2	Θ_2	0.00000	3.33333	6.83333	14.66667	44.66667	13.10000	16.87195
2	Θ_3	0.00000	2.46667	5.96667	13.93333	54.86667	12.63333	18.18570
2	Θ_4	0.00000	0.80000	3.70000	35.60000	89.66667	34.96667	39.28609
2	$D_{4->1}$	2.20000	15.86667	28.23333	47.73333	90.06667	48.96667	49.31379
2	$S_{4->1}$	5.93333	36.00000	45.30000	58.66667	98.40000	51.63333	51.62568
2	$D_{4->2}$	1.86667	16.60000	31.03333	40.66667	95.13333	48.90000	49.10817
2	$S_{4->2}$	5.66667	46.40000	50.16667	55.40000	98.40000	51.70000	51.64185
2	$D_{4->3}$	1.93333	6.33333	33.90000	49.26667	90.80000	47.10000	48.26352
2	$S_{4->3}$	8.00000	53.40000	61.90000	72.40000	98.20000	51.63333	51.38389
3	Θ_1	0.00000	1.13333	3.16667	5.86667	21.60000	5.03333	6.86507
3	Θ_2	0.00000	1.20000	3.63333	7.13333	27.26667	6.36667	8.85226
3	Θ_3	0.26667	3.40000	7.63333	19.80000	72.13333	18.30000	25.53206
3	Θ_4	0.00000	0.53333	3.76667	33.66667	85.60000	33.23333	38.06944
3	$D_{4->1}$	1.93333	24.66667	44.50000	49.26667	89.06667	49.30000	49.42389
3	$S_{4->1}$	8.53333	61.13333	64.56667	68.93333	98.00000	50.96667	50.90132
3	$D_{4->2}$	1.33333	1.73333	4.30000	36.46667	85.00000	46.63333	47.48744
3	$S_{4->2}$	5.33333	32.53333	35.83333	65.60000	98.06667	50.36667	50.51581
3	$D_{4->3}$	1.86667	19.26667	22.76667	30.00000	84.33333	48.03333	48.57096
3	$S_{4->3}$	4.80000	73.13333	79.96667	83.66667	98.00000	51.30000	51.00898
4	Θ_1	0.00000	1.00000	3.30000	6.86667	22.40000	6.10000	7.94495
4	Θ_2	0.00000	1.00000	2.90000	5.26667	17.40000	4.56667	5.66555
4	Θ_3	0.00000	0.86667	2.56667	4.66667	14.80000	4.03333	4.76520

Locus	Parameter	2.5%	25.0%	Mode	75.0%	97.5%	Median	Mean
4	Θ_4	0.00000	0.66667	3.63333	36.60000	90.93333	36.03333	40.17967
4	$D_{4\to1}$	2.26667	8.46667	27.56667	37.40000	82.20000	48.90000	49.32101
4	$S_{4\to1}$	7.86667	78.53333	93.76667	96.66667	97.53333	50.43333	50.42471
4	$D_{4\to2}$	2.40000	46.66667	50.63333	57.33333	94.73333	48.30000	48.68359
4	$S_{4\to2}$	4.73333	41.33333	54.43333	58.86667	97.86667	51.03333	50.67224
4	$D_{4\to3}$	1.60000	2.46667	5.03333	21.73333	88.00000	47.03333	47.91818
4	$S_{4\to3}$	4.86667	29.26667	41.90000	47.46667	97.93333	50.03333	50.43709
5	Θ_1	0.00000	0.66667	2.30000	4.26667	15.26667	3.76667	4.44859
5	Θ_2	0.00000	0.73333	2.03333	3.26667	7.40000	2.70000	2.33908
5	Θ_3	0.00000	1.20000	4.10000	9.13333	42.80000	8.30000	12.81575
5	Θ_4	0.66667	2.20000	16.90000	37.80000	88.80000	38.16667	42.18910
5	$D_{4\to1}$	2.86667	25.26667	40.56667	56.73333	90.86667	48.76667	49.27541
5	$S_{4\to1}$	6.80000	64.53333	67.83333	71.86667	98.46667	52.10000	51.99491
5	$D_{4\to2}$	1.33333	3.20000	8.90000	36.80000	92.20000	46.70000	47.55789
5	$S_{4\to2}$	6.80000	66.60000	77.63333	97.00000	98.66667	52.70000	52.39307
5	$D_{4\to3}$	2.66667	29.33333	37.16667	46.06667	95.66667	49.30000	49.48789
5	$S_{4\to3}$	7.00000	58.66667	62.76667	65.73333	98.60000	52.16667	52.14773
6	Θ_1	3.40000	10.46667	19.76667	37.66667	84.73333	33.30000	37.85264
6	Θ_2	0.80000	5.26667	9.83333	22.33333	60.73333	20.03333	24.66096
6	Θ_3	12.33333	21.33333	29.56667	54.66667	93.80000	47.30000	49.88206
6	Θ_4	1.60000	6.66667	18.76667	42.26667	90.66667	38.10000	42.01122
6	$D_{4\to1}$	1.33333	2.46667	24.50000	46.86667	94.20000	45.96667	47.29336
6	$S_{4\to1}$	9.40000	42.60000	49.76667	54.33333	99.20000	54.23333	54.21051
6	$D_{4\to2}$	0.80000	2.26667	8.10000	43.06667	91.20000	42.50000	44.86557
6	$S_{4\to2}$	9.13333	62.06667	83.23333	97.33333	99.13333	55.56667	54.61670
6	$D_{4\to3}$	1.80000	5.53333	32.56667	41.73333	94.46667	46.56667	47.65316
6	$S_{4\to3}$	8.06667	65.26667	80.43333	96.80000	99.00000	53.90000	53.41243
7	Θ_1	0.00000	3.20000	10.03333	22.80000	70.53333	21.16667	26.86479
7	Θ_2	3.06667	8.80000	18.23333	33.13333	79.73333	29.63333	34.74170
7	Θ_3	7.13333	14.66667	30.16667	46.86667	90.20000	41.10000	44.44450
7	Θ_4	0.86667	4.13333	10.43333	38.46667	82.00000	35.83333	40.39867
7	$D_{4\to1}$	1.46667	13.13333	24.03333	51.20000	94.13333	46.36667	47.43514
7	$S_{4\to1}$	8.13333	67.00000	78.90000	97.73333	99.00000	54.03333	53.42837
7	$D_{4\to2}$	1.86667	26.66667	36.70000	55.53333	86.93333	48.03333	48.65451
7	$S_{4\to2}$	8.00000	81.73333	94.23333	97.33333	99.00000	53.96667	53.41676
7	$D_{4\to3}$	2.00000	39.00000	45.16667	49.33333	93.66667	47.56667	48.55282
7	$S_{4\to3}$	7.80000	40.20000	42.36667	56.33333	98.60000	53.23333	53.04913

|								
All	Θ_1	0.40000	1.93333	2.96667	3.93333	5.46667	3.10000	3.12542
All	Θ_2	2.40000	4.93333	6.50000	8.06667	11.93333	6.90000	7.06436
All	Θ_3	5.33333	9.40000	11.70000	15.80000	27.40000	13.83333	14.94474
All	Θ_4	2.00000	8.86667	17.63333	23.33333	45.73333	19.23333	21.30078
All	$D_{4->1}$	1.20000	11.86667	26.83333	39.93333	86.73333	37.10000	40.49427
All	$S_{4->1}$	22.00000	76.40000	94.56667	97.13333	98.66667	61.10000	60.20047
All	$D_{4->2}$	0.86667	5.86667	19.70000	36.20000	82.93333	32.70000	36.92010
All	$S_{4->2}$	18.46667	65.06667	69.36667	78.66667	98.80000	62.10000	60.10014
All	$D_{4->3}$	1.00000	9.26667	33.23333	41.00000	82.93333	34.83333	37.96066
All	$S_{4->3}$	20.66667	74.60000	80.23333	84.80000	98.60000	61.03333	60.24782

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

Freq

$\Delta_{4\to2}$

Freq

$\sigma_{4\to2}$

Freq

$\Delta_{4\to3}$

Freq

$\sigma_{4\to3}$
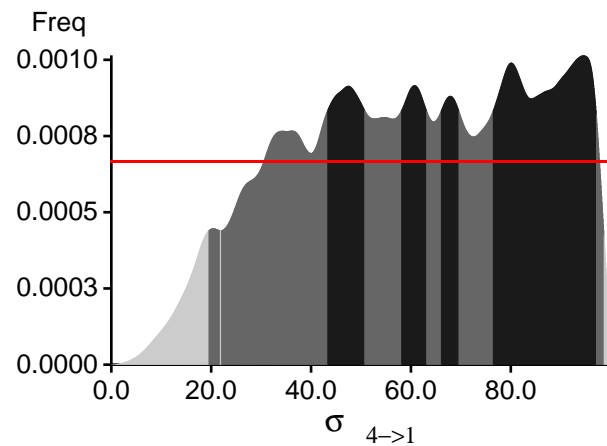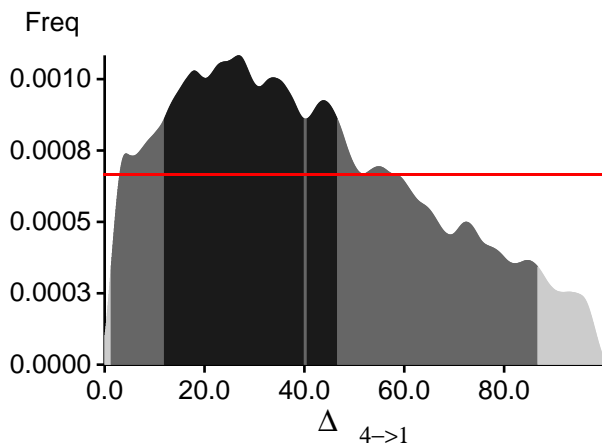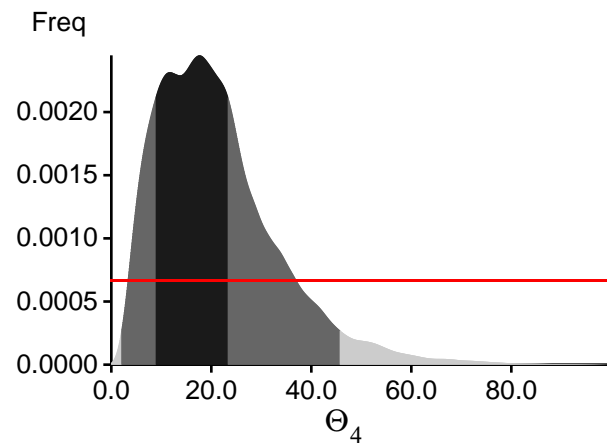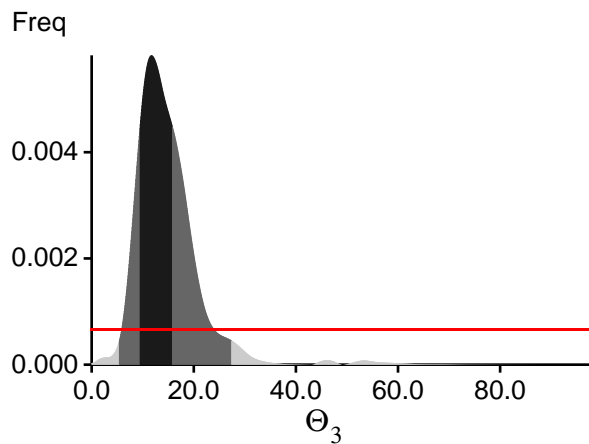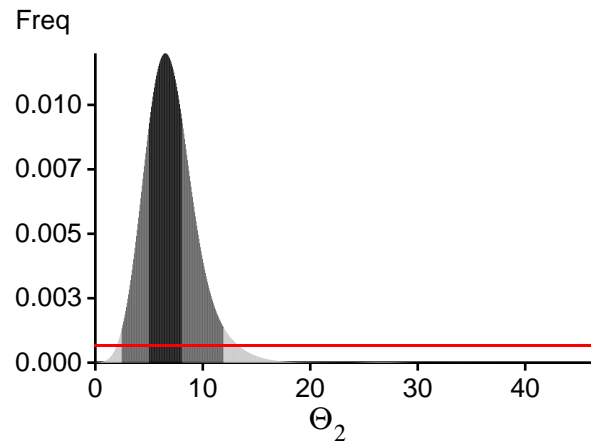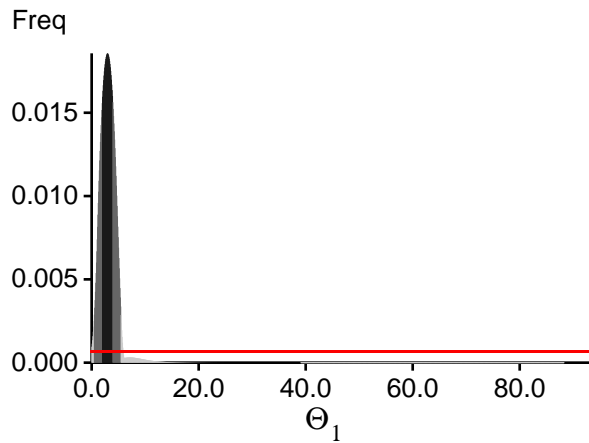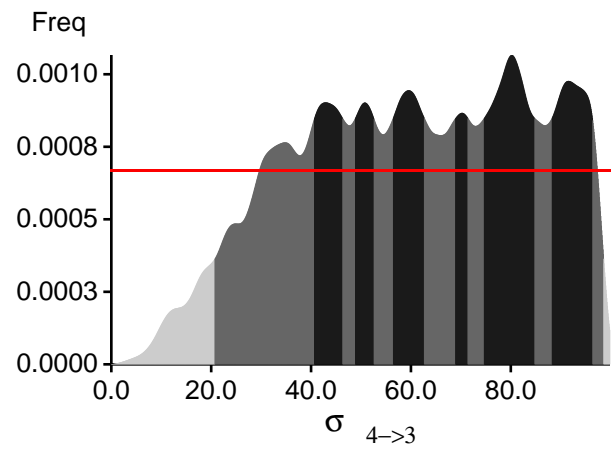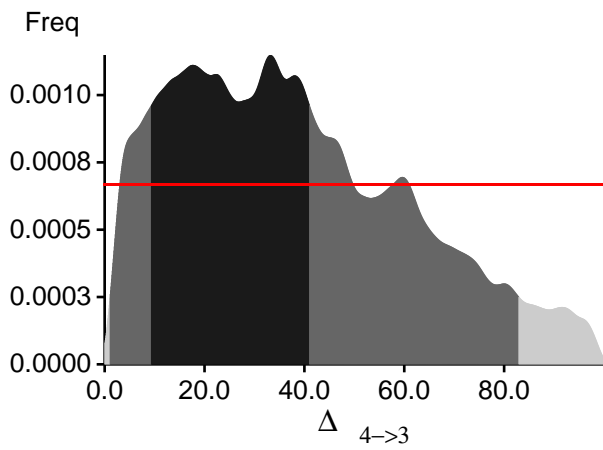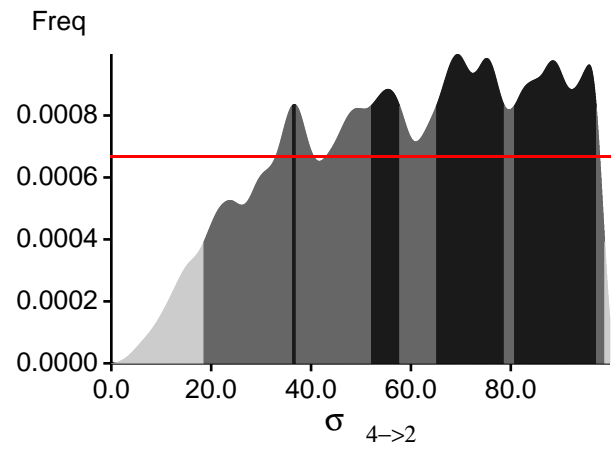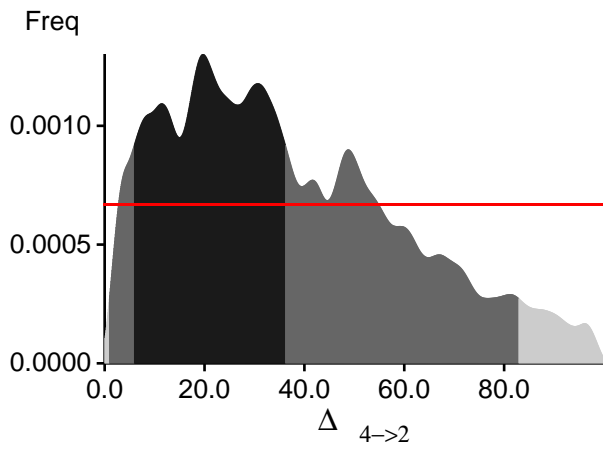
Log-Probability of the data given the model (marginal likelihood)

Use this value for Bayes factor calculations:

BF = Exp[ln(Prob(D | thisModel) - ln(Prob(D | otherModel)

or as LBF = 2 (ln(Prob(D | thisModel) - ln(Prob(D | otherModel))

shows the support for thisModel]

Locus	TI(1a)	BTI(1b)	HS(3)
1	-551.49	-164.79	-88.77
2	-125.56	-79.05	-70.01
3	-152.31	-84.15	-67.48
4	-82.01	-63.46	-56.14
5	-42.80	-41.16	-44.63
6	-230.79	-104.86	-81.55
7	-179.04	-95.19	-80.05
All	-1383.25	-651.91	-507.89

(1a) TI: Thermodynamic integration: log(Prob(D|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 = -19.252720]

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	250271/466775	0.53617
Θ_2	234645/466087	0.50344
Θ_3	239058/467179	0.51171
Θ_4	289257/467610	0.61859
$\Delta_{4->1}$	384631/467488	0.82276
$\sigma_{4->1}$	378614/466999	0.81074
$\Delta_{4->2}$	381539/466712	0.81750
$\sigma_{4->2}$	376784/466607	0.80750
$\Delta_{4->3}$	379019/466296	0.81283
$\sigma_{4->3}$	373653/467167	0.79983
Genealogies	4450298/9331080	0.47693

MCMC-Autocorrelation and Effective MCMC Sample Size

Parameter	Autocorrelation	Effective Sampe Size
Θ_1	0.83025	14008.55
Θ_2	0.84392	12380.43
Θ_3	0.79726	16564.98
Θ_4	0.68002	26823.22
$\Delta_{4\rightarrow1}$	0.54008	42308.48
$\sigma_{4\rightarrow1}$	0.52718	43873.30
$\Delta_{4\rightarrow2}$	0.53810	42492.06
$\sigma_{4\rightarrow2}$	0.52837	43644.55
$\Delta_{4\rightarrow3}$	0.54790	41341.81
$\sigma_{4\rightarrow3}$	0.53262	43107.23
Genealogies	0.83025	14008.55

Average temperatures during the run

Chain	Temperatures
1	0.00000
2	0.00000
3	0.00000
4	0.00000

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. Whith many parameters in a multilocus analysi   s, it is very common that some parameters for some loci will not be very informative, triggering suggestions (for example to increase the prior ran   ge) that are not sensible. This suggestion tool will improve with time, therefore do not blindly follow its suggestions. If some parameters are fla gged, inspect the tables carefully and judge wether an action is required. For example, if you run a Bayesian inference with sequence data, for mac   roscopic 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 rou tes 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 20 (Locus 1): Upper prior boundary seems too low!
Param 22 (Locus 1): Upper prior boundary seems too low!
Param 18 (Locus 4): Upper prior boundary seems too low!
Param 20 (Locus 5): Upper prior boundary seems too low!
Param 20 (Locus 6): Upper prior boundary seems too low!
Param 22 (Locus 6): Upper prior boundary seems too low!
Param 18 (Locus 7): Upper prior boundary seems too low!
Param 20 (Locus 7): Upper prior boundary seems too low!
Param 18 (all loci): Upper prior boundary seems too low!

Summary Assignment of Individuals to Populations

Individual	Population			
	1	2	3	4
?63	0.251	0.631	0.116	0.002

Detailed Assignment of Individuals to Populations

Individual	Locus	Population 1	2	3	4
?63	1	0.284	0.319	0.216	0.181
?63	2	0.267	0.309	0.289	0.135
?63	3	0.209	0.366	0.275	0.150
?63	4	0.302	0.306	0.292	0.100
?63	5	0.326	0.334	0.270	0.069
?63	6	0.279	0.305	0.207	0.209
?63	7	0.313	0.303	0.224	0.159
?63	All	0.251	0.631	0.116	0.002