AUTO

POPULATION SIZE, MIGRATION, DIVERGENCE, ASSIGNMENT, HISTORY

Bayesian inference using the structured coalescent

Migrate-n version 5.0.0a [May-20-2017]

Using Intel AVX (Advanced Vector Extensions)

Compiled for PARALLEL computer architectures

One master and 100 compute nodes are available.

Program started at Sun Aug 13 09:22:42 2017

Program finished at Sun Aug 13 13:17:13 2017 [Runtime:0000:03:54:31]



Options

Datatype: DNA sequence data

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: (with internal timer) 2012323978

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

1

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

Population

1 Romanshorn 0 '

Order of parameters:

1 Θ_1 <displayed>

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

Analysis strategy: Bayesian inference

Exponential Distribution -Population size estimation:

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 Delta Prior Minimum Mean Maximum Bins UpdateFreq Theta -11 Uniform 0.000000 0.050 0.100 0.010 1500 0.20000

[-1 -1 means priors were set globally]

Markov chain settings: Long chain

Number of chains 50000 Recorded steps [a] 200 Increment (record every x step [b] Number of concurrent chains (replicates) [c]

20000000 Visited (sampled) parameter values [a*b*c] 10000 Number of discard trees per chain (burn-in)

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.0.8

Haplotyping is turned on: NO

Output file: outfile_0.8_0.4

Posterior distribution raw histogram file: bayesfile

bayesallfile_0.8_0.4 Print data: No

Print genealogies [only some for some data type]: None

Raw data from the MCMC run:

Data summary

Data file: infile.0.8
Datatype: Sequence data
Number of loci: 100

Mutation	model:			
Locus S		Mutationmodel	Mutationmodel parameters	
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1	1	Jukes-Cantor	[Basefreq: =0.25]	
2	1	Jukes-Cantor	[Basefreq: =0.25]	
3	1	Jukes-Cantor	[Basefreq: =0.25]	
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[Basefreq: =0.25]

Jukes-Cantor

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1	1 1	1.000	1.000	1.000	
2	1 1	1.000	1.000	1.000	
3	1 1	1.000	1.000	1.000	
4	1 1	1.000	1.000	1.000	
5	1 1	1.000	1.000	1.000	
6	1 1	1.000	1.000	1.000	

7	1	1	1.000	1.000	1.000	
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9	1	1	1.000	1.000	1.000	
10	1	1	1.000	1.000	1.000	
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12	1	1	1.000	1.000	1.000	
13	1	1	1.000	1.000	1.000	
14	1	1	1.000	1.000	1.000	
15	1	1	1.000	1.000	1.000	
16	1	1	1.000	1.000	1.000	
17	1	1	1.000	1.000	1.000	
18	1	1	1.000	1.000	1.000	
19	1	1	1.000	1.000	1.000	
20	1	1	1.000	1.000	1.000	
21	1	1	1.000	1.000	1.000	
22	1	1	1.000	1.000	1.000	
23	1	1	1.000	1.000	1.000	
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31	1	1	1.000	1.000	1.000	
32	1	1	1.000	1.000	1.000	
33	1	1	1.000	1.000	1.000	
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64	1	1	1.000	1.000	1.000	
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86	1	1	1.000	1.000	1.000	
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89	1	1	1.000	1.000	1.000	
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97	1	1	1.000	1.000	1.000	
98	1	1	1.000	1.000	1.000	
99	1	1	1.000	1.000	1.000	
100	1	1	1.000	1.000	1.000	
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l rioma	10110111_0				2	10
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Bayesian Analysis: Posterior distribution table

Locus	Parameter	2.5%	25.0%	Mode	75.0%	97.5%	Median	Mean
1	Θ_1	0.03427	0.04520	0.04803	0.05007	0.05153	0.04617	0.08791
2	Θ_1	0.03527	0.04473	0.04810	0.04987	0.05187	0.04590	0.08798
3	Θ_1	0.03393	0.04453	0.04803	0.04987	0.05167	0.04570	0.08800
4	Θ_1	0.03213	0.04387	0.04790	0.04993	0.05153	0.04497	0.08422
5	Θ_1	0.03360	0.04447	0.04783	0.04973	0.05160	0.04563	0.08621
6	Θ_1	0.03433	0.04480	0.04790	0.04987	0.05167	0.04590	0.08620
7	Θ_1	0.03307	0.04347	0.04797	0.05013	0.05167	0.04537	0.08453
8	Θ_1	0.03227	0.04507	0.04790	0.04960	0.05167	0.04523	0.08397
9	Θ_1	0.03353	0.04513	0.04803	0.04987	0.05173	0.04557	0.08629
10	Θ_1	0.03420	0.04420	0.04790	0.04973	0.05160	0.04543	0.08578
11	Θ_1	0.03273	0.04400	0.04783	0.04980	0.05153	0.04517	0.08470
12	Θ_1	0.03527	0.04473	0.04797	0.04980	0.05167	0.04590	0.08721
13	Θ_1	0.03693	0.04533	0.04830	0.05007	0.05167	0.04637	0.08841
14	Θ_1	0.03580	0.04487	0.04797	0.04993	0.05160	0.04603	0.08741
15	Θ_1	0.03293	0.04400	0.04790	0.04987	0.05167	0.04517	0.08478
16	Θ_1	0.03313	0.04460	0.04797	0.04993	0.05167	0.04563	0.08635
17	Θ_1	0.03433	0.04487	0.04790	0.04993	0.05173	0.04597	0.08610
18	Θ_1	0.03273	0.04413	0.04803	0.04993	0.05167	0.04530	0.08531

Migrate 5.0.0a: (http://popgen.sc.fsu.edu) [program run on 09:22:42]

19	Θ_1	0.03220	0.04347	0.04783	0.04967	0.05167	0.04477	0.08436
20	Θ_1	0.03360	0.04427	0.04803	0.04987	0.05173	0.04543	0.08474
21	Θ_1	0.03433	0.04467	0.04797	0.04987	0.05173	0.04583	0.08806
22	Θ_1	0.03567	0.04467	0.04803	0.04973	0.05153	0.04590	0.08773
23	Θ_1	0.03380	0.04440	0.04790	0.04973	0.05167	0.04563	0.08674
24	Θ_1	0.03167	0.04393	0.04790	0.04993	0.05160	0.04503	0.08522
25	Θ_1	0.03247	0.04407	0.04790	0.04980	0.05160	0.04523	0.08420
26	Θ_1	0.03413	0.04487	0.04790	0.04973	0.05167	0.04603	0.08761
27	Θ_1	0.03413	0.04460	0.04797	0.04987	0.05173	0.04570	0.08722
28	Θ_1	0.03407	0.04533	0.04783	0.04933	0.05167	0.04550	0.08609
29	Θ_1	0.03273	0.04440	0.04803	0.05000	0.05167	0.04543	0.08508
30	Θ_1	0.03260	0.04513	0.04797	0.04967	0.05160	0.04530	0.08481
31	Θ_1	0.03307	0.04447	0.04783	0.04973	0.05160	0.04563	0.08624
32	Θ_1	0.03460	0.04453	0.04817	0.04993	0.05160	0.04570	0.08671
33	Θ_1	0.03347	0.04407	0.04777	0.04960	0.05173	0.04530	0.08758
34	Θ_1	0.03480	0.04460	0.04803	0.05000	0.05160	0.04570	0.08703
35	Θ_1	0.03353	0.04453	0.04783	0.04980	0.05167	0.04570	0.08760
36	Θ_1	0.03480	0.04560	0.04803	0.04967	0.05160	0.04577	0.08639
37	Θ_1	0.03207	0.04367	0.04790	0.04980	0.05160	0.04490	0.08323
38	Θ_1	0.03127	0.04380	0.04790	0.04980	0.05167	0.04503	0.08407
39	Θ_1	0.03307	0.04473	0.04783	0.04987	0.05160	0.04577	0.08641
40	Θ_1	0.03320	0.04447	0.04797	0.05000	0.05167	0.04557	0.08561
41	Θ_1	0.03173	0.04407	0.04790	0.04987	0.05167	0.04523	0.08485

_ocus	Parameter	2.5%	25.0%	Mode	75.0%	97.5%	Median	Mean
42	Θ_1	0.03480	0.04493	0.04803	0.05007	0.05173	0.04597	0.08757
43	Θ_1	0.03273	0.04387	0.04783	0.04967	0.05167	0.04510	0.08383
44	Θ_1	0.03280	0.04460	0.04783	0.04993	0.05160	0.04563	0.08635
45	Θ_1	0.03427	0.04540	0.04810	0.04973	0.05173	0.04563	0.08659
46	Θ_1	0.03513	0.04467	0.04790	0.04980	0.05153	0.04583	0.08741
47	Θ_1	0.03373	0.04440	0.04790	0.04973	0.05173	0.04557	0.08598
48	Θ_1	0.03340	0.04427	0.04790	0.04993	0.05167	0.04543	0.08601
49	Θ_1	0.03267	0.04393	0.04797	0.04993	0.05167	0.04503	0.08505
50	Θ_1	0.03240	0.04407	0.04783	0.04980	0.05153	0.04517	0.08603
51	Θ_1	0.03180	0.04393	0.04770	0.04980	0.05153	0.04510	0.08346
52	Θ_1	0.03367	0.04433	0.04783	0.04987	0.05160	0.04543	0.08600
53	Θ_1	0.03387	0.04447	0.04797	0.05000	0.05167	0.04557	0.08577
54	Θ_1	0.03280	0.04527	0.04790	0.04953	0.05180	0.04563	0.08613
55	Θ_1	0.03107	0.04427	0.04777	0.04940	0.05160	0.04443	0.08089
56	Θ_1	0.03260	0.04440	0.04783	0.04987	0.05160	0.04550	0.08622
57	Θ_1	0.03653	0.04447	0.04797	0.04973	0.05167	0.04570	0.08784
58	Θ_1	0.03460	0.04487	0.04790	0.04987	0.05160	0.04597	0.08677
59	Θ_1	0.03393	0.04440	0.04803	0.04987	0.05167	0.04557	0.08601
60	Θ_1	0.03433	0.04480	0.04803	0.05007	0.05173	0.04583	0.08686
61	Θ_1	0.03273	0.04507	0.04797	0.04973	0.05180	0.04550	0.08651

62	Θ_1	0.03467	0.04547	0.04810	0.04967	0.05167	0.04563	0.08623
63	Θ_1	0.03387	0.04453	0.04803	0.05000	0.05160	0.04557	0.08537
64	Θ_1	0.03320	0.04413	0.04790	0.04973	0.05167	0.04537	0.08556
65	Θ_1	0.03320	0.03980	0.04783	0.05067	0.05147	0.04523	0.08405
66	Θ_1	0.03373	0.04547	0.04803	0.04967	0.05173	0.04563	0.08664
67	Θ_1	0.03227	0.04393	0.04777	0.04960	0.05160	0.04517	0.08410
68	Θ_1	0.03167	0.04373	0.04797	0.04973	0.05173	0.04497	0.08408
69	Θ_1	0.03373	0.04453	0.04783	0.04980	0.05160	0.04570	0.08711
70	Θ_1	0.03453	0.04480	0.04783	0.04980	0.05173	0.04590	0.08713
71	Θ_1	0.03460	0.04493	0.04790	0.04967	0.05160	0.04610	0.08808
72	Θ_1	0.03360	0.04427	0.04783	0.04973	0.05160	0.04543	0.08587
73	Θ_1	0.03373	0.04453	0.04797	0.04993	0.05167	0.04563	0.08542
74	Θ_1	0.03420	0.04440	0.04790	0.04980	0.05160	0.04557	0.08653
75	Θ_1	0.03133	0.04380	0.04790	0.04980	0.05160	0.04497	0.08435
76	Θ_1	0.03267	0.04447	0.04803	0.05007	0.05160	0.04550	0.08502
77	Θ_1	0.03413	0.04520	0.04790	0.04953	0.05160	0.04543	0.08557
78	Θ_1	0.03147	0.04320	0.04790	0.04973	0.05167	0.04443	0.08416
79	Θ_1	0.03553	0.04513	0.04817	0.04993	0.05180	0.04630	0.08788
80	Θ_1	0.03327	0.04440	0.04790	0.04980	0.05167	0.04557	0.08494
81	Θ_1	0.03353	0.04420	0.04790	0.04973	0.05160	0.04537	0.08546
82	Θ_1	0.03247	0.04440	0.04783	0.04993	0.05160	0.04543	0.08596
83	Θ_1	0.03413	0.04480	0.04810	0.05000	0.05173	0.04590	0.08607
84	Θ_1	0.03393	0.04480	0.04790	0.04987	0.05160	0.04590	0.08810

Locus	Parameter	2.5%	25.0%	Mode	75.0%	97.5%	Median	Mean
85	Θ_1	0.03300	0.04440	0.04797	0.04987	0.05160	0.04550	0.08586
86	Θ_1	0.03400	0.04527	0.04797	0.04967	0.05147	0.04543	0.08561
87	Θ_1	0.03173	0.04473	0.04790	0.04947	0.05167	0.04503	0.08421
88	Θ_1	0.03200	0.04487	0.04817	0.05007	0.05180	0.04597	0.08765
89	Θ_1	0.03240	0.04493	0.04790	0.04953	0.05167	0.04517	0.08442
90	Θ_1	0.03473	0.04573	0.04797	0.04953	0.05167	0.04590	0.08683
91	Θ_1	0.03233	0.04427	0.04783	0.04967	0.05173	0.04550	0.08523
92	Θ_1	0.03420	0.04447	0.04770	0.04960	0.05160	0.04563	0.08799
93	Θ_1	0.03540	0.04520	0.04803	0.05000	0.05153	0.04623	0.08818
94	Θ_1	0.03320	0.04407	0.04803	0.04987	0.05167	0.04523	0.08540
95	Θ_1	0.03173	0.04387	0.04790	0.04980	0.05153	0.04503	0.08415
96	Θ_1	0.03340	0.04440	0.04790	0.04973	0.05153	0.04557	0.08702
97	Θ_1	0.03467	0.04493	0.04790	0.04987	0.05160	0.04597	0.08720
98	Θ_1	0.03380	0.04473	0.04803	0.04980	0.05173	0.04597	0.08731
99	Θ_1	0.03447	0.04487	0.04810	0.04993	0.05180	0.04597	0.08736
100	Θ_1	0.03307	0.04393	0.04790	0.04967	0.05147	0.04510	0.08613
All	Θ_1	0.01120	0.01547	0.01737	0.01907	0.02133	0.01697	0.09976

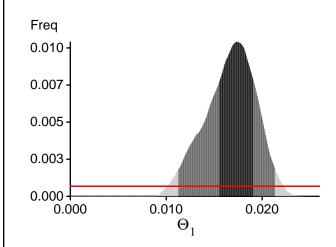
Citation suggestions:

Beerli P., 2006. Comparison of Bayesian and maximum-likelihood inference of population genetic parameters. Bioinformatics 22:341-345

Beerli P., 2007. Estimation of the population scaled mutation rate from microsatellite data, Genetics, 177:1967-1968.

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: $BF = Exp[\ ln(Prob(D \mid thisModel) - ln(\ Prob(\ D \mid otherModel)) \\ or \ as \ LBF = 2 \ (ln(Prob(D \mid thisModel) - ln(\ Prob(\ D \mid otherModel))) \\ shows the \ support for \ thisModel]$

Locus	TI(1a)	BTI(1b)	SS(2)	HS(3)
1	-16038.75	-15064.46	-14988.55	-15054.33
2	-15425.98	-14874.37	-14882.38	-14945.08
3	-14886.96	-14516.09	-14546.05	-14618.85
4	-14474.28	-14266.20	-14300.35	-14389.63
5	-14350.06	-14105.24	-14150.82	-14224.96
6	-16123.97	-15524.15	-15520.53	-15593.02
7	-14554.74	-14250.76	-14286.99	-14361.71
8	-14459.50	-14123.84	-14142.48	-14226.92
9	-25004.82	-21145.76	-20586.17	-20653.70
10	-14587.47	-14229.22	-14251.01	-14326.71
11	-14190.34	-14004.26	-14054.03	-14135.82
12	-15203.84	-14828.27	-14864.74	-14931.91
13	-17294.76	-15899.26	-15753.11	-15817.95
14	-16068.33	-15290.51	-15257.92	-15322.16
15	-14386.15	-14151.47	-14197.34	-14275.30
16	-14960.37	-14613.61	-14649.70	-14718.93
17	-14431.57	-14128.35	-14163.49	-14236.62
18	-14277.38	-14088.16	-14137.23	-14214.83
19	-14151.25	-13954.11	-14005.55	-14082.18
20	-14184.94	-13980.88	-14029.31	-14109.04
21	-15630.16	-15110.62	-15114.68	-15185.67
22	-19548.08	-17298.67	-17007.54	-17072.28
23	-15684.67	-15048.08	-15029.30	-15102.00
24	-15551.40	-14914.45	-14891.33	-14967.78
25	-14288.36	-14024.80	-14059.10	-14140.36
26	-16094.88	-15362.26	-15340.51	-15405.70
27	-15628.51	-14902.63	-14864.10	-14938.14
28	-14750.54	-14416.38	-14450.03	-14520.00
29	-14219.12	-14023.24	-14071.99	-14151.58

Migrate 5.0.0a: (http://popgen.sc.fsu.edu) [program run on 09:22:42]

30	-14226.69	-14014.98	-14063.65	-14141.42
31	-17478.30	-15870.99	-15678.83	-15749.31
32	-15944.81	-14949.82	-14860.68	-14935.98
33	-15450.94	-14891.41	-14896.91	-14958.39
34	-14858.51	-14441.76	-14462.54	-14531.28
35	-20489.16	-18921.32	-18767.04	-18826.46
36	-14375.72	-14127.70	-14174.75	-14247.20
37	-14025.42	-13866.38	-13919.32	-14000.84
38	-14235.15	-14040.48	-14086.98	-14166.64
39	-15132.81	-14545.52	-14532.36	-14604.69
40	-14436.96	-14193.32	-14227.49	-14310.37
41	-16191.69	-15548.31	-15524.71	-15600.40
42	-47424.65	-35876.39	-33959.53	-34037.72
43	-14152.55	-13962.54	-14013.94	-14092.59
44	-15128.92	-14544.62	-14522.66	-14604.35
45	-14546.82	-14239.99	-14276.30	-14351.55
46	-14940.80	-14535.56	-14551.37	-14628.66
47	-15556.11	-15006.28	-15006.99	-15078.29
48	-14423.80	-14170.40	-14214.77	-14286.51
49	-14439.63	-14202.78	-14250.90	-14325.01
50	-27652.80	-23467.15	-22844.04	-22923.12
51	-14056.22	-13891.47	-13941.91	-14024.05
52	-14785.93	-14405.59	-14432.92	-14504.81
53	-14706.17	-14328.13	-14353.41	-14425.85
54	-14609.76	-14333.44	-14379.82	-14448.92
55	-14628.55	-14317.35	-14346.54	-14428.37
56	-14328.81	-14104.48	-14150.61	-14227.05
57	-15041.08	-14561.63	-14576.50	-14639.74
58	-15821.65	-15336.62	-15334.51	-15417.10
59	-15312.30	-15022.93	-15035.46	-15126.96
60	-16358.56	-15363.19	-15283.61	-15350.74
61	-15147.47	-14784.34	-14818.40	-14888.14
62	-14295.28	-14091.88	-14139.96	-14216.25
63	-14304.54	-14049.06	-14091.67	-14165.65
64	-14337.95	-14117.14	-14169.18	-14241.85
65	-14140.76	-13959.46	-14007.20	-14090.20
66	-14542.18	-14208.19	-14237.46	-14309.71
67	-14330.33	-14132.10	-14172.25	-14256.75
68	-14329.94	-14074.79	-14116.08	-14199.39
69	-80707.76	-39566.39	-30523.00	-32401.91
70	-14373.21	-14149.08	-14201.14	-14269.46
71	-22548.58	-18702.41	-18116.03	-18179.66
72	-15270.45	-14900.05	-14929.99	-15002.87
73	-14275.31	-14028.94	-14074.05	-14149.12
74	-14545.11	-14251.92	-14293.51	-14361.87

All	-1658102.15	-1540860.23	-1527385.79	-1536607.22
100	-14707.60	-14357.56	-14388.33	-14461.49
99	-18093.83	-17025.55	-16945.02	-17009.45
98	-14691.85	-14461.60	-14505.33	-14582.14
97	-15427.36	-14900.34	-14901.64	-14972.80
96	-15062.52	-14734.71	-14777.00	-14837.76
95	-15692.34	-14979.31	-14940.26	-15020.41
94	-14560.26	-14287.21	-14326.86	-14403.52
93	-24577.13	-20141.68	-19465.34	-19521.89
92	-27728.58	-21317.22	-20268.10	-20332.81
91	-14219.54	-14031.51	-14083.90	-14164.08
90	-14894.19	-14428.61	-14438.44	-14509.05
89	-14452.52	-14187.75	-14221.42	-14304.10
88	-14892.52	-14594.87	-14633.72	-14703.54
87	-14428.08	-14211.02	-14253.91	-14334.59
86	-14450.91	-14159.92	-14196.08	-14269.70
85	-14232.28	-14028.14	-14080.81	-14156.05
84	-15061.07	-14629.28	-14658.09	-14718.23
83	-14493.88	-14173.66	-14202.97	-14279.92
82	-22041.03	-20337.18	-20114.92	-20219.48
81	-14697.16	-14340.91	-14371.33	-14444.33
80	-14344.49	-14047.00	-14079.31	-14156.94
79	-15881.62	-15073.38	-15027.69	-15093.87
78	-14192.09	-13987.44	-14039.40	-14114.58
77	-14318.38	-14062.63	-14105.11	-14182.63
76	-14282.38	-14067.15	-14107.53	-14190.62
75	-14478.15	-14217.13	-14256.88	-14333.72

- (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 = 160.884212]

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	371661452/399992737	0.92917
Genealogies	167074760/1600007263	0.10442

MCMC-Autocorrelation and Effective MCMC Sample Size

Parameter	Autocorrelation	Effective Sampe Size
Θ_1 Genealogies	0.44766 0.47489	3824215.13 3765002.18

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.
No warning was recorded during the run