AUTO

POPULATION SIZE, MIGRATION, DIVERGENCE, ASSIGNMENT, HISTORY

Bayesian inference using the structured coalescent

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

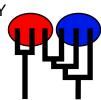
Using Intel AVX (Advanced Vector Extensions)

Compiled for PARALLEL computer architectures

One master and 100 compute nodes are available.

Program started at Sun Aug 13 04:32:36 2017

Program finished at Sun Aug 13 05:45:34 2017 [Runtime:0000:01:12:58]



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) 2408667578

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.0.9 NO

Haplotyping is turned on:

Output file: outfile_0.9_1.0

Posterior distribution raw histogram file: bayesfile

bayesallfile_0.9_1.0 Print data: No

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

Raw data from the MCMC run:

Data summary

Data file: infile.0.9
Datatype: Sequence data
Number of loci: 100

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Mutation	model:			
Locus Su	ublocus	Mutationmodel	Mutationmodel parameters	
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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Jukes-Cantor

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3	1 1	1.000	1.000	1.000	
4	1 1	1.000	1.000	1.000	
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6	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	
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46	1	1	1.000	1.000	1.000	
47	1	1	1.000	1.000	1.000	
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52	1	1	1.000	1.000	1.000	
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61	1	1	1.000	1.000	1.000	
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63	1	1	1.000	1.000	1.000	
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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	0.00127	0.00420	0.00583	0.00773	0.01560	0.00657	0.00704
2	Θ_1	0.00187	0.00433	0.00597	0.00793	0.01360	0.00677	0.00724
3	Θ_1	0.00247	0.00493	0.00557	0.00627	0.01000	0.00630	0.00673
4	Θ_1	0.00027	0.00227	0.00357	0.00480	0.00780	0.00383	0.00398
5	Θ_1	0.00107	0.00327	0.00483	0.00633	0.01073	0.00530	0.00564
6	Θ_1	0.00000	0.00080	0.00183	0.00267	0.00433	0.00203	0.00187
7	Θ_1	0.00407	0.00613	0.00737	0.00880	0.01247	0.00850	0.00912
8	Θ_1	0.00040	0.00240	0.00377	0.00500	0.00820	0.00403	0.00419
9	Θ_1	0.00067	0.00280	0.00417	0.00560	0.00927	0.00457	0.00480
10	Θ_1	0.00373	0.00680	0.00903	0.01187	0.02067	0.01043	0.01128
11	Θ_1	0.00100	0.00393	0.00443	0.00487	0.00913	0.00483	0.00509
12	Θ_1	0.00067	0.00280	0.00423	0.00560	0.00933	0.00463	0.00484
13	Θ_1	0.00173	0.00420	0.00583	0.00780	0.01327	0.00663	0.00708
14	Θ_1	0.00040	0.00240	0.00383	0.00507	0.00833	0.00410	0.00427
15	Θ_1	0.00327	0.00613	0.00697	0.00780	0.01280	0.00790	0.00850
16	Θ_1	0.00007	0.00200	0.00330	0.00447	0.00713	0.00350	0.00362
17	Θ_1	0.00133	0.00367	0.00523	0.00693	0.01173	0.00583	0.00619
18	Θ_1	0.00340	0.00633	0.00850	0.01113	0.01940	0.00977	0.01052

19	Θ_1	0.00367	0.00547	0.00690	0.00853	0.01160	0.00783	0.00844
20	Θ_1	0.00053	0.00260	0.00403	0.00533	0.00887	0.00437	0.00458
21	Θ_1	0.00047	0.00247	0.00383	0.00513	0.00847	0.00417	0.00433
22	Θ_1	0.00033	0.00120	0.00223	0.00327	0.00393	0.00243	0.00237
23	Θ_1	0.00227	0.00293	0.00590	0.01020	0.01167	0.00670	0.00713
24	Θ_1	0.00213	0.00467	0.00643	0.00847	0.01447	0.00730	0.00778
25	Θ_1	0.00033	0.00233	0.00363	0.00493	0.00800	0.00397	0.00409
26	Θ_1	0.00327	0.00647	0.00870	0.01140	0.02093	0.01003	0.01081
27	Θ_1	0.00033	0.00227	0.00363	0.00480	0.00787	0.00390	0.00401
28	Θ_1	0.00033	0.00227	0.00363	0.00487	0.00800	0.00390	0.00405
29	Θ_1	0.00200	0.00447	0.00623	0.00820	0.01407	0.00703	0.00754
30	Θ_1	0.00013	0.00200	0.00330	0.00447	0.00720	0.00350	0.00362
31	Θ_1	0.00327	0.00620	0.00830	0.01093	0.01913	0.00957	0.01034
32	Θ_1	0.00013	0.00207	0.00337	0.00453	0.00740	0.00363	0.00375
33	Θ_1	0.00460	0.00800	0.01057	0.01387	0.02440	0.01230	0.01335
34	Θ_1	0.00080	0.00293	0.00437	0.00580	0.00980	0.00483	0.00508
35	Θ_1	0.00047	0.00253	0.00390	0.00520	0.00853	0.00423	0.00439
36	Θ_1	0.00047	0.00253	0.00390	0.00520	0.00867	0.00423	0.00444
37	Θ_1	0.00013	0.00200	0.00330	0.00447	0.00720	0.00357	0.00365
38	Θ_1	0.00013	0.00200	0.00330	0.00440	0.00707	0.00350	0.00358
39	Θ_1	0.00053	0.00253	0.00397	0.00527	0.00873	0.00430	0.00448
40	Θ_1	0.00113	0.00340	0.00490	0.00647	0.01087	0.00543	0.00575
41	Θ_1	0.00040	0.00240	0.00377	0.00507	0.00840	0.00410	0.00426

Locus	Parameter	2.5%	25.0%	Mode	75.0%	97.5%	Median	Mean
42	Θ_1	0.00040	0.00247	0.00383	0.00513	0.00840	0.00417	0.00432
43	Θ_1	0.01500	0.01907	0.02530	0.03393	0.04600	0.02843	0.03216
44	Θ_1	0.00133	0.00367	0.00523	0.00693	0.01180	0.00590	0.00624
45	Θ_1	0.00000	0.00080	0.00170	0.00260	0.00413	0.00197	0.00177
46	Θ_1	0.00107	0.00333	0.00483	0.00640	0.01080	0.00537	0.00564
47	Θ_1	0.00887	0.01507	0.01697	0.01893	0.03527	0.01963	0.02155
48	Θ_1	0.00333	0.00633	0.00843	0.01107	0.01927	0.00970	0.01049
49	Θ_1	0.00400	0.00720	0.00943	0.01247	0.02173	0.01097	0.01187
50	Θ_1	0.00100	0.00320	0.00463	0.00620	0.01033	0.00510	0.00541
51	Θ_1	0.00080	0.00293	0.00437	0.00587	0.00980	0.00483	0.00508
52	Θ_1	0.00453	0.00647	0.00817	0.01007	0.01380	0.00937	0.01012
53	Θ_1	0.00007	0.00187	0.00317	0.00427	0.00673	0.00337	0.00342
54	Θ_1	0.00187	0.00380	0.00543	0.00713	0.01100	0.00610	0.00648
55	Θ_1	0.00287	0.00427	0.00590	0.00780	0.01040	0.00670	0.00715
56	Θ_1	0.00020	0.00213	0.00350	0.00467	0.00753	0.00370	0.00384
57	Θ_1	0.00073	0.00287	0.00430	0.00573	0.00953	0.00470	0.00492
58	Θ_1	0.00007	0.00187	0.00317	0.00427	0.00687	0.00337	0.00346
59	Θ_1	0.00007	0.00193	0.00323	0.00433	0.00693	0.00343	0.00351
60	Θ_1	0.00013	0.00193	0.00323	0.00433	0.00693	0.00343	0.00351
61	Θ_1	0.00013	0.00200	0.00330	0.00447	0.00720	0.00357	0.00365

62	Θ_1	0.00087	0.00300	0.00450	0.00593	0.00993	0.00490	0.00517
63	Θ_1	0.00140	0.00373	0.00537	0.00707	0.01193	0.00597	0.00634
64	Θ_1	0.00460	0.00940	0.01230	0.01613	0.03587	0.01430	0.01558
65	Θ_1	0.00000	0.00033	0.00110	0.00187	0.00333	0.00157	0.00113
66	Θ_1	0.00133	0.00367	0.00523	0.00693	0.01173	0.00583	0.00622
67	Θ_1	0.00000	0.00173	0.00297	0.00407	0.00627	0.00317	0.00317
68	Θ_1	0.00127	0.00360	0.00510	0.00680	0.01153	0.00570	0.00606
69	Θ_1	0.01380	0.01907	0.02530	0.03180	0.04800	0.02777	0.03121
70	Θ_1	0.00000	0.00167	0.00290	0.00393	0.00620	0.00310	0.00311
71	Θ_1	0.00000	0.00080	0.00177	0.00267	0.00427	0.00203	0.00184
72	Θ_1	0.00273	0.00553	0.00743	0.00987	0.01720	0.00857	0.00924
73	Θ_1	0.00200	0.00447	0.00617	0.00813	0.01407	0.00703	0.00750
74	Θ_1	0.00093	0.00313	0.00463	0.00613	0.01027	0.00510	0.00538
75	Θ_1	0.00047	0.00253	0.00390	0.00520	0.00860	0.00423	0.00440
76	Θ_1	0.00140	0.00367	0.00523	0.00693	0.01180	0.00590	0.00624
77	Θ_1	0.00060	0.00273	0.00410	0.00553	0.00913	0.00450	0.00472
78	Θ_1	0.00033	0.00227	0.00363	0.00487	0.00800	0.00390	0.00408
79	Θ_1	0.00140	0.00467	0.00643	0.00853	0.01887	0.00737	0.00788
80	Θ_1	0.00020	0.00207	0.00337	0.00453	0.00733	0.00363	0.00372
81	Θ_1	0.00000	0.00147	0.00263	0.00367	0.00567	0.00283	0.00279
82	Θ_1	0.00020	0.00207	0.00337	0.00453	0.00727	0.00363	0.00370
83	Θ_1	0.00100	0.00320	0.00463	0.00620	0.01033	0.00517	0.00541
84	Θ_1	0.00353	0.00527	0.00717	0.00947	0.01327	0.00823	0.00890

Migrate 5.0.0a: (http://popgen.sc.fsu.edu) [program run on 04:32:36]

Locus	Parameter	2.5%	25.0%	Mode	75.0%	97.5%	Median	Mean
85	Θ_1	0.00007	0.00193	0.00323	0.00433	0.00693	0.00343	0.00351
86	Θ_1	0.00247	0.00513	0.00697	0.00913	0.01580	0.00797	0.00854
87	Θ_1	0.00000	0.00180	0.00303	0.00413	0.00653	0.00323	0.00330
88	Θ_1	0.00807	0.01280	0.01643	0.02153	0.03720	0.01917	0.02098
89	Θ_1	0.00147	0.00387	0.00543	0.00720	0.01227	0.00610	0.00649
90	Θ_1	0.00067	0.00280	0.00423	0.00560	0.00940	0.00463	0.00487
91	Θ_1	0.00013	0.00207	0.00337	0.00453	0.00727	0.00357	0.00369
92	Θ_1	0.00127	0.00353	0.00510	0.00680	0.01153	0.00570	0.00606
93	Θ_1	0.00087	0.00307	0.00450	0.00600	0.01007	0.00497	0.00523
94	Θ_1	0.00613	0.00787	0.01037	0.01373	0.01760	0.01210	0.01316
95	Θ_1	0.00120	0.00347	0.00497	0.00660	0.01120	0.00557	0.00589
96	Θ_1	0.00533	0.00893	0.01163	0.01533	0.02713	0.01363	0.01484
97	Θ_1	0.00060	0.00267	0.00410	0.00547	0.00913	0.00450	0.00468
98	Θ_1	0.00000	0.00187	0.00317	0.00427	0.00680	0.00337	0.00345
99	Θ_1	0.00167	0.00440	0.00610	0.00807	0.01527	0.00697	0.00742
100	Θ_1	0.03087	0.04167	0.04757	0.04913	0.05120	0.04317	0.06287
All	Θ_1	0.00193	0.00313	0.00410	0.00500	0.00620	0.00417	0.00408

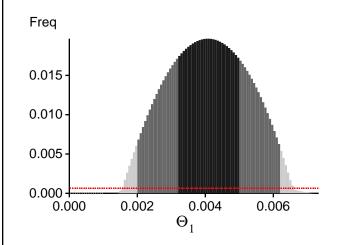
Citation suggestions:

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

ocus.	TI(1a)	BTI(1b)	SS(2)	HS(3)
1	-16860.30	-16016.02	-15992.17	-16043.57
2	-16313.08	-15844.72	-15892.20	-15943.28
3	-15692.25	-15140.09	-15161.61	-15214.12
4	-15438.58	-14933.10	-14956.90	-15013.38
5	-16169.97	-15408.26	-15392.06	-15445.29
6	-14490.95	-14115.74	-14148.08	-14210.92
7	-16055.64	-15463.82	-15486.30	-15536.23
8	-15178.66	-14730.79	-14765.01	-14820.55
9	-15227.48	-14830.79	-14876.32	-14931.80
10	-16846.72	-16192.19	-16211.77	-16263.12
11	-15015.46	-14616.81	-14658.94	-14714.12
12	-15390.38	-14908.92	-14939.65	-14993.86
13	-15557.17	-15099.38	-15140.50	-15190.56
14	-15191.24	-14773.91	-14815.15	-14871.22
15	-15809.21	-15295.89	-15329.07	-15379.01
16	-14954.27	-14526.93	-14559.93	-14617.26
17	-15462.03	-15061.23	-15110.76	-15163.39
18	-17530.18	-16459.19	-16400.48	-16449.35
19	-16381.21	-15810.87	-15840.64	-15888.85
20	-15454.65	-14936.61	-14959.24	-15013.72
21	-15020.43	-14614.03	-14653.75	-14709.82
22	-14755.17	-14326.27	-14353.99	-14414.10
23	-15947.16	-15344.09	-15359.45	-15409.99
24	-16574.55	-15897.14	-15906.56	-15955.57
25	-15309.54	-14838.09	-14868.91	-14923.46
26	-16887.50	-16110.29	-16105.88	-16152.26
27	-15928.73	-15165.40	-15143.34	-15199.26
28	-14905.43	-14542.27	-14588.80	-14644.41
29	-15974.20	-15437.10	-15467.04	-15518.06

Migrate 5.0.0a: (http://popgen.sc.fsu.edu) [program run on 04:32:36]

30	-14837.32	-14425.16	-14460.05	-14516.94
31	-15615.40	-15179.31	-15227.42	-15274.92
32	-14999.44	-14543.22	-14572.39	-14629.01
33	-16827.51	-16150.92	-16167.67	-16214.38
34	-15242.96	-14805.86	-14842.78	-14898.40
35	-15075.59	-14630.28	-14662.74	-14719.51
36	-15084.43	-14636.12	-14668.76	-14723.36
37	-14904.44	-14478.35	-14512.22	-14569.38
38	-15151.05	-14651.24	-14672.83	-14729.45
39	-15625.53	-15021.85	-15028.20	-15083.12
40	-16562.14	-15715.94	-15686.19	-15738.62
41	-14715.55	-14352.91	-14396.60	-14452.47
42	-14810.01	-14449.00	-14493.10	-14552.37
43	-18305.36	-17702.22	-17759.03	-17799.54
44	-15359.73	-14883.33	-14915.62	-14968.60
45	-14632.29	-14221.62	-14247.70	-14311.05
46	-15108.04	-14699.79	-14740.32	-14794.72
47	-22928.62	-19898.53	-19510.88	-19552.63
48	-16886.46	-16267.13	-16294.24	-16342.55
49	-19158.60	-17333.25	-17142.25	-17187.52
50	-15978.83	-15268.33	-15260.55	-15313.25
51	-15164.73	-14712.28	-14744.86	-14800.61
52	-15566.81	-15145.35	-15193.60	-15243.32
53	-15382.47	-14884.95	-14909.47	-14966.22
54	-15480.57	-15087.84	-15140.41	-15191.00
55	-16368.42	-15738.70	-15754.52	-15804.86
56	-15211.42	-14770.61	-14805.13	-14864.12
57	-15146.19	-14694.25	-14727.35	-14781.33
58	-14809.25	-14437.28	-14480.04	-14537.56
59	-14953.31	-14524.70	-14557.89	-14614.43
60	-15174.03	-14773.76	-14815.00	-14871.81
61	-14904.95	-14533.28	-14577.50	-14635.36
62	-15888.77	-15231.36	-15233.48	-15286.07
63	-15423.61	-14946.64	-14980.04	-15032.50
64	-18960.38	-18194.21	-18219.97	-18262.77
65	-14400.37	-14025.38	-14051.39	-14119.85
66	-15958.99	-15341.39	-15352.44	-15404.85
67	-14865.73	-14448.19	-14481.32	-14539.79
68	-15280.52	-14872.96	-14917.56	-14969.94
69	-28494.21	-22311.79	-21346.00	-21384.06
70	-15123.10	-14626.35	-14645.74	-14705.69
71	-14494.13	-14120.97	-14153.06	-14216.54
72	-16090.95	-15565.42	-15600.88	-15648.72
73	-15874.11	-15367.86	-15402.50	-15452.87
74	-15637.42	-15131.22	-15159.60	-15213.10

75	-14908.89	-14509.19	-14549.45	-14604.56
76	-16111.32	-15399.62	-15393.05	-15444.43
77	-15026.81	-14604.59	-14640.54	-14698.20
78	-15163.62	-14686.51	-14713.65	-14769.33
79	-16187.93	-15535.86	-15545.54	-15594.56
80	-15249.70	-14738.86	-14759.98	-14815.95
81	-14991.50	-14494.79	-14512.45	-14571.07
82	-15262.38	-14737.03	-14754.52	-14810.98
83	-15559.00	-15043.11	-15069.36	-15122.30
84	-15648.31	-15184.36	-15227.19	-15275.45
85	-14736.41	-14358.43	-14398.07	-14456.41
86	-18504.37	-16813.29	-16636.09	-16689.31
87	-15204.66	-14673.33	-14688.30	-14745.68
88	-18022.99	-17343.13	-17375.33	-17416.72
89	-15562.94	-15149.51	-15198.58	-15250.58
90	-15084.79	-14672.59	-14713.42	-14766.46
91	-15093.57	-14678.27	-14715.76	-14775.48
92	-15196.07	-14779.77	-14822.29	-14876.03
93	-15305.45	-14860.11	-14898.09	-14952.45
94	-15793.72	-15397.07	-15454.38	-15504.08
95	-15562.74	-15033.94	-15057.15	-15111.84
96	-15928.86	-15492.24	-15543.91	-15590.84
97	-15037.87	-14612.68	-14650.73	-14705.19
98	-14673.95	-14317.98	-14360.92	-14418.67
99	-16402.15	-15658.92	-15650.10	-15705.29
100	-20675.52	-19853.63	-19897.96	-19929.24
All	-1589475.62	-1527664.05	-1528616.86	-1533944.95

- (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 = 205.816611]

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 Genealogies	209421912/400016459 95556957/1599983541	0.52353 0.05972

MCMC-Autocorrelation and Effective MCMC Sample Size

Parameter	Autocorrelation	Effective Sampe Size
Θ_1	0.06309	8931068.88
Genealogies	0.22420	6405821.77

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