AUTO

POPULATION SIZE, MIGRATION, DIVERGENCE, ASSIGNMENT, HISTORY

Bayesian inference using the structured coalescent

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

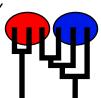
Using Intel AVX (Advanced Vector Extensions)

Compiled for PARALLEL computer architectures

One master and 100 compute nodes are available.

Program started at Sun Aug 13 04:10:39 2017

Program finished at Sun Aug 13 05:45:22 2017 [Runtime:0000:01:34:43]



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) 3448204046

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_0.7

Posterior distribution raw histogram file: bayesfile Raw data from the MCMC run: bayesallfile_0.9_0.7

Print data: No

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

Data summary

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

Mutationmode	٠ı٠
Mutationmode	7I.

Mutationmodel:				
Locus Si	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]	
4	1	Jukes-Cantor	[Basefreq: =0.25]	
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34	1	Jukes-Cantor	[Basefreq: =0.25]	

Migrate 5.0.0a: (http://popgen.sc.fsu.edu) [program run on 04:10:39]

35	1	Jukes-Cantor	[Pagefreg: -0.25]
36	1 1	Jukes-Cantor	[Basefreq: =0.25] [Basefreq: =0.25]
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100	1	Jukes-Cantor	[Basefreq: =0.25]	
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Locus	Sites
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Site rate	e variation and probat	oilities:			
Locus S	Sublocus Region type	Rate of change	Probability	Patch size	
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	
8	1	1	1.000	1.000	1.000	
9	1	1	1.000	1.000	1.000	
10	1	1	1.000	1.000	1.000	
11	1	1	1.000	1.000	1.000	
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	
24	1	1	1.000	1.000	1.000	
25	1	1	1.000	1.000	1.000	
26	1	1	1.000	1.000	1.000	
27	1	1	1.000	1.000	1.000	
28	1	1	1.000	1.000	1.000	
29	1	1	1.000	1.000	1.000	
30	1	1	1.000	1.000	1.000	
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	
34	1	1	1.000	1.000	1.000	
35	1	1	1.000	1.000	1.000	
36	1	1	1.000	1.000	1.000	
37	1	1	1.000	1.000	1.000	
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39	1	1	1.000	1.000	1.000	
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42	1	1	1.000	1.000	1.000	
43	1	1	1.000	1.000	1.000	
44	1	1	1.000	1.000	1.000	
45	1	1	1.000	1.000	1.000	
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47	1	1	1.000	1.000	1.000	
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50	1	1	1.000	1.000	1.000	
51	1	1	1.000	1.000	1.000	

52	1	1	1.000	1.000	1.000	
53	1	1	1.000	1.000	1.000	
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57	1	1	1.000	1.000	1.000	
58	1	1	1.000	1.000	1.000	
59	1	1	1.000	1.000	1.000	
60	1	1	1.000	1.000	1.000	
61	1	1	1.000	1.000	1.000	
62	1	1	1.000	1.000	1.000	
63	1	1	1.000	1.000	1.000	
64	1	1	1.000	1.000	1.000	
65	1	1	1.000	1.000	1.000	
66	1	1	1.000	1.000	1.000	
67	1	1	1.000	1.000	1.000	
68	1	1	1.000	1.000	1.000	
69	1	1	1.000	1.000	1.000	
70	1	1	1.000	1.000	1.000	
71	1	1	1.000	1.000	1.000	
72	1	1	1.000	1.000	1.000	
73	1	1	1.000	1.000	1.000	
74	1	1	1.000	1.000	1.000	
75	1	1	1.000	1.000	1.000	
76	1	1	1.000	1.000	1.000	
77	1	1	1.000	1.000	1.000	
78	1	1	1.000	1.000	1.000	
79	1	1	1.000	1.000	1.000	
80	1	1	1.000	1.000	1.000	
81	1	1	1.000	1.000	1.000	
82	1	1	1.000	1.000	1.000	
83	1	1	1.000	1.000	1.000	
84	1	1	1.000	1.000	1.000	
85	1	1	1.000	1.000	1.000	
86	1	1	1.000	1.000	1.000	
87	1	1	1.000	1.000	1.000	
88	1	1	1.000	1.000	1.000	
89	1	1	1.000	1.000	1.000	
90	1	1	1.000	1.000	1.000	
91	1	1	1.000	1.000	1.000	
92	1	1	1.000	1.000	1.000	
93	1	1	1.000	1.000	1.000	
94	1	1	1.000	1.000	1.000	
95	1	1	1.000	1.000	1.000	
96	1	1	1.000	1.000	1.000	

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	
Population		ı	1.000	1.000	Locus	Gene copies
1 Roman					1	10
i Koman	3110111_0				2	10
					3	10
					4	10
					5	10
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41	10
42	2 10
43	3 10
44	10
45	5 10
46	3 10
47	7 10
48	3 10
49	9 10
50	10
51	10
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53	3 10
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	93	10	
	94	10	
	95	10	
	96	10	
	97	10	
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Total of all populations	1	10	
	2	10	
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	92	10
	93	10
	94	10
	95	10
	96	10
	97	10
	98	10
	99	10
10	00	10

Bayesian Analysis: Posterior distribution table

Locus	Parameter	2.5%	25.0%	Mode	75.0%	97.5%	Median	Mean
1	Θ_1	0.01893	0.03147	0.03683	0.04513	0.05033	0.03570	0.04783
2	Θ_1	0.02060	0.03713	0.04483	0.04753	0.05073	0.03750	0.05192
3	Θ_1	0.02460	0.03947	0.04757	0.04920	0.05120	0.04090	0.06275
4	Θ_1	0.01960	0.02993	0.03623	0.04580	0.05027	0.03570	0.04676
5	Θ_1	0.02453	0.03873	0.04750	0.04880	0.05100	0.04003	0.05811
6	Θ_1	0.01227	0.01593	0.02317	0.03413	0.04320	0.02690	0.03179
7	Θ_1	0.02913	0.04233	0.04770	0.04960	0.05147	0.04363	0.07233
8	Θ_1	0.02253	0.03847	0.04497	0.04800	0.05080	0.03870	0.05416
9	Θ_1	0.01993	0.03447	0.04163	0.04580	0.05060	0.03683	0.05082
10	Θ_1	0.02607	0.04060	0.04763	0.04940	0.05133	0.04203	0.06809
11	Θ_1	0.02113	0.03760	0.04737	0.04827	0.05080	0.03823	0.05525
12	Θ_1	0.02253	0.03713	0.04743	0.04860	0.05080	0.03877	0.05458
13	Θ_1	0.02547	0.03993	0.04757	0.04920	0.05127	0.04137	0.06478
14	Θ_1	0.02147	0.03700	0.04357	0.04640	0.05067	0.03777	0.05226
15	Θ_1	0.02673	0.04187	0.04763	0.04927	0.05133	0.04203	0.06737
16	Θ_1	0.02027	0.03207	0.03663	0.04567	0.05047	0.03637	0.04890
17	Θ_1	0.02320	0.03953	0.04750	0.04873	0.05100	0.03970	0.05961
18	Θ_1	0.02680	0.04173	0.04763	0.04927	0.05133	0.04217	0.06686

19	Θ_1	0.02767	0.04220	0.04770	0.04907	0.05133	0.04237	0.06676
20	Θ_1	0.02180	0.03740	0.04117	0.04780	0.05067	0.03790	0.05232
21	Θ_1	0.01747	0.02840	0.03617	0.04313	0.05007	0.03430	0.04575
22	Θ_1	0.01587	0.02307	0.02930	0.03453	0.04873	0.03097	0.03793
23	Θ_1	0.02573	0.04120	0.04757	0.04907	0.05120	0.04143	0.06334
24	Θ_1	0.02727	0.04080	0.04763	0.04927	0.05133	0.04223	0.06585
25	Θ_1	0.02087	0.03487	0.03777	0.04647	0.05053	0.03710	0.05025
26	Θ_1	0.03033	0.04253	0.04777	0.04960	0.05147	0.04377	0.07380
27	Θ_1	0.01833	0.02700	0.03403	0.04267	0.04987	0.03417	0.04354
28	Θ_1	0.01980	0.03173	0.04030	0.04747	0.05040	0.03637	0.04883
29	Θ_1	0.02473	0.03947	0.04757	0.04920	0.05120	0.04090	0.06272
30	Θ_1	0.01847	0.03187	0.03917	0.04587	0.05047	0.03577	0.04803
31	Θ_1	0.02333	0.03993	0.04750	0.04887	0.05113	0.04017	0.06321
32	Θ_1	0.01940	0.03193	0.03803	0.04540	0.05040	0.03597	0.04851
33	Θ_1	0.02700	0.04120	0.04763	0.04953	0.05133	0.04250	0.07055
34	Θ_1	0.01733	0.03620	0.04383	0.04813	0.05133	0.03790	0.05319
35	Θ_1	0.01727	0.02813	0.03730	0.04387	0.05013	0.03437	0.04540
36	Θ_1	0.02120	0.03573	0.04443	0.04827	0.05073	0.03770	0.05318
37	Θ_1	0.02047	0.03427	0.04063	0.04647	0.05047	0.03683	0.04985
38	Θ_1	0.02080	0.03033	0.04103	0.04840	0.05047	0.03683	0.04931
39	Θ_1	0.01987	0.03207	0.03797	0.04760	0.05047	0.03637	0.04896
40	Θ_1	0.02007	0.03120	0.04043	0.04667	0.05040	0.03637	0.04875
41	Θ_1	0.01973	0.03487	0.04170	0.04747	0.05053	0.03670	0.05140

_ocus	Parameter	2.5%	25.0%	Mode	75.0%	97.5%	Median	Mean
42	Θ_1	0.01827	0.03347	0.03977	0.04727	0.05053	0.03597	0.04973
43	Θ_1	0.02807	0.04167	0.04763	0.04947	0.05140	0.04303	0.07219
44	Θ_1	0.01980	0.03447	0.04157	0.04767	0.05053	0.03683	0.05233
45	Θ_1	0.01027	0.01547	0.02037	0.02647	0.03960	0.02410	0.02778
46	Θ_1	0.01473	0.02347	0.03197	0.03847	0.04967	0.03177	0.04198
47	Θ_1	0.02913	0.04207	0.04770	0.04960	0.05147	0.04337	0.07324
48	Θ_1	0.02720	0.04107	0.04757	0.04927	0.05127	0.04210	0.06676
49	Θ_1	0.02580	0.04027	0.04770	0.04927	0.05133	0.04150	0.06671
50	Θ_1	0.02480	0.03987	0.04557	0.04860	0.05100	0.04030	0.05867
51	Θ_1	0.02327	0.03820	0.04743	0.04880	0.05093	0.03943	0.05740
52	Θ_1	0.01787	0.03160	0.03790	0.04687	0.05047	0.03557	0.05049
53	Θ_1	0.01620	0.02307	0.03023	0.03860	0.04920	0.03183	0.03887
54	Θ_1	0.02560	0.03960	0.04757	0.04913	0.05113	0.04110	0.06312
55	Θ_1	0.02480	0.03913	0.04750	0.04900	0.05120	0.04070	0.06073
56	Θ_1	0.02013	0.03200	0.03630	0.04527	0.05027	0.03617	0.04785
57	Θ_1	0.01927	0.03280	0.04070	0.04820	0.05067	0.03677	0.05155
58	Θ_1	0.01933	0.03127	0.03983	0.04613	0.05047	0.03617	0.04841
59	Θ_1	0.01767	0.02813	0.03283	0.04153	0.05000	0.03417	0.04441
60	Θ_1	0.01713	0.02613	0.03370	0.04333	0.05027	0.03417	0.04352
61	Θ_1	0.01873	0.02993	0.03670	0.04333	0.05020	0.03523	0.04621

62	Θ_1	0.02367	0.03833	0.04750	0.04860	0.05087	0.03943	0.05646
63	Θ_1	0.01973	0.03747	0.04750	0.04847	0.05087	0.03777	0.05493
64	Θ_1	0.02767	0.04233	0.04763	0.04920	0.05120	0.04250	0.06882
65	Θ_1	0.00527	0.00607	0.01483	0.03353	0.03720	0.01810	0.02041
66	Θ_1	0.02133	0.03787	0.04390	0.04787	0.05073	0.03803	0.05426
67	Θ_1	0.01533	0.02320	0.03170	0.03980	0.04973	0.03210	0.04032
68	Θ_1	0.02307	0.03927	0.04750	0.04867	0.05093	0.03943	0.05834
69	Θ_1	0.02660	0.04200	0.04763	0.04920	0.05133	0.04217	0.06929
70	Θ_1	0.01580	0.02333	0.02950	0.03760	0.04920	0.03163	0.03937
71	Θ_1	0.00920	0.01727	0.02237	0.02920	0.04933	0.02623	0.03089
72	Θ_1	0.02447	0.04007	0.04750	0.04893	0.05113	0.04063	0.06312
73	Θ_1	0.02387	0.03920	0.04750	0.04913	0.05120	0.04063	0.06240
74	Θ_1	0.01780	0.02920	0.03677	0.04467	0.05033	0.03497	0.04703
75	Θ_1	0.02180	0.03820	0.04483	0.04833	0.05087	0.03850	0.05464
76	Θ_1	0.02147	0.03640	0.04450	0.04840	0.05073	0.03817	0.05424
77	Θ_1	0.01573	0.02493	0.03063	0.04153	0.04987	0.03283	0.04312
78	Θ_1	0.02093	0.03587	0.04137	0.04773	0.05060	0.03737	0.05066
79	Θ_1	0.02827	0.04180	0.04763	0.04953	0.05140	0.04303	0.06929
80	Θ_1	0.01907	0.03220	0.03530	0.04240	0.05053	0.03583	0.04774
81	Θ_1	0.01613	0.02387	0.02917	0.03700	0.04913	0.03177	0.03934
82	Θ_1	0.01447	0.02040	0.02783	0.03593	0.04853	0.03010	0.03714
83	Θ_1	0.02213	0.03793	0.04463	0.04847	0.05087	0.03877	0.05501
84	Θ_1	0.02900	0.04207	0.04770	0.04953	0.05147	0.04337	0.07191

Migrate 5.0.0a: (http://popgen.sc.fsu.edu) [program run on 04:10:39]

_ocus	Parameter	2.5%	25.0%	Mode	75.0%	97.5%	Median	Mean
85	Θ_1	0.01287	0.02400	0.03383	0.04173	0.05047	0.03243	0.04202
86	Θ_1	0.01987	0.03447	0.04337	0.04780	0.05060	0.03677	0.05053
87	Θ_1	0.01373	0.02920	0.03430	0.04167	0.05140	0.03483	0.04456
88	Θ_1	0.02147	0.03820	0.04737	0.04873	0.05100	0.03897	0.05947
89	Θ_1	0.02507	0.03947	0.04757	0.04913	0.05113	0.04097	0.06236
90	Θ_1	0.02373	0.03660	0.04750	0.04920	0.05100	0.03990	0.05795
91	Θ_1	0.01853	0.02980	0.03670	0.04367	0.05033	0.03530	0.04582
92	Θ_1	0.02307	0.03953	0.04750	0.04887	0.05107	0.03997	0.06027
93	Θ_1	0.02373	0.03947	0.04750	0.04860	0.05093	0.03970	0.05792
94	Θ_1	0.02133	0.03827	0.04757	0.04920	0.05113	0.03957	0.06435
95	Θ_1	0.01953	0.03460	0.04010	0.04787	0.05053	0.03657	0.05097
96	Θ_1	0.01307	0.02233	0.03210	0.04040	0.04973	0.03130	0.04275
97	Θ_1	0.02140	0.03800	0.04370	0.04827	0.05080	0.03817	0.05494
98	Θ_1	0.01573	0.02533	0.03057	0.04060	0.04973	0.03263	0.04263
99	Θ_1	0.02413	0.03960	0.04757	0.04907	0.05113	0.04050	0.06120
100	Θ_1	0.01773	0.02507	0.03650	0.04853	0.05020	0.03477	0.04834
All	Θ_1	0.04047	0.04333	0.04477	0.04633	0.04933	0.04490	0.04492

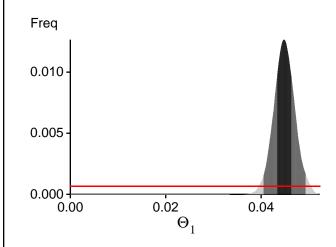
Citation suggestions:

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	-17040.48	-16042.72	-15986.10	-16041.68
2	-16296.44	-15839.98	-15887.60	-15941.53
3	-15674.83	-15137.32	-15162.85	-15213.39
4	-15383.75	-14924.02	-14956.05	-15013.03
5	-16269.25	-15423.99	-15392.77	-15444.04
6	-14315.91	-14087.87	-14148.80	-14211.22
7	-16077.66	-15468.51	-15489.00	-15534.68
8	-15080.59	-14715.39	-14767.45	-14821.25
9	-15113.41	-14811.43	-14874.39	-14929.65
10	-16944.24	-16206.97	-16210.11	-16258.52
11	-14884.20	-14595.34	-14658.72	-14715.00
12	-15317.92	-14897.03	-14940.13	-14993.68
13	-15493.72	-15089.60	-15141.55	-15191.58
14	-15076.95	-14755.73	-14816.34	-14872.64
15	-15779.56	-15290.43	-15329.47	-15378.23
16	-14828.12	-14507.15	-14562.37	-14620.16
17	-15362.91	-15044.92	-15110.16	-15164.03
18	-17858.25	-16510.63	-16398.52	-16447.18
19	-16413.31	-15815.47	-15840.13	-15889.05
20	-15403.09	-14927.91	-14959.15	-15013.30
21	-14894.31	-14593.33	-14650.89	-14708.83
22	-14619.32	-14304.69	-14355.79	-14416.18
23	-15967.98	-15346.94	-15359.91	-15409.77
24	-16666.33	-15911.53	-15906.43	-15955.63
25	-15231.94	-14825.83	-14869.34	-14924.34
26	-17044.68	-16135.60	-16107.43	-16153.89
27	-16012.56	-15178.22	-15141.61	-15198.77
28	-14750.20	-14517.16	-14589.39	-14645.87
29	-15966.26	-15435.31	-15467.02	-15517.13

Migrate 5.0.0a: (http://popgen.sc.fsu.edu) [program run on 04:10:39]

30	-14699.29	-14403.13	-14460.62	-14517.45
31	-15537.26	-15166.25	-15225.12	-15274.81
32	-14892.63	-14526.76	-14573.54	-14628.50
33	-16941.70	-16168.49	-16165.97	-16213.11
34	-15145.33	-14789.32	-14842.53	-14896.60
35	-14965.26	-14611.17	-14659.52	-14716.63
36	-14980.49	-14619.76	-14669.47	-14723.63
37	-14778.87	-14458.66	-14514.91	-14569.49
38	-15073.54	-14639.09	-14675.28	-14729.33
39	-15621.62	-15021.77	-15027.33	-15085.28
40	-16726.11	-15740.62	-15682.39	-15739.41
41	-14547.62	-14326.35	-14398.07	-14457.96
42	-14654.32	-14423.83	-14492.75	-14549.57
43	-18480.86	-17728.70	-17752.13	-17794.60
44	-15283.30	-14870.19	-14913.52	-14967.65
45	-14484.12	-14197.15	-14246.63	-14311.23
46	-14991.17	-14678.72	-14733.52	-14792.49
47	-24443.16	-20141.73	-19506.06	-19551.88
48	-16974.47	-16280.56	-16292.40	-16340.59
49	-19920.90	-17455.77	-17138.96	-17190.32
50	-16046.87	-15279.32	-15261.68	-15314.93
51	-15068.37	-14697.78	-14747.27	-14799.69
52	-15482.65	-15129.76	-15187.25	-15240.55
53	-15317.62	-14873.54	-14907.22	-14964.69
54	-15379.36	-15071.50	-15141.75	-15191.99
55	-16421.58	-15746.60	-15753.19	-15804.30
56	-15111.89	-14754.19	-14805.59	-14860.54
57	-15046.94	-14677.98	-14725.96	-14781.48
58	-14654.75	-14413.02	-14482.70	-14537.76
59	-14830.58	-14504.31	-14557.35	-14613.97
60	-15056.90	-14753.92	-14813.60	-14870.65
61	-14755.40	-14508.89	-14577.32	-14633.69
62	-15929.85	-15238.30	-15234.45	-15287.04
63	-15358.60	-14935.85	-14977.80	-15031.43
64	-19246.66	-18240.22	-18216.22	-18263.70
65	-14216.61	-13995.42	-14050.52	-14121.33
66	-15982.39	-15344.31	-15349.72	-15403.44
67	-14731.07	-14425.78	-14479.95	-14538.89
68	-15171.12	-14854.96	-14917.53	-14972.50
69	-31711.86	-22825.93	-21335.40	-21383.99
70	-15042.84	-14613.42	-14644.55	-14704.45
71	-14318.72	-14092.72	-14153.58	-14216.29
72	-16087.93	-15565.06	-15599.64	-15652.69
73	-15845.83	-15362.45	-15400.72	-15452.50
74	-15595.32	-15123.02	-15155.77	-15213.54

75	-14769.26	-14486.89	-14551.13	-14605.15
76	-16189.82	-15411.21	-15390.77	-15445.82
77	-14908.22	-14583.99	-14636.47	-14694.92
78	-15078.51	-14672.83	-14714.21	-14769.41
79	-16242.58	-15545.01	-15547.60	-15594.87
80	-15181.71	-14728.08	-14760.83	-14817.77
81	-14898.90	-14479.96	-14512.88	-14571.68
82	-15202.89	-14726.47	-14750.84	-14810.77
83	-15512.85	-15035.18	-15068.80	-15121.79
84	-15587.79	-15176.24	-15230.09	-15277.44
85	-14579.69	-14332.75	-14394.56	-14455.04
86	-19160.08	-16916.18	-16628.73	-16684.33
87	-15141.69	-14663.06	-14689.03	-14745.16
88	-18213.61	-17374.13	-17366.50	-17419.09
89	-15476.71	-15135.63	-15199.16	-15251.48
90	-14966.65	-14653.76	-14715.45	-14767.98
91	-14978.07	-14659.03	-14715.04	-14771.54
92	-15084.04	-14761.48	-14822.78	-14875.18
93	-15213.47	-14845.57	-14898.72	-14951.44
94	-15715.44	-15384.52	-15452.13	-15502.35
95	-15521.65	-15026.64	-15053.94	-15110.41
96	-15870.75	-15479.43	-15528.84	-15591.04
97	-14919.44	-14593.90	-14651.94	-14704.77
98	-14502.38	-14290.23	-14358.87	-14419.19
99	-16512.25	-15675.93	-15649.31	-15700.88
100	-21102.37	-19918.31	-19875.93	-19928.22
All	-1591816.07	-1528137.08	-1528654.85	-1534081.91

- (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 = 36.612214]

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	379826779/400025986	0.94951
Genealogies	99415890/1599974014	0.06214

MCMC-Autocorrelation and Effective MCMC Sample Size

Parameter	Autocorrelation	Effective Sampe Size
Θ_1 Genealogies	0.65876 0.21477	2063302.36 6499233.19

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		