Scoli-Holton: Linguistic phylogenies support back-migration from Beringia to Asia

MCMC Runs without Haida Outgroup in matrix

| Constraint                                      | Count |
|-------------------------------------------------|-------|
| With Na-Dene Ingroup Constraint                 | 2     |
| Without Na-Dene Ingroup Constraint              | 27    |
| Alternate Yeniseian without Kott and without Ket| 53    |
| Alternate Na-Dene without Eyak                   | 84    |
MrBayes v3.2.1 x64
(Bayesian Analysis of Phylogeny)
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Type "help" or "help <command>" for information on the commands that are available.
Type "about" for authorship and general information about the program.

MrBayes > exe /Users/msicoli/Yeniseian-NaDene-Typlogical_noHAX.nex

Executing file "/Users/msicoli/Yeniseian-NaDene-Typlogical_noHAX.nex"
UNIX line termination
Longest line length = 123
Parsing file
Expecting NEXUS formatted file
Reading data block
  Allocated taxon set
  Allocated matrix
  Defining new matrix with 39 taxa and 116 characters
  Data is Standard
  Missing data coded as ?
  Gaps coded as -
  Data matrix is not interleaved
Taxon  1 -> gwi
Taxon  2 -> dgr
Taxon  3 -> scsh
Taxon  4 -> xsl
Taxon  5 -> bea
Taxon  6 -> crx
Taxon  7 -> chp
Taxon  8 -> txc
Taxon  9 -> haa
Taxon 10 -> ing
Taxon 11 -> kuu
Taxon 12 -> hoi
Taxon 13 -> koy
Taxon 14 -> taa
Taxon 15 -> aht
Taxon 16 -> tfn
Taxon 17 -> kkz
Taxon 18 -> tcb
Taxon 19 -> tau
Taxon 20 -> ttmN
Taxon 21 -> tceS
Taxon 22 -> eya
Taxon 23 -> tli
Taxon 24 -> gce
Taxon 25 -> tol
Taxon 26 -> cco
Taxon 27 -> hup
Taxon 28 -> mtl
Taxon 29 -> wlk
Taxon 30 -> kto
Taxon 31 -> apc
Taxon 32 -> apw
Taxon 33 -> apj
Taxon 34 -> nav
Taxon 35 -> apk
Taxon 36 -> apl
Taxon 37 -> srs
Taxon 38 -> ket
Taxon 39 -> zko

Successfully read matrix
Setting default partition (does not divide up characters)
Setting model defaults
Seed (for generating default start values) = 1388062882
Adding dummy characters (unobserved site patterns) for division 1
WARNING: There are 32 characters incompatible with the specified coding bias. These characters will be excluded.

Setting output file names to "'/Users/msicoli/Yeniseian-NaDene-Typlogical_noMAX.nex.run<i>.<p/t>"
Exiting data block
Reached end of file

MrBayes > lset nst=6 rates=gamma

Setting Rates to Gamma
Successfully set likelihood model parameters
Adding dummy characters (unobserved site patterns) for division 1
WARNING: There are 32 characters incompatible with the specified coding bias. These characters will be excluded.

MrBayes > prset brlenspr=clock:uniform

Setting Brlenspr to Clock:Uniform
Successfully set prior model parameters
Adding dummy characters (unobserved site patterns) for division 1
WARNING: There are 32 characters incompatible with the specified coding bias. These characters will be excluded.

MrBayes > constraint ingroup = 1-37

Defining constraint called 'ingroup'

MrBayes > prset topologypr = constraints(ingroup)

Setting Topologypr to Constraints
Successfully set prior model parameters
Adding dummy characters (unobserved site patterns) for division 1
WARNING: There are 32 characters incompatible with the specified coding bias. These characters will be excluded.

MrBayes > mcmcp ngen=2000000 printfreq=10000 samplefreq=500 nruns=1 nchains=4 savebrlens=yes filename=DY-26Dec-strict-Yout

Setting number of generations to 2000000
Setting print frequency to 10000
Setting sample frequency to 500
Setting number of runs to 1
Setting number of chains to 4
Setting chain output file names to "DY-26Dec-strict-Yout.<p/t>"
Successfully set chain parameters
Running Markov chain
MCMC stamp = 4319925389
Seed = 810709782
Swapseed = 1388062882
Model settings:

Data not partitioned --
Datatype = Standard
Coding = Variable
# States = Variable, up to 10
  State frequencies are fixed to be equal
Rates = Gamma
  Gamma shape parameter is uniformly distributed on the interval (0.00,200.00).
  Gamma distribution is approximated using 4 categories.
Likelihood summarized over all rate categories in each generation.

Active parameters:

Parameters
------------------
Statefreq        1
Shape            2
Ratemultiplier   3
Topology         4
Brlens           5
Clockrate        6
------------------

1 -- Parameter = Alpha_symdir
   Type = Symmetric dirichlet/beta distribution alpha_i parameter
   Prior = Symmetric dirichlet with fixed(-1.00) variance parameter

2 -- Parameter = Alpha
   Type = Shape of scaled gamma distribution of site rates
   Prior = Uniform(0.00,200.00)

3 -- Parameter = Ratemultiplier
   Type = Partition-specific rate multiplier
   Prior = Fixed(1.0)

4 -- Parameter = Tau
   Type = Topology
   Prior = Prior on topologies obeys constraints
   Subparam. = V

5 -- Parameter = V
   Type = Branch lengths
   Prior = Clock:Uniform
   Tree age has an Exponential(1.000) distribution
   Node ages are not constrained

6 -- Parameter = Clockrate
   Type = Base rate of clock
   Prior = Fixed(1.000000)
   The clock rate is constant (strict clock)
Number of taxa = 39
Number of characters = 116

The MCMC sampler will use the following moves:

- With prob. Chain will use move
  - 2.38 % Multiplier(Alpha)
  - 11.90 % ExtSprClock(Tau,V)
  - 23.81 % NNIClock(Tau,V)
  - 11.90 % ParsSPRClock(Tau,V)
  - 47.62 % NodesliderClock(V)
  - 2.38 % TreeStretch(V)

Division 1 has 78 unique site patterns

Initializing conditional likelihoods
Using standard non-SSE likelihood calculator for division 1 (single-precision)

Initial log likelihoods and log prior probs:
Chain 1 -- -1428.020263 -- -90.228070
Chain 2 -- -1465.865890 -- -90.228070
Chain 3 -- -1507.829723 -- -90.228070
Chain 4 -- -1413.110454 -- -90.228070

Chain results (2000000 generations requested):

0 -- [-1428.020] (-1465.866) (-1507.830) (-1413.110)
10000 -- (-956.661) [-939.240] (-961.285) (-900.588) -- 0:16:35
20000 -- (-953.753) [-946.552] (-936.552) (-901.812) -- 0:18:09
30000 -- (-939.339) [-947.392] (-949.050) (-951.806) -- 0:19:42
40000 -- [-936.517] (-945.195) (-948.670) (-950.461) -- 0:18:47
50000 -- [-943.559] (-964.183) [-941.975] (-939.836) -- 0:18:51
60000 -- (-939.353) [-942.526] (-942.406) (-945.524) -- 0:18:51
70000 -- [-941.974] (-938.978) [-941.328] (-936.462) -- 0:19:18
80000 -- [-942.158] (-946.194) (-945.313) [-931.431] -- 0:19:12
90000 -- [-955.578] (-948.217) [-939.845] (-937.648) -- 0:18:44
100000 -- (-941.252) [-958.785] (-947.829) [-942.538] -- 0:18:41
110000 -- [-941.237] (-954.540) (-948.089) [-957.763] -- 0:18:36
120000 -- [-935.957] (-960.215) [-966.662] [-942.538] -- 0:18:32
130000 -- [-945.721] (-948.508) [-938.421] [-932.228] -- 0:18:27
140000 -- [-949.544] (-937.795) [-947.729] [-925.346] -- 0:18:22
150000 -- [-951.360] (-942.294) [-943.788] [-939.384] -- 0:18:17
160000 -- [-958.394] [-943.516] [-933.970] [-948.273] -- 0:18:01
170000 -- [-945.436] [-944.757] [-944.179] [-947.381] -- 0:17:56
180000 -- [-946.648] [-937.378] [-942.479] [-952.588] -- 0:17:51
190000 -- [-951.638] [-930.265] [-940.257] [-927.867] -- 0:17:46
200000 -- [-956.614] [-955.130] [-954.071] [-937.399] -- 0:17:42
210000 -- [-952.975] [-957.294] [-935.846] [-952.279] -- 0:17:36
220000 -- [-958.620] [-949.538] [-946.000] [-926.777] -- 0:17:31
230000 -- [-947.648] [-943.248] [-949.371] [-940.165] -- 0:17:34
240000 -- [-956.921] [-961.981] [-932.126] [-947.126] -- 0:17:28
250000 -- [-958.487] [-953.354] [-957.314] [-947.301] -- 0:17:23
260000 -- [-948.357] [-938.603] [-935.215] [-936.103] -- 0:17:24
270000 -- [-941.035] [-944.919] [-941.173] [-952.686] -- 0:17:11
280000 -- [-955.508] [-941.948] [-937.136] [-961.092] -- 0:17:05
290000 -- [-931.322] [-941.578] [-941.169] [-955.148] -- 0:17:00
300000 -- [-936.619] [-944.377] [-943.901] [-958.164] -- 0:16:54
310000 -- [-947.575] [-939.666] [-943.495] [-929.893] -- 0:16:48
320000 -- [-946.062] [-956.364] [-938.728] [-956.746] -- 0:16:42
330000 -- [-962.891] [-938.246] [-936.199] [-947.301] -- 0:16:36
340000 -- [-964.655] [-964.656] [-957.760] [-940.143] -- 0:16:31
350000 -- [-950.653] [-940.270] [-945.548] [-958.307] -- 0:16:29
Continue with analysis? (yes/no): n

Analysis completed in 19 mins 24 seconds
Analysis used 1070.60 seconds of CPU time
Log likelihood of best state for "cold" chain was -919.19

Acceptance rates for the moves in the "cold" chain:
With prob. (last 100) chain accepted proposals by move
 40.1 % ( 33 %) Multiplier(Alpha)
 18.6 % ( 14 %) ExtSprClock(Tau,V)
 44.8 % ( 54 %) NNIClock(Tau,V)
 15.5 % ( 10 %) ParsSPRClock(Tau,V)
 70.3 % ( 69 %) NodesliderClock(V)
 70.6 % ( 24 %) TreeStretch(V)

Chain swap information:
Upper diagonal: Proportion of successful state exchanges between chains
Lower diagonal: Number of attempted state exchanges between chains

Chain information:
ID -- Heat
-------------------
1 -- 1.00 (cold chain)
2 -- 0.91
3 -- 0.83
4 -- 0.77

Heat = 1 / (1 + T * (ID - 1))
(where T = 0.10 is the temperature and ID is the chain number)

MrBayes > sumt relburnin=yes

Using relative burnin (a fraction of samples discarded).
Summarizing trees in file "DY-26Dec-strict-Yout.t"
Using relative burnin ('relburnin=yes'), discarding the first 25 % of sampled trees
Writing statistics to files DY-26Dec-strict-Yout.<parts|tstat|vstat|trprobs|con>
Examining file ...
Found one tree block in file "DY-26Dec-strict-Yout.t" with 4001 trees in last block

Tree reading status:
0 10 20 30 40 50 60 70 80 90 100
v----v----v----v----v----v----v----v----v----v
*********************************************************************************
Read 4001 trees from last tree block (sampling 3001 of them)

General explanation:
In an unrooted tree, a taxon bipartition (split) is specified by removing a branch, thereby dividing the species into those to the left and those to the right of the branch. Here, taxa to one side of the removed branch are denoted '.' and those to the other side are denoted '*'. Specifically, the '.' symbol is used for the taxa on the same side as the outgroup.

In a rooted or clock tree, the tree is rooted using the model and not by reference to an outgroup. Each bipartition therefore corresponds to a clade, that is, a group that includes all the descendants of a particular branch in the tree. Taxa that are included in each clade are denoted using '***', and taxa that are not included are denoted using the '.' symbol.

The output first includes a key to all the bipartitions with frequency larger or equal to (Minpartfreq) in at least one run. Minpartfreq is a parameter to sumt command and currently it is set to 0.10. This is followed by a table with statistics for the informative bipartitions (those including at least two taxa), sorted from highest to lowest probability. For each bipartition, the table gives the number of times the partition or split was observed in all runs (#obs) and the posterior probability of the bipartition (Probab.), which
is the same as the split frequency. If several runs are summarized, this is followed by the minimum split frequency (\(\text{Min}(s)\)), the maximum frequency (\(\text{Max}(s)\)), and the standard deviation of frequencies (\(\text{Stddev}(s)\)) across runs. The latter value should approach 0 for all bipartitions as MCMC runs converge.

This is followed by a table summarizing branch lengths, node heights (if a clock model was used) and relaxed clock parameters (if a relaxed clock model was used). The mean, variance, and 95% credible interval are given for each of these parameters. If several runs are summarized, the potential scale reduction factor (PSRF) is also given; it should approach 1 as runs converge. Node heights will take calibration points into account, if such points were used in the analysis.

Note that Stddev may be unreliable if the partition is not present in all runs (the last column indicates the number of runs that sampled the partition if more than one run is summarized). The PSRF is not calculated at all if the partition is not present in all runs. The PSRF is also sensitive to small sample sizes and it should only be considered a rough guide to convergence since some of the assumptions allowing one to interpret it as a true potential scale reduction factor are violated in MrBayes.

List of taxa in bipartitions:

1 -- gwi
2 -- dgr
3 -- scsh
4 -- xsl
5 -- bea
6 -- crx
7 -- chp
8 -- txc
9 -- haa
10 -- ing
11 -- kuu
12 -- hoi
13 -- koy
14 -- taa
15 -- aht
16 -- tfn
17 -- kkz
18 -- tcb
19 -- tau
20 -- ttmN
21 -- tceS
22 -- eya
23 -- tli
24 -- gce
25 -- tol
26 -- cco
27 -- hup
28 -- mtl
29 -- wilk
30 -- kto
31 -- apc
32 -- apw
33 -- apj
34 -- nav
35 -- apk
36 -- apl
37 -- srs
38 -- ket
Key to taxon bipartitions (saved to file "DY-26Dec-strict-Yout.parts"):

| ID | Partition |
|----|-----------|
| 0  | *************************************** |
| 1  | *...................................... |
| 2  | *...................................... |
| 3  | *...................................... |
| 4  | *...................................... |
| 5  | *...................................... |
| 6  | *...................................... |
| 7  | *...................................... |
| 8  | *...................................... |
| 9  | *...................................... |
| 10 | *...................................... |
| 11 | *...................................... |
| 12 | *...................................... |
| 13 | *...................................... |
| 14 | *...................................... |
| 15 | *...................................... |
| 16 | *...................................... |
| 17 | *...................................... |
| 18 | *...................................... |
| 19 | *...................................... |
| 20 | *...................................... |
| 21 | *...................................... |
| 22 | *...................................... |
| 23 | *...................................... |
| 24 | *...................................... |
| 25 | *...................................... |
| 26 | *...................................... |
| 27 | *...................................... |
| 28 | *...................................... |
| 29 | *...................................... |
| 30 | *...................................... |
| 31 | *...................................... |
| 32 | *...................................... |
| 33 | *...................................... |
| 34 | *...................................... |
| 35 | *...................................... |
| 36 | *...................................... |
| 37 | *...................................... |
| 38 | *...................................... |
| 39 | *...................................... |
| 40 | *************************************.. |
| 41 | ......................................** |
| 42 | ..................................**... |
| 43 | ..........................*******..
| 44 | .............*...**.................... |
| 45 | ................................****. |
| 46 | ....................................**** |
| 47 | ......................................**** |
| 48 | ................................***. |
| 49 | ......................................* |
| 50 | ......................................* |
| 51 | ........................................* |
| 52 | ......................................* |
| 53 | ......................................* |
| 54 | ......................................* |
Summary statistics for informative taxon bipartitions (clades)
(saved to file "DY-26Dec-strict-Yout.tstat"):

| ID | #obs | Probab.    |
|----|------|------------|
| 40 | 3001 | 1.000000   |
| 41 | 3001 | 1.000000   |
| 42 | 3000 | 0.999667   |
| 43 | 2767 | 0.922026   |
| 44 | 2696 | 0.898367   |
| 45 | 2622 | 0.873709   |
| 46 | 2539 | 0.846051   |
| 47 | 2522 | 0.840387   |
| 48 | 2518 | 0.839054   |
| 49 | 2396 | 0.798401   |
| 50 | 2217 | 0.738754   |
| 51 | 2067 | 0.688770   |
| 52 | 2040 | 0.679773   |
| 53 | 2037 | 0.678774   |
| 54 | 1801 | 0.600133   |
| 55 | 1767 | 0.588804   |
| 56 | 1715 | 0.571476   |
| 57 | 1686 | 0.561813   |
| 58 | 1647 | 0.548817   |
| 59 | 1608 | 0.535821   |
| 60 | 1594 | 0.531156   |
| 61 | 1580 | 0.526491   |
| 62 | 1577 | 0.525492   |
| 63 | 1384 | 0.461180   |
| 64 | 1361 | 0.453515   |
| 65 | 1309 | 0.436188   |
| 66 | 1282 | 0.427191   |
| 67 | 1272 | 0.423859   |
| 68 | 1225 | 0.408197   |
| 69 | 1202 | 0.400533   |
| 70 | 1136 | 0.378540   |
| 71 | 1131 | 0.376874   |
| 72 | 943  | 0.314229   |
| 73 | 869  | 0.289570   |
| 74 | 855  | 0.284905   |
| 75 | 849  | 0.282906   |
| 76 | 822  | 0.273909   |
| 77 | 777  | 0.258914   |
| 78 | 768  | 0.255915   |
| 79 | 756  | 0.251916   |
| 80 | 741  | 0.246918   |
| 81 | 690  | 0.229923   |
| 82 | 609  | 0.202932   |
| 83 | 606  | 0.201933   |
| 84 | 589  | 0.196268   |
| 85 | 585  | 0.194935   |
| 86 | 564  | 0.187937   |
| 87 | 554  | 0.184605   |
| 88 | 553  | 0.184272   |
| 89 | 550  | 0.183272   |
| 90 | 533  | 0.177607   |
| 91 | 532  | 0.177274   |
| 92 | 526  | 0.175275   |
| 93 | 520  | 0.173276   |
| 94 | 498  | 0.165945   |
| 95 | 481  | 0.160280   |
Summary statistics for branch and node parameters
(saved to file "DY-26Dec-strict-Yout.vstat"):

| Parameter   | Mean      | Variance | Lower     | Upper     | Median   |
|-------------|-----------|----------|-----------|-----------|----------|
| length[1]   | 0.048019  | 0.000374 | 0.012385  | 0.084269  | 0.046128 |
| length[2]   | 0.050230  | 0.000529 | 0.012989  | 0.098331  | 0.046047 |
| length[3]   | 0.043713  | 0.000352 | 0.011244  | 0.080542  | 0.041384 |
| length[4]   | 0.042629  | 0.000654 | 0.007309  | 0.098330  | 0.036828 |
| length[5]   | 0.032730  | 0.000234 | 0.008190  | 0.062968  | 0.030478 |
| length[6]   | 0.043334  | 0.000253 | 0.015299  | 0.074194  | 0.041820 |
| length[7]   | 0.034178  | 0.000225 | 0.007689  | 0.066031  | 0.033154 |
| length[8]   | 0.047581  | 0.000233 | 0.018304  | 0.077108  | 0.047113 |
| length[9]   | 0.047953  | 0.000478 | 0.011545  | 0.089664  | 0.044194 |
| length[10]  | 0.077381  | 0.000905 | 0.021743  | 0.138188  | 0.075436 |
| length[11]  | 0.035462  | 0.000248 | 0.007991  | 0.066125  | 0.033154 |
| length[12]  | 0.036355  | 0.000273 | 0.007897  | 0.067311  | 0.033864 |
| length[13]  | 0.027673  | 0.000214 | 0.005571  | 0.058083  | 0.024950 |
| length[14]  | 0.094470  | 0.000881 | 0.039486  | 0.152294  | 0.094379 |
| length[15]  | 0.091397  | 0.000887 | 0.035261  | 0.147808  | 0.091357 |
| length[16]  | 0.036138  | 0.000258 | 0.009314  | 0.067995  | 0.034239 |
| length[17]  | 0.024711  | 0.000170 | 0.004349  | 0.049862  | 0.022045 |
| length[18]  | 0.030469  | 0.000239 | 0.005634  | 0.061502  | 0.027956 |
| length[19]  | 0.033689  | 0.000195 | 0.010236  | 0.062464  | 0.032016 |
| length[20]  | 0.035897  | 0.000223 | 0.009668  | 0.064411  | 0.034185 |
| length[21]  | 0.097014  | 0.000144 | 0.037673  | 0.165628  | 0.093576 |
| length[22]  | 0.099618  | 0.000138 | 0.033374  | 0.172188  | 0.094912 |
| length[23]  | 0.087039  | 0.000105 | 0.022049  | 0.154714  | 0.083948 |
| length[24]  | 0.075774  | 0.000895 | 0.025982  | 0.137985  | 0.071399 |
| length[25]  | 0.083066  | 0.000993 | 0.025470  | 0.143234  | 0.080296 |
| length[26]  | 0.090926  | 0.001201 | 0.027278  | 0.159159  | 0.086512 |
| length[27]  | 0.085646  | 0.001044 | 0.023525  | 0.149109  | 0.081732 |
| length[28]  | 0.044674  | 0.000420 | 0.011405  | 0.084643  | 0.041759 |
| length[29]  | 0.046055  | 0.000510 | 0.011240  | 0.091675  | 0.042223 |
| length[30]  | 0.088930  | 0.000632 | 0.000006  | 0.024855  | 0.006662 |
| length[31]  | 0.088922  | 0.000626 | 0.000006  | 0.024552  | 0.006644 |
| length[32]  | 0.014789  | 0.000096 | 0.003596  | 0.033753  | 0.012848 |
| length[33]  | 0.028931  | 0.000173 | 0.006547  | 0.053453  | 0.027011 |
| length[96] | 0.014836 | 0.000123 | 0.000146 | 0.036064 | 0.012021 |
| length[97] | 0.007722 | 0.000067 | 0.000002 | 0.025652 | 0.005010 |
| length[98] | 0.031997 | 0.000343 | 0.000752 | 0.065665 | 0.029096 |
| length[99] | 0.008762 | 0.000073 | 0.000088 | 0.025437 | 0.006355 |
| length[100] | 0.017243 | 0.000188 | 0.000278 | 0.044028 | 0.013108 |
| length[101] | 0.021578 | 0.000284 | 0.000136 | 0.053594 | 0.018178 |
| length[102] | 0.007575 | 0.000064 | 0.000006 | 0.023018 | 0.004943 |
| length[103] | 0.018035 | 0.000162 | 0.000342 | 0.044510 | 0.015812 |
| height[0] | 0.183142 | 0.001638 | 0.087549 | 0.254876 | 0.186298 |
| height[1] | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 |
| height[2] | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 |
| height[3] | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 |
| height[4] | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 |
| height[5] | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 |
| height[6] | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 |
| height[7] | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 |
| height[8] | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 |
| height[9] | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 |
| height[10] | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 |
| height[11] | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 |
| height[12] | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 |
| height[13] | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 |
| height[14] | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 |
| height[15] | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 |
| height[16] | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 |
| height[17] | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 |
| height[18] | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 |
| height[19] | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 |
| height[20] | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 |
| height[21] | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 |
| height[22] | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 |
| height[23] | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 |
| height[24] | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 |
| height[25] | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 |
| height[26] | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 |
| height[27] | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 |
| height[28] | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 |
| height[29] | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 |
| height[30] | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 |
| height[31] | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 |
| height[32] | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 |
| height[33] | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 |
| height[34] | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 |
| height[35] | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 |
| height[36] | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 |
| height[37] | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 |
| height[38] | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 |
| height[39] | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 |
| height[40] | 0.167999 | 0.01317 | 0.081373 | 0.229592 | 0.171755 |
| height[41] | 0.082629 | 0.000685 | 0.029604 | 0.130430 | 0.080783 |
| height[42] | 0.005295 | 0.000039 | 0.016085 | 0.03673 | 0.003673 |
Clade credibility values:

```
/---------- ket (38)

/---------------------------100---------------------------+-
          \----- zko (39)

/----------------------------- gwi (1)
          \--------------- dgr (2)

/----------------------------- scsh (3)
          \--------------- bea (5)
          \--------------- crx (6)

/----------------------------- xsl (4)
          \--------------- kkz (17)

/----------------------------- chp (7)
          \--------------- ttmN (20)
          \--------------- tceS (21)

+          \--------------- haa (9)
          \--------------- taa (14)
          \--------------- tcb (18)
          \--------------- tau (19)

/----------------------------- txc (8)
          \--------------- ing (10)
          \--------------- hoi (12)
          \--------------- koy (13)
          \--------------- kuu (11)
          \--------------- aht (15)
```

```
Phylogram (based on median node depths):

```
|                       |----------------------------------------------------------- tfn (16) |
|                       |
| \---100---           |----------------------------------------------------------- eya (22) |
|                       |\-------------- tli (23) |
|                       |\-------------- gce (24) |
|                       |\-------------- tol (25) |
|                       |\-------------- cco (26) |
|                       | /-------------- hup (27) |
|                       |\-------------- mtl (28) |
|                       |----------------------------------------------------------- olk (29) |
|                       |\-------------- kto (30) |
|                       |\-------------- apc (31) |
|                       |\-------------- apw (32) |
|                       |\-------------- apj (33) |
|                       |\-------------- nav (34) |
|                       |\-------------- apk (35) |
|                       |\-------------- apl (36) |
|                       |\-------------- srs (37) |
|                       |
|                       |\------------------------- ket (38) |
|                       |\------------------------- zko (39) |
|                       |\-------------- gwi (1) |
|                       |\-------------- dgr (2) |
|                       |\-------------- scsh (3) |
|                       |\-------------- bea (5) |
|                       |\-------------- crx (6) |
|                       |\-------------- xsl (4) |
|                       |\-------------- kkz (17) |
|                       |\-------------- chp (7) |
|                       |\-------------- ttmN (20) |
|                       |\-------------- tceS (21) |
```

Phylogram (based on median node depths):
Calculating tree probabilities...
Credible sets of trees (3001 trees sampled):
  50 % credible set contains 1501 trees
  90 % credible set contains 2701 trees
  95 % credible set contains 2851 trees
  99 % credible set contains 2971 trees

MrBayes > sump relburnin=yes

Using relative burnin (a fraction of samples discarded).
Summarizing parameters in file DY-26Dec-strict-Yout.p
Writing summary statistics to file DY-26Dec-strict-Yout.pstat
Using relative burnin ('relburnin=yes'), discarding the first 25 % of samples

Below is a rough plot of the generation (x-axis) versus the log probability of observing the data (y-axis). You can use this graph to determine what the burn in for your analysis should be. When the log probability starts to plateau you may be at stationarity. Sample trees and parameters after the log probability plateaus. Of course, this is not a guarantee that you are at stationarity. When possible, run multiple analyses starting from different random trees; if the inferences you make for independent analyses are the same, this is reasonable evidence that the chains have converged. You can use MrBayes to run several independent analyses simultaneously. During such a run, MrBayes will monitor the convergence of topologies. After the run has been completed, the 'sumt' and 'sump' functions will provide additional convergence diagnostics for all the parameters in your model. Remember that the burn in is the number of samples to discard. There are a total of ngen / samplefreq samples taken during a MCMC analysis.

Estimated marginal likelihoods for run sampled in file "DY-26Dec-strict-Yout.p":
(Use the harmonic mean for Bayes factor comparisons of models)
(Values are saved to the file /Users/msicoli/Yeniseian-NaDene-Typological_noHAX.nex.lstat)

| Arithmetic mean | Harmonic mean |
|-----------------|---------------|
| -928.25         | -957.98       |
Model parameter summaries for run sampled in file "DY-26Dec-strict-Yout":
Based on a total of 3001 samples out of a total of 4001 samples
from this analysis.
Parameter summaries saved to file "/Users/msicoli/Yeniseian-NaDene-Typlogical_noHAX.nex.pstat".

95% HPD Interval

| Parameter | Mean   | Variance | Lower   | Upper   | Median  | ESS*   |
|-----------|--------|----------|---------|---------|---------|--------|
| TH        | 0.183142 | 0.001638 | 0.087549 | 0.254876 | 0.186298 | 283.23 |
| TL        | 2.917361 | 0.341884 | 1.479322 | 3.862267 | 3.003610 | 258.33 |
| alpha     | 7.814915 | 618.921256 | 0.128622 | 34.662511 | 1.840312 | 2060.16 |

* Convergence diagnostic (ESS = Estimated Sample Size); ESS value
below 100 may indicate that the parameter is undersampled.

MrBayes > ssp ngen=100000 diagnfreq=1000 filename=YND-Typ-NoHax-Yout-ss

Setting number of generations to 100000
Setting diagnosing frequency to 1000

MrBayes > ss

Setting chain output file names to "YND-Typ-NoHax-Yout-ss.<p/t>"
Running Markov chain
MCMC stamp = 9313293518
Seed = 500640120
Swapseed = 1325479247
Model settings:

Data not partitioned --
Datatype = Standard
Coding = Variable
# States = Variable, up to 10
  State frequencies are fixed to be equal
Rates = Gamma
  Gamma shape parameter is uniformly dist-
  ributed on the interval (0.00,200.00).
  Gamma distribution is approximated using 4 categories.
  Likelihood summarized over all rate categories in each generation.

Active parameters:

Parameters
------------------
Statefreq | 1
Shape      | 2
Ratemultiplier | 3
Topology   | 4
Brlens     | 5
Clockrate  | 6
------------------

1 -- Parameter = Alpha_symdir
  Type = Symmetric dirichlet/beta distribution alpha_i parameter
  Prior = Symmetric dirichlet with fixed(-1.00) variance parameter
Parameter = Alpha
Type = Shape of scaled gamma distribution of site rates
Prior = Uniform(0.00,200.00)

Parameter = Ratemultiplier
Type = Partition-specific rate multiplier
Prior = Fixed(1.0)

Parameter = Tau
Type = Topology
Prior = Prior on topologies obeys constraints
Subparam. = V

Parameter = V
Type = Branch lengths
Prior = Clock:Uniform
  Tree age has an Exponential(1.000) distribution
  Node ages are not constrained

Parameter = Clockrate
Type = Base rate of clock
Prior = Fixed(1.000000)
The clock rate is constant (strict clock)

Number of taxa = 39
Number of characters = 116

The MCMC sampler will use the following moves:
  With prob. Chain will use move
    2.38 % Multiplier(Alpha)
    11.90 % ExtSprClock(Tau,V)
    23.81 % NNIClock(Tau,V)
    11.90 % ParsSPRClock(Tau,V)
    47.62 % NodesliderClock(V)
    2.38 % TreeStretch(V)

Division 1 has 78 unique site patterns
Initializing conditional likelihoods
Using standard non-SSE likelihood calculator for division 1 (single-precision)

Initial log likelihoods and log prior probs:
  Chain 1 -- -940.276105 -- -25.105876
  Chain 2 -- -937.127525 -- -30.598855
  Chain 3 -- -953.540022 -- -35.491175
  Chain 4 -- -935.883526 -- -31.235408

Starting stepping-stone sampling to estimate marginal likelihood.
50 steps will be used with 1500 generations (3 samples) within each step.
Total of 76500 generations (153 samples) will be collected while first
1500 generations (3 samples) will be discarded as initial burnin.
Additionally at the beginning of each step 0 generations (0 samples)
will be discarded as burnin.
Sampling from posterior to prior, i.e. first step samples from close to
posterior.
NOTE: Number of generation of each step is reduced to the closest multiple
  of sampling frequency. That is why, in total it will be taken 76500 genera-
  tions instead of requested 100000.
Chain results (76500 generations requested):

    0 -- [-940.276] (-937.128) (-953.540) (-935.884)
Sampling step 1 out of 50 steps...
Sampling step 2 out of 50 steps...
Sampling step 3 out of 50 steps...
Sampling step 4 out of 50 steps...
Sampling step 5 out of 50 steps...
Sampling step 6 out of 50 steps...

10000 -- (-983.462) (-954.663) [-960.939] (-953.831) -- 0:00:33
Sampling step 7 out of 50 steps...
Sampling step 8 out of 50 steps...
Sampling step 9 out of 50 steps...
Sampling step 10 out of 50 steps...
Sampling step 11 out of 50 steps...
Sampling step 12 out of 50 steps...
Sampling step 13 out of 50 steps...

20000 -- (-992.849) [-982.415] (-1116.329) (-1053.194) -- 0:00:31
Sampling step 14 out of 50 steps...
Sampling step 15 out of 50 steps...
Sampling step 16 out of 50 steps...
Sampling step 17 out of 50 steps...
Sampling step 18 out of 50 steps...
Sampling step 19 out of 50 steps...

30000 -- (-1116.901) (-1228.345) (-1069.047) [-1082.594] -- 0:00:24
Sampling step 20 out of 50 steps...
Sampling step 21 out of 50 steps...
Sampling step 22 out of 50 steps...
Sampling step 23 out of 50 steps...
Sampling step 24 out of 50 steps...
Sampling step 25 out of 50 steps...
Sampling step 26 out of 50 steps...

40000 -- (-1183.647) (-1240.637) (-1265.053) [-1159.604] -- 0:00:19
Sampling step 27 out of 50 steps...
Sampling step 28 out of 50 steps...
Sampling step 29 out of 50 steps...
Sampling step 30 out of 50 steps...
Sampling step 31 out of 50 steps...
Sampling step 32 out of 50 steps...
Sampling step 33 out of 50 steps...

50000 -- (-1257.997) (-1328.011) (-1322.755) [-1307.306] -- 0:00:14
Sampling step 34 out of 50 steps...
Sampling step 35 out of 50 steps...
Sampling step 36 out of 50 steps...
Sampling step 37 out of 50 steps...
Sampling step 38 out of 50 steps...
Sampling step 39 out of 50 steps...

60000 -- (-1312.262) (-1318.707) (-1303.586) [-1328.344] -- 0:00:09
Sampling step 40 out of 50 steps...
Sampling step 41 out of 50 steps...
Sampling step 42 out of 50 steps...
Sampling step 43 out of 50 steps...
Sampling step 44 out of 50 steps...
Sampling step 45 out of 50 steps...
Sampling step 46 out of 50 steps...

70000 -- (-2065.694) (-2060.396) (-2043.780) [-1442.593] -- 0:00:03
Sampling step 47 out of 50 steps...
Sampling step 48 out of 50 steps...
Sampling step 49 out of 50 steps...
Sampling step 50 out of 50 steps...

Analysis completed in 41 seconds
Analysis used 40.26 seconds of CPU time
Log likelihood of best state for "cold" chain was -926.40

Marginal likelihood (in natural log units) estimated using stepping-stone sampling based on 50 steps with 1500 generations (3 samples) within each step.

| Run | Marginal likelihood (ln) |
|-----|--------------------------|
| 1   | -1044.58                 |
More statistics on stepping-stone sampling is dumped to YND-Typ-NoHax-Yout-ss.ss file.

Plot of average standard deviation of split frequencies across steps. Points at -1.0 (y-axis) indicate that there were no splits above minimum frequency for corresponding step.

Acceptance rates for the moves in the "cold" chain:
With prob. (last 100) chain accepted proposals by move
  44.7 % ( 43 %) Multiplier(Alpha)
  42.8 % ( 62 %) ExtSprClock(Tau,V)
  78.3 % ( 96 %) NNClock(Tau,V)
  33.9 % ( 32 %) ParsSPRClock(Tau,V)
  86.4 % ( 97 %) NodesliderClock(V)
  52.6 % ( 83 %) TreeStretch(V)

Chain swap information:

|   | 1 | 2 | 3 | 4 |
|---|---|---|---|---|
| 1 | 0.26 | 0.09 | 0.04 |
| 2 | 12529 | 0.33 | 0.10 |
| 3 | 12772 | 12801 | 0.41 |
| 4 | 12816 | 12721 | 12861 |

Upper diagonal: Proportion of successful state exchanges between chains
Lower diagonal: Number of attempted state exchanges between chains

Chain information:

| ID  | Heat  |
|-----|-------|
| 1   | 1.00  (cold chain) |
| 2   | 0.91  |
| 3   | 0.83  |
| 4   | 0.77  |

Heat = 1 / (1 + T * (ID - 1))
(where T = 0.10 is the temperature and ID is the chain number)
MrBayes v3.2.1 x64
(Bayesian Analysis of Phylogeny)
Distributed under the GNU General Public License

Type "help" or "help <command>" for information on the commands that are available.
Type "about" for authorship and general information about the program.

MrBayes > exe /Users/msicoli/Yeniseian-NaDene-Typlogical_noHAX.nex

Executing file "/Users/msicoli/Yeniseian-NaDene-Typlogical_noHAX.nex"
UNIX line termination
Longest line length = 123
Parsing file
Expecting NEXUS formatted file
Reading data block
   Allocated taxon set
   Allocated matrix
   Defining new matrix with 39 taxa and 116 characters
   Data is Standard
   Missing data coded as ?
   Gaps coded as -
   Data matrix is not interleaved
Taxon 1 -> gwi
Taxon 2 -> dgr
Taxon 3 -> scsh
Taxon 4 -> xsl
Taxon 5 -> bea
Taxon 6 -> crx
Taxon 7 -> chp
Taxon 8 -> txc
Taxon 9 -> haa
Taxon 10 -> ing
Taxon 11 -> kuu
Taxon 12 -> hoi
Taxon 13 -> koy
Taxon 14 -> taq
Taxon 15 -> aht
Taxon 16 -> tfn
Taxon 17 -> kkz
Taxon 18 -> tcb
Taxon 19 -> tau
Taxon 20 -> ttmN
Taxon 21 -> tceS
Taxon 22 -> eya
Taxon 23 -> tli
Taxon 24 -> gce
Taxon 25 -> tol
Taxon 26 -> cco
Taxon 27 -> hup
Taxon 28 -> mtl
Taxon 29 -> wil
Taxon 30 -> kto
Taxon 31 -> apc
Taxon 32 -> apw
Taxon 33 -> apj
Taxon 34 -> nav
Taxon 35 -> apk
Taxon 36 -> apl
Taxon 37 -> srs
Taxon 38 -> ket
Taxon 39 -> zko
Successfully read matrix
Setting default partition (does not divide up characters)
Setting model defaults
Seed (for generating default start values) = 1387987200
Adding dummy characters (unobserved site patterns) for division 1
WARNING: There are 32 characters incompatible with the specified
coding bias. These characters will be excluded.
Setting output file names to "/Users/msicoli/Yeniseian-NaDene-Typological_noHAX.nex.run<i>.<p|t>"
Exiting data block
Reached end of file

MrBayes > lset nst=6 rates=gamma

Setting Rates to Gamma
Successfully set likelihood model parameters
Adding dummy characters (unobserved site patterns) for division 1
WARNING: There are 32 characters incompatible with the specified
coding bias. These characters will be excluded.

MrBayes > prset brlenspr=clock:uniform

Setting Brlenspr to Clock:Uniform
Successfully set prior model parameters
Adding dummy characters (unobserved site patterns) for division 1
WARNING: There are 32 characters incompatible with the specified
coding bias. These characters will be excluded.

MrBayes > mcmcp ngen=2000000 printfreq=10000 samplefreq=500 nruns=1 nchains=4 savebrlens=yes
filename=DY-25Dec-strictNOHAX

Setting number of generations to 2000000
Setting print frequency to 10000
Setting sample frequency to 500
Setting number of runs to 1
Setting number of chains to 4
Setting chain output file names to "DY-25Dec-strictNOHAX.<p/t>"
Successfully set chain parameters

MrBayes > mcmc

Running Markov chain
MCMC stamp = 9243191534
Seed = 1101468095
Swapseed = 1387987200
Model settings:

Data not partitioned --
Datatype = Standard
Coding = Variable
# States = Variable, up to 10
   State frequencies are fixed to be equal
Rates = Gamma
   Gamma shape parameter is uniformly distributed on the interval (0.00,200.00).
   Gamma distribution is approximated using 4 categories.
   Likelihood summarized over all rate categories in each generation.

Active parameters:

Parameters
------------------
Statefreq        1
Shape            2
Ratemultiplier   3
Topology         4
Brlens           5
Clockrate        6
------------------

1 -- Parameter = Alpha_symdir
   Type = Symmetric dirichlet/beta distribution alpha_i parameter
   Prior = Symmetric dirichlet with fixed(-1.00) variance parameter

2 -- Parameter = Alpha
   Type = Shape of scaled gamma distribution of site rates
   Prior = Uniform(0.00,200.00)

3 -- Parameter = Ratemultiplier
   Type = Partition-specific rate multiplier
   Prior = Fixed(1.0)

4 -- Parameter = Tau
   Type = Topology
   Prior = All topologies equally probable a priori
   Subparam. = V

5 -- Parameter = V
   Type = Branch lengths
   Prior = Clock:Uniform
       Tree age has an Exponential(1.000) distribution
       Node ages are not constrained

6 -- Parameter = Clockrate
   Type = Base rate of clock
   Prior = Fixed(1.000000)
       The clock rate is constant (strict clock)

Number of taxa = 39
Number of characters = 116
The MCMC sampler will use the following moves:
With prob. Chain will use move
  2.38 % Multiplier(Alpha)
  11.90 % ExtSprClock(Tau,V)
  23.81 % NNIClock(Tau,V)
  11.90 % ParsSPRClock(Tau,V)
Division 1 has 78 unique site patterns
Initializing conditional likelihoods
Using standard non-SSE likelihood calculator for division 1 (single-precision)

Initial log likelihoods and log prior probs:
- Chain 1: -1491.863997, -90.228070
- Chain 2: -1591.318217, -90.228070
- Chain 3: -1549.036671, -90.228070
- Chain 4: -1553.401708, -90.228070

Chain results (2000000 generations requested):
- Chain 1: -1491.864, -1591.318, -1549.037, -1553.402
- Chain 2: -937.355, -942.024, -963.513, -947.137
- Chain 3: -931.394, -947.608, -935.664, -968.341
- Chain 4: -954.203, -947.643, -944.162, -952.468

...
| Value  | X1     | X2     | X3     | X4     |
|--------|--------|--------|--------|--------|
| 430000 | -948.190 | -931.362 | -951.487 | -942.069 |
| 440000 | -956.419 | -949.344 | -955.221 | -945.501 |
| 450000 | -949.060 | -963.003 | -944.955 | -940.969 |
| 460000 | -953.972 | -944.687 | -943.767 | -958.391 |
| 470000 | -965.498 | -955.830 | -933.433 | -950.290 |
| 480000 | -950.727 | -959.634 | -952.038 | -946.686 |
| 490000 | -952.605 | -980.507 | -945.860 | -946.559 |
| 500000 | -951.101 | -936.082 | -944.782 | -957.836 |
| 510000 | -953.972 | -966.495 | -968.744 | -943.081 |
| 520000 | -961.576 | -942.323 | -964.328 | -944.200 |
| 530000 | -945.171 | -935.074 | -969.792 | -950.026 |
| 540000 | -967.644 | -942.136 | -951.312 | -950.994 |
| 550000 | -935.048 | -936.408 | -956.076 | -942.144 |
| 560000 | -965.434 | -935.725 | -956.447 | -956.846 |
| 570000 | -951.101 | -936.082 | -944.782 | -957.836 |
| 580000 | -961.879 | -953.709 | -964.860 | -953.055 |
| 590000 | -961.666 | -940.598 | -956.277 | -940.207 |
| 600000 | -967.548 | -939.136 | -938.238 | -937.428 |
| 610000 | -947.072 | -953.853 | -945.162 | -961.193 |
| 620000 | -947.103 | -945.870 | -942.390 | -967.242 |
| 630000 | -952.460 | -947.100 | -943.427 | -947.625 |
| 640000 | -974.147 | -948.559 | -951.161 | -953.197 |
| 650000 | -951.343 | -961.887 | -937.799 | -952.649 |
| 660000 | -959.785 | -940.668 | -961.349 | -933.157 |
| 670000 | -951.860 | -944.644 | -936.300 | -940.611 |
| 680000 | -933.585 | -943.479 | -940.807 | -971.696 |
| 690000 | -944.020 | -932.168 | -950.626 | -963.962 |
| 700000 | -979.578 | -935.104 | -946.969 | -976.455 |
| 710000 | -943.342 | -947.840 | -956.041 | -957.019 |
| 720000 | -955.619 | -956.604 | -938.917 | -950.457 |
| 730000 | -953.708 | -945.322 | -960.383 | -934.581 |
| 740000 | -953.175 | -952.847 | -942.552 | -960.200 |
| 750000 | -947.945 | -952.417 | -941.755 | -944.997 |
| 760000 | -953.298 | -951.212 | -949.528 | -949.182 |
| 770000 | -964.228 | -937.635 | -970.198 | -946.546 |
| 780000 | -952.428 | -957.455 | -955.931 | -938.665 |
| 790000 | -959.384 | -931.940 | -952.530 | -939.868 |
| 800000 | -944.044 | -943.402 | -940.504 | -936.578 |
| 810000 | -948.214 | -951.265 | -948.531 | -939.789 |
| 820000 | -936.333 | -940.802 | -963.623 | -956.137 |
| 830000 | -943.295 | -949.373 | -931.339 | -944.642 |
| 840000 | -944.600 | -971.124 | -956.322 | -941.198 |
| 850000 | -952.086 | -958.467 | -944.276 | -944.528 |
| 860000 | -935.019 | -963.331 | -954.709 | -934.909 |
| 870000 | -955.367 | -961.971 | -940.293 | -946.221 |
| 880000 | -944.956 | -952.784 | -948.711 | -946.135 |
| 890000 | -941.351 | -958.436 | -941.965 | -965.844 |
| 900000 | -943.845 | -949.997 | -957.026 | -966.243 |
| 910000 | -947.958 | -952.685 | -948.906 | -966.185 |
| 920000 | -943.547 | -944.791 | -953.795 | -958.219 |
| 930000 | -948.664 | -937.475 | -953.963 | -951.974 |
| 940000 | -945.228 | -943.000 | -940.391 | -958.682 |
| 950000 | -942.721 | -955.005 | -943.118 | -948.029 |
| 960000 | -949.308 | -958.432 | -944.956 | -947.329 |
| 970000 | -963.763 | -942.600 | -939.282 | -941.277 |
| 980000 | -956.826 | -952.028 | -958.046 | -951.130 |
Continue with analysis? (yes/no): n

Analysis completed in 16 mins 36 seconds
Analysis used 968.47 seconds of CPU time
Log likelihood of best state for "cold" chain was -919.51

Acceptance rates for the moves in the "cold" chain:
With prob. (last 100) chain accepted proposals by move
Multiplier(Alpha) 39.6 % (24 %) 39.6 % (24 %)
ExtSprClock(Tau,V) 18.4 % (15 %) 18.4 % (15 %)
NNIClock(Tau,V) 44.3 % (41 %) 44.3 % (41 %)
 ParsSPRClock(Tau,V) 15.1 % (16 %) 15.1 % (16 %)
NodesliderClock(V) 70.0 % (77 %) 70.0 % (77 %)
TreeStretch(V) 69.9 % (33 %) 69.9 % (33 %)

Chain swap information:

1 2 3 4
| ID | 0.51 | 0.24 | 0.10 |
|----|------|------|------|
| 2  | 333100 | 0.59 | 0.31 |
| 3  | 332474 | 333374 | 0.62 |
| 4  | 333812 | 344026 | 333214 |

Upper diagonal: Proportion of successful state exchanges between chains
Lower diagonal: Number of attempted state exchanges between chains

Chain information:

ID -- Heat

---
1 -- 1.00 (cold chain)
2 -- 0.91
3 -- 0.83
4 -- 0.77

Heat = 1 / (1 + T * (ID - 1))

(where T = 0.10 is the temperature and ID is the chain number)

MrBayes > sumt relburnin=yes

Using relative burnin (a fraction of samples discarded).
Summarizing trees in file "DY-25Dec-strictNOHAX.t"
Using relative burnin ('relburnin=yes'), discarding the first 25% of sampled trees
Writing statistics to files DY-25Dec-strictNOHAX.<parts|tstat|vstat|trprobs|con>
Examining file ...
Found one tree block in file "DY-25Dec-strictNOHAX.t" with 4001 trees in last block

Tree reading status:
0 10 20 30 40 50 60 70 80 90 100
v-------v-------v-------v-------v-------v-------v-------v-------v-------v-------v
*********************************************************************************
Read 4001 trees from last tree block (sampling 3001 of them)

General explanation:

In an unrooted tree, a taxon bipartition (split) is specified by removing a branch, thereby dividing the species into those to the left and those to the right of the branch. Here, taxa to one side of the removed branch are denoted '. ' and those to the other side are denoted '*'. Specifically, the '.' symbol is used for the taxa on the same side as the outgroup.

In a rooted or clock tree, the tree is rooted using the model and not by reference to an outgroup. Each bipartition therefore corresponds to a clade, that is, a group that includes all the descendants of a particular branch in the tree. Taxa that are included in each clade are denoted using '*', and taxa that are not included are denoted using the '.' symbol.

The output first includes a key to all the bipartitions with frequency larger or equal to (Minpartfreq) in at least one run. Minpartfreq is a parameter to sumt command and currently it is set to 0.10. This is followed by a table with statistics for the informative bipartitions (those including at least two taxa), sorted from highest to lowest probability. For each bipartition, the table gives the number of times the partition or split was observed in all
runs (#obs) and the posterior probability of the bipartition (Probab.), which
is the same as the split frequency. If several runs are summarized, this is
followed by the minimum split frequency (Min(s)), the maximum frequency
(Max(s)), and the standard deviation of frequencies (Stddev(s)) across runs.
The latter value should approach 0 for all bipartitions as MCMC runs converge.

This is followed by a table summarizing branch lengths, node heights (if a
clock model was used) and relaxed clock parameters (if a relaxed clock model
was used). The mean, variance, and 95% credible interval are given for each
of these parameters. If several runs are summarized, the potential scale
reduction factor (PSRF) is also given; it should approach 1 as runs converge.
Node heights will take calibration points into account, if such points were
used in the analysis.

Note that Stddev may be unreliable if the partition is not present in all
runs (the last column indicates the number of runs that sampled the partition
if more than one run is summarized). The PSRF is not calculated at all if
the partition is not present in all runs. The PSRF is also sensitive to small
sample sizes and it should only be considered a rough guide to convergence
since some of the assumptions allowing one to interpret it as a true potential
scale reduction factor are violated in MrBayes.

List of taxa in bipartitions:

1 -- gwi
2 -- dgr
3 -- scsh
4 -- xsl
5 -- bea
6 -- crx
7 -- chp
8 -- txc
9 -- haa
10 -- ing
11 -- kuu
12 -- hoi
13 -- koy
14 -- taa
15 -- aht
16 -- tfn
17 -- kkz
18 -- tcb
19 -- tau
20 -- ttmN
21 -- tceS
22 -- eya
23 -- tli
24 -- gce
25 -- tol
26 -- cco
27 -- hup
28 -- mtl
29 -- wlk
30 -- kto
31 -- apc
32 -- apw
33 -- apj
34 -- nav
35 -- apk
Key to taxon bipartitions (saved to file "DY-25Dec-strictNOHAX.parts"):

| ID | Partition |
|----|-----------|
| 0  | ****************************************** |
| 1  | *........................................ |
| 2  | *........................................ |
| 3  | *........................................ |
| 4  | *........................................ |
| 5  | *........................................ |
| 6  | *........................................ |
| 7  | *........................................ |
| 8  | *........................................ |
| 9  | *........................................ |
| 10 | *........................................ |
| 11 | *........................................ |
| 12 | *........................................ |
| 13 | *........................................ |
| 14 | *........................................ |
| 15 | *........................................ |
| 16 | *........................................ |
| 17 | *........................................ |
| 18 | *........................................ |
| 19 | *........................................ |
| 20 | *........................................ |
| 21 | *........................................ |
| 22 | *........................................ |
| 23 | *........................................ |
| 24 | *........................................ |
| 25 | *........................................ |
| 26 | *........................................ |
| 27 | *........................................ |
| 28 | *........................................ |
| 29 | *........................................ |
| 30 | *........................................ |
| 31 | *........................................ |
| 32 | *........................................ |
| 33 | *........................................ |
| 34 | *........................................ |
| 35 | *........................................ |
| 36 | *........................................ |
| 37 | *........................................ |
| 38 | *........................................ |
| 39 | *........................................ |
| 40 | *........................................ |
| 41 | *........................................ |
| 42 | *........................................ |
| 43 | ***..................................... |
| 44 | ***..................................... |
| 45 | ***..................................... |
| 46 | *****................................... |
| 47 | *****................................... |
| 48 | *****................................... |
| 49 | *****................................... |
Summary statistics for informative taxon bipartitions (clades)
(saved to file "DY-25Dec-strictNOHAX.tstat"):

| ID | #obs | Probab. |
|----|------|---------|
| 40 | 3001 | 1.000000 |
| 41 | 3001 | 1.000000 |
| 42 | 2784 | 0.927691 |
| 43 | 2711 | 0.903366 |
| 44 | 2584 | 0.861046 |
| 45 | 2541 | 0.846718 |
| 46 | 2519 | 0.839387 |
| 47 | 2342 | 0.780407 |
| 48 | 2334 | 0.777741 |
| 49 | 2173 | 0.724092 |
| 50 | 2132 | 0.710430 |
| 51 | 1993 | 0.664112 |
| 52 | 1920 | 0.639787 |
| 53 | 1840 | 0.613129 |
| 54 | 1809 | 0.602799 |
| 55 | 1804 | 0.601133 |
| 56 | 1779 | 0.592802 |
| 57 | 1639 | 0.546151 |
| 58 | 1629 | 0.542153 |
| 59 | 1627 | 0.542153 |
| 60 | 1624 | 0.541153 |
| 61 | 1554 | 0.517827 |
| 62 | 1535 | 0.511496 |
| 63 | 1422 | 0.473842 |
| 64 | 1381 | 0.460180 |
| 65 | 1338 | 0.445851 |
| 66 | 1256 | 0.418527 |
| 67 | 1249 | 0.416195 |
| 68 | 1196 | 0.398534 |
| 69 | 1187 | 0.395535 |
| 70 | 1180 | 0.393202 |
| 71 | 1134 | 0.377874 |
| 72 | 941  | 0.313562 |
| 73 | 930  | 0.309897 |
| 74 | 869  | 0.289570 |
| 75 | 845  | 0.281573 |
| 76 | 824  | 0.274575 |
| 77 | 808  | 0.269244 |
| 78 | 785  | 0.261579 |
| 79 | 736  | 0.245252 |
| 80 | 699  | 0.232922 |
| 81 | 697  | 0.232256 |
| 82 | 688  | 0.229257 |
| 83 | 660  | 0.219927 |
| 84 | 601  | 0.200267 |
| 85 | 573  | 0.190936 |
Summary statistics for branch and node parameters (saved to file "DY-25Dec-strictNOHAX.vstat"):

| Parameter | Mean   | Variance | Lower  | Upper  | Median |
|-----------|--------|----------|--------|--------|--------|
| length[1] | 0.047745 | 0.000397 | 0.012193 | 0.085901 | 0.045633 |
| length[2] | 0.049778 | 0.000533 | 0.011875 | 0.095301 | 0.046044 |
| length[3] | 0.043071 | 0.000362 | 0.011180 | 0.081444 | 0.040694 |
| length[4] | 0.033754 | 0.000242 | 0.007330 | 0.063727 | 0.031843 |
| length[5] | 0.040812 | 0.000601 | 0.005040 | 0.090257 | 0.035076 |
| length[6] | 0.032351 | 0.000250 | 0.005307 | 0.063883 | 0.030330 |
| length[7] | 0.043983 | 0.000278 | 0.014654 | 0.076065 | 0.042258 |
| length[8] | 0.098026 | 0.000954 | 0.034813 | 0.153322 | 0.098731 |
| length[9] | 0.047818 | 0.000243 | 0.015838 | 0.075966 | 0.044319 |
| length[10] | 0.048222 | 0.000497 | 0.009746 | 0.090153 | 0.044319 |
| length[11] | 0.077783 | 0.000976 | 0.018206 | 0.136765 | 0.076645 |
| length[12] | 0.035971 | 0.000260 | 0.008248 | 0.066786 | 0.034006 |
| length[13] | 0.036680 | 0.000282 | 0.007374 | 0.068520 | 0.034504 |
| length[14] | 0.027762 | 0.000223 | 0.004573 | 0.058179 | 0.024764 |
| length[15] | 0.095056 | 0.000962 | 0.034479 | 0.153684 | 0.094637 |
| length[16] | 0.091624 | 0.000941 | 0.029883 | 0.145360 | 0.091530 |
| length[17] | 0.035727 | 0.000253 | 0.007822 | 0.066391 | 0.033831 |
| length[18] | 0.024754 | 0.000182 | 0.003119 | 0.051212 | 0.022009 |
| length[19] | 0.030594 | 0.000251 | 0.004945 | 0.061505 | 0.027774 |
| length[20] | 0.033979 | 0.000207 | 0.008007 | 0.061703 | 0.032561 |
| length[21] | 0.035973 | 0.000216 | 0.008395 | 0.063505 | 0.034805 |
|       | length[22] | length[23] | length[24] | length[25] | length[26] | length[27] | length[28] | length[29] | length[30] | length[31] | length[32] | length[33] | length[34] | length[35] | length[36] | length[37] | length[38] | length[39] | length[40] | length[41] | length[42] | length[43] | length[44] | length[45] | length[46] | length[47] | length[48] | length[49] | length[50] | length[51] | length[52] | length[53] | length[54] | length[55] | length[56] | length[57] | length[58] | length[59] | length[60] | length[61] | length[62] | length[63] | length[64] | length[65] | length[66] | length[67] | length[68] | length[69] | length[70] | length[71] | length[72] | length[73] | length[74] | length[75] | length[76] | length[77] | length[78] | length[79] | length[80] |
|-------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
Clade credibility values:

/--------------------------------------------------------------------- txc (8)
|--------------------------------------------------------------------- kuu (11)
|--------------------------------------------------------------------- aht (15)
|--------------------------------------------------------------------- tfn (16)
|
|                |--60---+
|                |
|    /-----66-----+
|    |
|    \----84----+
|    |
|    \----72----+
|    |
|----93----+
|    |
|    \----------------100---------------+ apl (36)
|    |
|    \--------------------------------------------------------- srs (37)
Phylogram (based on median node depths):
Calculating tree probabilities...

Credible sets of trees (3001 trees sampled):
50 % credible set contains 1501 trees
90 % credible set contains 2701 trees
95 % credible set contains 2851 trees
99 % credible set contains 2971 trees

MrBayes > sump relburnin=yes

Using relative burnin (a fraction of samples discarded).
Summarizing parameters in file DY-25Dec-strictNOHAX.p
Writing summary statistics to file DY-25Dec-strictNOHAX.pstat
Using relative burnin ('relburnin=yes'), discarding the first 25 % of samples

Below is a rough plot of the generation (x-axis) versus the log probability of observing the data (y-axis). You can use this graph to determine what the burn in for your analysis should be. When the log probability starts to plateau you may be at stationarity. Sample trees and parameters after the log probability plateaus. Of course, this is not a guarantee that you are at stationarity. When possible, run multiple analyses starting from different random trees; if the inferences you make for independent analyses are the same, this is reasonable evidence that the chains have converged. You can use MrBayes to run several independent analyses simultaneously. During such a run, MrBayes will monitor the convergence of topologies. After the run has been completed, the 'sumt' and 'sump' functions will provide additional convergence diagnostics for all the parameters in your model. Remember that the burn in is the number of samples to discard. There are a total of ngen / samplefreq samples taken during a MCMC analysis.
Estimated marginal likelihoods for run sampled in file "DY-25Dec-strictNOHAX.p":  
(Use the harmonic mean for Bayes factor comparisons of models)  
(Values are saved to the file /Users/msicoli/Yeniseian-NaDene-Typlogical_noHAX.nex.lstat)

Arithmetic mean   Harmonic mean
--------------------------------
-929.96          -965.14
--------------------------------

Model parameter summaries for run sampled in file "DY-25Dec-strictNOHAX":  
Based on a total of 3001 samples out of a total of 4001 samples from this analysis.  
Parameter summaries saved to file "/Users/msicoli/Yeniseian-NaDene-Typlogical_noHAX.nex.pstat".

95% HPD Interval
-------------------------------
| Parameter | Mean     | Variance | Lower   | Upper   | Median   | ESS*    |
-------------------------------
| TH        | 0.167205 | 0.001492 | 0.064714| 0.226702| 0.171668| 319.44  |
| TL        | 2.854755 | 0.366821 | 1.394540| 3.892517| 2.963303| 284.19  |
| alpha     | 9.210757 | 772.797996| 0.087496| 56.401044| 1.903306| 2500.96 |
-------------------------------

* Convergence diagnostic (ESS = Estimated Sample Size); ESS value below 100 may indicate that the parameter is undersampled.

MrBayes > ssp ngen=100000 diagnfreq=1000 filename=YND-Typ-NoHax-ss

Could not find parameter "ngen=100000"

MrBayes > ssp ngen=100000 diagnfreq=1000 filename=YND-Typ-NoHax-ss

Setting number of generations to 100000  
Setting diagnosing frequency to 1000
MrBayes > ss

Setting chain output file names to "YND-Typ-NoHax-ss.<p/t>"
Running Markov chain
MCMC stamp = 7908113950
Seed = 1878978649
Swapseed = 1031120143
Model settings:

Data not partitioned --
  Datatype = Standard
  Coding = Variable
  # States = Variable, up to 10
    State frequencies are fixed to be equal
  Rates = Gamma
    Gamma shape parameter is uniformly distributed on the interval (0.00,200.00).
    Gamma distribution is approximated using 4 categories.
    Likelihood summarized over all rate categories in each generation.

Active parameters:

Parameters
------------------
Statefreq 1
Shape 2
Ratemultiplier 3
Topology 4
BrLens 5
Clockrate 6
------------------

1 -- Parameter = Alpha_symdir
  Type = Symmetric dirichlet/beta distribution alpha_i parameter
  Prior = Symmetric dirichlet with fixed(-1.00) variance parameter

2 -- Parameter = Alpha
  Type = Shape of scaled gamma distribution of site rates
  Prior = Uniform(0.00,200.00)

3 -- Parameter = Ratemultiplier
  Type = Partition-specific rate multiplier
  Prior = Fixed(1.0)

4 -- Parameter = Tau
  Type = Topology
  Prior = All topologies equally probable a priori
  Subparam. = V

5 -- Parameter = V
  Type = Branch lengths
  Prior = Clock:Uniform
    Tree age has an Exponential(1.000) distribution
    Node ages are not constrained

6 -- Parameter = Clockrate
  Type = Base rate of clock
  Prior = Fixed(1.000000)
    The clock rate is constant (strict clock)
Number of taxa = 39
Number of characters = 116

The MCMC sampler will use the following moves:
With prob. Chain will use move
2.38 % Multiplier(Alpha)
11.90 % ExtSprClock(Tau,V)
23.81 % NNIClock(Tau,V)
11.90 % ParsSPRClock(Tau,V)
47.62 % NodesliderClock(V)
2.38 % TreeStretch(V)

Division 1 has 78 unique site patterns
Initializing conditional likelihoods
Using standard non-SSE likelihood calculator for division 1 (single-precision)

Initial log likelihoods and log prior probs:
Chain 1 -- -937.554390 -- -17.664652
Chain 2 -- -941.921722 -- -36.467720
Chain 3 -- -945.920556 -- -31.420523
Chain 4 -- -968.722535 -- -27.744449

Starting stepping-stone sampling to estimate marginal likelihood.
50 steps will be used with 1500 generations (3 samples) within each step.
Total of 76500 generations (153 samples) will be collected while first
1500 generations (3 samples) will be discarded as initial burnin.
Additionally at the beginning of each step 0 generations (0 samples)
will be discarded as burnin.
Sampling from posterior to prior, i.e. first step samples from close to
posterior.
NOTE: Number of generation of each step is reduced to the closest multiple
of sampling frequency. That is why, in total it will be taken 76500 gene-
ations instead of requested 100000.

Chain results (76500 generations requested):

0 -- [-937.554] (-941.922) (-945.921) (-968.723)

Sampling step 1 out of 50 steps...
Sampling step 2 out of 50 steps...
Sampling step 3 out of 50 steps...
Sampling step 4 out of 50 steps...
Sampling step 5 out of 50 steps...
Sampling step 6 out of 50 steps...
Sampling step 7 out of 50 steps...
Sampling step 8 out of 50 steps...

10000 -- (-966.909) [-971.576] (-960.096) (-1012.739) -- 0:00:33
Sampling step 9 out of 50 steps...
Sampling step 10 out of 50 steps...
Sampling step 11 out of 50 steps...
Sampling step 12 out of 50 steps...
Sampling step 13 out of 50 steps...

20000 -- (-1040.425) (-1044.518) [-1011.347] (-1010.900) -- 0:00:28
Sampling step 14 out of 50 steps...
Sampling step 15 out of 50 steps...
Sampling step 16 out of 50 steps...
Sampling step 17 out of 50 steps...
Sampling step 18 out of 50 steps...
Sampling step 19 out of 50 steps...

30000 -- [-1056.473] (-1214.950) (-1120.707) (-1102.046) -- 0:00:23
Sampling step 20 out of 50 steps...
Sampling step 21 out of 50 steps...
Sampling step 22 out of 50 steps...
Sampling step 23 out of 50 steps...
Sampling step 24 out of 50 steps...
Sampling step 25 out of 50 steps...
Sampling step 26 out of 50 steps...

40000 -- (-1295.848) (-1294.247) [-1179.106] (-1254.753) -- 0:00:18
Sampling step 27 out of 50 steps...
Sampling step 28 out of 50 steps...
Sampling step 29 out of 50 steps...
Sampling step 30 out of 50 steps...
Sampling step 31 out of 50 steps...
Sampling step 32 out of 50 steps...
Sampling step 33 out of 50 steps...

50000 -- (-1389.502) (-1378.487) (-1326.617) [-1299.880] -- 0:00:13
Sampling step 34 out of 50 steps...
Sampling step 35 out of 50 steps...
Sampling step 36 out of 50 steps...
Sampling step 37 out of 50 steps...

Sampling step 38 out of 50 steps...

Sampling step 39 out of 50 steps...

60000 -- (-1391.943) (-1388.422) (-1364.142) [-1477.828] -- 0:00:08

Sampling step 40 out of 50 steps...

Sampling step 41 out of 50 steps...

Sampling step 42 out of 50 steps...

Sampling step 43 out of 50 steps...

Sampling step 44 out of 50 steps...

Sampling step 45 out of 50 steps...

Sampling step 46 out of 50 steps...

70000 -- (-1987.933) (-2082.221) (-2084.316) [-1834.352] -- 0:00:03

Sampling step 47 out of 50 steps...

Sampling step 48 out of 50 steps...

Sampling step 49 out of 50 steps...

Sampling step 50 out of 50 steps...

Analysis completed in 39 seconds
Analysis used 37.13 seconds of CPU time
Log likelihood of best state for "cold" chain was -929.82

Marginal likelihood (in natural log units) estimated using stepping-stone sampling based on
50 steps with 1500 generations (3 samples) within each step.

| Run | Marginal likelihood (ln) |
|-----|--------------------------|
| 1   | -1050.61                 |

More statistics on stepping-stone sampling is dumped to YND-Typ-NoMax-ss.ss file.

Plot of average standard deviation of split frequencies across steps.
Points at -1.0 (y-axis) indicate that there were no splits
above minimum frequency for corresponding step.
Acceptance rates for the moves in the "cold" chain:

With prob. (last 100) chain accepted proposals by move:

- Multiplier(Alpha) 44.6% (36%)
- ExtSprClock(Tau,V) 43.5% (63%)
- NNIClock(Tau,V) 78.2% (100%)
- ParsSPRClock(Tau,V) 33.3% (35%)
- NodesliderClock(V) 85.7% (99%)
- TreeStretch(V) 52.1% (80%)

Chain swap information:

| 1 | 2 | 3 | 4 |
|---|---|---|---|
| 1 | 0.25 | 0.07 | 0.02 |
| 2 | 12661 | 0.32 | 0.10 |
| 3 | 12779 | 12794 | 0.40 |
| 4 | 12805 | 12805 | 12656 |

Upper diagonal: Proportion of successful state exchanges between chains
Lower diagonal: Number of attempted state exchanges between chains

Chain information:

| ID | Heat |
|----|------|
| 1  | 1.00 | (cold chain) |
| 2  | 0.91 |
| 3  | 0.83 |
| 4  | 0.77 |

Heat = 1 / (1 + T * (ID - 1))
(where T = 0.10 is the temperature and ID is the chain number)

MrBayes >
MrBayes v3.2.1 x64

(Bayesian Analysis of Phylogeny)

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Type "help" or "help <command>" for information on the commands that are available.

Type "about" for authorship and general information about the program.

MrBayes > exe /Users/msicoli/Ket-NaDene-Typlogical_noHAX.nex

Executing file "/Users/msicoli/Ket-NaDene-Typlogical_noHAX.nex"
UNIX line termination
Longest line length = 123
Parsing file
Expecting NEXUS formatted file
Reading data block
Allocated taxon set
Allocated matrix
Defining new matrix with 38 taxa and 116 characters
Data is Standard
Missing data coded as ?
Gaps coded as -
Data matrix is not interleaved
Taxon 1 -> gwi
Taxon 2 -> dgr
Taxon 3 -> scsh
Taxon 4 -> xsl
Taxon 5 -> bea
Taxon 6 -> crx
Taxon 7 -> chp
Taxon 8 -> txc
Taxon 9 -> haa
Taxon 10 -> ing
Taxon 11 -> kuu
Taxon 12 -> hoi
Taxon 13 -> koy
Taxon 14 -> taa
Taxon 15 -> aht
Taxon 16 -> tfn
Taxon 17 -> kkz
Taxon 18 -> tcb
Taxon 19 -> tau
Taxon 20 -> ttmN
Taxon 21 -> tceS
Taxon 22 -> eya
Taxon 23 -> tli
Taxon 24 -> gce
Taxon 25 -> tol
Taxon 26 -> cco
Taxon 27 -> hup
Taxon 28 -> mtl
Taxon 29 -> wlk
Taxon 30 -> kto
Taxon 31 -> apc
Taxon 32 -> apw
Taxon 33 -> apj
Taxon 34 -> nav
Taxon 35 -> apk
Taxon 36 -> apl
Taxon 37 -> srs
Taxon 38 -> ket
Successfully read matrix
Setting default partition (does not divide up characters)
Setting model defaults
Seed (for generating default start values) = 1388163552
Adding dummy characters (unobserved site patterns) for division 1
WARNING: There are 38 characters incompatible with the specified
coding bias. These characters will be excluded.
Setting output file names to "/Users/msicoli/Ket-NaDene-Typlogical_noHAX.nex.run<i>.<p|t>"
Exiting data block
Reached end of file

MrBayes > lset nst=6 rates=gamma
Setting Rates to Gamma
Successfully set likelihood model parameters
Adding dummy characters (unobserved site patterns) for division 1
WARNING: There are 38 characters incompatible with the specified
coding bias. These characters will be excluded.

MrBayes > prset brlenspr=clock:uniform
Setting Brlenspr to Clock:Uniform
Successfully set prior model parameters
Adding dummy characters (unobserved site patterns) for division 1
WARNING: There are 38 characters incompatible with the specified
coding bias. These characters will be excluded.

MrBayes > mcmcp ngen=2000000 printfreq=10000 samplefreq=500 nruns=1 nchains=4 savebrlens=yes
filename=DY-27Dec-strict-H-KottOut
Setting number of generations to 2000000
Setting print frequency to 10000
Setting sample frequency to 500
Setting number of runs to 1
Setting number of chains to 4
Setting chain output file names to "DY-27Dec-strict-H-KottOut.<p/t>"
Successfully set chain parameters

MrBayes > mcmc
Running Markov chain
MCMC stamp = 2292685654
Seed = 2059386170
Swapseed = 1388163552
Model settings:

Data not partitioned --
Datatype = Standard
Coding = Variable
# States = Variable, up to 10
    State frequencies are fixed to be equal
Rates = Gamma
    Gamma shape parameter is uniformly dist-
ributed on the interval (0.00, 200.00).
Gamma distribution is approximated using 4 categories.
Likelihood summarized over all rate categories in each generation.

Active parameters:

Parameters
------------------
Statefreq        1  
Shape            2  
Ratemultiplier   3  
Topology         4  
Brlns           5  
Clockrate       6  
------------------

1 -- Parameter  = Alpha_symdir
   Type       = Symmetric dirichlet/beta distribution alpha_i parameter
   Prior      = Symmetric dirichlet with fixed(-1.00) variance parameter

2 -- Parameter  = Alpha
   Type       = Shape of scaled gamma distribution of site rates
   Prior      = Uniform(0.00, 200.00)

3 -- Parameter  = Ratemultiplier
   Type       = Partition-specific rate multiplier
   Prior      = Fixed(1.0)

4 -- Parameter  = Tau
   Type       = Topology
   Prior      = All topologies equally probable a priori
   Subparam.  = V

5 -- Parameter  = V
   Type       = Branch lengths
   Prior      = Clock:Uniform
                 Tree age has an Exponential(1.000) distribution
                 Node ages are not constrained

6 -- Parameter  = Clockrate
   Type       = Base rate of clock
   Prior      = Fixed(1.000000)
                 The clock rate is constant (strict clock)

Number of taxa = 38
Number of characters = 116

The MCMC sampler will use the following moves:
With prob.  Chain will use move
  2.38 %   Multiplier(Alpha)
  11.90 %  ExtSprClock(Tau,V)
  23.81 %  NNIClock(Tau,V)
  11.90 %  ParsSPRClock(Tau,V)
  47.62 %  NodesliderClock(V)
  2.38 %   TreeStretch(V)

Division 1 has 71 unique site patterns
Initializing conditional likelihoods
Using standard non-SSE likelihood calculator for division 1 (single-precision)
Initial log likelihoods and log prior probs:
Chain 1 -- -1417.300608 -- -87.230988
Chain 2 -- -1434.196678 -- -87.230988
Chain 3 -- -1393.517948 -- -87.230988
Chain 4 -- -1476.315409 -- -87.230988

Chain results (2000000 generations requested):
0 -- [-1417.301] (-1434.197) (-1393.518) (-1476.315)
FILE TRUNCATED
2000000 -- [-887.857] (-889.472) (-887.144) (-885.737) -- 0:00:00
Continue with analysis? (yes/no): n
Analysis completed in 15 mins 30 seconds
Analysis used 866.52 seconds of CPU time
Log likelihood of best state for "cold" chain was -855.15
Acceptance rates for the moves in the "cold" chain:
With prob.   (last 100)   chain accepted proposals by move
 46.0 %     ( 27 %)     Multiplier(Alpha)
 19.5 %     ( 23 %)     ExtSprClock(Tau,V)
 45.6 %     ( 50 %)     NNIClock(Tau,V)
 16.2 %     ( 21 %)     ParsSPRClock(Tau,V)
 71.0 %     ( 73 %)     NodesliderClock(V)
 69.6 %     ( 27 %)     TreeStretch(V)
Chain swap information:

|   | 1       | 2       | 3       | 4       |
|---|---------|---------|---------|---------|
| 1 | 0.57    | 0.29    | 0.13    |
| 2 | 333501  | 0.62    | 0.34    |
| 3 | 334725  | 332669  | 0.64    |
| 4 | 333645  | 333423  | 332037  |

Upper diagonal: Proportion of successful state exchanges between chains
Lower diagonal: Number of attempted state exchanges between chains

Chain information:

| ID | Heat |
|----|------|
| 1  | 1.00 (cold chain) |
| 2  | 0.91 |
| 3  | 0.83 |
| 4  | 0.77 |

Heat = 1 / (1 + T * (ID - 1))
(where T = 0.10 is the temperature and ID is the chain number)

MrBayes > sumt relburnin=yes
Using relative burnin (a fraction of samples discarded).
Summarizing trees in file "DY-27Dec-strict-H-KottOut.t"
Using relative burnin ("relburnin=yes"), discarding the first 25 % of sampled trees
Writing statistics to files DY-27Dec-strict-H-KottOut.<parts|tstat|vstat|trprobs|con>
Examining file ...
Found one tree block in file "DY-27Dec-strict-H-KottOut.t" with 4001 trees in last block

Tree reading status:

0 10 20 30 40 50 60 70 80 90 100
v-------v-------v-------v-------v-------v-------v-------v-------v-------v-------v
*********************************************************************************
Read 4001 trees from last tree block (sampling 3001 of them)

General explanation:

In an unrooted tree, a taxon bipartition (split) is specified by removing a branch, thereby dividing the species into those to the left and those to the right of the branch. Here, taxa to one side of the removed branch are denoted '.' and those to the other side are denoted '*'. Specifically, the '.' symbol is used for the taxa on the same side as the outgroup.

In a rooted or clock tree, the tree is rooted using the model and not by reference to an outgroup. Each bipartition therefore corresponds to a clade, that is, a group that includes all the descendants of a particular branch in the tree. Taxa that are included in each clade are denoted using '*', and taxa that are not included are denoted using the '.' symbol.

The output first includes a key to all the bipartitions with frequency larger or equal to (Minpartfreq) in at least one run. Minpartfreq is a parameter to sumt command and currently it is set to 0.10. This is followed by a table with statistics for the informative bipartitions (those including at least two taxa), sorted from highest to lowest probability. For each bipartition, the table gives the number of times the partition or split was observed in all runs (#obs) and the posterior probability of the bipartition (Probab.), which is the same as the split frequency. If several runs are summarized, this is followed by the minimum split frequency (Min(s)), the maximum frequency (Max(s)), and the standard deviation of frequencies (Stddev(s)) across runs. The latter value should approach 0 for all bipartitions as MCMC runs converge.

This is followed by a table summarizing branch lengths, node heights (if a clock model was used) and relaxed clock parameters (if a relaxed clock model was used). The mean, variance, and 95% credible interval are given for each of these parameters. If several runs are summarized, the potential scale reduction factor (PSRF) is also given; it should approach 1 as runs converge. Node heights will take calibration points into account, if such points were used in the analysis.

Note that Stddev may be unreliable if the partition is not present in all runs (the last column indicates the number of runs that sampled the partition if more than one run is summarized). The PSRF is not calculated at all if the partition is not present in all runs. The PSRF is also sensitive to small sample sizes and it should only be considered a rough guide to convergence since some of the assumptions allowing one to interpret it as a true potential scale reduction factor are violated in MrBayes.

List of taxa in bipartitions:

1 -- gwi
2 -- dgr
3 -- scsh
4 -- xsl
5 -- bea
6 -- crx
| ID | Partition |
|----|-----------|
| 0  | ****************************************** |
| 1  | *........................................ |
| 2  | *........................................ |
| 3  | *........................................ |
| 4  | *........................................ |
| 5  | *........................................ |
| 6  | *........................................ |
| 7  | *........................................ |
| 8  | *........................................ |
| 9  | *........................................ |
| 10 | *........................................ |
| 11 | *........................................ |
| 12 | *........................................ |
| 13 | *........................................ |
| 14 | *........................................ |
| 15 | *........................................ |
| 16 | *........................................ |
| 17 | *........................................ |
| 18 | *........................................ |
| 19 | *........................................ |
| 20 | *........................................ |
| 21 | *........................................ |
| 22 | *........................................ |
| 23 | *........................................ |

Key to taxon bipartitions (saved to file "DY-27Dec-strict-H-KottOut.parts"): 

7 -- chp  
8 -- txc  
9 -- haa  
10 -- ing  
11 -- kuu  
12 -- hoi  
13 -- koy  
14 -- taa  
15 -- aht  
16 -- tfn  
17 -- kkz  
18 -- tcb  
19 -- tau  
20 -- ttmN  
21 -- tceS  
22 --eya  
23 -- tli  
24 -- gce  
25 -- tol  
26 -- cco  
27 -- hup  
28 -- mtl  
29 -- wlk  
30 -- kto  
31 -- apc  
32 -- apw  
33 -- apj  
34 -- nav  
35 -- apk  
36 -- apl  
37 -- srs  
38 -- ket
Summary statistics for informative taxon bipartitions (clades)
(saved to file "DY-27Dec-strict-H-KottOut.tstat"):

| ID | #obs | Probab.    |
|----|------|-----------|
| 39 | 2999 | 0.999334  |
| 40 | 2808 | 0.935688  |
| 41 | 2736 | 0.911696  |
| 42 | 2734 | 0.911030  |
| 43 | 2579 | 0.859380  |
| 44 | 2469 | 0.822726  |
| 45 | 2427 | 0.808730  |
| 46 | 2232 | 0.743752  |
| 47 | 2176 | 0.725092  |
| 48 | 2028 | 0.675775  |
| 49 | 1942 | 0.647118  |
| 50 | 1923 | 0.640786  |
| 51 | 1839 | 0.612796  |
| 52 | 1784 | 0.594469  |
| 53 | 1779 | 0.590137  |
| 54 | 1715 | 0.571476  |
| 55 | 1676 | 0.558481  |
| 56 | 1664 | 0.554482  |
| 57 | 1585 | 0.528157  |
| 58 | 1584 | 0.527824  |
| 59 | 1454 | 0.484505  |
| 60 | 1406 | 0.468510  |
| 61 | 1331 | 0.443519  |
| 62 | 1258 | 0.419194  |
| 63 | 1234 | 0.411196  |
| 64 | 1221 | 0.406864  |
Summary statistics for branch and node parameters
(saved to file "DY-27Dec-strict-H-KottOut.vstat"):

| Parameter | Mean    | Variance | Lower  | Upper  | Median |
|-----------|---------|----------|--------|--------|--------|
| length[1] | 0.054449| 0.000423 | 0.018219| 0.095083| 0.052436|
| length[2] | 0.055576| 0.000605 | 0.014802| 0.102980| 0.051390|
| length[3] | 0.048364| 0.000402 | 0.012873| 0.086119| 0.046138|
| length[4] | 0.037867| 0.000271 | 0.010269| 0.071812| 0.036148|
| length[5] | 0.046347| 0.000705 | 0.018219| 0.105083| 0.052436|
| length[6] | 0.036925| 0.000287 | 0.007704| 0.070282| 0.034539|
| length[68] | 0.026477 | 0.000263 | 0.000840 | 0.057212 | 0.023941 |
| length[69] | 0.016362 | 0.000127 | 0.000444 | 0.038932 | 0.014060 |
| length[70] | 0.015587 | 0.000209 | 0.000031 | 0.044570 | 0.010729 |
| length[71] | 0.015888 | 0.000122 | 0.000135 | 0.037971 | 0.013718 |
| length[72] | 0.030459 | 0.000478 | 0.000068 | 0.069929 | 0.026451 |
| length[73] | 0.024863 | 0.000314 | 0.000022 | 0.057158 | 0.022064 |
| length[74] | 0.016257 | 0.000240 | 0.000076 | 0.042638 | 0.012599 |
| length[75] | 0.010750 | 0.000080 | 0.000067 | 0.029945 | 0.008432 |
| length[76] | 0.021499 | 0.000226 | 0.000123 | 0.048659 | 0.018963 |
| length[77] | 0.021349 | 0.000209 | 0.000239 | 0.049232 | 0.018843 |
| length[78] | 0.015384 | 0.000143 | 0.000184 | 0.038514 | 0.012599 |
| length[79] | 0.031338 | 0.000485 | 0.000571 | 0.075600 | 0.025821 |
| length[80] | 0.011779 | 0.000083 | 0.000012 | 0.028151 | 0.009912 |
| length[81] | 0.011318 | 0.000080 | 0.000067 | 0.029903 | 0.008608 |
| length[82] | 0.020761 | 0.000262 | 0.000019 | 0.052820 | 0.017270 |
| length[83] | 0.034349 | 0.000351 | 0.003689 | 0.072965 | 0.032539 |
| length[84] | 0.008866 | 0.000078 | 0.000014 | 0.025897 | 0.006174 |
| length[85] | 0.024760 | 0.000256 | 0.000165 | 0.054461 | 0.022623 |
| length[86] | 0.009192 | 0.000078 | 0.000067 | 0.027520 | 0.009912 |
| length[87] | 0.009517 | 0.000083 | 0.000010 | 0.027803 | 0.008608 |
| height[0]  | 0.172294 | 0.000916 | 0.113402 | 0.233284 | 0.174672 |
| height[1]  | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 |
| height[2]  | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 |
| height[3]  | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 |
| height[4]  | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 |
| height[5]  | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 |
| height[6]  | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 |
| height[7]  | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 |
| height[8]  | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 |
| height[9]  | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 |
| height[10] | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 |
| height[11] | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 |
| height[12] | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 |
| height[13] | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 |
| height[14] | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 |
| height[15] | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 |
| height[16] | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 |
Clade credibility values:

```
txc (8)
|----------------------------------------------- kuu (11)
|--------------------- aht (15)
|--------------------- tfn (16)
  |--------------------- apc (31)
  |--------------------- apw (32)
  |--------------------- apj (33)
  |--------------------- nav (34)
  |--------------------- apk (35)
  |--------------------- apl (36)
```
Phylogram (based on median node depths):

|--|---|---|---|---|
|---|---|---|---|---|

Phylogram (based on median node depths):
Calculating tree probabilities...

Credible sets of trees (3001 trees sampled):
  50 % credible set contains 1501 trees
  90 % credible set contains 2701 trees
  95 % credible set contains 2851 trees
  99 % credible set contains 2971 trees

MrBayes v3.2.1 x64

(Bayesian Analysis of Phylogeny)

Distributed under the GNU General Public License

Type "help" or "help <command>" for information on the commands that are available.

Type "about" for authorship and general information about the program.

MrBayes > exe /Users/msicoli/Kott-NaDene-Typlogical_noHAX.nex

Executing file "/Users/msicoli/Kott-NaDene-Typlogical_noHAX.nex"
UNIX line termination
Longest line length = 123
Parsing file
Expecting NEXUS formatted file
Reading data block
  Allocated taxon set
  Allocated matrix
  Defining new matrix with 38 taxa and 116 characters
  Data is Standard
  Missing data coded as ?
  Gaps coded as -
  Data matrix is not interleaved
  Taxon 1 -> gwi
  Taxon 2 -> dgr
Taxon 3 -> scsh
Taxon 4 -> xsl
Taxon 5 -> bea
Taxon 6 -> crx
Taxon 7 -> chp
Taxon 8 -> txc
Taxon 9 -> haa
Taxon 10 -> ing
Taxon 11 -> kuu
Taxon 12 -> hoi
Taxon 13 -> koy
Taxon 14 -> taa
Taxon 15 -> aht
Taxon 16 -> tfn
Taxon 17 -> kkz
Taxon 18 -> tfn
Taxon 19 -> tau
Taxon 20 -> ttmN
Taxon 21 -> tceS
Taxon 22 -> eya
Taxon 23 -> tli
Taxon 24 -> gce
Taxon 25 -> tol
Taxon 26 -> cco
Taxon 27 -> hup
Taxon 28 -> mtl
Taxon 29 -> wlk
Taxon 30 -> kto
Taxon 31 -> apc
Taxon 32 -> apw
Taxon 33 -> apj
Taxon 34 -> nav
Taxon 35 -> apk
Taxon 36 -> apl
Taxon 37 -> srs
Taxon 38 -> zko

Successfully read matrix
Setting default partition (does not divide up characters)
Setting model defaults
Seed (for generating default start values) = 1388166360
Adding dummy characters (unobserved site patterns) for division 1
WARNING: There are 37 characters incompatible with the specified
coding bias. These characters will be excluded.

Setting output file names to "/Users/msicoli/Kott-NaDene-Typological_noHAX.nex.run<i>.<p|t>

Exiting data block
Reached end of file

MrBayes > lset nst=6 rates=gamma

Setting Rates to Gamma
Successfully set likelihood model parameters
Adding dummy characters (unobserved site patterns) for division 1
WARNING: There are 37 characters incompatible with the specified
coding bias. These characters will be excluded.

MrBayes > prset brlenspr=clock:uniform

Setting Brlnsenpr to Clock:Uniform
Successfully set prior model parameters
Adding dummy characters (unobserved site patterns) for division 1
WARNING: There are 37 characters incompatible with the specified
coding bias. These characters will be excluded.

MrBayes > mcmcp ngen=2000000 printfreq=10000 samplefreq=500 nruns=1 nchains=4 savebrlens=yes filename=DY-27Dec-strict-H-Ketout

Setting number of generations to 2000000
Setting print frequency to 10000
Setting sample frequency to 500
Setting number of runs to 1
Setting number of chains to 4
Setting chain output file names to "DY-27Dec-strict-H-Ketout.
Successfully set chain parameters

MrBayes > mcmc

Running Markov chain
MCMC stamp = 3571666900
Seed = 498838383
Swapseed = 1388166360
Model settings:

Data not partitioned --
  Datatype = Standard
  Coding = Variable
  # States = Variable, up to 10
      State frequencies are fixed to be equal
  Rates = Gamma
      Gamma shape parameter is uniformly distributed on the interval (0.00,200.00).
      Gamma distribution is approximated using 4 categories.
      Likelihood summarized over all rate categories in each generation.

Active parameters:

Parameters
-------------
Statefreq  1
Shape      2
Ratemultiplier  3
Topology   4
Brlns     5
Clockrate  6
-------------

1 -- Parameter = Alpha_symdir
   Type = Symmetric dirichlet/beta distribution alpha_i parameter
   Prior = Symmetric dirichlet with fixed(-1.00) variance parameter

2 -- Parameter = Alpha
   Type = Shape of scaled gamma distribution of site rates
   Prior = Uniform(0.00,200.00)

3 -- Parameter = Ratemultiplier
   Type = Partition-specific rate multiplier
   Prior = Fixed(1.0)

4 -- Parameter = Tau
   Type = Topology
   Prior = All topologies equally probable a priori
   Subparam. = V
5 -- Parameter = V  
Type = Branch lengths  
Prior = Clock:Uniform  
Tree age has an Exponential(1.000) distribution  
Node ages are not constrained

6 -- Parameter = Clockrate  
Type = Base rate of clock  
Prior = Fixed(1.000000)  
The clock rate is constant (strict clock)

Number of taxa = 38  
Number of characters = 116

The MCMC sampler will use the following moves:  
With prob. Chain will use move
  2.38 % Multiplier(Alpha)  
  11.90 % ExtSprClock(Tau,V)  
  23.81 % NNIClock(Tau,V)  
  11.90 % ParsSPRClock(Tau,V)  
  47.62 % NodesliderClock(V)  
  2.38 % TreeStretch(V)

Division 1 has 73 unique site patterns  
Initializing conditional likelihoods  
Using standard non-SSE likelihood calculator for division 1 (single-precision)

Initial log likelihoods and log prior probs:  
Chain 1 -- -1436.616125 -- -87.230988  
Chain 2 -- -1499.059192 -- -87.230988  
Chain 3 -- -1473.869674 -- -87.230988  
Chain 4 -- -1572.409710 -- -87.230988

Chain results (2000000 generations requested):  
0 -- [-1436.616] (-1499.059) (-1473.870) (-1572.410)

FILE TRUNCATED

2000000 -- (-900.513) (-901.708) (-905.373) [-897.352] -- 0:00:00

Continue with analysis? (yes/no): n

Analysis completed in 15 mins 25 seconds  
Analysis used 898.11 seconds of CPU time  
Log likelihood of best state for "cold" chain was -867.29

Acceptance rates for the moves in the "cold" chain:  
With prob. (last 100) chain accepted proposals by move
  39.8 % ( 30 %) Multiplier(Alpha)  
  19.9 % ( 17 %) ExtSprClock(Tau,V)  
  45.9 % ( 48 %) NNIClock(Tau,V)  
  16.2 % ( 16 %) ParsSPRClock(Tau,V)  
  71.2 % ( 74 %) NodesliderClock(V)  
  69.8 % ( 28 %) TreeStretch(V)

Chain swap information:  
  1  2  3  4
Upper diagonal: Proportion of successful state exchanges between chains
Lower diagonal: Number of attempted state exchanges between chains

Chain information:

ID -- Heat
-----------
1 -- 1.00  (cold chain)
2 -- 0.91
3 -- 0.83
4 -- 0.77

Heat = 1 / (1 + T * (ID - 1))  
(where T = 0.10 is the temperature and ID is the chain number)

MrBayes > sumt relburnin=yes
Using relative burnin (a fraction of samples discarded).
Summarizing trees in file "DY-27Dec-strict-H-Ketout.t"
Using relative burnin ('relburnin=yes'), discarding the first 25 % of sampled trees
Writing statistics to files DY-27Dec-strict-H-Ketout.<parts|tstat|vstat|trprobs|con>
Examining file ...
Found one tree block in file "DY-27Dec-strict-H-Ketout.t" with 4001 trees in last block

General explanation:

In an unrooted tree, a taxon bipartition (split) is specified by removing a branch, thereby dividing the species into those to the left and those to the right of the branch. Here, taxa to one side of the removed branch are denoted '.' and those to the other side are denoted '*'. Specifically, the '.' symbol is used for the taxa on the same side as the outgroup.

In a rooted or clock tree, the tree is rooted using the model and not by reference to an outgroup. Each bipartition therefore corresponds to a clade, that is, a group that includes all the descendants of a particular branch in the tree. Taxa that are included in each clade are denoted using '*', and taxa that are not included are denoted using the '.' symbol.

The output first includes a key to all the bipartitions with frequency larger or equal to (Minpartfreq) in at least one run. Minpartfreq is a parameter to sumt command and currently it is set to 0.10. This is followed by a table with statistics for the informative bipartitions (those including at least two taxa), sorted from highest to lowest probability. For each bipartition, the table gives the number of times the partition or split was observed in all runs (#obs) and the posterior probability of the bipartition (Probab.), which is the same as the split frequency. If several runs are summarized, this is
followed by the minimum split frequency (Min(s)), the maximum frequency (Max(s)), and the standard deviation of frequencies (Stddev(s)) across runs. The latter value should approach 0 for all bipartitions as MCMC runs converge.

This is followed by a table summarizing branch lengths, node heights (if a clock model was used) and relaxed clock parameters (if a relaxed clock model was used). The mean, variance, and 95% credible interval are given for each of these parameters. If several runs are summarized, the potential scale reduction factor (PSRF) is also given; it should approach 1 as runs converge. Node heights will take calibration points into account, if such points were used in the analysis.

Note that Stddev may be unreliable if the partition is not present in all runs (the last column indicates the number of runs that sampled the partition if more than one run is summarized). The PSRF is not calculated at all if the partition is not present in all runs. The PSRF is also sensitive to small sample sizes and it should only be considered a rough guide to convergence since some of the assumptions allowing one to interpret it as a true potential scale reduction factor are violated in MrBayes.

List of taxa in bipartitions:

1 -- gwi
2 -- dgr
3 -- scsh
4 -- xsl
5 -- bea
6 -- crx
7 -- chp
8 -- txc
9 -- haa
10 -- ing
11 -- kuu
12 -- hoi
13 -- koy
14 -- taa
15 -- aht
16 -- tfn
17 -- kkz
18 -- tcb
19 -- tau
20 -- ttmN
21 -- tceS
22 -- eya
23 -- tli
24 -- gce
25 -- tol
26 -- cco
27 -- hup
28 -- mtl
29 -- wlk
30 -- kto
31 -- apc
32 -- apw
33 -- apj
34 -- nav
35 -- apk
36 -- apl
37 -- srs
38 -- zko
Key to taxon bipartitions (saved to file "DY-27Dec-strict-H-Ketout.parts"):

| ID | Partition |
|----|-----------|
| 0  | ************************************** |
| 1  | *.................................... |
| 2  | ................................... |
| 3  | ................................... |
| 4  | ................................... |
| 5  | ................................... |
| 6  | ................................... |
| 7  | ................................... |
| 8  | ................................... |
| 9  | ................................... |
| 10 | ................................... |
| 11 | ................................... |
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| 21 | ................................... |
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| 23 | ................................... |
| 24 | ................................... |
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| 30 | ................................... |
| 31 | ................................... |
| 32 | ................................... |
| 33 | ................................... |
| 34 | ................................... |
| 35 | ................................... |
| 36 | ................................... |
| 37 | ................................... |
| 38 | ................................... |
| 39 | ................................... |
| 40 | ......................********* |
| 41 | .................................... |
| 42 | .................................... |
| 43 | .................................... |
| 44 | .................................... |
| 45 | .................................... |
| 46 | .................................... |
| 47 | .................................... |
| 48 | .................................... |
| 49 | .................................... |
| 50 | .................................... |
| 51 | .................................... |
| 52 | .................................... |
| 53 | .................................... |
| 54 | .................................... |
| 55 | .................................... |
| 56 | .................................... |
Summary statistics for informative taxon bipartitions (clades)
(saved to file "DY-27Dec-strict-H-Ketout.tstat"):

| ID | #obs | Probab. |
|----|------|---------|

---
|   |    |          |
|---|----|----------|
| 39 | 3000 | 0.999667 |
| 40 | 2770 | 0.923026 |
| 41 | 2616 | 0.871709 |
| 42 | 2536 | 0.845052 |
| 43 | 2493 | 0.830723 |
| 44 | 2469 | 0.822726 |
| 45 | 2273 | 0.757414 |
| 46 | 2208 | 0.735755 |
| 47 | 2091 | 0.696768 |
| 48 | 1990 | 0.663112 |
| 49 | 1873 | 0.624125 |
| 50 | 1848 | 0.615795 |
| 51 | 1826 | 0.604664 |
| 52 | 1802 | 0.604667 |
| 53 | 1723 | 0.574142 |
| 54 | 1642 | 0.547151 |
| 55 | 1611 | 0.536821 |
| 56 | 1536 | 0.511829 |
| 57 | 1529 | 0.509497 |
| 58 | 1492 | 0.497168 |
| 59 | 1310 | 0.436521 |
| 60 | 1275 | 0.424858 |
| 61 | 1247 | 0.415528 |
| 62 | 1172 | 0.390536 |
| 63 | 1146 | 0.381873 |
| 64 | 1144 | 0.381206 |
| 65 | 1129 | 0.376208 |
| 66 | 1110 | 0.369877 |
| 67 | 1052 | 0.350550 |
| 68 | 945  | 0.314895 |
| 69 | 920  | 0.306564 |
| 70 | 859  | 0.286238 |
| 71 | 843  | 0.280906 |
| 72 | 778  | 0.259247 |
| 73 | 758  | 0.252582 |
| 74 | 741  | 0.246918 |
| 75 | 725  | 0.241586 |
| 76 | 712  | 0.237254 |
| 77 | 701  | 0.233589 |
| 78 | 680  | 0.226591 |
| 79 | 674  | 0.224592 |
| 80 | 664  | 0.221260 |
| 81 | 580  | 0.193269 |
| 82 | 576  | 0.191936 |
| 83 | 554  | 0.184605 |
| 84 | 552  | 0.183939 |
| 85 | 543  | 0.180940 |
| 86 | 537  | 0.178940 |
| 87 | 533  | 0.177607 |
| 88 | 512  | 0.170610 |
| 89 | 488  | 0.162612 |
| 90 | 474  | 0.157947 |
| 91 | 471  | 0.156948 |
| 92 | 452  | 0.150616 |
| 93 | 420  | 0.139953 |
| 94 | 418  | 0.139287 |
| 95 | 416  | 0.138620 |
| 96 | 413  | 0.137621 |
| 97 | 403  | 0.134289 |
Summary statistics for branch and node parameters
(saved to file "DY-27Dec-strict-H-Ketout.vstat"):

| Parameter | Mean       | Variance   | Lower       | Upper       | Median     |
|-----------|------------|------------|-------------|-------------|------------|
| length[1] | 0.052545   | 0.000471   | 0.011730    | 0.093428    | 0.050256   |
| length[2] | 0.053626   | 0.000632   | 0.014504    | 0.105335    | 0.049081   |
| length[3] | 0.046066   | 0.000415   | 0.011731    | 0.085941    | 0.044023   |
| length[4] | 0.035983   | 0.000287   | 0.008153    | 0.070499    | 0.033569   |
| length[5] | 0.044289   | 0.000742   | 0.005749    | 0.101774    | 0.037527   |
| length[6] | 0.035011   | 0.000301   | 0.006534    | 0.069443    | 0.032513   |
| length[7] | 0.046579   | 0.000874   | 0.012562    | 0.102167    | 0.039973   |
| length[8] | 0.106981   | 0.001158   | 0.037343    | 0.167190    | 0.107333   |
| length[9] | 0.051025   | 0.000296   | 0.016946    | 0.100596    | 0.048617   |
| length[10]| 0.052613   | 0.000605   | 0.011542    | 0.100596    | 0.049555   |
| length[11]| 0.085711   | 0.001215   | 0.022021    | 0.152710    | 0.084126   |
| length[12]| 0.053626   | 0.000632   | 0.014504    | 0.105335    | 0.049081   |
| length[13]| 0.035983   | 0.000287   | 0.008153    | 0.070499    | 0.033569   |
| length[14]| 0.050125   | 0.000296   | 0.016946    | 0.102167    | 0.049973   |
| length[15]| 0.103577   | 0.000471   | 0.022021    | 0.152710    | 0.084126   |
| length[16]| 0.100245   | 0.000605   | 0.011542    | 0.100596    | 0.049555   |
| length[17]| 0.085711   | 0.001215   | 0.022021    | 0.152710    | 0.084126   |
| length[18]| 0.035983   | 0.000287   | 0.008153    | 0.070499    | 0.033569   |
| length[19]| 0.051025   | 0.000296   | 0.016946    | 0.102167    | 0.049973   |
| length[20]| 0.100245   | 0.000605   | 0.011542    | 0.100596    | 0.049555   |
| length[21]| 0.085711   | 0.001215   | 0.022021    | 0.152710    | 0.084126   |
| length[22]| 0.051025   | 0.000296   | 0.016946    | 0.102167    | 0.049973   |
| length[23]| 0.085711   | 0.001215   | 0.022021    | 0.152710    | 0.084126   |
| length[24]| 0.035983   | 0.000287   | 0.008153    | 0.070499    | 0.033569   |
| length[25]| 0.051025   | 0.000296   | 0.016946    | 0.102167    | 0.049973   |
| length[26]| 0.085711   | 0.001215   | 0.022021    | 0.152710    | 0.084126   |
| length[27]| 0.035983   | 0.000287   | 0.008153    | 0.070499    | 0.033569   |
| length[28]| 0.051025   | 0.000296   | 0.016946    | 0.102167    | 0.049973   |
| length[29]| 0.085711   | 0.001215   | 0.022021    | 0.152710    | 0.084126   |
| length[30]| 0.035983   | 0.000287   | 0.008153    | 0.070499    | 0.033569   |
| length[31]| 0.051025   | 0.000296   | 0.016946    | 0.102167    | 0.049973   |
| length[32]| 0.085711   | 0.001215   | 0.022021    | 0.152710    | 0.084126   |
| length[33]| 0.035983   | 0.000287   | 0.008153    | 0.070499    | 0.033569   |
| length[34]| 0.051025   | 0.000296   | 0.016946    | 0.102167    | 0.049973   |
| length[35]| 0.085711   | 0.001215   | 0.022021    | 0.152710    | 0.084126   |
| length[36]| 0.035983   | 0.000287   | 0.008153    | 0.070499    | 0.033569   |
| length[37]| 0.051025   | 0.000296   | 0.016946    | 0.102167    | 0.049973   |
| length[38]| 0.085711   | 0.001215   | 0.022021    | 0.152710    | 0.084126   |
| length[39]| 0.035983   | 0.000287   | 0.008153    | 0.070499    | 0.033569   |

95% HPD Interval
Clade credibility values:

| Clade | Credibility |
|-------|-------------|
| txc   | 8           |
| kuu   | 11          |
| aht   | 15          |
| tfn   | 16          |
| zko   | 38          |
| apc   | 31          |
| apw   | 32          |
| apj   | 33          |
| nav   | 34          |
| apk   | 35          |
| apl   | 36          |
| srs   | 37          |
| eya   | 22          |
| hup   | 27          |
| mtl   | 28          |
| wlk   | 29          |
| kto   | 30          |
| ing   | 10          |
| hoi   | 12          |
| koy   | 13          |
| gwi   | 1           |
| dgr   | 2           |
| scsh  | 3           |
| bea   | 5           |
| crx   | 6           |
| xsl   | 4           |
Phylogram (based on median node depths):

/--------------- txc (8)
|-------------------- kuu (11)
|--------------------- aht (15)
|--------------------- tfn (16)
|--------------------- zko (38)

       /-- apc (31)
       |       /-- apw (32)
       |       |       /-- apj (33)
       |       |       |       /-- nav (34)
       |       |       |       |       /-- apk (35)
       |       |       |       |       |       ----- apl (36)
       |       |       |       |       |       |       srs (37)
       |       |       |       |       |       |       |       |       |       |       |       |       eya (22)

/------------------- tli (23)
|--------------------- hup (27)
|--------------------- mtl (28)

/------------------- wlk (29)
|------------------- kto (30)
Calculating tree probabilities...

Credible sets of trees (3001 trees sampled):

- 50% credible set contains 1501 trees
- 90% credible set contains 2701 trees
- 95% credible set contains 2851 trees
- 99% credible set contains 2971 trees
MrBayes > exe /Users/msicoli/Yeniseian-NaDene-Typ_noHAXNoEYA.nex

Executing file "/Users/msicoli/Yeniseian-NaDene-Typ_noHAXNoEYA.nex"
UNIX line termination
Longest line length = 123
Parsing file
Expecting NEXUS formatted file
Reading data block
  Allocated taxon set
  Allocated matrix
  Defining new matrix with 38 taxa and 116 characters
  Data is Standard
  Missing data coded as ?
  Gaps coded as -
  Data matrix is not interleaved
Taxon 1 -> gwi
Taxon 2 -> dgr
Taxon 3 -> scsh
Taxon 4 -> xsl
Taxon 5 -> bea
Taxon 6 -> crx
Taxon 7 -> chp
Taxon 8 -> txc
Taxon 9 -> haa
Taxon 10 -> ing
Taxon 11 -> kuu
Taxon 12 -> hoi
Taxon 13 -> koy
Taxon 14 -> taa
Taxon 15 -> aht
Taxon 16 -> tfn
Taxon 17 -> kkz
Taxon 18 -> tcb
Taxon 19 -> tau
Taxon 20 -> ttmN
Taxon 21 -> tceS
Taxon 22 -> tli
Taxon 23 -> gce
Taxon 24 -> tol
Taxon 25 -> cco
Taxon 26 -> hup
Taxon 27 -> mtl
Taxon 28 -> wlk
Taxon 29 -> kto
Taxon 30 -> apc
Taxon 31 -> apw
Taxon 32 -> apj
Taxon 33 -> nav
Taxon 34 -> apk
Taxon 35 -> apl
MrBayes > lset nst=6 rates=gamma

Setting Rates to Gamma
Successfully set likelihood model parameters
Adding dummy characters (unobserved site patterns) for division 1
WARNING: There are 32 characters incompatible with the specified coding bias. These characters will be excluded.

MrBayes > prset brlenspr=clock:uniform

Setting Brlnspr to Clock:Uniform
Successfully set prior model parameters
Adding dummy characters (unobserved site patterns) for division 1
WARNING: There are 32 characters incompatible with the specified coding bias. These characters will be excluded.

MrBayes > mcmcp ngen=2000000 printfreq=10000 samplefreq=500 nruns=1 nchains=4 savebrlens=yes
filename=DY-27Dec-strict-H-EOut

Setting number of generations to 2000000
Setting print frequency to 10000
Setting sample frequency to 500
Setting number of runs to 1
Setting number of chains to 4
Setting chain output file names to "DY-27Dec-strict-H-EOut.<p/t>"
Successfully set chain parameters

MrBayes > mcmc

Running Markov chain
MCMC stamp = 3445309595
Seed = 583544739
Swapseed = 1388169385
Model settings:

Data not partitioned --
Datatype = Standard
Coding = Variable
# States = Variable, up to 10
State frequencies are fixed to be equal
Rates = Gamma
Gamma shape parameter is uniformly distributed on the interval (0.00,200.00).
Gamma distribution is approximated using 4 categories.
Likelihood summarized over all rate categories in each generation.

Active parameters:

Parameters
--------------
Statefreq  1
Shape            2
Ratemultiplier   3
Topology         4
BrLens           5
Clockrate        6
------------------

1 -- Parameter = Alpha_symdir
   Type = Symmetric dirichlet/beta distribution alpha_i parameter
   Prior = Symmetric dirichlet with fixed(-1.00) variance parameter

2 -- Parameter = Alpha
   Type = Shape of scaled gamma distribution of site rates
   Prior = Uniform(0.00,200.00)

3 -- Parameter = Ratemultiplier
   Type = Partition-specific rate multiplier
   Prior = Fixed(1.0)

4 -- Parameter = Tau
   Type = Topology
   Prior = All topologies equally probable a priori
   Subparam. = V

5 -- Parameter = V
   Type = Branch lengths
   Prior = Clock:Uniform
          Tree age has an Exponential(1.000) distribution
          Node ages are not constrained

6 -- Parameter = Clockrate
   Type = Base rate of clock
   Prior = Fixed(1.000000)
          The clock rate is constant (strict clock)

Number of taxa = 38
Number of characters = 116

The MCMC sampler will use the following moves:
   With prob. Chain will use move
   2.38 % Multiplier(Alpha)
   11.90 % ExtSprClock(Tau,V)
   23.81 % NNIClock(Tau,V)
   11.90 % ParsSPRClock(Tau,V)
   47.62 % NodesliderClock(V)
   2.38 % TreeStretch(V)

Division 1 has 77 unique site patterns
Initializing conditional likelihoods
Using standard non-SSE likelihood calculator for division 1 (single-precision)

Initial log likelihoods and log prior probs:
   Chain 1 -- -1529.584402 -- -87.230988
   Chain 2 -- -1536.001745 -- -87.230988
   Chain 3 -- -1493.848213 -- -87.230988
   Chain 4 -- -1568.572229 -- -87.230988

Chain results (2000000 generations requested):
   0 -- [-1529.584] (-1536.002) (-1493.848) (-1568.572)

[OMITTED GENERATIONS]
Continue with analysis? (yes/no): n

Analysis completed in 16 mins 36 seconds
Analysis used 951.77 seconds of CPU time
Log likelihood of best state for "cold" chain was -893.59

Acceptance rates for the moves in the "cold" chain:

With prob. (last 100) chain accepted proposals by move
38.2 % ( 25 %) Multiplier(Alpha)
19.3 % ( 27 %) ExtSprClock(Tau,V)
45.0 % ( 43 %) NNIClock(Tau,V)
15.4 % ( 17 %) ParsSPRClock(Tau,V)
70.4 % ( 71 %) NodesliderClock(V)
71.2 % ( 26 %) TreeStretch(V)

Chain swap information:

|   | 1   | 2   | 3   | 4   |
|---|-----|-----|-----|-----|
| 1 | 0.53| 0.26| 0.11|
| 2 | 334295 | 0.60| 0.33|
| 3 | 332184 333798 | 0.64|
| 4 | 332815 334284 332624 |

Upper diagonal: Proportion of successful state exchanges between chains
Lower diagonal: Number of attempted state exchanges between chains

Chain information:

| ID | Heat |
|----|------|
| 1  | 1.00 (cold chain) |
| 2  | 0.91 |
| 3  | 0.83 |
| 4  | 0.77 |

Heat = 1 / (1 + T * (ID - 1))

where T = 0.10 is the temperature and ID is the chain number

Using relative burnin (a fraction of samples discarded).
Summarizing trees in file "DY-27Dec-strict-H-EOut.t"
Using relative burnin ('relburnin=yes'), discarding the first 25 % of sampled trees
Writing statistics to files DY-27Dec-strict-H-EOut.<parts|tstat|vstat|trprobs|con>
Examining file ...
Found one tree block in file "DY-27Dec-strict-H-EOut.t" with 4001 trees in last block

Tree reading status:

Read 4001 trees from last tree block (sampling 3001 of them)

General explanation:

In an unrooted tree, a taxon bipartition (split) is specified by removing a branch, thereby dividing the species into those to the left and those to the right of the branch. Here, taxa to one side of the removed branch are denoted '.' and those to the other side are denoted '***'. Specifically, the '.' symbol
is used for the taxa on the same side as the outgroup.

In a rooted or clock tree, the tree is rooted using the model and not by reference to an outgroup. Each bipartition therefore corresponds to a clade, that is, a group that includes all the descendants of a particular branch in the tree. Taxa that are included in each clade are denoted using '"', and taxa that are not included are denoted using the '.' symbol.

The output first includes a key to all the bipartitions with frequency larger or equal to (Minpartfreq) in at least one run. Minpartfreq is a parameter to sumt command and currently it is set to 0.10. This is followed by a table with statistics for the informative bipartitions (those including at least two taxa), sorted from highest to lowest probability. For each bipartition, the table gives the number of times the partition or split was observed in all runs (#obs) and the posterior probability of the bipartition (Probab.), which is the same as the split frequency. If several runs are summarized, this is followed by the minimum split frequency (Min(s)), the maximum frequency (Max(s)), and the standard deviation of frequencies (Stddev(s)) across runs. The latter value should approach 0 for all bipartitions as MCMC runs converge.

This is followed by a table summarizing branch lengths, node heights (if a clock model was used) and relaxed clock parameters (if a relaxed clock model was used). The mean, variance, and 95% credible interval are given for each of these parameters. If several runs are summarized, the potential scale reduction factor (PSRF) is also given; it should approach 1 as runs converge. Node heights will take calibration points into account, if such points were used in the analysis.

Note that Stddev may be unreliable if the partition is not present in all runs (the last column indicates the number of runs that sampled the partition if more than one run is summarized). The PSRF is not calculated at all if the partition is not present in all runs. The PSRF is also sensitive to small sample sizes and it should only be considered a rough guide to convergence since some of the assumptions allowing one to interpret it as a true potential scale reduction factor are violated in MrBayes.

Clade credibility values:

```
/--------------------------------------------------------------------- txc (8)
|--------------------------------------------------------------------- kuu (11)
|--------------------------------------------------------------------- aht (15)
|--------------------------------------------------------------------- tfn (16)
|--------------------------------------------------------------------- tli (22)
|--------------------------------------------------------------------- ket (37)
/---------------------------100---------------------------+
|--------------------------------------------------------------------- zko (38)
|--------------------------------------------------------------------- apc (30)
/-----61-----+
|--------------------------------------------------------------------- apw (31)
/-----69-----+
|--------------------------------------------------------------------- apj (32)
/-----84-----+
|--------------------------------------------------------------------- nav (33)
/-----73-----+
|--------------------100---------------------------+
|--------------------------------------------------------------------- apk (34)
/-----92-----+
```
[Expected changes per site]

Calculating tree probabilities...

Credible sets of trees (3001 trees sampled):
50 % credible set contains 1501 trees
90 % credible set contains 2701 trees
95 % credible set contains 2851 trees
99 % credible set contains 2971 trees

MrBayes > sump relburnin=yes

Using relative burnin (a fraction of samples discarded).
Summarizing parameters in file DY-27Dec-strict-H-EOut.p
Writing summary statistics to file DY-27Dec-strict-H-EOut.pstat
Using relative burnin ('relburnin=yes'), discarding the first 25 % of samples

Below is a rough plot of the generation (x-axis) versus the log probability of observing the data (y-axis). You can use this graph to determine what the burn in for your analysis should be. When the log probability starts to plateau you may be at stationarity. Sample trees and parameters after the log probability plateaus. Of course, this is not a guarantee that you are at stationarity. When the log probability starts to plateau, you may be at stationarity. When possible, run multiple analyses starting from different random trees; if the inferences you make for independent analyses are the same, this is reasonable evidence that the chains have converged. You can use MrBayes to run several independent analyses simultaneously. During such a run, MrBayes will monitor the convergence of topologies. After the run has been completed, the 'sumt' and 'sump' functions will provide additional convergence diagnostics for all the parameters in your model. Remember that the burn in is the number of samples to discard. There are a total of ngen / samplefreq samples taken during a MCMC analysis.

Estimated marginal likelihoods for run sampled in file "DY-27Dec-strict-H-EOut.p":
(Use the harmonic mean for Bayes factor comparisons of models)
(Values are saved to the file /Users/msicoli/Yeniseian-NaDene-Typ_noHAXNoEYA.nex.lstat)

Arithmetic mean  Harmonic mean
Model parameter summaries for run sampled in file "DY-27Dec-strict-H-EOut":
Based on a total of 3001 samples out of a total of 4001 samples
from this analysis.
Parameter summaries saved to file "/Users/msicoli/Yeniseian-NaDene-Typ_noHAXNoEYA.nex.pstat".

| Parameter | Mean   | Variance | Lower  | Upper  | Median | ESS*  |
|-----------|--------|----------|--------|--------|--------|-------|
| TH        | 0.175288 | 0.001509 | 0.086786 | 0.243660 | 0.176903 | 435.06 |
| TL        | 2.788269 | 0.305848 | 1.474125 | 3.694101 | 2.854921 | 399.02 |
| alpha     | 4.785785 | 305.551597 | 0.162164 | 9.106779 | 1.576508 | 2663.77 |

* Convergence diagnostic (ESS = Estimated Sample Size); ESS value below 100 may indicate that the parameter is undersampled.