MCMC Runs for Fig. 2 (with Haida Outgroup)

(2a) With Na-Dene Ingroup Constraint	2
(2b) Without Na-Dene Ingroup Constraint	40

```
                            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/DY-Typlogical_binary_bayes-2.nex

   Executing file "/Users/msicoli/DY-Typlogical_binary_bayes-2.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 40 taxa and 116 characters
      Data is Standard
      Missing data coded as ?
      Gaps coded as -
      Data matrix is not interleaved
      Taxon  1 -> hax
      Taxon  2 -> gwi
      Taxon  3 -> dgr
      Taxon  4 -> scsh
      Taxon  5 -> xsl
      Taxon  6 -> bea
      Taxon  7 -> crx
      Taxon  8 -> chp
      Taxon  9 -> txc
      Taxon 10 -> haa
      Taxon 11 -> ing
      Taxon 12 -> kuu
      Taxon 13 -> hoi
      Taxon 14 -> koy
      Taxon 15 -> taa
      Taxon 16 -> aht
      Taxon 17 -> tfn
      Taxon 18 -> kkz
      Taxon 19 -> tcb
      Taxon 20 -> tau
      Taxon 21 -> ttmN
      Taxon 22 -> tceS
      Taxon 23 -> eya
      Taxon 24 -> tli
      Taxon 25 -> gce
      Taxon 26 -> tol
      Taxon 27 -> cco
```

```
      Taxon 28 -> hup
      Taxon 29 -> mtl
      Taxon 30 -> wlk
      Taxon 31 -> kto
      Taxon 32 -> apc
      Taxon 33 -> apw
      Taxon 34 -> apj
      Taxon 35 -> nav
      Taxon 36 -> apk
      Taxon 37 -> apl
      Taxon 38 -> srs
      Taxon 39 -> ket
      Taxon 40 -> zko
      Successfully read matrix
      Setting default partition (does not divide up characters)
      Setting model defaults
      Seed (for generating default start values) = 1388071270
      Adding dummy characters (unobserved site patterns) for division 1
      WARNING: There are 26 characters incompatible with the specified
               coding bias. These characters will be excluded.
      Setting output file names to "/Users/msicoli/DY-Typlogical_binary_bayes-2.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 26 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 26 characters incompatible with the specified
            coding bias. These characters will be excluded.

MrBayes > outgroup 1

   Setting outgroup to taxon "hax"

MrBayes > constraint ingroup = 2-38

   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 26 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-Hout-Ynotin

   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-Hout-Ynotin.<p/t>"
   Successfully set chain parameters

MrBayes > mcmc

   Running Markov chain
   MCMC stamp = 5611881771
   Seed = 1248079053
   Swapseed = 1388071270
   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 diricihlet/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 = 40
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 81 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 -- -1621.647120 -- -93.249778
   Chain 2 -- -1592.249470 -- -93.249778
   Chain 3 -- -1633.133426 -- -93.249778
   Chain 4 -- -1575.340102 -- -93.249778


Chain results (2000000 generations requested):

    0 -- [-1621.647] (-1592.249) (-1633.133) (-1575.340)
10000 -- (-1028.739) (-1036.015) (-1042.466) [-1020.536] -- 0:19:54
20000 -- (-1045.088) (-1012.996) (-1046.210) [-1000.570] -- 0:19:48
30000 -- (-1020.521) (-1002.542) (-1016.358) [-1003.863] -- 0:19:42
40000 -- (-1023.325) (-1013.502) [-995.452] (-1014.276) -- 0:19:36
50000 -- (-1017.019) (-1015.170) [-990.457] (-1020.263) -- 0:19:30
60000 -- (-1025.688) [-1001.691] (-1020.365) (-1017.846) -- 0:19:24
70000 -- (-1010.197) [-1009.446] (-1003.460) (-1016.008) -- 0:18:50
80000 -- [-1011.420] (-1014.188) (-1019.493) (-1014.499) -- 0:18:48
90000 -- (-1006.714) [-1003.648] (-1019.475) (-1006.100) -- 0:18:44
100000 -- (-1011.789) (-1015.559) (-1016.683) [-1009.579] -- 0:18:41
110000 -- [-1005.796] (-1017.809) (-1024.687) (-1014.136) -- 0:18:36
120000 -- (-1016.930) (-1007.096) (-1021.067) [-1004.768] -- 0:18:32
130000 -- [-1023.588] (-1027.211) (-1019.895) (-1012.184) -- 0:18:27
140000 -- (-1005.673) (-1010.089) (-1015.651) [-1009.047] -- 0:18:22
150000 -- (-1020.893) (-1006.895) [-991.682] (-1033.428) -- 0:18:05
160000 -- (-1015.701) (-1011.841) [-1013.735] (-1002.196) -- 0:18:01
170000 -- (-1017.437) (-1044.298) (-1005.647) [-1009.599] -- 0:17:56
180000 -- (-1021.359) (-1002.082) (-1016.087) [-1002.729] -- 0:17:51
190000 -- (-1022.265) (-1009.941) (-1010.601) [-1000.119] -- 0:17:46
200000 -- (-1029.121) (-1027.367) [-1003.992] (-1021.071) -- 0:17:33
```

```
210000 -- (-1008.409) (-1009.661) (-1018.253) [-1014.320] -- 0:17:45
220000 -- (-1023.948) [-995.109] (-1022.535) (-1010.661) -- 0:17:39
230000 -- (-1003.654) (-1010.333) [-1003.976] (-1012.312) -- 0:17:34
240000 -- (-1006.234) (-997.865) (-1017.299) [-1008.493] -- 0:17:28
250000 -- (-1011.312) (-1016.119) [-1026.958] (-1017.007) -- 0:17:23
260000 -- (-999.963) (-1027.636) (-1015.583) [-1006.645] -- 0:17:17
270000 -- (-1025.851) [-1004.928] (-1026.834) (-1000.745) -- 0:17:05
280000 -- (-1025.845) (-996.241) (-1013.331) [-1014.689] -- 0:16:59
290000 -- (-1009.085) [-1011.515] (-1017.801) (-1007.360) -- 0:16:54
300000 -- (-1011.249) (-1016.287) [-1004.812] (-1029.991) -- 0:16:43
310000 -- (-1015.481) (-1007.481) [-1007.868] (-1019.198) -- 0:16:37
320000 -- (-1012.726) (-1016.447) [-1016.620] (-1015.538) -- 0:16:32
330000 -- (-1011.591) (-1014.093) (-1024.598) [-1027.289] -- 0:16:26
340000 -- (-1007.399) (-1009.124) (-1004.371) [-1003.718] -- 0:16:21
350000 -- (-1005.471) (-1005.793) [-998.373] (-1033.099) -- 0:16:11
360000 -- (-1026.010) [-1004.184] (-1015.620) (-1005.896) -- 0:16:05
370000 -- (-1024.046) (-1019.174) [-996.148] (-1011.345) -- 0:16:00
380000 -- [-1009.413] (-1008.610) (-1006.646) (-1013.255) -- 0:15:54
390000 -- [-1011.596] (-1013.265) (-1016.090) (-1029.346) -- 0:15:45
400000 -- [-1005.069] (-1007.953) (-1022.807) (-1017.452) -- 0:15:44
410000 -- (-1022.164) (-1002.936) (-1019.030) [-1004.159] -- 0:15:38
420000 -- (-1017.577) (-1009.683) (-1018.047) [-1006.836] -- 0:15:32
430000 -- (-1014.977) (-1014.136) [-1007.215] (-1002.965) -- 0:15:23
440000 -- [-1001.969] (-1005.414) (-1002.851) (-1020.846) -- 0:15:18
450000 -- [-1010.898] (-1024.177) (-1013.844) (-1004.979) -- 0:15:12
460000 -- [-1007.375] (-1024.528) (-1013.980) (-1010.060) -- 0:15:07
470000 -- (-1016.171) [-1021.828] (-1029.044) (-1009.960) -- 0:15:01
480000 -- (-1027.665) (-1025.530) (-1005.897) [-1011.579] -- 0:14:53
490000 -- (-1042.298) (-1013.445) [-993.752] (-1022.066) -- 0:14:47
500000 -- [-1006.274] (-1006.998) (-1020.058) (-1012.929) -- 0:14:42
510000 -- (-1013.059) (-1020.123) [-1018.778] (-1033.993) -- 0:14:39
520000 -- [-1005.962] (-1015.984) (-1013.603) (-1010.642) -- 0:14:33
530000 -- (-1033.233) (-1008.576) [-1018.045] (-1023.188) -- 0:14:28
540000 -- [-1005.473] (-1022.940) (-1019.235) (-1020.007) -- 0:14:22
550000 -- (-1024.444) (-1005.461) [-1003.346] (-1019.444) -- 0:14:16
560000 -- (-1013.884) (-1027.105) [-1002.710] (-1017.864) -- 0:14:08
570000 -- [-1004.944] (-1005.922) (-1003.306) (-1025.436) -- 0:14:02
580000 -- (-1011.828) (-1003.024) [-1004.551] (-1024.916) -- 0:13:57
590000 -- (-1008.870) [-1008.526] (-1014.506) (-1016.521) -- 0:13:51
600000 -- [-1006.229] (-1004.051) (-1014.935) (-1022.570) -- 0:13:46
610000 -- (-1009.967) (-1008.053) [-1002.212] (-1009.617) -- 0:13:40
620000 -- [-1014.093] (-1006.169) (-1011.886) (-1009.182) -- 0:13:34
630000 -- [-1006.522] (-1032.301) (-1025.145) (-1017.590) -- 0:13:28
640000 -- (-1011.318) (-1015.783) (-1010.288) [-1014.531] -- 0:13:23
650000 -- (-1020.133) [-1009.421] (-1021.844) (-1011.591) -- 0:13:17
660000 -- [-1005.344] (-1020.831) (-1028.511) (-1029.863) -- 0:13:09
670000 -- (-996.378) (-1021.608) (-1008.217) [-993.651] -- 0:13:04
680000 -- (-1018.575) (-1032.091) (-1015.942) [-1019.182] -- 0:12:58
690000 -- [-1008.255] (-1012.471) (-1031.978) (-1026.745) -- 0:12:54
700000 -- [-1003.531] (-999.518) (-1007.559) (-1003.923) -- 0:12:48
710000 -- (-1012.906) [-1004.163] (-1034.484) (-1008.115) -- 0:12:43
720000 -- [-1014.379] (-1010.820) (-1032.175) (-1016.982) -- 0:12:37
730000 -- (-1013.607) (-1007.597) (-1018.865) [-1014.726] -- 0:12:31
740000 -- (-1016.461) [-1011.403] (-1007.873) (-1000.126) -- 0:12:25
750000 -- [-1003.508] (-1008.402) (-1021.492) (-1031.679) -- 0:12:20
760000 -- (-1008.858) [-1005.331] (-1009.687) (-1014.012) -- 0:12:12
770000 -- (-1024.606) (-1008.203) (-1004.744) [-1011.825] -- 0:12:06
780000 -- [-1004.854] (-1020.586) (-1011.578) (-1005.325) -- 0:12:01
```

```
790000 -- (-1017.457) (-1018.735) (-1007.303) [-998.554] -- 0:11:55
800000 -- (-1009.723) (-1021.077) [-998.028] (-997.442) -- 0:11:49
810000 -- (-1003.867) (-1008.095) (-1011.783) [-1013.459] -- 0:11:46
820000 -- (-1035.514) [-1010.655] (-1010.580) (-1001.138) -- 0:11:39
830000 -- [-997.851] (-1002.037) (-1018.289) (-1008.216) -- 0:11:33
840000 -- (-1006.676) (-1010.737) (-1010.589) [-1010.792] -- 0:11:27
850000 -- (-1018.364) (-1008.317) (-1014.378) [-1001.501] -- 0:11:21
860000 -- (-1021.436) [-1010.950] (-1005.742) (-1037.870) -- 0:11:16
870000 -- (-1001.760) (-1013.312) (-1029.281) [-1001.023] -- 0:11:10
880000 -- (-1006.871) (-1007.812) [-1015.737] (-1009.957) -- 0:11:04
890000 -- (-1008.353) (-1019.206) (-1031.399) [-1001.545] -- 0:10:58
900000 -- (-1012.013) [-1004.281] (-1016.681) (-1021.461) -- 0:10:51
910000 -- [-1005.411] (-1008.072) (-1008.114) (-1012.823) -- 0:10:45
920000 -- (-1021.312) (-1014.828) [-1002.497] (-1012.104) -- 0:10:39
930000 -- (-1010.929) (-1023.528) (-1011.387) [-1009.112] -- 0:10:33
940000 -- (-996.431) [-1003.137] (-1026.287) (-1014.202) -- 0:10:28
950000 -- (-1024.055) [-1009.419] (-1020.389) (-1024.903) -- 0:10:22
960000 -- (-1041.328) (-1010.456) (-1023.506) [-997.472] -- 0:10:15
970000 -- (-1014.609) [-1001.060] (-1023.159) (-1024.159) -- 0:10:09
980000 -- (-1011.301) (-1054.548) [-1012.624] (-1010.832) -- 0:10:03
990000 -- [-1002.612] (-1014.374) (-1019.434) (-1002.944) -- 0:09:58
1000000 -- (-1003.871) (-1015.941) [-995.716] (-1025.840) -- 0:09:52
1010000 -- (-1002.151) [-1002.526] (-1014.542) (-1003.980) -- 0:09:46
1020000 -- (-1005.365) (-1007.142) (-1014.304) [-1011.118] -- 0:09:40
1030000 -- (-1018.665) (-1009.684) (-1015.946) [-1008.804] -- 0:09:34
1040000 -- [-999.383] (-1021.723) (-1028.371) (-1007.834) -- 0:09:28
1050000 -- (-1004.099) (-1024.959) (-1001.189) [-1007.905] -- 0:09:22
1060000 -- [-988.730] (-1004.434) (-1015.640) (-1006.683) -- 0:09:16
1070000 -- [-999.262] (-1004.973) (-1006.749) (-1005.523) -- 0:09:10
1080000 -- (-1013.961) (-1020.744) [-1031.183] (-1010.001) -- 0:09:04
1090000 -- (-1006.529) [-998.654] (-1007.874) (-1024.007) -- 0:08:58
1100000 -- (-1024.376) (-1002.335) (-1029.549) [-1009.602] -- 0:08:52
1110000 -- (-1012.109) (-1014.298) (-1019.636) [-1000.842] -- 0:08:46
1120000 -- (-1009.900) (-1010.068) (-1014.760) [-1001.766] -- 0:08:40
1130000 -- (-1017.094) (-1021.225) (-1004.484) [-1008.108] -- 0:08:35
1140000 -- [-1006.385] (-1007.006) (-1005.314) (-1017.679) -- 0:08:29
1150000 -- (-1003.342) [-1001.221] (-994.584) (-1025.503) -- 0:08:23
1160000 -- [-1006.083] (-1003.030) (-1022.906) (-1013.355) -- 0:08:16
1170000 -- (-1004.192) (-1015.177) [-999.339] (-1009.493) -- 0:08:10
1180000 -- (-1020.845) (-1015.033) (-1018.270) [-1002.128] -- 0:08:05
1190000 -- [-1003.126] (-1016.569) (-1002.137) (-1019.438) -- 0:07:59
1200000 -- [-996.806] (-999.814) (-1002.764) (-1013.049) -- 0:07:53
1210000 -- [-1001.722] (-1026.365) (-1016.175) (-1018.902) -- 0:07:47
1220000 -- (-1015.995) [-1001.441] (-1009.432) (-1012.153) -- 0:07:41
1230000 -- (-998.193) (-1006.988) (-1050.419) [-1010.159] -- 0:07:35
1240000 -- (-1024.412) (-1008.028) [-1003.617] (-1023.794) -- 0:07:29
1250000 -- (-1031.945) [-1006.180] (-1008.428) (-1006.075) -- 0:07:23
1260000 -- (-1014.436) (-1011.536) [-994.617] (-1007.333) -- 0:07:17
1270000 -- (-1016.975) (-1015.365) (-1025.255) [-1003.032] -- 0:07:11
1280000 -- [-1002.847] (-1017.189) (-1022.756) (-1020.052) -- 0:07:05
1290000 -- (-1011.274) (-1016.510) [-1013.226] (-1002.231) -- 0:06:59
1300000 -- (-1020.554) [-1006.932] (-1010.887) (-1011.382) -- 0:06:54
1310000 -- (-1017.449) [-1013.921] (-997.515) (-1032.533) -- 0:06:48
1320000 -- (-1023.736) [-1013.262] (-1012.495) (-1017.343) -- 0:06:42
1330000 -- [-1000.716] (-1001.966) (-1013.990) (-1009.810) -- 0:06:36
1340000 -- [-1004.158] (-998.993) (-1026.247) (-1011.871) -- 0:06:30
1350000 -- (-1012.705) (-1021.766) [-1011.275] (-1020.113) -- 0:06:24
1360000 -- [-1010.105] (-1019.915) (-1025.295) (-1003.399) -- 0:06:18
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```
1370000 -- [-1006.823] (-1009.164) (-1025.643) (-1000.132) -- 0:06:12
1380000 -- (-1009.512) (-1009.387) [-1011.366] (-1001.077) -- 0:06:06
1390000 -- [-1004.520] (-999.380) (-1004.833) (-1012.013) -- 0:06:00
1400000 -- (-1017.817) (-1002.724) (-1025.263) [-1001.223] -- 0:05:54
1410000 -- (-1007.228) (-1007.793) (-1012.588) [-1013.835] -- 0:05:48
1420000 -- (-1014.598) [-1014.575] (-1027.825) (-1014.534) -- 0:05:43
1430000 -- (-1024.554) (-1005.007) [-996.712] (-1008.030) -- 0:05:38
1440000 -- [-1002.040] (-1017.625) (-1014.425) (-1021.520) -- 0:05:32
1450000 -- (-1005.877) [-1006.654] (-1015.587) (-1006.798) -- 0:05:26
1460000 -- (-1024.343) [-1002.998] (-1009.389) (-1039.435) -- 0:05:20
1470000 -- (-1024.162) (-1004.402) (-1027.136) [-1015.784] -- 0:05:14
1480000 -- [-1000.024] (-1007.262) (-1003.811) (-1022.153) -- 0:05:08
1490000 -- (-1008.800) [-1001.139] (-1043.617) (-1029.495) -- 0:05:02
1500000 -- [-1007.570] (-1023.487) (-1013.776) (-1017.848) -- 0:04:56
1510000 -- (-1005.390) [-1015.025] (-1010.639) (-1016.422) -- 0:04:50
1520000 -- (-1025.913) [-1002.642] (-1023.501) (-1001.147) -- 0:04:44
1530000 -- (-1006.004) [-1001.935] (-1010.789) (-1010.275) -- 0:04:38
1540000 -- (-1012.211) [-1003.551] (-1019.575) (-1010.811) -- 0:04:32
1550000 -- (-999.041) [-995.241] (-1002.874) (-1014.930) -- 0:04:26
1560000 -- [-1020.326] (-1024.716) (-1020.863) (-1011.956) -- 0:04:20
1570000 -- (-1025.741) (-1008.577) (-1001.349) [-1002.617] -- 0:04:14
1580000 -- (-1020.624) (-1013.267) [-997.932] (-1007.265) -- 0:04:09
1590000 -- (-1004.218) (-1001.517) (-1013.014) [-1008.366] -- 0:04:02
1600000 -- [-1009.095] (-1021.691) (-996.973) (-1007.550) -- 0:03:57
1610000 -- (-999.023) [-994.537] (-1018.087) (-1013.087) -- 0:03:51
1620000 -- [-1004.278] (-1016.845) (-1028.289) (-1026.997) -- 0:03:45
1630000 -- (-1032.487) [-1001.177] (-1010.564) (-1018.761) -- 0:03:39
1640000 -- [-1006.698] (-1000.865) (-1013.335) (-1005.854) -- 0:03:33
1650000 -- [-996.261] (-1025.257) (-1013.089) (-1009.581) -- 0:03:27
1660000 -- (-1020.400) (-1011.972) (-1015.072) [-1005.024] -- 0:03:21
1670000 -- (-1017.090) [-1003.633] (-1019.213) (-1013.811) -- 0:03:15
1680000 -- (-1019.155) (-1008.609) [-1004.857] (-1018.926) -- 0:03:09
1690000 -- (-1025.212) [-1004.459] (-998.700) (-1012.996) -- 0:03:03
1700000 -- (-1014.646) (-1015.331) [-1000.895] (-1011.521) -- 0:02:57
1710000 -- (-1030.510) (-1028.287) (-1021.928) [-1001.915] -- 0:02:51
1720000 -- [-1004.680] (-1017.617) (-1013.717) (-1015.702) -- 0:02:45
1730000 -- [-1002.523] (-1028.054) (-1007.812) (-1009.944) -- 0:02:39
1740000 -- (-998.520) [-1020.882] (-1003.923) (-1016.380) -- 0:02:34
1750000 -- [-1015.786] (-1011.427) (-1003.391) (-1016.979) -- 0:02:28
1760000 -- (-1017.366) (-1017.620) (-1024.564) [-996.259] -- 0:02:22
1770000 -- (-1034.838) [-996.995] (-1016.746) (-1024.201) -- 0:02:16
1780000 -- (-1013.279) (-1008.245) [-1011.540] (-1013.103) -- 0:02:10
1790000 -- [-1002.172] (-1020.978) (-1030.276) (-1020.570) -- 0:02:04
1800000 -- (-1014.146) (-1028.866) [-1004.756] (-1013.892) -- 0:01:58
1810000 -- (-1007.502) [-1007.299] (-1012.769) (-1014.627) -- 0:01:52
1820000 -- (-1030.790) (-1007.458) (-1013.781) [-1010.303] -- 0:01:46
1830000 -- (-1014.613) (-1036.172) (-1006.008) [-1004.677] -- 0:01:40
1840000 -- (-1009.741) (-1023.893) (-1016.996) [-1008.143] -- 0:01:34
1850000 -- [-1009.368] (-1031.814) (-1024.418) (-1005.719) -- 0:01:28
1860000 -- (-1029.335) (-1017.162) (-1022.860) [-1006.332] -- 0:01:22
1870000 -- (-1017.730) [-1008.731] (-1005.959) (-1031.870) -- 0:01:16
1880000 -- (-1005.006) [-995.934] (-1038.465) (-1014.510) -- 0:01:11
1890000 -- [-1003.061] (-1006.095) (-1032.343) (-1037.317) -- 0:01:05
1900000 -- (-1007.907) (-1004.618) (-1018.096) [-1009.068] -- 0:00:59
1910000 -- (-1024.493) (-1011.079) (-1013.591) [-998.495] -- 0:00:53
1920000 -- (-1017.997) [-1010.508] (-1012.281) (-1034.992) -- 0:00:47
1930000 -- (-1014.825) (-1020.206) (-1011.872) [-996.885] -- 0:00:41
1940000 -- (-1006.821) (-1011.509) (-1029.874) [-997.373] -- 0:00:35
```

```
   1950000 -- (-1014.504) (-998.218) [-1008.689] (-1015.510) -- 0:00:29
   1960000 -- [-1000.227] (-1024.644) (-1018.482) (-1002.619) -- 0:00:23
   1970000 -- [-1009.259] (-1022.689) (-1020.227) (-1005.425) -- 0:00:17
   1980000 -- (-1006.788) [-1005.542] (-1000.144) (-1030.185) -- 0:00:11
   1990000 -- [-1009.699] (-1013.423) (-1016.056) (-1009.990) -- 0:00:05
   2000000 -- (-999.693) [-999.653] (-1018.502) (-1022.327) -- 0:00:00

   Continue with analysis? (yes/no): n

   Analysis completed in 19 mins 45 seconds
   Analysis used 1148.54 seconds of CPU time
   Log likelihood of best state for "cold" chain was -983.67

   Acceptance rates for the moves in the "cold" chain:
      With prob.   (last 100)   chain accepted proposals by move
         34.5 %     ( 31 %)     Multiplier(Alpha)
         18.6 %     ( 17 %)     ExtSprClock(Tau,V)
         44.4 %     ( 58 %)     NNIClock(Tau,V)
         15.9 %     ( 27 %)     ParsSPRClock(Tau,V)
         70.1 %     ( 74 %)     NodesliderClock(V)
         71.1 %     ( 31 %)     TreeStretch(V)

   Chain swap information:

                1       2       3       4
        ----------------------------------
      1 |            0.46    0.20    0.07
      2 |  333336            0.57    0.27
      3 |  332812  332788            0.60
      4 |  333315  334718  333031

   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-Hout-Ynotin.t"
   Using relative burnin ('relburnin=yes'), discarding the first 25 % of sampled trees
   Writing statistics to files DY-26Dec-strict-Hout-Ynotin.<parts|tstat|vstat|trprobs|con>
   Examining file ...
   Found one tree block in file "DY-26Dec-strict-Hout-Ynotin.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 equual to (Minpartfreq) in at least one run. Minpartfreq is a paramiter 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.

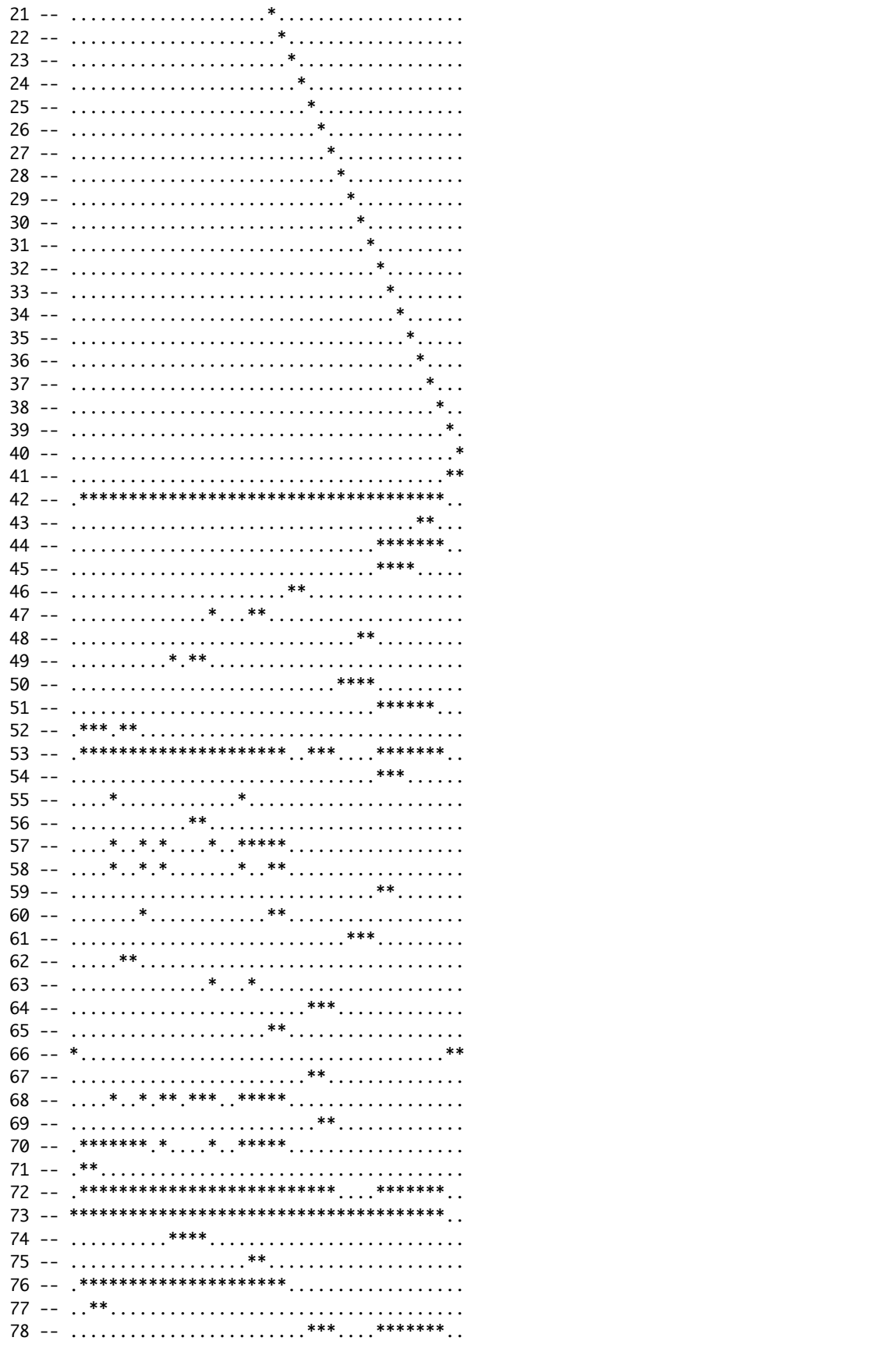
List of taxa in bipartitions:

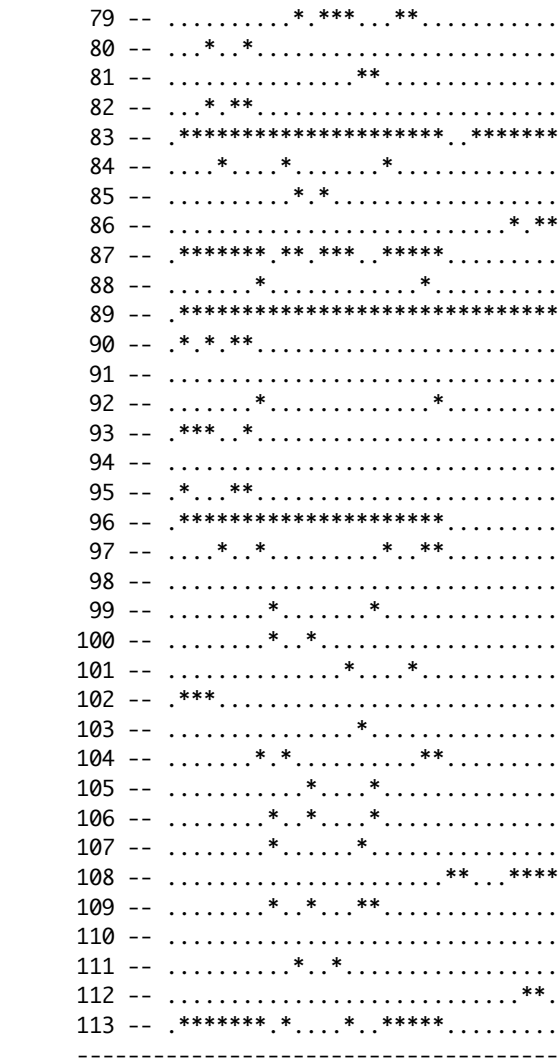
```
   1 -- hax
   2 -- gwi
   3 -- dgr
   4 -- scsh
   5 -- xsl
   6 -- bea
   7 -- crx
   8 -- chp
```

```
  9 -- txc
 10 -- haa
 11 -- ing
 12 -- kuu
 13 -- hoi
 14 -- koy
 15 -- taa
 16 -- aht
 17 -- tfn
 18 -- kkz
 19 -- tcb
 20 -- tau
 21 -- ttmN
 22 -- tceS
 23 -- eya
 24 -- tli
 25 -- gce
 26 -- tol
 27 -- cco
 28 -- hup
 29 -- mtl
 30 -- wlk
 31 -- kto
 32 -- apc
 33 -- apw
 34 -- apj
 35 -- nav
 36 -- apk
 37 -- apl
 38 -- srs
 39 -- ket
 40 -- zko

Key to taxon bipartitions (saved to file "DY-26Dec-strict-Hout-Ynotin.parts"):

 ID -- Partition
------------------------------------------------
  0 -- ***************************************
  1 -- *.....................................
  2 -- .*....................................
  3 -- ..*...................................
  4 -- ...*..................................
  5 -- ....*.................................
  6 -- .....*................................
  7 -- ......*...............................
  8 -- .......*..............................
  9 -- ........*.............................
 10 -- .........*............................
 11 -- ..........*...........................
 12 -- ...........*..........................
 13 -- ............*.........................
 14 -- .............*........................
 15 -- ..............*.......................
 16 -- ...............*......................
 17 -- ................*.....................
 18 -- .................*....................
 19 -- ..................*...................
 20 -- ...................*..................
```





Summary statistics for informative taxon bipartitions (clades)
   (saved to file "DY-26Dec-strict-Hout-Ynotin.tstat"):

ID	#obs	Probab.
41	3001	1.000000
42	3001	1.000000
43	3000	0.999667
44	2742	0.913695
45	2596	0.865045
46	2489	0.829390
47	2453	0.817394
48	2427	0.808730
49	2386	0.795068
50	2363	0.787404
51	2223	0.740753
52	2189	0.729424
53	2101	0.700100
54	2095	0.698101
55	1902	0.633789
56	1840	0.613129

57	1815	0.604798
58	1780	0.593136
59	1779	0.592802
60	1753	0.584139
61	1711	0.570143
62	1678	0.559147
63	1550	0.516495
64	1550	0.516495
65	1344	0.447851
66	1315	0.438187
67	1308	0.435855
68	1259	0.419527
69	1233	0.410863
70	1232	0.410530
71	1224	0.407864
72	1208	0.402532
73	1103	0.367544
74	940	0.313229
75	938	0.312562
76	898	0.299234
77	896	0.298567
78	854	0.284572
79	800	0.266578
80	796	0.265245
81	790	0.263246
82	767	0.255581
83	766	0.255248
84	717	0.238920
85	667	0.222259
86	660	0.219927
87	598	0.199267
88	595	0.198267
89	583	0.194269
90	572	0.190603
91	571	0.190270
92	566	0.188604
93	562	0.187271
94	554	0.184605
95	543	0.180940
96	512	0.170610
97	504	0.167944
98	489	0.162946
99	484	0.161280
100	437	0.145618
101	434	0.144618
102	423	0.140953
103	411	0.136954
104	403	0.134289
105	388	0.129290
106	367	0.122293
107	367	0.122293
108	349	0.116295
109	336	0.111963
110	317	0.105631
111	314	0.104632
112	302	0.100633
113	302	0.100633

Summary statistics for branch and node parameters
   (saved to file "DY-26Dec-strict-Hout-Ynotin.vstat"):

			95% HPD Interval		
Parameter	Mean	Variance	Lower	Upper	Median
length[1]	0.149021	0.001667	0.072231	0.222138	0.151446
length[2]	0.037315	0.000264	0.011224	0.070794	0.035081
length[3]	0.038527	0.000369	0.007472	0.075756	0.034763
length[4]	0.033894	0.000254	0.007696	0.066035	0.031258
length[5]	0.026910	0.000176	0.005262	0.053406	0.024800
length[6]	0.033928	0.000429	0.004540	0.077011	0.028675
length[7]	0.026087	0.000173	0.004540	0.052278	0.023711
length[8]	0.033943	0.000199	0.011678	0.062474	0.032088
length[9]	0.077738	0.000760	0.030209	0.130939	0.075027
length[10]	0.038054	0.000193	0.012807	0.064171	0.036822
length[11]	0.038798	0.000323	0.008381	0.073478	0.036493
length[12]	0.064047	0.000692	0.016491	0.115895	0.061844
length[13]	0.028292	0.000182	0.005960	0.054777	0.026238
length[14]	0.028895	0.000191	0.007661	0.058405	0.026620
length[15]	0.023359	0.000173	0.003215	0.050568	0.020581
length[16]	0.077707	0.000732	0.028646	0.129054	0.076062
length[17]	0.072818	0.000698	0.025545	0.123010	0.070354
length[18]	0.028083	0.000181	0.006291	0.054987	0.026166
length[19]	0.020803	0.000138	0.003021	0.043345	0.018432
length[20]	0.025653	0.000191	0.004518	0.054617	0.022889
length[21]	0.026936	0.000145	0.004764	0.048626	0.025352
length[22]	0.028276	0.000161	0.006865	0.052930	0.026578
length[23]	0.089295	0.001117	0.031513	0.158939	0.086111
length[24]	0.090682	0.001172	0.028811	0.158415	0.087102
length[25]	0.065840	0.000718	0.020920	0.119430	0.062619
length[26]	0.056992	0.000558	0.015092	0.101862	0.054247
length[27]	0.064051	0.000686	0.016303	0.112871	0.060695
length[28]	0.080657	0.001067	0.025057	0.144264	0.077095
length[29]	0.064110	0.000724	0.019062	0.115421	0.060244
length[30]	0.036410	0.000333	0.007256	0.071157	0.032948
length[31]	0.036934	0.000366	0.007550	0.074490	0.033083
length[32]	0.007055	0.000044	0.000003	0.020263	0.005045
length[33]	0.007046	0.000042	0.000003	0.019914	0.005019
length[34]	0.011777	0.000070	0.000212	0.027996	0.009934
length[35]	0.023291	0.000135	0.004389	0.045547	0.021076
length[36]	0.004294	0.000020	0.000005	0.012891	0.002917
length[37]	0.004297	0.000021	0.000005	0.012891	0.002917
length[38]	0.052303	0.000442	0.016462	0.092904	0.049761
length[39]	0.067992	0.000609	0.024310	0.114645	0.065959
length[40]	0.067992	0.000609	0.024310	0.114645	0.065959
length[41]	0.083565	0.000789	0.033112	0.138799	0.081689
length[42]	0.011059	0.000103	0.000007	0.031243	0.008255
length[43]	0.031191	0.000209	0.006132	0.058524	0.029229
length[44]	0.035025	0.000345	0.004089	0.072495	0.033027
length[45]	0.015662	0.000112	0.000032	0.036319	0.013492
length[46]	0.046171	0.000652	0.000026	0.092932	0.042852
length[47]	0.020892	0.000159	0.000051	0.044779	0.018939
length[48]	0.029713	0.000343	0.000032	0.064265	0.026263
length[49]	0.024321	0.000280	0.000588	0.056311	0.020545
length[50]	0.050135	0.000652	0.005136	0.098935	0.047728

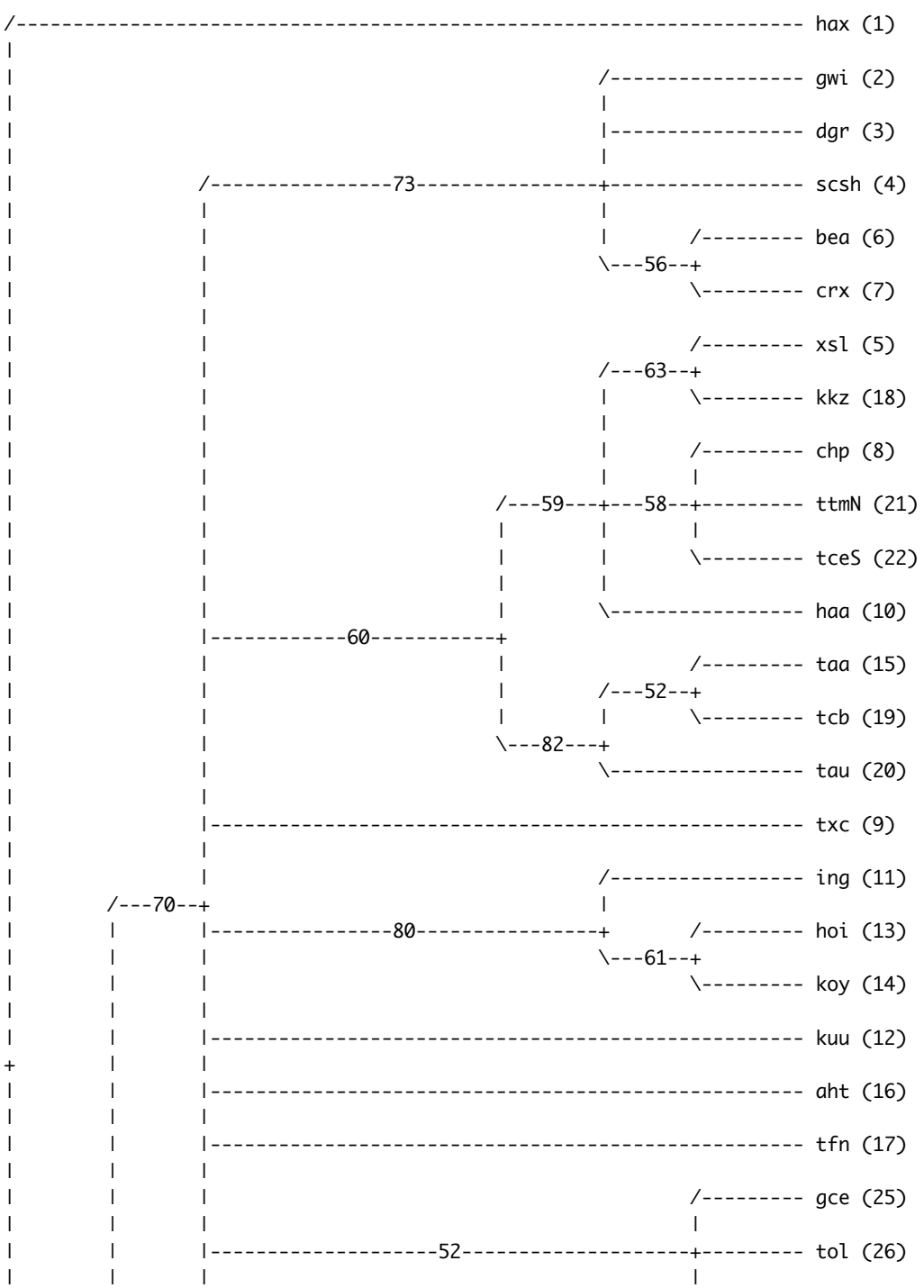
length[51]	0.021255	0.000222	0.000000	0.050305	0.018035
length[52]	0.021715	0.000244	0.000025	0.051070	0.019143
length[53]	0.019680	0.000151	0.000500	0.042915	0.017724
length[54]	0.012477	0.000096	0.000010	0.030689	0.010411
length[55]	0.016073	0.000110	0.000049	0.035806	0.014099
length[56]	0.015520	0.000136	0.000013	0.037846	0.012913
length[57]	0.016845	0.000103	0.000020	0.036035	0.015330
length[58]	0.014319	0.000090	0.000002	0.032932	0.012389
length[59]	0.010344	0.000073	0.000006	0.027120	0.008221
length[60]	0.009909	0.000055	0.000015	0.024532	0.008123
length[61]	0.032698	0.000573	0.000020	0.078916	0.027677
length[62]	0.021247	0.000211	0.000047	0.049778	0.018108
length[63]	0.011110	0.000092	0.000001	0.032586	0.008380
length[64]	0.026648	0.000295	0.000242	0.059169	0.023628
length[65]	0.010455	0.000070	0.000003	0.027521	0.008473
length[66]	0.009861	0.000081	0.000001	0.028046	0.007320
length[67]	0.027749	0.000400	0.000049	0.064813	0.023567
length[68]	0.019607	0.000104	0.003609	0.039578	0.017873
length[69]	0.029171	0.000425	0.000003	0.070205	0.025185
length[70]	0.023988	0.000182	0.000012	0.048041	0.022047
length[71]	0.017695	0.000143	0.000033	0.040986	0.015014
length[72]	0.013520	0.000104	0.000019	0.033348	0.011502
length[73]	0.009464	0.000082	0.000011	0.027601	0.006911
length[74]	0.025928	0.000291	0.000155	0.059801	0.022213
length[75]	0.013537	0.000158	0.000004	0.039193	0.009806
length[76]	0.012032	0.000069	0.000399	0.028022	0.010446
length[77]	0.018103	0.000164	0.000149	0.042929	0.015221
length[78]	0.016401	0.000142	0.000052	0.038212	0.013832
length[79]	0.016363	0.000177	0.000030	0.045584	0.012601
length[80]	0.014973	0.000135	0.000151	0.037706	0.012228
length[81]	0.022266	0.000253	0.000025	0.051567	0.018872
length[82]	0.016329	0.000186	0.000085	0.041764	0.012490
length[83]	0.012805	0.000104	0.000020	0.033383	0.010634
length[84]	0.007727	0.000055	0.000003	0.021404	0.005682
length[85]	0.009915	0.000089	0.000008	0.027907	0.007351
length[86]	0.022317	0.000336	0.000004	0.055773	0.018183
length[87]	0.014097	0.000126	0.000018	0.034915	0.011341
length[88]	0.006395	0.000036	0.000001	0.018014	0.004654
length[89]	0.004851	0.000025	0.000004	0.013239	0.003163
length[90]	0.018262	0.000176	0.000112	0.044099	0.015558
length[91]	0.006172	0.000034	0.000078	0.017461	0.004189
length[92]	0.005610	0.000030	0.000011	0.016308	0.003758
length[93]	0.014938	0.000133	0.000002	0.036110	0.012744
length[94]	0.006281	0.000033	0.000044	0.018665	0.004719
length[95]	0.014357	0.000136	0.000025	0.037513	0.011685
length[96]	0.011795	0.000097	0.000016	0.030274	0.009212
length[97]	0.006223	0.000042	0.000007	0.021221	0.004177
length[98]	0.011134	0.000079	0.000025	0.028473	0.008597
length[99]	0.018275	0.000259	0.000102	0.052328	0.013932
length[100]	0.018077	0.000227	0.000034	0.047424	0.014468
length[101]	0.006733	0.000054	0.000001	0.022404	0.004621
length[102]	0.010688	0.000100	0.000010	0.027235	0.008518
length[103]	0.019679	0.000181	0.000353	0.044838	0.017205
length[104]	0.005498	0.000030	0.000004	0.015555	0.004063
length[105]	0.017864	0.000195	0.000050	0.043065	0.015390
length[106]	0.018512	0.000188	0.000026	0.043973	0.016105
length[107]	0.016268	0.000172	0.000026	0.040762	0.012532
length[108]	0.009846	0.000081	0.000012	0.028003	0.007204

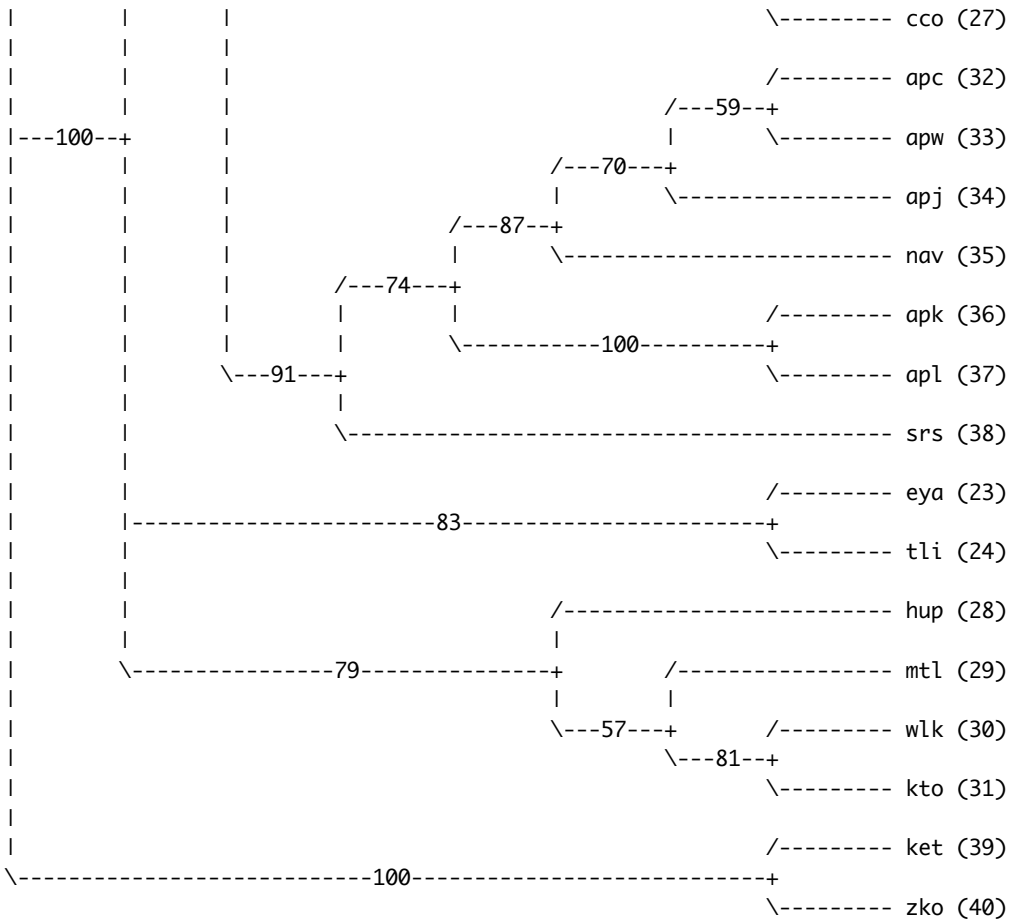
length[109]	0.013688	0.000129	0.000100	0.036721	0.010733
length[110]	0.005015	0.000029	0.000005	0.015598	0.003206
length[111]	0.007695	0.000059	0.000002	0.022708	0.005417
length[112]	0.028003	0.000725	0.000054	0.080112	0.019495
length[113]	0.014249	0.000100	0.000114	0.033999	0.011688
height[0]	0.156820	0.001784	0.078873	0.234185	0.159286
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]	0.000000	0.000000	0.000000	0.000000	0.000000
height[41]	0.067992	0.000609	0.024310	0.114645	0.065959
height[42]	0.141341	0.001419	0.067422	0.205022	0.145099
height[43]	0.004281	0.000020	0.000005	0.012770	0.002917
height[44]	0.053039	0.000342	0.020080	0.088245	0.051486
height[45]	0.023192	0.000106	0.006107	0.043449	0.021450
height[46]	0.084963	0.000938	0.028866	0.143800	0.083234
height[47]	0.027546	0.000156	0.007971	0.054617	0.025780
height[48]	0.032323	0.000215	0.007256	0.059388	0.030329
height[49]	0.038862	0.000245	0.011268	0.068063	0.037434
height[50]	0.083481	0.000886	0.029882	0.138897	0.081104
height[51]	0.035366	0.000176	0.012133	0.060569	0.033874
height[52]	0.053903	0.000319	0.022109	0.088277	0.053051

height[53]	0.112288	0.000875	0.053280	0.161754	0.114688
height[54]	0.012070	0.000052	0.001183	0.026022	0.010610
height[55]	0.023238	0.000117	0.006090	0.045362	0.021779
height[56]	0.025763	0.000141	0.005809	0.048093	0.024152
height[57]	0.052377	0.000247	0.022749	0.080302	0.052209
height[58]	0.043490	0.000191	0.018538	0.069192	0.042577
height[59]	0.004792	0.000021	0.000003	0.013665	0.003414
height[60]	0.032005	0.000132	0.012350	0.054066	0.031159
height[61]	0.057803	0.000455	0.018761	0.096093	0.056069
height[62]	0.022643	0.000127	0.003093	0.044245	0.020810
height[63]	0.018462	0.000094	0.002962	0.037406	0.016665
height[64]	0.072050	0.000555	0.027783	0.114274	0.071492
height[65]	0.023267	0.000112	0.006279	0.043142	0.021456
height[66]	0.144380	0.001577	0.070668	0.217572	0.146430
height[67]	0.053607	0.000433	0.015092	0.090608	0.051747
height[68]	0.064398	0.000355	0.033779	0.101876	0.062733
height[69]	0.053603	0.000436	0.018318	0.093609	0.051536
height[70]	0.071347	0.000427	0.030631	0.106287	0.072726
height[71]	0.031559	0.000201	0.008133	0.059098	0.029277
height[72]	0.128446	0.001260	0.057051	0.190155	0.131043
height[73]	0.151020	0.001621	0.075716	0.222711	0.153386
height[74]	0.059943	0.000470	0.020006	0.100306	0.058630
height[75]	0.020132	0.000122	0.003021	0.040456	0.018180
height[76]	0.101123	0.000646	0.048505	0.142494	0.102860
height[77]	0.031641	0.000190	0.007815	0.057848	0.029938
height[78]	0.094250	0.000689	0.047780	0.144646	0.094428
height[79]	0.050883	0.000294	0.020615	0.082825	0.049033
height[80]	0.025551	0.000134	0.007696	0.049627	0.023524
height[81]	0.065526	0.000463	0.029278	0.108143	0.063638
height[82]	0.037122	0.000214	0.012800	0.065197	0.035473
height[83]	0.130663	0.001227	0.062344	0.187474	0.136262
height[84]	0.035449	0.000150	0.013317	0.058154	0.033652
height[85]	0.028830	0.000176	0.005256	0.052964	0.027352
height[86]	0.062723	0.000498	0.023960	0.104471	0.061056
height[87]	0.077580	0.000493	0.037065	0.117100	0.076215
height[88]	0.028856	0.000128	0.011165	0.051318	0.028065
height[89]	0.150856	0.001735	0.066047	0.220686	0.154328
height[90]	0.043581	0.000235	0.017986	0.072589	0.042282
height[91]	0.006946	0.000030	0.000090	0.017741	0.005178
height[92]	0.028649	0.000126	0.009347	0.048488	0.027106
height[93]	0.044330	0.000225	0.018636	0.073373	0.043547
height[94]	0.006529	0.000025	0.000130	0.016044	0.005274
height[95]	0.040516	0.000221	0.014266	0.069173	0.039093
height[96]	0.102403	0.000774	0.045180	0.146079	0.104675
height[97]	0.040255	0.000178	0.015671	0.064084	0.039728
height[98]	0.037310	0.000195	0.012862	0.065803	0.035321
height[99]	0.066238	0.000588	0.024187	0.111913	0.064915
height[100]	0.062714	0.000538	0.023678	0.108604	0.060137
height[101]	0.020730	0.000098	0.004400	0.039674	0.019319
height[102]	0.042927	0.000249	0.013160	0.070348	0.041114
height[103]	0.072805	0.000622	0.028826	0.119901	0.070774
height[104]	0.038953	0.000164	0.017486	0.064967	0.038606
height[105]	0.060349	0.000475	0.023550	0.103502	0.057746
height[106]	0.068859	0.000502	0.033260	0.112444	0.066800
height[107]	0.073714	0.000598	0.031600	0.121944	0.073715
height[108]	0.129556	0.001227	0.059111	0.183467	0.132371
height[109]	0.081265	0.000548	0.045171	0.126128	0.079243
height[110]	0.017989	0.000077	0.004771	0.035068	0.016609

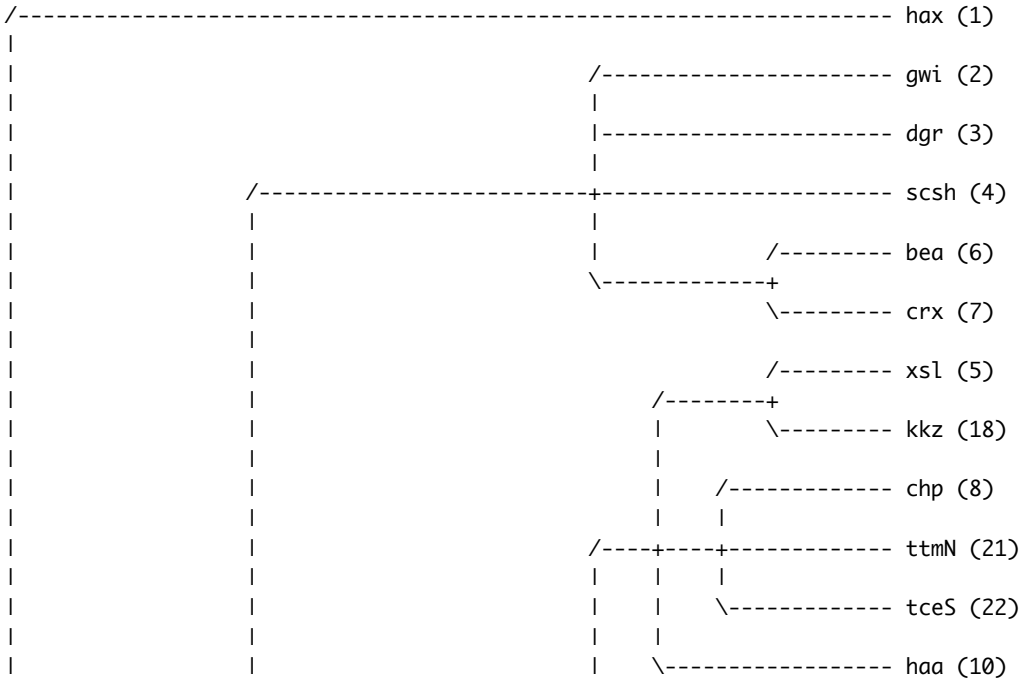
height[111]	0.028995	0.000172	0.008107	0.053429	0.026667
height[112]	0.052437	0.000472	0.013294	0.093269	0.051143
height[113]	0.088344	0.000667	0.037493	0.131650	0.090559

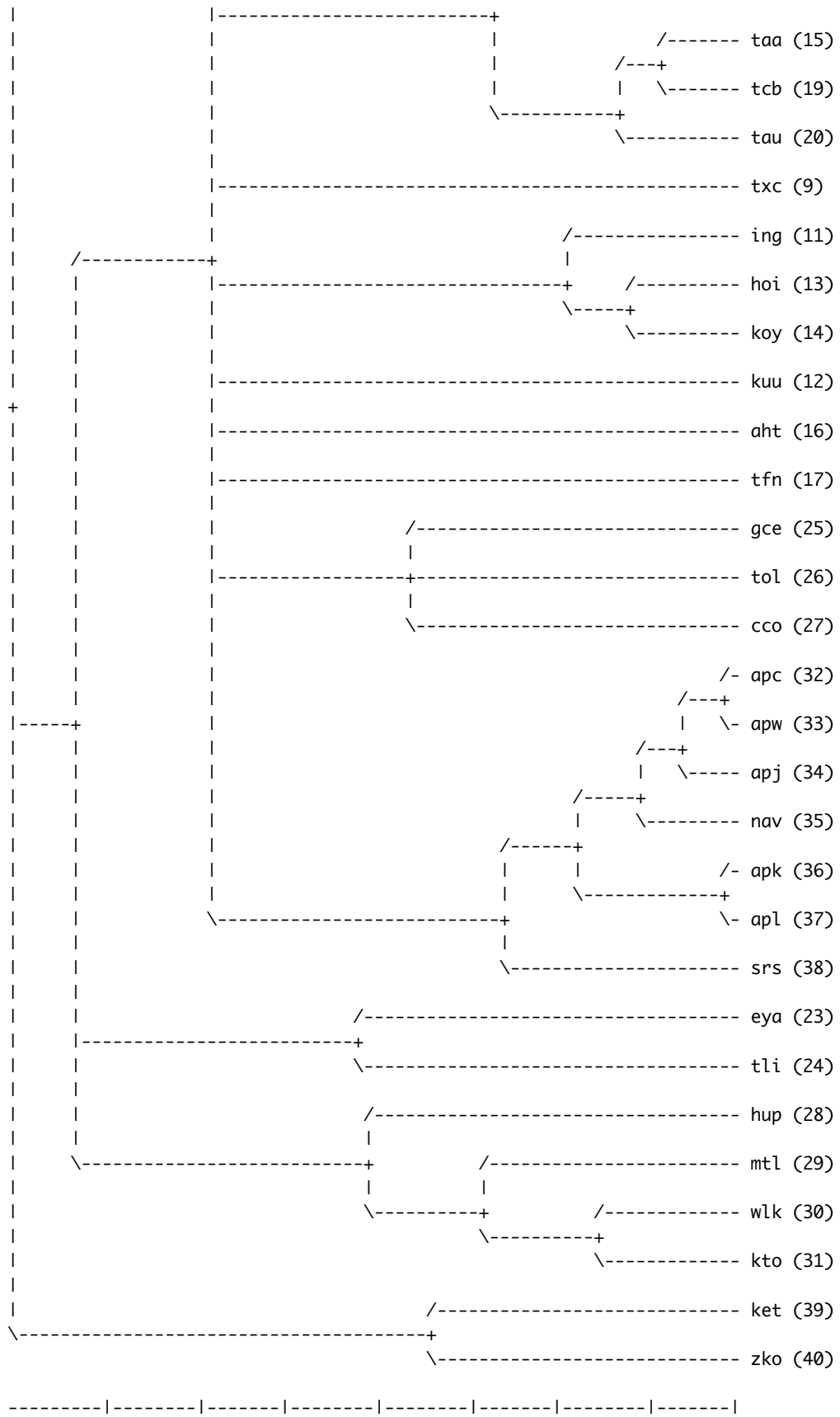
Clade credibility values:





Phylogram (based on median node depths):




taa (15)
tcb (19)
tau (20)
txc (9)
ing (11)
hoi (13)
koy (14)
kuu (12)
aht (16)
tfn (17)
gce (25)
tol (26)
cco (27)
apc (32)
apw (33)
apj (34)
nav (35)
apk (36)
apl (37)
srs (38)
eya (23)
tli (24)
hup (28)
mtl (29)
wlk (30)
kto (31)
ket (39)
zko (40)

```
         0.14     0.12    0.10     0.08     0.06    0.04     0.02    -0.00

   [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-26Dec-strict-Hout-Ynotin.p
   Writing summary statistics to file DY-26Dec-strict-Hout-Ynotin.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 station-
   arity. Sample trees and parameters after the log probability
   plateaus. Of course, this is not a guarantee that you are at sta-
   analysis should be. When the log probability starts to plateau
   tionarity. When possible, run multiple analyses starting from dif-
   ferent 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 conver-
   gence 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.

   +-------------------------------------------------------------+ -1002.152
   |                                                 *           |
   |                                                             |
   |             *               *                               |
   |            *                                                |
   |    *     *     * *   *    *                     *    *     |
   |           *                                  *        * *   |
   |                              *   * *         * *     *     *|
   |* **             *        *       * *    **        *    *   |
   |        **     *    **  **                        *         |
   | *     *      *                         *   *       *       |
   |                   *            *                        * |
   |     *                      *        * *                     |
   |                               *      *                     |
   |                                           *                 |
   |      *               *                                      |
   +------+-----+-----+-----+-----+-----+-----+-----+-----+-----+ -1009.401
   ^                                                             ^
   500000                                                        2000000
```

```
   Estimated marginal likelihoods for run sampled in file "DY-26Dec-strict-Hout-Ynotin.p":
      (Use the harmonic mean for Bayes factor comparisons of models)
      (Values are saved to the file /Users/msicoli/DY-Typlogical_binary_bayes-2.nex.lstat)

   Arithmetic mean   Harmonic mean
   --------------------------------
       -994.93         -1029.49
   --------------------------------


   Model parameter summaries for run sampled in file "DY-26Dec-strict-Hout-Ynotin":
      Based on a total of 3001 samples out of a total of 4001 samples
         from this analysis.
      Parameter summaries saved to file "/Users/msicoli/DY-Typlogical_binary_bayes-2.nex.pstat".

                                       95% HPD Interval
                                      -------------------
   Parameter      Mean      Variance     Lower       Upper       Median     ESS*
   ----------------------------------------------------------------------------
   TH          0.156820    0.001784    0.078873    0.234185    0.159286    384.87
   TL          2.527047    0.419954    1.269098    3.627597    2.598859    375.61
   alpha       1.211592    7.561679    0.126431    2.664872    0.928030   2141.27
   ----------------------------------------------------------------------------
   * 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-Hout-YnotinND-ss

   Setting number of generations to 100000
   Setting diagnosing frequency to 1000

MrBayes > ss

   Setting chain output file names to "YND-Typ-Hout-YnotinND-ss.<p/t>"
   Running Markov chain
   MCMC stamp = 7233609125
   Seed = 208011611
   Swapseed = 1272127178
   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 diricihlet/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 = 40
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 81 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 -- -999.653079 -- -8.415782
   Chain 2 -- -999.693164 -- -35.880936
   Chain 3 -- -1022.327222 -- -32.409647
   Chain 4 -- -1018.502047 -- -36.524456
```

```
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 begining 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-
rations instead of requested 100000.


Chain results (76500 generations requested):

    0 -- [-999.653] (-999.693) (-1022.327) (-1018.502)

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 -- [-1014.688] (-1036.589) (-1027.784) (-1025.635) -- 0:00:46
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 -- (-1104.824) [-1079.987] (-1054.040) (-1059.171) -- 0:00:39
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 -- (-1209.043) (-1184.110) [-1177.874] (-1288.336) -- 0:00:31
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 -- (-1246.398) [-1217.938] (-1401.095) (-1334.210) -- 0:00:23
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 -- [-1331.447] (-1391.716) (-1377.776) (-1371.829) -- 0:00:16
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 -- (-1451.355) (-1343.767) [-1521.399] (-1416.850) -- 0:00:10
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 -- (-2313.645) (-1450.966) [-1508.777] (-2264.034) -- 0:00:04
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 49 seconds
Analysis used 47.91 seconds of CPU time
Log likelihood of best state for "cold" chain was -988.36

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     -1118.81
    ------------------------------
More statistics on stepping-stone sampling is dumped to YND-Typ-Hout-YnotinND-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.
+------------------------------------------------------------+ 0.000
|                                                            |
|                                                            |
|                                                            |
|                                                            |
|                                                            |
|                                                            |
|                                                            |
|                                                            |
|                                                            |
|                                                            |
|                                                            |
|                                                            |
|                                                            |
|                                                            |
|***** **** ***** **** ***** **** ***** **** ***** **** *****|
+------+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 0.000
^                                                           ^
1                                                          50


Acceptance rates for the moves in the "cold" chain:
   With prob.   (last 100)   chain accepted proposals by move
      48.3 %     ( 56 %)     Multiplier(Alpha)
      44.0 %     ( 68 %)     ExtSprClock(Tau,V)
      78.0 %     (100 %)     NNIClock(Tau,V)
      34.2 %     ( 32 %)     ParsSPRClock(Tau,V)
      85.9 %     ( 98 %)     NodesliderClock(V)
      52.3 %     ( 87 %)     TreeStretch(V)

Chain swap information:
```

```
             1      2      3      4
      ------------------------------
    1 |          0.22   0.07   0.02
    2 |  12788          0.32   0.09
    3 |  12613  12830          0.41
    4 |  12848  12764  12657

   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 > ss

   Running Markov chain
   MCMC stamp = 7068357459
   Seed = 1721729764
   Swapseed = 370168243
   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 diricihlet/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 = 40
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 81 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 -- -1680.778432 -- -40.364893
   Chain 2 -- -2231.300002 -- -144.822360
   Chain 3 -- -2285.777987 -- -202.533686
   Chain 4 -- -2300.315466 -- -201.910542


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 begining 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.
```

```
   There are results from a previous run saved using the same filename(s).
   Do you want to overwrite these results? (yes/no): n

   Please specify a different file name before running the mcmc analysis.
      You can do that using 'mcmc filename=<name>'. You can also move or
      rename the old result files.
   Error preparing print files
   Error in command "Ss"

MrBayes > ss

   Running Markov chain
   MCMC stamp = 2928313836
   Seed = 1721729764
   Swapseed = 370168243
   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 diricihlet/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 = 40
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 81 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 -- -1680.778432 -- -40.364893
   Chain 2 -- -2231.300002 -- -144.822360
   Chain 3 -- -2285.777987 -- -202.533686
   Chain 4 -- -2300.315466 -- -201.910542


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 begining 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.


Chain results (76500 generations requested):

    0 -- [-1680.778] (-2231.300) (-2285.778) (-2300.315)

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 -- [-1044.196] (-1021.140) (-1043.047) (-1032.717) -- 0:00:46
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 -- (-1113.119) (-1109.920) [-1067.840] (-1075.641) -- 0:00:36
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 -- [-1122.192] (-1107.338) (-1337.333) (-1138.509) -- 0:00:29
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 -- (-1311.252) (-1365.492) (-1334.048) [-1205.317] -- 0:00:23
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 -- (-1361.075) (-1397.984) [-1355.495] (-1411.142) -- 0:00:16
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 -- [-1412.985] (-1420.651) (-1454.691) (-1428.179) -- 0:00:10
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 -- [-1462.462] (-2239.231) (-2297.458) (-2235.560) -- 0:00:04
Sampling step 47 out of 50 steps...

Sampling step 48 out of 50 steps...

Sampling step 49 out of 50 steps...

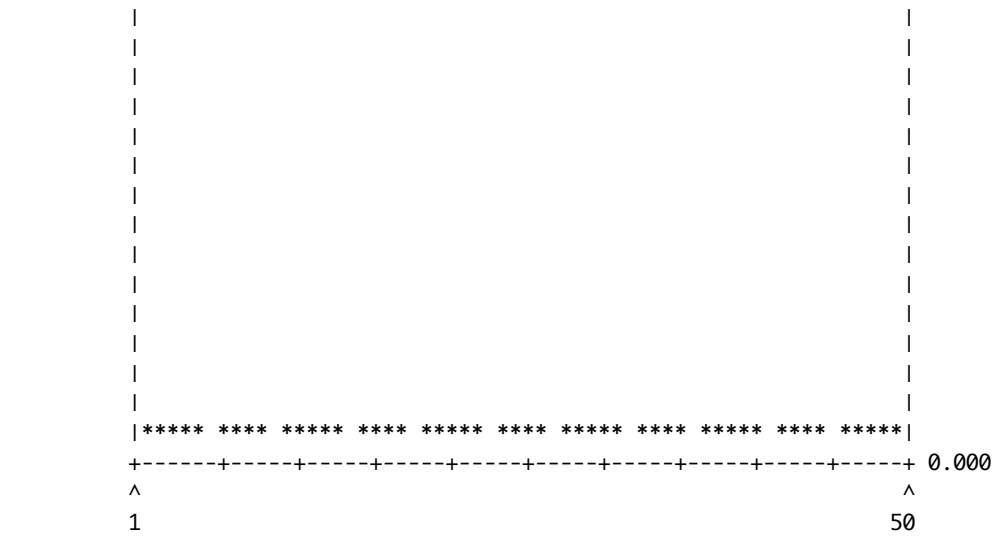
Sampling step 50 out of 50 steps...


Analysis completed in 49 seconds
Analysis used 48.09 seconds of CPU time
Log likelihood of best state for "cold" chain was -994.86

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     -1117.61
    ----------------------------
More statistics on stepping-stone sampling is dumped to YND-Typ-Hout-YnotinND-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.
+------------------------------------------------------------+ 0.000
```



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

With prob.	(last 100)	chain accepted proposals by move
43.4 %	(51 %)	Multiplier(Alpha)
43.2 %	(54 %)	ExtSprClock(Tau,V)
78.5 %	(100 %)	NNIClock(Tau,V)
33.4 %	(35 %)	ParsSPRClock(Tau,V)
85.8 %	(97 %)	NodesliderClock(V)
55.5 %	(87 %)	TreeStretch(V)

Chain swap information:

	1	2	3	4
1		0.20	0.05	0.01
2	12695		0.33	0.08
3	12671	12460		0.36
4	12990	12941	12743	

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 > ss

Running Markov chain
MCMC stamp = 6626483590

```
Seed = 1467775986
Swapseed = 171795935
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 diricihlet/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 = 40
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 81 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 -- -1620.166632 -- -3.810897
   Chain 2 -- -2300.560644 -- -166.199913
   Chain 3 -- -2156.594090 -- -129.082657
   Chain 4 -- -2293.230285 -- -186.740403


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 begining 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.


Chain results (76500 generations requested):

    0 -- [-1620.167] (-2300.561) (-2156.594) (-2293.230)

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 -- (-1031.570) (-1031.802) [-1018.638] (-1030.281) -- 0:00:39
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 -- (-1088.182) (-1143.689) (-1100.753) [-1091.231] -- 0:00:36
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 -- (-1158.099) (-1140.219) (-1239.290) [-1143.877] -- 0:00:29
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 -- (-1374.730) [-1266.760] (-1340.195) (-1343.404) -- 0:00:22
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 -- [-1335.118] (-1420.152) (-1393.019) (-1430.997) -- 0:00:16
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 -- [-1466.984] (-1352.105) (-1466.098) (-1425.234) -- 0:00:10
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 -- (-2221.032) (-2280.157) [-1945.455] (-2305.220) -- 0:00:04
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 48 seconds
Analysis used 47.53 seconds of CPU time
Log likelihood of best state for "cold" chain was -990.81

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     -1118.19
    ----------------------------
More statistics on stepping-stone sampling is dumped to YND-Typ-Hout-YnotinND-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.
+------------------------------------------------------------+ 0.000
|                                                            |
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```

```
   |***** **** ***** **** ***** **** ***** **** ***** **** *****|
   +------+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 0.000
   ^                                                             ^
   1                                                            50


   Acceptance rates for the moves in the "cold" chain:
      With prob.   (last 100)   chain accepted proposals by move
         41.9 %     ( 50 %)     Multiplier(Alpha)
         42.4 %     ( 59 %)     ExtSprClock(Tau,V)
         77.5 %     (100 %)     NNIClock(Tau,V)
         33.5 %     ( 35 %)     ParsSPRClock(Tau,V)
         85.7 %     ( 95 %)     NodesliderClock(V)
         53.1 %     ( 85 %)     TreeStretch(V)

   Chain swap information:

               1      2      3      4
        ------------------------------
      1 |          0.21   0.05   0.02
      2 |  12607          0.31   0.10
      3 |  12680  12749          0.41
      4 |  12875  12718  12871

   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 >
```

```
Last login: Thu Dec 26 10:15:42 on ttys000
msicoli-m1:~ msicoli$ mb


                            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/DY-Typlogical_binary_bayes-2.nex

   Executing file "/Users/msicoli/DY-Typlogical_binary_bayes-2.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 40 taxa and 116 characters
      Data is Standard
      Missing data coded as ?
      Gaps coded as -
      Data matrix is not interleaved
      Taxon  1 -> hax
      Taxon  2 -> gwi
      Taxon  3 -> dgr
      Taxon  4 -> scsh
      Taxon  5 -> xsl
      Taxon  6 -> bea
      Taxon  7 -> crx
      Taxon  8 -> chp
      Taxon  9 -> txc
      Taxon 10 -> haa
      Taxon 11 -> ing
      Taxon 12 -> kuu
      Taxon 13 -> hoi
      Taxon 14 -> koy
      Taxon 15 -> taa
      Taxon 16 -> aht
      Taxon 17 -> tfn
      Taxon 18 -> kkz
      Taxon 19 -> tcb
      Taxon 20 -> tau
      Taxon 21 -> ttmN
      Taxon 22 -> tceS
      Taxon 23 -> eya
```

```
      Taxon 24 -> tli
      Taxon 25 -> gce
      Taxon 26 -> tol
      Taxon 27 -> cco
      Taxon 28 -> hup
      Taxon 29 -> mtl
      Taxon 30 -> wlk
      Taxon 31 -> kto
      Taxon 32 -> apc
      Taxon 33 -> apw
      Taxon 34 -> apj
      Taxon 35 -> nav
      Taxon 36 -> apk
      Taxon 37 -> apl
      Taxon 38 -> srs
      Taxon 39 -> ket
      Taxon 40 -> zko
      Successfully read matrix
      Setting default partition (does not divide up characters)
      Setting model defaults
      Seed (for generating default start values) = 1388074477
      Adding dummy characters (unobserved site patterns) for division 1
      WARNING: There are 26 characters incompatible with the specified
               coding bias. These characters will be excluded.
      Setting output file names to "/Users/msicoli/DY-Typlogical_binary_bayes-2.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 26 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 26 characters incompatible with the specified
            coding bias. These characters will be excluded.

MrBayes > outgroup 1

   Setting outgroup to taxon "hax"

MrBayes > mcmcp ngen=2000000 printfreq=10000 samplefreq=500 nruns=1 nchains=4 savebrlens=yes
filename=DY-26Dec-strict-Hout2

   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-Hout2.<p/t>"
   Successfully set chain parameters

MrBayes > mcmc

   Running Markov chain
   MCMC stamp = 5449400826
   Seed = 1134458959
   Swapseed = 1388074477
   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 diricihlet/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 = 40
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 81 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 -- -1722.625492 -- -93.249778
   Chain 2 -- -1718.765922 -- -93.249778
   Chain 3 -- -1763.021428 -- -93.249778
   Chain 4 -- -1699.399305 -- -93.249778


Chain results (2000000 generations requested):

    0 -- [-1722.625] (-1718.766) (-1763.021) (-1699.399)
10000 -- (-1014.497) [-1017.643] (-1026.649) (-1008.923) -- 0:19:54
20000 -- (-1023.607) [-1013.409] (-1018.200) (-1008.476) -- 0:18:09
30000 -- [-1009.691] (-1014.904) (-1004.985) (-1006.906) -- 0:17:30
40000 -- (-1000.719) [-1010.092] (-1032.720) (-1021.775) -- 0:17:58
50000 -- (-1007.770) (-1020.555) [-1002.901] (-1038.949) -- 0:17:33
60000 -- [-1020.223] (-1009.007) (-1025.374) (-1003.929) -- 0:17:14
70000 -- (-1015.731) [-1009.247] (-1022.190) (-1022.128) -- 0:17:27
80000 -- (-1039.822) [-1021.826] (-1035.211) (-1000.508) -- 0:17:12
90000 -- (-1004.443) (-1013.859) (-1030.251) [-1020.982] -- 0:16:58
100000 -- (-1018.126) [-1004.591] (-1039.582) (-1022.379) -- 0:16:47
110000 -- (-1017.186) [-1009.560] (-1012.467) (-1005.066) -- 0:16:36
120000 -- (-1019.255) (-1025.618) [-1017.007] (-1016.738) -- 0:16:42
130000 -- [-1006.890] (-1028.668) (-1031.914) (-1004.633) -- 0:16:32
140000 -- (-1010.654) (-1015.918) [-1017.700] (-1013.347) -- 0:16:23
150000 -- (-1010.203) [-1006.789] (-1017.817) (-1018.112) -- 0:16:14
160000 -- [-1015.614] (-1019.639) (-1006.314) (-1025.479) -- 0:16:17
170000 -- (-1008.275) (-1017.001) [-1015.255] (-1016.792) -- 0:16:08
180000 -- (-1011.301) (-1012.343) [-1001.411] (-997.635) -- 0:16:00
190000 -- (-1037.016) (-1049.374) (-1018.325) [-1007.851] -- 0:16:02
200000 -- (-1023.995) (-1010.542) [-1000.898] (-1025.257) -- 0:15:54
210000 -- (-1014.727) (-1008.522) [-1001.171] (-1016.649) -- 0:15:46
220000 -- (-1018.374) (-1008.238) [-1005.388] (-1020.628) -- 0:15:46
```

```
230000 -- (-1014.622) [-1011.231] (-1009.556) (-1025.645) -- 0:15:38
240000 -- (-1021.399) (-1013.098) (-1021.066) [-1002.608] -- 0:15:31
250000 -- [-1009.901] (-1016.430) (-1015.178) (-1019.061) -- 0:15:24
260000 -- [-1001.343] (-1018.803) (-1012.355) (-1012.520) -- 0:15:16
270000 -- (-1025.207) (-1023.010) [-1006.626] (-995.819) -- 0:15:16
280000 -- (-1014.451) (-1021.193) (-1021.774) [-1014.267] -- 0:15:09
290000 -- (-1011.260) (-1005.571) [-1000.168] (-1010.005) -- 0:15:02
300000 -- (-1019.810) (-1014.776) [-1017.279] (-1028.504) -- 0:14:55
310000 -- [-1016.670] (-1012.246) (-1004.450) (-1008.476) -- 0:14:48
320000 -- (-1012.119) (-1024.311) [-1002.453] (-1026.813) -- 0:14:47
330000 -- (-1002.951) (-1011.099) [-1007.507] (-1004.218) -- 0:14:40
340000 -- (-1018.460) [-1000.701] (-1019.192) (-1015.460) -- 0:14:33
350000 -- (-1030.001) (-1016.537) (-1030.786) [-1020.008] -- 0:14:27
360000 -- (-1014.125) (-1025.268) (-1015.349) [-997.903] -- 0:14:21
370000 -- (-1006.544) (-1011.025) (-1010.609) [-1006.273] -- 0:14:19
380000 -- (-1011.312) (-1012.179) (-1009.748) [-1009.483] -- 0:14:12
390000 -- (-1008.134) (-1000.728) (-1038.844) [-998.146] -- 0:14:06
400000 -- (-1008.622) [-1009.413] (-1031.074) (-1005.924) -- 0:14:00
410000 -- [-1017.732] (-1008.041) (-1008.604) (-1026.424) -- 0:13:57
420000 -- [-1009.748] (-1043.303) (-1032.086) (-1008.092) -- 0:13:55
430000 -- [-1008.585] (-1024.107) (-1023.771) (-1009.831) -- 0:13:48
440000 -- (-994.937) [-995.373] (-1023.578) (-1028.488) -- 0:13:42
450000 -- (-1022.909) [-1029.937] (-1027.270) (-1005.861) -- 0:13:36
460000 -- (-1010.687) [-1008.994] (-1011.370) (-1034.851) -- 0:13:33
470000 -- (-1015.857) [-993.718] (-1041.442) (-1034.086) -- 0:13:27
480000 -- (-1013.218) [-1007.604] (-1038.061) (-1043.153) -- 0:13:21
490000 -- (-1012.241) [-1009.545] (-1029.787) (-1012.800) -- 0:13:18
500000 -- (-1033.317) [-1005.032] (-1011.921) (-1024.422) -- 0:13:12
510000 -- (-1025.198) [-1003.453] (-1019.197) (-1006.196) -- 0:13:05
520000 -- (-1010.933) (-1033.139) (-1023.603) [-1013.213] -- 0:12:59
530000 -- [-1005.216] (-1010.108) (-1019.806) (-1026.298) -- 0:12:53
540000 -- (-1019.579) [-1000.290] (-1019.684) (-1035.709) -- 0:12:50
550000 -- (-1017.249) [-1019.785] (-1024.485) (-1009.594) -- 0:12:44
560000 -- (-1005.997) (-1017.492) (-1039.417) [-1008.990] -- 0:12:38
570000 -- (-1027.129) (-1024.355) [-1013.148] (-1009.800) -- 0:12:32
580000 -- (-1037.588) (-1009.415) (-1015.059) [-1004.082] -- 0:12:29
590000 -- [-1019.528] (-1028.921) (-1020.814) (-1014.146) -- 0:12:23
600000 -- (-1017.486) (-1010.667) (-1013.812) [-1002.857] -- 0:12:17
610000 -- (-1019.989) (-1015.176) (-1030.724) [-1024.469] -- 0:12:11
620000 -- (-1019.025) (-1019.801) (-1013.647) [-992.001] -- 0:12:07
630000 -- (-1003.820) (-1035.340) (-1009.398) [-1003.366] -- 0:12:01
640000 -- (-1007.256) (-1029.314) (-1034.223) [-1019.918] -- 0:11:56
650000 -- (-1002.209) (-1012.760) (-1022.167) [-1012.788] -- 0:11:50
660000 -- (-1017.339) (-1015.947) (-1006.872) [-1016.495] -- 0:11:46
670000 -- (-1012.967) (-1024.409) [-1009.490] (-1007.301) -- 0:11:40
680000 -- (-1014.410) [-1013.084] (-1020.691) (-1021.829) -- 0:11:34
690000 -- (-1013.685) (-1013.432) (-1015.364) [-1027.233] -- 0:11:29
700000 -- (-1012.444) (-1016.996) [-1007.776] (-1016.672) -- 0:11:25
710000 -- (-1018.351) (-1016.554) (-1019.551) [-1013.677] -- 0:11:19
720000 -- (-1010.182) (-1024.488) (-1017.271) [-1005.163] -- 0:11:13
730000 -- [-1019.983] (-1015.347) (-1013.144) (-1027.756) -- 0:11:09
740000 -- [-1012.556] (-1021.014) (-1013.157) (-1010.041) -- 0:11:04
750000 -- [-1002.333] (-1042.517) (-1026.245) (-1002.412) -- 0:10:58
760000 -- (-1014.582) [-1013.034] (-1041.131) (-1005.686) -- 0:10:52
770000 -- (-1039.470) (-1004.469) (-1030.238) [-1007.420] -- 0:10:48
780000 -- (-1009.201) (-1037.511) (-1025.141) [-1009.637] -- 0:10:42
```

```
790000 -- (-1016.466) (-1018.118) [-1003.285] (-1029.998) -- 0:10:38
800000 -- (-1014.863) (-1009.890) [-1005.414] (-1005.042) -- 0:10:33
810000 -- [-1025.364] (-1027.859) (-1027.980) (-1020.011) -- 0:10:28
820000 -- [-1014.305] (-1014.964) (-1019.369) (-1002.666) -- 0:10:24
830000 -- (-1014.827) (-1008.108) [-1002.654] (-1016.085) -- 0:10:20
840000 -- (-1029.498) (-1012.174) [-1006.895] (-1024.971) -- 0:10:15
850000 -- (-1013.892) (-1016.781) (-1016.324) [-1009.748] -- 0:10:11
860000 -- (-1029.290) [-1003.779] (-1007.581) (-1016.285) -- 0:10:08
870000 -- (-1024.128) [-1005.391] (-1025.886) (-1010.730) -- 0:10:03
880000 -- (-1013.029) (-1009.380) [-1012.462] (-1009.819) -- 0:10:02
890000 -- (-1026.780) (-1004.365) [-1011.945] (-1015.154) -- 0:09:59
900000 -- (-1020.583) (-1024.687) (-1012.239) [-1028.622] -- 0:09:56
910000 -- (-1024.604) (-1014.801) [-1007.021] (-1013.390) -- 0:09:51
920000 -- (-1012.418) (-1015.645) [-1009.110] (-1035.222) -- 0:09:46
930000 -- (-1019.296) [-1008.446] (-1022.754) (-1017.964) -- 0:09:42
940000 -- [-1027.978] (-1021.167) (-1028.275) (-1011.273) -- 0:09:38
950000 -- [-1002.200] (-1020.174) (-1020.285) (-1023.198) -- 0:09:33
960000 -- (-1017.045) (-1011.769) [-996.005] (-996.040) -- 0:09:28
970000 -- (-1012.987) (-1016.354) (-1015.832) [-1006.497] -- 0:09:24
980000 -- (-1019.631) (-1009.587) (-1005.708) [-1020.112] -- 0:09:22
990000 -- (-1031.461) [-1003.500] (-1015.792) (-1019.421) -- 0:09:16
1000000 -- (-1006.903) [-999.303] (-1025.471) (-1017.260) -- 0:09:11
1010000 -- (-1002.770) (-1015.160) [-1004.507] (-1011.023) -- 0:09:05
1020000 -- (-1024.943) [-1008.650] (-1019.406) (-1013.561) -- 0:09:01
1030000 -- [-1011.039] (-1021.357) (-1024.012) (-1002.341) -- 0:08:56
1040000 -- [-998.166] (-1037.070) (-1019.062) (-1015.013) -- 0:08:50
1050000 -- (-1024.994) (-1018.720) [-1012.092] (-1007.999) -- 0:08:45
1060000 -- (-1017.209) (-1025.473) (-1011.543) [-998.992] -- 0:08:39
1070000 -- (-1001.184) (-1031.488) (-1022.035) [-1011.884] -- 0:08:34
1080000 -- [-999.890] (-1017.439) (-1006.941) (-1024.010) -- 0:08:28
1090000 -- (-1021.220) (-1016.798) [-1004.127] (-1010.098) -- 0:08:23
1100000 -- (-1028.519) (-1015.129) (-1017.016) [-1006.862] -- 0:08:19
1110000 -- [-1008.586] (-1021.477) (-1007.312) (-1015.056) -- 0:08:13
1120000 -- (-1022.880) (-1022.586) [-1016.760] (-1014.455) -- 0:08:10
1130000 -- (-1022.089) (-1011.151) (-1013.911) [-1007.817] -- 0:08:04
1140000 -- (-1011.862) (-1023.743) (-1023.192) [-1007.247] -- 0:07:59
1150000 -- (-1008.716) (-1013.480) [-1015.629] (-1017.107) -- 0:07:53
1160000 -- (-1026.803) [-1003.091] (-1022.967) (-1027.048) -- 0:07:47
1170000 -- (-1036.550) [-1010.462] (-1018.270) (-1002.477) -- 0:07:41
1180000 -- (-1035.019) (-1009.291) [-1011.227] (-1017.696) -- 0:07:35
1190000 -- (-1003.703) (-1021.246) [-992.147] (-1022.614) -- 0:07:31
1200000 -- [-1006.231] (-1010.943) (-1024.686) (-1006.088) -- 0:07:27
1210000 -- (-1014.149) [-1006.125] (-1014.461) (-1021.700) -- 0:07:23
1220000 -- (-1013.580) (-1011.293) [-1010.426] (-1013.179) -- 0:07:18
1230000 -- (-1017.776) [-993.012] (-1017.211) (-1019.230) -- 0:07:13
1240000 -- (-1003.576) (-1019.999) (-1023.753) [-1002.404] -- 0:07:08
1250000 -- (-1014.268) (-1038.050) [-1004.300] (-1003.180) -- 0:07:03
1260000 -- (-1012.634) (-1004.616) [-1006.035] (-1045.469) -- 0:06:57
1270000 -- (-1020.266) (-1017.449) [-1019.072] (-1028.054) -- 0:06:52
1280000 -- (-1028.537) [-1003.297] (-1039.640) (-1002.714) -- 0:06:46
1290000 -- (-1016.104) (-1015.200) [-1003.932] (-1016.838) -- 0:06:41
1300000 -- (-1015.873) (-1037.335) (-1006.258) [-1009.561] -- 0:06:35
1310000 -- (-1023.971) (-1009.974) [-1000.289] (-1015.560) -- 0:06:30
1320000 -- (-1033.882) [-1003.444] (-1009.753) (-1023.020) -- 0:06:24
1330000 -- (-1033.917) [-1014.760] (-1008.434) (-1039.305) -- 0:06:19
1340000 -- (-1006.140) [-1014.717] (-1017.292) (-1012.027) -- 0:06:13
```

```
1350000 -- (-1011.184) (-1015.369) [-1002.331] (-997.588) -- 0:06:08
1360000 -- (-1026.054) (-1015.572) [-1009.717] (-1021.713) -- 0:06:02
1370000 -- [-1007.505] (-1016.394) (-1017.961) (-1007.594) -- 0:05:57
1380000 -- (-1022.354) (-1006.005) [-1013.648] (-1017.233) -- 0:05:51
1390000 -- (-1008.898) (-1015.117) (-1006.989) [-1007.117] -- 0:05:47
1400000 -- (-1008.579) (-1015.636) [-1007.892] (-1030.924) -- 0:05:41
1410000 -- (-1012.460) [-1009.506] (-1012.407) (-1016.835) -- 0:05:36
1420000 -- [-1019.580] (-1016.090) (-1013.985) (-1011.427) -- 0:05:30
1430000 -- [-1006.685] (-1017.280) (-1011.769) (-1010.057) -- 0:05:25
1440000 -- (-1016.079) (-1014.731) (-1004.142) [-994.172] -- 0:05:19
1450000 -- [-1012.352] (-1031.939) (-1020.686) (-1012.811) -- 0:05:14
1460000 -- (-1012.028) (-1024.041) (-1019.289) [-1006.290] -- 0:05:08
1470000 -- (-1019.205) [-1009.648] (-1018.238) (-1008.048) -- 0:05:03
1480000 -- (-1018.225) [-1012.728] (-1029.428) (-1000.139) -- 0:04:57
1490000 -- (-1014.965) [-1009.722] (-1025.361) (-1030.039) -- 0:04:52
1500000 -- (-1033.445) (-1038.528) (-1016.186) [-1003.708] -- 0:04:46
1510000 -- (-1007.107) (-1013.430) [-1018.213] (-1007.367) -- 0:04:41
1520000 -- [-1002.590] (-1026.793) (-1008.335) (-1010.402) -- 0:04:35
1530000 -- (-1024.057) [-1004.905] (-1015.341) (-1009.141) -- 0:04:29
1540000 -- [-1005.775] (-1020.795) (-1016.775) (-998.706) -- 0:04:24
1550000 -- (-1011.082) (-1023.640) [-1001.394] (-1019.481) -- 0:04:18
1560000 -- (-1020.186) (-1053.092) [-1017.984] (-1013.622) -- 0:04:12
1570000 -- (-1009.287) (-1029.065) [-1016.064] (-1012.643) -- 0:04:07
1580000 -- [-1008.630] (-1017.484) (-1002.180) (-1017.557) -- 0:04:01
1590000 -- [-1010.918] (-1032.854) (-1018.106) (-1003.309) -- 0:03:55
1600000 -- (-1033.674) (-1024.527) [-1015.395] (-998.339) -- 0:03:50
1610000 -- (-1011.190) [-1015.395] (-1041.313) (-1008.084) -- 0:03:44
1620000 -- [-1005.289] (-1023.030) (-1006.672) (-1022.442) -- 0:03:38
1630000 -- (-1027.760) [-1012.656] (-1035.150) (-1006.086) -- 0:03:33
1640000 -- (-1006.304) [-1010.373] (-1005.114) (-1028.728) -- 0:03:27
1650000 -- (-1007.852) (-1021.388) [-1005.000] (-1022.408) -- 0:03:21
1660000 -- (-1006.677) (-1021.786) [-1013.038] (-1019.849) -- 0:03:16
1670000 -- (-1007.426) [-1003.562] (-1015.111) (-1024.981) -- 0:03:10
1680000 -- [-1008.550] (-1019.964) (-1021.046) (-1019.105) -- 0:03:04
1690000 -- (-1027.676) [-1027.736] (-1029.223) (-1014.990) -- 0:02:59
1700000 -- [-1004.450] (-1020.914) (-1017.062) (-1009.281) -- 0:02:53
1710000 -- (-1011.764) (-1005.248) (-1005.678) [-996.778] -- 0:02:47
1720000 -- [-1005.713] (-1026.591) (-1005.158) (-1013.104) -- 0:02:41
1730000 -- [-1014.851] (-1022.463) (-1001.089) (-1021.421) -- 0:02:36
1740000 -- (-1017.310) (-1036.472) [-1001.289] (-1014.162) -- 0:02:30
1750000 -- [-1020.465] (-1008.300) (-1015.938) (-1019.812) -- 0:02:24
1760000 -- (-1017.193) [-1001.525] (-1028.825) (-1019.178) -- 0:02:18
1770000 -- (-1023.535) [-999.780] (-1013.175) (-1017.314) -- 0:02:12
1780000 -- (-1039.640) (-1019.189) [-1017.200] (-1012.867) -- 0:02:06
1790000 -- (-1013.331) [-1008.762] (-1004.943) (-1032.596) -- 0:02:01
1800000 -- (-1022.281) [-1002.268] (-1013.067) (-1009.214) -- 0:01:55
1810000 -- (-1013.634) [-1019.998] (-1008.382) (-1016.517) -- 0:01:49
1820000 -- (-1009.430) [-1007.118] (-1043.366) (-1031.810) -- 0:01:43
1830000 -- (-1023.136) (-1003.273) [-1005.204] (-1005.465) -- 0:01:37
1840000 -- (-1031.059) [-1002.310] (-1019.906) (-1016.444) -- 0:01:32
1850000 -- (-1022.153) [-1006.872] (-1015.255) (-1019.787) -- 0:01:26
1860000 -- [-1004.272] (-1029.433) (-1012.534) (-1002.912) -- 0:01:20
1870000 -- (-1034.550) (-1018.303) [-1002.689] (-1011.167) -- 0:01:14
1880000 -- (-1023.759) (-1019.318) [-995.984] (-1013.254) -- 0:01:08
1890000 -- [-1002.934] (-1012.205) (-1013.271) (-1006.149) -- 0:01:03
1900000 -- [-1009.840] (-1022.766) (-1023.288) (-1028.966) -- 0:00:57
```

```
   1910000 -- (-1008.129) (-1026.136) [-1006.252] (-1012.397) -- 0:00:51
   1920000 -- (-1006.634) (-1026.334) [-1007.913] (-1007.945) -- 0:00:45
   1930000 -- (-1011.529) (-1015.872) (-1021.593) [-1014.711] -- 0:00:40
   1940000 -- [-1013.537] (-1027.924) (-1007.607) (-1033.956) -- 0:00:34
   1950000 -- (-1011.710) [-1006.317] (-1028.062) (-1005.585) -- 0:00:28
   1960000 -- (-1007.740) (-1023.011) (-1034.228) [-995.187] -- 0:00:22
   1970000 -- (-1003.515) (-1010.789) (-1018.642) [-1008.914] -- 0:00:17
   1980000 -- [-1007.155] (-1017.143) (-1034.538) (-1008.662) -- 0:00:11
   1990000 -- [-1018.314] (-1012.037) (-1021.902) (-1016.872) -- 0:00:05
   2000000 -- (-1007.355) [-1001.127] (-1009.912) (-1020.594) -- 0:00:00

   Continue with analysis? (yes/no): n

   Analysis completed in 19 mins 5 seconds
   Analysis used 1054.63 seconds of CPU time
   Log likelihood of best state for "cold" chain was -985.06

   Acceptance rates for the moves in the "cold" chain:
      With prob.   (last 100)   chain accepted proposals by move
         34.3 %     ( 16 %)     Multiplier(Alpha)
         19.0 %     ( 26 %)     ExtSprClock(Tau,V)
         44.9 %     ( 35 %)     NNIClock(Tau,V)
         15.6 %     ( 16 %)     ParsSPRClock(Tau,V)
         70.3 %     ( 74 %)     NodesliderClock(V)
         71.0 %     ( 32 %)     TreeStretch(V)

   Chain swap information:

                1       2       3       4
        ----------------------------------
      1 |            0.45    0.19    0.07
      2 |  332602            0.56    0.27
      3 |  334113  333671            0.60
      4 |  333117  332681  333816

   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-Hout2.t"
   Using relative burnin ('relburnin=yes'), discarding the first 25 % of sampled trees
```

```
Writing statistics to files DY-26Dec-strict-Hout2.<parts|tstat|vstat|trprobs|con>
Examining file ...
Found one tree block in file "DY-26Dec-strict-Hout2.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 equual to (Minpartfreq) in at least one run. Minpartfreq is a paramiter 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.

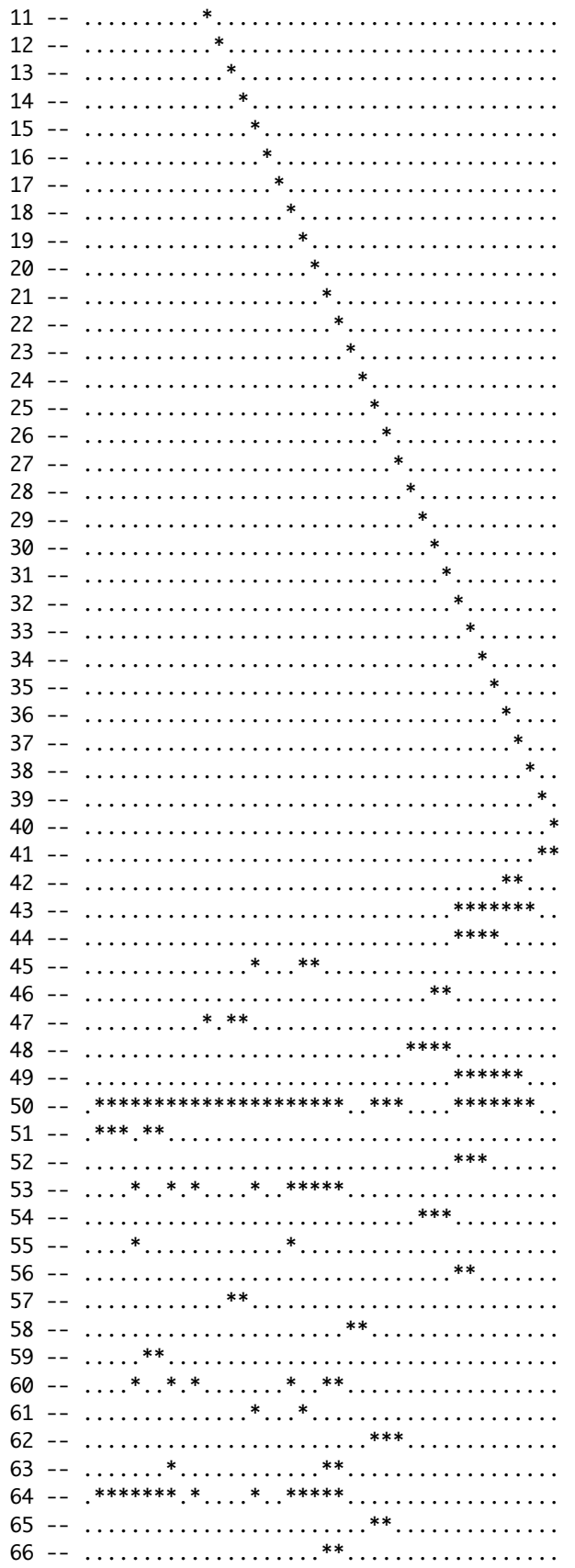
Note that Stddev may be unreliable if the partition is not present in all
runs (the last column indicates the number of runs that sampled the partition
if more than one run is summarized). The PSRF is not calculated at all if
the partition is not present in all runs.The PSRF is also sensitive to small
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.

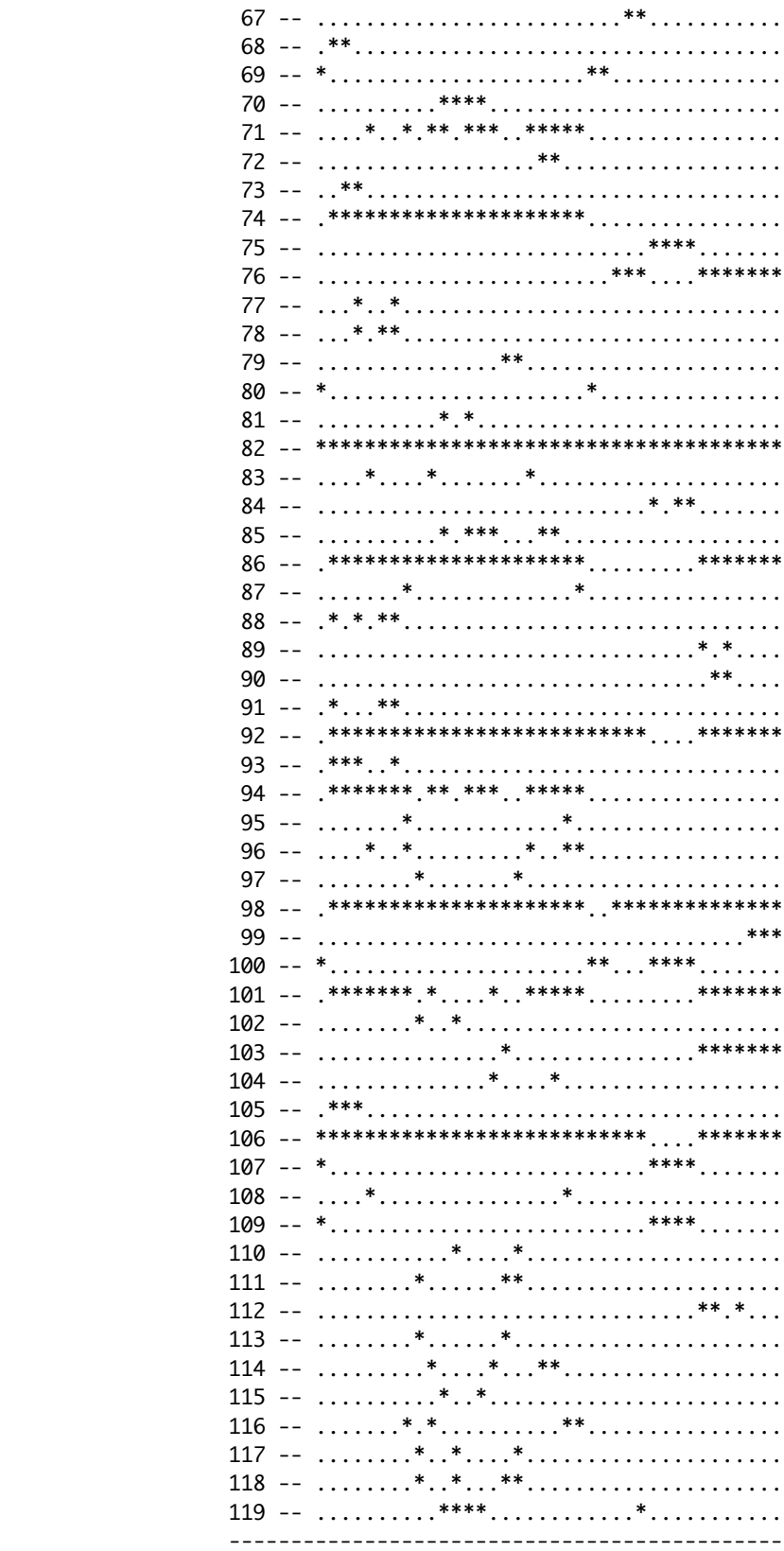
List of taxa in bipartitions:
```

```
  1 -- hax
  2 -- gwi
  3 -- dgr
  4 -- scsh
  5 -- xsl
  6 -- bea
  7 -- crx
  8 -- chp
  9 -- txc
 10 -- haa
 11 -- ing
 12 -- kuu
 13 -- hoi
 14 -- koy
 15 -- taa
 16 -- aht
 17 -- tfn
 18 -- kkz
 19 -- tcb
 20 -- tau
 21 -- ttmN
 22 -- tceS
 23 -- eya
 24 -- tli
 25 -- gce
 26 -- tol
 27 -- cco
 28 -- hup
 29 -- mtl
 30 -- wlk
 31 -- kto
 32 -- apc
 33 -- apw
 34 -- apj
 35 -- nav
 36 -- apk
 37 -- apl
 38 -- srs
 39 -- ket
 40 -- zko

Key to taxon bipartitions (saved to file "DY-26Dec-strict-Hout2.parts"):

 ID -- Partition
------------------------------------------------
  0 -- ****************************************
  1 -- *.....................................
  2 -- .*....................................
  3 -- ..*...................................
  4 -- ...*..................................
  5 -- ....*.................................
  6 -- .....*................................
  7 -- ......*...............................
  8 -- .......*..............................
  9 -- ........*.............................
 10 -- .........*............................
```





Summary statistics for informative taxon bipartitions (clades)

(saved to file "DY-26Dec-strict-Hout2.tstat"):

ID	#obs	Probab.
41	3001	1.000000
42	2997	0.998667
43	2776	0.925025
44	2616	0.871709
45	2564	0.854382
46	2527	0.842053
47	2441	0.813396
48	2250	0.749750
49	2241	0.746751
50	2238	0.745751
51	2118	0.705765
52	2043	0.680773
53	1984	0.661113
54	1836	0.611796
55	1826	0.608464
56	1789	0.596135
57	1760	0.586471
58	1758	0.585805
59	1695	0.564812
60	1588	0.529157
61	1586	0.528491
62	1583	0.527491
63	1572	0.523825
64	1448	0.482506
65	1406	0.468510
66	1289	0.429523
67	1202	0.400533
68	1170	0.389870
69	1067	0.355548
70	1066	0.355215
71	1053	0.350883
72	941	0.313562
73	931	0.310230
74	924	0.307897
75	921	0.306898
76	880	0.293236
77	806	0.268577
78	801	0.266911
79	783	0.260913
80	731	0.243585
81	730	0.243252
82	660	0.219927
83	658	0.219260
84	654	0.217927
85	637	0.212263
86	580	0.193269
87	580	0.193269
88	555	0.184938
89	555	0.184938
90	555	0.184938
91	552	0.183939
92	551	0.183605

```
 93   529    0.176275
 94   520    0.173276
 95   518    0.172609
 96   506    0.168610
 97   503    0.167611
 98   487    0.162279
 99   460    0.153282
100   456    0.151949
101   443    0.147617
102   430    0.143286
103   412    0.137288
104   410    0.136621
105   397    0.132289
106   385    0.128291
107   377    0.125625
108   373    0.124292
109   369    0.122959
110   368    0.122626
111   356    0.118627
112   356    0.118627
113   355    0.118294
114   352    0.117294
115   350    0.116628
116   335    0.111629
117   333    0.110963
118   310    0.103299
119   304    0.101300
---------------------

Summary statistics for branch and node parameters
   (saved to file "DY-26Dec-strict-Hout2.vstat"):

                                      95% HPD Interval
                                     -------------------
Parameter       Mean       Variance     Lower       Upper       Median
-------------------------------------------------------------------------
length[1]      0.114690    0.001561    0.046758    0.189851    0.112184
length[2]      0.037719    0.000299    0.009372    0.071696    0.034830
length[3]      0.038457    0.000364    0.009583    0.079175    0.034806
length[4]      0.033569    0.000275    0.007822    0.065881    0.030545
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length[6]      0.033752    0.000470    0.003749    0.078995    0.028476
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length[8]      0.034227    0.000205    0.010211    0.062754    0.032086
length[9]      0.077158    0.000804    0.027178    0.132055    0.075157
length[10]     0.037659    0.000207    0.012679    0.065648    0.036050
length[11]     0.038082    0.000362    0.007724    0.074951    0.034214
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length[17]     0.072553    0.000779    0.026308    0.127393    0.069223
length[18]     0.028093    0.000201    0.005710    0.056587    0.025475
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length[40]	0.059751	0.000504	0.022647	0.103790	0.057580
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length[90]	0.006533	0.000042	0.000016	0.020109	0.004647
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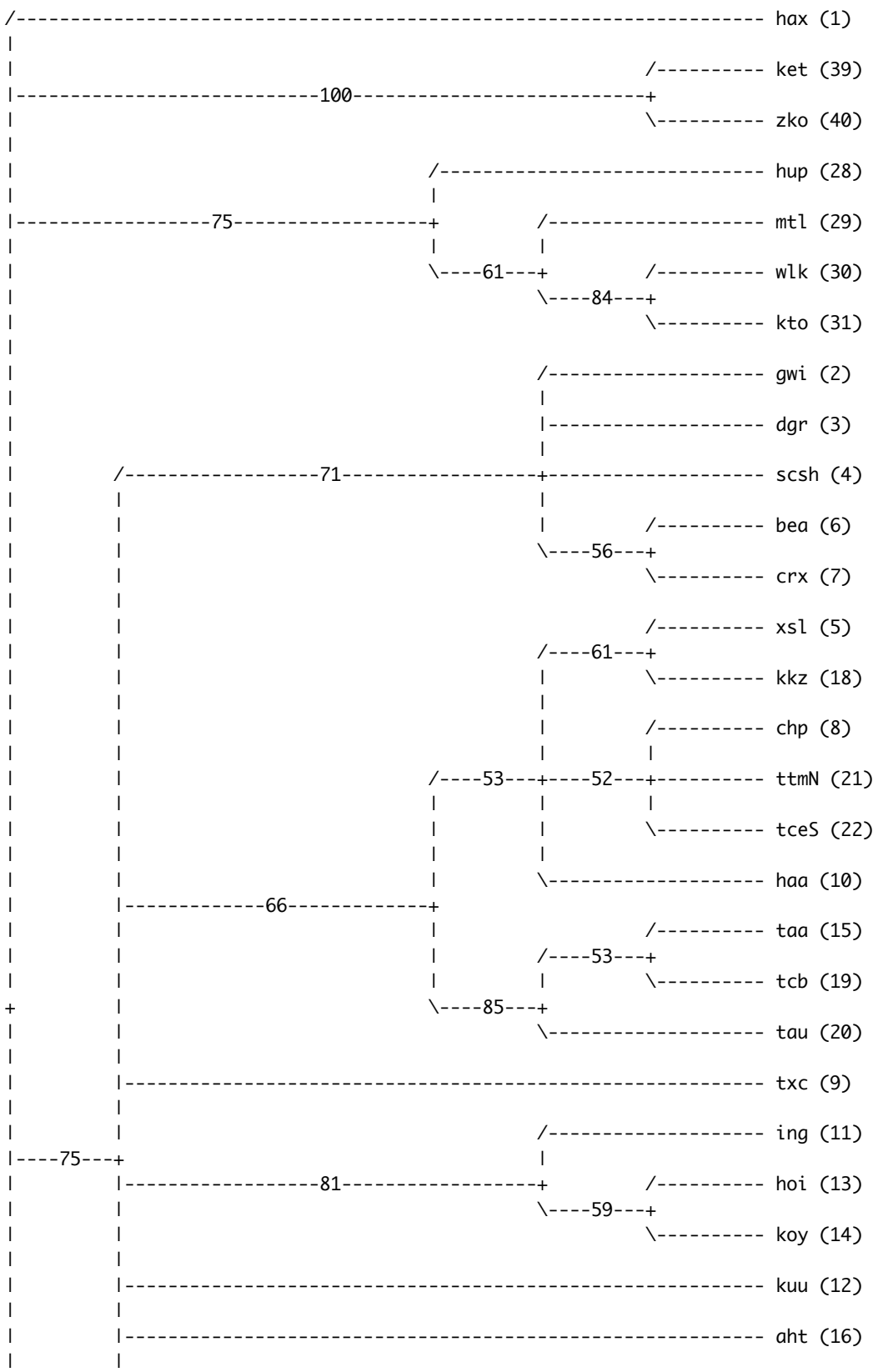
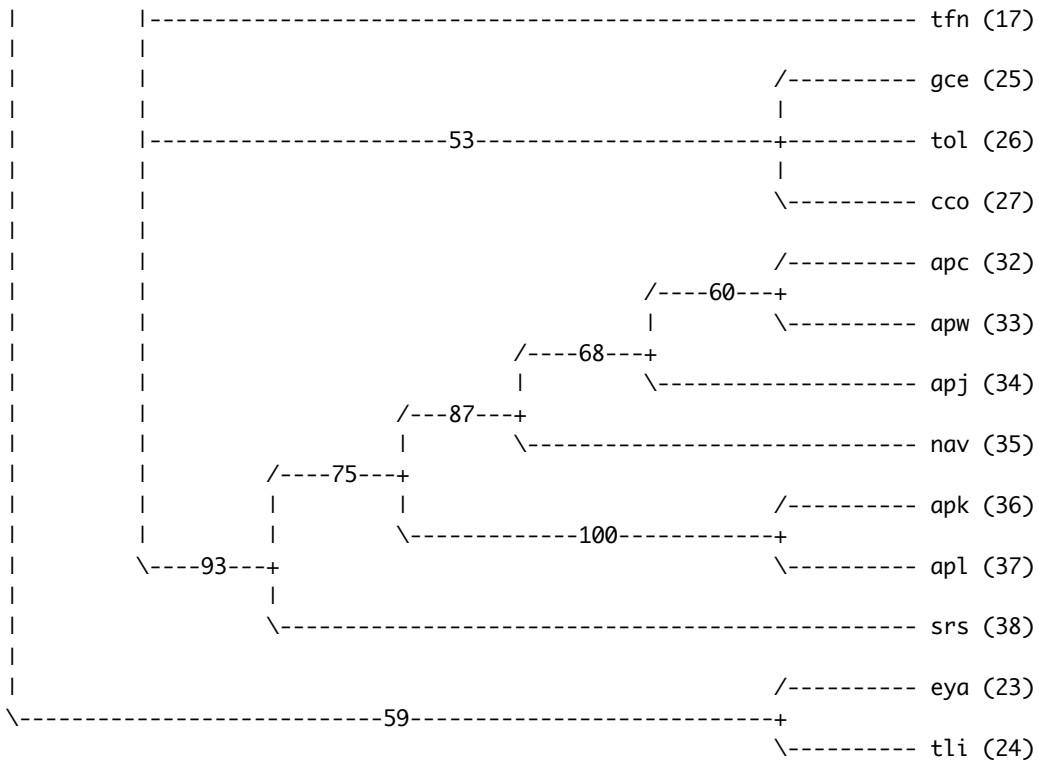
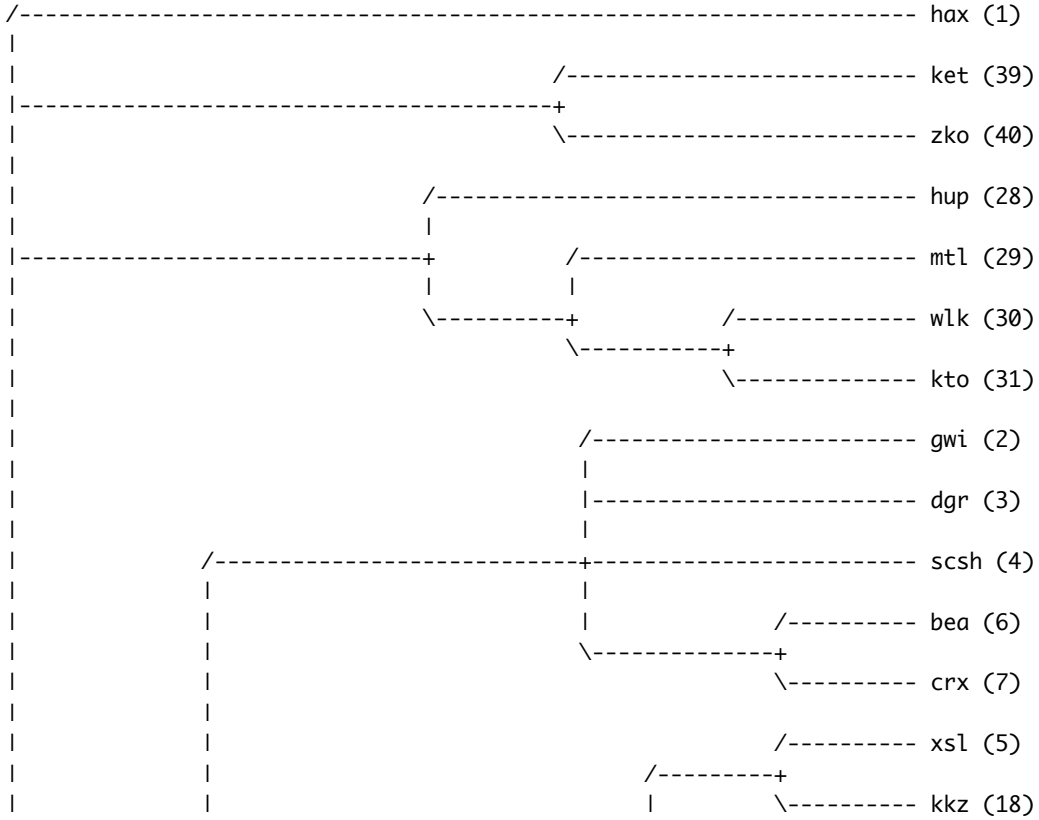
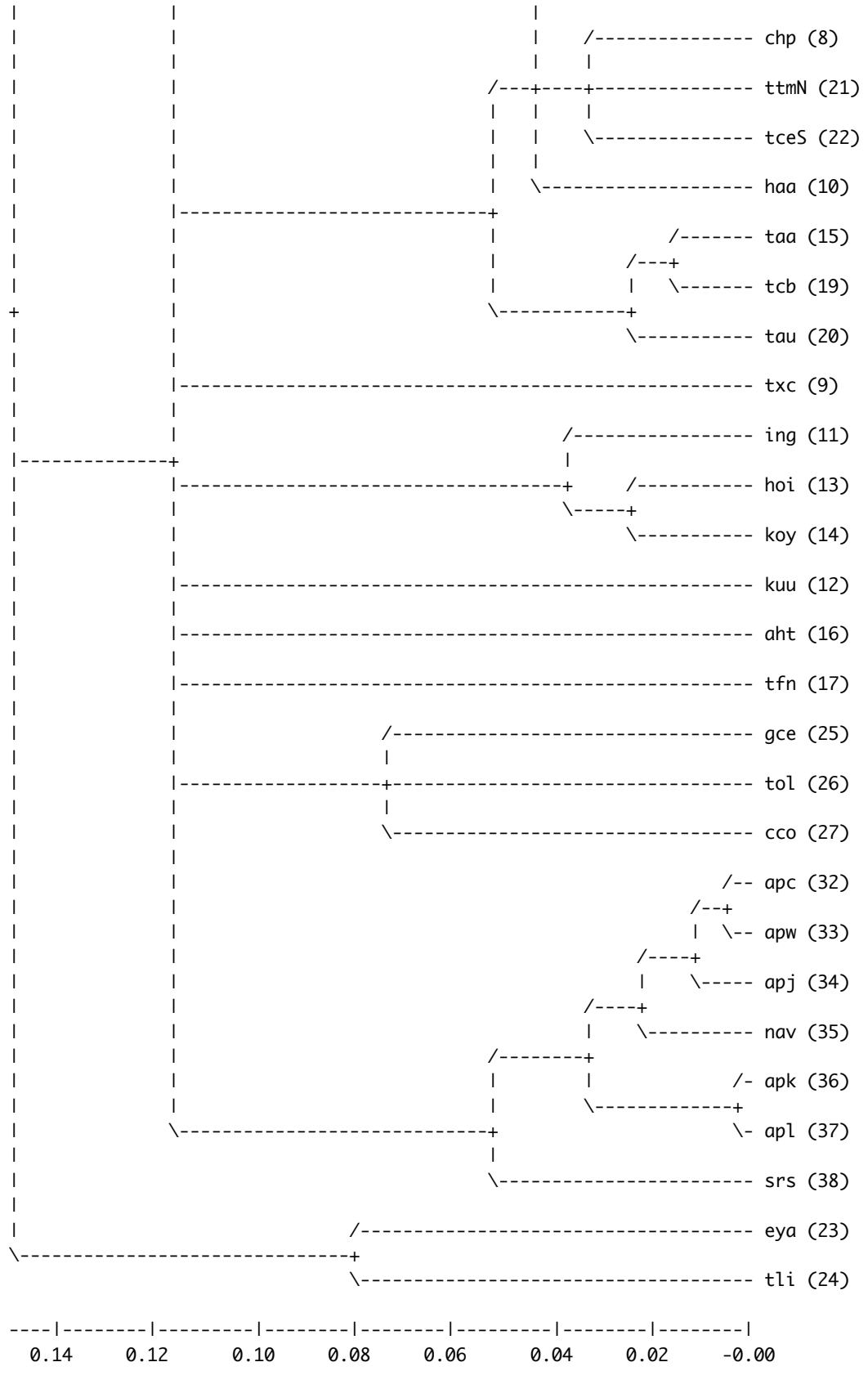
Clade credibility values:





Phylogram (based on median node depths):

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eya (23)
tli (24)
0.14
0.12
0.10
0.08
0.06
0.04
0.02
-0.00

```
   [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-26Dec-strict-Hout2.p
   Writing summary statistics to file DY-26Dec-strict-Hout2.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 station-
   arity. Sample trees and parameters after the log probability
   plateaus. Of course, this is not a guarantee that you are at sta-
   analysis should be. When the log probability starts to plateau
   tionarity. When possible, run multiple analyses starting from dif-
   ferent 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 conver-
   gence 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.

   +-------------------------------------------------------------+ -1004.822
   |                       *      *                              |
   |           *                                                 |
   |             *     *                             *           |
   |  *   *                **                              * *  |
   |                  *       *         *                        |
   |   **        *      *           *    **                   **|
   |                             * **                 *          |
   | *   *                                              *   *    |
   |*        **                *      * *      **   *  *  *     |
   |                ** *             *      *        *          |
   |       *      *                                *             |
   |        *            *    *            *  *                 |
   |                                        *                    |
   |                                              *              |
   |                                                        *  * |
   +------+-----+-----+-----+-----+-----+-----+-----+-----+-----+ -1011.995
   ^                                                             ^
   500000                                                        2000000
```

```
   Estimated marginal likelihoods for run sampled in file "DY-26Dec-strict-Hout2.p":
      (Use the harmonic mean for Bayes factor comparisons of models)
      (Values are saved to the file /Users/msicoli/DY-Typological_binary_bayes-2.nex.lstat)

   Arithmetic mean   Harmonic mean
   --------------------------------
       -996.18         -1027.76
   --------------------------------


   Model parameter summaries for run sampled in file "DY-26Dec-strict-Hout2":
      Based on a total of 3001 samples out of a total of 4001 samples
         from this analysis.
      Parameter summaries saved to file "/Users/msicoli/DY-
Typological_binary_bayes-2.nex.pstat".

                                       95% HPD Interval
                                      --------------------
   Parameter      Mean      Variance     Lower       Upper       Median     ESS*
   ----------------------------------------------------------------------------
   TH          0.143615    0.001725    0.068256    0.212151    0.147314    243.95
   TL          2.439625    0.459764    1.230095    3.583763    2.512555    223.79
   alpha       1.086565    0.816773    0.128740    2.635880    0.896767    413.73
   ----------------------------------------------------------------------------
   * 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-Hout2-ss

   Setting number of generations to 100000
   Setting diagnosing frequency to 1000

MrBayes > ss

   Setting chain output file names to "YND-Typ-Hout2-ss.<p/t>"
   Running Markov chain
   MCMC stamp = 6022182788
   Seed = 780705211
   Swapseed = 1290899819
   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 diricihlet/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 = 40
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 81 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 -- -1001.127181 -- -12.625325
   Chain 2 -- -1007.355276 -- -30.294350
   Chain 3 -- -1009.911630 -- -29.733445
   Chain 4 -- -1020.593917 -- -43.326549


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 begining 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-
rations instead of requested 100000.


Chain results (76500 generations requested):

    0 -- [-1001.127] (-1007.355) (-1009.912) (-1020.594)

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 -- (-1052.155) (-1046.580) [-1031.839] (-1040.015) -- 0:00:39
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 -- (-1051.856) (-1100.553) [-1047.227] (-1131.271) -- 0:00:33
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 -- (-1296.567) (-1245.607) (-1147.229) [-1142.151] -- 0:00:27
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 -- (-1462.189) [-1320.794] (-1322.051) (-1349.255) -- 0:00:22
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 -- (-1444.965) (-1431.647) [-1346.870] (-1403.867) -- 0:00:16
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 -- (-1503.649) (-1454.469) [-1457.306] (-1492.975) -- 0:00:10
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 -- (-2210.742) (-2278.530) [-2175.981] (-2049.667) -- 0:00:04
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 48 seconds
Analysis used 44.62 seconds of CPU time
Log likelihood of best state for "cold" chain was -992.96

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     -1127.56
    ------------------------------
More statistics on stepping-stone sampling is dumped to YND-Typ-Hout2-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.
+------------------------------------------------------------+ 0.000
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|*****  ****  *****  ****  *****  ****  *****  ****  *****  ****  *****|
+------+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 0.000
^                                                            ^
1                                                           50
```

```
   Acceptance rates for the moves in the "cold" chain:
      With prob.   (last 100)   chain accepted proposals by move
         49.8 %     ( 61 %)     Multiplier(Alpha)
         43.2 %     ( 59 %)     ExtSprClock(Tau,V)
         78.4 %     (100 %)     NNIClock(Tau,V)
         33.1 %     ( 29 %)     ParsSPRClock(Tau,V)
         86.1 %     ( 97 %)     NodesliderClock(V)
         54.7 %     ( 85 %)     TreeStretch(V)

   Chain swap information:

               1      2      3      4
        ------------------------------
      1 |          0.21   0.04   0.01
      2 |  12713          0.31   0.08
      3 |  12860  12787          0.36
      4 |  12542  12762  12836

   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 > ss

   Running Markov chain
   MCMC stamp = 6548936566
   Seed = 231125092
   Swapseed = 1717525018
   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 diricihlet/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 = 40
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 81 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 -- -1700.896933 -- -70.642544
   Chain 2 -- -2266.130972 -- -171.769429
   Chain 3 -- -2280.289285 -- -222.262241
   Chain 4 -- -2308.118309 -- -203.827352


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 begining 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.


Chain results (76500 generations requested):

    0 -- [-1700.897] (-2266.131) (-2280.289) (-2308.118)

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 -- (-1035.938) (-1029.248) [-1010.146] (-1029.447) -- 0:00:39
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 -- (-1128.993) (-1088.452) (-1098.992) [-1056.226] -- 0:00:33
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 -- (-1180.920) (-1293.324) [-1152.954] (-1182.539) -- 0:00:26
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 -- [-1228.154] (-1381.908) (-1361.579) (-1382.597) -- 0:00:21
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 -- (-1399.794) (-1424.915) [-1466.781] (-1453.575) -- 0:00:15
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 -- (-1627.987) (-1471.007) [-1466.831] (-1546.448) -- 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 -- (-2307.970) [-1665.981] (-2265.110) (-1983.707) -- 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 45 seconds
Analysis used 44.36 seconds of CPU time
Log likelihood of best state for "cold" chain was -1003.68

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     -1127.07
    ------------------------------
More statistics on stepping-stone sampling is dumped to YND-Typ-Hout2-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.
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^                                                            ^
1                                                           50


Acceptance rates for the moves in the "cold" chain:
   With prob.   (last 100)   chain accepted proposals by move
      43.8 %     ( 54 %)     Multiplier(Alpha)
```

```
      43.4 %     ( 64 %)     ExtSprClock(Tau,V)
      78.8 %     (100 %)     NNIClock(Tau,V)
      32.9 %     ( 25 %)     ParsSPRClock(Tau,V)
      86.0 %     ( 98 %)     NodesliderClock(V)
      53.6 %     ( 81 %)     TreeStretch(V)

   Chain swap information:

            1      2      3      4
     ------------------------------
   1 |          0.23   0.05   0.01
   2 |  12719          0.30   0.07
   3 |  12663  12921          0.35
   4 |  12905  12609  12683

   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 > ss

   Running Markov chain
   MCMC stamp = 6390972662
   Seed = 1735696387
   Swapseed = 147486170
   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 diricihlet/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 = 40
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 81 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 -- -1750.544444 -- -81.031598
   Chain 2 -- -2269.986807 -- -189.910093
   Chain 3 -- -2295.411042 -- -191.476033
   Chain 4 -- -2277.901644 -- -199.106113
```

```
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 begining 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.


Chain results (76500 generations requested):

    0 -- [-1750.544] (-2269.987) (-2295.411) (-2277.902)

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 -- (-1031.442) [-1016.888] (-1049.916) (-1047.454) -- 0:00:39
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 -- [-1078.900] (-1159.212) (-1080.756) (-1083.329) -- 0:00:36
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 -- (-1267.103) [-1118.587] (-1225.274) (-1241.654) -- 0:00:27
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 -- (-1356.317) [-1207.039] (-1354.253) (-1404.918) -- 0:00:21
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 -- (-1444.109) (-1362.327) (-1467.370) [-1339.991] -- 0:00:15
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 -- (-1506.013) (-1465.573) (-1484.749) [-1449.323] -- 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 -- (-2300.140) [-1590.175] (-2286.516) (-2258.392) -- 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 45 seconds
Analysis used 44.39 seconds of CPU time
Log likelihood of best state for "cold" chain was -1002.80

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     -1125.48
    ------------------------------
More statistics on stepping-stone sampling is dumped to YND-Typ-Hout2-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.
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+------+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 0.000
^                                                            ^
1                                                           50


Acceptance rates for the moves in the "cold" chain:
   With prob.   (last 100)   chain accepted proposals by move
      43.3 %     ( 51 %)     Multiplier(Alpha)
      43.2 %     ( 53 %)     ExtSprClock(Tau,V)
      78.8 %     (100 %)     NNIClock(Tau,V)
      33.0 %     ( 27 %)     ParsSPRClock(Tau,V)
      86.0 %     (100 %)     NodesliderClock(V)
```

```
      52.3 %     ( 91 %)     TreeStretch(V)

   Chain swap information:

            1      2      3      4
     ------------------------------
   1 |          0.18   0.05   0.01
   2 |  12763          0.31   0.08
   3 |  12778  12783          0.37
   4 |  12663  12704  12809

   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 >
```