Exercise 3 help file: The box below contains part of the results output by codeml for a ML analysis. This box indicates the log likelihood score required to carry out the likelihood ratio tests of exercise 3.

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.
.
TREE #  1:  (1, 2, (5, ((3, 4), (((6, (8, 9)), (7, 10)), (11, 12)))));    MP score: -1
check convergence..
lnL(ntime: 21  np: 23):   -6018.633010          +0.0000
   13..1     13..2     13..14    14..5     14..15                           15..17   17..18    18..19
19..6     19..20    20..8     20..9     18..21                           22..11    22..12
 0.165986 0.145030 0.060255 0.252090 0.030239                     68 0.125411 0.692353 0.249467
0.205980 0.294515 0.131299 0.213038 0.174959                      0 0.290395 0.356760 2.401783
0.136656


Note: Branch length is defined as number of n                 er codon (not per nucleotide
site).


tree length =    4.50360


(1: 0.165986, 2: 0.145030, (5: 0.252090, ((3: 0.133936, 4: 0.101768): 0.230094, (((6: 0.205980, (8:
0.131299, 9: 0.213038): 0.294515): 0.249467, (7: 0.155890, 10: 0.172753): 0.174959): 0.692353, (11:
0.290395, 12: 0.356760): 0.321380): 0.125411): 0.030239): 0.060255);


(X02152Hom: 0.165986, U07178Sus: 0.145030, (M22585rab: 0.252090, ((NM017025Rat: 0.133936, U13687Mus:
0.101768): 0.230094, (((AF070995C: 0.205980, (X04752Mus: 0.131299, U07177Rat: 0.213038): 0.294515):
0.249467, (U95378Sus: 0.155890, U13680Hom: 0.172753): 0.174959): 0.692353, (X53828OG1: 0.290395,
U28410OG2: 0.356760): 0.321380): 0.125411): 0.030239): 0.060255);
.
.
.
```

> This is the log likelihood score (lnL) computed for a dataset of 12 sequences.
>
> The likelihood was computed for a user-supplied tree topology. That topology is shown in newick format in the line starting with "TREE # 1:"

Note: The next page contains a different part of the results for the same analysis. That output will help you identify the branch specific estimates of ω under H1, H2 and H3.

Exercise 3 help file: The box below contains output that can be found at the very bottom of the result file. These results are for a model having the same ω in all branches of the tree. Your "branch models" (specified as H1, H2 & H3) will have different ω's for different branches, and the column marked "dN/dS" will have different values in your files (depending on the model).

Branches labeled **A0** in figure (pro-orthologous *Ldh-A* sequences)

Branches labeled **C0** in figure (the proximal post-duplication branch for *Ldh-C*)

Branches labeled **C1** in figure (the distal post-duplication branches for *Ldh-C*)

Branches labeled **A1** in figure (post-duplication event *Ldh-A* sequences)

```
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.

dN & dS for each branch

 branch           t         N        S     dN/dS       dN       dS    N*dN    S*dS

  13..1       0.166     729.3    269.7    0.1367    0.0205   0.1497    14.9    40.4
  13..2       0.145     729.3    269.7    0.1367    0.0179   0.1308    13.0    35.3
  13..14      0.060     729.3    269.7    0.1367    0.0074   0.0543     5.4    14.7
  14..5       0.252     729.3    269.7    0.1367    0.0311   0.2273    22.7    61.3
  14..15      0.030     729.3    269.7    0.1367    0.0037   0.0273     2.7     7.4
  15..16      0.230     729.3    269.7    0.1367    0.0283   0.2075    20.7    55.9
  16..3       0.134     729.3    269.7    0.1367    0.0165   0.1208    12.0    32.6
  16..4       0.102     729.3    269.7    0.1367    0.0125   0.0918     9.1    24.7
  15..17      0.125     729.3    269.7    0.1367    0.0155   0.1131    11.3    30.5
  17..18      0.692     729.3    269.7    0.1367    0.0853   0.6242    62.2   168.3
  18..19      0.249     729.3    269.7    0.1367    0.0307   0.2249    22.4    60.7
  19..6       0.206     729.3    269.7    0.1367    0.0254   0.1857    18.5    50.1
  19..20      0.295     729.3    269.7    0.1367    0.0363   0.2655    26.5    71.6
  20..8       0.131     729.3    269.7    0.1367    0.0162   0.1184    11.8    31.9
  20..9       0.213     729.3    269.7    0.1367    0.0262   0.1921    19.1    51.8
  18..21      0.175     729.3    269.7    0.1367    0.0216   0.1577    15.7    42.5
  21..7       0.156     729.3    269.7    0.1367    0.0192   0.1406    14.0    37.9
  21..10      0.173     729.3    269.7    0.1367    0.0213   0.1558    15.5    42.0
  17..22      0.321     729.3    269.7    0.1367    0.0396   0.2898    28.9    78.1
  22..11      0.290     729.3    269.7    0.1367    0.0358   0.2618    26.1    70.6
  22..12      0.357     729.3    269.7    0.1367    0.0440   0.3217    32.1    86.7

tree length for dN:      0.55489
tree length for dS:      4.06047
.
.
```