```
seqfile = seqfile.txt    * sequence data filename
treefile = tree.HO.txt    * tree structure file name [CHANGE THIS]
 outfile = results.txt  * main result file name
 * 0:user defined tree
 seqtype = 1
               * 1:codons
               * 0:equal, 1:F1X4, 2:F3X4, 3:F61
CodonFreq = 2
   model = 0
              * 0:one omega ratio for all branches [FOR MODEL H0]
               * 1:separate omega for each branch
               * 2:user specified dN/dS ratios for branches [FOR MODELS H1-H3]
 NSsites = 0
   icode = 0
              * 0:universal code
kappa = 2
              * initial or fixed kappa
fix omega = 0
               * 1:omega fixed, 0:omega to be estimated
   omega = 0.2 * initial omega
```

NOTE: By changing the treefile read by codeml, you are changing among "branch models" represented within the different treefiles shown below. Remember that these "tree models" specify different biological hypotheses testable via LRTs. Each "branch model" differs according to the branch, or branches, that are identified with a "branch mark" (i.e., #1, #2, etc.) as having unique selection pressure (d_N/d_S) .

```
* tree.H0.txt (H_0 in Table 3):
* model = 0
*(X02152Hom, U07178Sus, (M22585rab, ((NM017025Rat, U13687Mus),
*(((AF070995C,(X04752Mus,U07177Rat)),(U95378Sus,U13680Hom)),(X538280G1,
* U284100G2))));
* tree.H1.txt (H<sub>1</sub> in Table 3):
* model = 2
*(X02152Hom, U07178Sus, (M22585rab, ((NM017025Rat, U13687Mus), (((AF070995C,
*(X04752Mus,U07177Rat)),(U95378Sus,U13680Hom))#1,(X538280G1,U284100G2))
* )));
* tree.H2.txt (H2 in Table 3):
* model = 2
* (X02152Hom, U07178Sus, (M22585rab, ((NM017025Rat, U13687Mus), (((AF070995C
* #1, (X04752Mus #1, U07177Rat #1) #1, (U95378Sus #1, U13680Hom #1)
* #1) #1, (X538280G1, U284100G2)))));
* tree.H0.txt (H3 in Table 3):
* model = 2
* (X02152Hom, U07178Sus, (M22585rab, ((NM017025Rat, U13687Mus), (((AF070995C
* #1, (X04752Mus #1, U07177Rat #1) #1, (U95378Sus #1, U13680Hom #1)
* #1) #1, (X538280G1 #2, U284100G2 #2) #2))));
```