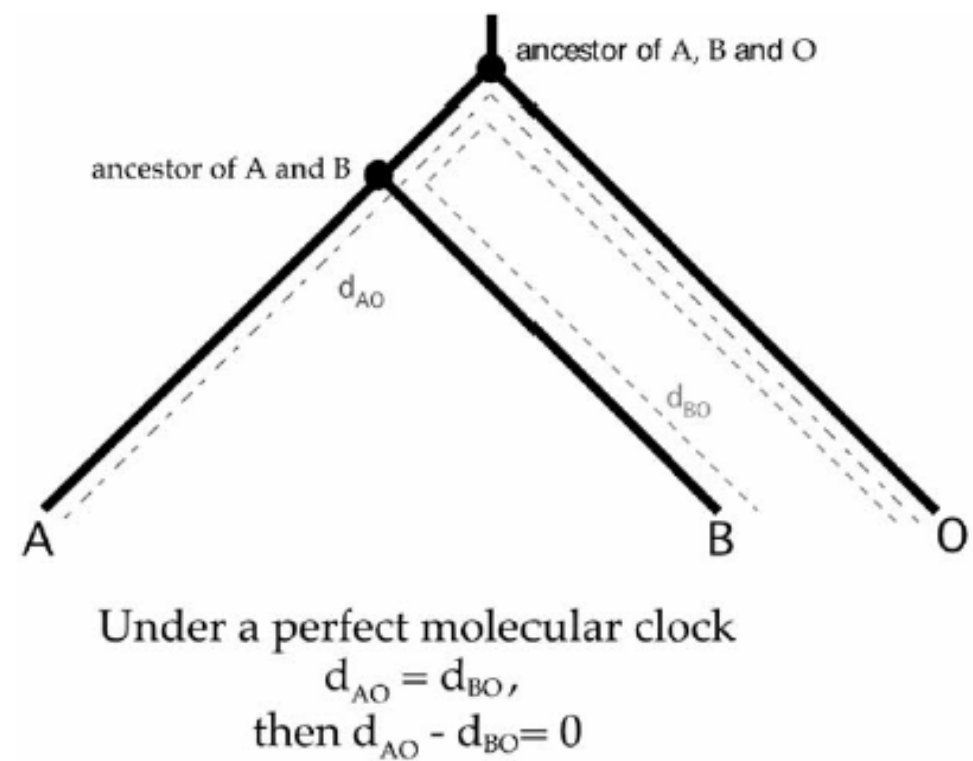
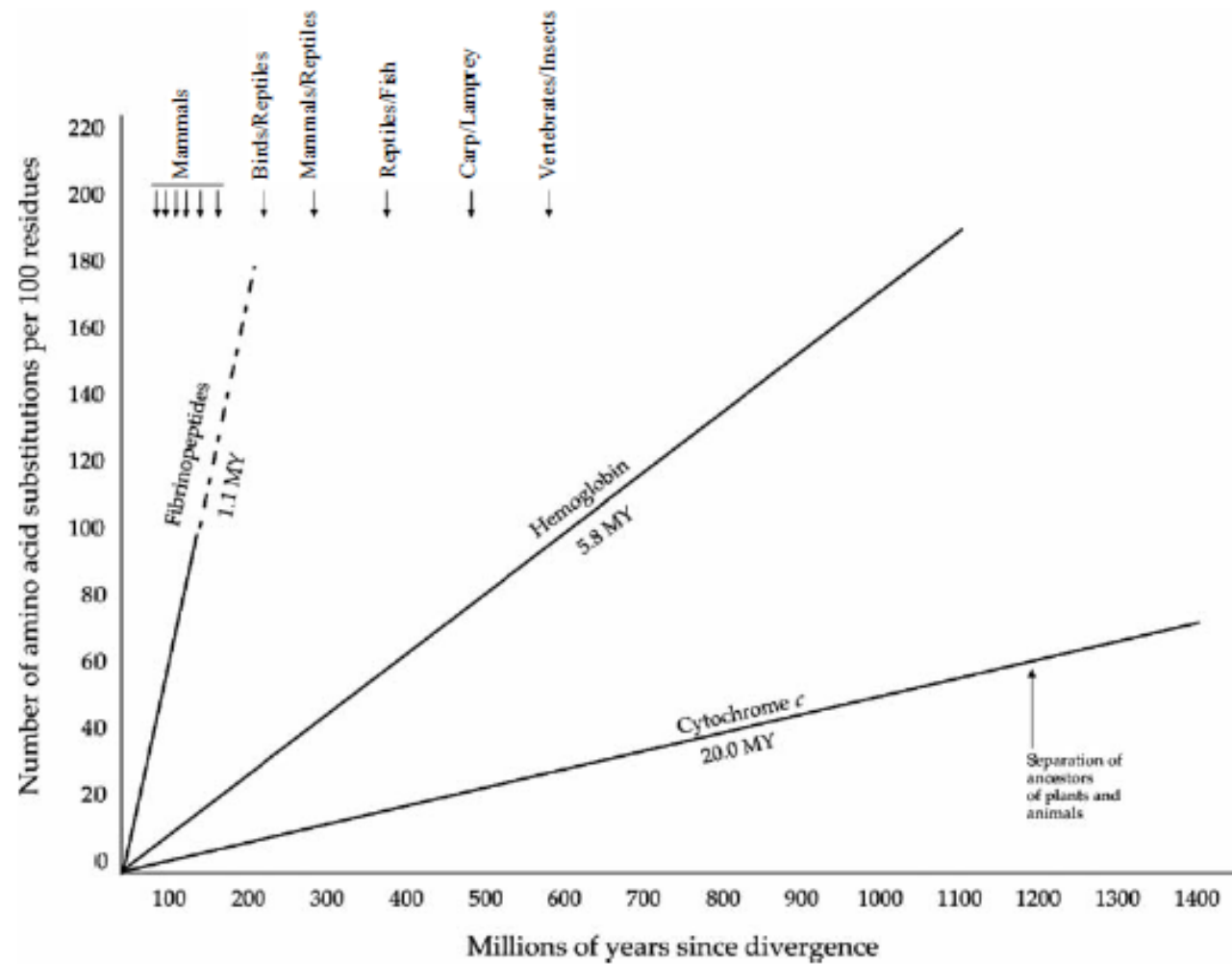
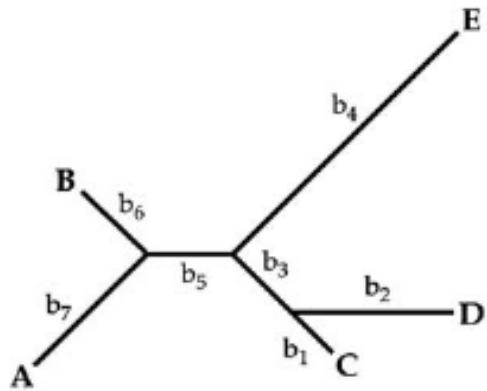


# 11. Moleküler saat analizi



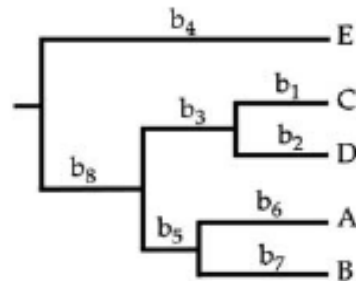
(a)  
**Non-clock-like phylogenetic tree**  
*n* taxa = 5



unrooted tree  
 $2n-3$  independent branches

All  $b_1, b_2, b_3, b_4, b_5, b_6$  and  $b_7$   
 need to be estimated

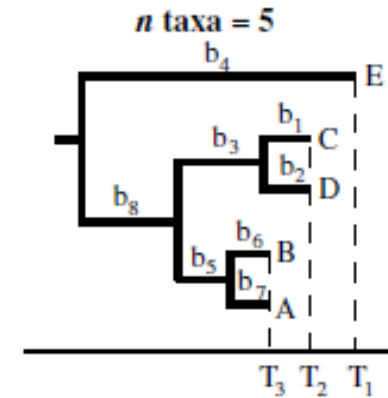
(b)  
**Clock-like phylogenetic tree**  
*n* taxa = 5



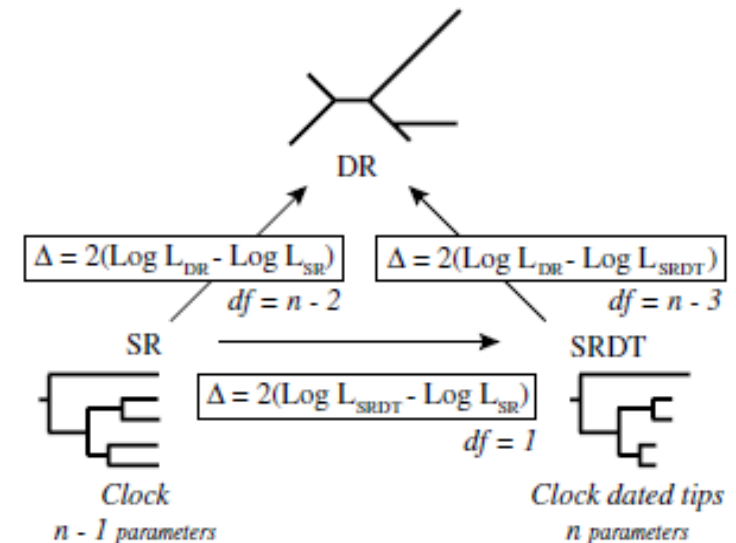
rooted tree  
 $n-1$  independent branches

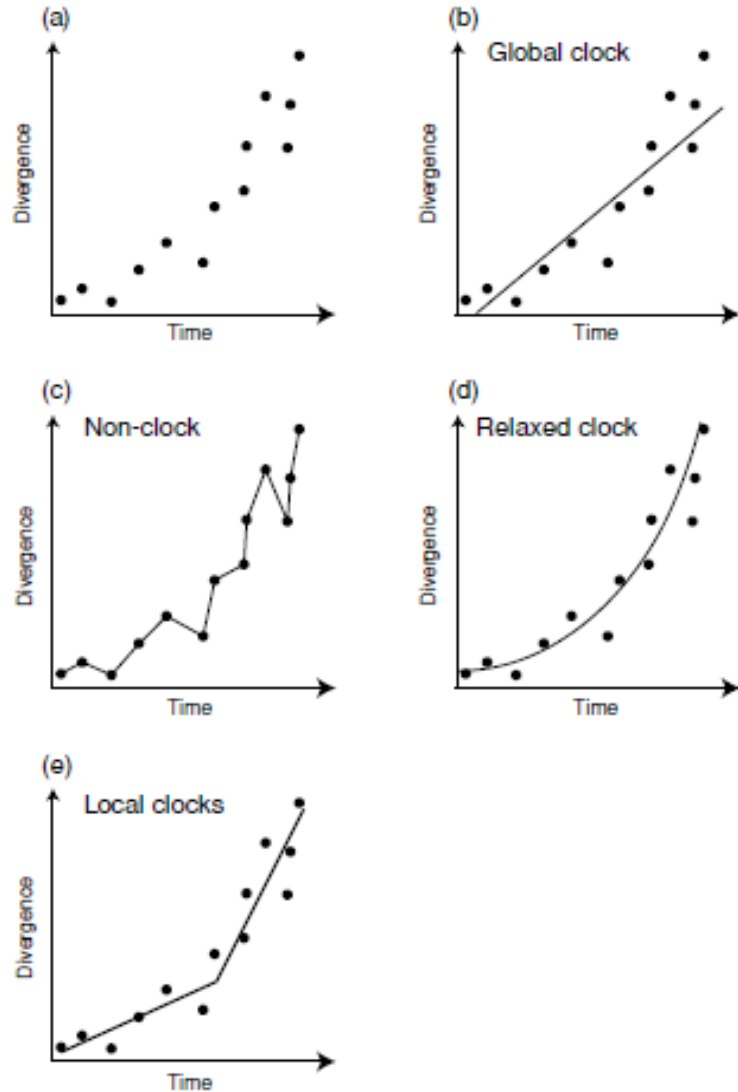
Only  $b_1, b_3, b_4$  and  $b_6$   
 for example, need to be estimated,  
 since under the molecular clock:

$$\begin{aligned} b_2 &= b_1 \\ b_5 &= b_1 + b_3 - b_6 \\ b_7 &= b_6 \\ b_8 &= b_4 - b_5 - b_6 \end{aligned}$$



Non-clock  
 $2n-3$  parameters





```

seqfile = primates.phy
treefile = primates_unrooted.tre

outfile = mlb * main result file
noisy = 9 * 0,1,2,3: how much rubbish on the screen
verbose = 0 * 1: detailed output, 0: concise output
runmode = 0 * 0: user tree; 1: semi-automatic; 2: automatic
           * 3: StepwiseAddition; (4,5):PerturbationNNI

model = 7 * 0:JC69, 1:K80, 2:F81, 3:F84, 4:HKY85
         * 5:T92, 6:TN93, 7:REV, 8:UNREST, 9:REVu; 10:UNRESTu

Mgene = 0 * 0:rates, 1:separate; 2:diff pi, 3:diff kapa, 4:all diff

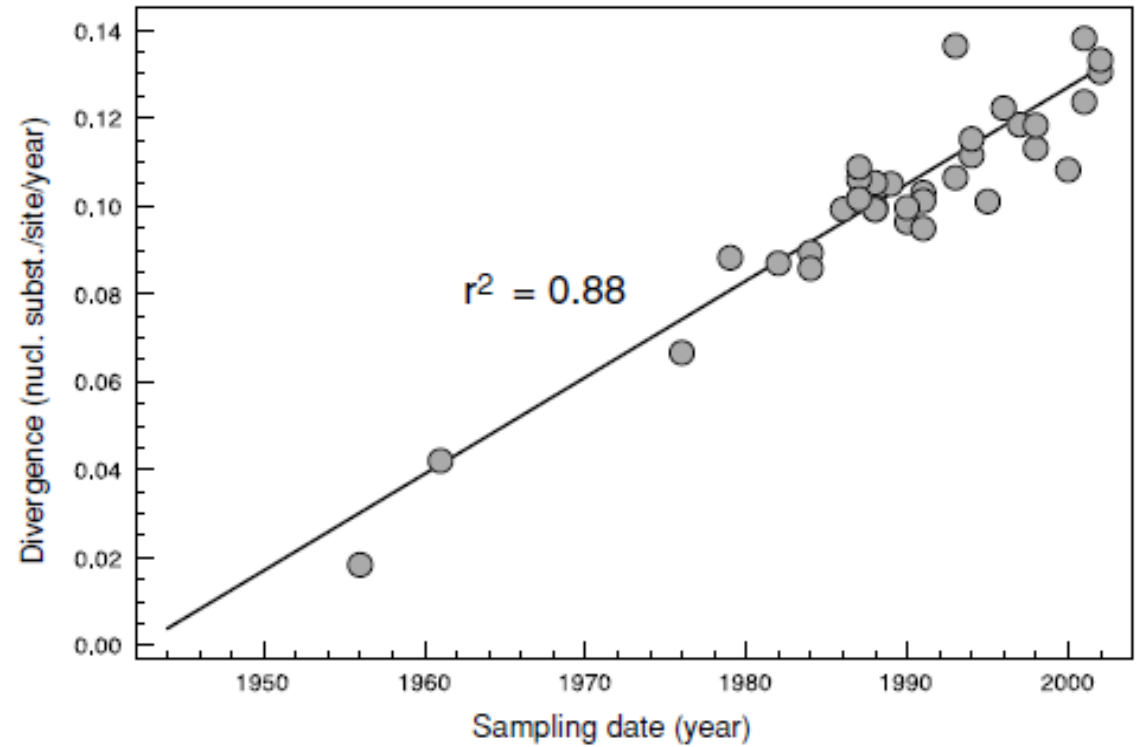
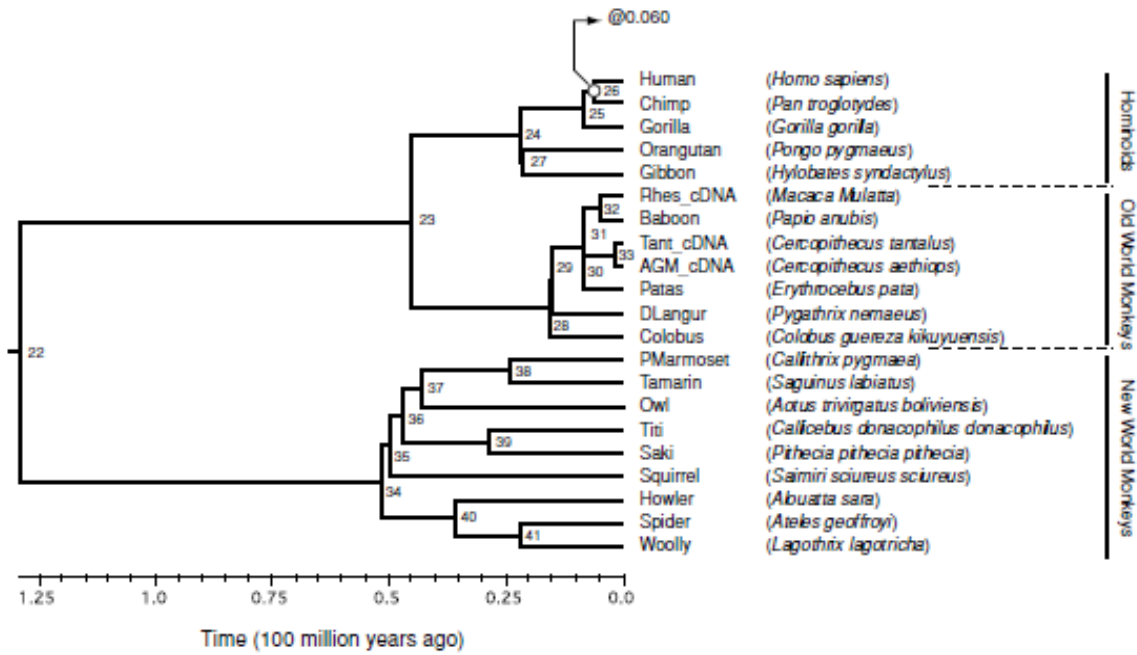
*
ndata = 5
clock = 0 * 0:no clock, 1:clock; 2:local clock; 3:CombinedAnalysis
fix_kappa = 0 * 0: estimate kappa; 1: fix kappa at value below
kappa = 5 * initial or fixed kappa

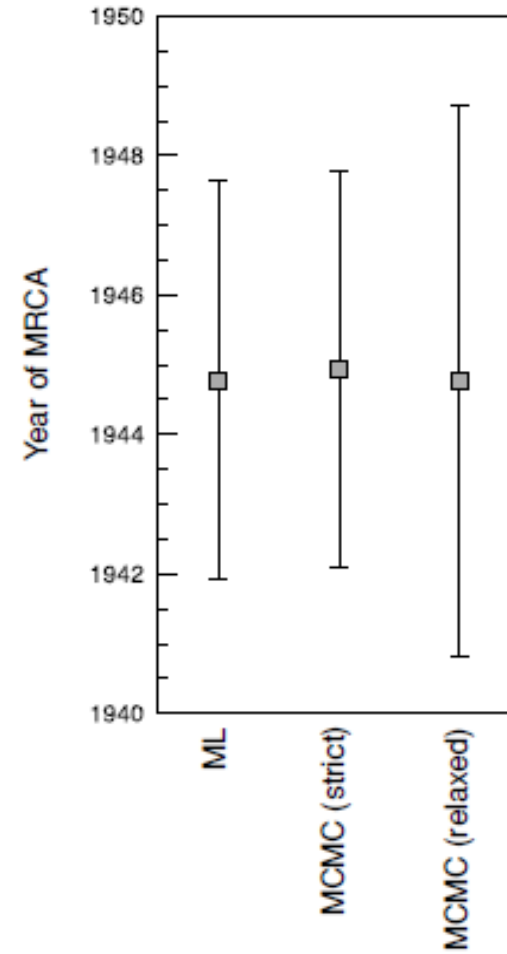
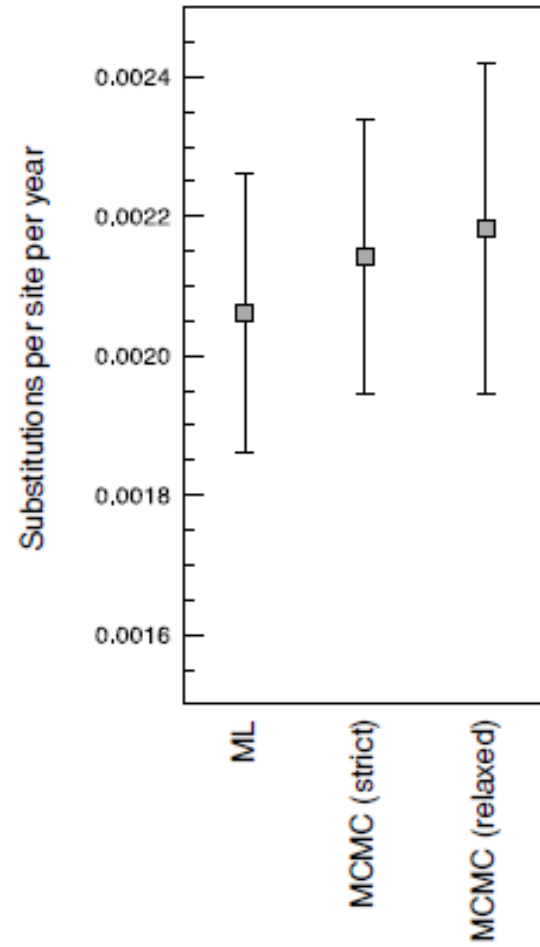
fix_alpha = 0 * 0: estimate alpha; 1: fix alpha at value below
alpha = 0.5 * initial or fixed alpha, 0:infinity (constant rate)
Malpha = 0 * 1: different alpha's for genes, 0: one alpha
ncatG = 6 * # of categories in the dG, AdG, or nparK models of
          rates
nparK = 0 * rate-class models. 1:rK, 2:rK fK, 3:rK MK(1/K), 4:rK MK

nhomo = 0 * 0 1: homogeneous, 2: kappa for branches, 3: N1, 4: N2
getSE = 0 * 0: don't want them, 1: want S.E.s of estimates
RateAncestor = 1 * (0,1,2): rates (alpha>0) or ancestral states

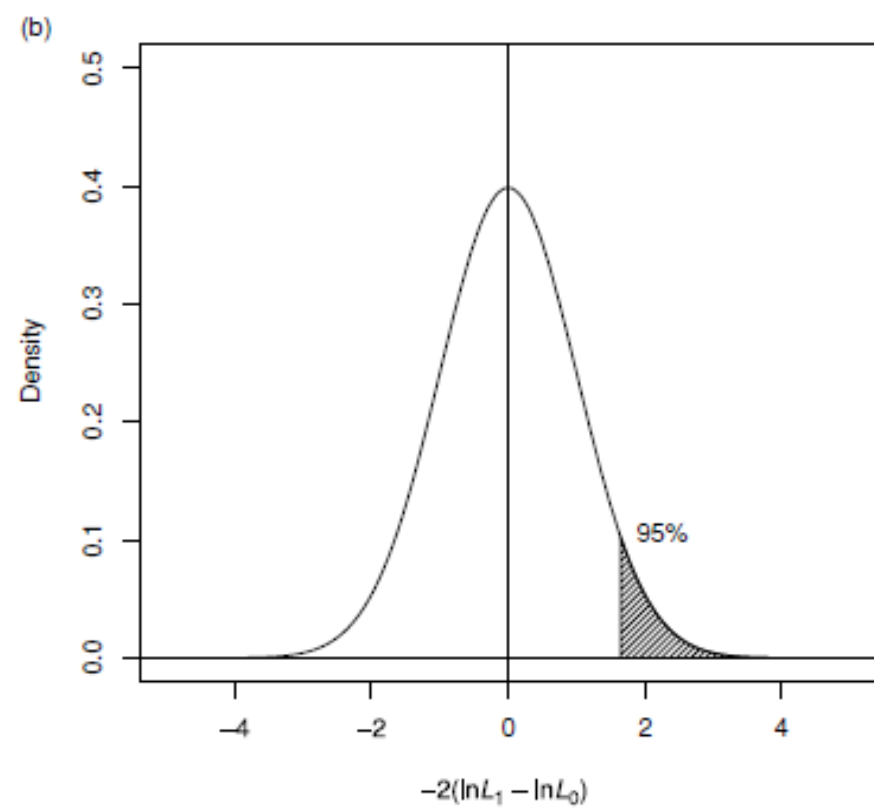
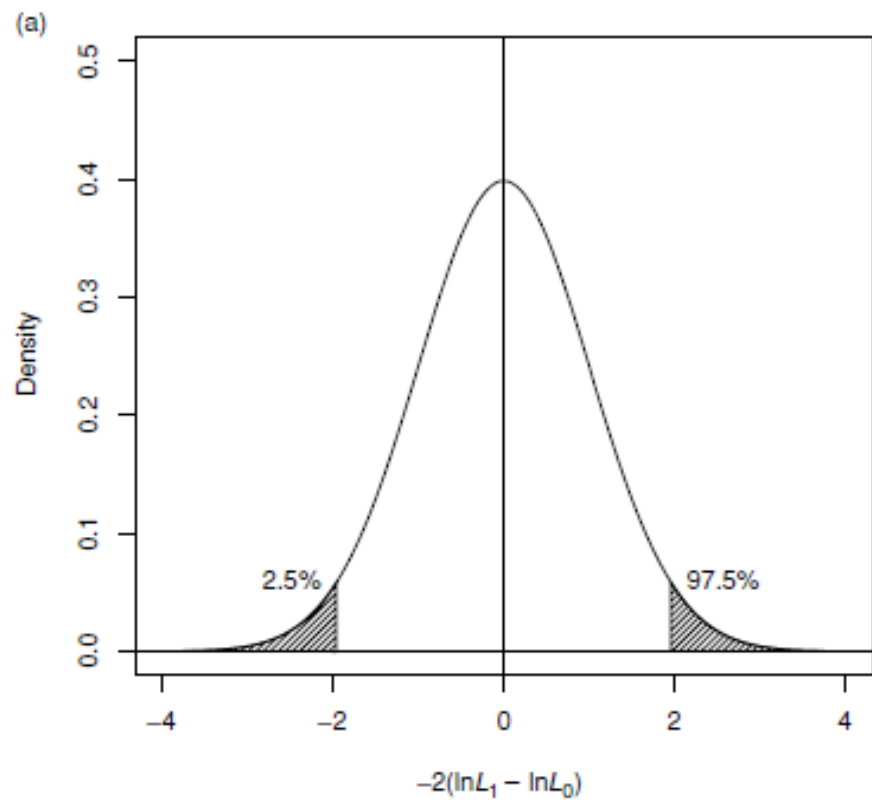
Small_Diff = 7e-6
cleandata = 0 * remove sites with ambiguity data (1:yes, 0:no)?
*
icode = 0 * (with RateAncestor=1. try "GC" In data,model=4,Mgene=4)

```

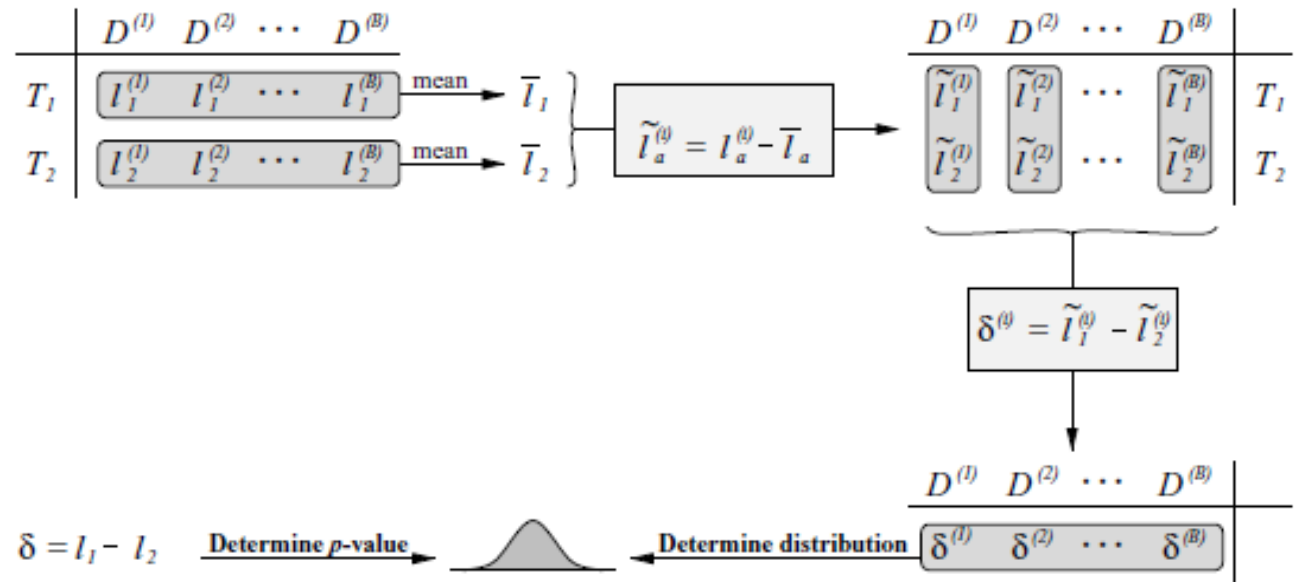
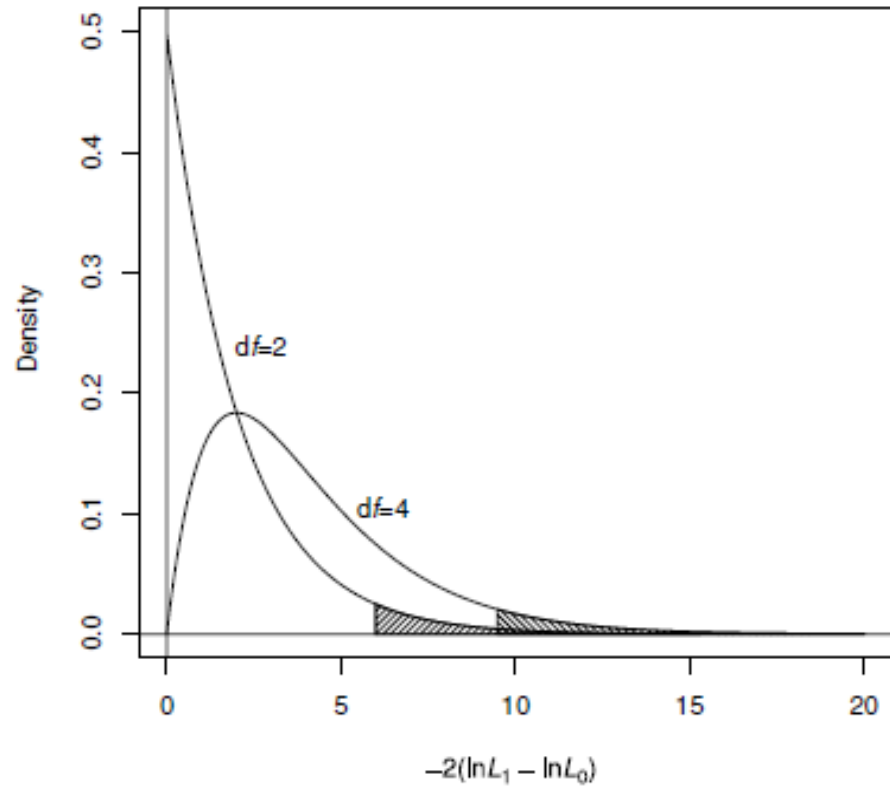


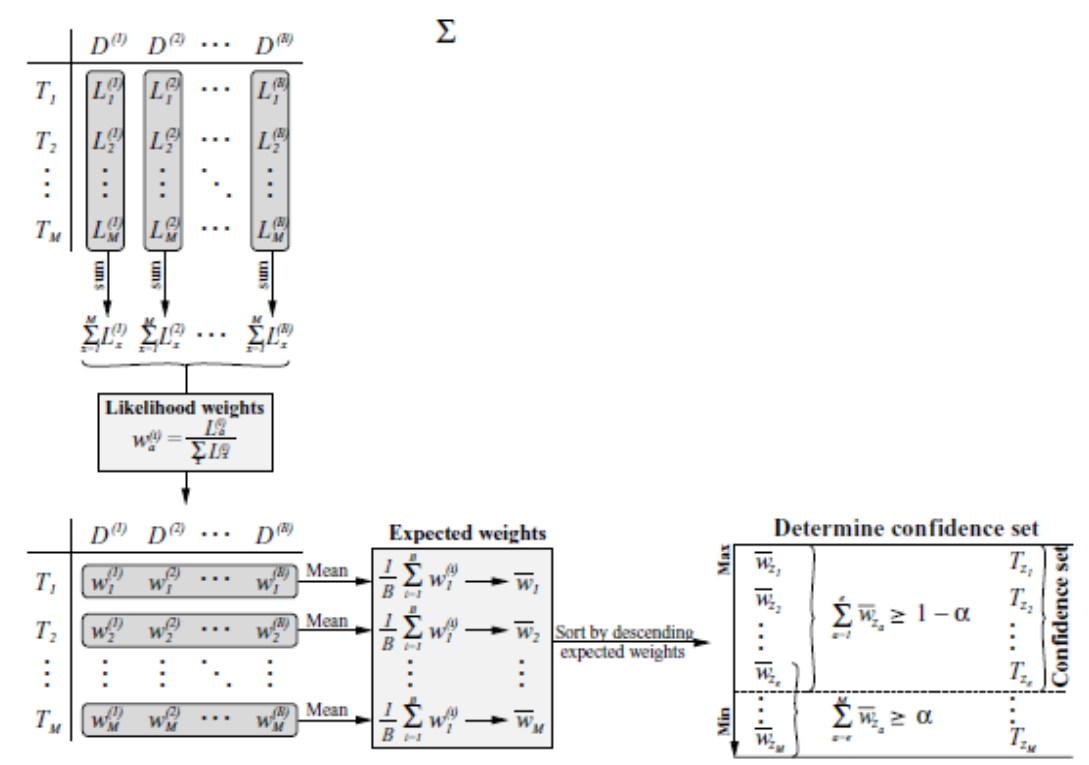
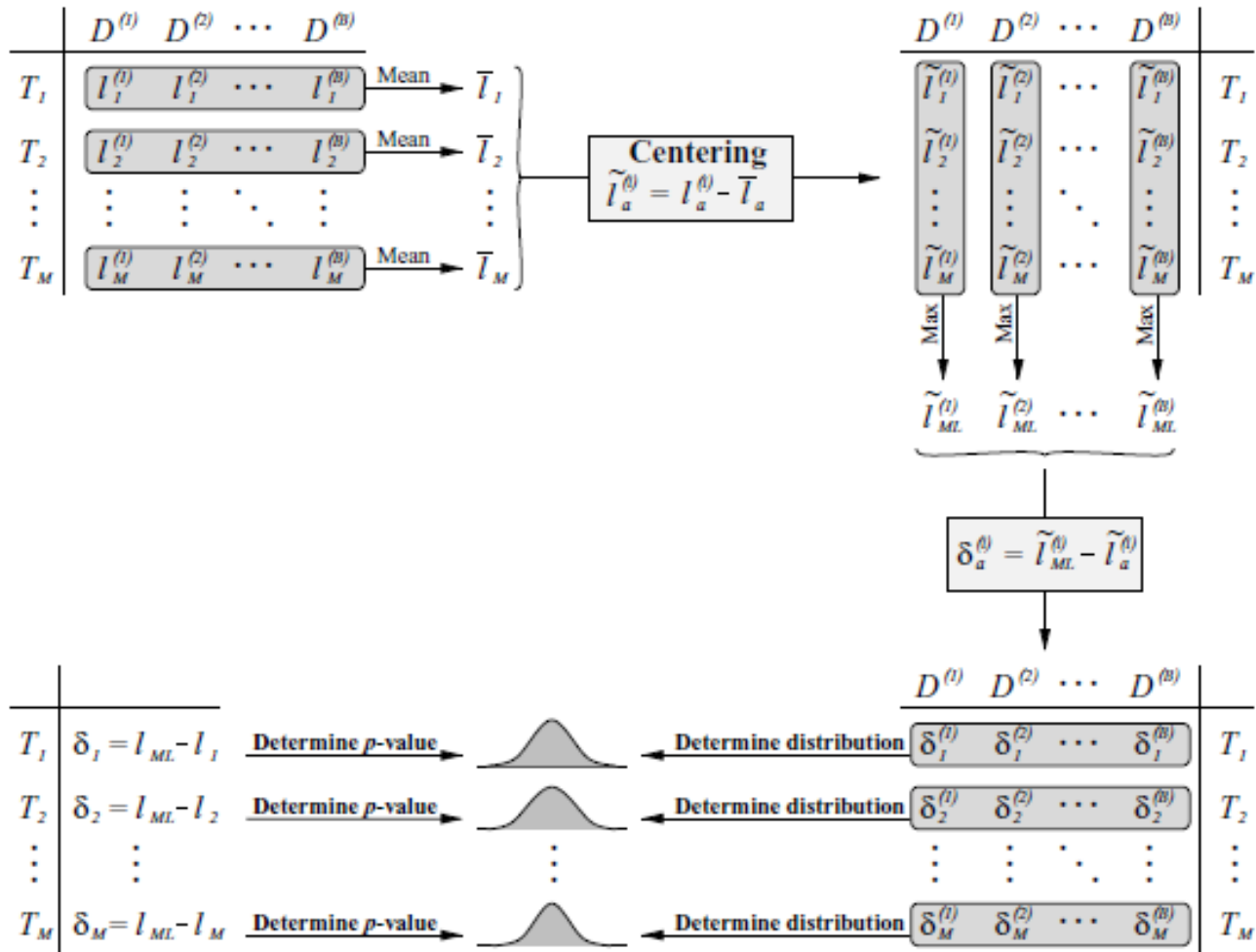


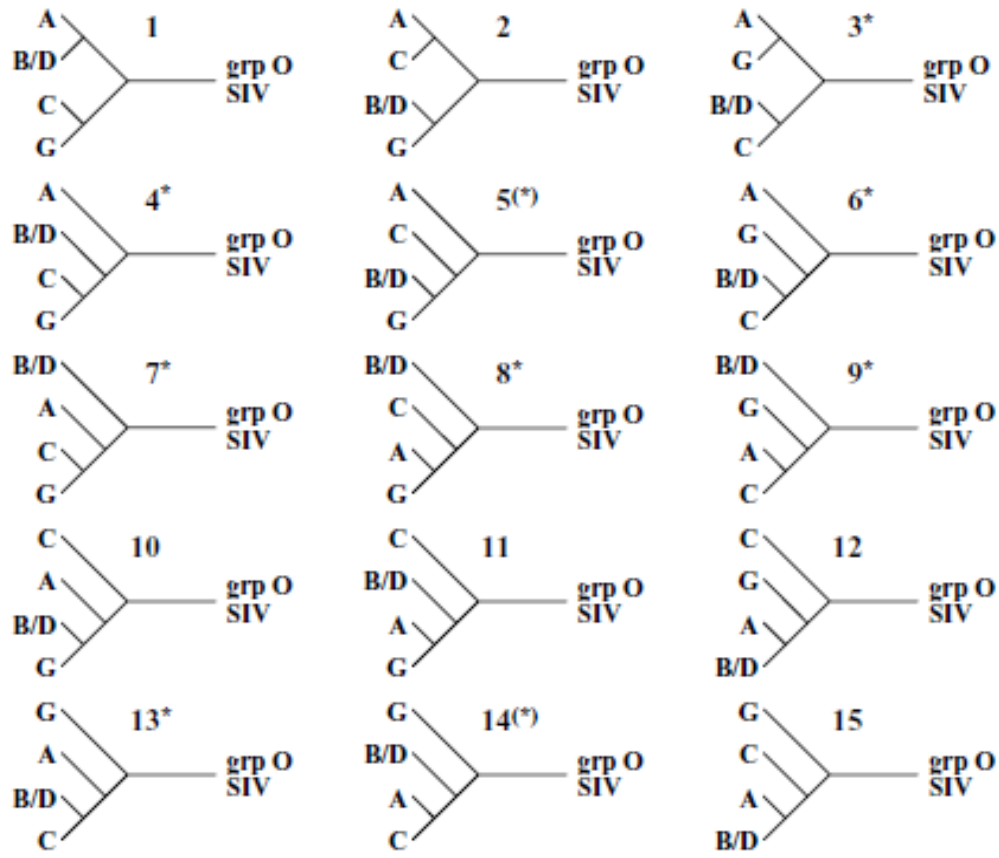
# 12. Ağaç topolojilerinin test edilmesi











COMPARISON OF USER TREES (NO CLOCK)

| Tree | log L     | difference | S.E.        | p-1sKH   | p-SH     | c-ELW    | 2sKH |
|------|-----------|------------|-------------|----------|----------|----------|------|
| 1    | -17405.05 | 12.13      | 9.0392      | 0.0960 + | 0.1870 + | 0.0051 - | +    |
| 2    | -17405.90 | 12.99      | 8.9989      | 0.0780 + | 0.1760 + | 0.0027 - | +    |
| 3    | -17395.02 | 2.11       | 3.4895      | 0.2600 + | 0.7860 + | 0.1147 + | +    |
| 4    | -17401.24 | 8.33       | 8.2551      | 0.1580 + | 0.3830 + | 0.0704 + | +    |
| 5    | -17404.03 | 11.12      | 7.4308      | 0.0720 + | 0.2290 + | 0.0097 - | +    |
| 6    | -17392.91 | 0.00       | <----- best | 1.0000 + | 1.0000 + | 0.4437 + | best |
| 7    | -17401.49 | 8.58       | 9.7675      | 0.1780 + | 0.3760 + | 0.0587 + | +    |
| 8    | -17396.14 | 3.22       | 6.8145      | 0.3160 + | 0.7170 + | 0.1770 + | +    |
| 9    | -17401.98 | 9.07       | 9.7895      | 0.1700 + | 0.3400 + | 0.0460 + | +    |
| 10   | -17408.52 | 15.61      | 8.3014      | 0.0380 - | 0.0780 + | 0.0003 - | +    |
| 11   | -17399.72 | 6.81       | 5.7552      | 0.1170 + | 0.4840 + | 0.0085 - | +    |
| 12   | -17408.66 | 15.75      | 8.3151      | 0.0250 - | 0.0740 + | 0.0003 - | +    |
| 13   | -17396.12 | 3.21       | 2.9334      | 0.1280 + | 0.6930 + | 0.0580 + | +    |
| 14   | -17405.43 | 12.52      | 8.9404      | 0.0670 + | 0.1910 + | 0.0042 - | +    |
| 15   | -17408.24 | 15.33      | 8.2263      | 0.0370 - | 0.0860 + | 0.0009 - | +    |

```

# $Id: consel.c,v 1.19 2004/11/11 08:14:09 shimo Exp $
# reading hivALN.rmt.....
# K:10
# R:0.5 0.599915 0.69983 0.799745 0.89966 1 1.09991 1.19983 1.29974 1.39966
# B:10000 10000 10000 10000 10000 10000 10000 10000 10000 10000
# M:15
# generate the identity association
# CM:15
# MC-TEST STARTS
# centering the replicates
# calculating kh-pvalue.....
# calculating mc-pvalue.....
# calculating the variances.....
# calculating weighted kh-pvalue.....
# calculating weighted mc-pvalue.....
# MC-TEST DONE
# calculate replicates of the statistics.....
# BP-TEST STARTS - DONE
# AU-TEST STARTS
# sorting the replicates.....
# calculating approximately unbiased p-values by MLE (fast) fit-
ting.....
# time elapsed for AU test is t=0.05 sec
# ALPHA:0.05 0.1 0.5 0.9 0.95
# calculating confidence intervals.....
# AU-TEST DONE
# writing hivALN.pv
# writing hivALN.ci
# exit normally

```

|    | TREE-PUZZLE |          |        |        |         | CONSEL |        |        |        |        |
|----|-------------|----------|--------|--------|---------|--------|--------|--------|--------|--------|
|    | $l$         | $\delta$ | KH     | SH     | ELW     | AU     | KH     | SH     | WKH    | WSH    |
| 1  | -17405.05   | 12.13    | 0.096+ | 0.187+ | 0.0051  | 0.030  | 0.094+ | 0.193+ | 0.094+ | 0.419+ |
| 2  | -17405.90   | 12.99    | 0.078+ | 0.176+ | 0.0027  | 0.044  | 0.076+ | 0.159+ | 0.076+ | 0.396+ |
| 3  | -17395.02   | 2.11     | 0.260+ | 0.786+ | 0.1147+ | 0.433+ | 0.272+ | 0.793+ | 0.272+ | 0.768+ |
| 4  | -17401.24   | 8.33     | 0.158+ | 0.383+ | 0.0704+ | 0.235+ | 0.164+ | 0.384+ | 0.164+ | 0.520+ |
| 5  | -17404.03   | 11.12    | 0.072+ | 0.229+ | 0.0097  | 0.072+ | 0.072+ | 0.227+ | 0.072+ | 0.322+ |
| 6  | -17392.91   | 0.00     | 1.000+ | 1.000+ | 0.4437+ | 0.826+ | 0.728+ | 0.960+ | 0.681+ | 0.961+ |
| 7  | -17401.49   | 8.58     | 0.178+ | 0.376+ | 0.0587+ | 0.281+ | 0.190+ | 0.370+ | 0.190+ | 0.578+ |
| 8  | -17396.14   | 3.22     | 0.316+ | 0.717+ | 0.1770+ | 0.475+ | 0.319+ | 0.721+ | 0.319+ | 0.745+ |
| 9  | -17401.98   | 9.07     | 0.170+ | 0.340+ | 0.0460+ | 0.272+ | 0.175+ | 0.339+ | 0.175+ | 0.551+ |
| 10 | -17408.52   | 15.61    | 0.038  | 0.078+ | 0.0003  | 0.005  | 0.034  | 0.072+ | 0.034  | 0.216+ |
| 11 | -17399.72   | 6.81     | 0.117+ | 0.484+ | 0.0085  | 0.042  | 0.121+ | 0.487+ | 0.089+ | 0.380+ |
| 12 | -17408.66   | 15.75    | 0.025  | 0.074+ | 0.0003  | 0.040  | 0.034  | 0.064+ | 0.034  | 0.225+ |
| 13 | -17396.12   | 3.21     | 0.128+ | 0.693+ | 0.0580+ | 0.141+ | 0.135+ | 0.695+ | 0.135+ | 0.492+ |
| 14 | -17405.43   | 12.52    | 0.067+ | 0.191+ | 0.0042  | 0.074+ | 0.082+ | 0.177+ | 0.082+ | 0.393+ |
| 15 | -17408.24   | 15.33    | 0.037  | 0.086+ | 0.0009  | 0.033  | 0.037  | 0.075+ | 0.037  | 0.227+ |