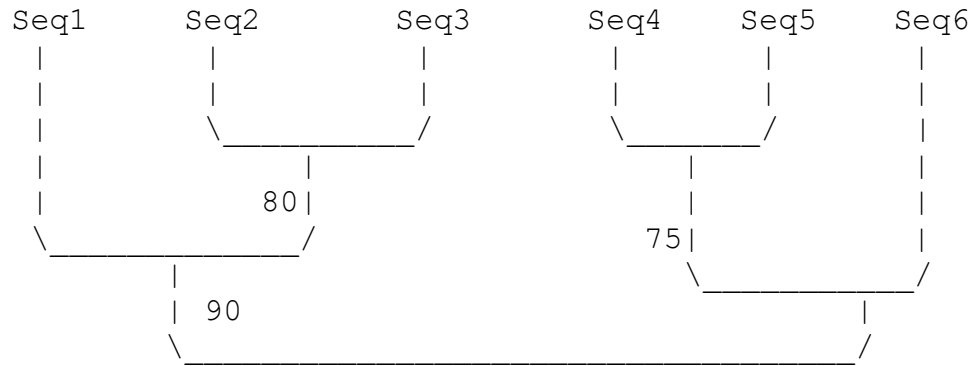


# Training questions

that may be not obvious from the online take-home exams

Given this tree:



While depicted as rooted, the tree should be considered as unrooted

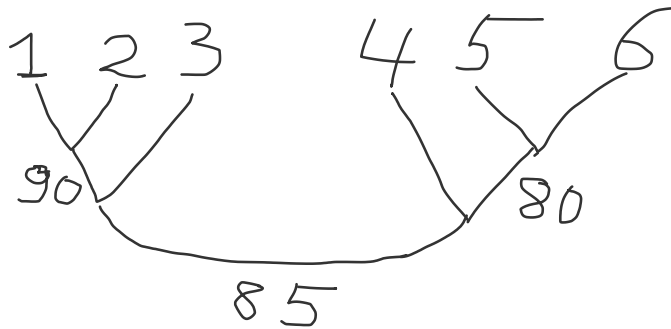
Write down the bipartition table corresponding to this tree. Assume that the order of OTUs is

- Seq1
- Seq2
- Seq3
- Seq4
- Seq5
- Seq6
- . \*\* . . .
- \* \* \* . . .
- . . . \* \*

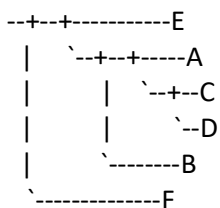
Draw the tree that corresponds to the following bipartition table:

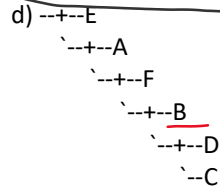
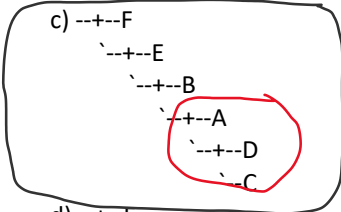
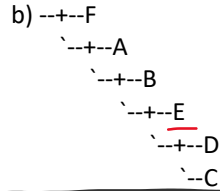
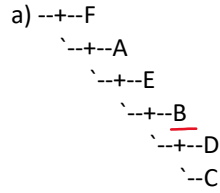
OTUs in order:

Seq1	
Seq2	
Seq3	
Seq4	
Seq5	
Seq6	
* *	. . . . . 90
. . . * * *	85
. . . . * *	80

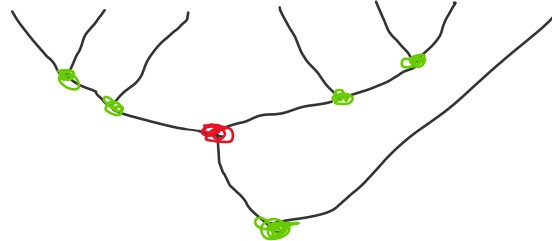


Which of the tree given in a) b) c) d) has identical topology to the tree depicted bellow?





Use the **rooted** tree (((Aalpha, Balpha), Calpha), ((Cbeta, (Bbeta, Abeta))), Dxyz) for the following questions.  
 Draw the tree here

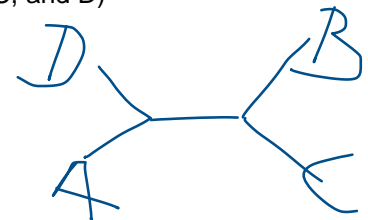
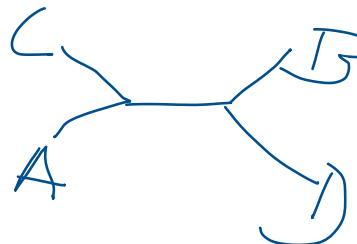
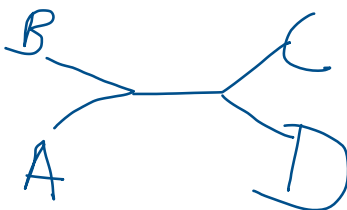


Speciation  
 Duplication

In your answers assume that the split between Dxyz and the other sequences represents a speciation event, and that the split between the alpha and beta sequences represent a gene duplication.

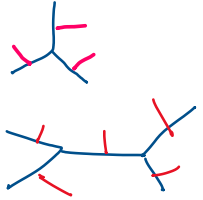
- TRUE or  FALSE: Dxyz is an orthologs to Abeta and to Aalpha
- TRUE or  FALSE: Dxyz is an orthologs to Aalpha and to Balpha
- TRUE or  FALSE: Calpha and Bbeta could be orthologs
- TRUE or  FALSE: Abeta is an orthologs to Cbeta
- TRUE or  FALSE: Abeta is an orthologs to Aalpha
- TRUE or  FALSE: Dxyz is a paralog to Calpha and to Cbeta
- TRUE or  FALSE: Abeta is an ortholog to Dxyz

Draw the possible distinct tree topologies that are possible for 4 OTUs (A, B, C, and D)



Given a specific topology of one unrooted tree with 3 OTUs, how many rooted phylogenies are possible that conform to the given topology.

- A) 3, B) 5, C) 6, D) 7, E) 9



Given a specific topology of one unrooted tree with 4 OTUs, how many rooted phylogenies are possible that conform to the given topology.

- A) 3, B) 5, C) 6, D) 7, E) 9

Which of the following groups is the closest phylogenetic relative to the mitochondrial endosymbiont?

- A. protist  
B. Archaea  
C. The same as that of the nuclear genome from which the mitochondria came.  
D. Alphaproteobacteria  
E. Cyanobacteria

Same question but closest phylogenetic relative to the plastids of Archaeplastida

Which of the following is one of the possible fates of a duplicated gene ?

- A. Decay, lost, and deletion.  
B. Sit around for some time as junk DNA.  
C. Subfunctionalization (Both copies retain only part of the original function).  
D. Neofunctionalization (Acquires a new function).  
E. All of the above.

Which is the most common fate of one of the genes following a gene duplication.

- A. Non-functionalization  
B. Polyfunctionalization  
C. Subfunctionalization.  
D. Neofunctionalization

In a rooted gene tree, which of the following types of homologs best specifies homology, when the basal bifurcation separating the homologs is reflects a speciation event?

- A. xenolog  
B. ortholog  
C. hololog  
D. paralog  
E. homeolog

#### True/False Questions:

- T A phylogenetic tree can define clades ONLY if the phylogeny is rooted  
F In human and plant genes introns occur frequently; however, there are always slightly more nucleotides in the exon than in the intron sequences.  
T Rotating branches of a phylogenetic tree around a node does NOT change the meaning of that tree  
F Every possible bipartition produced from a bootstrap analysis can always be depicted on a single tree.