Additional questions to study for final:

Which is a solution to the bipartition paradox (i.e., the more OTUs are added to a phylogenetic reconstruction, the shorter the internal branches become, the lower the support values of the branches becomes)?
A. Add more sequences to the tree
B. There is no solution
C. Ignore bootstrap values
D. Use embedded quartets

TRUE or FALSE: In a Lento plot, values above and below the x-axis represent values of support and values of conflict, respectively.

Which is the most abundant oxygenic phototroph in the ocean?
A. Thermotoga
B. Halobacterium
C. Prochlorococcus
D. Synechococcus

TRUE or **FALSE**: The supermatrix approach outperforms the supertree approach when there are high amounts of gene transfer (up to 45% of the genes), especially in case of highways of gene sharing.
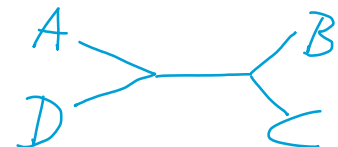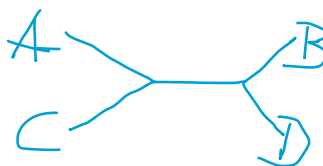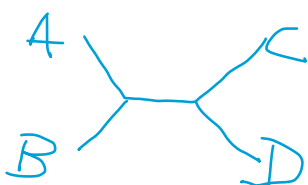
TRUE or **FALSE**: The supertree approach outperforms the supertree approach when there is no horizontal gene transfer, but very high or very low substitution rates.

You perform two independent maximum likelihood (ML) analyses of a multiple alignment containing 5 sequences. Assuming the order of taxa is identical in the bipartition tables resulting from both runs, you discover that one bipartition in each run has 100% bootstrap support. The bipartition in the first run is identified as "∗∗∗.." and the bipartition in the second run is identified as "...∗∗"
This indicates that
A) In one analysis the tree "flipped" to an alternative evolutionary history, probably because some sequences contain an intein
B) In one of the ML analyses the tree heuristics probably got stuck in a local optimum, because a "lucky" NNI operation can eventually escape to a more likely tree
C) In one of the ML analyses the tree heuristics probably got stuck in a local optimum, because a "lucky" SPR operation can eventually escape to a more likely tree
D) In one of the ML analyses the tree heuristics probably got stuck in a local optimum, because a "lucky" TBR operation can eventually escape to a more likely tree
E) These bipartitions are identical

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

HGT was suggested to have contributed to which of the following (more than one answer correct):
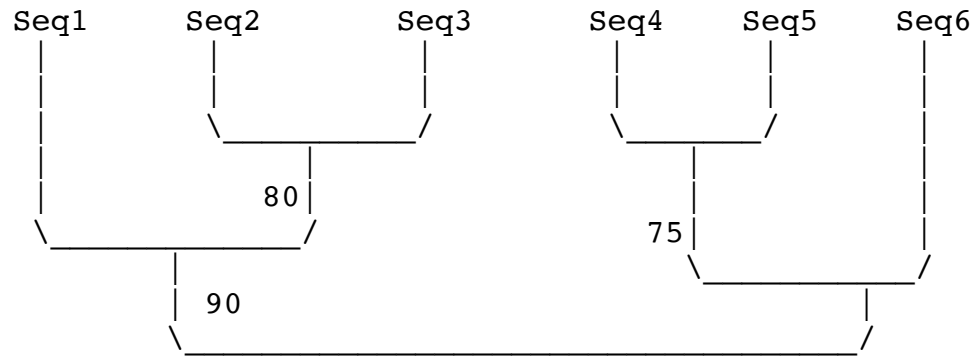
    TCA cycle
    electron transport chain in photosynthesis that can use water as electron donor
    electron transport chain in bacterial respiration
    Acetoclastic methanogenesis
    methylaspartate cycle in haloarchaea

Given this tree:

```
Seq1        Seq2          Seq3      Seq4      Seq5      Seq6
 |           |             |         |         |         |
 |           |             |         |         |         |
 |           _____/          _____/          |
 |                 |                      |               |
 |               80|                      |               |
 _____/                    75|               |
          |                               _____/
          |  90                                  |
          _____ /
```

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
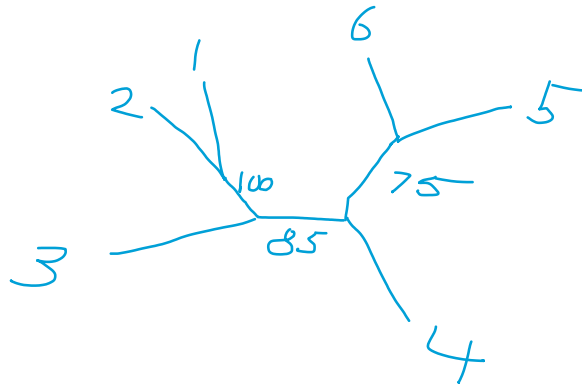Seq1
Seq2
Seq3
Seq4
Seq5

.**... 80
***... 90
***..* 75

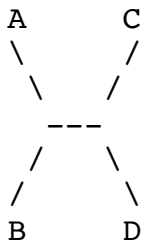Draw the tree that corresponds to the following bipartition table:
OUT in order:
Seq1
Seq2
Seq3
Seq4
Seq5
Seq6

```
*  *  .  .  .  .      100
.  .  .  *  *  *       85
.  .  .  .  *  *       75
```

Given the tree

```
A        C
 \      /
  \    /
   ---
  /    \
 /      \
B        D
```
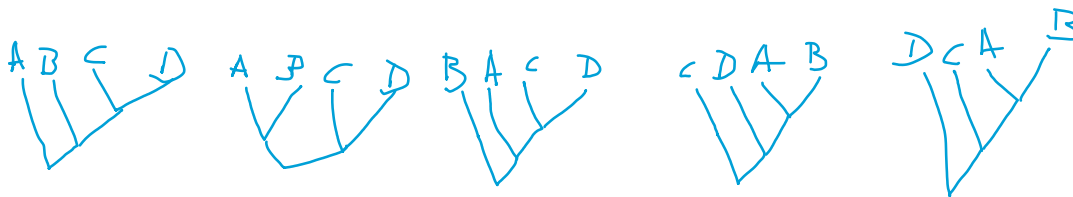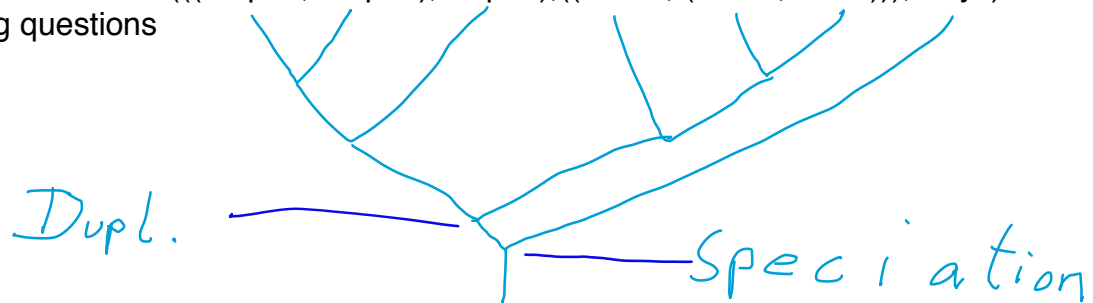
How many different rooted trees have the same topology when considered as unrooted?

5

Draw these trees.

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

Dupl. ——

——Speciation

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

TRUE or FALSE: Dxyz is an orthologs to Aalpha

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