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

Given this tree:

```
Seq1          Seq2           Seq3         Seq4        Seq5        Seq6
 |             |              |            |           |           |
 |             |              |            |           |           |
 |             _____/            _____/           |
 |                    |                          |                 |
 |                  80|                          |                 |
 _____/                       75|                 |
          |                                      _____/
          | 90                                            |
          _____/
```
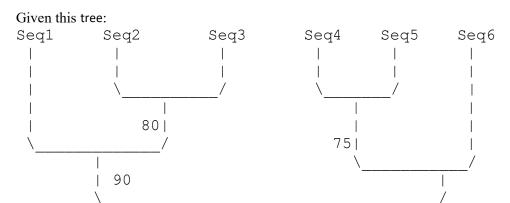
While depicted as rooted, the tree should be considered as unrooted

Write down the bipartition table corresponding to this tree. Assume that the order of OTUs is
Seq1
Seq2
Seq3
Seq4
Seq5
Seq6

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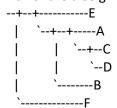
OTUs in order:
Seq1
Seq2
Seq3
Seq4
Seq5
Seq6

```
*  *  .  .  .  .     90
.  .  .  *  *  *     85
.  .  .  .  *  *     80
```

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

```
--+--+----------E
  |    `--+--+-----A
  |       |  `--+--C
  |       |     `--D
  |       `-------B
  `-------------F
```

a)
```
--+--F
  `--+--A
     `--+--E
        `--+--B
           `--+--D
              `--C
```

b)
```
--+--F
  `--+--A
     `--+--B
        `--+--E
           `--+--D
              `--C
```

c)
```
--+--F
  `--+--E
     `--+--B
        `--+--A
           `--+--D
              `--C
```

d)
```
--+--E
  `--+--A
     `--+--F
        `--+--B
           `--+--D
              `--C
```

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

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

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 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. Subfuctionalization.
        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

What is a Go domain?
- A. A protein domain that has Glucose Oxidase activity.
- B. A compact part of a protein that was defined using the approach of Mitiko Gō as a part of the protein where the protein sequence remains local
- C. A compact part of a protein that is similar to a domain in the Japanese board game of Go
- D. A compact part of a protein that self-splices out of a host protein and **GO**es on to do its own thing.

Which of the following are considered to reflect positive or diversifying selection?
- a. Selective Sweeps
- b. High dN
- c. dN/dS larger than 1
- d. SNPs in the allele are not in linkage equilibrium
- e. all of the above
- f. b and c

Which of the following is true of scaled branches on a phylogenetic tree? (1 point)
- A. they take into account changes that occurred over time
- B. they are always preferable to unscaled branches
- C. they give information about how much change has occurred
- D. all of the above

Which viral amino acids are most likely to be under positive selection due to interactions with the immune system and the subsequent need to change to evade capture?
- A. The ones bound to the viral genome (DNA or RNA)
- B. The ones responsible for the conformation change that releases the genome into the cell
- C. The ones on the outside of the capsid
- D. The ones on the inside of the capsid
- E. All of the above

Which of the following IS an example how a new gene can be created?
- a) Through mutations in non-coding DNA
- b) Left over DNA of viruses or other genetic parasites being repurposed
- c) Genome rearrangement shuffling exons and bringing together existing domains into a new combination
- d) Gene duplication followed by neofunctionalization
- e) All of the above

The discovery of a predicted intron in the triose phosphate isomerase of the Mosquito was considered verification for introns separating proteins domains. The distribution of this intron on a phylogenetic tree of eukaryotes supports which of the following?

A. HGT of the intron into mosquito
B. LBA, caused by the intron sequence being highly divergent
C. the *intron late* hypothesis
D. the *intron early* hypothesis
E. None of the above

Which of the following is a possible benefit of having introns?
      A. Exon shuffling
      B. Alternative splicing
      C. One gene can turn into several different products
      D. The nonsense mediated decay pathway can be triggered
      E. All of the above
      F. A-C is correct

Which role does exon shuffling play in the maturation of the human immune system?

Which of the following is NOT a proper taxonomic groups (i.e., they do NOT form a clade in the "traditional" version of tree of life)?
    A. Prokaryotes
    B. photo-synthetic Eukaryotes
    C. Primates
    D. Reptiles
    E. All of the above
    F. Protists
    G. Fish
    H. Vertebrates

In a phylogenetic tree, OTU is NOT synonymous with which of the following term(s)?
    A. Leaf
    B. Taxa
    C. Terminal Node
    D. Branch
    E. Species

True/False Questions:

A phylogenetic tree can define clades ONLY if the phylogeny is rooted

In human and plant genes introns occur frequently; however, there are always slightly more nucleotides in the exon than in the intron sequences.

Rotating branches of a phylogenetic tree around a node does NOT change the meaning of that tree

All bipartition produced from a bootstrap analysis are always part of the consensus tree.