

Additional questions to consider in preparation for the final:

Which is a solution to the bipartition paradox (i.e., the more OTUs are added to an phylogenetic reconstruction, the shorter the internal branches become, the lower the support values of the braches 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 bipartition or Lento plot, values above and below the x-axis represent values of support and values of conflict, respectively.

Which is the most abundant genus of oxygenic phototroph in the ocean?

- A. Thermotoga
- B. Halobacterium
- C. Prochlorococcus
- D. Synechococcus

TRUE or FALSE: The supertree approach outperforms the supermatrix 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 supermatrix approach outperforms the supertree approach when there is no horizontal gene transfer, but very high or 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

Which of the following are ~~not~~ considered methods to detect positive selection?

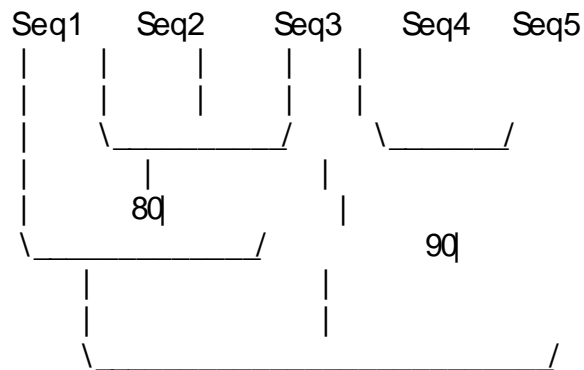
- a. Selective Sweeps

- 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 NOT a lesson learned from the genome of the tardigrade?

- A) sequence data is only as good as the specimen
- B) secrecy in science detracts from identifying problems early on
- C) 1/6 of the tardigrade genome is from HGT
- D) A&B

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, Seq 5.

Draw the tree that corresponds to the following bipartition table:

OUT in order:

- Seq1
- Seq2
- Seq3
- Seq4
- Seq5
- Seq6

* * 100
 * * * 85
 * * 75
 * * * . * * 95

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

Given the tree



How many different rooted trees have the same topology when considered as unrooted?

Draw these trees.

Use the rooted tree $((((A_{\alpha}, B_{\alpha}), C_{\alpha}), ((C_{\beta}, (B_{\beta}, A_{\beta}))), D_{xyz})$ for the following questions

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