

Additional questions to study for the Final

Which of the following is a technique to identify transferred genes and not just putatively transferred genes?

- a. Gene presence absence data for closely related genomes (if a gene is absent in many deeper branching relatives, then a gene showing up in a single lineage as been created in that lineage, likely through HGT. If you compare to many closely related genomes, the presence absence analysis results is somewhat like a phylogenetic conflict)
- b. Phylogenetic conflict
- c. Composition based analyses
- d. Taxplot at NCBI
- e. All of the above
- f. a+b

When performing a Taxplot of one bacterial genome as query and one other bacterial genome and one archaeal genome for comparison, what do the hits that are closer to the archaeal genome represent?

- A. Horizontal gene transfers
- B. Long branch attractions
- C. Putative HGTs that must be verified, for example by making phylogenetic trees, or a gene presence absence analysis using a larger taxon sampling.
- D. Lineage specific gene sorting
- E. Errors in gene calling

It was once thought that Y-Chromosome Adam lived ~40,000 years ago. What happened to this story?

- A) Further studied proved that there was a massive migration of men from China into sub-Saharan Africa and this story totally makes sense to someone, despite the lack of fossils showing such a migration.
- B) An African American was found whose genome had all of the ancestral states, which finally made people think that it might be a good idea to sequence a few more sub-Saharan Africans. Y-Chromosome Adam now dates back to well over 200,000 years.
- C) The genome of the Neanderthals revealed that it really goes back to only 30,000 years.

To recapitulate the evolutionary history of genomes, Supermatrix approaches are advantageous (as compared to supertree approaches)

- A) In the presence of gene transfer
- B) In case sequences are close to being saturated with substitution events
- C) In case of closely related organisms.

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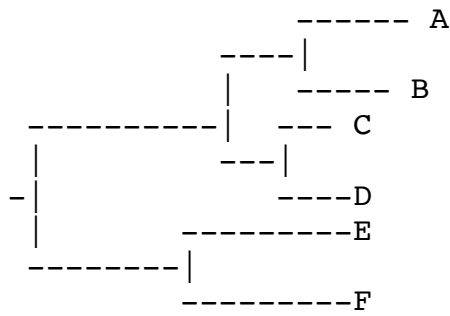
True / False Bipartition based analysis of gene trees to identify phylogenetic conflict with the species tree has the problem that the more sequences one includes in an analysis, the lower the average bootstrap of the individual branches becomes.

True / **False** Embedded quartet based analysis of gene trees to identify phylogenetic conflict with the species tree has the problem that the more sequences one includes in an analysis, the lower the average bootstrap of the individual branches becomes.

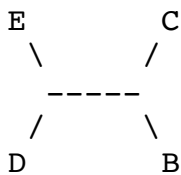
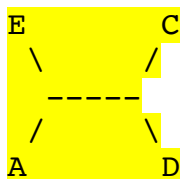
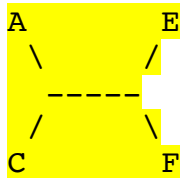
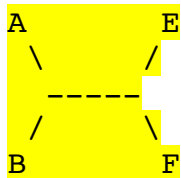
True / False Bipartition and quartet spectra are a good starting point to reconstruct the relationship between genomes.

Which of the following bipartitions are incompatible with **** .*** . . .** (Note: the questions is not are they compatible with one another)

- ***** . . .
- . . .*** . . .
- ** * . .**
- ***** . * .
- ***** . .



Which quartets are embedded in the above tree?



True **False** – Some Tardigrades contain over 15% bacterial genes in their nuclear genomes

True False - Publication of the erroneous finding of massive transfer of bacterial genes into a Tardigrade could have been avoided, if scientist would have taken notice of the work of others.