

## QUESTION 1

Bootstrap values belong to which of the following?

- A. Taxa, Species, or OTUs
- B. Leaves
- C. Splits or bipartitions**
- D. The ancestral sequence
- E. None of the above

## QUESTION 2

Given a specific topology of one unrooted tree with 6 OTUs, how many rooted phylogenies are possible that conform to the given topology.

- A. 6,
- B. 7,
- C. 9,**
- D. 105,
- E. 945

## QUESTION 3

How many rooted trees with 4 taxa can be collapsed down into a single unrooted tree?

- A. 1,
- B. 2,
- C. 3,
- D. 4,
- E. 5,**
- F. None of the above

## QUESTION 4

You slice an alignment up by columns, put each column in a hat, and pick a column from the hat at random, writing it into a new dataset. You put the column back in the hat and randomly pick another, repeating this process until you have the same number of columns as the original dataset. What have you created?

- A. Crap
- B. A jackknife sample
- C. A single nonparametric bootstrap sample**
- D. A phylogenetic tree
- E. A single parametric bootstrap sample

## QUESTION 5

If evolutionary parameters are estimated from a dataset and associated tree and those parameters are then used to simulate a new dataset, what is this dataset?

- A. Crap
- B. A jackknife sample
- C. A single nonparametric bootstrap sample
- D. A phylogenetic tree
- E. A single parametric bootstrap sample**

## QUESTION 6

In the PHYLIP package, Trees written onto "outtree" are in the:

- A. Newick format**
- B. Matlab Format
- C. Java Format
- D. C++ Format
- E. PHYLIP Format

## QUESTION 7

Maximum likelihood aims to build the tree

- A. that is most probable given the data.
- B. that explains the evolutionary history that gave rise to the aligned sequences with the least number of substitution events.
- C. that is in the best possible agreement with the observed number of substitutions observed between the sequences.
- D. that makes the data set (e.g., aligned sequences) most probable.**

## QUESTION 8

Parsimony aims to build the tree

- A. under which the data set (e.g., aligned sequences) is most probable.
- B. that is most probable given the data.
- C. that explains the evolutionary history that gave rise to the aligned sequences with the least number of substitution events.**
- D. is in the best possible agreement with the observed number of substitutions observed between the sequences.

## QUESTION 9

The place of the root in the tree of life was first determined using which molecule?

- A. Inteins
- B. The signal recognition particle and receptor
- C. ATPsynthase catalytic and non-catalytic subunits**
- D. rRNA
- E. None of the above

## QUESTION 10

True/False All tree building programs (excepting UPGMA which is awful) have their advantages and disadvantages over other programs, which is why more than one should always be used to analyze any dataset, to verify that the findings are independent of the program used.

- True**
- False

## QUESTION 11

True/False Parsimony does a better job handling gaps than Neighbor Joining, but Neighbor Joining can do better with long branches (provided a correction for multiple substitutions is applied).

- True**
- False

## QUESTION 12

True/False Phylogenetic reconstruction using Metropolis coupled Markov chain Monte Carlo sampling aims to find the phylogenetic tree that is most probable given the data by walking around in tree space with a biased walk and sampling the trees.

- True**
- False

## QUESTION 13

True/False Rotating branches of a phylogenetic tree around a node changes the meaning of that tree.

- True
- False**

## QUESTION 14

True/False. Phylogenetic analysis is an inference of evolutionary relationships between organisms.

- True
- False

## QUESTION 15

True/False: Bootstrap analysis can be used for more than just neighbor joining tree calculations.

- True
- False

## QUESTION 16

What does an internal node on a phylogenetic tree represent?

- A. Time
- B. A common ancestor**
- C. Rate of evolution
- D. Total evolution
- E. A species or sequence present today

## QUESTION 17

What happens when a dataset is not first aligned using a Multiple Sequence Alignment program?

- A. An error is produced and the program refuses to calculate the tree
- B. A strange tree is produced, sometimes with 100% bootstrap support**
- C. The program alerts you to the problem and suggests that you do an alignment
- D. The program calculates a tree, but it is a random tree with 0% bootstrap support

## QUESTION 18

Which approach finds the "true" tree?

- A. Parsimony
- B. Maximum Likelihood
- C. Bayesian Inference
- D. Neighbor Joining
- E. All of the above
- F. None of the above**

## QUESTION 19

Which comes first in phylogenetic analysis?

- A. Tree evaluation
- B. Determination of substitution model
- C. Alignment
- D. Tree building
- E. Compilation of a sequence dataset**

## QUESTION 20

Which of the follow term(s) is often used as a synonym for the splits of a tree?

- A. Bifurcation
- B. Branch
- C. Bipartition
- D. clann
- E. All of the above
- F. A, B and C**

## QUESTION 21

Which of the following are approaches to build trees from of alignments?

- A. Neighbor Joining
- B. UPGMA (Although this one should NEVER be used)
- C. Maximum Likelihood
- D. Bayesian Inference
- E. Parsimony
- F. All of the above**

## QUESTION 22

Which of the following is a tree reconstruction artifact?

- A. Incomplete lineage sorting
- B. Horizontal gene transfer
- C. Insufficient phylogenetic signal
- D. Long branch attraction**
- E. Unrecognized paralogy
- F. Saturation with substitutions
- G. Among Site Rate Variation

### QUESTION 23

Which of the following programs uses a guide tree to align sequences?

- A. Muscle
- B. Clustal**
- C. GBlocks
- D. BLAST
- E. Needleman Wunsch (as applied in C++)

### QUESTION 24

Which of the following is a factor when calculating the bootstrap support of a branch in a phylogenetic tree?

- A. Branch lengths
- B. The number of times a split is recovered in a set of bootstrap samples**
- C. The Gamma parameter and among site rate variation
- D. Lineage sorting

### QUESTION 25

Which of the following programs produces a guaranteed optimal alignment (as measured by the alignment score), but with the possibility that there might be many equally optimal pathways/traces through the scoring table?

- A. Muscle
- B. Needleman-Wunch algorithm**
- C. Clustal
- D. Seaview
- E. Jalview

### QUESTION 26

Which of the following bipartitions is not compatible with the others (i.e., it could not exist on the same tree as the others)?

- A. ....\*\*\*
- B. ...\*\*\*\*\*
- C. \*\*\*.....
- D. ....\*\*
- E. ...\*\*....**
- F. ....\*\*...

## QUESTION 27

Which of the following can be used to root the tree of life?

- A. Rock
- B. Virus
- C. Random sequence
- D. Unrelated sequence
- E. Paralogs that diverged Pre-LUCA (Last Universal Common cellular Ancestor)**
- F. Composition of reconstructed sequences that reflect a more primitive state (symplesiomorphy) closer to the early expansion of the genetic code.

## QUESTION 28

True/False Both group 2 intron and spliceosomal introns form lariat loops.

- True**
- False

## QUESTION 29

For alternative splicing to work without introducing frameshifts, introns need to be in the same phase.

- True**
- False

## QUESTION 30

Go plots:

- A. use Gene Ontology information to identify protein domains
- B. were named after Japanese scientist Mitiko Gō**
- C. identify domains in a protein structure that are formed by continuous stretches of the peptide backbone**
- D. reliably pinpoint intron insertion sites.

## QUESTION 31

Which of the following is true with respect to the outgroup of a phylogenetic tree?

- A. To minimize LBA artifacts, it should be as closely related to the ingroup as possible
- B. To minimize LBA artifacts, more than one sequence could be used in the outgroup.
- C. It can be a random sequence
- D. A and B**

## QUESTION 32

Which of the following are reasons a gene tree may not match the species tree? (MORE THAN ONE ANSWER MAY BE CORRECT)

- A. Incomplete lineage sorting**
- B. Unrecognized gene duplication followed by gene loss**
- C. Long branch attraction**
- D. Insufficient phylogenetic signal**