Take Home Exam 5 Answers.

Question 1

In the evolutionary history leading to mammals for several rounds of whole genome duplication occurred. What is the total number of duplication events that have occurred in the lineage leading humans?

A. 0
B. 1
C. 2
D. 3
E. 4

Question 2

What is the total number of duplication events that have occurred in the lineage leading bonyfish?

A. 0
B. 1
C. 2
D. 3
E. 4

Question 3

In the principle component analysis, JALVIEW uses which of the following to define protein space?

A. The presence or absence of a conserved sequence motif to define protein space.
B. A tree based on percent identity to define groups that are close to each other in sequence space.
C. Each alignment column as a dimension to define protein space.
D. GC bias on the leading versus lagging strand.
E. None of the above.

Question 4

In dotlet regions of low complexity appear as

A. grey or black squares
B. as two diagonal lines that cross in the center of the region of low complexity
C. as multiple grey or black diagonals very close to one another
D. as multiple grey or black diagonals that are spaced one repeat unit appart.

Question 5

Both group 2 intron and spliceosomal introns form lariat loops.

True
False

Question 6

There are many unrelated Eukaryotes that acquired the ability to photosynthesize by capturing as an endosymbiont an Eukaryote with a plastid endosymbiont. This is called secondary endosymbiosis.

True
False

Question 7

Dotlet can do DNA-DNA comparisons

True
False

Question 8

Dotlet can calculate comparisons between a protein sequence and a DNA sequence

True
False

Question 9

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

True
False

Question 10

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?

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

Question 11

Why is photosynthesis not a good shared derived character to define a eukaryotic group called "algae"?

Using photosynthesis as the shared character would include other groups as part of the algae family (as photosynthesis is not restricted to algae alone). Photosynthetic bacteria, and organisms which form a symbiosis with chloroplasts (i.e. all land plants), would then be included.

Question 12

Which of the following can lead to gene family* expansions (more than one correct answer is possible). [* a gene family is group of homologous genes present in a genome]

A. Tandem gene duplication
B. Gene duplication through an mRNA intermediate
C. polyploidization
D. Gene loss
E. Acquisition of a new gene through horizontal gene transfer
F. Aneupolyploidization
G. Rearrangement of chromosomes

Question 13

What is the most common fate of one of the genes created in a gene duplication event?

A. Neofunctionalizatin
B. Subfunctionalization
C. Nonfunctionalization
D. Polyfunctionalization

Question 14

What is the immediate selective advantage for an organism following subfunctionalization?

There is no IMMEDIATE advantage to subfunctionalization. Any form of benefit takes a long time to take shape via evolutionary forces.

Question 15

Brown Algae and Diatoms have which type of plastids?

A. Primary (i.e. endosymbiosis with a Cyanobacterium)
B. Secondary (i.e. an endosymbiosis with a Eukaryote with a primary plastid)
C. Tertiary (i.e. an endosymbiosis with a secondary plastid)
D. Quaternary (i.e. an endosymbiosis with a tertiary plastid)
E. None. Photosynthesis occurs across the primary cell membrane

Question 16

Which of the following is true for progressive alignment algorithms?

A. clustalw is a progressive alignment algorithm
B. progressive alignment algorithms calculate an optimal global alignment.
C. progressive alignments are global alignments
D. alignments calculated through a progressive alignment algorithms usually are a more faithful reflection of similarities in protein structure than pairwise alignments.
E. progressive alignments use a guide tree calculated from pairwise sequence comparisons
F. progressive alignments often contain a strong bias in favor of the phylogeny that is used as the guide tree.
G. alignment calculated via the program muscle are considered preferable for reconstructing molecular evolution.

Question 17

What is a Principle Component Analysis?

A. A way to visualize n-dimensional protein space by projecting it onto a 2-dimensional screen.
B. BLAST is used to identify common motifs that together using domain shuffling make up the components of a large number of proteins.
C. A measure of how many rearrangements a genome has undergone.
D. A method for detecting duplicated genes.
E. None of the above.

Question 18

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 horrible tree is produced, sometimes with strong support values
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 that will have no statistical support.