Name: _____

Score: _____ / _____

Exam 3

Dear All,

Here is your exam for Bioinformatics (Bio300/CS300). This exam is closed notes and closed book; you are not allowed to run any code on any computer to answer any questions. Unless you have made arrangements with the instructor, it is assumed that you will have 75 minutes to complete this exam. The exam is to be completed in Alden hall only. By the submission of your exam, you are agreeing to adhere to the honor code pledge.

Best of luck to all,
 Dr. Bonham-Carter

Part 1

1

What is a silent mutation? Justify your answer.

A. A mutation and change at the DNA level in which the resulting protein is the same as a wild-type protein.　　Feedback: --------

B. A mutation in which the damage is readily noticeable.　　Feedback: --------

C. A mutation which is deactivated by a biological machinery handling mutation prevention system.　　Feedback: --------

D. A mutation and change occurring strictly at the protein level where all folding was prevented.　　Feedback: --------

Answer Point Value: 10.0 points
Answer Key: A
Correct Feedback: --------
Incorrect Feedback: --------

What is an alignment-based prediction algorithm used for? Justify your answer.

○ A. The determination and search for specific sequences such as ORFs by locating their start and stop codons.   Feedback: --------

○ B. The determination of sequence similarity to previously identified genes of the same organism.   Feedback: --------

○ C. The identification of the placement of genetic sequence identifiers and other biological multi-purpose repair machinery regions (using BLAST).   Feedback: --------

○ D. The determination of sequence similarity to previously identified genes of other organisms (using BLAST).   Feedback: --------

Answer Point Value: 10.0 points
Answer Key: D
Correct Feedback: --------
Incorrect Feedback: --------

True/False: Exons are non-coding segments of genetic sequence material.

○ True

○ False

Answer Point Value: 10.0 points
Answer Key: False
Correct Feedback: --------
Incorrect Feedback: --------

4

What is an intron? Justify your answer.

○ A. An intron is a sequence of amino acids which enables protein folding.

Feedback: --------

○ B. An intron a coding section of an RNA transcript.

Feedback: --------

○ C. An intron is any nucleotide sequence within a gene that remains in the mRNA sequence.

Feedback: --------

○ D. An intron is any nucleotide sequence within a gene that is removed by RNA splicing during maturation of the final RNA product.

Feedback: --------

Answer Point Value: 10.0 points
Answer Key: D
Correct Feedback: --------
Incorrect Feedback: --------

5

True/False: The frequencies of codon usage do not exhibit much variation across organisms.

○ True
○ False

Answer Point Value: 10.0 points
Answer Key: False
Correct Feedback: --------
Incorrect Feedback: --------

6

What is the output of the following code in python. Explain your reasoning.

```
from Bio.SeqUtils import GC
seq = "GTCT"
GC(seq)
```

Answer Point Value: 10.0 points
Model Short Answer: --------
Feedback: --------

7

In a BLAST search, an E-value is given. What is this value used for?

Answer Point Value: 10.0 points
Model Short Answer: --------
Feedback: --------

8

Describe two major differences between the information content of UniProt and the Protein Data Bank.

Answer Point Value: 10.0 points
Model Short Answer: --------
Feedback: --------

9

Why is it important to understand what folded protein looks like?

Answer Point Value: 10.0 points
Model Short Answer: --------
Feedback: --------

10

Describe the use of JMol for investigating folded proteins.

Answer Point Value: 10.0 points
Model Short Answer: --------
Feedback: --------