Assignment 12

The due date for submitting this assignment has passed. As per our records you have not submitted this assignment.

1) Which statements are correct? 1 point
- During metagenomics, all the genetic elements are sequenced.
- Typically maintaining a comprehensive genomic database and analyzing the metagenomic data is computationally challenging.
- Nextera and Nanopore are sequencing platforms.
- All the statements above are true.

No, the answer is incorrect.
Score: 0
Accepted Answers:
All the statements above are true.

2) Which are not the nucleotide sequence/ amino acid databases? 1 point
- TIGR
- Genbank (NCBI)
- Bacteria
- PIR
- Yeast
- GenPept

No, the answer is incorrect.
Score: 0
Accepted Answers:
Bacteria

3) Which are incorrect matches? 1 point
- Bioinformatics I
- Bioinformatics II
- Bioinformatics III

No, the answer is incorrect.
Score: 0
Accepted Answers:
<table>
<thead>
<tr>
<th>A. Microarray</th>
<th>1. Analysis of the complete set of epigenetic modifications on the genetic material of a cell is done.</th>
</tr>
</thead>
<tbody>
<tr>
<td>B. Proteomics</td>
<td>2. RNA levels of every gene in the genome analyzed in parallel.</td>
</tr>
<tr>
<td>C. Epigenomics</td>
<td>3. Global metabolite analysis is done.</td>
</tr>
<tr>
<td>D. Metabolomics</td>
<td>4. Global protein analysis is generated by large mass spectra libraries.</td>
</tr>
</tbody>
</table>

- A-2, C-1
- A-3, B-4
- C-1, D-2
- B-4, D-3

No, the answer is incorrect.
Score: 0
Accepted Answers:
A-3, B-4
C-1, D-2

4) State True or False: 1 point

Bioinformatics is the retrieval and analysis of biochemical and biological data using mathematics and computer science.

- TRUE
- FALSE

No, the answer is incorrect.
Score: 0
Accepted Answers:
TRUE

5) How Bioinformatics is helpful in analyzing Central dogma: 1 point

- It can give the information of RNA function & structure.
- It can give the information of protein function, sequence & structure.
- We can get the phenotypic information of the organism.
- In all of the above cases.

No, the answer is incorrect.
Score: 0
Accepted Answers:
In all of the above cases.

6) Which of the conversions of these sequences are correctly matched with their percentage similarity? 1 point

<table>
<thead>
<tr>
<th>Sequence conversions</th>
<th>Percentage similarity</th>
</tr>
</thead>
<tbody>
<tr>
<td>1. ATGCTAAACT → TTGGAATCA</td>
<td>70</td>
</tr>
<tr>
<td>2. TACGGCATY → TACGGATMA</td>
<td>50</td>
</tr>
</tbody>
</table>

- Only 1
- Only 2
- Both
- None
7) Which of these are correct for the following alignment?

prin-ciple → principlal

- No. of mismatches= 2, No. of gaps= 1
- No. of mismatches= 3, No. of gaps= 2
- No. of mismatches= 1, No. of gaps= 2
- No. of mismatches= 2, No. of gaps= 3

No, the answer is incorrect.
Score: 0
Accepted Answers:
None

8) The widely used local similarity algorithms are:

- Smith-Waterman
- Basic Local Alignment Search Tool (BLAST)
- Fast Alignment (FASTA)
- All of the above.

No, the answer is incorrect.
Score: 0
Accepted Answers:
All of the above.

9) Match the following:

<p>| | | |</p>
<table>
<thead>
<tr>
<th></th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>BLAST</td>
<td>a. Compares a DNA query to DNA database.</td>
</tr>
<tr>
<td>2</td>
<td>BLASTX</td>
<td>b. Compares the 6-frame translations of DNA query to the 6-frame translations of a DNA database.</td>
</tr>
<tr>
<td>3</td>
<td>FASTX</td>
<td>c. Compares the 6-frame translations of DNA query to protein database.</td>
</tr>
<tr>
<td>4</td>
<td>TBLASTX</td>
<td>d. Compares a protein query to protein database.</td>
</tr>
<tr>
<td>5</td>
<td>BLASTN</td>
<td>e. Compares a translated DNA query to a protein database.</td>
</tr>
</tbody>
</table>

- 1- d, 2- c, 3- e, 4- b, 5- a
- 1- d, 2- b, 3- e, 4- c, 5- a
- 1- d, 2- c, 3- e, 4- b, 5- a
- 1- e, 2- c, 3- a, 4- b, 5- a

No, the answer is incorrect.
Score: 0
Accepted Answers:
1- d, 2- c, 3- e, 4- b, 5- a

10) State true or false:

T-COFFEE, b2sequ and LALIGN are the algorithms/sites that are used to translate DNA sequence to a particular protein.

- True
No, the answer is incorrect.
Score: 0
Accepted Answers: False