BIOINFORMATICS QUESTION BANK FOR OBE 2020

Instructions to the students:

Your semester end theory exam will be open book examination which will be of 75 marks.

*Each exam will be of **2 hours**. You will be provided with 1 extra hour to scan your answersheets and upload it.*

*Every question paper will comprise of 6 questions of equal marks i.e. **18.75** marks; out of which you have to perform any **four**.*

Questions can be analytical whose straight answer you won't get in any book. That is why the answers are expected to be simple, to the point and non lengthy.

1. What is PIR? Describe the various resources and databases of PIR.

2. Define DDBJ. Give an account of all the resources and data submission in DDBJ

3. Give the applications of bioinformatics in drug discovery, QSAR, microbial genome and crop improvement.

4. What is phylogeny? What are the various methods for phylogenetic analysis? Give differences between NJ, MP and ML trees.

5. Classify biological databases based on data type, maintainer status, data access, data source, database design and Organism. Explain and give examples.

6. What is bioinformatics? What are the branches, scope and aim of bioinformatics?

7. What is BLAST? Give the different categories into which BLAST tools can be categorised. What are the different parameters you observe after running any BLAST exercise. Define them. Give a brief of specialised tools and databases of NCBI.

8. What do you understand by sequence alignment? Differentiate between global and local alignment. Explain the various scoring matrices. Give differences between PAM and BLOSUM. Also explain the relationship shared between BLOSUM and PAM substitution matrices w.r.t their number.

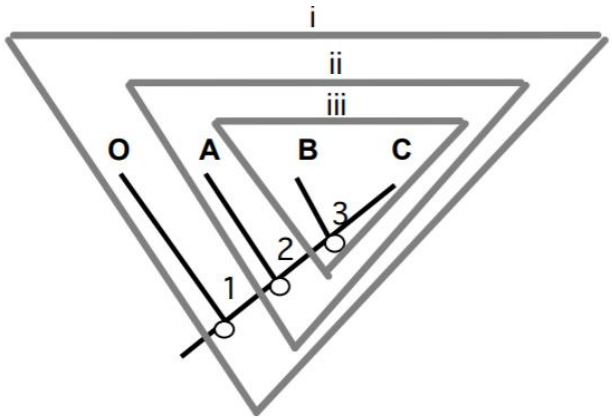
9. What is Entrez? Schematically represent the architecture of Entrez System, briefly explaining each of them.

10. Which three databases constitute the INSDC? Schematically give an idea of all its resources. Also highlight some of its primary and derivative databases.

11. If you have a gene sequence of an organism whose genome is yet to be annotated, how will you proceed forward via in silico analysis to trace a specific region with a known function. Which tool will be useful? Explain the concept and different categories of that tool in detail.

12. What are scoring matrices and what are they used for? Name and differentiate between two commonly used amino acid substitution matrices. If you have more divergent sequences then which substitution matrix one should use and with high or low number?

13. Answer the following questions according to the phylogenetic tree given below:



i. Taxon B is sister to Taxon …….

ii. Taxon (iii) is a monophyletic group consisting of ancestor…….. , and all of its descendents, ……...

iii. Taxon (iii) and …….are sister groups.

iv. The most recent common ancestor of taxa A, B, and C is ……...

v. The most recent common ancestor of taxa O, A, B, and C is ……...

True or false?

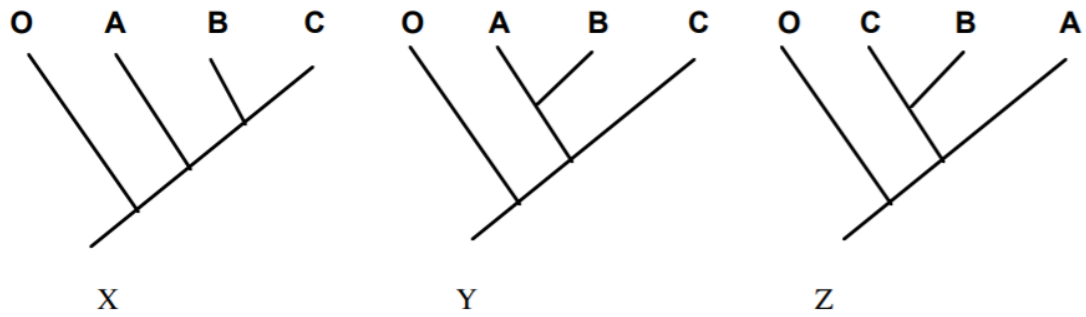
vi. Taxa A and B share a more recent common ancestor than do Taxa A and O.

vii. Taxa O, A, and B form a monophyletic group.

viii. Taxa A, B, and C form a non-monophyletic group.

ix. Taxa B and C share a more recent common ancestor than either does with A.

x. As in the tree above, mark the three nested clades on the trees below, mark them i, ii, iii, starting with the most inclusive group. Mark the trees (if any) that depict the same history.



Tree X may be depicted as follows: (0, (A, (B,C))). Depict trees Y and Z the same way.