KATHMANDU UNIVERSITY
End Semester Examination
September 2024

Marks Scored:

Level : B.Sc.
Year : I

Course : BINF 101
Semester : II

Exam Roll No. :

Time: 30 mins.

F. M. : 10

Registration No.:

Date : 13 SEP 2024

SECTION "A"
[20 Q. × 0.5 = 10 marks]

Choose and mark [X] the most appropriate answer. Symbols have their usual meanings.

1. Which of the following is characterized as sequence analysis component of Bioinformatics?
   [ ] Protein Structure Prediction
   [ ] Metabolic Pathway Modeling
   [ ] Phylogeny
   [ ] protein Interaction Prediction

2. The direction of nucleotides in DNA is read from:
   [ ] 5` to 3` end
   [ ] 3` to 5` end
   [ ] N-terminal to C-terminal end
   [ ] C-terminal to N-terminal end

3. The small subunit of ribosome contains:
   [ ] 5s rRNA [ ] 28s rRNA [ ] 23s rRNA [ ] 16s rRNA

4. Tandem DNA repeats from 8 to 100 nucleotides long are:
   [ ] short tandem repeats
   [ ] microsatellite
   [ ] simple sequence repeats
   [ ] minisatellite

5. The sequence identifier used in FASTA file downloaded from NCBI reference sequence is:
   [ ] gi|gi_number|gb|accession.version|locus
   [ ] ref|accession|locus
   [ ] sp|accession|locus
   [ ] pir|entry

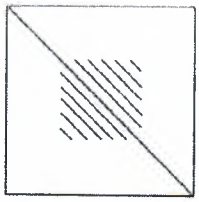
6. The Phred quality score for the probability of error is 5 in 100 will be (rounded off):
   [ ] 11 [ ] 12 [ ] 13 [ ] 14

7. Which of the following is not an example of secondary database?
   [ ] SWISS-PROT [ ] PROSITE [ ] BLOCKS [ ] PDB

8. Calculate sequence similarity for the sequences:
   a)ATCGATCGATCG
   b) ATCGGCTAATCG
   [ ] 75% [ ] 66.66% [ ] 25% [ ] 33.33%

9. Which of the gap penalty is independent of the length of the gap?
   [ ] Constant penalty
   [ ] Affine penalty
   [ ] Proportional penalty
   [ ] Extension penalty

10. The following pattern was visualized during pairwise sequence alignment. Interpretation of the plot hints that the pattern is due to:



[ ] palindrome
[ ] partial palindrome
[ ] microsatellites
[ ] minisatellites

11. PAM 80 matrix corresponds to _____ amino acid identity
[ ] 80% [ ] 20% [ ] 50% [ ] 100%

12. Which matrix is preferred to compare highly divergent proteins?
[ ] BLOSUM 90 [ ] BLOSUM 80 [ ] BLOSUM 62 [ ] BLOSUM 45

13. BLAST algorithm that takes nucleotide query translates in all 6 reading frame and compares with a protein databases is:
[ ] BLASTP [ ] BLASTN [ ] BLASTX [ ] TBLASTN

14. The consensus telomere sequence in humans is:
[ ] TTAGGG [ ] TTGGGG [ ] TAGGG [ ] TTTAGGG

15. The set of all coding and no-coding RNA is called as
[ ] Genome [ ] Transcriptome [ ] Proteome [ ] Metabolome

16. Base pairings between which nucleotides are not permitted during RNA folding:
[ ] G-C [ ] A-U [ ] G-U [ ] A-C

17. Which of the following amino acid is positively charged?
[ ] Arginine [ ] Aspartic acid [ ] Aspartate [ ] Phenylalanine

18. Calculate the alpha helix parameter if 30 of 50 Alanine are in alpha helix where a total of 400 amino acids out of 1000 were in alpha helix?
[ ] 1 [ ] 1.25 [ ] 1.5 [ ] 1.75

19. An unnatural group that does not include the most recent common ancestor is:
[ ] monophyletic group [ ] polyphyletic group
[ ] paraphyletic group [ ] anaphyletic group

20. Which substitution model assumes that all nucleotides occur in equal frequency (25%) and are substituted with equal probability?
[ ] Jukes Cantor model [ ] Kimura two parameter model
[ ] Hasegawa Kishono Yano model [ ] General Time Reversible model

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13 SEP 2024

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SECTION "B"
[3Q. × 7 = 21 marks]

Attempt *ANY THREE* questions.

1. Explain the distance-based tree building Method UPGMA. Produce an UPGMA tree of 5 OTUs considering the following observed evolutionary distances. Also, indicate branch Lengths between OTUs and all internal nodes.

	A	B	C	D	E
A	-				
B	19	-			
C	19	8	-		
D	17	19	19	-	
E	11	19	19	17	-

2. Explain each of the individual steps behind DNA sequencing method of Sanger sequencing. Provide your answers with detailed figures.

3. How does alignment using dynamic programming differ for global and local alignment? Create TWO possible alignment for the below provided sequences; considering score for match = 2, mismatch = 0 and gap penalty = -1.
   Seq #1: TGCATGTATTA
   Seq #2: CCATCTATTA

4. Explain the features of prokaryotic and eukaryotic DNA that are used for gene prediction.

SECTION "C"
[19 marks]

5. Write short notes on: (***ANY FIVE***) [5Q. × 3 = 15 marks]
   a. Polymerase Chain Reaction
   b. Draw the structures of: Cytosine, Adenine and Tyrosine
   c. BLAST
   d. Ramachandran Plot
   e. DNA microarray
   f. Application of Bioinformatics

6. Give major differences between: [2Q. × 2 = 4 marks]
   a. Exhaustive and Heuristic algorithm
   b. Maximum Parsimony and UPGMA