KATHMANDU UNIVERSITY
End Semester Examination [C]
June/July, 2023

Marks Scored:

Level : B.Tech.
Year : III
Course : BIOT 305
Semester : II

Exam Roll No. :
Time: 30 mins.
F. M. : 10

Registration No.:
Date : 27 JUN 2023

SECTION "A"

[20 Q. × 0.5 = 10 marks]

Choose and tick [✓] the most appropriate answer.

1. Which kind of information is not found in RNA sequences?
   [ ] Localization signals
   [ ] Stability signals
   [ ] Splice site signals
   [ ] Nucleosome positioning signals

2. The study of the relationship of genomic structures of different species is made under:
   [ ] Gene Expression Profiling
   [ ] Comparative Genomics
   [ ] Drug Discovery
   [ ] Biotechnology

3. The chain extension step in Sanger Sequencing will stop when using:
   [ ] Adenosine Triphosphate
   [ ] Deoxyadenosine triphosphate
   [ ] Dideoxyadenosine triphosphate
   [ ] Monooxyadenosine triphosphate

4. Which of the sequencing platform has an average read length of 2000 nucleotides?
   [ ] ABI Sanger Sequencing
   [ ] Roche 454 Pyrosequencing
   [ ] SOLiD Sequencing by ligation
   [ ] PacBio Single Molecule Sequencing

5. Which of the following is not a term that described under Gene Ontology?
   [ ] Molecular Function
   [ ] Biological Process
   [ ] Cellular Component
   [ ] Protein transport

6. Which website does contain of entries describing the protein families, domains and functional sites?
   [ ] Expasy
   [ ] PDB
   [ ] Prosite
   [ ] KEGG

7. The sequence identifier for NCBI reference sequence is:
   [ ] gi|gi_number|gb|accession.version|locus
   [ ] ref|accession|locus
   [ ] sp|accession|locus
   [ ] gi|gi_number|embl|accession.version|locus

8. The Phred quality score for the probability of error is 1 in 50 will be (rounded off):
   [ ] 15
   [ ] 16
   [ ] 17
   [ ] 18

9. A copy of a gene can be found in the same organism, this is due to:
   [ ] Gene mutation
   [ ] Gene duplication
   [ ] Gene translocation
   [ ] Gene recombination

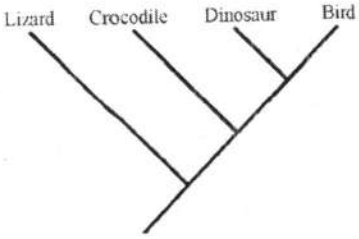
10. Which of the following substitution matrix should be chosen if the sequences have little to no divergence between them?
[ ] PAM 250 [ ] PAM 200 [ ] BLOSUM 40 [ ] BLOSUM 90

11. If the word size is increased for the parameter in BLAST search, which of the following will be true?
[ ] sensitivity will increase [ ] sensitivity will decrease
[ ] search speed will be faster [ ] no change in search speed

12. Which of the following implements block based method for multiple sequence alignment?
[ ] DIALIGN2 [ ] PRRN [ ] ClustalW [ ] MUSCLE

13. Which of the assumptions is incorrect for molecular phylogenetics?
[ ] Sequences used should be homologous
[ ] Phylogenetic divergence is bifurcating
[ ] Alignment positions evolve independently
[ ] Homoplasy estimates true evolution

14. Which of the following is an accurate statement by looking at the tree provided?
[ ] A crocodile is more closely related to a lizard than to a bird
[ ] A crocodile is more closely related to a bird than to a lizard
[ ] A crocodile is equally related to a lizard and a bird
[ ] A crocodile is related to a lizard, but is not related to a bird



15. The number of different rooted trees that can be drawn using 7 taxa is
[ ] 105 [ ] 905 [ ] 10395 [ ] 5695

16. What parameter in Bootstrap method is defined to be a confidence interval within which is contained not the true phylogeny, but the phylogeny that would be estimated on repeated sampling of many characters from the underlying pool of characters?
[ ] Accuracy [ ] Repeatability [ ] Precision [ ] Phylogeny

17. The consensus motif of Shine-Delgarno sequence can be represented as:
[ ] GCCACCatgG [ ] (C/T)(C/T)CA(C/T)(C/T)
[ ] AGGAGGT [ ] (Py)$_{12}$NCAG

18. Which gene prediction program uses conditional maximum likelihood to differentiate coding from noncoding features?
[ ] HMMgene [ ] GENSCAN [ ] GRAIL [ ] GeneMark

19. Which amino acids provide sites for aromatic packing interactions?
[ ] Glycine [ ] Glutamine [ ] Tryptophan [ ] Histidine

20. Which of the amino acid has higher tendency to be found in alpha helix secondary structure?
[ ] Methionine [ ] Valine [ ] proline [ ] Isoleucine

KATHMANDU UNIVERSITY
End Semester Examination [C]
June/July, 2023

27 JUN 2023

Level : B.Tech.
Year : III
Time : 2 hrs. 30 mins.

Course : BIOT 305
Semester : II
F. M. : 40

SECTION "B"

[4Q × 6 = 24 marks]

Attempt *ANY FOUR* 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. [3+3]

	A	**B**	**C**	**D**	**E**
A	-				
B	17	-			
C	21	30	-		
D	31	34	28	-	
E	12	21	39	43	-

2. Create a PSSM matrix based on the position of the nucleotides in the provide sequence and evaluate the probability of sequence CCACACCACA fitting to that matrix. [6]

Position	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**
Seq. 1	A	T	A	T	A	C	A	C	A	G
Seq. 2	T	T	G	A	T	A	C	T	A	A
Seq. 3	C	T	G	C	C	T	C	A	A	T
Seq. 4	A	C	A	C	G	C	C	A	T	T
Seq. 5	T	G	G	A	A	T	G	T	C	T

3. Explain each of the individual steps behind DNA sequencing method of Sanger sequencing. Provide your answer with detailed figures. [6]

4. Explain the process by which matrices such as PAM or BLOSUM that are used to calculate sequence similarity are created? Create **TWO** possible alignment for the below provided sequences; considering score for match = 1, mismatch= -1and gap penalty = -1. [3+3]

   Seq #1: **ATCTGATCGG**
   Seq #2: **ACTCATACG**

5. Explain the features of the prokaryotic genes. How gene prediction is going to be different between prokaryotes and eukaryotes? [3+3]

SECTION "C"

[8Q. × 2 =16 marks]

Attempt *ANY EIGHT* questions.

6. What are the various applications of Bioinformatics?

7. Differentiate between the shotgun and hierarchical approach used for whole genome sequencing.

8. Explain the FASTQ format and its constituents.

9. How does the length of the sequence alignments matter to determine homology?

10. Explain the various types of BLAST available in NCBI database.

11. Differentiate the various types of clades that can be inferred from a phylogenetic tree.

12. How does Bootstrap indicates the stability of individual clades in the tree.

13. How does the codon usage bias differentiate the coding and non-coding regions?

14. Explain how the protein packaging or folding would occur.