(University of Choice)

MASINDE MULIRO UNIVERSITY OF SCIENCE AND TECHNOLOGY (MMUST)

MAIN CAMPUS

UNIVERSITY EXAMINATIONS
2019/2020 ACADEMIC YEAR

FOURTH YEAR SECOND SEMESTER EXAMINATIONS

FOR THE DEGREE
OF
BACHELOR OF MEDICAL LABORATORY SCIENCES/MEDICAL BIOTECHNOLOGY

SPECIAL/SUPPLEMENTARY EXAMINATION

COURSE CODE: BML 421

COURSE TITLE: BIO-INFORMATICS AND BIO-COMPUTING

DATE: 15th October 2020   **TIME**: 8.00 AM -10.00 AM

INSTRUCTIONS TO CANDIDATES

This paper is divided into three sections, **A B** and **C,** carrying respectively: Multiple Choice questions (**MCQs**), short answer questions (**SAQs**) and long answer questions (**LAQs**).

TIME: 2 Hours

MMUST observes ZERO tolerance to examination cheating

This Paper Consists of 4 Printed Pages. Please Turn Over.

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SECTION A: MULTIPLE CHOICE QUESTIONS (MCQs)

1. Bioinformatics and bio-computation field involve the following EXCEPT?
   a) The discovery of therapeutic products
   b) Biotechnology and recombinant technology
   c) The study of molecular pathways and drug resistance
   d) Improving the genetic code
2. Core genome comprises which of the following?
   a) Set of unique genes that allow speciation and are not conserved across same genus.
   b) Set of unique genes shared by all genomes that are conserved across all species in a genus.
   c) A set of non-essential genes in an organism
   d) The genome that is found in all organisms
3. Which of the following best describes the pan-genome of an organism?
   a) Set of genes forming up a single strain
   b) Essential genes in a specie
   c) Complete set of all complement genes present in all strains of a specie
   d) All sets of genes that are comprised in a genus.
4. Which of the following is NOT a functional macromolecule in cellular processes?
   a) mRNA
   b) SiRNA
   c) tRNA
   d) Ribosomal RNA
5. Which of the following is a BLAST program for a protein sequence in translated nucleotide database?
   a) tBLASTx
   b) BLASTn
   c) BLASTx
   d) tBLASTn
6. What does OMIM represent in bioinformatics?
   a) Multiple sequence alignment tool
   b) Organization of mammalian genetic trees
   c) Database for Mendelian inheritance in man
   d) Objects for microorganism inheritance
7. PDB as applied in bioinformatics is a
   a) Primer design program
   b) Data bank for proteins and their structures
   c) Phylogenetic database
   d) Phosphorylating dimer of biomolecules
8. Orthologous genes
   a) Similar genes in the same genus that result from gene duplication.
   b) Genes that have lost function over time in ancestry.
   c) Similar genes in different genus that results from gene ancestral inheritance.
   d) Acquired genes from other organisms that were not part of the genus ancestry.
9. Which of the following best describes a core genome?
   a) Set of unique genes that allow speciation and are not conserved across same genus.
   b) Set of unique genes that are conserved across the genus.
   c) A set of non-essential genes in an organism

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d) The genome that is found in all organisms

10. Which of the following is a BLAST program for a protein sequence in a protein database?
    a) BLASTp
    b) BLASTn
    c) BLASTx
    d) tBLASTn

11. Which of the following is a BLAST program for a nucleotide sequence in a nucleotide database?
    a) BLASTp
    b) BLASTn
    c) BLASTx
    d) TBLASTn

12. Which of the following describes paralogous genes?
    a) Similar genes in the same genus that result from gene duplication.
    b) Similar genes in different genus that results from gene ancestral inheritance.
    c) Genes that have lost function over time in ancestry.
    d) Acquired genes from other organisms that were not part of the genus ancestry.

13. Clustal W is a suitable software for computational analysis of
    a) Pairwise sequence alignment
    b) Multiple sequence alignment
    c) Gene expression profiles
    d) Protein folding into tertiary structures

14. EXPASY is
    a) Database for expression profiles of genes
    b) Database for gene transcripts
    c) Computational Software for protein analysis
    d) Bank for expression regulatory molecules

15. Which of the following is a BLAST program for translated nucleotide sequence in a translated nucleotide database?
    a) tBLASTx
    b) BLASTn
    c) BLASTx
    d) tBLASTn

16. Dispensable genome
    a) Set of unique genes that are conserved across the genus.
    b) A set of non-essential genes in an organism
    c) The genome that is found in all organisms
    d) Set of unique genes that allow speciation and are not conserved across same genus.

17. A bioinformatician would like to study expressed genes and their abundance. Where can he find this information
    a) ENTREZ

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b) UNI GENE
c) BLAST
d) Protein data bank

18. During computational translation the software will stop the peptide sequence translation when it encounters the following EXCEPT?
a) AUG
b) UGA
c) UAG
d) UAA

19. Which of the following is FALSE about RNA splicing?
a) It is a process through which bacteria produce mature mRNA
b) It involves removal of non-coding regions of RNA
c) It is a post-transcription process
d) RNA editing process for eukaryotes

20. Which of the following is a BLAST program for a translated nucleotide sequence in protein database?
a) BLASTp
b) BLASTn
c) BLASTx
d) TBLASTn

SECTION B: SHORT ANSWER QUESTIONS (40 MARKS)
1. Giving relevant examples, describe the use of databases in bioinformatics.
(8 Marks).
2. List types of bioinformatics databases giving examples of the databases in each case. (8 Marks).
3. In the EMBL database format, what do the following lines represent; ID, AC, NI, DE, KW, DT, OS, OC, RN, FT, SQ, CC, RP, RX, RA, RL.
(8 Marks).
4. Describe the tasks that the ExPASy database can enable you perform.
(8 Marks).
5. Describe the stepwise process of performing a blast of a DNA sequence.
(8 Marks).

SECTION C: LONG ANSWER QUESTIONS (40 Marks)

1. Discuss the some of the common algorithms used in sequence analysis.
(20 Marks).

2. Compare and contrast BLAST and FastA platforms during sequence homology searches. (20 Marks).

3. Discuss the major points to consider before submitting sequences to databases.
(20 Marks).

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