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University Examinations 2024/2025

FOURTH YEAR FIRST SEMESTER EXAMINATION FOR THE DEGREE OF BACHELOR OF MEDICAL LABORATORY SCIENCES AND MEDICAL MICROBIOLOGY

HML 3417/HMM 3416: GENOMICS AND BIOINFORMATICS

DATE: JANUARY 2025 **TIME: 3 HOURS**

INSTRUCTIONS:
Answer ***All*** *questions*
Ensure that all your answers are properly numbered
Part I multiple Choice Questions (MCQ): Write the correct answer on the space provided in the answer booklet. Each MCQ is one mark
Part II: Short Answer Questions – Answer questions following each other on the answer booklet
Part III: Long Answer Questions – Answer each question on the answer booklet

SECTION A: MULTIPLE CHOICE QUESTIONS (20 marks)

1. How do changes in nucleotide sequences (mutations) affect protein structure?
   A. They always lead to beneficial changes.
   B. They can alter amino acid sequences, potentially affecting protein function.
   C. They only occur in non-coding regions of DNA.
   D. They always result in the production of non-functional proteins.
2. Which of the following best describes the relationship between a genome and a gene?
   A. A genome is a subset of genes.

B. A genome is made up of all of an organism's genes.

C. Genes are sequences of RNA that create a genome.

D. A gene contains a genome.

3. What is the main purpose of DNA in living organisms?

A. Store instructions for protein synthesis

B. Convert RNA into proteins

C. Break down carbohydrates

D. Provide energy for cell metabolism

4. Which of the following is an advantage of NGS over traditional sequencing methods?

A. It is less expensive for sequencing a few genes.

B. It sequences multiple DNA fragments simultaneously, saving time.

C. It eliminates the need for DNA extraction.

D. It cannot be used for whole-genome sequencing.

5. How is genetic variation significant in a population?

A. It reduces adaptability to changing environments.

B. It increases diversity and allows for natural selection.

C. It is a cause of many metabolic errors.

D. It has no impact on evolutionary processes.

6. The chain termination method used in Sanger sequencing is dependent on the use of:

A. Modified nucleotides that stop the DNA replication process

B. Enzymes that repair DNA strands

C. RNA molecules as templates

D. DNA ligase

7. What is one advantage of next-generation sequencing over Sanger sequencing?

A. It uses fluorescent dyes instead of radioactive labeling.

B. It sequences DNA molecules one at a time.

C. It can process millions of DNA fragments in parallel.

D. It is more accurate for sequencing short fragments.

8. Which best describes bioinformatics workflows?
   A. A set of laboratory protocols for DNA extraction
   B. A series of computational processes to analyze biological data
   C. A method for manually editing gene sequences
   D. A diagnostic procedure for identifying infections
9. One critical function of bioinformatics in genomics is:
   A. Cloning genes for expression in other species
   B. Creating 3D images of protein structures
   C. Storing, analyzing, and interpreting large-scale genomic data
   D. Isolating bacterial cultures from patient samples
10. In the context of genomics, bioinformatics helps to:
   A. Visualize evolutionary relationships
   B. Measure physical properties of genes
   C. Facilitate large-scale sequence comparisons
   D. Perform real-time PCR
11. Proteomics is essential for understanding:
   A. How proteins are encoded in DNA
   B. The entire set of proteins expressed in a cell or tissue
   C. DNA replication mechanisms
   D. The formation of RNA molecules
12. Why is protein structure important in biology?
   A. It determines the size of a cell.
   B. It directly influences protein function and interactions.
   C. It is involved in DNA transcription.
   D. It prevents mutations.

13. A major role of bioinformatics tools such as BLAST is to:
    A. Design primers for PCR experiments
    B. Detect similarities between DNA or protein sequences
    C. Construct protein folding models
    D. Measure gene expression levels
14. Which database provides comprehensive access to annotated genomic sequences?
    A. PCR Bank
    B. Ensembl Genome Browser
    C. LipidBase
    D. PDB (Protein Data Bank)
15. Why is sequence alignment important in bioinformatics?
    A. It determines the primary structure of proteins.
    B. It helps identify homologous sequences across different species.
    C. It eliminates the need for PCR amplification.
    D. It improves the quality of DNA extraction.
16. When visualizing genomic data, which type of feature would you typically observe?
    A. RNA transcripts only
    B. Protein tertiary structures
    C. Gene locations, exons, and regulatory regions
    D. Chromosome karyotypes
17. Genomic data visualization is often achieved using tools like:
    A. Mass spectrometry
    B. Microscopy
    C. Genome browsers
    D. PCR machines
18. What information can be inferred from the branching pattern of a phylogenetic
    A. The physical distances between species

B. The evolutionary history and relatedness of different species

C. The rate of DNA replication in an organism

D. The chromosomal number of each species

19. The use of genomic data in personalized medicine allows physicians to:

A. Tailor treatment based on an individual's genetic makeup

B. Treat all patients with the same condition similarly

C. Diagnose diseases using only physical examination

D. Eliminate all genetic diseases completely

20. Which of the following best describes the central role of RNA in gene expression?

A. It stores genetic information for inheritance.

B. It acts as an intermediate between DNA and proteins.

C. It directly controls cell division

D. It breaks down during mitosis

SECTION B: SHORT ANSWER ALL QUESTIONS (40 MARKS)

a) With examples, describe consequences of genetic variation (6 marks)

b) Tabulate the difference between DNA and RNA (6 marks)

c) Describe the importance of Bioinformatics in Genomics (6 marks)

d) Explain the importance of sequence alignment (4 marks)

e) Describe the key Components of Bioinformatics Workflows (5 marks)

f) Explain how phylogenetic trees can be interpreted to reflect different aspects of evolutionary biology (5marks)

g) Describe the types of RNA (4 marks)

h) Explain the ethical issues in Genomics (4 marks)

SECTION C: LONG ANSWER TWO QUESTIONS (40 MARKS)

QUESTION ONE

a) Discuss the key steps in DNA/RNA extraction (10 marks)

b) Describe the steps in Polymerase chain reactions (10 marks)

QUESTION TWO

Describe the main sequencing platforms used in whole genome sequencing (20 marks)

QUESTION THREE

Discuss genome structure and variation (20 marks)