

VU Learning HUB

BIF401 Quiz File

Chapter-wise Solved MCQs

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Chapter 1: Introduction to Bioinformatics

Q1. According to Chapter 1, approximately how many genes are present in the human genome? A) 10,000 B) 25,000 C) 50,000 D) 100,000

Q2. From 1982 to 2002, the size of GenBank grew from 2 billion base pairs to how many base pairs? A) 10 billion base pairs B) 25 billion base pairs C) 56 billion base pairs D) 100 billion base pairs

Q3. Which three domains comprise the phylogenetic "tree of life" described in Chapter 1? A) Viruses, Bacteria, and Fungi B) Bacteria, Archaea, and Eucarya C) Prokaryotes, Eukaryotes, and Protists D) Animals, Plants, and Microorganisms

Q4. Which public sequence database is identified as the repository for DNA and RNA sequences maintained by the NIH? A) UniProt B) Swiss-Prot C) GenBank D) ExPASy

Answer Key

B — The handout states that the human genome contains over 25,000 genes.

C — GenBank expanded from 2 billion base pairs in 1982 to 56 billion base pairs by 2002.

B — The three domains of the tree of life listed in the text are Bacteria, Archaea, and Eucarya.

C — GenBank (maintained by the NIH) is the public sequence database for DNA and RNA.

Chapter 2: Sequence Analysis

Q1. Which algorithm is used specifically for global pairwise sequence alignment? A) Smith-Waterman Algorithm B) Needleman-Wunsch Algorithm C) Chou-Fasman Algorithm D) Zuker's Algorithm

Q2. What does the acronym PAM stand for in sequence alignment scoring matrices? A) Protein Alignment Matrix B) Pairwise Amino-acid Match C) Point Accepted Mutation D) Probabilistic Alignment Model

Q3. Which alignment search tool was developed at NCBI in 1990 for rapid local sequence database searching? A) FASTA B) BLAST C) CLUSTALW D) PROSITE

Q4. Which tool developed by EMBL-EBI uses progressive alignment to construct Multiple Sequence Alignments (MSA)? A) Smith-Waterman B) Needleman-Wunsch C) CLUSTALW D) BLAST

Answer Key

B — The Needleman-Wunsch algorithm is designed to compute global sequence alignments.

C — PAM stands for Point Accepted Mutation, representing amino acid substitutions that conserve function.

B — BLAST (Basic Local Alignment Search Tool) was developed in 1990 by NCBI.

C — CLUSTALW is a tool developed by EMBL-EBI that uses progressive alignment for MSA.

Chapter 3: Molecular Evolution

Q1. In a phylogenetic tree diagram, what do the internal nodes represent? A) Genes from living species B) Inferred common ancestors C) Terminal leaf nodes D) Outgroup species

Q2. UPGMA belongs to which major category of tree construction methods? A) Objective-based methods B) Maximum Likelihood methods C) Clustering approaches D) Maximum Parsimony methods

Q3. What does the acronym UPGMA stand for? A) Universal Pair Group Matching Algorithm B) Unweighted Pair Group Method with Arithmetic Mean C) Unified Phylogenetic Group Maximum Alignment D) Unrooted Pair Group Molecular Analysis

Q4. In the UPGMA clustering process, which pair of sequences or clusters is combined first? A) The pair with the largest evolutionary distance B) The pair with the shortest evolutionary distance C) The pair with the highest number of gaps D) The pair located at the outer edges of the matrix

Answer Key

B — Internal nodes on a phylogenetic tree represent common ancestors inferred from sequence data.

C — UPGMA is categorized under clustering approaches for building phylogenetic trees.

B — UPGMA stands for Unweighted Pair Group Method with Arithmetic Mean.

B — UPGMA merges the pair of sequences or clusters with the shortest evolutionary distance first.

Chapter 4: RNA Secondary Structure Prediction

Q1. What thermodynamic property is used to evaluate the stability of an RNA secondary structure? A) Activation Energy B) Gibbs Free Energy C) Kinetic Energy D) Enthalpy of Vapourisation

Q2. In RNA energy calculations, base pairing releases energy and contributes which type of value? A) Positive destabilizing energy B) Negative stabilizing energy C) Neutral structural energy D) Zero net energy

Q3. Which algorithm predicts optimal RNA secondary structure by calculating stabilizing and destabilizing energies to select the structure with the overall lowest free energy? A) Needleman-Wunsch Algorithm B) Smith-Waterman Algorithm C) Zuker's Algorithm D) Chou-Fasman Algorithm

Q4. The web server MFOLD is an online tool developed as an upgraded implementation of which algorithm? A) Zuker's Algorithm B) Needleman-Wunsch Algorithm C) UPGMA D) BLAST

Answer Key

B — Gibbs Free Energy determines RNA folding stability, with structures favoring lower energy states.

B — Base pairing of complementary nucleotides releases energy, contributing negative stabilizing energy values.

C — Zuker's algorithm calculates stabilizing and destabilizing energies to find the RNA structure with lowest overall energy.

A — The MFOLD web server is an online tool developed as an upgraded version of Zuker's algorithm.

Chapter 5: Protein Sequences

Q1. What is the process of converting DNA information into RNA called in the central dogma? A) Translation B) Transcription C) Replication D) Ionization

Q2. What does MS1 in mass spectrometry measure for precursor proteins or peptides? A) Fragment sequence tags B) Intact protein/peptide mass C) Amino acid side-chain charge D) Isoelectric point only

Q3. Tandem Mass Spectrometry (MS2 or MS/MS) is primarily used for which purpose in protein identification? A) Measuring total DNA concentration B) Generating peptide fragments and peptide sequence tags C) Calculating Gibbs Free Energy D) Predicting RNA secondary loops

Q4. What does the file format acronym MGF stand for in proteomics search tools? A) Molecular Gel Format B) Mascot Generic Format C) Mass Gradient File D) Matrix Grid Format

Answer Key

B — In the central dogma, converting DNA information to RNA is known as transcription.

B — MS1 measures the intact mass of precursor proteins or peptides.

B — Tandem MS (MS2) fragments intact peptides to generate peptide sequence tags for protein identification.

B — MGF stands for Mascot Generic Format, developed by Matrix Science for MS/MS data.

Chapter 6: Protein Structures

Q1. Secondary structures of proteins, such as Alpha Helices and Beta Sheets, are primarily stabilized by which type of bond? A) Disulphide bridges B) Hydrogen bonds in the protein backbone C) Ionic bonds between R-groups D) Hydrophobic interactions only

Q2. Which diagram is used to analyze allowed protein backbone bond angles (Phi and Psi)? A) Dot Plot B) Ramachandran Plot C) Hydrophobicity Plot D) Zuker Plot

Q3. Which structural level occurs specifically in multimeric proteins composed of multiple polypeptide chains? A) Primary (1') structure B) Secondary (2') structure C) Tertiary (3') structure D) Quaternary (4') structure

Q4. The Chou-Fasman algorithm is used to predict which structural feature of proteins? A) Intact mass from MS data B) Secondary structures (Alpha Helices, Beta Sheets, and Turns) C) Phylogenetic trees from sequence distance D) Open Reading Frames in DNA

Answer Key

B — Secondary structures (Alpha Helices and Beta Sheets) are stabilized by hydrogen bonds in the protein backbone.

B — The Ramachandran Plot visualizes allowed backbone bond angles in protein structures.

D — Quaternary (4') structures are formed by the interaction of multiple polypeptide chains in multimeric proteins.

B — The Chou-Fasman algorithm uses amino acid propensities to predict secondary structures like alpha helices and beta sheets.

End of Quiz

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