NATIONAL OPEN UNIVERSITY OF NIGERIA
Plot 91, Cadastral Zone, Nnamdi Azikiwe Expressway, Jabi - Abuja
Faculty of Science
DEPARTMENT OF BIOLOGICAL SCIENCES
2024_2 EXAMINATION

COURSE CODE: BIO316
COURSE TITLE: INTRODUCTION TO BIOINFORMATICS
CREDIT UNIT: 2 UNITS
TIME ALLOWED: 2 HOURS
INSTRUCTION: ANSWER QUESTION ONE AND ANY TWO OTHERS.

Q1

a. Enumerate the scope of phylogenetic analysis (3marks)
b. What is Phylogeny? (4marks)
c. Explain two (2) statistical significance of FASTA (6marks)
d. Justify the use of ENTREZ as sequence retrieval tool. (8marks)
e. List and explain any three (3) biopharmaceutical companies that uses bioinformatics and their products. (9marks)

Q2

a. Itemize four (4) knowledge areas of bioinformatics. (2marks)
b. State the objectives of sequence alignment analysis. (4marks)
c. List and explain the two (2) types of sequence analysis. (4marks)
d. Explain the importance of scripting language. (5marks)
e. List and explain five (5) uses of BLAST. (5marks)

Q3

a. Describe flatfile format. (8marks)
b. List and explain any (5) bioinformatic projects. (12marks)

Q4

a. Discuss the limitations of bioinformatics. (10marks)
b. Concisely explain the pitfall of biological database. (10marks)

Q5

a. Itemize eight (8) applications of data mining in bioinformatics. (8marks)
b. Justify the use of any two (2) bioinformatics tools in biotechnology (12marks)
   i. Construction of the Phylogenetic Tree
   ii. Prediction of RNA Secondary Structure
   iii. Gene Designing and Codon Optimization

Q6

a. Provide the difference between pairwise alignment and multiple sequence alignment under the following;

  i. Description
  ii. Category
  iii. Algorithm
  iv. Techniques (10marks)

b. Explain the fundamental steps of phylogenetic study. (10marks)