NATIONAL OPEN UNIVERSITY OF NIGERIA

14-16 AHMADU BELLO WAY, VICTORIA ISLAND LAGOS

SCHOOL OF SCIENCE AND TECHNOLOGY

MARCH/APRIL 2015 EXAMINATION

COURSE CODE: **BIO 316 MARKING SCHEME**

COURSE TITLE: **INTRODUCTION TO BIOINFORMATICS**

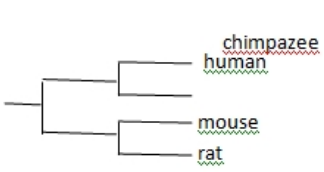
TIME ALLOWED **(2 HRS)**

INSTRUCTION: **Answer any 4 questions**

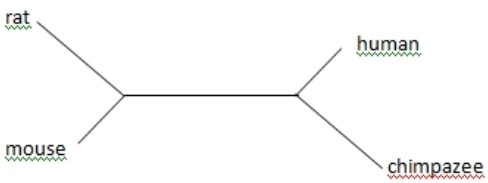
QUESTION ONE

a. What is bioinformatics (2 Mrks)

a. Consider the two phylogenetic trees below:



A: Rooted Tree



B: Unrooted Tree

Give brief analysis of the two trees (4 Marks)

a.

Complete the table below. (6 Mrks)

Program	**Query**	**Database**
BLASTP		
	Nucleotide: 6 frame translation	
TBLASTN		Nucleotide: 6 frame translation
TBLASTX	Nucleotide: 6 frame translation	

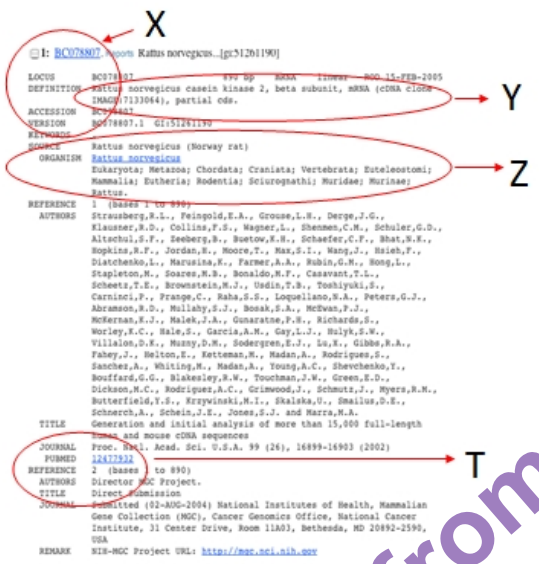
1 Mrk for each correct entry

a. Itemize any five examples of phylogenetic Softwares. (5 Mrks)

b. Data mining does notgives biological meaning to a search. (True or False) (½ Mrk)

QUESTION TWO

a. Identify what X,Y, Z and T are from the figure below? (6 Marks)



b.

Two kinds of alignment: global and local. Briefly explain when each type of alignment is the appropriate choice. (10 Mrks)

c.

i. List one common phylogenetic analytical methods . (1Mrk)

ii. The dotplot is a table of matrix representing a visual representation of similarities between two sequences. (True or False) (½ Mrk)

QUESTION THREE

a. Fill out the dynamic programming table for determining the optimum global alignment between sequences ACTG and CGGA. Assume that a match is scored +3 and that mismatches and spaces are scored −1 each. (12Mrks).

a. What is the optimum alignment corresponding to the table in part (a) and what is its score? (5½Mrks).

QUESTION FOUR

a.

i. Explain the circumstance that led to the development of bioinformatics (3 Mrks)

ii. What are databases? (2 Mrks)

a. Draw a diagram to show data flow for submissions and updates between the databases. (6 Mrks)

a. List three ways in which sequence alignment helps scientists. (6 Mrks)

a. You intend to carry out an investigation on a molecule called human neutrophil elastase. How will you start to search for relevant entries on this enzyme and get a detail information including the sequence of the enzyme? (½Mrks)

QUESTION FIVE

a. The GENSCAN is a type of what **program** and uses what type of **hidden model**?

(2Mrks)

a. What is parsimony? (3 Mrks)

a. What is the key difference between the initial phases of BLAST and FASTA? (5 Mrks)

b. Explain why neither FASTA nor BLAST are guaranteed to return a sequence that has maximum similarity score with respect to the query sequence. (7Mrks).

a. Is PUDMED one of the biomedical search engines? (Yes or No) (½Mrks)

QUESTION SIX

a. Explain what you understand by Online Mendelian Inheritance in Man, OMIM. . (8Mrks).

a. For the parsimony problem, suppose we start with some tree T for the given set of species. Next, we do a series of nearest-neighbor interchange (NNI) operations. Each time, we see if the tree T' obtained has better parsimony score than the current tree T. If so, we replace T by T' ; otherwise, we stop. Is the final tree obtained in this fashion guaranteed to be optimum (i.e., have the best possible parsimony score)? (6 Mrks)

a.

List the three classifications of database (3 Mrks)

d. Flatfile format is the basic unit of information within the primary data bases. (True or False)(½Mrks