Technical University of Mombasa

Faculty of Applied and Health Sciences

DEPARTMENT OF PURE AND APPLIED SCIENCES

UNIVERSITY EXAMINATION FOR THE DEGREE OF BACHELOR OF TECHNOLOGY IN INDUSTRIAL MICROBIOLOGY AND BIOTECHNOLOGY

BTMBT 10M Y4 S2

ABT 4405: BIOINFORMATICS

SEMESTER EXAMINATION

DECEMBER 2013 SERIES 2 HOURS

Instructions to candidates:

This paper consist of **FIVE** questions
Answer question **ONE** (compulsory) and any other **TWO** questions

QUESTION ONE

a) Define the following terminologies

I. Bioinformatics **(1mark)**

II. Identifier **(1mark)**

b) Distinguish between FASTQ and NEXUS formats. **(6marks)**

c) You are given the following pair of sequences:

1. VWEDNW DDD
2. VSEDNRDDD

3. VWDDNWDED
4. VWEDNWDDD
5. VWDDNWDED
6. VSEDNRDDD

(i) Calculate similarity scores between these sequences using an identity matrix (assume mismatch = -1, and match = 2). **(6marks)**

(ii) Make comparisons from the results obtained. **(2marks)**

d) Distinguish between an identifier and accession code (Accession number). **(2marks)**

e) Briefly explain the THREE main steps in clustal W program. **(6marks)**

f) Describe the bioinformatic Sequence Markup language (BSLM) Format. **(6marks)**

QUESTION TWO (20marks)

Use the given information below to solve the following questions.

BLOSUM 62 and PAM 250 substitution matrices

	A	R	N	D	C	Q	E	G	H	I	L	K	M	F	P	S	T	W	Y	V
A	4	-1	-2	-2	0	-1	-1	0	-2	-1	-1	-1	-1	-2	-1	1	0	-3	-2	0
R	-1	5	0	-2	-3	1	0	-2	0	-3	-2	2	-1	-3	-2	-1	-1	-3	-2	-3
N	-2	0	6	1	3	0	0	0	1	-3	-3	0	-2	-3	-2	1	0	-4	-2	-3
D	-2	-2	1	6	-3	0	2	-1	-1	-3	-4	-1	-3	-3	-1	0	-1	-4	-3	-3
C																				

You are given the following pair of sequences:

1. KAWSADV
2. KDWSAEV

1. KAWSADV
2. KYWSAEV

1. KDWSAEV
2. KYWSAEV

a) Calculate similarity scores between these sequences using:

   (i) Identify matrix (assume mismatch = -1, and match = 2)
   (ii) BLOSUM62
   (iii) PAM250

(15marks)

b) Make comparisons between the results obtained from BLOSUM62 and PAM250.
(5marks)

QUESTION THREE

a) Explain any SIX significances of the Human Genome project. **(12marks)**
b) Describe any FOUR bioinformatics tools you would use when performing multiple alignments analysis. **(8marks)**

QUESTION FOUR

Briefly discuss the following secondary protein sequence databases:

a) Prosite
b) Block
c) Interpro
d) Pfam
e) SMART

(20marks)

QUESTION FIVE

Explain the following basics local Alignment search tool (BLAST) programs:

(i) Blastp
(ii) Blastx
(iii) tBlastn
(iv) tBlastx
(v) Position specific iterative-Blast (PSI-Blast)

(20marks)