TECHNICAL UNIVERSITY OF MOMBASA

FACULTY OF APPLIED AND HEALTH SCIENCES

DEPARTMENT OF PURE & APPLIED SCIENCES

UNIVERSITY EXAMINATION FOR:

MSC IN BIOTECHNOLOGY

ABT 5106: ADVANCED BIOINFORMATICS

SPECIAL/ SUPPLEMENTARY EXAMINATIONS

SERIES: SEPTEMBER 2018

TIME: 3 HOURS

DATE: SEP 2018

Instructions to Candidates

You should have the following for this examination

-Answer Booklet, examination pass and student ID

This paper consists of **SIX** questions, each **25 marks**. Attempt any FOUR questions Choose instruction.

Do not write on the question paper.

Question ONE (25 marks)

a. Outline the limitations of bioinformatics. 8 marks

b. Explain the application of bioinformatics in the following fields;

i. Microbial genome applications 5 marks

ii. Comparative Studies 5 marks

iii. Health and Drug discovery 7 marks

Question TWO (25 marks)

a. Outline the factor to consider when designing primers. 8 marks

b. Describe any FIVE bioinformatic tools you would use to design primers. 10 marks

c. Distinguish between unigene and locus link. 7 marks

Question THREE (25 marks)

Explain the three primary nucleotide sequence databases. 25 marks

Question FOUR (25 marks)

a. Use the following substitution matrices to solve the following questions

BLOSUM 62

	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	0	-3	-3	-3	9	-3	-4	-3	-3	-1	-1	-3	-1	-2	-3	-1	-1	-2	-2	-1
Q	-1	1	0	0	-3	5	2	-2	0	-3	-2	1	0	-3	-1	0	-1	-2	-1	-2
E	-1	0	0	2	-4	2	5	-2	0	-3	-3	1	-2	-3	-1	0	-1	-3	-2	-2
G	0	-2	0	-1	-3	-2	-2	6	-2	-4	-4	-2	-3	-3	-2	0	-2	-2	-3	-3
H	-2	0	1	-1	-3	0	0	-2	8	-3	-3	-1	-2	-1	-2	-1	-2	-2	2	-3
I	-1	-3	-3	-3	-1	-3	-3	-4	-3	4	2	-3	1	0	-3	-2	-1	-3	-1	3
L	-1	-2	-3	-4	-1	-2	-3	-4	-3	2	4	-2	2	0	-3	-2	-1	-2	-1	1
K	-1	2	0	-1	-3	1	1	-2	-1	-3	-2	5	-1	-3	-1	0	-1	-3	-2	-2
M	-1	-1	-2	-3	-1	0	-2	-3	-2	1	2	-1	5	0	-2	-1	-1	-1	-1	1
F	-2	-3	-3	-3	-2	-3	-3	-3	-1	0	0	-3	0	6	-4	-2	-2	1	3	-1
P	-1	-2	-2	-1	-3	-1	-1	-2	-2	-3	-3	-1	-2	-4	7	-1	-1	-4	-3	-2
S	1	-1	1	0	-1	0	0	0	-1	-2	-2	0	-1	-2	-1	4	1	-3	-2	-2
T	0	-1	0	-1	-1	-1	-1	-2	-2	-1	-1	-1	-1	-2	-1	1	5	-2	-2	0
W	-3	-3	-4	-4	-2	-2	-3	-2	-2	-3	-2	-3	-1	1	-4	-3	-2	11	2	-3
Y	-2	-2	-2	-3	-2	-1	-2	-3	2	-1	-1	-2	-1	3	-3	-2	-2	2	7	-1
V	0	-3	-3	-3	-1	-2	-2	-3	-3	3	1	-2	1	-1	-2	-2	0	-3	-1	4

PAM250

	A	R	N	D	C	Q	E	G	H	I	L	K	M	F	P	S	T	W	Y	V
A	2	-2	0	0	-2	0	0	1	-1	-1	-2	-1	-1	-3	1	1	1	-6	-3	0
R	-2	6	0	-1	-4	1	-1	-3	2	-2	-3	3	0	-4	0	0	-1	2	-4	-2
N	0	0	2	2	-4	1	1	0	2	-2	-3	1	-2	-3	0	1	0	-4	-2	-2
D	0	-1	2	4	-5	2	3	1	1	-2	-4	0	-3	-6	-1	0	0	-7	-4	-2
C	-2	-4	-4	-5	12	-5	-5	-3	-3	-2	-6	-5	-5	-4	-3	0	-2	-8	0	-2
Q	0	1	1	2	-5	4	2	-1	3	-2	-2	1	-1	-5	0	-1	-1	-5	-4	-2
E	0	-1	1	3	-5	2	4	0	1	-2	-3	0	-2	-5	-1	0	0	-7	-4	-2
G	1	-3	0	1	-3	-1	0	5	-2	-3	-4	-2	-3	-5	0	1	0	-7	-5	-1
H	-1	2	2	1	-3	3	1	-2	6	-2	-2	0	-2	-2	0	-1	-1	-3	0	-2
I	-1	-2	-2	-2	-2	-2	-2	-3	-2	5	2	-2	2	1	-2	-1	0	-5	-1	4
L	-2	-3	-3	-4	-6	-2	-3	-4	-2	2	6	-3	4	2	-3	-3	-2	-2	-1	2
K	-1	3	1	0	-5	1	0	-2	0	-2	-3	5	0	-5	-1	0	0	-3	-4	-2
M	-1	0	-2	-3	-5	-1	-2	-3	-2	2	4	0	6	0	-2	-2	-1	-4	-2	2
F	-3	-4	-3	-6	-4	-5	-5	-5	-2	1	2	-5	0	9	-5	-3	-3	0	7	-1
P	1	0	0	-1	-3	0	-1	0	0	-2	-3	-1	-2	-5	6	1	0	-6	-5	-1
S	1	0	1	0	0	-1	0	1	-1	-1	-3	0	-2	-3	1	2	1	-2	-3	-1
T	1	-1	0	0	-2	-1	0	0	-1	0	-2	0	-1	-3	0	1	3	-5	-3	0
W	-6	2	-4	-7	-8	-5	-7	-7	-3	-5	-2	-3	-4	0	-6	-2	-5	17	0	-6
Y	-3	-4	-2	-4	0	-4	-4	-5	0	-1	-1	-4	-2	7	-5	-3	-3	0	10	-2
V	0	-2	-2	-2	-2	-2	-2	-1	-2	4	2	-2	2	-1	-1	-1	0	-6	-2	4

Given the following pairs of sequences below;

i. KYWSAVYA
ii. KKAWVDVA

i. DWSAEVKK
ii. AWSADVKY

Calculate similarity scores between these sequences using:

i. Identity matrix (assume match = 2, and mismatch = 1) 4 marks
ii. PAM250 matrix 4 marks

iii. BLOSUM 62 matrix 4 marks

b. Describe the needleman-Wunsch algorithm 10 marks

c. Distinguish between an identifier and accession code 3 marks

Question FIVE (25 marks)

a. Use the Standard Code for Information Interchange table below to solve the following.

	30	40	50	60	70	80	90	100	110	120
0		(	2	<	F	P	Z	d	n	x
1		)	3	=	G	Q	[	e	o	y
2		*	4	>	H	R	\	f	p	z
3	!	+	5	?	I	S	]	g	q	{
4	”	,	6	@	J	T	^	h	r	|
5	#	-	7	A	K	U	_	i	s	}
6	$	.	8	B	L	V		j	t	~
7	%	/	9	C	M	W	a	k	u	DEL
8	&	0	:	D	N	X	b	l	v	
9	’	1	;	E	O	Y	c	m	w	

Given characters ‘k’ and ‘Y’

Calculate in each case the corresponding Phred quality score based on

i. The fastq-sanger format. 6 marks

ii. The Solexa/Illumina read format. 6 marks

b. Describe the tBLASTn bioinfomatic tool 7 marks

c. Using an illustration, describe the position specific iterative-BLAST (PSI-BLAST) approach. 6 marks

Question SIX (25 marks)

a. Distinguish between MEGABLAST and BLASTn bioinformatic tools. 6 marks

b. Contrast Parsimony and Maximum likelihood tree building algorithms. 5 marks

c. Distinguish between ENZYME and REBASA databases. 14 marks