TECHNICAL UNIVERSITY OF **MOMBASA**

FACULTY OF APPLIED AND HEALTH SCIENCES
DEPARTMENT OF PURE & APPLIED SCIENCES
UNIVERSITY EXAMINATION FOR:
BMLS
AAB 4411: BIOINFORMATICS PAPER 2
SPECIAL/SUPPLEMENTARY EXAMINATION
SERIES: SEPTEMBER 2018
TIME: 2 HOURS
DATE: Pick Date Sep2018

Instructions to Candidates
You should have the following for this examination
Answer Booklet, examination pass and student ID
This paper consists of **FIVE** questions. Attemptquestion ONE (Compulsory) and any other TWO questions.
Do not write on the question paper.

Question ONE

a) Give the full meaning of the following abbreviations as used in Bioinformatics.

i. XML (1 mark)

ii. SAM (1 mark)

iii. ASN (1 mark)

b) You are given the following pairs of sequences:

i. DDBICEKDDATU
ii. DRBICEKADATM

i. CBOCADACTUMD
ii. CKECADAGTUUD

Calculate similarity scores between the pair of sequences using an identity matrix (assume mismatch=0, and match=1). (4 marks)

c) Distinguish between coding sequence and open reading frame. (4 marks)

d) Describe the use of the following bioinformatic tools.

i. Bl2seq (1 mark)

ii. Needle (2 marks)

iii. Water (2 marks)

e) Describe the FASTA file format. (5 marks)

f) Differentiate between MEGABLAST and Blastn bioinformatic programs. (5 marks)

g) Describe the progressive alignment principle in ClustalW. (4 marks)

Question TWO (25 marks)

a. Describe any FIVE bioinformatics tools you would use to perform restriction analysis of nucleotide sequences. (10 marks)

a. Explain tBlastx program. (10 marks)

Question THREE (25 marks)

a. Use the American 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 a character ‘W’, Calculate the corresponding Phred quality score based on the following file formats:

i. Fastq-solexa format. (4 marks)

ii. Fastq-illumina format. (3 marks)

b. Contrast Parsimony and Maximum likelihood tree building algorithms. (6 marks)

c. Describe the CATH database. (7 marks)

Question FOUR (25 marks)

a. Discuss the FSSP protein sequence databases. (10 marks)

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

Question FIVE

a. Use the BLOSUM 62 and PAM250 substitution matrices below 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 pairs of sequences below;

i. DWSDEVKA
ii. YWSDEVKA

i. DEVKDWSA
ii. DEKVDWSS

Calculate similarity scores between these sequences using:

i. PAM250 matrix (2 marks)

ii. BLOSUM 62 matrix (2 marks)

b. Outline EIGHT factors to consider when designing primers. (8 marks)

c. Explain the importance of performing Multiple Sequence Alignment. (8 marks)