

HW3 Alex Zhang

problem 1.

a)

	-	T	A	G	A
-	0	-2	-4	-6	-8
T	-2	1	-1	-3	-5
A	-4	-1	2	0	-2
C	-6	-3	0	1	-1
C	-8	-5	-2	-1	0
A	-10	-7	-4	-3	0
C	-12	-9	-6	-5	-2

b)

After tracing back the matrix, alignment that produce optimal value will be:

① T A C C A C
T A - G A -

② T A C C A C
T A G - A -

c)

	-	T	A	G	A
-	0	-5	-10	-15	-20
T	-5	2	-3	-8	-13
T	-10	-3	4	-1	-6
C	-15	-8	-1	-3	-8
C	-20	-13	-6	-8	-10
A	-25	-18	-11	-11	-6
C	-30	-23	-16	-16	-11

The same alignment is produced.

problem 2

a) The modification for local alignment is changing every negative entry into zero and find the relative maximum score in matrix instead of bottom right.

The relation is

$$a(i, j) = \max \begin{cases} a(i-1, j-1) + p(S(i), T(j)) \\ a(i, j-1) + p(-, T(j)) \\ a(i-1, j) + p(S(i), -) \\ 0 \end{cases}$$

and match is 1, mismatch is -1, gap is -2
(Obtained in Dr. Khuri's lecture).

b) From slide 33, the local alignment is gained by the sequence in grey. which is

Local Alignments

Therefore, the optimal local alignment will be

A C G G A G G
A C G T A G G

		G	A	A	C	G	T	A	G	G	C	G	T	A	T
A	0	0	1	1	0	0	0	1	0	0	0	0	0	1	0
T	0	0	0	0	0	0	1	0	0	0	0	0	1	0	2
A	0	0	1	1	0	0	0	2	0	0	0	0	0	2	0
C	0	0	0	0	2	0	0	0	1	0	1	0	0	0	1
T	0	0	0	0	0	1	1	0	0	0	0	0	1	0	1
A	0	0	1	1	0	0	0	2	0	0	0	0	0	2	0
C	0	0	0	0	2	0	0	0	0	0	1	0	0	0	0
G	0	1	0	0	0	3	1	0	1	1	0	2	0	0	0
G	0	1	0	0	0	1	2	0	0	2	0	1	1	0	0
A	0	0	2	1	0	0	0	1	1	0	0	0	0	2	0
G	0	1	0	0	0	1	0	0	2	0	1	0	0	0	0
G	0	1	0	0	0	1	0	0	1	3	1	0	0	0	0
G	0	1	0	0	0	1	0	0	1	2	4	4	2	0	0

Thus, the best local alignment achieved from the above Dynamic Programming is:

A C G G A G G
A C G T A G G

problem 3

a)

-	-	M	D	R	I	V	E	R
-	0	-12	-24	-36	-48	-60	-72	-84
M	↑ -12	6	-6	-18	-30	-42	-54	-66
I	↑ -24	↑ -6	4	-8	-13	-25	-37	-49
S	↑ -36	↑ -18	↑ -6	4	-8	-14	-25	-37
L	↑ -48	↑ -30	↑ -18	↑ -8	6	-6	-17	-28
Q	↑ -60	↑ -42	↑ -28	↑ -17	↑ -6	4	-4	-16

The global alignments will be

- ① M D R I V E R ② M D R I V E R
 M - - I S L Q M I S - L Q -

- ③ M D R I V E R
 M I S L - Q -

b)

-	-	M	D	R	I	V	E	R
-	0	0	0	0	0	0	0	0
M	0	6	0	0	2	2	0	0
I	0	2	4	0	5	6	0	0
S	0	0	0	4	0	4	6	0
L	0	4	0	0	6	2	1	3
Q	0	0	6	1	0	4	4	2

The local alignment will be

① - MD
SLQ

② M
M

(3) - MDPI
- MISL

(4) RIV
-MI

⑤ RIVE
- MIS

Extra credit:

B)

- M D R I V E R

$$\begin{array}{cccccccccccc}
 & & \leftarrow & \nwarrow & \nwarrow & \nwarrow & \nwarrow & \nwarrow & \nwarrow & \nwarrow & \nwarrow & \\
 - & 0 & -12 & -16 & -20 & -24 & -28 & -32 & -36 & & & \\
 M \uparrow & & \nwarrow & 6 & -6 & -10 & -14 & -18 & -22 & -26 & & \\
 & -12 & & & & & & & & & & \\
 I \uparrow & & \uparrow & \nearrow & 4 & -8 & -5 & -10 & -20 & -24 & & \\
 & -16 & & & & & & & & & & \\
 S \uparrow & & \uparrow & \nearrow & \nearrow & 4 & -9 & -6 & -10 & -20 & & \\
 & -20 & & & & & & & & & & \\
 L \uparrow & & \uparrow & \nearrow & -14 & -8 & 6 & -6 & -9 & -13 & & \\
 & -24 & & & & & & & & & & \\
 Q \uparrow & & \uparrow & \nearrow & \nearrow & \nearrow & \nearrow & \nearrow & \nearrow & \nearrow & & \\
 & -28 & & & & & & & & & & \\
 & -18 & & & & & & & & & & \\
 & -12 & & & & & & & & & & \\
 & -6 & & & & & & & & & & \\
 & -4 & & & & & & & & & & \\
 & -4 & & & & & & & & & & \\
 & -8 & & & & & & & & & &
 \end{array}$$

The global alignment will be:

MDRIVER

$$M - I \leq Q$$

The local alignment will be

	-	M	D	R	I	VER
-	0	0	0	0	0	0
M	0	6	0	0	2	0
I	0	2	4	0	5	6
S	0	0	0	4	0	4
L	0	4	0	0	6	2
Q	0	0	6	1	0	4

which is the same as previous one

- | | | | |
|----------------|----------|------------------|--------------|
| ① -MD
SLQ | ② M
M | ③ -MDRI
-MISL | ④ RIV
-MI |
| ⑤ RIVE
-MIS | | | |

problem 4

1) The substitutions have no effect on first five amino acids. they are all the same. we can conclude that this is a. Synonymous substitution between DNAs.

2)

There are more transitions than transversions

3)

The amino acids are different in each column. but they still share the same physicochemical properties, with the mutations

4)

a)

From column 38 to 46, all nucleotides have transitions not transversion. we can create gaps in order for better alignments. if not gaps. this may create transversions which will decrease the score: Also. with transversion, the protein created will have different physicochemical property.

b)

If no gaps, there will exist both G & C, T in the same column, which cause transversions. Also A and T will in the same column. causing transversion. The physicochemical property of amino acid will differ.