

Question 1.

For Smith-Waterman local alignment algorithm, recurrence relation is $F(i,j) = \max [0, F(i,j-1) + \text{gap score}, F(i-1,j) + \text{gap score}, F(i-1,j-1) + \text{match or mismatch score}]$ where the F is the score matrix.

With the above information, matrix[1,5] where the first matching is encountered has score 7. This obtained by matrix[0,4] + match score. Then **match score is 7**.

Gap penalty can be find, if the matrix[1,6] is viewed. matrix[1,5] + gap score = 3. matrix[1,5] is 7 and it can be seen **gap score is -4**.

If matrix[2,6] is viewed, mismatch score can be find since letter A and letter E mismatch. matrix[1,5] + mismatch score = matrix[2,6]. matrix[1,5] is 7 then **mismatch score -6**.

Score is 24 as it can be seen on the table as a maximum value.

An alignment of two sequences:

M	A	G	E	D
M	A	-	E	D
7	7	-4	7	7

Score Matrix

	-	M	I	M	A	G	E	D	I	L
-	0	0	0	0	0	0	0	0	0	0
G	0	0	0	0	0	7	3	0	0	0
A	0	0	0	0	7	3	1	0	0	0
M	0	7	3	7	3	1	0	0	0	0
A	0	3	1	3	14	10	6	2	0	0
E	0	0	0	0	10	8	17	13	9	5
D	0	0	0	0	6	4	13	24	20	16
K	0	0	0	0	2	0	9	20	18	14

Question 2.

Score Matrix

	-	M	C	G	M	G	C	M	E	L
-	0	-4	-8	-12	-16	-20	-24	-28	-32	-36
G	-4	-3	-7	-2	-6	-10	-14	-18	-22	-26
M	-8	1	-3	-6	3	-1	-5	-9	-13	-17
C	-12	-3	10	6	2	0	8	4	0	-4
M	-16	-7	6	7	11	7	4	13	9	5
E	-20	-11	2	4	7	9	5	9	18	14
D	-24	-15	-2	1	3	6	6	5	14	10
L	-28	-19	-6	-3	3	2	5	8	10	18

Traceback Matrix

	-	M	C	G	M	G	C	M	E	L
-	0	left	left	-12	-16	-20	-24	-28	-32	-36
G	-4	opleft	left/ opleft	opleft	left	left/ opleft	left	left	left	left
M	-8	opleft	left	top	opleft	left	left	left/ opleft	left	left
C	-12	top	opleft	left	left	opleft	opleft	left	left	left
M	-16	opleft	top	opleft	opleft	left	top	opleft	left	left
E	-20	top	top	opleft	top	opleft	left	top	opleft	left
D	-24	top	top	opleft	top	opleft	opleft	top	top	left / top
L	-28	top	top	opleft	opleft	top	opleft	opleft	top	opleft

Each number in the table is obtained by the previous cells. Recurrence relation is like the local assignment without zero. So traceback matrix represents the value is obtained from which cell.

Best alignment of two sequences:

M	C	G	M	G	C	M	E	_	L
_	_	 	 	_	 	 	 	_	
G	M	G	C	M	E	D	L		
-4	-4	6	5	-4	9	5	5	-4	4