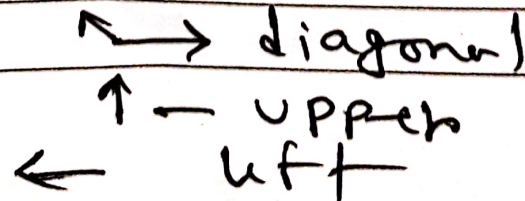


#Needleman-Wunseh Algorithm for  
global alignment.steps:

1. Add a gap penalty to all cells
2. For a particular cell, (initialization)  
add gap penalty with—
  - (i) Horizontally (left adjacent)
  - (ii) Vertically (upper adjacent)
- ③ Now, considering the the diagonal checking, check whether ~~match~~ the nucleotides match or mismatch.
- (ii) add the value of match or mismatch with the immediate diagonal cell.
- ③ find maximum among (i), (ii), and (iii) for the cell.
- ④ for each calculation mark with an arrow from which you have found the maximum value. the arrows might have  

  - ↖ diagonal
  - ↑ upper
  - ← left

⑤

1	0
3	5

exactly match

3	0
3	2

mismatch

-3	0
3	5

or

3	0
3	5

Gap

(1,3) matrix filling  
(9,5) trace back

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

Trace back

A T G C T } motif  
 A - A C T }  
 →



Perform local alignment by applying Smith-Waterman algorithm on the following sequence -

RS = AGCGTAG  
LS = CTCGTC

Here,  
Match = +1  
Mismatch = -1  
Gap = -2

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

Alignment Score: 3

Local Alignment = CGT