

1. What is global alignment?

Global alignment is an alignment of every amino acid or nucleotide in the sequence

2. What is local alignment?

Local alignment is also alignment of every amino acid or nucleotide in the sequence, but it doesn't include the entire sequence, it can be achieved by aligning similar portions and ignoring the rest of the sequence

3. What is the difference between local and global alignment?

The main difference is in global alignment we select the entire sequence and do the aligning, but in local alignment the entire sequence isn't required, some parts of the sequence can be similar and can give more precision when the overall score is calculated.

4) match score = +5  
mismatch = -4  
gap = -4

a) A HCTTG GCAT

	-	A	C	T	T	G
-	0	-4	-8	-12	-16	-20
G	-4	5	-1	-5	-9	-11
C	-8	-1	5	-3	-7	-11
T	-12	-5	-3	5	-1	-5
A	-20	-11	-7	-1	4	7

HCTTG  
GCTTA  
optimal alignment  
local

B) GCTGG A HGGCAT TTAGCHCG

	-	A	A	G	G	C	A	T
-	0	-4	-8	-12	-16	-20	-24	-28
T	-4	5	-1	-5	-9	-13	-17	-21
T	-8	-1	5	-5	-9	-13	-17	-21
A	-12	-5	-1	5	-9	-13	-17	-21
G	-16	-9	-5	5	5	-9	-13	-17
C	-20	-13	-9	-5	-9	5	-9	-13
A	-24	-17	-13	-9	-13	-9	5	-9
C	-28	-21	-17	-13	-17	-13	-9	5
G	-32	-25	-21	-17	-21	-17	-13	-9

A-HGGCAT- optimal  
TTAG-CHCG local alignment

3) match score = +5  
 mismatch = -4  
 gap = -4

B)

	-	G	C	T	G	G	A	A	G	G	C	A	T
-	0	-4	-8	-12	-16	-20	-24	-28	-32	-36	-40	-44	-48
G	-4	5	-1	-5	5	5	-1	-5	5	5	-1	-5	-9
C	-8	-1	5	-1	-5	-9	5	5	-1	-5	5	5	-1
A	-12	-5	-1	5	-1	-5	5	5	-1	-5	5	5	-1
G	-16	5	-1	-5	5	5	-1	-5	5	5	-1	-5	-9
A	-20	-1	-5	5	-1	-5	5	5	-1	-5	5	5	-1
G	-24	5	-1	-5	5	5	-1	-5	5	5	-1	-5	-9
C	-28	-1	5	-1	-5	-9	5	5	-1	-5	5	5	-1
A	-32	-5	-1	5	-1	-5	5	5	-1	-5	5	5	-1
C	-36	-1	5	-1	-5	-9	5	5	-1	-5	5	5	-1
G	-40	5	-1	-5	5	5	-1	-5	5	5	-1	-5	-9

GCTGGAAAGCAT -  
 GCA G - A - G - C A C G

optimal alignment

3) match score = +5  
 mismatch = -4  
 gap = -4

a)

	-	A	A	C	T	T	G	G	C	A	T
-	0	-4	-8	-12	-16	-20	-24	-28	-32	-36	-40
C	-4	-4	-8	-3	-7	-11	-15	-19	-23	-27	-31
G	-8	-8	-12	-7	-11	-15	-6	-10	-14	-18	-22
C	-12	-12	-16	-2	-11	-15	-10	-14	-5	-9	-13
T	-16	-16	-20	-11	-2	-6	-10	-14	-9	-9	-4
T	-20	-20	-24	-15	-6	+3	-1	-5	-9	-13	-4
A	-24	-15	-15	-19	-10	-1	-5	-9	-9	-4	-8
G	-28	-19	-19	-23	-14	-5	+4	0	-4	-8	-9

A A C T T G G C A T

~~TTG~~  
~~TTG~~

optimal alignment

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