

Global Pairwise Sequence Alignment

Input :- Two sequences X & Y

Output :- Alignment of X & Y

Eg :- X = GTAC, Y = ACAGC, eg. Align = $\begin{array}{c} -GTAC \\ ACAGC \end{array} \mid \begin{array}{c} G-TAC \\ ACAGC \end{array} \mid \begin{array}{c} G--TAC \\ ACA-GC \end{array}$

Conditions (feasibility)

- Both have to be of same length
- A '-' can not map with '-' in the other
- Removing '-' should give the original sequences back.

Calculating optimal ones (Scoring Matrix)

	A	C	G	T	-
A	10	4	4	4	-4
C	4	10	4	4	-4
G	4	4	10	4	-4
T	4	4	4	10	-4
-	-4	-4	-4	-4	10

$$\begin{array}{r} X = G-TAC \\ Y = ACAGC \\ \hline 4 \quad -4 \quad 4 \quad 4 \quad 10 \\ \hline \downarrow \\ \text{Score} = 18 \end{array}$$

$$\begin{array}{r} X = G--TAC \\ Y = ACA-GC \\ \hline 4 \quad -4 \quad -4 \quad -4 \quad 10 \\ \hline \downarrow \\ \text{Score} = 6 \end{array}$$

Local Pairwise Sequence Alignment

X = - - - (AG - A) - - - - -
Y = T T T (A G G A) T T T T T

10 10 -10 10

↓
20 local score

⇒ -80 global score

Looking at every possible substring of X, every possible substring of Y, align them globally. And now from every possible combination of substring from these two strings, finding the one that gives us the highest possible score.

→ Optimal Alignment is the one with highest score.

↳ the optimal alignment "Score" is always unique.

↳ There may be more alignments with the same score though.

Eg. →

$$\begin{array}{r} A G - A \\ A G G A \\ \hline \text{Score} = 20 \end{array}$$

$$\begin{array}{r} A - G A \\ A G G A \\ \hline \text{Score} = 20 \end{array}$$

Different alignment but same score.

in such case pick an arbitrary alignment.
