Sequence Alignment Report Mohab Olayan

Time Analysis :The time analysis of my approach is O(mn) where m and n are length of x and y.

Description: My approach is that to iterate through each position and check for score if i matched or inserted gap in X or inserted gap in Y
And then store the maximum of the scores in my tmp 2d array so in this way i know where to add gap or keep it the same pair and get the best alignment score for each position.
Then after finishing filling the array i traceback the tmp to reconstruct my alignment and get the score of the alignment and display both.

Code: I created 2 methods to implement my approach Alignment and GetIndex .Alignment creates the tmp and fills it using the help of GetIndex and reconstructs the Sequence also using the help if get index. GetIndex takes as parameter char returns the index of the char in score matrix.

Conclusion:In conclusion i used Dynamic programming to get the best alignment between two gene sequences according to the score matrix.