CSEN703:ANALYSIS AND DESIGN OF ALGORITHMS

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I solved this problem using dynamic programing , we start by creating a dynamic matrix to store the dynamic programing values which will be the size of (n+1)x(m+1): N being the size of the first gene sequence and m being the size of the second gene sequence ,then i iterated through each cell of the dynamic matrix and calculate the score for the 3 possible actions : delete , match , insert then i find the maximum of the 3 and put it in the dynamic matrix , and then during the traceback, we go from the bottom-right to the top-left of the DP matrix. We choose the direction at each step based on the highest score, we add characters to the aligned sequences alignx and aligny .The final aligned sequences alignmentx and alignmenty are printed.In summary, the code uses dynamic programming to compute the highest-scoring alignment of two gene sequences based on a given scoring matrix. The traceback then reconstructs the aligned sequences, and the results are printed.

Time Analysis : this code has time complexity of O(NxM) because of the nested loops where N is the size of the first gene sequence and m is the size of the second gene

Inputs
N = “TCCCAGTTATGTCAGGGGACACGAGCATGCAGAGAC”
M = “AATTGCCGCCGTCGTTTTCAGCAGTTATGTCAGATC”

Outputs
Gene X= “---TCCCAGTTATGTCAGGGGACACG-AG-CATG-CAGAGAC”
Gene Y= “ AATTGCC-G-C-CGTC-GTTTTCA-GCAGTTATGTCAGAT-C”