Assignment 4: Dynamic Programming, Greedy Algorithms

Abstract:

I have implemented the bottom-up version of the Smith-Waterman algorithm given by the recursive definition of the function 'M' (as seen on the slides).

I have implemented the top-down with memoization version of the Smith-Waterman algorithm given by the recursive definition of the function 'M'.

Also, I, then recursively print the matching sequence that is derived from both 'X' and 'Y'. I have found the maximum alignment for a specific value of 'X' and 'Y' by using the Smith-Waterman algorithm.

Result:

A. The maximum alignment for X = dcdcbacbbb and Y= acdccabdbb by using the Smith-Waterman algorithm.

Bottom-up SW

Top-down SW

Discussion:

a. Bottom-up version of the Smith-Waterman algorithm

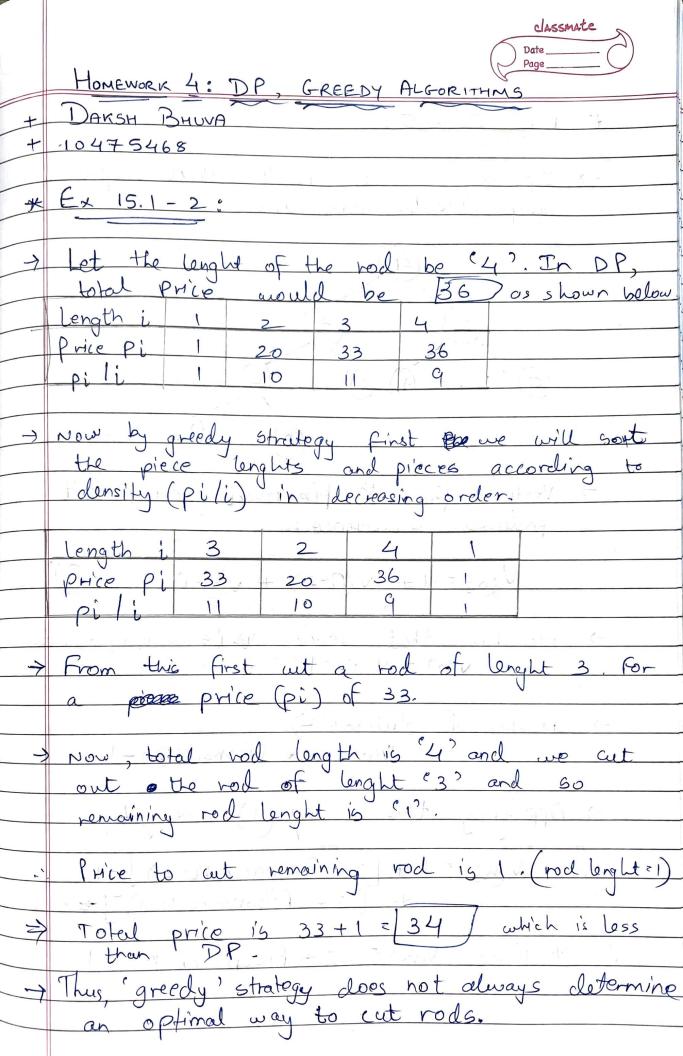
- I have implemented the pseudo-code as given on the lecture slides for bottom-up version with some minor changes.
- The time-complexity for Smith-Waterman algorithm is O (n x m) when n \neq m, and O (n²) or O (m²) when n = m.

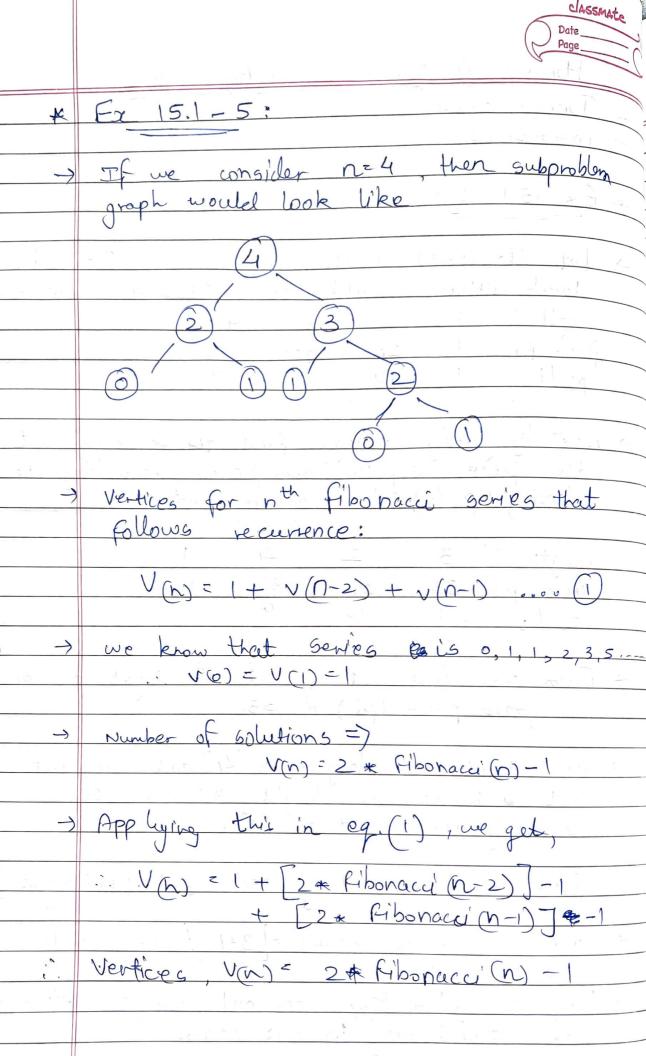
b. Top-down with memoization version of the Smith-Waterman algorithm

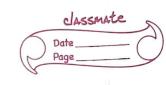
- I have implemented the top-down version using the Auxiliary recursive function for calling them.
- The time-complexity for Smith-Waterman algorithm is O (n x m) when n \neq m, and O (n²) or O (m²) when n = m.

Conclusion:

Thus, the Smith-Waterman algorithm is Dynamic Programming algorithm that performs a local sequence alignment. Its practical application is to determine similar regions between two nucleotide or protein sequences.







The 1000 number of edges that 1000000 .. E(n) = 2 + E(n-1) + E(n-2) - Similarly for portion. E(0) = 0 Applying it in eq. (2). Enj = 2 * Fibonacci (n) - 2 > Algorithm :-· Algo (FIBONACCI (X)) (1) let F[0... x+1) be an array. (2) F[0]=0 and F[1]=1 (3) for (2) 5 ix x) do 1 (4) Ri] = F(i-1] + F(i-2) (5) return F(x).

