

CMPS 102 — Fall 2018 — Homework 4

"I have read and agree to the collaboration policy." - Kevin Wang

Collaborators: *None*

Solution to Problem 2: DNA

2 DNA sequences $S = \{s_1, s_2, \dots, s_i, \dots, s_m\}$ and $T = \{t_1, t_2, \dots, t_j, \dots, t_n\}$ have lengths m and n respectively.

Let LCS be the longest common sub-sequence.

$LCS[i, j]$ is the length of the largest common sub-sequence, LCS , shared by two sequences of sizes i and j .

Base Case: An empty sequence does not share a common sub-sequence.

$$LCS[i, 0] = 0 \text{ and } LCS[0, j] = 0$$

Case 1: $s_i = t_j$; the element is a part of the LCS .

$$LCS[i, j] = 1 + LCS[i - 1, j - 1]$$

Case 2: $s_i \neq t_j$; we ignore one of the elements.

$$LCS[i, j] = \max(LCS[i - 1, j], LCS[i, j - 1])$$

Therefore, the LCS of S and T has length $LCS[m][n]$. We can then walk back through the matrix to find an LCS .

Continued...

Algorithm 1 Finds the *LCS* of two sequences *S* and *T* with sizes *m* and *n*, respectively

LCS (*m*, *n*):

Let $LCS[m][n]$ be the sub-sequence size matrix

for *i* = 0 to *m* **do**

for *j* = 0 to *n* **do**

if *i* = 0 or *j* = 0 **then**

$LCS[i][j] = 0$

else if $s_i = t_j$ **then**

$LCS[i][j] = LCS[i - 1][j - 1] + 1$

else

$LCS[i][j] = \max(LCS[i - 1][j] , LCS[i][j - 1])$

end if

end for

end for

$LCS[m][n]$ is the length of the *LCS*

Let *LCS* be an empty sub-sequence

Let *i* = *m* and *j* = *n*

while *i* > 0 and *j* > 0 **do**

if $s_i = t_j$ **then**

$s_i :: LCS$

$i --, j --$

else if $LCS[i - 1][j] \geq LCS[i][j - 1]$ **then**

 Using $LCS[i - 1][j] > LCS[i][j - 1]$ can return another different *LCS*

$i --$

else

$j --$

end if

end while

Time Complexity: $O(mn)$

The 2 for-loops iterate *m* and *n* times, respectively, taking time $O(mn)$. Iterating back through the matrix to find the elements of the *LCS* takes $O(m + n)$. Total time used is $O(mn + m + n)$.

Space Complexity: $O(mn)$

The *LCS* matrix takes size $O(mn)$. The *LCS* sequence, takes (at most) $O(\max(m, n))$. Total space used is $O(mn + \max(m, n))$.