Longest common subsequence (LCS): Biological afflications

Often need to compare the DNA of two (or more) different organisms. A strand of DNA consists of a string of molecules called bases. We formalize this last notion of similarity as the longest-common-subsequence problem. A subsequence of a given sequence is just the given sequence of zero or more elements lest out.

- Common subsequence: Z is said to be common subsequence to both X & Y.

EX

$$X = (A, B, B, A, B, B)$$

$$Y = (B, A, A, B, A, A)$$

$$Y = (B, A, A, B, A, A)$$

$$Y = (A, A) \cdot (CS) = (A, A) \cdot (CS)$$

$$CS_1 = (A, A), CS_2 = (B, B, B) \times, CS_3 = (A)$$

- Longest common subsequence: It's a longest common subsequence.

  Bubsequence from all the available common subsequence.
- · This section shows how to efficiently solve the LCS problem using dynamic programming.

In a boute-force approach to solving the LCS problem, we should enumerate all subsequences of X and check each subsequence to see whether it is also a subsequence of y, keeping track of the longest subsequence we find. Each subsequence of X corresponds to a subset of the indices {1,2,--, m} of X. Because X has 2m subsequences, this approach requires exponential time.

## -> Recursive solution:

$$C[i,j] = \begin{cases} 0 & \text{if } i = 0 \text{ of } j = 0, \\ C[i-1,j-1]+1 & \text{if } i,j \neq 0 \text{ for } x_i = y_j, \\ \max(c[i,j-1],c[i-1,j]) & \text{if } i,j \neq 0 \text{ for } x_i \neq y_i, \end{cases}$$

Procedure LCS-Length takes two sequence  $X = \{x_1, x_2, ---- x_m\}$  and  $Y = \{y_1, y_2, ---- y_n\}$  as imputs. It stores the C[i,1] vaue in a table C[o---m, o--n], and it computes the entries in your major order. The procedure also maintains the table b[i--m, i--n] to help us construct an optimal solution.

1. m = X. length

2. n = Y. length

3. Let b[1-m,1-n] and c[0-m,0-n] be new tables

4. For i= 1 to m

5. c[i, 0] = 0

6. por 1= 0 ton

7. ([01]) =0

11. If 
$$xi == y_j$$

12. 
$$C[i,j] = C[i-1,j-1]+1$$

15. 
$$c[i,j] = c[i-1,j]$$

We encounted the elements of this LCS in reverse order with this method. The following recursive procedure print out an LCS of X \$ 2 y in proper, forward order.

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0	ti	0	To		0	10		0	1	0	0	
1	A	0	0	1	0	0		1	1	1	1	
2	B	0	7	17	-	1	1	1	1.	9	2	
3	C	0	1	1	1	21	1:	24	2		2	
4	B	0	1	1		2	1:	2	3	7	3	
5	D	0	1	2		2	:	2	3	1	3	-
6	A	0	1	2		2		3 /	3		41	
7	B	0	1	2		2	-	3/	4		41	
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2	1	1	TA	1	21	1
-	11	1	1	1.	-	10
4	1	11	1	11	40	12
5	1	K	K	1	100	1
6	1	1	1	7	1	K
		,	-	,		1
7	7	1	11	1/	MA	
	-	-		San Charles		

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C[3,5] = max(c[2,5], c[3,4]) \Rightarrow 2
C[316] = max (c[216], c[316]) > 2
                                                             (5)
C[411] = c[310]+1 > 0+1 > 1
C[4,2] = max(C[3,2], C[4,1]) =1
C[413] = \max(C[313], C[412]) \Rightarrow 2
c[4,4] = max (c[3,4], c[4,3]) →2
c[415] = c[3,4]+1 ⇒ 2+1 ⇒3
C[4,6] = \max(C[316], C[415]) \Rightarrow 3
c[5,1] = max(c[4,1], c[5,0]) =1
c[5,2] = c[4,1]+1 ⇒ 2
c[5,3] = max(c[4,3], c[5,2]) ⇒2
c[5,4] = max(c[4,4], c[5,3]) =>2
c[5,5] = max(c[4,5], c[5,4]) =>3
c[5,6] = max (c[4,6], c[5,5]) =>3
c[6,1] = max (c[5,1], c[6,0]) ⇒1
C[6,2] = max (c[5,2], c[6,1]) => 2
c(6,3) = max (c[5,3], c[6,2]) ⇒2
C[6,4] = C[5,3]+1 => 2+1 => 3
c[6,5] = max[c[5,5], c[6,4]) => 3
C[6,6] = c[5,5]+1 ⇒ 3+1 ⇒ 4
C[7,1] = C[6,0]+1 > 0+1 >1
c[7,2] = max (c[6,2], c[7,1]) ⇒ 2
c[713] = max (c[6,3], c[7,2]) ⇒2
c[7,4] = max(c[6,4], c[713]) =>2
c[715] = c[6,4]+1 ⇒ 3+1 ⇒ 4
c[716] = max(c[6,6], c[7,5]) ⇒ 4
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TC = # 08 distinct function calls = m+n > 0(m+n)