More Pynamic Programming Tuesday, November 6, 2018 5:26 PM

1) DNA Matching

A DUA moleculu can be thought of as a long string over alphabet & +, T, Ca } (length · ~ o(10"))

A labor-intensive and ERRON-PRONE process to sequence DNA

KANTC

LONKEST COMMON SUBSEQUENCE PROBLEM

INPUT: two strongs x[0..n-1], 4[0..m-1]

OUTPUT: the length of a longest common subsequence of X, Y

Def: it subsequence 5 of a string X is obtained by remaining a subset of charaders in X.

Et . X = ABCBDAB Suborquences: ALDAB BDA

ABCBDAB

A subsequence is NOT a substring, which must be a single black

Def. Common subsequence X = A B C 3 B B

BDAB

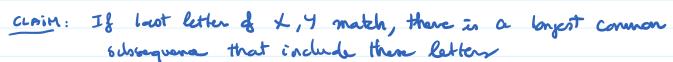
y = 00 C ABA

BCAB

A DYDAMIC PROGLAMMING SOLUTION

X =

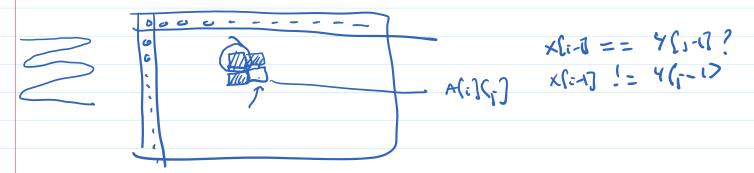
CLAIM: If lost letter of X, Y match, there is a longit common



Cure 2: last letters ab not match



Subproblems
$$f(i)$$
 = light of longest common subsequences of $\chi(0...i-1)$ and $\gamma(0...j-1)$

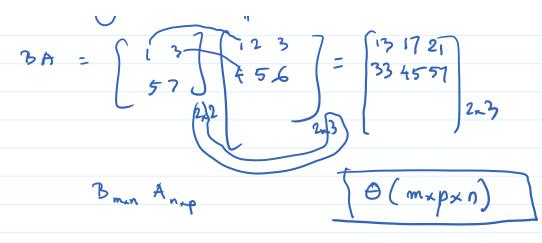


E. . X= ABCBDAB Y=DDCABA

					1			1		
,			A	ъ	C	Ъ	D	~	ъ	
		0	(6 M	0	0	0	0	0	٥	
	В	1011	0	11		1	1	1	١	
	D	6	0	1K	1	1	2	2	2	
					m	2/	_ 0 0	0	2	\vdash

-		UII		• /	•		•		•	
	D	6	0	1K	1	١	2	2	2	
	C	0	0		246	-26	- 2R	2	2	
	K	0	1	(20	2	2	30	3	
	77	0	1	2	2	34	-3 N	3	4	
	A	0	1	2	2	3	3	4 €	(4))
	1~									

Matrix
$$A = \begin{bmatrix} 1 & 2 & 3 \\ 4 & 5 & 6 \end{bmatrix}_{2 \times 3} B = \begin{bmatrix} 1 & 3 \\ 5 & 7 \end{bmatrix}_{2 \times 2}$$



Output. the least number of integer multiplications required to compute this product of motrices.

EX. MIOTRO MIOSES HEREO

100,5,50 = 25,000 10×100×20 =20,000 (15,000)

M. M. X Subproblens . (M, M2) X M2 M4 M5

> Slillil = lost anner for multiphyon M: -- M.

Bare cares 5(i)(i) = 0

K KI

