In normal implementation, Scm, n) can Sind one of optimal alignment. How to Sind out all of optimal alignments ?:

For Sinding all possible optimal alignments, we can use the approach of Needlman-

Week 7 410821316 養養子

Wunsch Algorithm:

$$s1 = sub1 + e1$$
,  $sa = sub2 + ea$ 

4 condition

1CS (S1, S2) =

max (10s(sub1, s2), 10s(s1, sub2), 10s(sub1, sub2)),

when e1 ≠ e2

LCS(sub1, sub2) + e1, when e1 = e2

Recursive Function

 $LCS(s1, s2) = \emptyset$ , when  $s1 \neq \emptyset$  or  $s2 \neq \emptyset$  initial

You can form a list using the algorithm. Within the forming progress, LCS might come from top, left, or top-left, store all the possible situation. In the tracing pack, traverse all of the possibilities and get all of the lCS, or optimal alignments.

How many optimal alignment may exist ? Please construct a set of input to explain your answer:

Input: ABCBJAB, BDCABA

Output: BCAB, BCBA, BDAB

3) Three optimal alignments exist.

Suppose both & and B are very long, that all m×n soores in we con't maintain Please find the way which only caches n values: Two-dimensional array length Itiliji, means first (i) elements of s1 and first (j) elements of S2. In order to reduce the cost of memory space, we have to improve the way we the list. For sorming a list, we only need the upper black, lefter block and the left-upper block. For calculation, we set to be from lest to right, then top to bottom. By doing so, we only need one array (upper now) and a single variable (lost-upper block), and its space complexity can be improved to  $O(\min(N, M))$ .

N and M to be the length of the sequence

Analyze space complexity, time complexity in best case and worst case in 0.1 and 0.2:

Time Complexity for Q1:

D(N×M)

N and M to be the sequence length \*

Space Complexity for Q1:

D(N×M)

N and M to be the sequence length \*

Time Complexity for Q2:

D (N×M)

N and M to be the sequence length \*

Space Complexity for Q2:

D(N×M)

N and M to be the sequence length \*