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**Week 7: Sequence Alignment**

The DNA sequence alignment is a longest common subsequence problem which accepts multiple answers. Given two DNA sequences in the form of strings, a longest common subsequence is required. Given that all the subsequences with the same maximum length are required, the strings must be analyzed both from start to end.

**Problem:**

The input file contains several test cases with a blank line between two consecutive inputs. The strings are at most 300 characters-long.

For each test case, print all the longest common sequences, one per line, in lexicographical order. If there isn't any common sequence between the two strings, just print: 'No common sequence.' Print a blank line between the output of consecutive datasets.

**Code:**

Text

Description automatically generated

**Discussion:**

Again, Dynamic programming is used to solve the problem. An array of size n\*m is created, n being the length of one string and m the length of the other. The array is traversed from start to end giving the value of 1 to the first common character found. If another common character follows this one then the value of it +1 is given to that place in the array. The variable next is a pointer so as it is updated then the place that’s being analyzed in the array is updated as well. The array contains the maximum length at that point. A Set of results is created because the results have to be printed in order, a set is by default sorted. If a new maximum length is found then the set is cleared and the new solution is added to the result array.

Time: O(n\*m)

Space: O(n\*m)

**Result:**

A picture containing logo

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