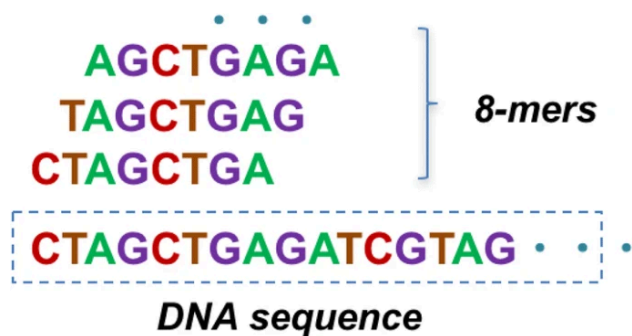


CSE 208  
Online 4 (Hashing)  
Section B  
Time: 20 minutes

Given a DNA sequence, find out the counts of all unique k-mers found in it. A DNA sequence is a string of nucleotides represented by the letters A (adenine), T (thymine), C (cytosine), and G (guanine). A k-mer is a substring of length k from a given DNA sequence. For instance, if k is 3, the k-mers from the sequence "ATCGATCGATCG" would be "ATC", "TCG", "CGA", "GAT", "ATC", "TCG", "CGA", "GAT", "ATC", "TCG". The value of k can be any positive integer. The k-mer count refers to the number of occurrences of each unique k-mer in the DNA sequence. For example, if we have the sequence "ATCGATCGATCG" and we are interested in 3-mers, the k-mer counts would be: "ATC": 3, "TCG": 3, "CGA": 3, "GAT": 3.

The run-time complexity of your solution program should be  $O(kn)$ .



\*\*

Input

The first line will contain two inputs  $l$  ( $1 \leq l \leq 100$ ) and  $k$  ( $1 \leq k \leq 100$ ;  $k \leq n$ ), where  $l$  is the length of the DNA sequence and  $k$  is the length of the k-mer substrings we want to count.

The second line contains the DNA sequence. The DNA sequences will be a string of length  $l$  and will have characters A, C, T and G.

Output

Your program should print all the unique k-mers and their counts in separate lines. The k-mers and counts should be separated by spaces. The k-mers can be printed in any order.

Sample Input/Output

Input	Output
5 3 ATGCA	ATG 1 TGC 1 GCA 1
12 3 ATCGATCGATCG	ATC 3 TCG 3 CGA 3 GAT 3

\*\* Image Source: <https://doi.org/10.1007/s12539-019-00348-5>