Create K-mers

Sahithi is a very picky girl and almost wants things to be very precise, be it her food choices or everyday activities. Her friends are fed up with her and decide to kill her. They call her to the BBC canteen at 3am and kill her. Kunal and Shaanjeet being good friends of sahithi, decide to solve the murder mystery. They go to crime scene and find a hair strand and reach to conclusion that it doesn't belong to sahithi. The decide to extract the DNA from hair strand and compare it with college DNA database. Help Kunal and Shaanjeet (though they are bonds and don't really need help) solve the following subtasks.

DNA sequence consists of base pairs namely adenine - A, guanine - G, cytosine - C, thymine - T. Since DNA is millions of base pairs long, its extracted as smaller fragments of base pairs (called reads). Then it is compared against a reference genome (already existing DNA sequence), and built back. But even among two similar species (like two humans) there is 1-2% difference in DNA due to evolution, which makes us different from each other, or there can be sequencing errors(errors while extracting), hence when comparing against a reference genome, we look for approximate matching rather than exact matching.

SUBTASK-1 (30)

For a given DNA sequence(say L), output K-mers of overlapping size m.

K-mers : Base pairs of length k.

Input:

First line contains L, K, m Second line contains the DNA sequence.

Output:

K-mers with overlap as m.

Constraints:

2 < L <=1e5

1 < K <=1e4

0 <= m <= K-1

Sample Input 1

931

AGCTCGATC

Sample Output 1

AGC

CTC

CGA

ATC

Sample Input 2

1053

AGCTACGTAC

Sample Output 2

CTACG

ACGTA

GTAC

Note: Last k-mer need not necessarily be of length k.

No clarifications have been made at this time.



Request clarification

Submit solution

My submissions All submissions Best submissions

✓ Points: 30 (partial)

② Time limit: 1.0s

Memory limit: 64M

✓ Allowed languages

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