
Subwords 1

X85229_en

A nucleic acid or amino acid sequence of length n can be seen as composed of a number of possibly overlapping k -mers or words of length k , for $1 \leq k \leq n$. An interesting problem is the generation of all the words of length k contained in a genomic sequence with n nucleotides, for all k with $1 \leq k \leq n$. That is, the generation of all the subwords of a genomic sequence of length n .

Write code for the subwords problem. The program must implement and use the SUBWORDS function in the pseudocode discussed in class, which is iterative and is not allowed to perform input/output operations. Make one submission with Python code and another submission with C++ code.

Input

The input is a string s over the alphabet $\Sigma = \{A, C, G, T\}$.

Output

The output is a sorted list of all the nonempty subwords of s , without repetitions.

Sample input

TATAAT

Sample output

A
AA
AAT
AT
ATA
ATAA
ATAAT
T
TA
TAA
TAAAT
TAT
TATA
TATAA
TATAAT

Problem information

Author : Gabriel Valiente

Generation : 2022-07-07 18:29:59

© Jutge.org, 2006–2022.

<https://jutge.org>