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The Virtual Learning Environment for Computer Programming

Subwords 2 X43423_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 $1 \le k \le n$. 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 $1 \le k \le n$. That is, the generation of all the subwords of a genomic sequence of length n.

Write pseudocode, Python code, and C++ code for the subwords problem. The program must implement and use the subwords function in the pseudocode, which must be recursive and is not allowed to perform input/output operations. Make two submissions, including the pseudocode as a comment to both the Python and the C++ code.

Input

The input is a string s (a genomic sequence) 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
ATA
ATAA
ATAAT
T
T
TA
TAA
TAAT
TATA
TATA
TATAA
TATAA
TATAAT

Problem information

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