
Read mapping 1

X89781_en

Sequence reads are mapped to a reference genome using some indexing data structure, one of which is the suffix array. The suffix array of a string is a sorted array of the suffixes of the string, that is, an array of the (starting) positions of the sorted suffixes of the string.

For example, the genomic sequence fragment TATAAT has the suffixes TATAAT at position 1, ATAAT at position 2, TAAT at position 3, AAT at position 4, AT at position 5, and T at position 6. The sorted suffixes are AAT at position 4, AT at position 5, ATAAT at position 2, T at position 6, TAAT at position 3, and TATAAT at position 1. Therefore, the suffix array of TATAAT is (4, 5, 2, 6, 3, 1).

Write code for the read mapping problem. The program must implement and use the SUFFIX-ARRAY 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 the suffix array of s .

Sample input

TATAAT

Sample output

4
5
2
6
3
1

Hint

Use the built-in sorting algorithm of Python or C++ to sort suffixes.

Problem information

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