# *Jutge.org*

The Virtual Learning Environment for Computer Programming

## Gene finding X66236_en

Recall that in prokaryotic genomes, the sequence coding for a protein occurs as one contiguous open reading frame, and that an open reading frame begins with the start codon ATG (methionine) in most species and ends with a stop codon TAA, TAG, or TGA.

For example, the DNA sequence of Bacteriophage $\phi$-X174, which was the first genome to be sequenced, has 117 open reading frames (11 of which are protein coding genes) within a circular single strand of 5,386 nucleotides.

Write code for the gene finding problem. The program must implement and use the GENE-FINDING 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 minimal substring of $s$ (an open reading frame) from a start codon to a stop codon.

### Sample input

```
GGTTTCTATGTGGCTAAATACGTTAACAAAAAGTCAGATATGGACCTTGCTGCTAAAGGTCTAGGAGCTAAAGAATGGAA
```

### Sample output

```
ATGTGGCTAAATACGTTAACAAAAAGTCAGATATGGACCTTGCTGCTAAAGGTCTAG
```

### Problem information

Author : Gabriel Valiente
Generation : 2022-07-07 18:27:10