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## Sliding window 2

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Recall that a string (genomic sequence) can be split in words of length 3 (codons) by sliding a window of size 3 over the string, with a step size of 3. More in general, a string can be split in overlapping words of length  $x$  and overlap size  $x - y$  by sliding a window of size  $x$  and step size  $y$  over the string. For example, sliding a window of size 3 and step size 2 over the string TATAAT gives the overlapping words TAT and TAA.

Write code for the sliding window problem. The program must implement and use the SLIDING-WINDOW function in the pseudocode discussed in class, which is recursive 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  $s$  (a genomic sequence) over the alphabet  $\Sigma = \{A, C, G, T\}$ , an integer  $x$  (the window size), and an integer  $y$  (the step size).

### Output

The output is all substrings of  $s$  of size  $x$  starting at positions  $1, 1 + y, 1 + 2y, \dots$

#### Sample input 1

```
ACGGTAGACCT
3
1
```

#### Sample output 1

```
ACG
CGG
GGT
GTA
TAG
AGA
GAC
ACC
CCT
```

#### Sample input 2

```
ACGGTAGACCT
3
3
```

#### Sample output 2

```
ACG
GTA
GAC
```

#### Sample input 3

```
ACGGTAGACCT
3
5
```

#### Sample output 3

```
ACG
AGA
```

#### Sample input 4

```
ACGGTAGACCT
5
2
```

#### Sample output 4

```
ACGGT
GGTAG
TAGAC
GACCT
```

**Hint**

Notice that there are no “partial” substrings of  $s$  (of size smaller than  $x$ ) in the output.

**Problem information**

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