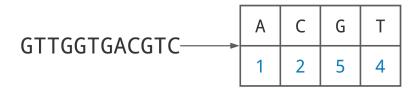
# 1K Generate the Frequency Array of a String

## Frequency Array Problem

Generate the frequency array of a DNA string.

**Input:** A DNA string *Text* and an integer *k*. **Output:** The frequency array of *k*-mers in *Text*.



# **Formatting**

**Input:** A DNA string *Text* and an integer *k*.

**Output:** A space-separated list of integers representing the frequency array of *k*-mers in *Text*).

#### **Constraints**

- The length of *Text* will be between 1 and  $10^3$ .
- The integer k will be between 1 and  $10^1$ .
- *Text* will be a DNA string.

# Test Cases 🖸

#### Case 1

**Description:** The sample dataset is not actually run on your code.

#### Input:

ACGCGGCTCTGAAA
2

#### **Output:**

2 1 0 0 0 0 2 2 1 2 1 0 0 1 1 0

#### Case 2

**Description:** This dataset checks if you have an off-by-one error at the end of Text (i.e. you are not counting the last k-mer in Text). There are three instances of AA (AAAAC, AAAAC, and AAAAC), but there is one instance of AC at the end (AAAAC).

#### Input:

AAAAC

2

#### Output:

3 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0

#### Case 3

**Description:** This dataset checks if you have an off-by-one error at the beginning of Text (i.e. you are not counting the first k-mer in Text). There are two instances of AA (TTAAA and TTAAA), but there is one instance of TA (TTAAA) and one instance of TT (TTAAA).

## Input:

TTAAA

2

#### **Output:**

2 0 0 0 0 0 0 0 0 0 0 1 0 0 1

#### Case 4

**Description:** This dataset checks if your code actually increments each count, or if your code instead just sets the count equal to one each time. In other words, this dataset checks if your code is doing something like array[k-mer] = 1 instead of array[k-mer] + 1.

## Input:

AAA

2

## **Output:**

#### Case 5

**Description:** A larger dataset of the same size as that provided by the randomized autograder.