

A DNA sequence can be represented as a string consisting of the letters A, C, G and T, which correspond to the types of successive nucleotides in the sequence. Each nucleotide has an *impact factor*, which is an integer. Nucleotides of types A, C, G and T have impact factors of 1, 2, 3 and 4, respectively. You are going to answer several queries of the form: What is the minimal impact factor of nucleotides contained in a particular part of the given DNA sequence?

The DNA sequence is given as a non-empty string  $S = S[0]S[1] \dots S[N-1]$  consisting of  $N$  characters. There are  $M$  queries, which are given in non-empty arrays  $P$  and  $Q$ , each consisting of  $M$  integers. The  $K$ -th query ( $0 \leq K < M$ ) requires you to find the minimal impact factor of nucleotides contained in the DNA sequence between positions  $P[K]$  and  $Q[K]$  (inclusive).

For example, consider string  $S = \text{CAGCCTA}$  and arrays  $P, Q$  such that:

```
P[0] = 2    Q[0] = 4
P[1] = 5    Q[1] = 5
P[2] = 0    Q[2] = 6
```

The answers to these  $M = 3$  queries are as follows:

- The part of the DNA between positions 2 and 4 contains nucleotides G and C (twice), whose impact factors are 3 and 2 respectively, so the answer is 2.
- The part between positions 5 and 5 contains a single nucleotide T, whose impact factor is 4, so the answer is 4.
- The part between positions 0 and 6 (the whole string) contains all nucleotides, in particular nucleotide A whose impact factor is 1, so the answer is 1.

Write a function:

```
function solution(S, P, Q);
```

that, given a non-empty zero-indexed string  $S$  consisting of  $N$  characters and two non-empty zero-indexed arrays  $P$  and  $Q$  consisting of  $M$  integers, returns an array consisting of  $M$  integers specifying the consecutive answers to all queries.

The sequence should be returned as:

- a Results structure (in C), or
- a vector of integers (in C++), or
- a Results record (in Pascal), or
- an array of integers (in any other programming language).

For example, given the string  $S = \text{CAGCCTA}$  and arrays  $P, Q$  such that:

```
P[0] = 2    Q[0] = 4
P[1] = 5    Q[1] = 5
P[2] = 0    Q[2] = 6
```

the function should return the values  $[2, 4, 1]$ , as explained above.

Assume that:

- $N$  is an integer within the range  $[1..100,000]$ ;
- $M$  is an integer within the range  $[1..50,000]$ ;
- each element of arrays  $P, Q$  is an integer within the range  $[0..N - 1]$ ;
- $P[K] \leq Q[K]$ , where  $0 \leq K < M$ ;
- string  $S$  consists only of upper-case English letters A, C, G, T.

Complexity:

- expected worst-case time complexity is  $O(N+M)$ ;
- expected worst-case space complexity is  $O(N)$ , beyond input storage (not counting the storage required for input arguments).

Elements of input arrays can be modified.

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