Codility_

CodeCheck Report: training69NA7M-VMU

Test Name:

Check out Codility training tasks

Summary Timeline

Tasks summary

Task	Time spent	Score
GenomicRangeQuery ⚠ Python	1 min	100%

Total score

100%

Tasks Details

Medium

1. GenomicRangeQuery
Find the minimal nucleotide from a range of sequence DNA.

Task Score	Correctness	Performance
100%	100%	100%

Task description

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]...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 ≤ 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 = 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
```

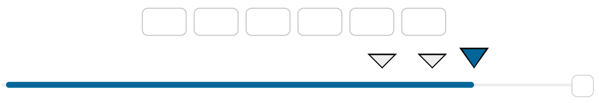
The answers to these M = 3 queries are as follows:

- 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

Solution

Programming language used:	Python	
Total time used:	1 minutes	?
Effective time used:	1 minutes	?
Notes:	*not defined yet*	

Task timeline ?



15:24:23 15:25:19

Code: 15:25:19 UTC, py, final, score: **100**

show code in pop-up

```python
# you can write to stdout for debugging purposes,
# print("this is a debug message")

def solution(S, P, Q):
    # Implement your solution here
    # pass
    nucleotides = {'A': 0, 'C': 1, 'G': 2, 'T': 3}
    sequence = [[0] * (len(S) + 1) for _ in range(

    for i in range(len(S)):
```

whose impact factor is 1, so the answer is 1.

Write a function:

```
def solution(S, P, Q)
```

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

Result array should be returned as an array of integers.

For example, given the string S = `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.

Write an **efficient** algorithm for the following assumptions:

- 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 and Q is an integer within the range [0..N − 1];
- P[K] ≤ Q[K], where 0 ≤ K < M;
- string S consists only of upper-case English letters `A, C, G, T`.

```
        nucleotide = nucleotides[S[i]]
        for j in range(4):
            sequence[j][i + 1] = sequence[j][i] +

    result = []
    for i in range(len(P)):
        start = P[i]
        end = Q[i]

        for j in range(4):
            if sequence[j][end + 1] - sequence[j][
                result.append(j + 1)
                break

    return result

```

Analysis summary

The solution obtained perfect score.

Analysis

Detected time complexity: **O(N + M)**

expand all	**Example tests**	
▶	example example test	✔ OK
expand all	**Correctness tests**	
▶	extreme_sinlge single character string	✔ OK
▶	extreme_double double character string	✔ OK
▶	simple simple tests	✔ OK
▶	small_length_string small length simple string	✔ OK
▶	small_random small random string, length = ~300	✔ OK
expand all	**Performance tests**	
▶	almost_all_same_letters GGGGGG..??..GGGGGG..??..GGGGGG	✔ OK
▶	large_random large random string, length	✔ OK
▶	extreme_large all max ranges	✔ OK