ADAMATCH - Ada and Nucleobase

#fast-fourier-transofm (/problems/tag/fast-fourier-transofm) #polynomial-multiplication (/problems/tag/polynomial-multiplication)

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Ada the Ladybug is helping her friend who is biologist. He examines DNA. Actually he has a long DNA of one bug, consisting of adenine, cytosine, guanine and thymine and he wants to know whether another bug might be relative to first bug. A bug is relative to another bug if his his DNA has very low Hamming Distance with some substring of the first bug.

Your job is to find the lowest hamming distance between second DNA and any substring of first DNA.

Input

Input contains only two lines: first DNA (**s**) and second DNA (**r**).

It is true that $\mathbf{0 < |r| \le |s| \le 5*10^5}$

|s| means length of string **s**.

All strings contains only **A, C, T, and G** .

Output

Print minimal Hamming Distance (https://en.wikipedia.org/wiki/Hamming_distance) (the number of mismatched nucleobases) of any substring of **s** and **r** (the substring MUST have length **|r|**)

Example Inputs

```
ACTGACTGACTG
ACCG
```

```
AAAAAACCA
AAACA
```

```
ACGC
GGG
```

```
ACTTTG
TTTGA
```

```
ACTGACTGACTG
ACTG
```

Example Output

```
1
```

```
1
```

```
2
```

```
3
```

```
0
```

Inputs explanation

```
ACTGACTGACTG
AAAAAACCA
ACGC
ACTTTG
ACTGACTGACTG
```

Added by:	Morass (/users/morass)
Date:	2017-02-09
Time limit:	6.5s
Source limit:	50000B
Memory limit:	1536MB
Cluster:	Cube (Intel G860) (/clusters/)
Languages:	All except: ASM64 GOSU

Evaluate this problem

Nobody has rated this problem yet, maybe you'll be the first?

Concept difficulty

easy normal hard extreme

Implementation difficulty

easy normal hard extreme

Recommend!

Own tags

# # # # # # # # # #

Tag name Add