

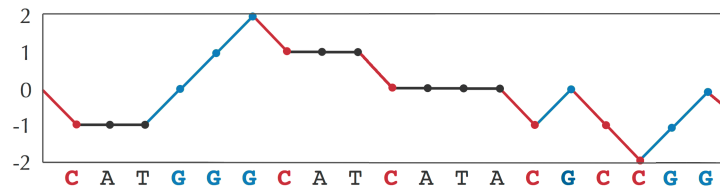
1F Find a Position in a Genome Minimizing the Skew

Minimum Skew Problem

Find a position in a genome minimizing the skew.

Input: A DNA string *Genome*.

Output: All integers i minimizing $\text{SKEW}(\text{PREFIX}_i(\text{Genome}))$ over all values of i (from 0 to $|\text{Genome}|$).



Formatting

Input: A DNA string *Genome*.

Output: A space-separated list of integers i minimizing $\text{SKEW}(\text{PREFIX}_i(\text{Genome}))$ over all values of i (from 0 to $|\text{Genome}|$).

Constraints

- The length of *Genome* will be between 1 and 10^5 .
- *Genome* will be a DNA string.

Test Cases

Case 1

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

Input:

TAAAGACTGCCGAGAGGCCAACACGAGTGCTAGAACGAGGGGCGTAAACGCGGGTCCGAT

Output:

11 24

Case 2

Description: This dataset checks if your code's indexing is off. Specifically, it verifies that your code is not returning an index 1 too high (i.e. 4) or 1 too low (i.e. 2).

Input:

ACCG

Output:

3

Case 3

Description: This dataset checks to see if your code is missing the last symbol of *Genome*.

Input:

ACCC

Output:

4

Case 4

Description: This dataset makes sure you're not accidentally finding the maximum skew instead of the minimum skew.

Input:

CCGGGT

Output:

2

Case 5

Description: First, this dataset checks if you are only finding 1 index (and not multiple indices). Then, it checks if you are using a delimiter to separate your indices (a space character).

Input:

CCGGCCGG

Output:

2 6

Case 6

Description: A larger dataset of the same size as that provided by the randomized autograder. Check input/output folders for this dataset.