Problem G
Genetic Sequence Searching

Time limit: 1 second
Memory limit: 2048 megabytes

Problem Description

Recently scientists have been looking into a new kind of pathogenic virus. To learn more about this virus, they did DNA sequencing on the samples and identified a typical pattern t in all the virus samples.

The scientists then want to identify the pattern in other DNA sequences. They just collected a DNA sequence s from cells of other organisms and were eager to discover all the occurrences of t in s. However, since DNA sequencing can go wrong, they want to find out the occurrences that differ in at most 1 character.

More formally, Let $s = s_1 s_2 \dots s_{|s|}$ and $t = t_1 t_2 \dots t_{|t|}$ are two DNA sequences. The scientists want to know all integers i between 1 and $|s| - |t| + 1$, such that substrings $s_i s_{i+1} \dots s_{i+|t|-1}$ and $t_1 t_2 \dots t_{|t|}$ have at most 1 different character.

Note that unlike usual DNAs, s and t may contain characters other than `ATCG`.

Input Format

The first line of the input contains the string s. The second line of the input contains the string t.

Output Format

Print the number of occurrences in the first line. If there is at least one occurrence in t, in the second line, print all i such that substrings $s_i s_{i+1} \dots s_{i+|t|-1}$ and $t_1 t_2 \dots t_{|t|}$ have at most 1 different character. Print the answers in increasing order.

Technical Specification

- $1 \le |t| \le |s| \le 10^6$
- Each character in s and t has an ASCII code in the rage $[33, 126]$. In other words, each character is one of `!"#$%&'()*+,-./0123456789:;<=>?@ABCDEFGHIJKLMNOPQRSTUVWXYZ[]^_`abcdefghijklmnopqrstuvwxyz{|}~`.

Sample Input 1

```
PCCA_Winter_Camp_2023
AC
```

Sample Output 1

```
4
1 2 4 12
```

Sample Input 2

```
meowmeow
owo
```

Sample Output 2

```
1
3
```