A DNA sequence consists of four letters, A, C, G, and T. The GC-ratio of a DNA sequence is the number of Cs and Gs of the sequence divided by the length of the sequence. GC-ratio is important in gene finding because DNA sequences with relatively high GC-ratios might be good candidates for the starting parts of genes. Given a very long DNA sequence, researchers are usually interested in locating a subsequence whose GC-ratio is maximum over all subsequences of the sequence. Since short subsequences with high GC-ratios are sometimes meaningless in gene finding, a length lower bound is given to ensure that a long subsequence with high GC-ratio could be found. If, in a DNA sequence, a 0 is assigned to every A and T and a 1 to every C and G, the DNA sequence is transformed into a binary sequence of the same length. GC-ratios in the DNA sequence are now equivalent to averages in the binary sequence.

| Position Index | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Sequence | 0 | 0 | 1 | 0 | 1 | 0 | 1 | 1 | 0 | 1 | 1 | 0 | 1 | 1 | 0 | 1 | 0 |

For the binary sequence above, if the length lower bound is 7, the maximum average is 6/8 which happens in the subsequence [7,14]. Its length is 8, which is greater than the length lower bound 7. If the length lower bound is 5, then the subsequence [7,11] gives the maximum average 4/5. The length is 5 which is equal to the length lower bound. For the subsequence [7,11], 7 is its starting index and 11 is its ending index.

Given a binary sequence and a length lower bound $L$, write a program to find a subsequence of the binary sequence whose length is at least $L$ and whose average is maximum over all subsequences of the binary sequence. If two or more subsequences have the maximum average, then find the shortest one; and if two or more shortest subsequences with the maximum average exist, then find the one with the smallest starting index.

## Input

Your program is to read from standard input. The input consists of $T$ test cases. The number of test cases $T$ is given in the first line of the input. Each test case starts with a line containing two integers $n$ ($1 \leq n \leq 100,000$) and $L$ ($1 \leq L \leq 1,000$) which are the length of a binary sequence and a length lower bound, respectively. In the next line, a string, binary sequence, of length $n$ is given.

## Output

Your program is to write to standard output. Print the starting and ending index of the subsequence.

## Sample Input

```
2
17 5
00101011011011010
20 4
11100111100111110000
```

## Sample Output

```
7 11
6 9
```