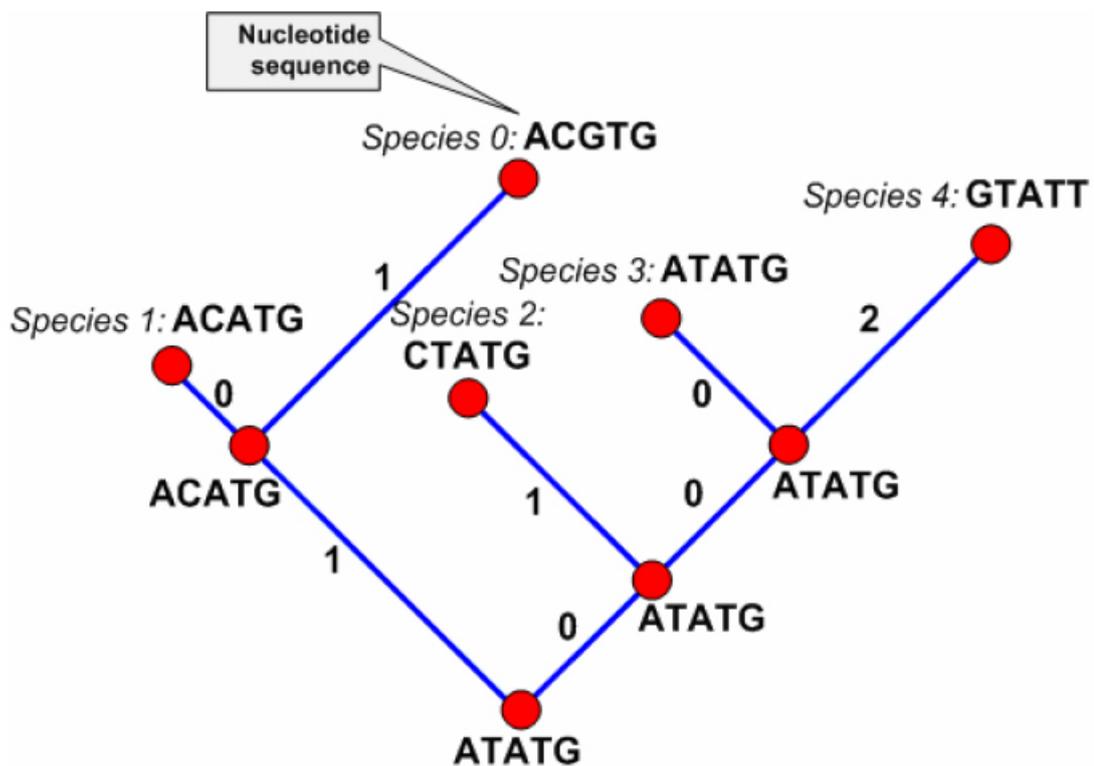


3672 Inferring Ancestors

Reconstructing the evolutionary relationships among species is one of major subjects in biology. Typically, each species is presented by a sequence over four nucleotide types: A, C, G, and T. A nucleotide mutation is said to be happened at position i between two sequences $X = (x_1, \dots, x_l)$ and $Y = (y_1, \dots, y_l)$ if $x_i \neq y_i$. The distance between two sequences X and Y is calculated as the total nucleotide mutations between them.

There are n contemporary species, which are labeled from 0 to $n-1$. The evolutionary relationships among species are depicted by a binary rooted tree where n leaves represent n contemporary species, internal nodes represent ancestor species, and branch lengths represent distances between species (see figure below). This tree can be represented in text form using brackets as $((0,1),((3,4),2))$.



An evolutionary tree of five species with the length of the tree of 5

Since nucleotide sequences are not available for ancestor species, our task is to determine one nucleotide sequence for each ancestor species such that the tree length (total branch lengths) is minimized.

Input

The input consists of several data sets. The first line of the input file contains the number of data sets which is a positive integer and is not bigger than 20. The following lines describe the data sets.

For each data set, the first line containing two integer numbers separated by space ($n \leq 10$, $l \leq 100$) indicating the number of contemporary species and the length of nucleotide sequences, respectively. The i -th line of the following n lines contains the nucleotide sequence of the contemporary species labeled $i-1$. The last line contains the text representation of the tree topology.

Output

For each data set, write in one line an integer number indicating the minimum length of the tree.

Sample Input

```
2
2 3
AGG
CGT
(0,1)
5 5
ACGTG
ACATG
CTATG
ATATG
GTATT
((0,1),(2,(3,4)))
```

Sample Output

```
2
5
```