

Tree of Life

You are a biologist studying an evolutionary tree. An evolutionary tree is a rooted tree showing the evolutionary relationships between several species. There are N nodes numbered 1 to N , each of which represents a different species. The tree is rooted from node 1. Two species are said to be *distant* if neither of their corresponding nodes are descendants of the other.

You have collected the DNA sequences of all N species in your evolutionary tree. The DNA of the species of node i is represented as a string S_i composed of the characters **A**, **C**, **G**, and **T** for $1 \leq i \leq N$. The *genetic similarity* of two species is the length of the longest common substring of their DNA sequences.

Find the largest genetic similarity between two distant species.

Constraints

S is the sum of the lengths of the N DNA sequences collected.

Subtask 1 [20%]

$$1 \leq N \leq 20\,000$$

$$1 \leq S \leq 100\,000$$

All DNA sequences only contain **A**.

Subtask 2 [80%]

$$1 \leq N \leq 20\,000$$

$$1 \leq S \leq 100\,000$$

Input Specification

The first line contains a single integer N .

The next $N - 1$ lines each contain a single integer. These integers represent the tree. The integer on the i^{th} of the $N - 1$ lines represents the node which is the parent of the node $i + 1$. For convenience, it is guaranteed that this number is less than $i + 1$.

The next N lines each contain a string composed of **G**, **C**, **A**, or **T**. The string on the i^{th} of the N lines is S_i , the DNA of the species represented by node i .

Output Specification

Output a single integer, the largest genetic similarity between two distant species. If there are no two distant species, output **-1**.

Sample Input 1

3
1
2
ACT
GG
AGG

Sample Output 1

-1

Sample Input 2

3
1
1
ACT
GG
AGG

Sample Output 2

2