

DNA of Space Dinosaurs

Problem Description

Two galactic paleontologists—the famously quarrelsome Dr. Glorb and Prof. Zax—are analyzing fossil DNA from several fossils from a distant planet. Cosmic radiation has scrambled the strands, but fragments remain. The paleontologists are highly competitive:

- Dr. Glorb insists the fossils belonged to the legendary Kaijurasaurus Rex,
- while Prof. Zax claims they were harmless Intergalactic Duckosaurs.
- They refuse to stop arguing until you, the programmer, compute how closely fossil DNA matches other strands of DNA to help identify the species.

To quantify how closely related two particular DNA strands are, the scientists start by aligning the DNA strands and finding the longest sequence of nucleotides that appears *in both strands in the same order* (not necessarily contiguously).

Formally, given two strings X and Y , a *subsequence* of X is any string obtained by deleting zero or more characters from X without changing the order of the remaining characters. The **Longest Common Subsequence (LCS)** of X and Y is a common subsequence of maximum possible length.

The scientists are going to give you n test cases. Each test case is described by two nucleotide sequences. Your task is to compute the *length* of the LCS for each test case.

Input

The first line contains an integer n indicating the number of test cases ($1 \leq n \leq 100$). The following $2n$ lines describe the inputs to the tests cases. Each test case is given by a string X on one line and a string Y on the following line. Each string X consists only of upper letter characters 'A' through 'Z' and has length between 1 and 1,000. Same constraints apply to Y .

Output

For each test case, output a single line:

Case [CASE_NUMBER]: [LCS_LENGTH]

Where [CASE_NUMBER] should be the number indicating the case (1-based), and [LCS_LENGTH] should be the length of the LCS of X and Y corresponding to that case.

Samples

Sample Input	Sample Output
2 ACGTGCTA CATGACTA XKCD KXCD	Case 1: 6 Case 2: 3