**Mutations of viruses**

Remember that the genetic code (see problem P36671) is a set of rules that translates sequences of nucleotides to proteins. Working with DNA instead of messenger RNA, the sequences of nucleotides change the base \( U \) for the base \( T \).

Often, as a reaction of resistance against drugs, the viruses mutate their ADN maintaining their functionality, that is, synthesizing the same protein. For instance, if a virus had the sequence

\[
\text{GCCAATGACTAAGGCCTAAAGA}
\]

then would synthesize the protein \( \text{Thr–Lys–Ala} \). If the virus mutates to

\[
\text{GCCAATGACCAACGCCTAAAGA}
\]

(the tenth base has changed from \( T \) to \( C \)), it would still synthesize \( \text{Thr–Lys–Ala} \). In this case, we say that one (or more) equivalent mutations have been produced.

However, if the virus mutated to

\[
\text{GCCAATGTCTAAGGCCTAAAGA}
\]

(the eighth base has changed from \( A \) to \( T \) and the fourteenth base has changed from \( G \) to \( A \)), then would synthesize \( \text{Ser–Lys–Leu} \), fact that is noticed indicating \( \text{Thr–1–Ser,Ala–3–Leu} \) (the number indicates in which codon the mutation has been produced).

Write a program that prints if pairs of DNA sequences represent equivalent mutations and, if not, prints which mutations have been produced. The program must print also how many different bases there are between the \( \text{ATG} \) codon and the Stop codon.

**Input**

Input starts with a natural number \( k \). After, come \( k \) pairs of DNA sequences of the same length. Each DNA sequence is formed by a strip of characters ‘A’, ‘C’, ‘T’ and ‘G’ in a line without spaces. All the DNA sequences have an \( \text{ATG} \) codon before a Stop codon. The \( \text{ATG} \) codon and the Stop codon never mutate in each pair of sequences nor any mutation can introduce a new Stop codon. The pairs of sequences always have the same length.

**Output**

For each pair of DNA sequences of the input, print if are or are not equivalent. In case that they are not equivalent, print the changes that mutations have produced according to standard notation described previously. The number of different bases must be written at the end of the line, in brackets.

Follow the format of the example.
Sample input

4

GCCAATGACTAAGGCCTAAAGA
GCCAATGACCAAGGCCTAAAGA

GCCAATGACTAAGGCCTAAAGA
GCCAATGTCTAAGACCTAAAGA

GCCAATGACTAAGGCCTAAAGA
GCCAATGTCTAAACCTAAAGA

GCCAATGACTAAGGCCTAAAGA
GCCAATGACTAAGGCCTAAAGA

Sample output

Equivalent (1)
Thr-1-Ser, Ala-3-Thr (2)
Thr-1-Ser, Ala-3-Thr (3)
Equivalent (0)

Problem information

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