

Problem A. Advanced Evolution Studies

Input file: *standard input*
 Output file: *standard output*
 Time limit: 2 seconds
 Memory limit: 1024 mebibytes

A phylogenetic tree is a diagram that shows the evolutionary relationships inferred based on the similarities and differences among various species or individuals, including physical and genetic characteristics. This diagram is represented as a rooted tree.

Through years of research, Ji-yeon has proposed m hypotheses that elucidate the correlations among n species. Each species is labeled by a unique positive integer from 1 to n . Ji-yeon wants to create a phylogenetic tree with n or more vertices to validate her research, with each species i corresponding to vertex i of the tree.

For two vertices x and y in a rooted tree, vertex x is considered an *ancestor* of vertex y if either they are the same or vertex x is an ancestor of the parent of vertex y . If vertex x is an ancestor of vertex y , then vertex y is a *descendant* of vertex x . The *lowest common ancestor* of two vertices x and y is the ancestor of both x and y that has the highest number of ancestors.

The hypotheses proposed by Ji-yeon are given in the form of (a, b, c, d) . Each hypothesis claims that, if the lowest common ancestor of vertices a and b is vertex x , and the lowest common ancestor of vertices c and d is vertex y , then vertex x is a descendant of vertex y , and vertices x and y are different.

Given m hypotheses for n species, create a phylogenetic tree that satisfies all the hypotheses, or determine that there is no such tree. Each vertex i of the tree should correspond to species i . Furthermore, the number of vertices n' in the tree should be from n to $2n$: it can be shown that, if an answer exists, there exists an answer with at most $2n$ vertices as well.

Input

The first line contains two integers, n and m : the number of species Ji-yeon studied and the number of hypotheses ($4 \leq N \leq 2000$; $1 \leq M \leq 2000$).

Then m lines follow. Each of them contains four integers, a , b , c , and d , representing a hypothesis ($1 \leq a, b, c, d \leq N$; $a \neq b$; $c \neq d$).

Output

If there is no phylogenetic tree t that satisfies all hypotheses, print -1 on the first line. Otherwise, on the first line, print the number of vertices n' that make up the phylogenetic tree ($n \leq n' \leq 2n$). On the second line, print n' integers $p_1, p_2, \dots, p_{n'}$ separated by spaces. Each p_i is the parent of vertex i , or 0 if vertex i is the root. The vertices are numbered from 1 to n' , with vertices from 1 to n corresponding to the species.

If there are multiple possible phylogenetic trees, print any one of them.

Examples

<i>standard input</i>	<i>standard output</i>
6 2 1 2 3 5 2 5 1 4	7 3 3 7 6 7 0 6
5 3 1 2 3 4 3 5 1 4 2 4 2 5	-1