Task 4: GENOME

In comparative genomic, biologists would like to find a gene sequence that is conserved among a set of species.

Let $\{1, 2, \ldots, n\}$ be a set of n integers in which each integer represents a gene. For the m species S_1, S_2, $\cdots$, S_m, each species S_i is identified by a permutation of $\{1, 2, \ldots, n\}$. The permutation represents the ordering of genes in S_i.

A subsequence of an integer sequence is obtained by omitting none, one, or more integers from the original sequence. An integer sequence $x_1, x_2, \ldots, x_k$ is a *conserved gene sequence* among the m species if $x_1, x_2, \ldots, x_k$ is a subsequence of S_i for all $i = 1, 2, \ldots, m$. Our aim is to find the length of the longest conserved gene sequences for the m species.

Example

Consider the following 3 species,

- $5, 3, 4, 1, 2$;
- $2, 5, 4, 3, 1$;
- $5, 2, 3, 1, 4$.

The following subsequences

- $5, 1$;
- $5, 3$;
- $5, 4$;
- $3, 1$;

are conserved gene sequences among the 3 species but are not longest. The longest conserved gene sequence of the 3 species is $5, 3, 1$.

Input File: GENOME.IN

The input file GENOME.IN contains $m + 1$ lines. The first line contains two integers n and m separated by spaces, where $1 \leq n \leq 100$ and $1 \leq m \leq 10$. Each of the next m lines contains a permutation of $1, 2, \ldots, n$, with spaces between two adjacent integers. For the given example, the input file contains:

```
5 3
5 3 4 1 2
2 5 4 3 1
5 2 3 1 4
```

Output File: GENOME.OUT

The output file GENOME.OUT contains an integer that gives the length of the longest conserved gene sequences. For the given example, the output file contains:

```
3
```