

# Infection Investigation

Time limit: 3 seconds  
Memory limit: 1024 megabytes

Isaac is a biologist who specializes in diagnosing viral diseases. The virus modifies the host genome (a sequence of genes) by altering it to suit its own needs. Isaac is writing a paper investigating viral infection in genomes. He has some samples and asks you to help analyze them.

For simplicity, we will assume that the viral genome consists of genes  $1, 2, \dots, n$  in this order. The host genome is a permutation of genes  $1, 2, \dots, n$ : it consists of genes  $a_1, a_2, \dots, a_n$  in this order.

Consider a genomic segment  $[l; r]$  consisting of genes  $a_l, a_{l+1}, \dots, a_r$ . The infection level of this segment is measured as the length of the longest subsequence of genes shared with the viral genome. Formally, the infection level is the maximum  $k$  such that there exist  $l \leq i_1 < i_2 < \dots < i_k \leq r$  for which the inequalities  $a_{i_1} < a_{i_2} < \dots < a_{i_k}$  hold.

To analyze the genome, Isaac needs to estimate the infection levels of  $q$  genomic segments. To secure the funding, Isaac only needs approximate results: an error factor of up to 1.5 is allowed.

## Input

Each test contains multiple test cases. The first line contains the number of test cases  $t$  ( $1 \leq t \leq 10^4$ ). The description of the test cases follows.

The first line of each test case contains two integers  $n$  and  $q$ , denoting the host genome length and the number of genomic segments Isaac is interested in ( $1 \leq n, q \leq 2 \cdot 10^5$ ).

The second line contains  $n$  distinct integers  $a_1, a_2, \dots, a_n$ , describing the host genome ( $1 \leq a_i \leq n$ ).

Each of the following  $q$  lines contains two integers  $l$  and  $r$ , denoting the boundaries of a genomic segment for which the infection level should be estimated ( $1 \leq l \leq r \leq n$ ).

It is guaranteed that the sum of  $n$  over all test cases does not exceed  $2 \cdot 10^5$ , and the sum of  $q$  over all test cases does not exceed  $2 \cdot 10^5$ .

## Output

For each test case, print  $q$  positive integers, denoting the infection levels of the corresponding genomic segments.

For each genomic segment, let your answer be  $x$  and let the true answer be  $y$ . Your answer will be considered correct if it differs from the true answer by a factor of at most 1.5, that is, if  $\max\left(\frac{x}{y}, \frac{y}{x}\right) \leq 1.5$ .

## Example

standard input	standard output
2	4
10 4	3
3 5 8 4 6 7 1 10 2 9	5
1 7	1
7 10	6
1 10	12
3 4	
8 2	
1 2 3 4 5 6 7 8	
1 8	
1 8	