# Problem I. 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 $1, 2, \ldots, n$ in this order. The host genome is a permutation of genes $1, 2, \ldots n$: it consists of genes $a_1, a_2, \ldots, a_n$ in this order.

Consider a genomic segment $[l; r]$ consisting of genes $a_l, a_{l+1}, \ldots, a_r$. 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 $l \le i_1 < i_2 < \cdots < i_k \le r$ for which the inequalities $a_{i_1} < a_{i_2} < \cdots < a_{i_k}$ 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 $t$ ($1 \le t \le 10^4$). 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 ($1 \le n, q \le 2 \cdot 10^5$).

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

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 ($1 \le l \le r \le n$).

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 $\max\left(\frac{x}{y}, \frac{y}{x}\right) \le 1.5$.

## Example

| standard input | standard output |
|---|---|
| 2<br>10 4<br>3 5 8 4 6 7 1 10 2 9<br>1 7<br>7 10<br>1 10<br>3 4<br>8 2<br>1 2 3 4 5 6 7 8<br>1 8<br>1 8 | 4<br>3<br>5<br>1<br>6<br>12 |