Шаг 2 из 10



2.4 Problem 3. Diagnosis 5 из 10 шагов пройдено 0 из 2 100 баллов получено



**Diagnosis**

Determining the correct diagnosis is a crucial step in patient treatment. However, it can be far from trivial, as the disease can have multiple phenotypic manifestations with different degrees of specifcity, partly overlapping with other conditions. To formalize the diagnostics process, Human Phenotype Ontology (HPO) was invented, using which both the disease manifestations and patient phenotypic traits can be described. In this problem, your task will be to identify the patients' diseases given their clinical phenotypes.

In this problem, you are given a human phenotype tree. Each vertex of this tree corresponds to a phenotypic abnormality. The abnormalities on the lower levels are more specifc, with the specifcity of the vertex ***v*** defned as information content ***IC***(***v***) value. Additionally, you are given descriptions of several diseases, each defned as a set of abnormalities, that is vertices of the phenotype tree. Finally, you are given descriptions of patients, similarly defned as sets of phenotype tree vertices, describing their clinical phenotypes.

Your task is to fnd for each of the patients their most likely disease. More precisely, for every patient ***p*** with the phenotype set ***Qp*** fnd the disease ***m*** with the phenotype set ***Dm*** which maximizes the value of

**∑ (** max ***IC*(*LCA***(***q***, ***d***)**))**,

***q***∈***Qp  d***∈***Dm***

where ***LCA***(***q***, ***d***) is the lowest common ancestor of phenotype vertex ***q*** and phenotype vertex ***d*** and ***IC***(***v***) is the information content of vertex ***v***. If there are several diseases with the same maximal value,then any of them can be returned.

**Input Format**

The frst line of the input fle contains one integer ***n*** — the number of vertices in the phenotype tree. The vertices are identifed by numbers 1, 2, … , ***n***, with vertex 1 being the root of the tree.

The second line contains ***n*** − 1 integers — the parent identifers for the vertices 2, 3, … , ***n***.

The third line contains ***n*** integers — information content values of the corresponding vertices 1, 2, … , ***n***. It is guaranteed that for every vertex ***v*** its information content ***IC***(***v***) is greater than the information content of its parent vertex.

The fourth line contains one integer ***m*** — the number of diseases.

Next ***m*** lines contain descriptions of diseases. The ***i***-th line contains an integer ***cmi***— the number of vertices in the phenotypes tree describing the ***i***-th disease, followed by ***cmi*** different integers — the identifers of vertices describing the ***i***-th disease.

The next line contains one integer ***nq*** — the number of patients.

Next ***nq*** lines contain descriptions of patients. The ***i***-th line contains an integer ***cqi***— the number of vertices in the phenotypes tree describing the ***i***-th patient, followed by ***cqi*** different integers — the identifers of vertices describing the ***i***-th patient.

**Output Format**

The output fle should contain ***nq*** lines. The ***i***-th line should contain one integer — the identifer of a disease of the ***i***-th patient. The indexing starts from 1.

**Scoring**

For all tests, you will receive points proportional to the number of diseases you recovered correctly.

**Sample Input**



**10**

**113344555**

**57813181415212029**

**2**

**2 4 2**

* **10**

**4**

**3598**

* **6**

**2710**

**1 10**

**Sample Output**



**2**

**1**

**2**

**2**

