

6285 Identification of Protein

A protein is a sequence of amino acids. One of the ways to sequence (i.e. to read) a protein is to use *Tandem mass spectrometry* (usually abbreviated as MS^2).

In this problem the following toy situation is considered:

- A protein is a sequence of at most 400 amino acids.
- There are only two types of amino acids, P and Q.
- Mass of P is 97.05276 daltons, mass of Q is 128.05858 daltons.

The result of an ideal measurement via MS^2 is a set of real numbers called peaks, which contains the mass of each prefix and each suffix of the protein (including the entire protein), and no other numbers.

But it's never ideal in practice. You're given the results of MS^2 experiment for an unknown protein. The following conditions hold:

- masses of some prefixes and/or some suffixes might be absent in the set.
- some peaks that do not correspond to any prefix/suffix mass might be included in the set (they are called noise peaks).
- all peaks are positive numbers.
- the largest peak in the set is equal to the mass of the entire protein.
- all peaks that correspond to prefix/suffix masses are exact measurements.

Reconstruct the protein that has the mass equal to the largest peak and minimizes the number of noise peaks (and thus maximizes the number of peaks that correspond to its suffixes or prefixes).

Input

The input will contain several test cases, each of them as described below.

The first line contains integer n ($1 \leq n \leq 100000$), the number of peaks in the given MS^2 experiment results.

Each of the next n lines contains a positive real number p_i , the mass of the i -th peak.

All of above conditions are guaranteed to be satisfied. All peaks are distinct. Each peak has no more than 5 digits after a decimal point.

Output

For each test case, write to the output on a line by itself.

Output a string of up to 400 characters consisting only of 'P' and 'Q' characters — the reconstructed protein. If there are multiple answers that minimize the number of noise peaks, output any one of them.

Note for the sample:

In the given example, the protein PQQ (or QQP) explains all peaks except two: 291.15828 and 353.16991.

Sample Input

6
225.11134
353.16992
353.16991
291.15828
97.05276
128.05858

Sample Output

PQQ