Q6: Search That Genome…

A genome is a nucleotide string of four symbols – A, C, G and T – representing the bases of DNA. For example "TACGTGCA" is a sample sequence. What if you wanted to determine whether a given sequence contained either "ACGTG" or "ACGTA" consecutively (the only difference being the last base)? In this case, your *search string* would be "ACGTR" because – using the table on the right – character "R" can represent either a "G" or an "A"; using this search string, a match is found in the sample sequence as shown below.

Search Symbol	Potential Matches
G	G
A	A
T	T
C	C
R	G or A
Y	T or C
M	A or C
K	G or T
S	G or C
W	A or T

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DNA sequence:   AAAATACGTGCATCGACGTCT
Search String:       ACGTR
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Write a program that takes a sample DNA sequence and a search string, and determines the first subsequence in the sample (i.e., from the left) that matches the search string. In the above search, the program identifies that subsequence "ACGTG" is a match, and reports it. When there is no match, you should report "NO MATCH".

Input

The first line of input contains a single genome string of no more than 140 "A", "C", "G", and "T" characters on the line by itself. The second line contains a search string (of no more than 10 characters) on the line by itself containing only characters in the first column of the above table.

Output

If there is a match, your output will consist of the matched subsequence within the input genome string on a line by itself; if there is no match, then the only line of input will be the string "NO MATCH".

Sample Input and Output

Input	Output
TACGTGCATCGACGTCT ACGTR	ACGTG
TACGTGCATCGACGTCT SSRSKW	CGACGT
TACGTGCATCGACGTCT MKSAT	NO MATCH
AAAACCCC RMWASMYC	AAAACCCC
AAAACCCC MW	AA
ACGTCGAACGTA RYSTR	ACGTA
ACTGA AYKGWR	NO MATCH