

All-Star Contest

ACSL DNA

PROBLEM: In a galaxy far, far away there is a planet called ACSL-land. The ACSloids who live there have DNA structures similar to those who inhabit Earth. Single strands consist of a sequence of 4 bases. The bases are A, C, S, and L. A and L are complementary bases, as are C and S. This means that when searching for an Inverted Repeat, A and L are interchanged and C and S are interchanged. Certain patterns can be found in adjacent (no other bases between) sequences and your mission is to identify all the unique patterns of a given type that are in each strand. These patterns are:

Direct Repeat (DR): ACSAL and ACSAL

Mirror Repeat (MR): ACSAL and LASCA - palindrome where the original sequence is 2 or more bases in length.

Inverted Repeat (IR): ACSAL and ALCSL - palindrome with complements - This means that when searching for an Inverted Repeat, A and L are interchanged and C and S are interchanged in the palindrome. The original sequence must be 2 or more characters in length.

Everted-Left, Everted-Right (EL or ER) - ACSAL and ACASL – In an odd numbered sequence of bases greater than or equal to 3, starting with the middle letter and following a sequence of left/right or right/left, the resulting string of bases is the same as the original. The example above is for EL.

INPUT: 10 strings representing the DNA strand followed by the type of repeat you are searching for (DR, MR, IR, EL, or ER).

OUTPUT: All the unique subsequences of the strand that include the original and the indicated repeat/evert. If there are none, then print NONE.

SAMPLE INPUT

1. ACACSLACSL, DR
2. CSLLSACAACSL, MR
3. AACSLACSLALAL, IR
4. SCACALACASL, EL
5. SCACALLSACA, ER

SAMPLE OUTPUT

1. ACAC, ACSLACSL
2. SLLS, CAAC, CSLLSC
SCAACS, LSCAACSL, LLSCAACSL
3. SLAC, ACSL, LALA, ALAL
ACSLACSL, CSLACS, LACSLA
4. ACSALACASL
SCACSA
5. ACSALLSACA
SALLSA