List of problems for eertree

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Problem 1

Consider an arbitrary string g. We will call this string as palindrome generator. The set of palindromes $P(g)$ that are generated by this string is determined as follows.

Let string length be n. For all i from 1 to n in $P(g)$ strings $g[1..i]g[1..i]^r$ and $g[1..i]g[1..i-1]^r$ are included, where α^r means α, written in reversed order.

For example if $g =$ "$olymp$", then $P(g) = \{$"oo","o","$ollo$","olo","$olyylo$","$olylo$", "$olymmylo$","$olymylo$","$olymppmylo$","$olympmylo$"$\}$.

For a given generator of palindromes g and the string s, it is required to find the number of occurrences of string from $P(g)$ in s as substrings. Namely, it is required to find the number of pairs (i, j) such that $s[i..j] \in P(g)$.

Example input	Example output
olymp olleolleolympmyolylomylo	7

Link to a problem

Problem 2

Each palindrome can be always created from the other palindromes, if a single character is also a palindrome. For example, the string "$malayalam$" can be created by some ways:

$$malayalam = m + ala + y + ala + m$$
$$malayalam = m + a + l + aya + l + a + m$$

We want to take the value of function $NumPal(s)$ which is the number of different palindromes that can be created using the string S by the above method. If the same palindrome occurs more than once then all of them should be counted separately.

Example input	Example output
malayalam	15

Link to a problem

Problem 3

For a given string S we want to find minimum number of continuous palindromes in which this string can be broken.

Example input	Example output
abacdc	2
ababa	1
ababbacababbad	5
abcd	4

Link to a problem

Problem 4

For a given string S we want to find total number of continuous palindromes in which this string can be broken.

Example input	Example output
aaa	6
aba	4

Link to a problem

Problem 5

For a given DNA sequence we want to find non palindrome of length n between 2 palindromes of length m. Can be practical for searching potential hairpins.

Problem 6

For a given DNA sequence we want to find mutations that leads to palindromic sequence and probability of these events.