The problem about task 1 is to calculate the number of exons.

Here is the biological importance.

If there are more exons in one sequence, it suggests that there will be more potential isoforms after alternative RNA splicing. Meanwhile, exon number can also h elp to judge the Splicing efficiency.

The challenge for this code is that the first and last exons do not necessarily have a splice acceptor. So as you can see the approach here, we firstly Find the first exon which does not Strat with AG, but end with GT. When we come to find the next exon, we found that if there is an AG in first exon or intron, we will get the wrong result. So in the second step, we remove the first exon and the first GT. Then, we can find the sequence start with AG and end with GT. Since we use the $, the last exon just not end with the AG will also be output.

Please input this sequence. And the exon number is 3.

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