AP CS A Recursion Assignment: RNA and protein alignments

Part I: RNA fragment alignment. For this assignment, you are to make a java package that takes two RNA fragments and prints out the top global alignment of the two strands along with the alignment score.

a) Indel penalty: -1; Match score: +1; mismatches are not allowed.

User Input: The two RNA fragments. The fragments can be of any length, but you may assume the user has entered acceptable fragments consisting entirely of a, g, u and c.

What should be output:

1. the alignment, one strand on top of the other with insertions signified with “-“.

2. The score for the alignment.

Your program must feature a recursive method.

Hint: Spend a lot of time on planning. Map out on “paper” with UMLs and pseudocode how you will be able to carry out the task. Think about how you determined the best alignment using the DP Scoring Matrix. Now see if you write out how a program might carry out the same logical, algorithmic steps that you took using pencil and paper.

Test out your methods as you go. Test out small chunks of code as you go. Use small test cases at first. I suggest *ugu* and *uua* as a good test case as you develop your program.

The output for this test case should be:

ugu-

u-ua

The score for this alignment is 0.

This task may well take 3 days. If you finish with it, show it to me and I will tell you what steps to take next for parts b and c.