CS302 - Programming Assignment 3

Due: Wed, Nov 1. Must be uploaded to Canvas before the beginning of class.

Please read the sections of the syllabus on programming assignments and honor code before starting this homework. I would also recommend reading the rubric for programming grading, so that you know how we will be grading this assignment.

1. [**30 points**] Create a Java class called SequenceAlign. It should be able to implement a dynamic programming algorithm for sequence alignment, based on the algorithm we discuss in class. For your objective functions, set $p_{gap} = p_{mm}$. Then use your program to try to classify the species of the first 5 unknown DNA sequences on this website, by comparing to the DNA sequences listed under the different groups. You should test your code on small sequences to make sure it is working correctly.

   Put a multiline comment at the beginning of your class. It should contain:

   - Your name
   - "Programming Assignment 2"
   - The name of anyone you worked with
   - Output from your program, for example:

     ```
     DNA 1 is likely from a xxxxx
     DNA 2 is likely from a xxxxx
     DNA 3 is likely from a xxxxx
     DNA 4 is likely from a xxxxx
     DNA 5 is likely from a xxxxx
     ```

     (Your output need not be exactly the same format as this, but should convey this information in some way.)