**CS 476 Bioinformatics Algorithms FA22**

**Project I: Sequence Alignment and Substitution Matrices (UG&G /G)**

**Demo Description**

In this project, I want you to record a 5~10 minutes demo video for your program.

1. **Test Input**

Seq\_1 =sequenceA1.txt

Seq\_2 =sequenceA2.txt

Submatrix = AAnucleoPP.txt

Gap penalty = -5

Gap\_open = -3

Gap\_extend = -1

1. **Demo Contents**
2. Upload and compile your program to home sever
3. Run your program with the given Test Input
4. The output under global, local, semi-global, and affine setting
5. Pick one of the alignment algorithms and briefly explain it in your code. (UG only)

Briefly explain global alignment with affine gap penalty in your code. If you didn’t complete this part, pick one of the alignment algorithms and briefly explain it in your code (G only)

1. If you attempt the Extra Credit, show me what you have done.