# **Final Project First Attempt**

CMSC 435 - Introduction to Data Science Group 9

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## **Section 1:** Knowledge Discovery Process

- Researched protein sequences and amino acids
- Developed a Python script using the Biopython package to read in the data to calculate length and molecular weight as features and generate a csv file with those features for each data object.
- Features
  - Length
    - Number of characters (AKA amino acids) in sequence.
  - Molecular Weight
    - Wrote a Python script to calculate using BioPython. If the sequence contained an X or Z, I predicted it as missing value since BioPython would throw an error for sequences with those amino acids. Otherwise, the sequence's molecular weight was calculated.
  - Most Frequent Amino Acid
    - Wrote Python script to removed non-natural residues from nonDRNA objects such as X, B, Z, U, since Pfeature cannot handle these values
    - Used Pfeature to find Amino Acid compositions for each data object
    - Wrote Python script to find the Amino Acid with the highest composition for each protein sequence
- Classification Algorithm
  - Chosen
    - Decision Tree
      - With default parameters
  - Attempted
    - Linear SVM

## **Section 2: Model Results**

**Accuracy: 89.08%** 

#### predicted

	DNA	RNA	DRNA	nonDRNA
DNA	8	4	0	379
RNA	7	6	0	510
DRNA	0	0	0	22
nonDR NA	17	21	0	7821

actual

#### DNA MCC:

- TP (True DNA): 8

- FP (False DNA): 7+17= 24

- TN: 7821 + 6 + 510 + 22 + 21 = 8380

- FN: 4 + 379 = 383

- MCC:  $(8 * 8380) - (24 * 383) / \sqrt{(8+24)(8+383)(8380+24)(8380+383)} =$ **0.060** 

#### RNA MCC:

- TP: **6** 

- TN: 8 + 379 + 17 + 22 + 7821= **8247** 

- FP: 7 + 0 + 510 = 517

- FN: 4 + 0 + 21 = 25

- MCC = **0.034** 

#### DRNA MCC:

- TP: 0
- TN: 8 + 4 + 7 + 6 + 17 + 21 + 379 + 510 + 7821 = 8773
- FP: **0**
- FN: **22**
- MCC =  $(0 * 8773) (0 * 22) / \sqrt{(0 * 0)(0 * 22)(8773 * 0)(8773 * 22)} = \mathbf{0}$

# nonDRNA MCC:

- TP: **7821**
- TN: 8 + 4 + 7 + 6 = 25
- FN: 17 + 21 = 38
- FP: 379 + 510 + 22 = **911**
- MCC = **0.07999**