

## **Biopython Lab:**

### **Instructions:**

1. ALL DUE TIMES ARE IN EST
2. Upload a Python file to this BB Assignment.
3. All answers must be in your own words, and copy-and-paste answers will receive no credit.
4. You must submit a **.py** file and the resulting **FilteredProteinFasta.fasta**
5. You are limited to 2 submissions
6. **You must be in the lab session to get the lab's credit.**
7. If you cannot submit the lab by the end of the day, you can still submit it by the end of the next day with a 25%penalty. Any lab submissions after two days of the lab class will be given a zero

### **1. Basic Parsing with BioPython**

- Write a Python script to parse a FASTA file named ProteinFasta.fasta using the SeqIO module and print each sequence's ID, sequence, and length.

### **2. Count Total Records**

- Modify your code to calculate and display the total number of records in the FASTA file.

### **3. Access Specific Records**

- Add functionality to your script to print the details (ID, sequence, and length) of:
  - The first record in the file.
  - The last record in the file.

### **4. Sequence Length Calculation**

- Write a Python script to calculate and print the total length of all sequences in the file.

### **5. Using BioPython's SeqIO module, create a new FASTA file from ProteinFasta.fasta. The new file should:**

- Include only sequences longer than 10 amino acids.
- Add "\_filtered" to the record IDs to indicate they were filtered.
- Save the output as FilteredProteinFasta.fasta.