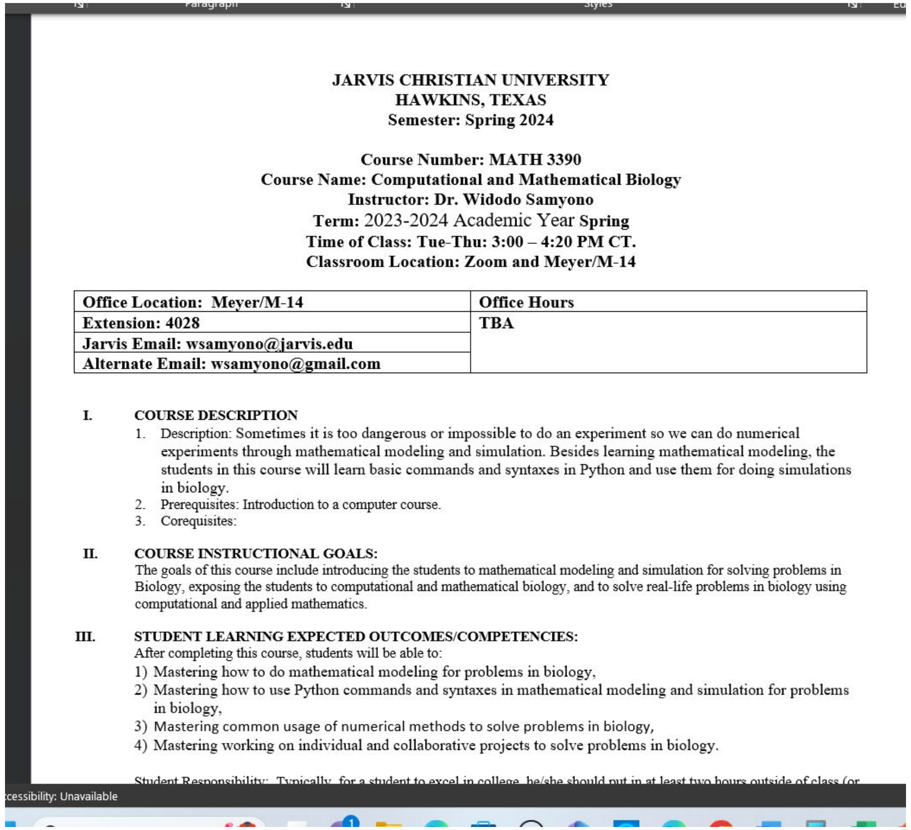
Jarvis Bulldog Team

Syllabus

https://github.com/wsamyono/BulldogTeamFacHackGA23/blob/d57bd2fa4c3138ea5ca917ae4cedd4927b4c8ebc/Spring%202024%20MATH%203390%20Course%20Syllabus%20WSamyono.docx



JARVIS CHRISTIAN UNIVERSITY
HAWKINS, TEXAS
Semester: Spring 2024

Course Number: MATH 3390
Course Name: Computational and Mathematical Biology
Instructor: Dr. Widodo Samyono
Term: 2023-2024 Academic Year **Spring**
Time of Class: Tue-Thu: 3:00 – 4:20 PM CT.
Classroom Location: Zoom and Meyer/M-14

Office Location: Meyer/M-14	**Office Hours**
Extension: 4028	**TBA**
Jarvis Email: wsamyono@jarvis.edu	
Alternate Email: wsamyono@gmail.com	

I. **COURSE DESCRIPTION**

1. Description: Sometimes it is too dangerous or impossible to do an experiment so we can do numerical experiments through mathematical modeling and simulation. Besides learning mathematical modeling, the students in this course will learn basic commands and syntaxes in Python and use them for doing simulations in biology.
2. Prerequisites: Introduction to a computer course.
3. Corequisites:

II. **COURSE INSTRUCTIONAL GOALS:**

The goals of this course include introducing the students to mathematical modeling and simulation for solving problems in Biology, exposing the students to computational and mathematical biology, and to solve real-life problems in biology using computational and applied mathematics.

III. **STUDENT LEARNING EXPECTED OUTCOMES/COMPETENCIES:**

After completing this course, students will be able to:

1) Mastering how to do mathematical modeling for problems in biology,
2) Mastering how to use Python commands and syntaxes in mathematical modeling and simulation for problems in biology,
3) Mastering common usage of numerical methods to solve problems in biology,
4) Mastering working on individual and collaborative projects to solve problems in biology.

Student Responsibility: Typically, for a student to excel in college, he/she should put in at least two hours outside of class (or

Team Member:
Widodo Samyono,
Jarvis Christian University

Team Mentor:
Je'aime Powell,
TACC

Team Theme Song: Hey Bulldog, The Beatles,
https://www.youtube.com/watch?v=M4vbJQ-MrKo

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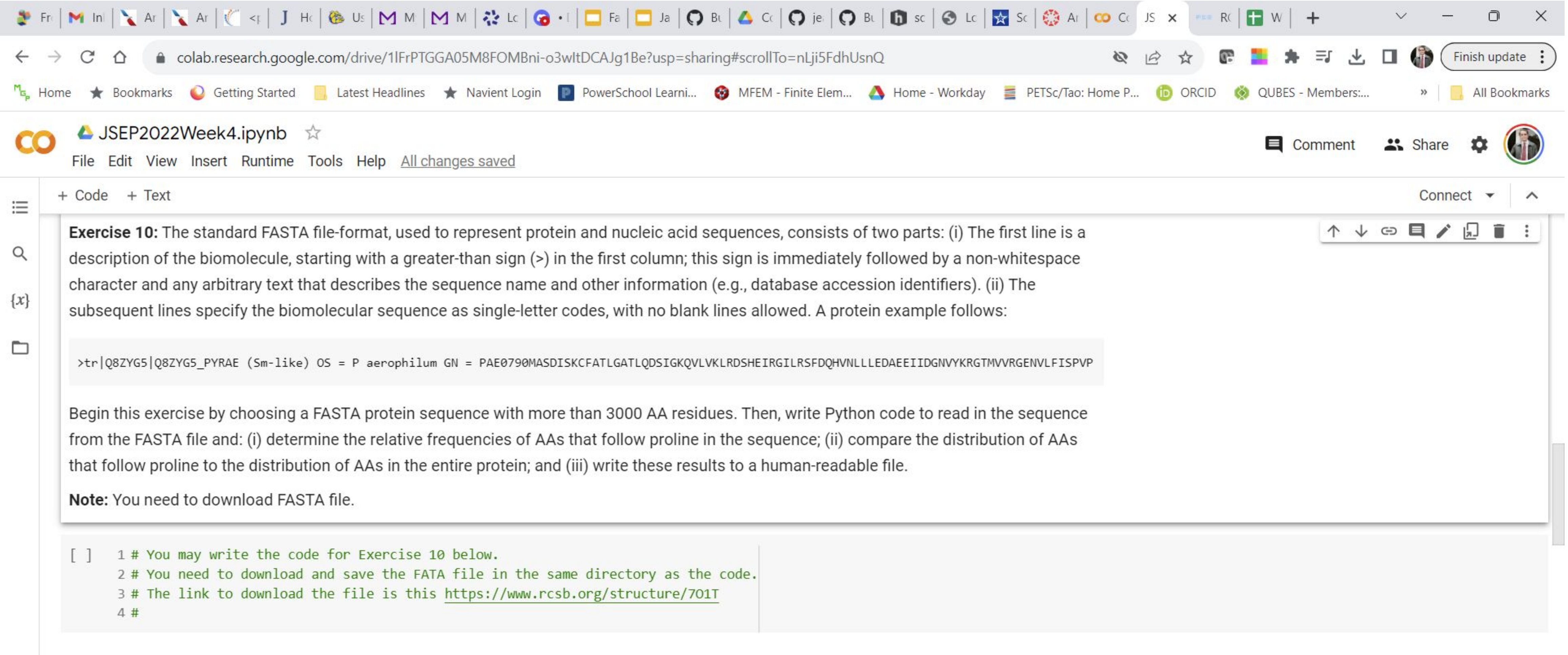
Sample Exercises



Exercise 10: The standard FASTA file-format, used to represent protein and nucleic acid sequences, consists of two parts: (i) The first line is a description of the biomolecule, starting with a greater-than sign (>) in the first column; this sign is immediately followed by a non-whitespace character and any arbitrary text that describes the sequence name and other information (e.g., database accession identifiers). (ii) The subsequent lines specify the biomolecular sequence as single-letter codes, with no blank lines allowed. A protein example follows:

```
>tr|Q8ZYG5|Q8ZYG5_PYRAE (Sm-like) OS = P aerophilum GN = PAE0790MASDISKCFATLGATLQDSIGKQVLVKLRDSHEIRGILRSFDQHVNLLLEDAEEIIDGNVYKRGTMVVRGENVLFISPVP
```

Begin this exercise by choosing a FASTA protein sequence with more than 3000 AA residues. Then, write Python code to read in the sequence from the FASTA file and: (i) determine the relative frequencies of AAs that follow proline in the sequence; (ii) compare the distribution of AAs that follow proline to the distribution of AAs in the entire protein; and (iii) write these results to a human-readable file.

Note: You need to download FASTA file.

[ ]

```
# You may write the code for Exercise 10 below.
# You need to download and save the FATA file in the same directory as the code.
# The link to download the file is this https://www.rcsb.org/structure/7O1T
#
```

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Supporting Gateways

1) SGX3 Science Gateways https://sciencegateways.org/education-training/resources#/
2) Design Safe Gateways https://www.designsafe-ci.org/
3) Texas Advanced Computing Center (TACC) https://www.tacc.utexas.edu/
4) Jetstream2 https://jetstream-cloud.org/index.html
5) ACCESS https://access-ci.org/