# Sample Syllabi – Subject to Change
# Mathematical and Computational Research in Biological Sciences
## An Introductory Hands-on Course in Application of Quantitative Methods in Biology

**Instructor:**     Esmael J. Haddadian, Ph.D.

**Lectures:**                 MTWRF: 9:30-11:00 AM
**Computer Labs:**           MTWRF: 12:30-3:30 PM

**Course description and objectives:** Using computation to model and study biological systems is one of the leading edges of current scientific research. This course is designed to provide a stimulating introduction to the application of computation to model and study biological systems. In this hands-on exploration of the latest techniques, students will learn how macromolecules, such as DNA, RNA, and proteins, perform their functions and how to visualize and quantify their behavior. This course will provide an introduction to the basics of computer coding for biological data analysis, and how to apply cutting-edge high performance computation to biological questions using the super computers at the University of Chicago Research Computing Center (RCC). Students will be instructed on how to use the internet to do literature searches, how to prepare a scientific poster and how to plan and deliver an oral presentation.

## Grading Components

26%     Computer lab reports

17%     Exam-1

17%     Exam-2

10%     Group projects, class presentations/participation

30%     Final project poster

**Final Project:** students will use the super computer Midway to process and analyze whole-exome next generation sequencing data. The exome is the part of the genome formed by exons, the sequences which when transcribed remain within the mature RNA after introns are removed by RNA splicing. Exome sequencing is a process by which the DNA from canonical coding regions (genes) is selectively captured and sequenced. Using state of the art tools, students will annotate large samples of exomes from the 1000 genome project in order to identify disease-relevant variants. They will subsequently prepare about their findings.

## Lab Software:
R:                  http://www.r-project.org
R-studio:           http://www.rstudio.com
Unix commands:      https://kb.iu.edu/d/afsk
                    http://mally.stanford.edu/~sr/computing/basic-unix.html
VMD is free software that can be downloaded from
http://www.ks.uiuc.edu/Development/Download/download.cgi?PackageName=VMD
VMD tutorial
http://www.ks.uiuc.edu/Training/Tutorials/vmd/tutorial-html/index.html

**Textbooks:** <u>Scans of these book's chapters will be available on Canvas</u>
1. Campbell, Biology (11<sup>th</sup> edition), Pearson Benjamin Cummings Publishers. ISBN: 978-0-13-409341-3.
2. Bioinformatics for Beginners: Genes, Genomes, Molecular Evolution, Databases and analytical Tools. Supratim Choudhuri. ISBN: 978-0-12-410471-6.
3. Understanding Bioinformatics. Marketa Zvelebil and Jeremy O. Baum. ISBN: 978-0-8153-4024-9

# Week 1
**Lectures:**
The chemical context of life
Water and life
Carbon and the molecular diversity of life
The structure and function of large biological molecules
Genomic technologies

**Labs:**
An introduction to computer programing
An introduction to R, a free software environment for statistical computing and graphics
Visualizing macromolecules in 3D

**Activities:**
Visiting DNA sequencing and genotyping facility

# Week 2
**Lectures:**
Amino acids, Proteins
Biological sequence alignment and analysis
An introduction to high performance computation and its application in biological sciences

**Labs:**
Writing an open reading frame code (ORF) to identify the coding part of a given DNA
DNA/protein sequence alignment and analysis
Introduction to UNIX commands as gateway to supercomputers

**Activities:**
Computational biology in the news, presentations on a topic in computational/ quantitative biology

# Week 3
**Lectures:**
Genome annotation
Biological data bases
Human Genetic Diseases

**Labs:**
Analyzing and annotating a large human genome data using the supercomputer Midway

**Activities:**
Visiting the university data center (supercomputer Midway)
Poster presentations

| Topic & Reading | Lab |
|---|---|
| The chemical context of life<br>Water and life<br>*Book: Chapters 2, 3, Campbell biology* | Intro-Programing-1:<br>Introduction to R |
| Carbon and the molecular diversity of life<br>The structure and function of large biological molecules<br>*Book: Chapters 4 and 5, Campbell biology* | Intro-Programing-2:<br>Vectors and matrices in R |
| The structure and function of large biological molecules<br>*Continued, Chapter 5, Campbell biology* | Intro-Programing-3: Lists, Data frames, and Functions |
| The molecular base of inheritance: DNA and RNA<br>*Book: Chapters 16, Campbell biology* | Intro-Programing-4:<br>Graphing in R |
| Genomic technologies<br>*Book: Chapter 20, Campbell biology* | Visualizing Macromolecules: Introduction to Vmd-1<br>**Visiting DNA sequencing and genotyping facility** |
| Amino acids, Proteins<br>*Chapter 2 Understanding Bioinformatics*<br>**Exam-1** | Introduction to Vmd-2<br>Open reading frame code, part-1 |
| Sequence alignment and similarity<br>*Book: Chapter 6, Bioinformatics for Beginners*<br>*Chapter 2 Understanding Bioinformatics* | Open reading frame code, part-2<br>Pairwise sequence alignment |
| Sequence alignment and similarity (continued)<br>*Book: Chapter 6, Bioinformatics for Beginners*<br>*Chapter 2 Understanding Bioinformatics* | Multiple sequence alignment |
| An introduction High performance computation-1 | Connecting to the supercomputer<br>*Midway*<br>Introduction to Unix |
| Genome annotation<br>An introduction High performance computation-2<br>**Exam-2** | Genome annotation-1<br>**Visiting university data center (super computer Midway)** |
| Data and databases search<br>*Book: Chapter 5, Bioinformatics for Beginners*<br>*Chapter 3 Understanding Bioinformatics* | Genome annotation-2 |
| Team poster preparation | Poster Preparation |
| Poster presentations | No-Lab |