

Introduction to Bioinformatics

This introductory bioinformatics course from INBRE is designed for undergraduate students to gain technical training in bioinformatics. This course is focused on providing students with the necessary skills to learn R programming and utilize this software in their own biological data analysis. Through hands-on exercises and practical examples, they will gain proficiency in utilizing R to process, manipulate, and visualize data. Additionally, this course will cover essential concepts and techniques for performing a general genome analysis. No prior experience with R is necessary and by the end of the course, students will be equipped with the foundational knowledge and practical skills required to integrate bioinformatics into their own research projects.

This course will be held via Zoom over a 9-Week period. Links to the Zoom sessions will be given at a later date.

Graduate Assistant:

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INBRE Bioinformatics Objectives:

Gain knowledge of bioinformatic data. Gain knowledge of basic R programming and common tools for processing bioinformatic data.

Course Objectives:

1. Use R to enter and edit expressions and scripts.
2. Read, subset, and reshape, tabular data.
3. Find and install external R packages.
4. Make figures and tables from data.
5. Knowledge of bioinformatic data, including types of data, types of data science, and current challenges in large bioinformatic data sets.
6. Know basic principles of designing a bioinformatic study.

Required Materials:

R Studio and Mega are required for this course. Both are free for download and can be found at the links below. We will download the software together in class, but feel free to do it prior too.

To begin working with R studio there are two programs that you must download. One being the core R software and the other being R studio where you will conduct all of your R coding.

<http://cran.r-project.org/>

<http://rstudio.com>

<https://mega.io/>

Course Format:

Week 1 Introduction	
<p>June 14, 2023</p>	<p>Intro to R programming</p> <ul style="list-style-type: none"> • Instillation • Onboarding • How to submit homework and R Markdown Documents <p>R Packages</p> <ul style="list-style-type: none"> • Package Databases • Installing Packages <p>Basic R Functions</p> <ul style="list-style-type: none"> • Basic Operations (Vectors, Variables) • Intro to ggplot2 <p>Assignments: HW1 – Intro to R and ggplot2, Quiz 1</p>
Week 2 Molecular Biology Introduction and Biological Databases	
<p>June 21, 2023</p> <p>Due: HW1</p> <p>Quiz 1</p>	<p>Molecular Biology Introduction</p> <ul style="list-style-type: none"> • Central Dogma of Molecular Biology • Human Genome • Introns/Exons • Mutations <p>Biological Databases Introduction</p> <ul style="list-style-type: none"> • Types of Databases • NCBI Introduction <p>Choose Project</p> <ul style="list-style-type: none"> • Hemoglobin • Cytochrome C • Histone H1 • Rheumatoid Factor

	<ul style="list-style-type: none"> • Beta-2 microglobulin • EGFR <p>Assignments: HW2 – NCBI & PubMed, Quiz 2</p>
Week 3	
Sequence Alignment in BLAST	
<p>June 28, 2023</p> <p>Due: HW2</p> <p>Quiz 2</p>	<p>Methods of Sequence Alignment</p> <ul style="list-style-type: none"> • Algorithms • Local vs. Global <p>R Tools for Sequence Alignment</p> <ul style="list-style-type: none"> • Biostrings <p>Assignments: HW3 – Biostrings, Quiz 3</p>
Week 4	
Multiple Sequence Alignment in R	
<p>July 5, 2023</p> <p>Due: HW3</p> <p>Quiz 3</p>	<p>Methods of Multiple Sequence Alignment</p> <ul style="list-style-type: none"> • MUSCLE • TCOFFEE <p>R Tools for Multiple Sequence Alignment</p> <ul style="list-style-type: none"> • MSA Package • Biostrings Package <p>Assignments: HW 4 – Multiple Sequence Alignment, Quiz 4</p>
Week 5	
Phylogenetic Trees	
<p>July 12, 2023</p> <p>Due: HW4</p> <p>Quiz 4</p>	<p>Phylogenetic Tree Construction</p> <ul style="list-style-type: none"> • Clustal Omega <p>Assignments: None! Practice/Prepare for Presentations</p>
Week 6	
Introduction to Molecular Phylogeny	

<p>July 19, 2023</p>	<p>Midterm Presentations: Present a cohort of at least 4 proteins with homology to your chosen protein.</p> <p>Assignments: Quiz 5</p>
<p>Week 7 MEGA</p>	
<p>July 26, 2023</p> <p>Due: Quiz 5</p>	<p>Midterm Presentations: Present a cohort of at least 4 proteins with homology to your chosen protein.</p> <p>MEGA: Molecular Evolutionary Genetics Analysis</p> <ul style="list-style-type: none"> • Understand features. • Interpret outputs. <p>Phylogenetic Tree Analysis</p> <ul style="list-style-type: none"> • Bootstrapping <p>Assignments: HW 5 – MEGA and Phylogenetics, Quiz 6</p>
<p>Week 8 Protein Structure/Function</p>	
<p>August 2, 2023</p> <p>Due: HW5</p> <p>Quiz 6</p>	<p>The Basics of Proteins</p> <ul style="list-style-type: none"> • Protein Structure (Primary, Secondary, Tertiary, Quaternary) • Post Translational Modifications • Predicting the 3-D shape of your favorite protein <p>Google’s Alphafold Algorithm for Protein Folding</p> <p>Assignments: HW6 – Protein Structure, Quiz 7, Final</p>
<p>Week 9 Guest Lecture and Final Project Due</p>	
<p>August 9, 2023</p> <p>Due: Final Paper/Poster</p> <p>Quiz 7</p>	<p>Guest Lecture: AI and Bioinformatics Dr. Bjarne Bartlett</p> <p>Final Paper</p> <ul style="list-style-type: none"> • 1-2 page research paper or alternatively a poster on your phylogenetic analysis of a particular protein group.

	Course Evaluation Survey
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Assignments:

Assignments are for students to measure progress learning the basics of bioinformatics. Assignments are required for a course certificate.

Final Project:

The final project will be chosen from a list of suggested projects and completed in groups. Individual/custom final projects are accepted/encouraged.

University of Hawaii Executive Policy 12.211

Reporting suspected academic, scientific and research misconduct is a shared and serious responsibility of all members of the academic community. Allegations should not be made capriciously, but indications or evidence of fraud or misconduct must not be ignored. Allegations of unethical conduct are serious and can ruin professional careers.