

BIMM 143: Introduction to Bioinformatics (Spring 2020)

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Course Website: https://bioboot.github.io/bimm143_S20/

***N.B.** For the Spring 2020 quarter, BIMM-143 will be offered online only*.*

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Overview: Bioinformatics - the application of computational and analytical methods to biological problems - is a rapidly maturing field that is driving the collection, analysis, and interpretation of the avalanche of data in modern life sciences and medical research.

This upper division 4-unit course is designed for biology majors and provides an introduction to the principles and practical approaches of bioinformatics as applied to genes and proteins. An integrated lecture/lab structure with hands-on exercises and small-scale projects emphasizes modern developments in genomics and proteomics. Major topics include: Genomic and biomolecular bioinformatic resources, Advances in sequencing technologies; Genome informatics, Structural informatics, and Transcriptomics. Computational tools, techniques and best practices that foster reproducible bioinformatics research will also be introduced. A comprehensive [website](#) containing all reading materials, screencasts and course notes will be maintained throughout the term.

Students completing this course will be able to apply leading existing bioinformatics tools to address biological questions. Our broader goal is to point towards perspectives that bioinformatics can expose for the integration and analysis of complex biological information.

Audience: Biology majors with upper division standing. A familiarity with basic biomedical concepts is essential (students should have successfully completed BILD1 and BILD4 or BIMM 101). No formal programming training or high level mathematical skills are required.

Requirements: To fully participate in this course students will be expected to use their own computers to access both class material and bioinformatics software and data resources that are freely available online.

Schedule: Video lectures and screencast hands-on sessions will be available on a weekly basis. Hands-on sessions will require both individual and small group based computational work.

Class announcements: All announcements regarding the course will be by email to your UCSD address. We will also be using [Piazza](#) to facilitate course communication, particularly around questions and answers. If you have a question outside of class or office hours, first check if it has already been asked on Piazza and if not post there. If you have a question or concern you don't feel comfortable posting on Piazza feel free to reach out via email.

Office hours: We will use [Zoom](#) on a weekly basis at a time to be determined from student polling. For now email me for a time and we will make it happen.

Textbook: There is no textbook for the course. **Lecture notes, homework assignments, grading criteria, video lectures, hands-on session screencasts** and required **reading material** will be available from our public facing [course website](#).

Piazza “clubhouse” forum: We will use [Piazza](#) to help facilitate course communication. If you have course related questions first check if they have already been asked on Piazza and if not post there. I also encourage students to post suggestions and strategies that can help their classmates cope with this most peculiar of quarters. Feel free to post something funny that relates to our course materials, your study skill suggestions, memes about our topics, videos, and, yes, the occasional complaint. My hope is that this "clubhouse" forum will allow us to support one another and give us all a feeling of camaraderie that we would experience in a traditional in-person class.

Course scope and syllabus outline: This is a tentative course schedule. The flow of topics might change slightly depending on how quickly/slowly it feels right to progress through them.

Week 1

Introduction to Bioinformatics and Key Online Bioinformatics Resources: NCBI & EBI

Biology is an information science, History of Bioinformatics, Types of data, Application areas: Introduction to upcoming segments, NCBI & EBI resources for the molecular domain of bioinformatics, Focus on GenBank, UniProt, Entrez and Gene Ontology.

Week 2

Sequence Alignment, DNA and Protein Database Searching

Homology, Sequence similarity, Local and global alignment, Database searching with BLAST, PSI-BLAST, Profiles and HMMs, Protein structure comparisons.

Week 3

Bioinformatics data analysis with R

Why do we use R for bioinformatics? R language basics and the RStudio IDE, Major R data structures and functions, Using R interactively from the RStudio console. Import biomolecular data in various formats (both local and from online sources).

Week 4

Data exploration and visualization in R

The exploratory data analysis mindset, Data visualization best practices, Simple base graphics (including scatterplots, histograms, bar graphs, dot charts, boxplots and heatmaps), Building more complex charts with ggplot.

Week 5

Writing your own R functions and working with R packages for bioinformatics

Using R scripts and Rmarkdown files, Import data in various formats both local and from online sources, The basics of writing your own functions that promote code robustness, reduce duplication and facilitate code re-use.

Week 6

Bioinformatics R packages from CRAN and BioConductor

More on how to write R functions with worked examples. Further extending functionality and utility with R packages, Obtaining R packages from CRAN and Bioconductor, Working with Bio3D for molecular data, Managing genome-scale data with bioconductor..

Week 7

Machine learning for bioinformatics

Unsupervised learning, K-means clustering, Hierarchical clustering, Heatmap representations. Dimensionality reduction, Principal Component Analysis (PCA). Longer hands-on session with unsupervised learning analysis of cancer cells further highlighting practical considerations and best practices for the analysis and visualization of high dimensional datasets.

Week 8

Genome informatics and high throughput sequencing

Searching genes and gene functions, Genome databases, Variation in the Genome, High-throughput sequencing technologies, biological applications, bioinformatics analysis methods. The Galaxy platform along with resources from the EBI & UCSC.

Week 9

Transcriptomics, RNA-Seq analysis, and the interpretation of gene lists

RNA-Seq aligners, Differential expression tests, RNA-Seq statistics, Counts and FPKMs and avoiding P-value misuse, Hands-on analysis of RNA-Seq data with R. Gene function annotation, Functional databases KEGG, InterPro, GO ontologies and functional enrichment analysis.

Week 10

Course wrap up, project completion

Summary of learning goals, Student course evaluation time; Find a gene assignment due. Open study or a student selected topic from those below:

Biological network analysis

Network based approaches for integrating and interpreting large heterogeneous high throughput data sets; Discovering relationships in 'omics' data; Network construction, manipulation, visualization and analysis; Major graph theory and network topology measures and concepts. Hands-on with Cytoscape and igraph packages.

Cancer genomics

Cancer genomics resources and bioinformatics tools for investigating the molecular basis of cancer. Mining the NCI Genomic Data Commons; Immunoinformatics and immunotherapy; Using genomics and bioinformatics to help design a personalized cancer vaccine. Implications for personalized medicine.

Hands-on with git

Hands-on introduction to git, currently the most popular version control system. We will learn how to perform common operations with git and RStudio. We will also cover the popular social code-hosting platforms GitHub, BitBucket and GitLab.

Essential statistics for bioinformatics

Review of data summary statistics; Inferential statistics; Significance testing; Two sample T-test; Power analysis; Multiple testing correction; and almost everything you wanted to know about p-values but were afraid to ask! Extensive R examples and applications.

Unix for bioinformatics

Bioinformatics on the command line, Why do we use UNIX for bioinformatics? UNIX philosophy, 21 Key commands, Understanding processes, File system structure, Connecting to remote servers, Redirection, streams and pipes, Workflows for batch processing, Organizing computational projects.

The future of bioinformatics

Applications of bioinformatics to translational medicine and the social impacts and ethical implications of how genomic sequence information is used in society. Example topics include: How to best balance privacy concerns with the desire to share and re-use data generated by taxpayer funded research? Should doctors know and preemptively act based on our genetic disease predispositions? How are racial DNA differences impacting racial prejudices?

Course Objectives:

At the end of this course students will:

- Understand the increasing necessity for computation in modern life sciences research.
- Be able to use and evaluate online bioinformatics resources including major biomolecular and genomic databases, search and analysis tools, genome browsers, structure viewers, and select quality control and analysis tools to solve problems in the biological sciences.
- Understand the process by which genomes are currently sequenced and the bioinformatics processing and analysis required for their interpretation.
- Be familiar with the research objectives of the bioinformatics related sub-disciplines of Genome informatics, Transcriptomics and Structural informatics.

In short, students will develop a solid foundational knowledge of bioinformatics and be able to evaluate new biomolecular and genomic information using existing bioinformatic tools and resources.

Specific Learning Goals

Teaching toward the specific learning goals below is expected to occupy 60%-70% of class time. The remaining course content is at the discretion of the instructor with student body input. This includes student selected topics for peer presentation as well one student selected guest lecture from an industry based genomic scientist.

All students who receive a passing grade should be able to:

- 1 Appreciate and describe in general terms the role of computation in hypothesis-driven discovery processes within the life sciences.

- 2 Be able to query, search, compare and contrast the data contained in major bioinformatics databases and describe how these databases intersect (GenBank, GENE, UniProt, PFAM, OMIM, PDB, UCSC, ENSEMBLE).
- 3 Describe how nucleotide and protein sequence and structure data are represented (FASTA, FASTQ, GenBank, UniProt, PDB).
- 4 Be able to describe how dynamic programming works for pairwise sequence alignment and appreciate the differences between global and local alignment along with their major application areas.
- 5 Calculate the alignment score between two nucleotide or protein sequences using a provided scoring matrix and be able to perform BLAST, PSI-BLAST, HMMER and protein structure based database searches and interpret the results in terms of the biological significance of an e-value.
- 6 Use R to read and parse comma-separated (.csv) formatted files ready for subsequent analysis.
- 7 Perform elementary statistical analysis on biomolecular and “omics” datasets with R and produce informative graphical displays and data summaries.
- 8 Appreciate and describe in general terms the rapid advances in sequencing technologies and the new areas of investigation that these advances have made accessible.
- 9 Understand the process by which genomes are currently sequenced and the bioinformatics processing and analysis required for their interpretation.
- 10 For a genomic region of interest (e.g. the neighborhood of a particular gene), use a genome browser to view nearby genes, transcription factor binding regions, epigenetic information, etc.
- 11 Given an RNA-Seq data file, find the set of significantly differentially expressed genes and use online tools to interpret gene lists and annotate potential gene functions.
- 12 Perform a GO analysis to identify the pathways relevant to a set of genes (e.g. identified by transcriptomic study or a proteomic experiment).
- 13 Use the KEGG pathway database to look up interaction pathways.
- 14 Understand the challenges in integrating and interpreting large heterogeneous high throughput data sets into their functional context.
- 15 Have an appreciation for the social impacts and ethical implications of how genomic sequence information is used in our society

Homework assignments and project:

Weekly homework will consist of online knowledge assessment quizzes and application assignments (a.k.a. "hands-on lab sections") together with pre-class reading and video screen-casts.

Specific grading criteria (assessment rubrics) for each homework will be given at the time of assignment. Weekly grades will be posted online. Each student is responsible for checking to ensure that a grade has been entered for their submissions. Documents submitted by email do not always arrive at their intended destination and late submissions will not be accepted after one week past the original due date. Collectively homework performance will account for 65% of the course grade.

A total of 35% of the course grade will be assigned based on the "*find-a-gene project assignment*". The purpose of this project assignment is for you to grasp the principles of database searching, sequence analysis, functional annotation and exploratory data analysis with R that we cover in the course (see additional details online). Further details will be given in class.

There will be no final exam for the Spring 2020 quarter.

Diversity and Inclusion.

I would like to create a learning environment for my students that supports a diversity of thoughts, perspectives and experiences, and honors your identities (including race, gender, class, sexuality, religion, ability, etc.) To help accomplish this:

- If you have a name and/or set of pronouns that differ from those that appear in your official UCSD records, please let me know!
- If you feel like your performance in the class is being impacted by your experiences outside of class, please don't hesitate to contact me. I want to be a resource for you. Remember that you can also submit anonymous feedback (which will lead to me making a general announcement to the class, if necessary to address your concerns).
- I (like many people) am still in the process of learning about diverse perspectives and identities. If something was said in class or online (by anyone) that made you feel uncomfortable, please talk to me about it. Again, anonymous feedback is always an option.
- As a participant in course discussions, you should also strive to honor the diversity of your classmates.
- Please contact me (in our person office hours or electronically) or submit anonymous feedback if you have any suggestions to improve the quality of the course materials or delivery mechanisms.

Ethics Code.

You are encouraged to collaborate with your fellow students. However, all material submitted to the instructor must be your own work.

"Academic Integrity is expected of everyone at UC San Diego. This means that you must be honest, fair, responsible, respectful, and trustworthy in all of your actions. Lying, cheating or any other forms of dishonesty will not be tolerated because they undermine learning and the

University's ability to certify students' knowledge and abilities. Thus, any attempt to get, or help another get, a grade by cheating, lying or dishonesty will be reported to the Academic Integrity Office and will result sanctions.

Sanctions can include an F in this class and suspension or dismissal from the University. So, think carefully before you act. Before you act, ask yourself the following questions: a) is my action honest, fair, respectful, responsible & trustworthy and, b) is my action authorized by the instructor? If you are unsure, don't ask a friend—ask your instructor, instructional assistant, or the Academic Integrity Office”.

You can learn more about academic integrity at academicintegrity.ucsd.edu
(Source: UCSD Academic Integrity Office, 2018)

***A note on COVID-19**

At the time of writing we are in the middle of a major COVID-19 pandemic crisis. Whilst we are making every effort to support your learning online, nothing is going to fully compensate for what we are going to lose in the next few months. My hope is that this online course can serve as a venue where we build a vibrant supportive community and utilize this forced distancing as a productive learning time.