BENG 183. Applied Genomic Technologies

Syllabus

Instructor: Sheng Zhong, Ph.D. Professor of Bioengineering.
Lectures: TuTh 2:00-3:20pm.
Classroom: PFBH 191.

TAs and emails:

- Joe Solvason, solvason@eng.ucsd.edu
- Gaoyuan Li, gaoyuan-li@ucsd.edu
- Joshua Burrows, jtburrow@ucsd.edu

TA office hours:

- Joe Solvason: Fri 2:30-3:30pm https://ucsd.zoom.us/j/4438298331#success
- Gaoyuan Li: Mon 3-4pm, https://ucsd.zoom.us/j/91438627959
- Joshua Burrows: Wed 4-5pm, https://ucsd.zoom.us/s/98354668940

Prerequisites

BIMM 100 or CHEM 114C, or consent of department.

Course Description

This course introduces genomics technologies and their biomedical applications. Students will learn and genome sequencing, RNA sequencing, and the computational methods for analyses of these data. Probability theory and applications together with the basics of machine learning methods will be introduced. Students will be able to formulate hypotheses and perform statistical tests. Students will be able to design gene expression analysis experiments, transform next-generation sequencing data into summary data matrix, identify differentially expressed genes, perform K-nearest neighbor classification, perform hierarchical clustering and K-means clustering. Contemporary research developments on personalized medicine and liquid biopsy analyses will be discussed.

Schedule

This course has six modules. This course will have a mixture of in-person lectures and pre-recorded lectures. Please only come to the classroom when a lecture is marked “in person”.

Pre-recorded lectures will be posted on the course website on or before the lecture date and time. Please do not come to the classroom for the pre-recorded lectures.

The lecturer has requested the in-person lectures be podcasted.

- Module 1: DNA sequencing, RNA sequencing, and ChIP sequencing
  - Lecture 1 – 4: 9/22: In person.
  - 9/27: Pre-recorded lecture.
  - 9/29: In person.
  - 10/4: pre-recorded lecture.
- Module 2: Analysis of RNA-seq data

    - Lectures 5 – 7: 10/6: Pre-recorded lecture.
    - 10/11: In person.
    - 10/13: Pre-recorded lecture.
- Midterm 1: 10/20, take home.
- Module 3: Genome interaction and a primer to precision medicine
    - Lectures 8 – 10: 10/18, 10/25: Pre-recorded lectures.
    - 10/27: In person.
- Module 4: Random variable and hypothesis testing
    - Lectures 11 – 13: 11/1, 11/3, 11/8: Pre-recorded lectures.
- Module 5: A primer to machine learning and applications to cancer classification.
    - Lectures 14 – 16: 11/10, 11/15: In person.
    - 11/17: Pre-recorded lecture.
- Midterm 2: 11/22, take home.
- Module 6: Group presentations.
    - Sessions 17 – 18: 11/29, 12/1. In person.

Course Calendar

Please check out the course calendar from the course website.

Textbook and Other Materials

Required Reading

1. Applied Genomic Technologies (course handout), https://github.com/Zhong-Lab-UCSD/BENG183_2022Fall_Applied-Genomic-Technologies
2. 3D Genome (eBook), Xingzhao Wen and Sheng Zhong, Open Access Publications from the University of California (eScholarship), https://zhonglab.gitbook.io/3dgenome
3. Introduction to Probability, Statistics, and Random Processes, Hossein Pishro-Nik, Kappa Research, LLC. August 24, 2014. ISBN-10: 0990637204. ISBN-13: 978-0990637202. Please note that the textbook is also freely available online: https://www.probabilitycourse.com/

Additional Materials

In addition to the textbook listed above, there is a plethora of available information on the Internet. This information includes peer-reviewed manuscripts, Wikipedia articles, YouTube videos of lectures from UCSD and/or other universities, and much more. A course handout will be provided. Students are strongly encouraged to review additional online materials prior to each lecture.

Course Outcomes

After successfully completing this class, a student will be able to:
1. Understand the technologies of Sanger sequencing, sequencing by synthesis, RNA sequencing, and extracellular-RNA sequencing.
2. Design genomic technologies to identify gene expression biomarkers.
3. Apply probability theory to solve real-life problems.
4. Formulate statistical hypotheses and perform hypothesis testing.

5. Identify differentially expressed genes from gene expression data.
6. Cluster data from a data matrix.
7. Perform classification of data from a data matrix.
8. Analyze RNA sequencing data with bioinformatic software.