

BIOF 521: Bioinformatics for Analysis of Data Generated by Next Generation Sequencing

In this course, students will learn to analyze data generated by a variety of sequencing techniques (such as DNaseq, RNAseq and CHIP-seq) particularly in relation to biomedical applications (such as analysis of gene expression and identification of medically relevant sequence variation). While recorded lectures and readings will provide necessary background, the course emphasizes hands-on, self-paced lessons featuring real-world data sets to give the learner experience with all major steps of sequencing analyses, from filtering of raw data to creating polished figures. As the course progresses, students will work on a term project in which they design a sequencing project based on their own research interests. To make this course accessible to all students, we will focus on the use of publicly available resources, such as the NCBI SRA and the Galaxy platform, that can be accessed from anywhere.

Learning Objectives

Students in the course will:

- Compare and contrast a variety of modern sequencing techniques and their applications.
- Utilize and compare several platforms for the analysis of sequencing data.
- Carry out bioinformatics analyses on biomedically relevant sequencing data sets.
- Interpret the results of these analyses by generating figures and written summaries.
- Develop a sequencing and analysis plan for a project relevant to their own research interests.

Credits: 2

Class Type: Graduate Course

Prerequisites:

This course has no official pre-requisites. However, the course material assumes that you are familiar with general genetics and statistics concepts at the level expected from undergraduate coursework. No prior knowledge of bioinformatics data analysis or programming languages is required.

Program: Bioinformatics and Data Science

Availability Summer 2022