

BIOS/BCB785: Statistical Methods for Gene Expression Analysis (Spring 2019)

Instructor

Yuchao Jiang

Assistant Professor

Department of Biostatistics & Department of Genetics

4115D McGavran-Greenberg Hall & 5112 Genetic Medicine Building

Email: yuchaoj@email.unc.edu

Classes meet

Tuesday and Thursday, 01/09/2019 - 04/26/2019

11:00am – 12:15pm, 1305 McGavran-Greenberg Hall

Office hours

Thursday 2:30pm – 3:30pm, 4115D McGavran-Greenberg Hall

Course description

This course is designed to provide graduate students interested in statistical genetics and genomics with an opportunity to gain or enhance knowledge in gene expression analysis by next-generation sequencing. The course is aimed at preparing students for conducting methodological research in high-throughput transcriptomic studies. The course includes two sections: bulk RNA-seq and single-cell RNA-seq (scRNA-seq). Each section starts with biological background, followed by statistical and computational methods, and finishes with biological interpretations and follow-ups. Topics include: data normalization, measurement of error models, dispersion shrinkage, dimensionality reduction, zero-inflated factor analysis, batch correction, clustering algorithm, deconvolution, pseudotime reconstruction, deep neural network, and autoencoder, etc.

Prerequisites

BIOS 661 and 663 or permission of the instructor.

Course content

The following course content is a tentative plan. We may not strictly follow it.

| Week | Date | Topics |
|------|---------------|--|
| 1 | 01/10 | Overview of molecular biology with emphasis on gene expression |
| 2 | 01/15 & 01/17 | Introduction to RNA-seq, normalization, differential expression |
| 3 | 01/22 & 01/24 | Allele-specific expression and isoform expression |
| 4 | 01/29 & 01/31 | Expression quantitative trait loci (eQTL) |
| 5 | 02/05 & 02/07 | Introduction to scRNA-seq |
| 6 | 02/12 & 02/14 | Dimensionality reduction, data visualization, and clustering |
| 7 | 02/19 & 02/21 | Noise modeling, normalization, and batch correction |
| 8 | 02/26 & 02/28 | Gene expression distribution, identifying differential distributions |
| 9 | 03/05 & 03/07 | Deep neural network for gene expression |
| 10 | 03/12 & 03/14 | No classes (spring break) |
| 11 | 03/19 & 03/21 | Autoencoder and transfer learning for scRNA-seq |
| 12 | 03/26 & 03/28 | Pseudo-time reconstruction |
| 13 | 04/02 & 04/04 | Gene expression deconvolution |
| 14 | 04/09 & 04/11 | scRNA-seq in cancer |
| 15 | 04/16 & 04/18 | Final project presentations |
| 16 | 04/23 & 04/25 | Final project presentations |