

# BIOS785 Statistical Methods for Gene Expression Analysis (Spring 2019)

## Instructor

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## Classes meet

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

11:00 AM - 12:30 PM

1305 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 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 bulk RNA-seq, normalization, differential expression
3	01/22 & 01/24	Allele-specific and isoform-specific 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, clustering
7	02/19 & 02/21	Noise modeling, normalization, batch correction
8	02/26 & 02/28	Gene expression distribution, identifying differential distributions
9	03/05 & 03/07	No classes (spring break)
10	03/12 & 03/14	Deep neural network for gene expression
11	03/19 & 03/21	Autoencoder for denoising
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