

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 sequencing and single-cell RNA sequencing (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

Week	Date	Topics
1	01/10	Overview of molecular biology with emphasis on transcription and 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