

BIOS/BCB785: Statistical Methods for Gene Expression Analysis (Fall 2020)

Instructor

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Classes meet

Monday and Wednesday, 08/10/2020 - 11/17/2020
09:20am – 10:35am
Remote teaching via Zoom

Office hours

Virtual via <https://whereby.com/yuchaoj>; time TBD.

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 website/slack

<https://github.com/yuchaojiang/BIOSBCB785>
<http://unc785fall2020.slack.com/>

Grading scale

Final course grades will be determined following [UNC Graduate School grading scale](#), based on attendance and class participation (20%), written reviews (30%), project proposal (10%), project presentation (20%), and project report (20%). Top 25% of the registered students will receive H.

Grader

TBD.

Course schedule (subject to change)

[Google sheet](#)