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 strictfly follow it.

Date	Lecture	Topic	Paper(s)	Note
01/10/19	1	Logistics and introduction to molecular biology with an emphasis on gene expression	NA	
01/15/19	2	Introduction to RNA-seq	Review: Conesa et al., Genome Biology, 2016	
01/17/19	3	Bulk gene expression data normalization	RUV: Risso et al., Nature Biotech., 2014	
01/22/19	4	Bulk gene expression batch correction	ComBat: Johnson et al., Biostatistics, 2007 svaseq: Leek, Nucleic Acids Research, 2014	
01/24/19	5	Isoform expression	Jiang & Wong, Bioinformatics, 2009	
01/29/19	6	Allele-specific expression and mapping of eQTLs	Sun, Biometrics, 2012	
01/31/19	7	Bulk gene expression deconvolution	csSAM: Shen-Orr et al., Nature Methods, 2010 CIBERSORT: Newman et al., Nature Methods, 2015	
02/05/19	8	Differential expression	DESeq2: Love et al., Genome Biology, 2014 LIMMA: Ritchie et al., Nucleic Acids Res., 2015	Guest lecture by Mike Love
02/07/19	9	Gene set enrichment analysis	Subramanian et al., PNAS, 2005	Guest lecture by Di Wu
02/12/19	10	Overview of scRNA-seq	Review: Stegle et al., Nature Reviews Genetics, 2015 Review: Kolodziejczyk et al., Molecular Cell, 2015	
02/14/19	11	scRNA-seq quality control	Scater: McCarthy et al., Bioinformatics, 2017	
02/19/19	12	Dimensionality reduction and data visualization	Becht et al., Nature Biotech., 2018	
02/21/19	13	scRNA-seq clustering	SAFE-clustering: Yang et al., Bioinformatics, 2018	Guest lecture by Yun Li
02/26/19	14	scRNA-seq data normalization	Review: Bacher & Kendziorski, Genome Biology, 2016 SCnorm: Bacher et al., Nature Methods, 2017	Guest lecture by Rhonda Bacher
02/28/19	15	scRNA-seq denoising and imputation	SAVER: Huang et al., Nature Methods, 2018 MAGIC: Dijk et al., Cell, 2018	
03/05/19	16	Batch correction by scRNA-seq	CCA: Butler et al., Nature Biotech., 2018 MNN: Haghverdi et al., Nature Biotech., 2018	
03/07/19	17	(Differential) Gene expression distribution	scDD: Korthauer et al., Genome Biology, 2016 DESCEND: Wang et al., PNAS, 2018	
03/12/19	Spring break	NA	NA	Spring break
03/14/19	Spring break	NA	NA	Spring break
03/19/19	18	Allele-specific gene expression by scRNA-seq	SCALE: Jiang et al., Genome Biology, 2017	
03/21/19	19	Introduction to deep neural network	Goodfellow et al., MIT Press, 2016	
03/26/19	20	Autoencoder and transfer learning for scRNA-seq	scVI: Lopez et al., Nature Methods, 2018 DCA: Eraslan et al., bioRxiv, 2018 SAVER-X: Wang et al., bioRxiv, 2018	ENAR 2019
03/28/19	21	Pseudotime reconstruction by scRNA-seq	TSCAN: Ji & Ji, Nucleic Acids Research, 2016 Monocle 2: Qiu et al., Nature Methods, 2017	
04/02/19	22	Gene expression deconvolution by scRNA-seq	Zhu et al., Annals of Applied Statistics, 2018 MuSiC: Wang et al., bioRxiv, 2018	Project proposal due before class
04/04/19	23	Multi-modal alignment of single-cell transcriptomic and epigenomic data	Duren et al., PNAS, 2018	
04/09/19	24	scRNA-seq for cancer genomics	Cardelino: McCarthy et al., bioRxiv, 2018	
04/11/19	25	Copy number variation detection by scRNA-seq	Patel et al., Science, 2014 Fan et al., Genome Research, 2018	
04/16/19	Final presentation	NA	NA	
04/18/19	Final presentation	NA	NA	
04/23/19	Final presentation	NA	NA	
04/25/19	Final presentation	NA	NA	Project final report due before class