



“Conceptualizing a pipeline from single cell data to predictive mathematical modeling”

**NorthShore University HealthSystem
Research Institute
1001 University Place, Evanston, IL
Conference Room 118**

PROGRAM

Wednesday, March 4, 2020

9:00 AM – 5:00 PM

Moderators

8.55 AM -9.00 AM - Welcome - Simon Hayward (NorthShore)/Timothy Ratliff (Purdue)

scRNAseq

9.00 AM – 9:45 AM - Douglas Strand (UT Southwestern)
A cellular atlas of the normal and diseased human prostate

9.45 AM – 10:30 AM - Renee Vickman (NorthShore)
“Deciphering human prostate carcinoma-associated fibroblast heterogeneity using scRNA-seq”

10.30-10.45 Coffee Break

Data Processing/Statistical Approaches

10.45 AM – 11:30 AM - Nadia Lanman (Purdue)
“Gaining insight into the heterogeneity of Benign Prostatic Hyperplasia using scRNA-Seq”

11.30 AM – 12:15 PM - Mengjie Chen (University of Chicago)
“How to pre-process single cell RNA-seq UMI data”

12.15-1.30 Lunch

Mathematical Approaches to Pathway Analysis

1.30 PM – 2:15 PM - Yuan Ji (University of Chicago)
“Bayesian graphical models with application to cancer genomics”

2.15 PM – 3:00 PM - Meaghan Broman (Purdue)
“Exploring immune cell interactions in benign prostatic hyperplasia”

3.00-3.15 Coffee Break

Cell-based mathematical models

3.15 pm- 4:00 PM - David Basanta (Moffitt Cancer Center, Tampa)
“Setting the stage for cancer: agent-based modeling in cancer and homeostasis”

4.00 PM – 4:45 PM – Alexander Anderson (Moffitt Cancer Center, Tampa)
“The role of reactive stroma in tumor evolution and drug resistance.”

4.45 PM – 5:00 PM - Comments and Discussion

5.00 PM - Meeting Adjourn