

# First Year RPG Discussion

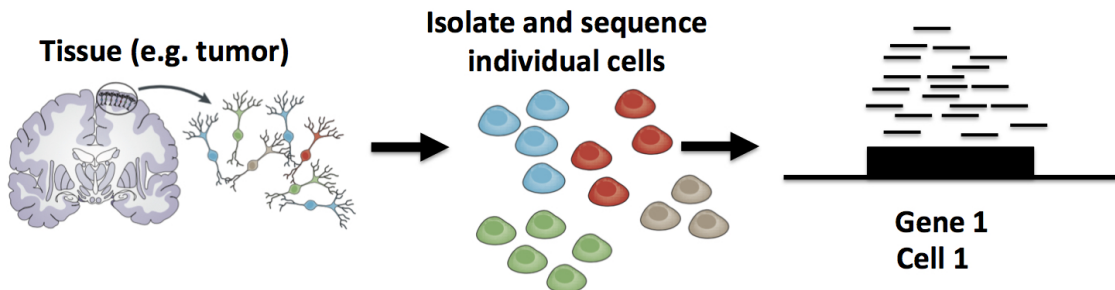
Xinyi Lin

Supervisor: Joshua Ho

2021/03/31 (updated: 2021-04-07)

# Background

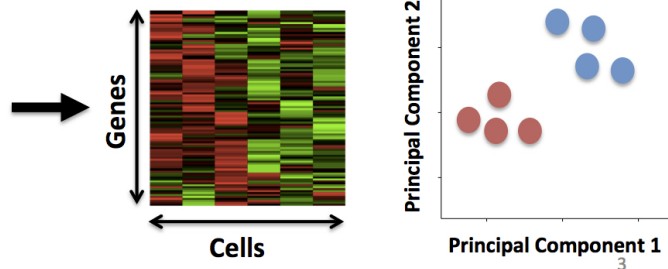
## Single-cell RNA-Seq (scRNA-Seq)



**Read Counts**

	Cell 1	Cell 2	...
Gene 1	18	0	
Gene 2	1010	506	
Gene 3	0	49	
Gene 4	22	0	
...			

**Compare gene expression profiles of single cells**



# Background

- Applications
  - cell development
  - tumor development
  - diseases' mechanism
- Challenges
  - cell clustering
  - dynamic changes on different cell types
  - trajectory analysis
  - data integration

# Background

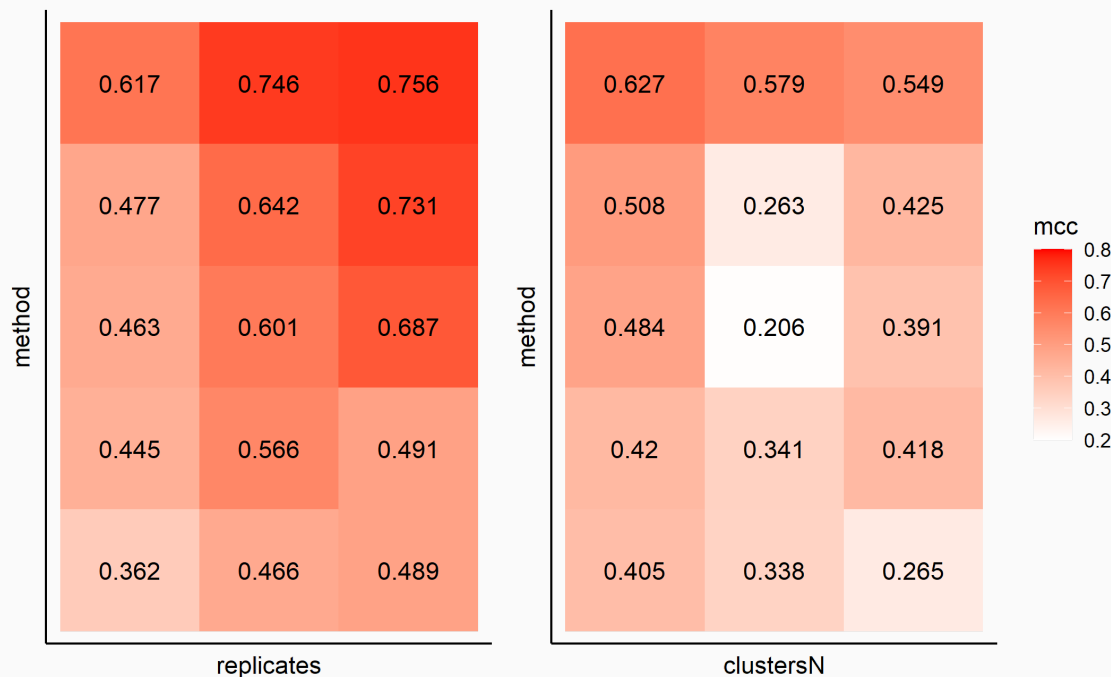
- Tissues are cellular heterogeneity
- Composition difference exists
- Interested in changes of proportions in dynamic process

# Current Project: DCATS

- R package designed for differential composition analysis on single cell data
- Basic assumptions
  - misclassification error exists
  - cell counts follow binomial distribution
- Input
  - cell counts matrices of samples coming from different conditions
  - a confusion matrix describing the misclassification error(user-input or calculated by DCATS)

# Current Projects: DCATS

- Simulation results

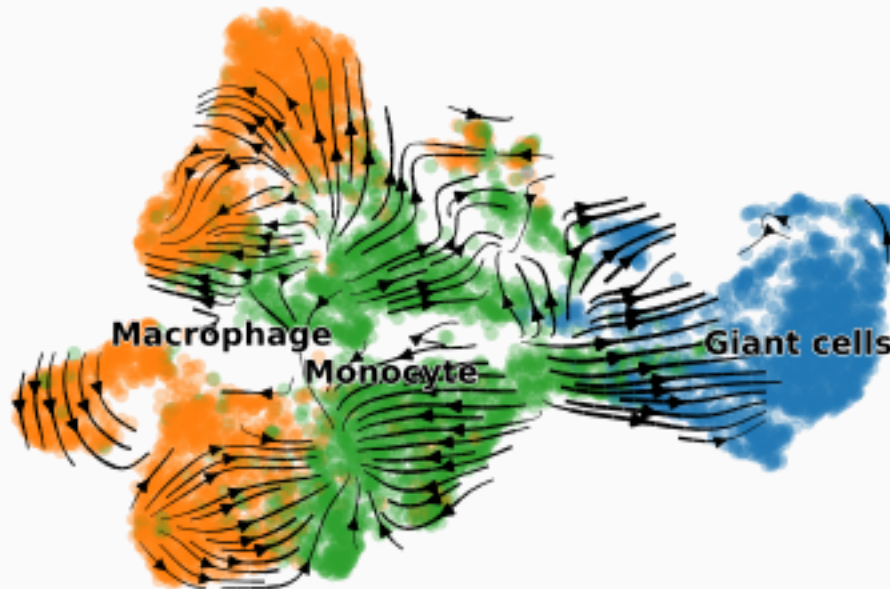


- Real world data analysis

- Give consistent conclusions as original papers: *Kang, Hyun Min, et al, 2018* and *Haber, Adam L., et al, 2017*

# Current Projects: other side projects(will be updated)

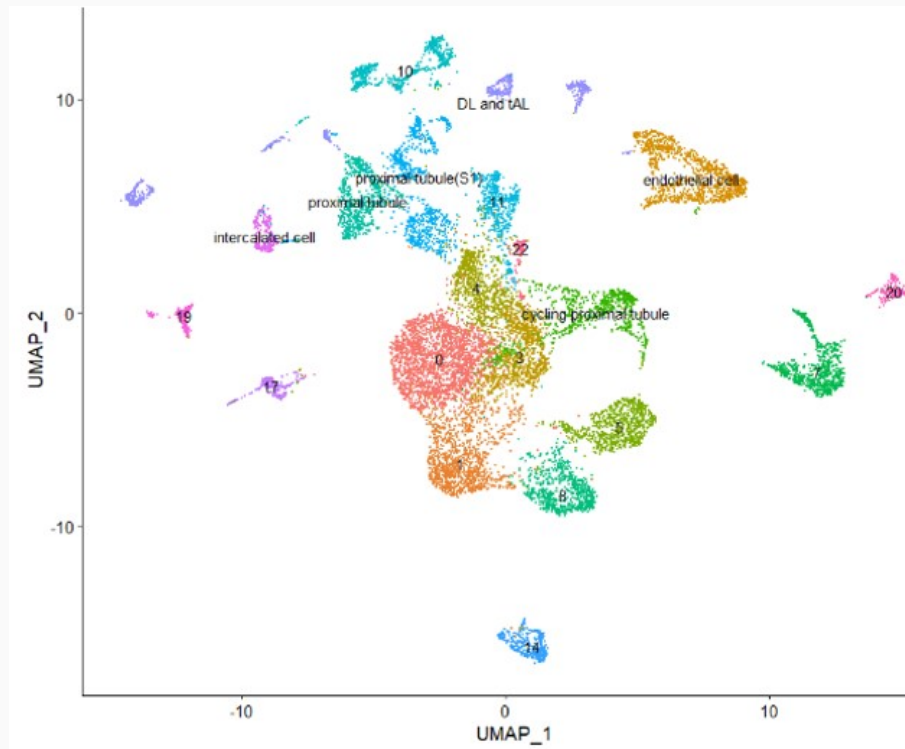
- Giant Cell Tumor of Bones(GCTB)
  - verify a somatic alterations(*H3F3A*, Gly34Val) on GCTB samples we have
  - trajectory analysis



Trajectory of myeloid cells

# Current Projects: other side projects(will be updated)

- Mouse's Kidneys
  - give a possible clustering result
  - identify some cell types based on the clustering result





# Future Plan: current projects

- DCATS: get it published
- Side projects
  - be familiar with computational tools related to scRNA-seq
  - finish related bioinformatics analysis
  - find out some new problems during collaboration
  - learn more biological knowledge

# Future Plan: exchange program

- Time: late 2022 or early 2023
- Duration: 3-6 months
- University: Peking University
- Goals: Collaborate with people there on some scRNA-seq related projects

# Future Plan: Other possible projects

- Comparing single cell information coming from mouse and human being
- Analyzing time series single cell information
- Statistical modeling for different types of single cell data

Thanks!