Several unanswered questions

1. Cancer: Cancer cell, stromal cells (fibroblast, blood vessel cells), immune cells (**TME**)

Goal: evaluate if **glutaminolysis** is the major energy source of cancer cells while immunes largely utilize **glucose** in XXX (e.g. XXX=kidney) cancer types.

Past studies

Existing limitations: The observation was made on mouse system, which could not reflect the metabolic characteristics of real human cancer.

Goal: we want to characterize or quantify the level of **glutaminolysis and glycolysis** in different cells collected from real human kidney cancer samples.

Data preparation: data downloading and filtering

Data processing: (to do 1 (Wennan), identify a method to predict and annotate cells in cancer microenvironments.)

You provide data -> Wennan

Data analysis (scFEA + manually organized pathways) -> Send results to you.

You will do the summary to check:

1. Which cell group or cluster has the more increased or decreased metabolic rate of which pathway or module？

Kidney cancer single cell data

**Branched chain amino acids metabolism** in cancer vs AD.

Products/Projects

R mark down:

1. Data downloading (Kevin)
2. Seurat (R)
3. scFEA try (Grace) (python notebook, pdf, html)
4. downstream analysis of scFEA analysis (R)
5. Association analysis (R)

Two backgrounds

1. Altered metabolism in human diseases and current limitations in understanding them. **Gene expression data**, scFEA(scFEA inputs and outputs) -> new capability. Input/Output. (Shaoyang)

Background + Literature review? \*\*\*\*

Whole study pipeline! \*\*\*\*

What did you do? \*\*

Long term research goal of the whole project. \*\*\*

1. Comprehensive collection of data sets (Kevin)

Single cell RNA-seq data \*\*

Background + Literature review + GEO database introduction? \*\*

Type of data sets and challenges, Availability of different types of experiments and how they contribute? \*\*\*\*

Method: R programming and text mining based data search and selection \*\*\*\*

Long term research goal. \*\*

Three (2.5) projects :

1. Branched chain amino acids metabolisms in cancer and Alzheimer’s diseases

Background, why we chose this topic \*\*\* (Noah)

Data \*\*

Analysis \*\*

Results \*\*

Conclusions \*\*

Future plans \*

1. Glytaminolysis/Glycolysis ratio in cancer vs normal tissue/cells through cancer types

Background, why we chose this topic \*\*\* (Jonathan)

Data \*\*

Analysis \*\*

Results \*\*\*\*!!!

Conclusions \*\*

Future plans \*

1. Glytaminolysis/Glycolysis ratio in different cell types of cancer

Background, why we chose this topic \*\*\* (Grace)

Data \*

Analysis \*

Results \*\*!!!

Conclusion of this study.\*

Conclusions of the whole team!!!\*\*\*\*

Future plans of the whole team\*\*\*\*