**Meeting: Oct 3, 2019 (12:00pm)**

* Additional questions about paper “Batch effects in single-cell Rna-sequencing data are corrected by matching mutual nearest neighbors”
  + The three assumptions in the paper do not have limitation or other words, these assumptions all make sense.
    - Assumption 1:
      * most of the time, the cells in different batches are from the same tissue or position. So these would be always at least one cell population presented in the batches
    - Assumption 2:
      * It is fair to say that the batch effect is orthogonal to the biological effect.
    - Assumption 3:
      * (Use figure 1 in the paper as reference)
  + Mathematics part:
    - The relationship between biological and batch effects is always additive.
* Limitation discussed about the paper:
  + The paper pair wisely compare the batches, what is the order to compare
  + Which group is regarded as the reference group to do the first batch effect comparison?
* Action plans:
  + Design simulation studies
  + Four time points as four batches
  + Each batch has 4, 5, 6, 7 cells types.

**Meeting: Sept 23, 2019 (12:30pm)**

* Questions about the following two papers:
  1. “Batch effects in single-cell Rna-sequencing data are corrected by matching mutual nearest neighbors”
  2. “bayNorm: Bayesian gene expression recovery, imputation and normalisation for single cell RNA-sequencing data”

**Meeting: Sept 13, 2019 (3:00pm)**

* Potential project
  1. Batch effect
* Read the following:
  1. “12 Grand Challenges in Single-Cell Data Science”
  2. \*\*\* “Batch effects in single-cell Rna-sequencing data are corrected by matching mutual nearest neighbors”
  3. \*\*\* “bayNorm: Bayesian gene expression recovery, imputation and normalisation for single cell RNA-sequencing data”
  4. “A test metric for assessing single-cell RNA-seq batch correction”

**Meeting: Sept 3, 2019 (3:00pm)**

* Read the following:

1. “Challenges in unsupervised clustering of single-cell RBA-seq data”
2. “Integrative single-cell analysis”

* Reading notes:
  1. “Challenges in unsupervised clustering of single-cell RBA-seq data”
     + Challenges in single-cell RNA data analysis
       - Technical
       - Computational
       - Biological
     + Important: Biological interpretation & annotation
  2. “Integrative single-cell analysis”
     + Biological terminologies to pick up
     + Relationship between DNA (which does not change in the cell) ----transcription---> RNA ----translation--> protein.