**Graduate Group in Epidemiology and Biostatistics**

**Lab Rotation (one page) Summary**

**Fall Semester 2019**

**Instructor: Mingyao Li**

**Student: Jiayi (Jessie) Tong**

**Project Title: Correcting gene expression batch effect in single-cell RNA-seq data**

**Overall Project Goals:** (What is the main objective of the project from the Lab or Mentor perspective)

The overall goal of this lab rotation is to expose the student to the latest development in single-cell RNA sequencing (scRNA-seq) technology, make the student understand statistical issues related to scRNA-seq data analysis, and teach the student to perform hands-on analysis of scRNA-seq data.

**Lab Rotation Student Goals:** (The specific piece(s) of the overall objective that the student will contribute to the overall goals).

* Develop an understanding of modern developments in scRNA-seq technology and the statistical issues related to it.
* Have a deeper understanding on gene expression batch effect correction algorithms.
* Evaluate different batch effect correction strategies using simulated benchmark datasets.

**Specific Tasks or Assignments:**

* Read key review papers on single-cell RNA-seq data analysis.
* Read methodology papers on batch effect correction of gene expression.
* Perform benchmark simulations to evaluate different batch effect correction strategies.
* If time permits, develop a better strategy to correct batch effect in gene expression.

**Expectations and Grading:**

* By the end of the rotation, the student should understand the technical and analytical challenges of scRNA-seq data analysis.
* The student is expected to perform simulations to evaluate the performance of different batch effect correction strategies.
* Grading: 1) The student will meet with the advisor once a week. The student is expected to read papers on single-cell RNA-seq data analysis and discuss with advisor on relevant statistical issues and biological interpretation (30%); 2) Simulations to evaluate batch effect correction strategies (60%); 3) Rotation project presentation (10%).

**Timeline:** First 3-4 weeks: read papers to have a broad understanding of single-cell technologies and statistical methods related to batch effect correction. Remaining weeks: perform simulations to explore various batch effect correction strategies.

**Innovation: (**statistical methodology, analytic technique or other)

Comparison of global correction and local correction for batch effect removal is novel in single-cell RNA-seq gene expression data analysis. Findings from this analysis have important implications for single-cell RNA-seq studies.

**Student Signature:** ­\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_ Date: \_\_\_\_\_09/23/2019\_\_\_\_\_\_\_\_\_

**Instructor Signature:** ­\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_ Date: \_\_\_\_\_\_\_\_09/21/2019\_\_\_\_\_\_