**Syllabus for Bioinformatics Bootcamp - Advanced Topics in Single Cell RNA-Seq (Spring 2020)**

**Dates and times:** Tuesdays 5-6:30PM, February 9th – March 16th

**Location**: <https://zoom.us/j/92316306974?pwd=OE55NXdZb2hFcFAxdlZpM29Wcm5yQT09>

**Instructor**: Henry Miller, M.S.  
**Title:** 3rd year graduate student, IBMS PhD Program  
**Email:** [millerh1@uthscsa.edu](mailto:millerh1@uthscsa.edu)

**Office hours:** <https://calendly.com/millerh1/30min>

**Advisor:** Yidong Chen, Ph.D.  
**Title:** Professor, Population Health Sciences  
**Email:** [cheny8@uthscsa.edu](mailto:cheny8@uthscsa.edu)

**Description and Learning Outcomes:**

This workshop will teach fundamental techniques in the analysis and interpretation of single cell RNA-Seq data. Most sessions will consist of a 30-40-minute lecture, followed by hands-on activities guided by the instructors which, if not completed before the workshop ends, will be finished for homework. In the final week, students will complete a final project which combines skills learned throughout the workshop.

This workshop is designed to teach you how to:

* Perform basic scRNA-Seq data preparation.
* Use manifold learning techniques to analyze cellular relationships in scRNA-Seq data.
* Find and interpret biologically-meaningful patterns in scRNA-Seq data.
* Integrate single cell data from multiple batches, studies, or modalities.
* Present the results of scRNA-Seq analyses with publication-quality figures.

**OF NOTE**: It is expected that all participants have working knowledge of R programming and basic RNA-Seq analysis. If you need to review these topics, please see the Fall 2020 Bioinformatics Bootcamp in which they are covered extensively: <https://uthscsa.box.com/s/bq936da9strq5u8g42y8sc9ppj3mq1jt>

**Course outline**

**Week 1: Orientation and introduction to single-cell RNA-Seq**

Activity/Homework: Install Seurat and load a dataset (provided) into R.

Date: Feb 9th

**Week 2: Preparing scRNA-Seq data**

Activity/Homework: Do QC steps, normalize/scale data, and do PCA along with all relevant plots using the provided dataset.

Date: Feb 16th

**Week 3: Uncovering dataset structure**

Activity/Homework: Perform TSNE, UMAP, and PHATE along with clustering; generate the relevant plots.

Date: Feb 23rd

**Week 4: scRNA-Seq biological interpretation**

Activity/Homework: Perform cluster marker analysis along with over-representation analysis; use sub clustering to further divide the dataset.

Date: Mar 2nd

**Week 5: Advanced topics in single cell analysis**

Activity/Homework: Form teams and begin the miniproject.

Date: Mar 9th

**Week 6: Miniproject presentations**

Activity: Miniprojects presentations and final thoughts.

Date: Mar 16th

**Additional information:**

* This workshop does not provide a grade and is not credit-bearing.
* **Zoom lectures will be recorded**
* It is expected that all participants have working knowledge of R programming and basic RNA-Seq analysis.
* For additional help, instructors may be reached by email at any time.
* Course materials, including zoom recordings, will be hosted on Box and/or youtube/github and a link will be provided to all attendees.