# Regulatory Genomics Lab

1. See Pythonic way to process single cell data on sample with both scRNA-seq and scATAC-seq
2. Look at normalization and signatures for scATAC-seq data
3. Identify differentially accessible peak intervals
4. Search for DNA sequence motifs under peaks

# Strategies for Success

1. No cell should take more than 3mins to run, but there is a lot to read, so pace yourself
2. The last sections rely on external tools, if there are long queues, just download prepared results
3. 13 “Check Your Understanding” questions meant to stop you to have you think about materials. Should be able to comment first line to continue