scRNA-seq Weekly Meeting Log

June 29, 2022

* How will Ansgar and Adrianne work (together) on the project?
* Building interface similar to Loupe browser?
  + Probably not feasible
  + Possible alternatives
    - Open-source python codes
    - Scanpy
    - Seurat (first choice)
* Summer project goals:
  + Compare experimental data from 2 different dates (ex. 4 hr uninfected/infected; for batch effect, technical replicates)
  + Analyze new data generated by Paola
  + Temporal analysis
  + Identify cell type/timepoint in clusters
* Make project “wish list”
  + Signal info (ex. pre-processed count data)
  + Identify single cells (ex. color by timepoint)
* Filtering tutorial with Albert for Ansgar and Adrianne
* No meeting next week
* Next steps
  + Albert will send tutorials

July 20, 2022

* Agenda:
  + Experiment Numbering (Albert)
  + Slides on step-by-step filtering and processing of sequenced data (Ansgar)
* Numbering Scheme:
  + New numbering scheme for experiments: 3A, 3B, 4
  + 3A and 3B are for technical replicates (twice sequenced) data from experiment 3
  + Experiment 4 showed signs of running faster than experiment 3 (infection happened more quickly)
  + We are no longer using data from Experiments 1 and 2.
  + Albert expects data from Exp. 4 to be available early next week.
* Filtering/Processing
  + Starting with default parameters set by Seurat. See: dataPipelineProcess.pptx in Box Folder/Github
  + May need to change the mitochondrial contamination (MT) parameter.
  + We are interested in some genes (TLR2, IL11) that are not highly expressed (Carol). Keep this in mind when doing filtering.
* Next Steps:
  + Find out which type of dim. Reduction (linear or non-linear) the dataset is suited to (Ansgar and Shuchin).
  + Integrate other clustering algorithm into Seurat data pipeline (Ansgar)
  + Conduct preliminary analysis of cluster biomarkers and use to identify cells in UMAP representation.