Johnson Lab meeting 12/17/19

SingleCell

Josh Campbell’s group- working with; software suite for single-cell analysis in a structured way, Campbell- human network atlas group, he’s the lead, (tumor). Scruff package- does alignment, BAM file, etc

Can we merge all these things? Data structures, utility functions, dimension reductions, etc?

We will: focus on building data structures,

SCTK will become the package, remove the shiny (it will become its own thing), QC, object-type conversion, visualizations functions, etc. Run function on data object.

Additional packages outside SCTK: batch, celda, methodA, …

Scruff processes sequencing data, exports sce object

Data object (SCE, MA, Co)

HSCs in human fetal liver analysis- Vanessa’s presentation

-no one marker that exclusively marks HSCs,

-CD34+ marks HSC, around 1%

-GPI-80 – 10-30%

-look into “UMAP”, clusters and distance

Cell detection Rate (CDR) the fraction of genes detected expressed in each cell

MAST vs t-test,

Gene Ontology enrichment analysis, Gorilla website (.www.cbl-gorilla.cs.technion.ac.il)

Imputation? MAGIC- markov affinity-based graph imputation of cells (impute\_seurat\_MAGIC() function)

Adaptively-thresholded low rank approximation – RunALRA() function