10X data were processed with cellranger pipeline to generate count matrix for downstream analysis.

Single cell genes: >30K, include lincRNAs besides coding genes

Datasets come from 10X genomics: (non-small cell lung cancer)

<https://www.10xgenomics.com/resources/datasets/>

Use PCA dimensions for t-SNE (use PCA to reduce the dimensions first, say use the first 20 PCA dimensions; and then use t-SNE for pretty visualization/clustering, which is essentially another dimension reduction)

Tutorial code:

<https://github.com/broadinstitute/CEGS-2018/blob/master/src/cegs_lab.Rmd>

Single Cell portal:

<https://portals.broadinstitute.org/single_cell>

github:

<https://github.com/seandavi/awesome-single-cell>

Single cell course:

<https://hemberg-lab.github.io/scRNA.seq.course/>