Seurat Object Notes for R

Useful Resources:
- Seurat: Spatial Transcriptomics
- Seurat webpage
  - Analysis, visualization, and integration of spatial datasets with Seurat
  - Analysis of Image-based Spatial Data in Seurat
- Satijalab/seurat Github
- The Seurat Class
- Fundamental scRNAseq: Chapter 3 Analysis Using Seurat
- Introduction to Single-cell RNA-seq - ARCHIVED

The Seurat object serves as a container that contains both data (like the count matrix) and analysis (like PCA, or clustering results) for a single-cell dataset

`meta.data`

Contains meta-information about each cell, starting with number of features detected (nFeature) and the original identity class (orig.ident); more information is added using `AddMetaData`

nFeature_RNA is the number of genes detected in each cell.
- number of genes detected per cell

nCount_RNA is the total number of molecules detected within a cell. And each dot in the following plots represents a cell.
- number of UMIs per cell

Resources for Assay Objects
- https://github.com/satijalab/seurat/wiki/Assay
- https://satijalab.org/seurat/reference/getassay

Resources for Images
- https://rdrr.io/cran/SeuratObject/man/Images.html