1. **Set up the Seurat Object**
   The Read10X function reads in the output of the cellranger pipeline from 10X, returning a unique molecular identified count matrix. Next use the count matrix to create a Seurat object.

2. **Pre-processing**
   - **QC and selecting cells for further analysis**: PercentageeFeatureSet(), removing unwanted cells from the dataset.
   - **Normalizing the data** NormalizeData(), a global-scaling normalization method.
   - Identification of highly variable features (feature selection): FindVariableFeatures(), will be used in downstream analysis.
   - **Scaling the data**: linear transformation: ScaleData(), a standard pre-processing step prior to dimensional reduction techniques like PCA. Shifts the expression of each gene, so the mean expression across cells is 0 and the variance across cells is 1. Gives equal weight in downstream analysis.
   - **Perform linear dimensional reduction**: perform PCA on the scaled data: RunPCA(). Only the previously determined variable features are used as input.
   - **Determine the dimensionality of the dataset**: JackStraw().

3. **Cluster the cells**
   FindNeighbors()---construct KNN graph and refine the edge weights between any 2 cells.
   FindClusters()---apply modularity optimization techniques

4. **Run non-linear dimensional reduction (UMAP/tSNE)**
   RunUMAP(), goal of these algorithms is to learn the underlying manifold of the data in order to place similar cells together in low-dimensional space.

5. **Finding differentially expressed features (cluster biomarkers).**
   FindMarkers(), find markers that define clusters via differential expression.

6. **Assigning cell type identity to clusters**