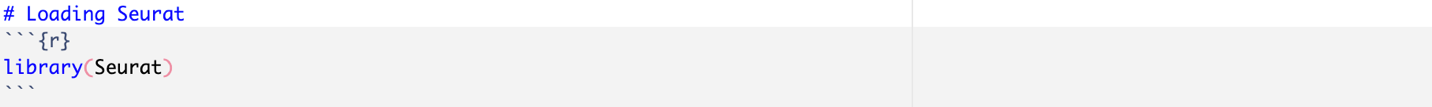
**Day7 worksheet**

**Covered in this worksheet:**

1. Loading Seurat package into R environment
2. Reading files into R (Seurat) that were mapped using Cellranger
3. Creating Seurat objects and adding metadata
4. Filtering out low-quality cells and doublets
5. Merging Seurat objects
6. Normalizing and scaling data, and identifying highly variable genes across single cells
7. Conducting principal component reduction (PCA)
8. Integrating Seurat objects by gender differences

**Code:**

1. Reading files into R (Seurat) that were mapped using Cellranger



1. Reading files into R (Seurat) that were mapped using Cellranger and creating Seurat objects

A screenshot of a computer

Description automatically generated

1. Adding metadata A screenshot of a computer code

   Description automatically generated
2. Cleaning dataA screenshot of a computer

   Description automatically generatedA screenshot of a computer screen

   Description automatically generated
3. Merging Seurat objects (prior to “integration”) A screenshot of a computer code

   Description automatically generated
4. Normalizing and scaling data, and identifying variable genes across cells and then conducting PCA reduction

A close-up of a computer code

Description automatically generated

1. Integrating data by gender

A screenshot of a computer program

Description automatically generated

**Day8 worksheet**

**Covered in this worksheet:**

1. Clustering integrated data and generating UMAP plot of single cells
2. Identifying differentially expressed genes across clusters
3. Visualizing gene expression across UMAP clusters
4. Rename clusters by putative cell types