# Introduction to Cell Ranger for scRNA-seq data analysis using Python

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## 0. `Demonstrations/cellranger_setup.md`

This file contains the instructions for setting up **Cell Ranger**.

## 1. `Data/cellranger_data/`

This directory contains the files necessary for demonstration practices. Our focus will primarily be on two folders:

### 1.1 `references/`

- `Homo_sapiens.GRCh38.dna.chromosome.21.fa` : A FASTA file for your genome reference.
- `gencode.v41.primary_assembly.annotation.chr21.gtf` : A GTF file with annotated genes.
- `cellranger_mkref.sh` : A script used to build the reference datasets.

### 1.2 `fastq/`

This folder contains the FASTQ files, which will be used to generate the count matrix.

### 1.3 `cellranger_count.sh`

This script will be used to generate the count matrix.

## 2. Run Cell Ranger commands

### 2.1 Building reference

To build the references, navigate to the `cellranger_data/references/` directory from the `Data/` folder and run the `cellranger_mkref.sh` script:

```
cd cellranger_data/references
sh cellranger_mkref.sh
```

### 2.2 Generating count matrix

After generating the reference, create the count matrix by running the `cellranger_count.sh` script in the `cellranger_data/` directory:

```
cd ..
sh cellranger_count.sh
```

## Acknowledgement

Slides and demonstration materials are primarily reused, with slight adaptation, from **Introduction to single-cell RNA-seq analysis, University of Cambridge** .