singlecell_Seurat_pipeline

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Single-cell RNA-Seq analysis pipeline (GEO format)

This is a pipeline to analyze single-cell RNA Seq data from GEO In this script the single cell RNA-Seq results from this paper is regenerated: https://pubmed.ncbi.nlm.nih.gov/34956864/ Title: Bulk and Single-Cell Profiling of Breast Tumors Identifies TREM-1 as a Dominant Immune Suppressive Marker Associated With Poor Outcomes

```r
message("You will not see the message.")
library(Seurat)
library(tidyverse)
library(GEOquery)
```

```r
# No need to perform the following two lines next time, as the folders are already created.
files <- getGEOSuppFiles("GSE188600")
untar("GSE188600_RAW.tar", exdir = 'data/')
```

```r
message("You will not see the message.")
```

```
## You will not see the message.
```