Long Covid study scRNA-seq, 24 month time point, data integration

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This pipeline is for analysis of scRNA-seq data from a publicly available data set.

Citation:

Phetsouphanh C, [. . .] Matthews GV. Improvement of immune dysregulation in individuals with long COVID at 24-months following SARS-CoV-2 infection. Nat Commun. 2024 Apr 17;15(1):3315. doi: 10.1038/s41467-024-47720-8. PMID: 38632311; PMCID: PMC11024141.

Click here to access the data from GEO

This script integrates the four libraries collected at 24 months.

```
library(Seurat)
```

```
## Loading required package: SeuratObject
```

```
## Loading required package: sp
```

```
##
## Attaching package: 'SeuratObject'
```

```
## The following objects are masked from 'package:base':
##
##     intersect, t
```

```
library(ggpubr)
```

```
## Loading required package: ggplot2
```

```
library(tidyverse)
```

```
## -- Attaching core tidyverse packages ------------------------ tidyverse 2.0.0 --
## v dplyr     1.1.4     v readr     2.1.5
## v forcats   1.0.0     v stringr   1.5.1
## v lubridate 1.9.4     v tibble    3.2.1
## v purrr     1.0.4     v tidyr     1.3.1
```

```
## -- Conflicts ------------------------------------------ tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()
## i Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to become errors
```

```
# Read in integration anchors generated by the previous script
anchors <- readRDS( "./data/covid/int_anchors_24mths.rds")

combo <- IntegrateData(anchorset = anchors,
                                    normalization.method = "SCT")
```

```
## [1] 1
```

```
## [1] 2
## [1] 3
## [1] 4
## Merging dataset 2 into 1
## Extracting anchors for merged samples
## Finding integration vectors
## Finding integration vector weights
## Integrating data
## Merging dataset 4 into 3
## Extracting anchors for merged samples
## Finding integration vectors
## Finding integration vector weights
## Integrating data
## Merging dataset 3 4 into 1 2
## Extracting anchors for merged samples
## Finding integration vectors
## Finding integration vector weights
## Integrating data
```

```r
# Export, to be used by future scripts
saveRDS(combo, "./data/covid/initial_combo_24mths.rds")
```