

# Software & installation

- Monocle3 runs in the R statistical computing environment
- Needs R version 3.5 or higher
- To install from the Trapnell Lab GitHub

```
devtools :: install_github('cole-trapnell-lab/monocle3')
```

- To test the installation

```
library(monocle3)
```

# Import your own data

- To create your own cds object, use gene x cell matrix (mat), gene data frame (gene\_meta) and cell data frame (cell\_meta):

```
cds <- new_cell_dataset(mat, cell_meta, gene_meta)
```

- Monocle3 can also import data from 10x experiments directly into cds objects

```
cds <- load_cellranger_data("cell_ranger_output")
```