

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")
```

Accessor functions for cds

- **exprs/counts**: A numeric matrix of expression values, where rows are genes and columns are cells
- **pData/colData**: An object where rows are cells and columns are cell attributes such as cell type, culture condition, etc
- **fData/rowData**: An object where rows are features (e.g. genes) and columns are gene attributes such as biotype, gc content, etc

`colData(cds)`

`rowData(cds)`

`counts(cds)`