

Next we cluster the cells

- The `cluster_cells` function of `monocle3` allows users to group similar cells according to global expression profiles
- In addition, partitions (super-clusters) are calculated for dividing distinct trajectories
- You can access values using the following:

```
cds <- cluster_cells(cds)
head(partitions(cds, reduction_method = "UMAP"))
head(clusters(cds, reduction_method = "UMAP"))
```

Group cells by partitions

Pre-process

Reduce
dimension

Cluster

