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)
```

colData(cds)

	cell_type	culture_cond	Size_Factor
cell_1			
cell_2			
cell_3			
cell_n			

rowData(cds)

	biotype	gc_content
gene_1		
gene_2		
gene_3		
gene_n		

```
Console   Terminal ×   Jobs ×

~/Documents/agogate/monocle3/

>
```