

Case study: Monocle 3

```
R/cell_data_set.R
```

```

#' Create a new cell_data_set object.
#'
#' @param expression_data expression data matrix for an experiment, can be a
#'   sparseMatrix.
#' @param cell_metadata data frame containing attributes of individual cells,
#'   where row.names(cell_metadata) = colnames(expression_data).
#' @param gene_metadata data frame containing attributes of features
#'   (e.g. genes), where
#'   row.names(gene_metadata) = row.names(expression_data).
#' @return a new cell_data_set object
#' @export
#' @examples
#' small_a549_colData_df <- readRDS(system.file("extdata",
#'                                             "small_a549_dex_pdata.rda",
#'                                             package = "monocle3"))
#' small_a549_rowData_df <- readRDS(system.file("extdata",
#'                                             "small_a549_dex_fdata.rda",
#'                                             package = "monocle3"))
#' small_a549_exprs <- readRDS(system.file("extdata",
#'                                         "small_a549_dex_exprs.rda",
#'                                         package = "monocle3"))
#' small_a549_exprs <- small_a549_exprs[,row.names(small_a549_colData_df)]
#' cds <- new_cell_data_set(expression_data = small_a549_exprs,
#'                          cell_metadata = small_a549_colData_df,
#'                          gene_metadata = small_a549_rowData_df)
#'
new_cell_data_set <- function(expression_data,
                              cell_metadata = NULL,
                              gene_metadata = NULL) {

```

The NAMESPACE file defines the API

NAMESPACE

```
export("fData<-")  
export("pData<-")  
export("principal_graph<-")  
export("principal_graph_aux<-")
```

```
...  
export(size_factors)  
export(top_markers)  
exportClasses(cell_data_set)  
exportMethods("fData<-")  
exportMethods("pData<-")
```

```
...  
exportMethods(pseudotime)  
import(ggplot2)  
importClassesFrom(S4Vectors,List)  
importFrom(S4Vectors,"metadata<-")  
importFrom(S4Vectors,SimpleList)  
importFrom(S4Vectors,metadata)  
importFrom(SingleCellExperiment,"reducedDim<-")  
importFrom(SingleCellExperiment,"reducedDims<-")  
importFrom(SingleCellExperiment,SingleCellExperiment)
```

Monocle functions that
become visible to the user

Functions from other packages
that become visible