# Case study: Monocle 3

`R/cell_data_set.R`

```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 \code{row.names(cell_metadata) = colnames(expression_data)}.
#' @param gene_metadata data frame containing attributes of features
#'    (e.g. genes), where
#'    \code{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) {
```

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#' @param cell_metadata data frame containing attributes of individual cells,
#'  where \code{row.names(cell_metadata) = colnames(expression_data)}.
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#'    (e.g. genes), where
#'    \code{row.names(gene_metadata) = row.names(expression_data)}.
#' @return a new cell_data_set object
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#' @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) {
```