


```
#' Add together two numbers.
#
#' @param x A number.
#' @param y A number.
#' @return The sum of x and y.
#' @examples
#' add(1, 1)
#' add(10, 1)
add <- function(x, y) {
  x + y
}
```

Roxy generates documents for you

`add {rvest}`

Add together two numbers

Description

Add together two numbers

Usage

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add(x, y)
```

Arguments

x A number

y A number

Value

The sum of **x** and **y**

Examples

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add(1, 1)
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```
add(10, 1)
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Rstudio will run Roxygen for you
on command

Roxygen comments document your code

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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) {

```