Case study: Monocle 3

R/cell_data_set.R

```r
new_cell_data_set <- function(expression_data,
                              cell_metadata = NULL,
                              gene_metadata = NULL) {

   assertthat::assert_that(class(expression_data) == "matrix" ||
                             is_sparse_matrix(expression_data),
                        msg = paste("Argument expression_data must be a",
                                    "matrix - either sparse from the",
                                    "Matrix package or dense"))
   …

   sce <- SingleCellExperiment(list(counts=methods::as(expression_data, "dgCMatrix")),
                             rowData = gene_metadata,
                             colData = cell_metadata)

   cds <- methods::new("cell_data_set",
           assays = SummarizedExperiment::Assays(
             list(counts=methods::as(expression_data, "dgCMatrix"))),
           colData = colData(sce),
           int_elementMetadata =int_elementMetadata(sce),
           int_colData = int_colData(sce),
           int_metadata = int_metadata(sce),
           metadata = metadata(sce),
           NAMES = NULL,
           elementMetadata = elementMetadata(sce)[,0],
           rowRanges = rowRanges(sce))

   metadata(cds)$cds_version <- Biobase::package.version("monocle3")
   clusters <- stats::setNames(SimpleList(), character(0))
   cds <- estimate_size_factors(cds)
   cds
}
```

The `DESCRIPTION` file contains high-level metadata

```
Package: mypackage
Title: What The Package Does (one line, title case required)
Version: 0.1
Authors@R: person("First", "Last", email = "first.last@example.com",
                  role = c("aut", "cre"))
Description: What the package does (one paragraph)
Depends: R (>= 3.1.0)
License: What license is it under?
LazyData: true
```