

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
```

Case study: Monocle 3

DESCRIPTION

```
Package: monocle3
Title: Clustering, differential expression, and trajectory analysis for single-
       cell RNA-Seq
Version: 0.2.1.3
Authors@R:
  person(given = "Hannah",
         family = "Pliner",
         role = c("aut", "cre"),
         email = "hpliner@uw.edu")
  person(given = "Xiaojie",
         family = "Qiu",
         role = c("aut", "cre"),
         email = "xqiu@uw.edu")
  person(given = "Cole",
         family = "Trapnell",
         role = c("aut", "cre"),
         email = "colettrap@uw.edu")
Description: Monocle 3 performs clustering, differential expression and
             trajectory analysis for single-cell expression experiments. It orders
             individual cells according to progress through a biological process,
             without knowing ahead of time which genes define progress through that
             process. Monocle 3 also performs differential expression analysis,
             clustering, visualization, and other useful tasks on single-cell expression
             data. It is designed to work with RNA-Seq data, but could be used with
             other types as well.
License: MIT + file LICENSE
Encoding: UTF-8
LazyData: true
```