

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
```

Case study: Monocle 3

DESCRIPTION

```
Roxygen: list(markdown = TRUE)
RoxygenNote: 7.1.0
LinkingTo:
  Rcpp
Depends:
  Biobase,
  SingleCellExperiment
Imports:
  assertthat (>= 0.2.1),
  batchelor,
  BiocGenerics (>= 0.28.0),
  DelayedArray (>= 0.8.0),
  ...
  testthat (>= 2.1.0),
  pryr (>= 0.1.4),
  ggrastr,
  knitr,
  rmarkdown,
  spelling,
  scran
VignetteBuilder: knitr
Language: en-US
Remotes:
  VPetukhov/ggrastr,
  cole-trapnell-lab/leidenbase
```