

Packages

Using the help search in RStudio, or `??` we can discover if the function is in an installed package. If so, we simply need to load the package first

```
library(MASS)
truehist(iris$Species)
```

If it's not in an installed package, we can try searching on [Rdocumentation.org](https://rdrr.io/) or [RSeek.org](https://www.rdocumentation.org/).

Installing Packages

CRAN packages can be installed from the RStudio Packages tab.

For Bioconductor packages, we source the `biocLite` function from the Bioconductor website, then run e.g.

```
source("https://bioconductor.org/biocLite.R")
biocLite("limma", "edgeR")
```

`biocLite` must be sourced in each session a Bioconductor package is to be installed. It ensures the Bioconductor and R versions are compatible.

GitHub packages are built from source, so require additional tools (see "Install R" notes). Once setup, we can use `install_github` from the `devtools` package, e.g.

```
library(devtools)
install_github("hadley/vctrs")
```

It may be necessary to install other packages the package depends on from GitHub/Bioconductor first.

Finding Out About Packages

Often we find out about packages from a book, paper or tutorial.

To find a package that implements a particular method, we can search on Rdocumentation.org or RSeek.org.

[CRAN Task Views](#) and [BiocViews](#) give overviews of packages relating to a particular application or type of method.

Navigating a Package

Help for a package can be found by clicking on the *Packages* tab. This lists the functions/topics with help pages in that package.

In addition the following may be available

DESCRIPTION Metadata for the package, including a short Description field

vignettes User guides or extended documentation on specific topics

demos Use e.g. `demo(package = "stats")` to see available demos

NEWS News of changes in each package release

pkg-package Overall help file for `pkg`