

## Install packages from

- · Bioconductor?
  - 1. First install BiocManager from CRAN
  - 2. Run the R command BiocManager::install("package\_name")
- · GitHub?
  - 1. Install devtools
  - 2. Run the R command devtools::install github("username/repository").
- · Source code?
  - 1. Put the source.tar.gz in your working directory...
  - 2. Run the R command install.package("source.tar.gz", repos = NULL, type =
    "source").

## Exercises

## **Install limma**

limma is the favorite package of anyone that wants to analyze gene expression data (microarray, RNA-seq, NanoString etc.)

Install it with the command

BiocManager::install("limma")

## Explore the package

```
1. Load: library(limma)
```

2. Look at the main help page

```
?`limma-package`
```

1. Look at the first vignette: vignette("intro", package = "limma")