

R Package Install

Michael P. Wilson

Computational Biology Core



R Versions

- 3.5.2
 - Exists inside a Singularity container
 - Contains bioconductor, IRanges, DESeq2, dplyr, gplots, ggplot2, RColorBrewer, genefilter, grDevices
 - Other libraries must be installed in user space
 - module load R/3.5.2
- Older versions
 - 2.14.2, 3.1.0, 3.1.2, 3.2.1, 3.2.3, 3.3.1, 3.3.2, 3.4.1, 3.4.3, 3.5.1, 3.5.1-MS



R Libraries

- Library
 - `> .Library`
 - `[1] "/usr/lib/R/library"`
- Library Paths:
 - `.libPaths()`
 - `.libPaths(c(.libPaths(), "~/myRLibrary"))`
 - `~/myRLibrary` must exist (`mkdir ~/myRLibrary`)



R Local Library

```
> .libPaths()
[1] "/library"          "/usr/local/lib/R/site-library"
[3] "/usr/lib/R/site-library"  "/usr/lib/R/library"
> BiocManager::install(c("rstanarm"))
Bioconductor version 3.8 (BiocManager 1.30.4), R 3.5.2 (2018-12-20)
Installing package(s) 'rstanarm'
Warning in install.packages(pkgs = doing, lib = lib, repos = repos, ...) :
  'lib = "/library"' is not writable
Would you like to use a personal library instead? (yes/No/cancel) yes
Would you like to create a personal library
'~/R/x86_64-pc-linux-gnu-library/3.5'
to install packages into? (yes/No/cancel) yes
```



R Package Install

- CRAN:
 - `install.packages("DESeq2")`
 - `install.packages("remeta", repos="http://cran.r-project.org", lib="~/local/R_libs/")`
- Bioconductor:
 - `BiocManager::install(c("Rcpp", "RcppArmadillo", "RcppParallel", "data.table", "SPAtest", "RcppEigen", "Matrix", "methods"))`

