R Package Install

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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"

> 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"))`