

Code Library

Ruhika Chatterjee

2024-12-07

Basic R Functions

R Data Structures

```
# Matrix  
x <- matrix(c(1, 2, 3, 4, 5, 6, 7, 8), nrow = 4, ncol = 2) #create matrix
```

R Packages

- Repositories: CRAN, BioConductor (bioinformatics), GitHub
- Search: <https://www.rdocumentation.org/>

```
version #R info version
```

```
##  
## platform      _  
## arch          x86_64-w64-mingw32  
## os            mingw32  
## crt           ucrt  
## system        x86_64, mingw32  
## status  
## major         4  
## minor         4.1  
## year          2024  
## month         06  
## day           14  
## svn rev       86737  
## language      R  
## version.string R version 4.4.1 (2024-06-14 ucrt)  
## nickname      Race for Your Life
```

```
sessionInfo() #R info version, packages
```

```
## R version 4.4.1 (2024-06-14 ucrt)  
## Platform: x86_64-w64-mingw32/x64  
## Running under: Windows 11 x64 (build 22631)
```

```
##
## Matrix products: default
##
##
## locale:
## [1] LC_COLLATE=English_United States.utf8
## [2] LC_CTYPE=English_United States.utf8
## [3] LC_MONETARY=English_United States.utf8
## [4] LC_NUMERIC=C
## [5] LC_TIME=English_United States.utf8
##
## time zone: America/New_York
## tzcode source: internal
##
## attached base packages:
## [1] stats      graphics  grDevices  utils      datasets  methods    base
##
## loaded via a namespace (and not attached):
## [1] compiler_4.4.1    fastmap_1.2.0     cli_3.6.3        tools_4.4.1
## [5] htmltools_0.5.8.1 rstudioapi_0.17.1 yaml_2.3.10       rmarkdown_2.29
## [9] knitr_1.49        xfun_0.49         digest_0.6.37    rlang_1.1.4
## [13] evaluate_1.0.1
```

```
# Install from CRAN:
# install.packages("ggplot2", repos = "http://cran.us.r-project.org") #install
# install.packages(c("labeling", "tibble"), repos = "http://cran.us.r-project.org") #multiple

# Install from Bioconductor
# install.packages("BiocManager", repos = "https://bioconductor.org/biocLite.R")
# BiocManager::install(c("GenomicFeatures", "AnnotationDbi")) #install package

# Install from GitHub (need package, author name)
# install.packages("devtools", repos = "http://cran.us.r-project.org") #only once
# library(devtools)
# install_github("author/package") #installs package

# library(ggplot2) # Load package, careful of dependencies
# installed.packages() #check installed packages
# library() #alternate
# old.packages(repos = "http://cran.us.r-project.org") #check packages to update
# update.packages(repos = "http://cran.us.r-project.org") #update all packages
# install.packages("ggplot2") #to update single package
# detach("package:ggplot2", unload=TRUE) #unload function
# remove.packages("ggtree") #remove package
# help(package = "ggplot2") #package info
# browseVignettes("ggplot2") #extended help files
```