

Course_Notes

Ruhika Chatterjee

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Notes taken from Johns Hopkins University Coursera course series Data Science Specialization.

Intro Information

Every Data Science Project starts with a question that is to be answered with data

- That means that forming the question is an important first step in the process.
- The second step is finding or generating the data you're going to use.
- With the question solidified and data in hand, the data are then analyzed first by exploring the data and then often by modeling the data.
- After drawing conclusions, the project has to be communicated to others.
- Most projects build off someone else's work. It's really important to give credit.

R project: Data, Scripts, Output

Troubleshooting

- Check error messages and outputs
- Talk to your rubber duck
- <https://www.r-project.org/help.html>
- Use `help()` function and `?` command (i.e. `help(lm)` or `help("lm")`, or `?lm` or `i`lm``)
- Use Google or search.r-project.org
- Check forums StackOverflow and CrossValidated

How to effectively ask questions on forums

- The question you are trying to answer
- How you approached the problem, what steps you have already taken

- What steps will reproduce the problem (including sample data!)
- What was the expected output
- What you saw instead (including any error messages you received!)
- What troubleshooting steps you have already tried
- Details about your set-up, eg: OS, Rversion, packages
- Be specific in the title of your questions!
- Read the forum posting guidelines, ask your question on an appropriate forum!
- Be explicit, detailed, courteous, and succinct
- Follow up on the post OR post the solution

Good to know: Know Thy System

- How much memory is available?
- Applications in use?
- Other users in the system?
- OS? 32 or 64-bit?
- memory used for numeric data frame = $2 * \text{rows} * \text{columns} * 8\text{byte/numeric} / 2^{20} \text{ bytes/MB} / 2^{10} \text{ GB/MB}$

Data Science Essentials

Types of Questions

- Descriptive: describe or summarize a set of data by generating simple summaries about the samples and their measurements, usually measures of central tendency (eg: mean, median, mode) or measures of variability (eg: range, standard deviations or variance). No interpretation involved.
- Exploratory: examine or explore the data and find relationships that weren't previously known, analyzing correlative (not causative) relationships. Allows formulation of hypotheses and can drive the design of future studies and data collection.
- Inferential: use a relatively small sample of data to infer or say something about the population at large through statistical modelling. Finding population-wide estimate and uncertainty using a representative sample.
- Predictive: use current data to make predictions about future data, or the likelihood of future outcomes, through past patterns of relevant variables. Best models involve more data and simple models, noting that prediction is based on correlative relationship.

- Causal: see what happens to one variable when we manipulate another variable, looking at the cause and effect of a relationship. Usually uses results of randomized studies that were designed to identify causation, using aggregate results (i.e. causation may not apply to everyone). Data collection is a challenge.
- Mechanistic: understand the exact changes in variables that lead to exact changes in other variables. In deterministic relationships for simple situations or in those that are nicely modeled by deterministic equations (i.e. only noise in measurement error). Cannot use for inference, only really used in physical or engineering sciences.

Experimental Design

- Organizing an experiment so that you have the correct and sufficient data. to clearly and effectively answer your data science question. Ask question, create setup, identify problems or sources of error, collect data.
- Keep track of independent and dependent variables, decide what variables you will measure, and which you will manipulate to effect changes in other measured variables.
- Develop your hypothesis, decide sample size.
- Determine confounders, control for it by measuring confounding variables or fixing the variable. Consider control groups, including blinding to combat placebo effect; randomization to remove confounder bias and systemic error; and replication to measure variability accurately and establish significance. These strategies remove the effect of confounding.
- Share data and code.
- Beware of p-hacking. p-value: value that tells you the probability that the results of your experiment were observed by chance, where significance is usually set below 0.05. p-hacking involves testing hypotheses till one reveals a statistically significant p-value.

Big Data

Difficulty in volume, velocity, and variety. Also move from structured data (long tables, spreadsheets, or databases with columns and rows of information that you can sum or average or analyse however you like within those confines) to unstructured data. Big data is big, changing, from many sources, and messy. But volume of data can counteract the messiness, changing data allows real-time analysis, can answer more type of questions, can uncover hidden correlations.

Intro to R

- CRAN: <https://cran.r-project.org/>
- RStudio: <https://posit.co/products/open-source/rstudio/>

History of R

- R is a dialect of S - language developed by John Chambers at Bell Labs for statistical analysis (lots of corporate acquisitions and versions)

- Developed to allow users to progress to programmers
- R developed in 1991 at Auckland, New Zealand by Ihaka and Gentleman.
- Similar syntax and superficial semantics to S, run on any standard OS, frequent releases. Lean base software, sophisticated graphics, interactive with powerful programming language, active community.
- Free and freedom to run program as desired, study and adapt program, redistribute copies, and improve program.
- Drawbacks: based on 40 year old tech, lacking dynamic/3D graphics, functionality based on consumer demand and user contribution, objects stored on physical memory, not always ideal.
- To understand computations in R, two slogans are helpful: 1. Everything that exists is an object. 2. Everything that happens is a function call.

Helpful Books

- Chambers (2008). *Software for Data Analysis*, Springer.
- Chambers (1998). *Programming with Data*, Springer.
- Venables & Ripley (2002). *Modern Applied Statistics with S*, Springer.
- Venables & Ripley (2000). *S Programming*, Springer.
- Pinheiro & Bates (2000). *Mixed-Effects Models in S and S-PLUS*, Springer.
- Murrell (2005). *R Graphics*, Chapman & Hall/CRC Press.
- Springer's series *Use R!*

R Markdown

- <https://rmarkdown.rstudio.com/>
- **bold** and *italics*
- Parameter {r Markdown, echo = False} to not print code
- Ctrl+Alt+I (Windows) to initiate code block
- note: add 2 spaces after bullet text

```
#install.packages("rmarkdown")
```

Coding Standards

- Write text in text editor
- Indent your code (4-8)

- Limit width of code (80 cols)
- Limit length of function (1 activity, single page)

Debugging

Problem

- message: no stop, message function.
- warning: unexpected, not fatal, end of function, warning function.
- error: fatal, stop function.
- Condition: classes listed above or creatable, generic.

```
log(-1) # returns NaN and warning about args
```

```
## Warning in log(-1): NaNs produced
```

```
## [1] NaN
```

```
printmessage <- function(x) {
  if (x > 0) print("x > 0")
  else print(" x <= 0")
  invisible(x) # return no print
}
#printmessage(NA) # comparison not possible, error
```

How to know something is wrong?

- What was the input? How was the function called?
- What was expected? i.e. output, message, other result
- What was done?
- What was the difference between expected and actual results?
- Were the expectations correct?
- Is the problem reproducible?

Tools

Use in commandline and in code `####traceback` - print function call stack after an error. Call immediately after error. Useful when functions call functions.

- `lm(y ~ x)`
- `traceback()`
- prints list of function calls, error is in the top function

debug

- flags function fro debug mode to step through execution line-by-line
- `debug(lm)`
- `lm(y ~ x)`
- prints function code then browser prompt (workspace in function environment).
- Press n for next to iterate through the lines. Can call debugger on functions inside debugger.

browser

- suspends execution of function wherever called and enters debug mode

trace

- insert debugging code into function in specific places

recover

- modify error behavior to browse function call stack. Set global option for all command-line calls
- `options(error = recover)`
- Prints call stack options, select level to browse environment of function

Version Control

- GitHub Repository Instruction: <https://docs.github.com/en/get-started/start-your-journey/hello-world>
- Git Download: <https://git-scm.com/downloads>

To configure Git in Git Bash

- `git config --global user.name "Jane Doe"`
- `git config --global user.email janedoe@gmail.com`
- `git config --list` confirm changes
- exit Terminal

Link

- Link RStudio to Git: Tools > Global Options > Git/SVN then confirm directory
- Link to GitHub: "Create RSA Key", close, "View public key", in GitHub Account Settings > "SSH and GPG keys" > "New SSH key", paste, title

Linking Repositories

- To Link Directly: Create repository in GitHub, copy URL, create new project in RStudio (Version control), Git as VC software, paste URL
- Stage, commit, push (with a message explaining what changed, why and by whom) Save, Git Tab check file as “Staged”, click Commit, Commit message, Commit, Push
- Clone Repository: RStudio File > New Project > Version Control, Git, URL, location, create

Add existing Project to GitHub

in Git Bash

- `cd ~/dir/name/of/path/to/file` #navigate Terminal
- `git init` #initializes as git repo
- `git add .` #adds directory files to repo
- `git commit -m “Initial commit”` #commit

in GitHub: create repo (same name, no .readme, .gitignore, license), select “Push an existing repository from the command line”, copy the code, reopen all

Swirl

<https://swirlstats.com/>

```
# install.packages("swirl", repos = "http://cran.us.r-project.org")
# install_from_swirl("R Programming") # install course
# library("swirl") # load interactive
# Swirl() # launch interactive
# help.start() # help
# play() # to leave lesson
# nxt() # to return to lesson
# Esc to return to R prompt
# bye() # exit and save
# skip() # skip current question
# main() # swirl main menu
# info() # display options
```

Scoping

```
search() # provides list for environments
```

```
## [1] ".GlobalEnv"      "package:stats"    "package:graphics"
## [4] "package:grDevices" "package:utils"    "package:datasets"
## [7] "package:methods"  "Autoloads"        "package:base"
```

- Global environment is the workspace.
- Scoping begins in global environment ends in base package, order depends on configuration of setup (loading package), inserts in slot 2 in reverse order.
- Separate namespace for function and non-function objects.
- Functions: Scoping in R is lexical/static scoping (also Python, Lisp). Local variables assigned in the body of a function. Formal arguments defined in args passed. Free variable not explicitly defined, in R looks in environment where function was defined then parent environments till reach global environment/namespace of package, then down from top-level environment to empty environment. Finally throws error if nothing found.
- Dynamic scoping looks in calling environment first.
- Environment: collection of symbol-value pairs.
- Every environment (except empty environment) has parent environment (can have multiple children).
- Parent environment: environment in which the function was called.
- Take function and associate with environment is a function closure.
- **THEREFORE:** define free variables in workspace and define function in global environment. EXCEPT when defining functions inside functions.
- R objects must be stored in memory. Functions carry pointer to defining environment.
- Optimization: pass function to functions optim, nlm, optimize. Object function depends on parameters and data.
- **Course 2, Module 2, scoping Rules- Optimization Example**
- Example:

```
make.power <- function(n) {
  pow <- function(x) { # x is free variable
    x^n
  }
  pow # returns function as object
}

cube <- make.power(3)
square <- make.power(2)
cube(3)
```

```
## [1] 27
```

```
square(3)
```

```
## [1] 9
```


R Packages

- Repositories: CRAN, BioConductor (bioinformatics), GitHub
- Search: <https://www.rdocumentation.org/>
- Base packages: utils, stats, datasets, graphics, grDevices, grid, methods, tools, parallel, compiler, splines, tcltk, stats4.
- Recommended packages: boot, class, cluster, codetools, foreign, KernSmooth, lattice, mgcv, nime, rpart, survival, MASS, spatial, nnet, Matrix.

```
# 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
```

```
## Warning: package 'ggplot2' was built under R version 4.4.2
```

```
installed.packages() #check installed packages
```

```
##               Package
## abind           "abind"
## AnnotationDbi   "AnnotationDbi"
## askpass         "askpass"
## backports       "backports"
## base64enc       "base64enc"
## BH              "BH"
## Biobase         "Biobase"
## BiocGenerics    "BiocGenerics"
## BiocIO          "BiocIO"
## BiocManager     "BiocManager"
## BiocParallel    "BiocParallel"
## BiocVersion     "BiocVersion"
## Biostrings      "Biostrings"
## bit             "bit"
## bit64           "bit64"
## bitops          "bitops"
## blob            "blob"
## brew            "brew"
## brio            "brio"
```

## broom	"broom"
## bslib	"bslib"
## cachem	"cachem"
## callr	"callr"
## cellranger	"cellranger"
## checkmate	"checkmate"
## cli	"cli"
## clipr	"clipr"
## colorspace	"colorspace"
## commonmark	"commonmark"
## conflicted	"conflicted"
## cpp11	"cpp11"
## crayon	"crayon"
## credentials	"credentials"
## curl	"curl"
## data.table	"data.table"
## DBI	"DBI"
## dbplyr	"dbplyr"
## DelayedArray	"DelayedArray"
## desc	"desc"
## devtools	"devtools"
## diffobj	"diffobj"
## digest	"digest"
## downlit	"downlit"
## dplyr	"dplyr"
## dtplyr	"dtplyr"
## ellipsis	"ellipsis"
## evaluate	"evaluate"
## fansi	"fansi"
## farver	"farver"
## fastmap	"fastmap"
## fontawesome	"fontawesome"
## forcats	"forcats"
## formatR	"formatR"
## Formula	"Formula"
## fs	"fs"
## futile.logger	"futile.logger"
## futile.options	"futile.options"
## gargle	"gargle"
## generics	"generics"
## GenomeInfoDb	"GenomeInfoDb"
## GenomeInfoDbData	"GenomeInfoDbData"
## GenomicAlignments	"GenomicAlignments"
## GenomicFeatures	"GenomicFeatures"
## GenomicRanges	"GenomicRanges"
## gert	"gert"
## ggplot2	"ggplot2"
## gh	"gh"
## gitcreds	"gitcreds"
## glue	"glue"
## googledrive	"googledrive"
## googlesheets4	"googlesheets4"
## gridExtra	"gridExtra"
## gtable	"gtable"

## haven	"haven"
## highr	"highr"
## Hmisc	"Hmisc"
## hms	"hms"
## htmlTable	"htmlTable"
## htmltools	"htmltools"
## htmlwidgets	"htmlwidgets"
## httpuv	"httpuv"
## httr	"httr"
## httr2	"httr2"
## ids	"ids"
## ini	"ini"
## IRanges	"IRanges"
## isoband	"isoband"
## jquerylib	"jquerylib"
## jsonlite	"jsonlite"
## KEGGREST	"KEGGREST"
## KernSmooth	"KernSmooth"
## knitr	"knitr"
## labeling	"labeling"
## lambda.r	"lambda.r"
## later	"later"
## lifecycle	"lifecycle"
## lubridate	"lubridate"
## magrittr	"magrittr"
## MatrixGenerics	"MatrixGenerics"
## matrixStats	"matrixStats"
## memoise	"memoise"
## mime	"mime"
## miniUI	"miniUI"
## modelr	"modelr"
## munsell	"munsell"
## name	"name"
## openssl	"openssl"
## pillar	"pillar"
## pkgbuild	"pkgbuild"
## pkgconfig	"pkgconfig"
## pkgdown	"pkgdown"
## pkgload	"pkgload"
## plogr	"plogr"
## plyr	"plyr"
## png	"png"
## praise	"praise"
## prettyunits	"prettyunits"
## processx	"processx"
## profvis	"profvis"
## progress	"progress"
## promises	"promises"
## ps	"ps"
## purrr	"purrr"
## R6	"R6"
## ragg	"ragg"
## rappdirs	"rappdirs"
## rcmdcheck	"rcmdcheck"

## RColorBrewer	"RColorBrewer"
## Rcpp	"Rcpp"
## RCurl	"RCurl"
## readr	"readr"
## readxl	"readxl"
## rematch	"rematch"
## rematch2	"rematch2"
## remotes	"remotes"
## reprex	"reprex"
## reshape2	"reshape2"
## restfulr	"restfulr"
## rhdf5	"rhdf5"
## rhdf5filters	"rhdf5filters"
## Rhdf5lib	"Rhdf5lib"
## Rhtslib	"Rhtslib"
## rJava	"rJava"
## rjson	"rjson"
## rlang	"rlang"
## rmarkdown	"rmarkdown"
## RMySQL	"RMySQL"
## roxygen2	"roxygen2"
## rprojroot	"rprojroot"
## Rsamtools	"Rsamtools"
## RSQLite	"RSQLite"
## rstudioapi	"rstudioapi"
## rtracklayer	"rtracklayer"
## rversions	"rversions"
## rvest	"rvest"
## S4Arrays	"S4Arrays"
## S4Vectors	"S4Vectors"
## sass	"sass"
## scales	"scales"
## selectr	"selectr"
## sessioninfo	"sessioninfo"
## shiny	"shiny"
## snow	"snow"
## sourcetools	"sourcetools"
## SparseArray	"SparseArray"
## stringi	"stringi"
## stringr	"stringr"
## SummarizedExperiment	"SummarizedExperiment"
## swirl	"swirl"
## sys	"sys"
## systemfonts	"systemfonts"
## testthat	"testthat"
## textshaping	"textshaping"
## tibble	"tibble"
## tidyr	"tidyr"
## tidyselect	"tidyselect"
## tidyverse	"tidyverse"
## timechange	"timechange"
## tinytex	"tinytex"
## tzdb	"tzdb"
## UCSC.utils	"UCSC.utils"

## urlchecker	"urlchecker"
## usethis	"usethis"
## utf8	"utf8"
## uuid	"uuid"
## vctr	"vctr"
## viridis	"viridis"
## viridisLite	"viridisLite"
## vroom	"vroom"
## waldo	"waldo"
## whisker	"whisker"
## withr	"withr"
## xfun	"xfun"
## XLConnect	"XLConnect"
## xlsx	"xlsx"
## xlsxjars	"xlsxjars"
## XML	"XML"
## xml2	"xml2"
## xopen	"xopen"
## xtable	"xtable"
## XVector	"XVector"
## yaml	"yaml"
## zip	"zip"
## zlibbioc	"zlibbioc"
## base	"base"
## boot	"boot"
## class	"class"
## cluster	"cluster"
## codetools	"codetools"
## compiler	"compiler"
## datasets	"datasets"
## foreign	"foreign"
## graphics	"graphics"
## grDevices	"grDevices"
## grid	"grid"
## KernSmooth	"KernSmooth"
## lattice	"lattice"
## MASS	"MASS"
## Matrix	"Matrix"
## methods	"methods"
## mgcv	"mgcv"
## nlme	"nlme"
## nnet	"nnet"
## parallel	"parallel"
## rpart	"rpart"
## spatial	"spatial"
## splines	"splines"
## stats	"stats"
## stats4	"stats4"
## survival	"survival"
## tcltk	"tcltk"
## tools	"tools"
## translations	"translations"
## utils	"utils"
##	LibPath

## abind	"C:/Users/Owner/AppData/Local/R/win-library/4.4"
## AnnotationDbi	"C:/Users/Owner/AppData/Local/R/win-library/4.4"
## askpass	"C:/Users/Owner/AppData/Local/R/win-library/4.4"
## backports	"C:/Users/Owner/AppData/Local/R/win-library/4.4"
## base64enc	"C:/Users/Owner/AppData/Local/R/win-library/4.4"
## BH	"C:/Users/Owner/AppData/Local/R/win-library/4.4"
## Biobase	"C:/Users/Owner/AppData/Local/R/win-library/4.4"
## BiocGenerics	"C:/Users/Owner/AppData/Local/R/win-library/4.4"
## BiocIO	"C:/Users/Owner/AppData/Local/R/win-library/4.4"
## BiocManager	"C:/Users/Owner/AppData/Local/R/win-library/4.4"
## BiocParallel	"C:/Users/Owner/AppData/Local/R/win-library/4.4"
## BiocVersion	"C:/Users/Owner/AppData/Local/R/win-library/4.4"
## Biostrings	"C:/Users/Owner/AppData/Local/R/win-library/4.4"
## bit	"C:/Users/Owner/AppData/Local/R/win-library/4.4"
## bit64	"C:/Users/Owner/AppData/Local/R/win-library/4.4"
## bitops	"C:/Users/Owner/AppData/Local/R/win-library/4.4"
## blob	"C:/Users/Owner/AppData/Local/R/win-library/4.4"
## brew	"C:/Users/Owner/AppData/Local/R/win-library/4.4"
## brio	"C:/Users/Owner/AppData/Local/R/win-library/4.4"
## broom	"C:/Users/Owner/AppData/Local/R/win-library/4.4"
## bslib	"C:/Users/Owner/AppData/Local/R/win-library/4.4"
## cachem	"C:/Users/Owner/AppData/Local/R/win-library/4.4"
## callr	"C:/Users/Owner/AppData/Local/R/win-library/4.4"
## cellranger	"C:/Users/Owner/AppData/Local/R/win-library/4.4"
## checkmate	"C:/Users/Owner/AppData/Local/R/win-library/4.4"
## cli	"C:/Users/Owner/AppData/Local/R/win-library/4.4"
## clipr	"C:/Users/Owner/AppData/Local/R/win-library/4.4"
## colorspace	"C:/Users/Owner/AppData/Local/R/win-library/4.4"
## commonmark	"C:/Users/Owner/AppData/Local/R/win-library/4.4"
## conflicted	"C:/Users/Owner/AppData/Local/R/win-library/4.4"
## cpp11	"C:/Users/Owner/AppData/Local/R/win-library/4.4"
## crayon	"C:/Users/Owner/AppData/Local/R/win-library/4.4"
## credentials	"C:/Users/Owner/AppData/Local/R/win-library/4.4"
## curl	"C:/Users/Owner/AppData/Local/R/win-library/4.4"
## data.table	"C:/Users/Owner/AppData/Local/R/win-library/4.4"
## DBI	"C:/Users/Owner/AppData/Local/R/win-library/4.4"
## dbplyr	"C:/Users/Owner/AppData/Local/R/win-library/4.4"
## DelayedArray	"C:/Users/Owner/AppData/Local/R/win-library/4.4"
## desc	"C:/Users/Owner/AppData/Local/R/win-library/4.4"
## devtools	"C:/Users/Owner/AppData/Local/R/win-library/4.4"
## diffobj	"C:/Users/Owner/AppData/Local/R/win-library/4.4"
## digest	"C:/Users/Owner/AppData/Local/R/win-library/4.4"
## downlit	"C:/Users/Owner/AppData/Local/R/win-library/4.4"
## dplyr	"C:/Users/Owner/AppData/Local/R/win-library/4.4"
## dtplyr	"C:/Users/Owner/AppData/Local/R/win-library/4.4"
## ellipsis	"C:/Users/Owner/AppData/Local/R/win-library/4.4"
## evaluate	"C:/Users/Owner/AppData/Local/R/win-library/4.4"
## fansi	"C:/Users/Owner/AppData/Local/R/win-library/4.4"
## farver	"C:/Users/Owner/AppData/Local/R/win-library/4.4"
## fastmap	"C:/Users/Owner/AppData/Local/R/win-library/4.4"
## fontawesome	"C:/Users/Owner/AppData/Local/R/win-library/4.4"
## forcats	"C:/Users/Owner/AppData/Local/R/win-library/4.4"
## formatR	"C:/Users/Owner/AppData/Local/R/win-library/4.4"
## Formula	"C:/Users/Owner/AppData/Local/R/win-library/4.4"

```

## fs "C:/Users/Owner/AppData/Local/R/win-library/4.4"
## futile.logger "C:/Users/Owner/AppData/Local/R/win-library/4.4"
## futile.options "C:/Users/Owner/AppData/Local/R/win-library/4.4"
## gargle "C:/Users/Owner/AppData/Local/R/win-library/4.4"
## generics "C:/Users/Owner/AppData/Local/R/win-library/4.4"
## GenomeInfoDb "C:/Users/Owner/AppData/Local/R/win-library/4.4"
## GenomeInfoDbData "C:/Users/Owner/AppData/Local/R/win-library/4.4"
## GenomicAlignments "C:/Users/Owner/AppData/Local/R/win-library/4.4"
## GenomicFeatures "C:/Users/Owner/AppData/Local/R/win-library/4.4"
## GenomicRanges "C:/Users/Owner/AppData/Local/R/win-library/4.4"
## gert "C:/Users/Owner/AppData/Local/R/win-library/4.4"
## ggplot2 "C:/Users/Owner/AppData/Local/R/win-library/4.4"
## gh "C:/Users/Owner/AppData/Local/R/win-library/4.4"
## gitcreds "C:/Users/Owner/AppData/Local/R/win-library/4.4"
## glue "C:/Users/Owner/AppData/Local/R/win-library/4.4"
## googledrive "C:/Users/Owner/AppData/Local/R/win-library/4.4"
## googlesheets4 "C:/Users/Owner/AppData/Local/R/win-library/4.4"
## gridExtra "C:/Users/Owner/AppData/Local/R/win-library/4.4"
## gtable "C:/Users/Owner/AppData/Local/R/win-library/4.4"
## haven "C:/Users/Owner/AppData/Local/R/win-library/4.4"
## highr "C:/Users/Owner/AppData/Local/R/win-library/4.4"
## Hmisc "C:/Users/Owner/AppData/Local/R/win-library/4.4"
## hms "C:/Users/Owner/AppData/Local/R/win-library/4.4"
## htmlTable "C:/Users/Owner/AppData/Local/R/win-library/4.4"
## htmltools "C:/Users/Owner/AppData/Local/R/win-library/4.4"
## htmlwidgets "C:/Users/Owner/AppData/Local/R/win-library/4.4"
## httpuv "C:/Users/Owner/AppData/Local/R/win-library/4.4"
## httr "C:/Users/Owner/AppData/Local/R/win-library/4.4"
## httr2 "C:/Users/Owner/AppData/Local/R/win-library/4.4"
## ids "C:/Users/Owner/AppData/Local/R/win-library/4.4"
## ini "C:/Users/Owner/AppData/Local/R/win-library/4.4"
## IRanges "C:/Users/Owner/AppData/Local/R/win-library/4.4"
## isoband "C:/Users/Owner/AppData/Local/R/win-library/4.4"
## jquerylib "C:/Users/Owner/AppData/Local/R/win-library/4.4"
## jsonlite "C:/Users/Owner/AppData/Local/R/win-library/4.4"
## KEGGREST "C:/Users/Owner/AppData/Local/R/win-library/4.4"
## KernSmooth "C:/Users/Owner/AppData/Local/R/win-library/4.4"
## knitr "C:/Users/Owner/AppData/Local/R/win-library/4.4"
## labeling "C:/Users/Owner/AppData/Local/R/win-library/4.4"
## lambda.r "C:/Users/Owner/AppData/Local/R/win-library/4.4"
## later "C:/Users/Owner/AppData/Local/R/win-library/4.4"
## lifecycle "C:/Users/Owner/AppData/Local/R/win-library/4.4"
## lubridate "C:/Users/Owner/AppData/Local/R/win-library/4.4"
## magrittr "C:/Users/Owner/AppData/Local/R/win-library/4.4"
## MatrixGenerics "C:/Users/Owner/AppData/Local/R/win-library/4.4"
## matrixStats "C:/Users/Owner/AppData/Local/R/win-library/4.4"
## memoise "C:/Users/Owner/AppData/Local/R/win-library/4.4"
## mime "C:/Users/Owner/AppData/Local/R/win-library/4.4"
## miniUI "C:/Users/Owner/AppData/Local/R/win-library/4.4"
## modelr "C:/Users/Owner/AppData/Local/R/win-library/4.4"
## munsell "C:/Users/Owner/AppData/Local/R/win-library/4.4"
## name "C:/Users/Owner/AppData/Local/R/win-library/4.4"
## openssl "C:/Users/Owner/AppData/Local/R/win-library/4.4"
## pillar "C:/Users/Owner/AppData/Local/R/win-library/4.4"

```

## pkgbuild	"C:/Users/Owner/AppData/Local/R/win-library/4.4"
## pkgconfig	"C:/Users/Owner/AppData/Local/R/win-library/4.4"
## pkgdown	"C:/Users/Owner/AppData/Local/R/win-library/4.4"
## pkgload	"C:/Users/Owner/AppData/Local/R/win-library/4.4"
## plogr	"C:/Users/Owner/AppData/Local/R/win-library/4.4"
## plyr	"C:/Users/Owner/AppData/Local/R/win-library/4.4"
## png	"C:/Users/Owner/AppData/Local/R/win-library/4.4"
## praise	"C:/Users/Owner/AppData/Local/R/win-library/4.4"
## prettyunits	"C:/Users/Owner/AppData/Local/R/win-library/4.4"
## processx	"C:/Users/Owner/AppData/Local/R/win-library/4.4"
## profvis	"C:/Users/Owner/AppData/Local/R/win-library/4.4"
## progress	"C:/Users/Owner/AppData/Local/R/win-library/4.4"
## promises	"C:/Users/Owner/AppData/Local/R/win-library/4.4"
## ps	"C:/Users/Owner/AppData/Local/R/win-library/4.4"
## purrr	"C:/Users/Owner/AppData/Local/R/win-library/4.4"
## R6	"C:/Users/Owner/AppData/Local/R/win-library/4.4"
## ragg	"C:/Users/Owner/AppData/Local/R/win-library/4.4"
## rappdirs	"C:/Users/Owner/AppData/Local/R/win-library/4.4"
## rcmdcheck	"C:/Users/Owner/AppData/Local/R/win-library/4.4"
## RColorBrewer	"C:/Users/Owner/AppData/Local/R/win-library/4.4"
## Rcpp	"C:/Users/Owner/AppData/Local/R/win-library/4.4"
## RCurl	"C:/Users/Owner/AppData/Local/R/win-library/4.4"
## readr	"C:/Users/Owner/AppData/Local/R/win-library/4.4"
## readxl	"C:/Users/Owner/AppData/Local/R/win-library/4.4"
## rematch	"C:/Users/Owner/AppData/Local/R/win-library/4.4"
## rematch2	"C:/Users/Owner/AppData/Local/R/win-library/4.4"
## remotes	"C:/Users/Owner/AppData/Local/R/win-library/4.4"
## reprex	"C:/Users/Owner/AppData/Local/R/win-library/4.4"
## reshape2	"C:/Users/Owner/AppData/Local/R/win-library/4.4"
## restfulr	"C:/Users/Owner/AppData/Local/R/win-library/4.4"
## rhdf5	"C:/Users/Owner/AppData/Local/R/win-library/4.4"
## rhdf5filters	"C:/Users/Owner/AppData/Local/R/win-library/4.4"
## Rhdf5lib	"C:/Users/Owner/AppData/Local/R/win-library/4.4"
## Rhtslib	"C:/Users/Owner/AppData/Local/R/win-library/4.4"
## rJava	"C:/Users/Owner/AppData/Local/R/win-library/4.4"
## rjson	"C:/Users/Owner/AppData/Local/R/win-library/4.4"
## rlang	"C:/Users/Owner/AppData/Local/R/win-library/4.4"
## rmarkdown	"C:/Users/Owner/AppData/Local/R/win-library/4.4"
## RMySQL	"C:/Users/Owner/AppData/Local/R/win-library/4.4"
## roxygen2	"C:/Users/Owner/AppData/Local/R/win-library/4.4"
## rprojroot	"C:/Users/Owner/AppData/Local/R/win-library/4.4"
## Rsamtools	"C:/Users/Owner/AppData/Local/R/win-library/4.4"
## RSQLite	"C:/Users/Owner/AppData/Local/R/win-library/4.4"
## rstudioapi	"C:/Users/Owner/AppData/Local/R/win-library/4.4"
## rtracklayer	"C:/Users/Owner/AppData/Local/R/win-library/4.4"
## rversions	"C:/Users/Owner/AppData/Local/R/win-library/4.4"
## rvest	"C:/Users/Owner/AppData/Local/R/win-library/4.4"
## S4Arrays	"C:/Users/Owner/AppData/Local/R/win-library/4.4"
## S4Vectors	"C:/Users/Owner/AppData/Local/R/win-library/4.4"
## sass	"C:/Users/Owner/AppData/Local/R/win-library/4.4"
## scales	"C:/Users/Owner/AppData/Local/R/win-library/4.4"
## selectr	"C:/Users/Owner/AppData/Local/R/win-library/4.4"
## sessioninfo	"C:/Users/Owner/AppData/Local/R/win-library/4.4"
## shiny	"C:/Users/Owner/AppData/Local/R/win-library/4.4"


```

## snow "C:/Users/Owner/AppData/Local/R/win-library/4.4"
## sourcetools "C:/Users/Owner/AppData/Local/R/win-library/4.4"
## SparseArray "C:/Users/Owner/AppData/Local/R/win-library/4.4"
## stringi "C:/Users/Owner/AppData/Local/R/win-library/4.4"
## stringr "C:/Users/Owner/AppData/Local/R/win-library/4.4"
## SummarizedExperiment "C:/Users/Owner/AppData/Local/R/win-library/4.4"
## swirl "C:/Users/Owner/AppData/Local/R/win-library/4.4"
## sys "C:/Users/Owner/AppData/Local/R/win-library/4.4"
## systemfonts "C:/Users/Owner/AppData/Local/R/win-library/4.4"
## testthat "C:/Users/Owner/AppData/Local/R/win-library/4.4"
## textshaping "C:/Users/Owner/AppData/Local/R/win-library/4.4"
## tibble "C:/Users/Owner/AppData/Local/R/win-library/4.4"
## tidyr "C:/Users/Owner/AppData/Local/R/win-library/4.4"
## tidyselect "C:/Users/Owner/AppData/Local/R/win-library/4.4"
## tidyverse "C:/Users/Owner/AppData/Local/R/win-library/4.4"
## timechange "C:/Users/Owner/AppData/Local/R/win-library/4.4"
## tinytex "C:/Users/Owner/AppData/Local/R/win-library/4.4"
## tzdb "C:/Users/Owner/AppData/Local/R/win-library/4.4"
## UCSC.utils "C:/Users/Owner/AppData/Local/R/win-library/4.4"
## urlchecker "C:/Users/Owner/AppData/Local/R/win-library/4.4"
## usethis "C:/Users/Owner/AppData/Local/R/win-library/4.4"
## utf8 "C:/Users/Owner/AppData/Local/R/win-library/4.4"
## uuid "C:/Users/Owner/AppData/Local/R/win-library/4.4"
## vctrs "C:/Users/Owner/AppData/Local/R/win-library/4.4"
## viridis "C:/Users/Owner/AppData/Local/R/win-library/4.4"
## viridisLite "C:/Users/Owner/AppData/Local/R/win-library/4.4"
## vroom "C:/Users/Owner/AppData/Local/R/win-library/4.4"
## waldo "C:/Users/Owner/AppData/Local/R/win-library/4.4"
## whisker "C:/Users/Owner/AppData/Local/R/win-library/4.4"
## withr "C:/Users/Owner/AppData/Local/R/win-library/4.4"
## xfun "C:/Users/Owner/AppData/Local/R/win-library/4.4"
## XLConnect "C:/Users/Owner/AppData/Local/R/win-library/4.4"
## xlsx "C:/Users/Owner/AppData/Local/R/win-library/4.4"
## xlsxjars "C:/Users/Owner/AppData/Local/R/win-library/4.4"
## XML "C:/Users/Owner/AppData/Local/R/win-library/4.4"
## xml2 "C:/Users/Owner/AppData/Local/R/win-library/4.4"
## xopen "C:/Users/Owner/AppData/Local/R/win-library/4.4"
## xtable "C:/Users/Owner/AppData/Local/R/win-library/4.4"
## XVector "C:/Users/Owner/AppData/Local/R/win-library/4.4"
## yaml "C:/Users/Owner/AppData/Local/R/win-library/4.4"
## zip "C:/Users/Owner/AppData/Local/R/win-library/4.4"
## zlibbioc "C:/Users/Owner/AppData/Local/R/win-library/4.4"
## base "C:/Program Files/R/R-4.4.1/library"
## boot "C:/Program Files/R/R-4.4.1/library"
## class "C:/Program Files/R/R-4.4.1/library"
## cluster "C:/Program Files/R/R-4.4.1/library"
## codetools "C:/Program Files/R/R-4.4.1/library"
## compiler "C:/Program Files/R/R-4.4.1/library"
## datasets "C:/Program Files/R/R-4.4.1/library"
## foreign "C:/Program Files/R/R-4.4.1/library"
## graphics "C:/Program Files/R/R-4.4.1/library"
## grDevices "C:/Program Files/R/R-4.4.1/library"
## grid "C:/Program Files/R/R-4.4.1/library"
## KernSmooth "C:/Program Files/R/R-4.4.1/library"

```

## lattice	"C:/Program Files/R/R-4.4.1/library"
## MASS	"C:/Program Files/R/R-4.4.1/library"
## Matrix	"C:/Program Files/R/R-4.4.1/library"
## methods	"C:/Program Files/R/R-4.4.1/library"
## mgcv	"C:/Program Files/R/R-4.4.1/library"
## nlme	"C:/Program Files/R/R-4.4.1/library"
## nnet	"C:/Program Files/R/R-4.4.1/library"
## parallel	"C:/Program Files/R/R-4.4.1/library"
## rpart	"C:/Program Files/R/R-4.4.1/library"
## spatial	"C:/Program Files/R/R-4.4.1/library"
## splines	"C:/Program Files/R/R-4.4.1/library"
## stats	"C:/Program Files/R/R-4.4.1/library"
## stats4	"C:/Program Files/R/R-4.4.1/library"
## survival	"C:/Program Files/R/R-4.4.1/library"
## tcltk	"C:/Program Files/R/R-4.4.1/library"
## tools	"C:/Program Files/R/R-4.4.1/library"
## translations	"C:/Program Files/R/R-4.4.1/library"
## utils	"C:/Program Files/R/R-4.4.1/library"
##	Version Priority
## abind	"1.4-8" NA
## AnnotationDbi	"1.68.0" NA
## askpass	"1.2.1" NA
## backports	"1.5.0" NA
## base64enc	"0.1-3" NA
## BH	"1.87.0-1" NA
## Biobase	"2.66.0" NA
## BiocGenerics	"0.52.0" NA
## BiocIO	"1.16.0" NA
## BiocManager	"1.30.25" NA
## BiocParallel	"1.40.0" NA
## BiocVersion	"3.20.0" NA
## Biostrings	"2.74.1" NA
## bit	"4.5.0.1" NA
## bit64	"4.6.0-1" NA
## bitops	"1.0-9" NA
## blob	"1.2.4" NA
## brew	"1.0-10" NA
## brio	"1.1.5" NA
## broom	"1.0.7" NA
## bslib	"0.8.0" NA
## cachem	"1.1.0" NA
## callr	"3.7.6" NA
## cellranger	"1.1.0" NA
## checkmate	"2.3.2" NA
## cli	"3.6.3" NA
## clipr	"0.8.0" NA
## colorspace	"2.1-1" NA
## commonmark	"1.9.2" NA
## conflicted	"1.2.0" NA
## cpp11	"0.5.1" NA
## crayon	"1.5.3" NA
## credentials	"2.0.2" NA
## curl	"6.1.0" NA
## data.table	"1.16.4" NA

## DBI	"1.2.3"	NA
## dbplyr	"2.5.0"	NA
## DelayedArray	"0.32.0"	NA
## desc	"1.4.3"	NA
## devtools	"2.4.5"	NA
## diffobj	"0.3.5"	NA
## digest	"0.6.37"	NA
## downlit	"0.4.4"	NA
## dplyr	"1.1.4"	NA
## dtplyr	"1.3.1"	NA
## ellipsis	"0.3.2"	NA
## evaluate	"1.0.3"	NA
## fansi	"1.0.6"	NA
## farver	"2.1.2"	NA
## fastmap	"1.2.0"	NA
## fontawesome	"0.5.3"	NA
## forcats	"1.0.0"	NA
## formatR	"1.14"	NA
## Formula	"1.2-5"	NA
## fs	"1.6.5"	NA
## futile.logger	"1.4.3"	NA
## futile.options	"1.0.1"	NA
## gargle	"1.5.2"	NA
## generics	"0.1.3"	NA
## GenomeInfoDb	"1.42.1"	NA
## GenomeInfoDbData	"1.2.13"	NA
## GenomicAlignments	"1.42.0"	NA
## GenomicFeatures	"1.58.0"	NA
## GenomicRanges	"1.58.0"	NA
## gert	"2.1.4"	NA
## ggplot2	"3.5.1"	NA
## gh	"1.4.1"	NA
## gitcreds	"0.1.2"	NA
## glue	"1.8.0"	NA
## googledrive	"2.1.1"	NA
## googlesheets4	"1.1.1"	NA
## gridExtra	"2.3"	NA
## gtable	"0.3.6"	NA
## haven	"2.5.4"	NA
## highr	"0.11"	NA
## Hmisc	"5.2-2"	NA
## hms	"1.1.3"	NA
## htmlTable	"2.4.3"	NA
## htmltools	"0.5.8.1"	NA
## htmlwidgets	"1.6.4"	NA
## httpuv	"1.6.15"	NA
## httr	"1.4.7"	NA
## httr2	"1.1.0"	NA
## ids	"1.0.1"	NA
## ini	"0.3.1"	NA
## IRanges	"2.40.1"	NA
## isoband	"0.2.7"	NA
## jquerylib	"0.1.4"	NA
## jsonlite	"1.8.9"	NA

## KEGGREST	"1.46.0"	NA
## KernSmooth	"2.23-26"	"recommended"
## knitr	"1.49"	NA
## labeling	"0.4.3"	NA
## lambda.r	"1.2.4"	NA
## later	"1.4.1"	NA
## lifecycle	"1.0.4"	NA
## lubridate	"1.9.4"	NA
## magrittr	"2.0.3"	NA
## MatrixGenerics	"1.18.1"	NA
## matrixStats	"1.5.0"	NA
## memoise	"2.0.1"	NA
## mime	"0.12"	NA
## miniUI	"0.1.1.1"	NA
## modelr	"0.1.11"	NA
## munsell	"0.5.1"	NA
## name	"0.0.1"	NA
## openssl	"2.3.1"	NA
## pillar	"1.10.1"	NA
## pkgbuild	"1.4.6"	NA
## pkgconfig	"2.0.3"	NA
## pkgdown	"2.1.1"	NA
## pkgload	"1.4.0"	NA
## plogr	"0.2.0"	NA
## plyr	"1.8.9"	NA
## png	"0.1-8"	NA
## praise	"1.0.0"	NA
## prettyunits	"1.2.0"	NA
## processx	"3.8.5"	NA
## profvis	"0.4.0"	NA
## progress	"1.2.3"	NA
## promises	"1.3.2"	NA
## ps	"1.8.1"	NA
## purrr	"1.0.2"	NA
## R6	"2.5.1"	NA
## ragg	"1.3.3"	NA
## rappdirs	"0.3.3"	NA
## rcmdcheck	"1.4.0"	NA
## RColorBrewer	"1.1-3"	NA
## Rcpp	"1.0.14"	NA
## RCurl	"1.98-1.16"	NA
## readr	"2.1.5"	NA
## readxl	"1.4.3"	NA
## rematch	"2.0.0"	NA
## rematch2	"2.1.2"	NA
## remotes	"2.5.0"	NA
## reprex	"2.1.1"	NA
## reshape2	"1.4.4"	NA
## restfulr	"0.0.15"	NA
## rhdf5	"2.50.2"	NA
## rhdf5filters	"1.18.0"	NA
## Rhdf5lib	"1.28.0"	NA
## Rhtslib	"3.2.0"	NA
## rJava	"1.0-11"	NA

## rjson	"0.2.23"	NA
## rlang	"1.1.4"	NA
## rmarkdown	"2.29"	NA
## RMySQL	"0.10.29"	NA
## roxygen2	"7.3.2"	NA
## rprojroot	"2.0.4"	NA
## Rsamtools	"2.22.0"	NA
## RSQLite	"2.3.9"	NA
## rstudioapi	"0.17.1"	NA
## rtracklayer	"1.66.0"	NA
## rversions	"2.1.2"	NA
## rvest	"1.0.4"	NA
## S4Arrays	"1.6.0"	NA
## S4Vectors	"0.44.0"	NA
## sass	"0.4.9"	NA
## scales	"1.3.0"	NA
## selectr	"0.4-2"	NA
## sessioninfo	"1.2.2"	NA
## shiny	"1.10.0"	NA
## snow	"0.4-4"	NA
## sourcetools	"0.1.7-1"	NA
## SparseArray	"1.6.0"	NA
## stringi	"1.8.4"	NA
## stringr	"1.5.1"	NA
## SummarizedExperiment	"1.36.0"	NA
## swirl	"2.4.5"	NA
## sys	"3.4.3"	NA
## systemfonts	"1.2.1"	NA
## testthat	"3.2.3"	NA
## textshaping	"1.0.0"	NA
## tibble	"3.2.1"	NA
## tidyr	"1.3.1"	NA
## tidyselect	"1.2.1"	NA
## tidyverse	"2.0.0"	NA
## timechange	"0.3.0"	NA
## tinytex	"0.54"	NA
## tzdb	"0.4.0"	NA
## UCSC.utils	"1.2.0"	NA
## urlchecker	"1.0.1"	NA
## usethis	"3.1.0"	NA
## utf8	"1.2.4"	NA
## uuid	"1.2-1"	NA
## vctrs	"0.6.5"	NA
## viridis	"0.6.5"	NA
## viridisLite	"0.4.2"	NA
## vroom	"1.6.5"	NA
## waldo	"0.6.1"	NA
## whisker	"0.4.1"	NA
## withr	"3.0.2"	NA
## xfun	"0.49"	NA
## XLConnect	"1.1.0"	NA
## xlsx	"0.6.5"	NA
## xlsxjars	"0.6.1"	NA
## XML	"3.99-0.18"	NA

## xml2	"1.3.6"	NA
## xopen	"1.0.1"	NA
## xtable	"1.8-4"	NA
## XVector	"0.46.0"	NA
## yaml	"2.3.10"	NA
## zip	"2.3.1"	NA
## zlibbioc	"1.52.0"	NA
## base	"4.4.1"	"base"
## boot	"1.3-30"	"recommended"
## class	"7.3-22"	"recommended"
## cluster	"2.1.6"	"recommended"
## codetools	"0.2-20"	"recommended"
## compiler	"4.4.1"	"base"
## datasets	"4.4.1"	"base"
## foreign	"0.8-86"	"recommended"
## graphics	"4.4.1"	"base"
## grDevices	"4.4.1"	"base"
## grid	"4.4.1"	"base"
## KernSmooth	"2.23-24"	"recommended"
## lattice	"0.22-6"	"recommended"
## MASS	"7.3-60.2"	"recommended"
## Matrix	"1.7-0"	"recommended"
## methods	"4.4.1"	"base"
## mgcv	"1.9-1"	"recommended"
## nlme	"3.1-164"	"recommended"
## nnet	"7.3-19"	"recommended"
## parallel	"4.4.1"	"base"
## rpart	"4.1.23"	"recommended"
## spatial	"7.3-17"	"recommended"
## splines	"4.4.1"	"base"
## stats	"4.4.1"	"base"
## stats4	"4.4.1"	"base"
## survival	"3.6-4"	"recommended"
## tcltk	"4.4.1"	"base"
## tools	"4.4.1"	"base"
## translations	"4.4.1"	NA
## utils	"4.4.1"	"base"
##	Depends	
## abind	"R (>= 1.5.0)"	
## AnnotationDbi	"R (>= 2.7.0), methods, stats4, BiocGenerics (>= 0.29.2),\nBiobase (>= 1.17.0),	
## askpass	NA	
## backports	"R (>= 3.0.0)"	
## base64enc	"R (>= 2.9.0)"	
## BH	NA	
## Biobase	"R (>= 2.10), BiocGenerics (>= 0.27.1), utils"	
## BiocGenerics	"R (>= 4.0.0), methods, utils, graphics, stats"	
## BiocIO	"R (>= 4.3.0)"	
## BiocManager	NA	
## BiocParallel	"methods, R (>= 3.5.0)"	
## BiocVersion	"R (>= 4.4.0)"	
## Biostrings	"R (>= 4.0.0), BiocGenerics (>= 0.37.0), S4Vectors (>=\n0.27.12), IRanges (>= 2	
## bit	"R (>= 3.4.0)"	
## bit64	"R (>= 3.4.0), bit (>= 4.0.0)"	
## bitops	NA	

```

## blob NA
## brew NA
## brio "R (>= 3.6)"
## broom "R (>= 3.5)"
## bslib "R (>= 2.10)"
## cachem NA
## callr "R (>= 3.4)"
## cellranger "R (>= 3.0.0)"
## checkmate "R (>= 3.0.0)"
## cli "R (>= 3.4)"
## clipr NA
## colorspace "R (>= 3.0.0), methods"
## commonmark NA
## conflicted "R (>= 3.2)"
## cpp11 "R (>= 4.0.0)"
## crayon NA
## credentials NA
## curl "R (>= 3.0.0)"
## data.table "R (>= 3.3.0)"
## DBI "methods, R (>= 3.0.0)"
## dbplyr "R (>= 3.6)"
## DelayedArray "R (>= 4.0.0), methods, stats4, Matrix, BiocGenerics (>=\n0.51.3), MatrixGeneri
## desc "R (>= 3.4)"
## devtools "R (>= 3.0.2), usethis (>= 2.1.6)"
## diffobj "R (>= 3.1.0)"
## digest "R (>= 3.3.0)"
## downlit "R (>= 4.0.0)"
## dplyr "R (>= 3.5.0)"
## dtplyr "R (>= 3.3)"
## ellipsis "R (>= 3.2)"
## evaluate "R (>= 3.6.0)"
## fansi "R (>= 3.1.0)"
## farver NA
## fastmap NA
## fontawesome "R (>= 3.3.0)"
## forcats "R (>= 3.4)"
## formatR "R (>= 3.2.3)"
## Formula "R (>= 2.0.0), stats"
## fs "R (>= 3.6)"
## futile.logger "R (>= 3.0.0)"
## futile.options "R (>= 2.8.0)"
## gargle "R (>= 3.6)"
## generics "R (>= 3.2)"
## GenomeInfoDb "R (>= 4.0.0), methods, BiocGenerics (>= 0.37.0), S4Vectors (>=\n0.25.12), IRang
## GenomeInfoDbData "R (>= 3.5.0)"
## GenomicAlignments "R (>= 4.0.0), methods, BiocGenerics (>= 0.37.0), S4Vectors (>=\n0.27.12), IRang
## GenomicFeatures "R (>= 3.5.0), BiocGenerics (>= 0.51.2), S4Vectors (>=\n0.17.29), IRanges (>= 2
## GenomicRanges "R (>= 4.0.0), methods, stats4, BiocGenerics (>= 0.37.0),\nS4Vectors (>= 0.27.1
## gert NA
## ggplot2 "R (>= 3.5)"
## gh "R (>= 3.6)"
## gitcreds "R (>= 3.4)"
## glue "R (>= 3.6)"
## googledrive "R (>= 3.6)"

```

```

## googlesheets4      "R (>= 3.6)"
## gridExtra          NA
## gtable              "R (>= 4.0)"
## haven               "R (>= 3.6)"
## highr               "R (>= 3.3.0)"
## Hmisc               "R (>= 4.2.0)"
## hms                NA
## htmlTable           "R (>= 4.1)"
## htmltools           "R (>= 2.14.1)"
## htmlwidgets        NA
## httpuv              "R (>= 2.15.1)"
## httr                "R (>= 3.5)"
## httr2               "R (>= 4.0)"
## ids                 NA
## ini                 NA
## IRanges             "R (>= 4.0.0), methods, utils, stats, BiocGenerics (>= 0.39.2), \nS4Vectors (>= 0.39.2)"
## isoband             NA
## jquerylib           NA
## jsonlite            "methods"
## KEGGREST            "R (>= 3.5.0)"
## KernSmooth          "R (>= 2.5.0), stats"
## knitr               "R (>= 3.6.0)"
## labeling            NA
## lambda.r            "R (>= 3.0.0)"
## later               NA
## lifecycle           "R (>= 3.6)"
## lubridate           "methods, R (>= 3.2)"
## magrittr            "R (>= 3.4.0)"
## MatrixGenerics      "matrixStats (>= 1.4.1)"
## matrixStats         "R (>= 3.4.0)"
## memoise             NA
## mime                NA
## miniUI              NA
## modelr              "R (>= 3.2)"
## munsell             NA
## name                "R (>= 4.1)"
## openssl             NA
## pillar              NA
## pkgbuild            "R (>= 3.5)"
## pkgconfig           NA
## pkgdown             "R (>= 4.0.0)"
## pkgload             "R (>= 3.4.0)"
## plogr               NA
## plyr                "R (>= 3.1.0)"
## png                 "R (>= 2.9.0)"
## praise              NA
## prettyunits         "R(>= 2.10)"
## processx            "R (>= 3.4.0)"
## profvis             "R (>= 4.0)"
## progress            "R (>= 3.6)"
## promises            NA
## ps                  "R (>= 3.4)"
## purrr               "R (>= 3.5.0)"
## R6                  "R (>= 3.0)"

```



```

## ragg NA
## rappdirs "R (>= 3.2)"
## rcmdcheck NA
## RColorBrewer "R (>= 2.0.0)"
## Rcpp NA
## RCurl "R (>= 3.4.0), methods"
## readr "R (>= 3.6)"
## readxl "R (>= 3.6)"
## rematch NA
## rematch2 NA
## remotes "R (>= 3.0.0)"
## reprex "R (>= 3.6)"
## reshape2 "R (>= 3.1)"
## restfulr "R (>= 3.4.0), methods"
## rhdf5 "R (>= 4.0.0), methods"
## rhdf5filters NA
## Rhdf5lib "R (>= 4.2.0)"
## Rhtslib NA
## rJava "R (>= 3.6.0), methods"
## rjson "R (>= 4.0.0)"
## rlang "R (>= 3.5.0)"
## rmarkdown "R (>= 3.0)"
## RMySQL "R (>= 2.8.0), DBI (>= 0.4)"
## roxygen2 "R (>= 3.6)"
## rprojroot "R (>= 3.0.0)"
## Rsamtools "methods, GenomeInfoDb (>= 1.1.3), GenomicRanges (>= 1.31.8),\nBiostrings (>= 2
## RSQLite "R (>= 3.1.0)"
## rstudioapi NA
## rtracklayer "R (>= 3.5.0), methods, GenomicRanges (>= 1.37.2)"
## rversions NA
## rvest "R (>= 3.6)"
## S4Arrays "R (>= 4.3.0), methods, Matrix, abind, BiocGenerics (>=\n0.45.2), S4Vectors, IR
## S4Vectors "R (>= 4.0.0), methods, utils, stats, stats4, BiocGenerics (>=\n0.37.0)"
## sass NA
## scales "R (>= 3.6)"
## selectr "R (>= 3.0)"
## sessioninfo "R (>= 2.10)"
## shiny "R (>= 3.0.2), methods"
## snow "R (>= 2.13.1), utils"
## sourcetools "R (>= 3.0.2)"
## SparseArray "R (>= 4.3.0), methods, Matrix, BiocGenerics (>= 0.43.1),\nMatrixGenerics (>= 1
## stringi "R (>= 3.4)"
## stringr "R (>= 3.6)"
## SummarizedExperiment "R (>= 4.0.0), methods, MatrixGenerics (>= 1.1.3),\nGenomicRanges (>= 1.55.2), I
## swirl "R (>= 3.1.0)"
## sys NA
## systemfonts "R (>= 3.2.0)"
## testthat "R (>= 3.6.0)"
## textshaping "R (>= 3.2.0)"
## tibble "R (>= 3.4.0)"
## tidyr "R (>= 3.6)"
## tidyselect "R (>= 3.4)"
## tidyverse "R (>= 3.3)"
## timechange "R (>= 3.3)"

```

## tinytex	NA
## tzdb	"R (>= 3.5.0)"
## UCSC.utils	NA
## urlchecker	"R (>= 3.3)"
## usethis	"R (>= 3.6)"
## utf8	"R (>= 2.10)"
## uuid	"R (>= 2.9.0)"
## vctrs	"R (>= 3.5.0)"
## viridis	"R (>= 2.10), viridisLite (>= 0.4.0)"
## viridisLite	"R (>= 2.10)"
## vroom	"R (>= 3.6)"
## waldo	"R (>= 4.0)"
## whisker	NA
## withr	"R (>= 3.6.0)"
## xfun	"R (>= 3.2.0)"
## XLConnect	"R (>= 3.6.0)"
## xlsx	NA
## xlsxjars	"rJava"
## XML	"R (>= 4.0.0), methods, utils"
## xml2	"R (>= 3.6.0)"
## xopen	"R (>= 3.1)"
## xtable	"R (>= 2.10.0)"
## XVector	"R (>= 4.0.0), methods, BiocGenerics (>= 0.37.0), S4Vectors (>=\n0.27.12), IRanges"
## yaml	NA
## zip	NA
## zlibbioc	NA
## base	NA
## boot	"R (>= 3.0.0), graphics, stats"
## class	"R (>= 3.0.0), stats, utils"
## cluster	"R (>= 3.5.0)"
## codetools	"R (>= 2.1)"
## compiler	NA
## datasets	NA
## foreign	"R (>= 4.0.0)"
## graphics	NA
## grDevices	NA
## grid	NA
## KernSmooth	"R (>= 2.5.0), stats"
## lattice	"R (>= 4.0.0)"
## MASS	"R (>= 4.4.0), grDevices, graphics, stats, utils"
## Matrix	"R (>= 4.4.0), methods"
## methods	NA
## mgcv	"R (>= 3.6.0), nlme (>= 3.1-64)"
## nlme	"R (>= 3.5.0)"
## nnet	"R (>= 3.0.0), stats, utils"
## parallel	NA
## rpart	"R (>= 2.15.0), graphics, stats, grDevices"
## spatial	"R (>= 3.0.0), graphics, stats, utils"
## splines	NA
## stats	NA
## stats4	NA
## survival	"R (>= 3.5.0)"
## tcltk	NA
## tools	NA

```

## translations      NA
## utils             NA
##                   Imports
## abind              "methods, utils"
## AnnotationDbi     "DBI, RSQLite, S4Vectors (>= 0.9.25), stats, KEGGREST"
## askpass            "sys (>= 2.1)"
## backports         NA
## base64enc         NA
## BH                NA
## Biobase            "methods"
## BiocGenerics       "methods, utils, graphics, stats"
## BiocIO             "BiocGenerics, S4Vectors, methods, tools"
## BiocManager        "utils"
## BiocParallel       "stats, utils, futile.logger, parallel, snow, codetools"
## BiocVersion        NA
## Biostrings         "methods, utils, grDevices, stats, crayon"
## bit               NA
## bit64              "graphics, methods, stats, utils"
## bitops            NA
## blob               "methods, rlang, vctrs (>= 0.2.1)"
## brew              NA
## brio               NA
## broom              "backports, dplyr (>= 1.0.0), generics (>= 0.0.2), glue,\nlifecycle, purrr, rlang"
## bslib              "base64enc, cachem, fastmap (>= 1.1.1), grDevices, htmltools\n(>= 0.5.8), jquery"
## cachem             "rlang, fastmap (>= 1.2.0)"
## callr              "processx (>= 3.6.1), R6, utils"
## cellranger         "rematch, tibble"
## checkmate          "backports (>= 1.1.0), utils"
## cli                "utils"
## clipr              "utils"
## colorspace         "graphics, grDevices, stats"
## commonmark         NA
## conflicted         "cli (>= 3.4.0), memoise, rlang (>= 1.0.0)"
## cpp11              NA
## crayon              "grDevices, methods, utils"
## credentials        "openssl (>= 1.3), sys (>= 2.1), curl, jsonlite, askpass"
## curl               NA
## data.table         "methods"
## DBI                NA
## dbplyr             "blob (>= 1.2.0), cli (>= 3.6.1), DBI (>= 1.1.3), dplyr (>=\n1.1.2), glue (>= 1.3.2)"
## DelayedArray       "stats"
## desc               "cli, R6, utils"
## devtools           "cli (>= 3.3.0), desc (>= 1.4.1), ellipsis (>= 0.3.2), fs (>=\n1.5.2), lifecycle, pkgbuild, pkgcheck, pkgdown, pkgload, pkgshiny, pkgtest, rcmdr, rlang, rmarkdown, rprojroot, rstudioapi, shiny, testthat, usethis, withr"
## diffobj            "crayon (>= 1.3.2), tools, methods, utils, stats"
## digest             "utils"
## downlit            "brio, desc, digest, evaluate, fansi, memoise, rlang, vctrs,\nwithr, yaml"
## dplyr              "cli (>= 3.4.0), generics, glue (>= 1.3.2), lifecycle (>=\n1.0.3), magrittr (>= 2.0.1), purrr, rlang, tibble, tidyr, vctrs"
## dtplyr             "cli (>= 3.4.0), data.table (>= 1.13.0), dplyr (>= 1.1.0),\nnglue, lifecycle, rlang"
## ellipsis           "rlang (>= 0.3.0)"
## evaluate           NA
## fansi              "grDevices, utils"
## farver             NA
## fastmap            NA
## fontawesome        "rlang (>= 1.0.6), htmltools (>= 0.5.1.1)"

```

```

## forcats "cli (>= 3.4.0), glue, lifecycle, magrittr, rlang (>= 1.0.0),\ntibble"
## formatR NA
## Formula NA
## fs "methods"
## futile.logger "utils, lambda.r (>= 1.1.0), futile.options"
## futile.options NA
## gargle "cli (>= 3.0.1), fs (>= 1.3.1), glue (>= 1.3.0), httr (>= 1.4.5), jsonlite, li
## generics "methods"
## GenomeInfoDb "stats, stats4, utils, UCSC.utils, GenomeInfoDbData"
## GenomeInfoDbData NA
## GenomicAlignments "methods, utils, stats, BiocGenerics, S4Vectors, IRanges,\nGenomicRanges, Biost
## GenomicFeatures "methods, utils, stats, DBI, XVector, Biostrings, rtracklayer"
## GenomicRanges "utils, stats, XVector (>= 0.29.2)"
## gert "askpass, credentials (>= 1.2.1), openssl (>= 2.0.3),\nrstudioapi (>= 0.11), sy
## ggplot2 "cli, glue, grDevices, grid, gtable (>= 0.1.1), isoband,\nlifecycle (> 1.0.1), l
## gh "cli (>= 3.0.1), gitcreds, glue, httr2, ini, jsonlite,\nlifecycle, rlang (>= 1.0
## gitcreds NA
## glue "methods"
## googledrive "cli (>= 3.0.0), gargle (>= 1.5.0), glue (>= 1.4.2), httr,\njsonlite, lifecycle
## googlesheets4 "cellranger, cli (>= 3.0.0), curl, gargle (>= 1.5.0), glue (>= 1.3.0), googled
## gridExtra "gtable, grid, grDevices, graphics, utils"
## gtable "cli, glue, grid, lifecycle, rlang (>= 1.1.0), stats"
## haven "cli (>= 3.0.0), forcats (>= 0.2.0), hms, lifecycle, methods,\nreadr (>= 0.1.0)
## highr "xfun (>= 0.18)"
## Hmisc "methods, ggplot2, cluster, rpart, nnet, foreign, gtable, grid,\ngridExtra, dat
## hms "lifecycle, methods, pkgconfig, rlang (>= 1.0.2), vctrs (>= 0.3.8)"
## htmlTable "stringr, knitr (>= 1.6), magrittr (>= 1.5), methods,\ncheckmate, htmlwidgets, l
## htmltools "base64enc, digest, fastmap (>= 1.1.0), grDevices, rlang (>= 1.0.0), utils"
## htmlwidgets "grDevices, htmltools (>= 0.5.7), jsonlite (>= 0.9.16), knitr\n(>= 1.8), rmarkd
## httpuv "later (>= 0.8.0), promises, R6, Rcpp (>= 1.0.7), utils"
## httr "curl (>= 5.0.2), jsonlite, mime, openssl (>= 0.8), R6"
## httr2 "cli (>= 3.0.0), curl (>= 6.1.0), glue, lifecycle, magrittr,\nopenssl, R6, rappo
## ids "openssl, uuid"
## ini NA
## IRanges "stats4"
## isoband "grid, utils"
## jquerylib "htmltools"
## jsonlite NA
## KEGGREST "methods, httr, png, Biostrings"
## KernSmooth NA
## knitr "evaluate (>= 0.15), highr (>= 0.11), methods, tools, xfun (>= 0.48), yaml (>=
## labeling "stats, graphics"
## lambda.r "formatR"
## later "Rcpp (>= 0.12.9), rlang"
## lifecycle "cli (>= 3.4.0), glue, rlang (>= 1.1.0)"
## lubridate "generics, timechange (>= 0.3.0)"
## magrittr NA
## MatrixGenerics "methods"
## matrixStats NA
## memoise "rlang (>= 0.4.10), cachem"
## mime "tools"
## miniUI "shiny (>= 0.13), htmltools (>= 0.3), utils"
## modelr "broom, magrittr, purrr (>= 0.2.2), rlang (>= 1.0.6), tibble,\ntidyr (>= 0.8.0)
## munsell "colorspace, methods"

```

```

## name "tibble, dplyr, stringr, tidyselect, rlang, cli"
## openssl "askpass"
## pillar "cli (>= 2.3.0), glue, lifecycle, rlang (>= 1.0.2), utf8 (>=\n1.1.0), utils, vc"
## pkgbuild "callr (>= 3.2.0), cli (>= 3.4.0), desc, processx, R6"
## pkgconfig "utils"
## pkgdown "bslib (>= 0.5.1), callr (>= 3.7.3), cli (>= 3.6.1), desc (>=\n1.4.0), digest, c"
## pkgload "cli (>= 3.3.0), desc, fs, glue, lifecycle, methods, pkgbuild,\nprocessx, rlang"
## plogr NA
## plyr "Rcpp (>= 0.11.0)"
## png NA
## praise NA
## prettyunits NA
## processx "ps (>= 1.2.0), R6, utils"
## profvis "htmlwidgets (>= 0.3.2), rlang (>= 1.1.0), vctrs"
## progress "crayon, hms, prettyunits, R6"
## promises "fastmap (>= 1.1.0), later, magrittr (>= 1.5), R6, Rcpp, rlang,\nstats"
## ps "utils"
## purrr "cli (>= 3.6.1), lifecycle (>= 1.0.3), magrittr (>= 1.5.0),\nrlang (>= 1.1.1), v"
## R6 NA
## ragg "systemfonts (>= 1.0.3), textshaping (>= 0.3.0)"
## rappdirs NA
## rcmdcheck "callr (>= 3.1.1.9000), cli (>= 3.0.0), curl, desc (>= 1.2.0),\nndigest, pkgbuild"
## RColorBrewer NA
## Rcpp "methods, utils"
## RCurl "bitops"
## readr "cli (>= 3.2.0), clipr, crayon, hms (>= 0.4.1), lifecycle (>=\n0.2.0), methods,"
## readxl "cellranger, tibble (>= 2.0.1), utils"
## rematch NA
## rematch2 "tibble"
## remotes "methods, stats, tools, utils"
## reprex "callr (>= 3.6.0), cli (>= 3.2.0), clipr (>= 0.4.0), fs, glue,\nknitr (>= 1.23)"
## reshape2 "plyr (>= 1.8.1), Rcpp, stringr"
## restfulr "XML, RCurl, rjson, S4Vectors (>= 0.13.15), yaml"
## rhdf5 "Rhdf5lib (>= 1.13.4), rhdf5filters (>= 1.15.5)"
## rhdf5filters NA
## Rhdf5lib NA
## Rhtslib "tools, zlibbioc"
## rJava NA
## rjson NA
## rlang "utils"
## rmarkdown "bslib (>= 0.2.5.1), evaluate (>= 0.13), fontawesome (>=\n0.5.0), htmltools (>="
## RMySQL "methods"
## roxygen2 "brew, cli (>= 3.3.0), commonmark, desc (>= 1.2.0), knitr,\nmethods, pkgload (>="
## rprojroot NA
## Rsamtools "utils, BiocGenerics (>= 0.25.1), S4Vectors (>= 0.17.25),\nIRanges (>= 2.13.12)"
## RSQLite "bit64, blob (>= 1.2.0), DBI (>= 1.2.0), memoise, methods,\nnpkgconfig, rlang"
## rstudioapi NA
## rtracklayer "XML (>= 1.98-0), BiocGenerics (>= 0.35.3), S4Vectors (>=\n0.23.18), IRanges (>="
## rversions "curl, utils, xml2 (>= 1.0.0)"
## rvest "cli, glue, httr (>= 0.5), lifecycle (>= 1.0.3), magrittr,\nrlang (>= 1.1.0), s"
## S4Arrays "stats, crayon"
## S4Vectors NA
## sass "fs (>= 1.2.4), rlang (>= 0.4.10), htmltools (>= 0.5.1), R6,\nrapprdirs"
## scales "cli, farver (>= 2.0.3), glue, labeling, lifecycle, munsell (>=\n0.5), R6, RCol"

```

```

## selectr "methods, stringr, R6"
## sessioninfo "cli (>= 3.1.0), tools, utils"
## shiny "utils, grDevices, httpuv (>= 1.5.2), mime (>= 0.3), jsonlite\n(>= 0.9.16), xtable"
## snow NA
## sourcetools NA
## SparseArray "utils, stats, matrixStats, IRanges, XVector"
## stringi "tools, utils, stats"
## stringr "cli, glue (>= 1.6.1), lifecycle (>= 1.0.3), magrittr, rlang\n(>= 1.0.0), stringr"
## SummarizedExperiment "utils, stats, tools, Matrix, BiocGenerics (>= 0.51.3),\nS4Vectors (>= 0.33.7), SummarizedExperiment"
## swirl "stringr, testthat (>= 1.0.2), httr (>= 1.1.0), yaml, RCurl,\ndigest, tools, methods"
## sys NA
## systemfonts "grid, jsonlite, lifecycle, tools, utils"
## testthat "brio (>= 1.1.3), callr (>= 3.7.3), cli (>= 3.6.1), desc (>= 1.4.2), digest (>= 0.6.29), devtools, lifecycle, rlang, testthat"
## textshaping "lifecycle, stats, stringi, systemfonts (>= 1.1.0), utils"
## tibble "fansi (>= 0.4.0), lifecycle (>= 1.0.0), magrittr, methods,\nnpillar (>= 1.8.1), tibble"
## tidyr "cli (>= 3.4.1), dplyr (>= 1.0.10), glue, lifecycle (>= 1.0.3),\nmagrittr, purrr"
## tidyselect "cli (>= 3.3.0), glue (>= 1.3.0), lifecycle (>= 1.0.3), rlang\n(>= 1.0.4), vctrs"
## tidyverse "broom (>= 1.0.3), conflicted (>= 1.2.0), cli (>= 3.6.0),\ndbplyr (>= 2.3.0), dplyr, forcats, ggplot2, hms, lifecycle, magrittr, methods, pillar, purrr, rlang, tidyr, tidyselect, tibble, tidyverse"
## timechange NA
## tinytex "xfun (>= 0.48)"
## tzdb NA
## UCSC.utils "methods, stats, httr, jsonlite, S4Vectors"
## urlchecker "cli, curl, tools, xml2"
## usethis "cli (>= 3.0.1), clipr (>= 0.3.0), crayon, curl (>= 2.7), desc\n(>= 1.4.2), fs, usethis"
## utf8 NA
## uuid NA
## vctrs "cli (>= 3.4.0), glue, lifecycle (>= 1.0.3), rlang (>= 1.1.0)"
## viridis "ggplot2 (>= 1.0.1), gridExtra"
## viridisLite NA
## vroom "bit64, cli (>= 3.2.0), crayon, glue, hms, lifecycle (>= 1.0.3), methods, rlang"
## waldo "cli, diffobj (>= 0.3.4), glue, methods, rlang (>= 1.1.0)"
## whisker NA
## withr "graphics, grDevices"
## xfun "grDevices, stats, tools"
## XLConnect "methods, rJava (>= 1.0-1)"
## xlsx "rJava, xlsxjars, grDevices, utils"
## xlsxjars NA
## XML NA
## xml2 "cli, methods, rlang (>= 1.1.0)"
## xopen "processx"
## xtable "stats, utils"
## XVector "methods, utils, tools, zlibbioc, BiocGenerics, S4Vectors,\nIRanges"
## yaml NA
## zip NA
## zlibbioc NA
## base NA
## boot NA
## class "MASS"
## cluster "graphics, grDevices, stats, utils"
## codetools NA
## compiler NA
## datasets NA
## foreign "methods, utils, stats"
## graphics "grDevices"

```

```

## grDevices      NA
## grid           "grDevices, utils"
## KernSmooth     NA
## lattice        "grid, grDevices, graphics, stats, utils"
## MASS           "methods"
## Matrix         "grDevices, graphics, grid, lattice, stats, utils"
## methods        "utils, stats"
## mgcv           "methods, stats, graphics, Matrix, splines, utils"
## nlme           "graphics, stats, utils, lattice"
## nnet           NA
## parallel       "tools, compiler"
## rpart          NA
## spatial        NA
## splines        "graphics, stats"
## stats          "utils, grDevices, graphics"
## stats4         "graphics, methods, stats"
## survival       "graphics, Matrix, methods, splines, stats, utils"
## tcltk          "utils"
## tools          NA
## translations   NA
## utils          NA
##               LinkingTo
## abind          NA
## AnnotationDbi  NA
## askpass        NA
## backports      NA
## base64enc      NA
## BH             NA
## Biobase        NA
## BiocGenerics   NA
## BiocIO         NA
## BiocManager    NA
## BiocParallel   "BH, cpp11"
## BiocVersion    NA
## Biostrings     "S4Vectors, IRanges, XVector"
## bit           NA
## bit64         NA
## bitops        NA
## blob          NA
## brew          NA
## brio          NA
## broom         NA
## bslib         NA
## cachem        NA
## callr         NA
## cellranger    NA
## checkmate     NA
## cli           NA
## clipr         NA
## colorspace    NA
## commonmark    NA
## conflicted    NA
## cpp11         NA
## crayon        NA

```

## credentials	NA
## curl	NA
## data.table	NA
## DBI	NA
## dbplyr	NA
## DelayedArray	"S4Vectors"
## desc	NA
## devtools	NA
## diffobj	NA
## digest	NA
## downlit	NA
## dplyr	NA
## dtplyr	NA
## ellipsis	NA
## evaluate	NA
## fansi	NA
## farver	NA
## fastmap	NA
## fontawesome	NA
## forcats	NA
## formatR	NA
## Formula	NA
## fs	NA
## futile.logger	NA
## futile.options	NA
## gargle	NA
## generics	NA
## GenomeInfoDb	NA
## GenomeInfoDbData	NA
## GenomicAlignments	"S4Vectors, IRanges"
## GenomicFeatures	NA
## GenomicRanges	"S4Vectors, IRanges"
## gert	NA
## ggplot2	NA
## gh	NA
## gitcreds	NA
## glue	NA
## googledrive	NA
## googlesheets4	NA
## gridExtra	NA
## gtable	NA
## haven	"cpp11"
## highr	NA
## Hmisc	NA
## hms	NA
## htmlTable	NA
## htmltools	NA
## htmlwidgets	NA
## httpuv	"later, Rcpp"
## httr	NA
## httr2	NA
## ids	NA
## ini	NA
## IRanges	"S4Vectors"

## isoband	NA
## jquerylib	NA
## jsonlite	NA
## KEGGREST	NA
## KernSmooth	NA
## knitr	NA
## labeling	NA
## lambda.r	NA
## later	"Rcpp"
## lifecycle	NA
## lubridate	NA
## magrittr	NA
## MatrixGenerics	NA
## matrixStats	NA
## memoise	NA
## mime	NA
## miniUI	NA
## modelr	NA
## munsell	NA
## name	NA
## openssl	NA
## pillar	NA
## pkgbuild	NA
## pkgconfig	NA
## pkgdown	NA
## pkgload	NA
## plogr	NA
## plyr	"Rcpp"
## png	NA
## praise	NA
## prettyunits	NA
## processx	NA
## profvis	NA
## progress	NA
## promises	"later, Rcpp"
## ps	NA
## purrr	"cli"
## R6	NA
## ragg	"systemfonts, textshaping"
## rappdirs	NA
## rcmdcheck	NA
## RColorBrewer	NA
## Rcpp	NA
## RCurl	NA
## readr	"cpp11, tzdb (>= 0.1.1)"
## readxl	"cpp11 (>= 0.4.0), progress"
## rematch	NA
## rematch2	NA
## remotes	NA
## reprex	NA
## reshape2	"Rcpp"
## restfulr	NA
## rhdf5	"Rhdf5lib"
## rhdf5filters	"Rhdf5lib"

## Rhdf5lib	NA
## Rhtslib	"zlibbioc"
## rJava	NA
## rjson	NA
## rlang	NA
## rmarkdown	NA
## RMySQL	NA
## roxygen2	"cpp11"
## rprojroot	NA
## Rsamtools	"Rhtslib (>= 2.99.1), S4Vectors, IRanges, XVector, Biostrings"
## RSQLite	"plogr (>= 0.2.0), cpp11 (>= 0.4.0)"
## rstudioapi	NA
## rtracklayer	"S4Vectors, IRanges, XVector"
## rversions	NA
## rvest	NA
## S4Arrays	"S4Vectors"
## S4Vectors	NA
## sass	NA
## scales	NA
## selectr	NA
## sessioninfo	NA
## shiny	NA
## snow	NA
## sourcetools	NA
## SparseArray	"S4Vectors, IRanges, XVector"
## stringi	NA
## stringr	NA
## SummarizedExperiment	NA
## swirl	NA
## sys	NA
## systemfonts	"cpp11 (>= 0.2.1)"
## testthat	NA
## textshaping	"cpp11 (>= 0.2.1), systemfonts (>= 1.0.0)"
## tibble	NA
## tidyr	"cpp11 (>= 0.4.0)"
## tidyselect	NA
## tidyverse	NA
## timechange	"cpp11 (>= 0.2.7)"
## tinytex	NA
## tzdb	"cpp11 (>= 0.4.2)"
## UCSC.utils	NA
## urlchecker	NA
## usethis	NA
## utf8	NA
## uuid	NA
## vctrs	NA
## viridis	NA
## viridisLite	NA
## vroom	"cpp11 (>= 0.2.0), progress (>= 1.2.1), tzdb (>= 0.1.1)"
## waldo	NA
## whisker	NA
## withr	NA
## xfun	NA
## XLConnect	NA

```

## xlsx NA
## xlsxjars NA
## XML NA
## xml2 NA
## xopen NA
## xtable NA
## XVector "S4Vectors, IRanges"
## yaml NA
## zip NA
## zlibbioc NA
## base NA
## boot NA
## class NA
## cluster NA
## codetools NA
## compiler NA
## datasets NA
## foreign NA
## graphics NA
## grDevices NA
## grid NA
## KernSmooth NA
## lattice NA
## MASS NA
## Matrix NA
## methods NA
## mgcv NA
## nlme NA
## nnet NA
## parallel NA
## rpart NA
## spatial NA
## splines NA
## stats NA
## stats4 NA
## survival NA
## tcltk NA
## tools NA
## translations NA
## utils NA
## Suggests
## abind NA
## AnnotationDbi "utils, hgu95av2.db, GO.db, org.Sc.sgd.db, org.At.tair.db,\nRUnit, TxDb.Hsapiens"
## askpass "testthat"
## backports NA
## base64enc NA
## BH NA
## Biobase "tools, tkWidgets, ALL, RUnit, golubEsets, BiocStyle, knitr,\nlimma"
## BiocGenerics "Biobase, S4Vectors, IRanges, S4Arrays, SparseArray,\nDelayedArray, HDF5Array, C"
## BiocIO "testthat, knitr, rmarkdown, BiocStyle"
## BiocManager "BiocVersion, BiocStyle, remotes, rmarkdown, testthat, withr,\nncurl, knitr"
## BiocParallel "BiocGenerics, tools, foreach, BBmisc, doParallel,\nGenomicRanges, RNAseqData.H"
## BiocVersion NA
## Biostrings "graphics, pwalgn, BSgenome (>= 1.13.14),\nBSgenome.Celegans.UCSC.ce2 (>= 1.3.

```

```

## bit "testthat (>= 0.11.0), roxygen2, knitr, markdown, rmarkdown,\nmicrobenchmark, b
## bit64 "testthat (>= 3.0.3), withr"
## bitops NA
## blob "covr, crayon, pillar (>= 1.2.1), testthat"
## brew "testthat (>= 3.0.0)"
## brio "covr, testthat (>= 3.0.0)"
## broom "AER, AUC, bbmle, betareg (>= 3.2-1), biglm, binGroup, boot,\nbtergm (>= 1.10.6)
## bslib "bsicons, curl, fontawesome, future, ggplot2, knitr, magrittr,\nrapprdirs, rmark
## cachem "testthat"
## callr "asciicast (>= 2.3.1), cli (>= 1.1.0), mockery, ps, rprojroot,\nspelling, testt
## cellranger "covr, testthat (>= 1.0.0), knitr, rmarkdown"
## checkmate "R6, fastmatch, data.table (>= 1.9.8), devtools, ggplot2,\nknitr, magrittr, mic
## cli "callr, covr, crayon, digest, glue (>= 1.6.0), grDevices,\nhtmltools, htmlwidg
## clipr "covr, knitr, rmarkdown, rstudioapi (>= 0.5), testthat (>= \n2.0.0)"
## colorspace "datasets, utils, KernSmooth, MASS, kernlab, mvtnorm, vcd,\ntcltk, shiny, shiny
## commonmark "curl, testthat, xml2"
## conflicted "callr, covr, dplyr, Matrix, methods, pkgload, testthat (>= \n3.0.0), withr"
## cpp11 "bench, brio, callr, cli, covr, decor, desc, ggplot2, glue,\nknitr, lobster, moc
## crayon "mockery, rstudioapi, testthat, withr"
## credentials "testthat, knitr, rmarkdown"
## curl "spelling, testthat (>= 1.0.0), knitr, jsonlite, later,\nrmmarkdown, httpuv (>=
## data.table "bit64 (>= 4.0.0), bit (>= 4.0.4), R.utils, xts, zoo (>= \n1.8-1), yaml, knitr, r
## DBI "arrow, blob, covr, DBItest, dbplyr, downlit, dplyr, glue,\nhms, knitr, magrittr
## dbplyr "bit64, covr, knitr, Lahman, nycflights13, odbc (>= 1.4.2),\nRMariaDB (>= 1.2.2)
## DelayedArray "BiocParallel, HDF5Array (>= 1.17.12), genefilter,\nSummarizedExperiment, airway
## desc "callr, covr, gh, spelling, testthat, whoami, withr"
## devtools "BiocManager (>= 1.30.18), callr (>= 3.7.1), covr (>= 3.5.1),\ncurl (>= 4.3.2),
## diffobj "knitr, rmarkdown"
## digest "tinytest, simplermardown"
## downlit "covr, htmltools, jsonlite, MASS, MassSpecWavelet, pkgload,\nrmmarkdown, testtha
## dplyr "bench, broom, callr, covr, DBI, dbplyr (>= 2.2.1), ggplot2,\nknitr, Lahman, lo
## dtplyr "bench, covr, knitr, rmarkdown, testthat (>= 3.1.2), tidyr (>= \n1.1.0), waldo (
## ellipsis "covr, testthat"
## evaluate "callr, covr, ggplot2 (>= 3.3.6), lattice, methods, pkgload,\nrlang, knitr, tes
## fansi "unitizer, knitr, rmarkdown"
## farver "covr, testthat (>= 3.0.0)"
## fastmap "testthat (>= 2.1.1)"
## fontawesome "covr, dplyr (>= 1.0.8), gt (>= 0.9.0), knitr (>= 1.31),\ntestthat (>= 3.0.0),
## forcats "covr, dplyr, ggplot2, knitr, readr, rmarkdown, testthat (>= \n3.0.0), withr"
## formatR "rstudioapi, shiny, testit, rmarkdown, knitr"
## Formula NA
## fs "covr, crayon, knitr, pillar (>= 1.0.0), rmarkdown, spelling,\ntestthat (>= 3.0
## futile.logger "testthat, jsonlite"
## futile.options NA
## gargle "aws.ec2metadata, aws.signature, covr, httpuv, knitr,\nrmmarkdown, sodium, spell
## generics "covr, pkgload, testthat (>= 3.0.0), tibble, withr"
## GenomeInfoDb "R.utils, data.table, GenomicRanges, Rsamtools,\nGenomicAlignments, GenomicFeat
## GenomeInfoDbData NA
## GenomicAlignments "ShortRead, rtracklayer, BSgenome, GenomicFeatures,\nRNAseqData.HNRNPC.bam.chr1
## GenomicFeatures "txdbmaker, org.Mm.eg.db, org.Hs.eg.db, BSgenome,\nBSgenome.Hsapiens.UCSC.hg19
## GenomicRanges "Matrix, Biobase, AnnotationDbi, annotate, Biostrings (>= \n2.25.3), SummarizedE
## gert "spelling, knitr, rmarkdown, testthat"
## ggplot2 "covr, dplyr, ggplot2movies, hexbin, Hmisc, knitr, mapproj,\nmaps, multcomp, mur
## gh "covr, knitr, mockery, rmarkdown, rprojroot, spelling,\ntestthat (>= 3.0.0), wi

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## gitcreds "codetools, covr, knitr, mockery, oskeyring, rmarkdown,\ntestthat (>= 3.0.0), w
## glue "crayon, DBI (>= 1.2.0), dplyr, knitr, magrittr, rlang,\nrmarkdown, RSQLite, tes
## googledrive "curl, dplyr (>= 1.0.0), knitr, mockr, rmarkdown, spelling,\ntestthat (>= 3.1.3
## googlesheets4 "readr, rmarkdown, spelling, testthat (>= 3.1.7)"
## gridExtra "ggplot2, egg, lattice, knitr, testthat"
## gtable "covr, ggplot2, knitr, profvis, rmarkdown, testthat (>= 3.0.0)"
## haven "covr, crayon, fs, knitr, pillar (>= 1.4.0), rmarkdown,\ntestthat (>= 3.0.0), u
## highr "knitr, markdown, testit"
## Hmisc "survival, qreport, acepack, chron, rms, mice, rstudioapi,\ntables, plotly (>= 4
## hms "crayon, lubridate, pillar (>= 1.1.0), testthat (>= 3.0.0)"
## htmlTable "testthat, XML, xml2, Hmisc, rmarkdown, chron, lubridate,\ntibble, purrr, tidys
## htmltools "Cairo, markdown, ragg, shiny, testthat, withr"
## htmlwidgets "testthat"
## httpuv "callr, curl, testthat, websocket"
## httr "covr, httpuv, jpeg, knitr, png, readr, rmarkdown, testthat\n(>= 0.8.0), xml2"
## httr2 "askpass, bench, clipr, covr, doctest, httpuv, jose, jsonlite,\nknitr, later (>=
## ids "knitr, rcorpora, rmarkdown, testthat"
## ini "testthat"
## IRanges "XVector, GenomicRanges, Rsamtools, GenomicAlignments,\nGenomicFeatures, BSGenom
## isoband "covr, ggplot2, knitr, magick, microbenchmark, rmarkdown, sf,\ntestthat, xml2"
## jquerylib "testthat"
## jsonlite "httr, vctrs, testthat, knitr, rmarkdown, R.rsp, sf"
## KEGGREST "RUnit, BiocGenerics, BiocStyle, knitr, markdown"
## KernSmooth "MASS, carData"
## knitr "bslib, codetools, DBI (>= 0.4-1), digest, formatR, gifski,\ngridSVG, htmlwidg
## labeling NA
## lambda.r "testit"
## later "knitr, nanonext, R6, rmarkdown, testthat (>= 2.1.0)"
## lifecycle "covr, crayon, knitr, lintr, rmarkdown, testthat (>= 3.0.1),\ntibble, tidyverse
## lubridate "covr, knitr, rmarkdown, testthat (>= 2.1.0), vctrs (>= 0.6.5)"
## magrittr "covr, knitr, rlang, rmarkdown, testthat"
## MatrixGenerics "Matrix, sparseMatrixStats, SparseArray, DelayedArray,\nDelayedMatrixStats, Summ
## matrixStats "utils, base64enc, ggplot2, knitr, markdown, microbenchmark,\nR.devices, R.rsp"
## memoise "digest, aws.s3, covr, googleAuthR, googleCloudStorageR, httr,\ntestthat"
## mime NA
## miniUI NA
## modelr "compiler, covr, ggplot2, testthat (>= 3.0.0)"
## munsell "ggplot2, testthat"
## name "testthat (>= 3.0.0)"
## openssl "curl, testthat (>= 2.1.0), digest, knitr, rmarkdown,\njsonlite, jose, sodium"
## pillar "bit64, DBI, debugme, DiagrammeR, dplyr, formattable, ggplot2,\nknitr, lubridate
## pkgbuild "covr, cpp11, knitr, Rcpp, rmarkdown, testthat (>= 3.2.0),\nwithr (>= 2.3.0)"
## pkgconfig "covr, testthat, disposables (>= 1.0.3)"
## pkgdown "covr, diffviewer, evaluate (>= 0.24.0), gert, gt, htmltools,\nhtmlwidgets, kni
## pkgload "bitops, jsonlite, mathjaxr, pak, Rcpp, remotes, rstudioapi,\ntestthat (>= 3.2.
## plogr "Rcpp"
## plyr "abind, covr, doParallel, foreach, iterators, itertools,\ntcltk, testthat"
## png NA
## praise "testthat"
## prettyunits "codetools, covr, testthat"
## processx "callr (>= 3.7.3), cli (>= 3.3.0), codetools, covr, curl,\ndebugme, parallel, r
## profvis "htmltools, knitr, rmarkdown, shiny, testthat (>= 3.0.0)"
## progress "Rcpp, testthat (>= 3.0.0), withr"
## promises "future (>= 1.21.0), knitr, purrr, rmarkdown, spelling,\ntestthat, vembedr"

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## ps "callr, covr, curl, pillar, pingr, processx (>= 3.1.0), R6,\nrlang, testthat (>= 3.0.0)"
## purrr "covr, dplyr (>= 0.7.8), httr, knitr, lubridate, rmarkdown,\ntestthat (>= 3.0.0)"
## R6 "testthat, pryr"
## ragg "covr, graphics, grid, testthat (>= 3.0.0)"
## rappdirs "roxygen2, testthat (>= 3.0.0), covr, withr"
## rcmdcheck "covr, knitr, mockery, processx, ps, rmarkdown, svglite,\ntestthat, webfakes"
## RColorBrewer NA
## Rcpp "tinytest, inline, rbenchmark, pkgKitten (>= 0.1.2)"
## RCurl "XML"
## readr "covr, curl, datasets, knitr, rmarkdown, spelling, stringi,\ntestthat (>= 3.2.0)"
## readxl "covr, knitr, rmarkdown, testthat (>= 3.1.6), withr"
## rematch "covr, testthat"
## rematch2 "covr, testthat"
## remotes "brew, callr, codetools, covr, curl, git2r (>= 0.23.0), knitr,\nmockery, pingr,
## reprex "covr, fortunes, miniUI, rprojroot, sessioninfo, shiny,\nspelling, styler (>= 1.0.0)"
## reshape2 "covr, lattice, testthat (>= 0.8.0)"
## restfulr "getPass, rsolr, RUnit"
## rhdf5 "bit64, BiocStyle, knitr, rmarkdown, testthat, bench, dplyr,\nggplot2, mockery,
## rhdf5filters "BiocStyle, knitr, rmarkdown, tinytest, rhdf5 (>= 2.47.7)"
## Rhdf5lib "BiocStyle, knitr, rmarkdown, tinytest, mockery"
## Rhtslib "knitr, rmarkdown, BiocStyle"
## rJava NA
## rjson NA
## rlang "cli (>= 3.1.0), covr, crayon, fs, glue, knitr, magrittr,\nmethods, pillar, rma
## rmarkdown "digest, dygraphs, fs, rsconnect, downlit (>= 0.4.0), katex\n(>= 1.4.0), sass (
## RMySQL "testthat, curl"
## roxygen2 "covr, R.methodsS3, R.oo, rmarkdown (>= 2.16), testthat (>=\n3.1.2), yaml"
## rprojroot "covr, knitr, lifecycle, mockr, rlang, rmarkdown, testthat (>=\n3.0.0), withr"
## Rsamtools "GenomicAlignments, ShortRead (>= 1.19.10), GenomicFeatures,\nTxDb.Dmelanogaster
## RSQLite "callr, cli, DBItest (>= 1.8.0), decor, gert, gh, hms, knitr,\nmagrittr, rmarkd
## rstudioapi "testthat, knitr, rmarkdown, clipr, covr"
## rtracklayer "BSgenome (>= 1.33.4), humanStemCell, microRNA (>= 1.1.1),\ngenefilter, limma,
## rversions "covr, mockery, testthat"
## rvest "chromote, covr, knitr, R6, readr, repurrrsive, rmarkdown,\nspelling, stringi (
## S4Arrays "BiocParallel, SparseArray (>= 0.0.4), DelayedArray, testthat,\nknitr, rmarkdow
## S4Vectors "IRanges, GenomicRanges, SummarizedExperiment, Matrix,\nDelayedArray, ShortRead
## sass "testthat, knitr, rmarkdown, withr, shiny, curl"
## scales "bit64, covr, dichromat, ggplot2, hms (>= 0.5.0), stringi,\ntestthat (>= 3.0.0)"
## selectr "testthat, XML, xml2"
## sessioninfo "callr, covr, mockery, reticulate, rmarkdown, testthat, withr"
## shiny "coro (>= 1.1.0), datasets, DT, Cairo (>= 1.5-5), testthat (>=\n3.0.0), knitr (
## snow "rlecuyer"
## sourcetools "testthat"
## SparseArray "HDF5Array, ExperimentHub, testthat, knitr, rmarkdown,\nBiocStyle"
## stringi NA
## stringr "covr, dplyr, gt, htmltools, htmlwidgets, knitr, rmarkdown,\ntestthat (>= 3.0.0)"
## SummarizedExperiment "jsonlite, rhdf5, HDF5Array (>= 1.7.5), annotate,\nAnnotationDbi, GenomicFeatur
## swirl "stringi"
## sys "unix (>= 1.4), spelling, testthat"
## systemfonts "covr, farver, graphics, knitr, rmarkdown, testthat (>= 2.1.0)"
## testthat "covr, curl (>= 0.9.5), diffviewer (>= 0.1.0), knitr,\nrmarkdown, rstudioapi, S
## textshaping "covr, grDevices, grid, knitr, rmarkdown, testthat (>= 3.0.0)"
## tibble "bench, bit64, blob, brio, callr, cli, covr, crayon (>=\n1.3.4), DiagrammeR, dp
## tidyr "covr, data.table, knitr, readr, repurrrsive (>= 1.1.0),\nrmarkdown, testthat (

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## tidyselect "covr, crayon, dplyr, knitr, magrittr, rmarkdown, stringr,\ntestthat (>= 3.1.1)
## tidyverse "covr (>= 3.6.1), feather (>= 0.3.5), glue (>= 1.6.2), mockr\n(>= 0.2.0), knitr
## timechange "testthat (>= 0.7.1.99), knitr"
## tinytex "testit, rstudioapi"
## tzdb "covr, testthat (>= 3.0.0)"
## UCSC.utils "DBI, RMariaDB, GenomeInfoDb, testthat, knitr, rmarkdown,\nBiocStyle"
## urlchecker "covr"
## usethis "covr, knitr, magick, pkgload (>= 1.3.2.1), rmarkdown,\nroxygen2 (>= 7.1.2), sp
## utf8 "cli, covr, knitr, rlang, rmarkdown, testthat (>= 3.0.0),\nwithr"
## uuid NA
## vctrs "bit64, covr, crayon, dplyr (>= 0.8.5), generics, knitr,\npillar (>= 1.4.4), pk
## viridis "hexbin (>= 1.27.0), scales, MASS, knitr, dichromat,\nncolorspace, httr, mapproj
## viridisLite "hexbin (>= 1.27.0), ggplot2 (>= 1.0.1), testthat, covr"
## vroom "archive, bench (>= 1.1.0), covr, curl, dplyr, forcats, fs,\nggplot2, knitr, pa
## waldo "bit64, R6, S7, testthat (>= 3.0.0), withr, xml2"
## whisker "markdown"
## withr "callr, DBI, knitr, methods, rlang, rmarkdown (>= 2.12),\nRSQLite, testthat (>=
## xfun "testit, parallel, codetools, methods, rstudioapi, tinytex (>=\n0.30), mime, li
## XLConnect "RUnit, lattice, ggplot2 (>= 0.9.3), zoo"
## xlsx "rprojroot, testthat, covr, tibble, knitr, rmarkdown"
## xlsxjars NA
## XML "bitops, RCurl"
## xml2 "covr, curl, httr, knitr, magrittr, mockery, rmarkdown,\ntestthat (>= 3.0.0)"
## xopen "ps, testthat (>= 3.0.0)"
## xtable "knitr, plm, zoo, survival"
## XVector "Biostrings, drosophila2probe, RUnit"
## yaml "RUnit"
## zip "covr, processx, R6, testthat, withr"
## zlibbioc "BiocStyle, knitr"
## base "methods"
## boot "MASS, survival"
## class NA
## cluster "MASS, Matrix"
## codetools NA
## compiler NA
## datasets NA
## foreign NA
## graphics NA
## grDevices "KernSmooth"
## grid NA
## KernSmooth "MASS, carData"
## lattice "KernSmooth, MASS, latticeExtra, colorspace"
## MASS "lattice, nlme, nnet, survival"
## Matrix "MASS, datasets, sfsmisc, tools"
## methods "codetools"
## mgcv "parallel, survival, MASS"
## nlme "Hmisc, MASS, SASmixed"
## nnet "MASS"
## parallel "methods"
## rpart "survival"
## spatial "MASS"
## splines "Matrix, methods"
## stats "MASS, Matrix, SuppDists, methods, stats4"
## stats4 NA

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## survival	NA
## tcltk	NA
## tools	"codetools, methods, xml2, curl, commonmark, knitr, xfun,\nmathjaxr, V8"
## translations	NA
## utils	"methods, xml2, commonmark, knitr, jsonlite"
##	Enhances
## abind	NA
## AnnotationDbi	NA
## askpass	NA
## backports	NA
## base64enc	"png"
## BH	NA
## Biobase	NA
## BiocGenerics	NA
## BiocIO	NA
## BiocManager	NA
## BiocParallel	"Rmpi"
## BiocVersion	NA
## Biostrings	NA
## bit	NA
## bit64	NA
## bitops	NA
## blob	NA
## brew	NA
## brio	NA
## broom	NA
## bslib	NA
## cachem	NA
## callr	NA
## cellranger	NA
## checkmate	NA
## cli	NA
## clipr	NA
## colorspace	NA
## commonmark	NA
## conflicted	NA
## cpp11	NA
## crayon	NA
## credentials	NA
## curl	NA
## data.table	NA
## DBI	NA
## dbplyr	NA
## DelayedArray	NA
## desc	NA
## devtools	NA
## diffobj	NA
## digest	NA
## downlit	NA
## dplyr	NA
## dtplyr	NA
## ellipsis	NA
## evaluate	NA
## fansi	NA

## farver	NA
## fastmap	NA
## fontawesome	NA
## forcats	NA
## formatR	NA
## Formula	NA
## fs	NA
## futile.logger	NA
## futile.options	NA
## gargle	NA
## generics	NA
## GenomeInfoDb	NA
## GenomeInfoDbData	NA
## GenomicAlignments	NA
## GenomicFeatures	NA
## GenomicRanges	NA
## gert	NA
## ggplot2	"sp"
## gh	NA
## gitcreds	NA
## glue	NA
## googledrive	NA
## googlesheets4	NA
## gridExtra	NA
## gtable	NA
## haven	NA
## highr	NA
## Hmisc	NA
## hms	NA
## htmlTable	NA
## htmltools	"knitr"
## htmlwidgets	"shiny (>= 1.1)"
## httpuv	NA
## httr	NA
## httr2	NA
## ids	NA
## ini	NA
## IRanges	NA
## isoband	NA
## jquerylib	NA
## jsonlite	NA
## KEGGREST	NA
## KernSmooth	NA
## knitr	NA
## labeling	NA
## lambda.r	NA
## later	NA
## lifecycle	NA
## lubridate	"chron, data.table, timeDate, tis, zoo"
## magrittr	NA
## MatrixGenerics	NA
## matrixStats	NA
## memoise	NA
## mime	NA

## miniUI	NA
## modelr	NA
## munsell	NA
## name	NA
## openssl	NA
## pillar	NA
## pkgbuild	NA
## pkgconfig	NA
## pkgdown	NA
## pkgload	NA
## plogr	NA
## plyr	NA
## png	NA
## praise	NA
## prettyunits	NA
## processx	NA
## profvis	NA
## progress	NA
## promises	NA
## ps	NA
## purrr	NA
## R6	NA
## ragg	NA
## rappdirs	NA
## rcmdcheck	NA
## RColorBrewer	NA
## Rcpp	NA
## RCurl	NA
## readr	NA
## readxl	NA
## rematch	NA
## rematch2	NA
## remotes	NA
## reprex	NA
## reshape2	NA
## restfulr	NA
## rhdf5	NA
## rhdf5filters	NA
## Rhdf5lib	NA
## Rhtslib	NA
## rJava	NA
## rjson	NA
## rlang	"winch"
## rmarkdown	NA
## RMySQL	NA
## roxygen2	NA
## rprojroot	NA
## Rsamtools	NA
## RSQLite	NA
## rstudioapi	NA
## rtracklayer	NA
## rversions	NA
## rvest	NA
## S4Arrays	NA

## S4Vectors	NA
## sass	NA
## scales	NA
## selectr	NA
## sessioninfo	NA
## shiny	NA
## snow	"Rmpi"
## sourcetools	NA
## SparseArray	NA
## stringi	NA
## stringr	NA
## SummarizedExperiment	NA
## swirl	NA
## sys	NA
## systemfonts	NA
## testthat	NA
## textshaping	NA
## tibble	NA
## tidyr	NA
## tidyselect	NA
## tidyverse	NA
## timechange	NA
## tinytex	NA
## tzdb	NA
## UCSC.utils	NA
## urlchecker	NA
## usethis	NA
## utf8	NA
## uuid	NA
## vctrs	NA
## viridis	NA
## viridisLite	NA
## vroom	NA
## waldo	NA
## whisker	NA
## withr	NA
## xfun	NA
## XLConnect	NA
## xlsx	NA
## xlsxjars	NA
## XML	NA
## xml2	NA
## xopen	NA
## xtable	NA
## XVector	NA
## yaml	NA
## zip	NA
## zlibbioc	NA
## base	"chron, date, round"
## boot	NA
## class	NA
## cluster	"mvoutlier, fpc, ellipse, sfsmisc"
## codetools	NA
## compiler	NA

## datasets	NA	
## foreign	NA	
## graphics	"vcd"	
## grDevices	NA	
## grid	NA	
## KernSmooth	NA	
## lattice	"chron, zoo"	
## MASS	NA	
## Matrix	"SparseM, graph"	
## methods	NA	
## mgcv	NA	
## nlme	NA	
## nnet	NA	
## parallel	"snow, Rmpi"	
## rpart	NA	
## spatial	NA	
## splines	NA	
## stats	"Kendall, coin, multcomp, pcaPP, pspearman, robustbase"	
## stats4	NA	
## survival	NA	
## tcltk	NA	
## tools	NA	
## translations	NA	
## utils	NA	
##	License	License_is_FOSS
## abind	"MIT + file LICENSE"	NA
## AnnotationDbi	"Artistic-2.0"	NA
## askpass	"MIT + file LICENSE"	NA
## backports	"GPL-2 GPL-3"	NA
## base64enc	"GPL-2 GPL-3"	NA
## BH	"BSL-1.0"	NA
## Biobase	"Artistic-2.0"	NA
## BiocGenerics	"Artistic-2.0"	NA
## BiocIO	"Artistic-2.0"	NA
## BiocManager	"Artistic-2.0"	NA
## BiocParallel	"GPL-2 GPL-3"	NA
## BiocVersion	"Artistic-2.0"	NA
## Biostrings	"Artistic-2.0"	NA
## bit	"GPL-2 GPL-3"	NA
## bit64	"GPL-2 GPL-3"	NA
## bitops	"GPL (>= 2)"	NA
## blob	"MIT + file LICENSE"	NA
## brew	"GPL (>= 2)"	NA
## brio	"MIT + file LICENSE"	NA
## broom	"MIT + file LICENSE"	NA
## bslib	"MIT + file LICENSE"	NA
## cachem	"MIT + file LICENSE"	NA
## callr	"MIT + file LICENSE"	NA
## cellranger	"MIT + file LICENSE"	NA
## checkmate	"BSD_3_clause + file LICENSE"	NA
## cli	"MIT + file LICENSE"	NA
## clipr	"GPL-3"	NA
## colorspace	"BSD_3_clause + file LICENSE"	NA
## commonmark	"BSD_2_clause + file LICENSE"	NA

## conflicted	"MIT + file LICENSE"	NA
## cpp11	"MIT + file LICENSE"	NA
## crayon	"MIT + file LICENSE"	NA
## credentials	"MIT + file LICENSE"	NA
## curl	"MIT + file LICENSE"	NA
## data.table	"MPL-2.0 file LICENSE"	NA
## DBI	"LGPL (>= 2.1)"	NA
## dbplyr	"MIT + file LICENSE"	NA
## DelayedArray	"Artistic-2.0"	NA
## desc	"MIT + file LICENSE"	NA
## devtools	"MIT + file LICENSE"	NA
## diffobj	"GPL-2 GPL-3"	NA
## digest	"GPL (>= 2)"	NA
## downlit	"MIT + file LICENSE"	NA
## dplyr	"MIT + file LICENSE"	NA
## dtplyr	"MIT + file LICENSE"	NA
## ellipsis	"MIT + file LICENSE"	NA
## evaluate	"MIT + file LICENSE"	NA
## fansi	"GPL-2 GPL-3"	NA
## farver	"MIT + file LICENSE"	NA
## fastmap	"MIT + file LICENSE"	NA
## fontawesome	"MIT + file LICENSE"	NA
## forcats	"MIT + file LICENSE"	NA
## formatR	"GPL"	NA
## Formula	"GPL-2 GPL-3"	NA
## fs	"MIT + file LICENSE"	NA
## futile.logger	"LGPL-3"	NA
## futile.options	"LGPL-3"	NA
## gargle	"MIT + file LICENSE"	NA
## generics	"MIT + file LICENSE"	NA
## GenomeInfoDb	"Artistic-2.0"	NA
## GenomeInfoDbData	"Artistic-2.0"	NA
## GenomicAlignments	"Artistic-2.0"	NA
## GenomicFeatures	"Artistic-2.0"	NA
## GenomicRanges	"Artistic-2.0"	NA
## gert	"MIT + file LICENSE"	NA
## ggplot2	"MIT + file LICENSE"	NA
## gh	"MIT + file LICENSE"	NA
## gitcreds	"MIT + file LICENSE"	NA
## glue	"MIT + file LICENSE"	NA
## googledrive	"MIT + file LICENSE"	NA
## googlesheets4	"MIT + file LICENSE"	NA
## gridExtra	"GPL (>= 2)"	NA
## gtable	"MIT + file LICENSE"	NA
## haven	"MIT + file LICENSE"	NA
## highr	"GPL"	NA
## Hmisc	"GPL (>= 2)"	NA
## hms	"MIT + file LICENSE"	NA
## htmlTable	"GPL (>= 3)"	NA
## htmltools	"GPL (>= 2)"	NA
## htmlwidgets	"MIT + file LICENSE"	NA
## httpuv	"GPL (>= 2) file LICENSE"	NA
## httr	"MIT + file LICENSE"	NA
## httr2	"MIT + file LICENSE"	NA

## ids	"MIT + file LICENSE"	NA
## ini	"GPL-3"	NA
## IRanges	"Artistic-2.0"	NA
## isoband	"MIT + file LICENSE"	NA
## jquerylib	"MIT + file LICENSE"	NA
## jsonlite	"MIT + file LICENSE"	NA
## KEGGREST	"Artistic-2.0"	NA
## KernSmooth	"Unlimited"	NA
## knitr	"GPL"	NA
## labeling	"MIT + file LICENSE Unlimited"	NA
## lambda.r	"LGPL-3"	NA
## later	"MIT + file LICENSE"	NA
## lifecycle	"MIT + file LICENSE"	NA
## lubridate	"GPL (>= 2)"	NA
## magrittr	"MIT + file LICENSE"	NA
## MatrixGenerics	"Artistic-2.0"	NA
## matrixStats	"Artistic-2.0"	NA
## memoise	"MIT + file LICENSE"	NA
## mime	"GPL"	NA
## miniUI	"GPL-3"	NA
## modelr	"GPL-3"	NA
## munsell	"MIT + file LICENSE"	NA
## name	"MIT + file LICENSE"	NA
## openssl	"MIT + file LICENSE"	NA
## pillar	"MIT + file LICENSE"	NA
## pkgbuild	"MIT + file LICENSE"	NA
## pkgconfig	"MIT + file LICENSE"	NA
## pkgdown	"MIT + file LICENSE"	NA
## pkgload	"GPL-3"	NA
## plogr	"MIT + file LICENSE"	NA
## plyr	"MIT + file LICENSE"	NA
## png	"GPL-2 GPL-3"	NA
## praise	"MIT + file LICENSE"	NA
## prettyunits	"MIT + file LICENSE"	NA
## processx	"MIT + file LICENSE"	NA
## profvis	"MIT + file LICENSE"	NA
## progress	"MIT + file LICENSE"	NA
## promises	"MIT + file LICENSE"	NA
## ps	"MIT + file LICENSE"	NA
## purrr	"MIT + file LICENSE"	NA
## R6	"MIT + file LICENSE"	NA
## ragg	"MIT + file LICENSE"	NA
## rappdirs	"MIT + file LICENSE"	NA
## rcmdcheck	"MIT + file LICENSE"	NA
## RColorBrewer	"Apache License 2.0"	NA
## Rcpp	"GPL (>= 2)"	NA
## RCurl	"BSD_3_clause + file LICENSE"	NA
## readr	"MIT + file LICENSE"	NA
## readxl	"MIT + file LICENSE"	NA
## rematch	"MIT + file LICENSE"	NA
## rematch2	"MIT + file LICENSE"	NA
## remotes	"MIT + file LICENSE"	NA
## reprex	"MIT + file LICENSE"	NA
## reshape2	"MIT + file LICENSE"	NA

## restfulr	"Artistic-2.0"	NA
## rhdf5	"Artistic-2.0"	NA
## rhdf5filters	"BSD_2_clause + file LICENSE"	NA
## Rhdf5lib	"Artistic-2.0"	NA
## Rhtslib	"LGPL (>= 2)"	NA
## rJava	"LGPL-2.1"	NA
## rjson	"GPL-2"	NA
## rlang	"MIT + file LICENSE"	NA
## rmarkdown	"GPL-3"	NA
## RMySQL	"GPL-2"	NA
## roxygen2	"MIT + file LICENSE"	NA
## rprojroot	"MIT + file LICENSE"	NA
## Rsamtools	"Artistic-2.0 file LICENSE"	NA
## RSQLite	"LGPL (>= 2.1)"	NA
## rstudioapi	"MIT + file LICENSE"	NA
## rtracklayer	"Artistic-2.0 + file LICENSE"	NA
## rversions	"MIT + file LICENSE"	NA
## rvest	"MIT + file LICENSE"	NA
## S4Arrays	"Artistic-2.0"	NA
## S4Vectors	"Artistic-2.0"	NA
## sass	"MIT + file LICENSE"	NA
## scales	"MIT + file LICENSE"	NA
## selectr	"BSD_3_clause + file LICENSE"	NA
## sessioninfo	"GPL-2"	NA
## shiny	"GPL-3 file LICENSE"	NA
## snow	"GPL"	NA
## sourcetools	"MIT + file LICENSE"	NA
## SparseArray	"Artistic-2.0"	NA
## stringi	"file LICENSE"	"yes"
## stringr	"MIT + file LICENSE"	NA
## SummarizedExperiment	"Artistic-2.0"	NA
## swirl	"MIT + file LICENSE"	NA
## sys	"MIT + file LICENSE"	NA
## systemfonts	"MIT + file LICENSE"	NA
## testthat	"MIT + file LICENSE"	NA
## textshaping	"MIT + file LICENSE"	NA
## tibble	"MIT + file LICENSE"	NA
## tidyr	"MIT + file LICENSE"	NA
## tidyselect	"MIT + file LICENSE"	NA
## tidyverse	"MIT + file LICENSE"	NA
## timechange	"GPL (>= 3)"	NA
## tinytex	"MIT + file LICENSE"	NA
## tzdb	"MIT + file LICENSE"	NA
## UCSC.utils	"Artistic-2.0"	NA
## urlchecker	"GPL-3"	NA
## usethis	"MIT + file LICENSE"	NA
## utf8	"Apache License (== 2.0) file LICENSE"	NA
## uuid	"MIT + file LICENSE"	NA
## vctrs	"MIT + file LICENSE"	NA
## viridis	"MIT + file LICENSE"	NA
## viridisLite	"MIT + file LICENSE"	NA
## vroom	"MIT + file LICENSE"	NA
## waldo	"MIT + file LICENSE"	NA
## whisker	"GPL-3"	NA

## withr	"MIT + file LICENSE"	NA
## xfun	"MIT + file LICENSE"	NA
## XLConnect	"GPL-3"	NA
## xlsx	"GPL-3"	NA
## xlsxjars	"GPL-3"	NA
## XML	"BSD_3_clause + file LICENSE"	NA
## xml2	"MIT + file LICENSE"	NA
## xopen	"MIT + file LICENSE"	NA
## xtable	"GPL (>= 2)"	NA
## XVector	"Artistic-2.0"	NA
## yaml	"BSD_3_clause + file LICENSE"	NA
## zip	"MIT + file LICENSE"	NA
## zlibbioc	"Artistic-2.0 + file LICENSE"	NA
## base	"Part of R 4.4.1"	NA
## boot	"Unlimited"	NA
## class	"GPL-2 GPL-3"	NA
## cluster	"GPL (>= 2)"	NA
## codetools	"GPL"	NA
## compiler	"Part of R 4.4.1"	NA
## datasets	"Part of R 4.4.1"	NA
## foreign	"GPL (>= 2)"	NA
## graphics	"Part of R 4.4.1"	NA
## grDevices	"Part of R 4.4.1"	NA
## grid	"Part of R 4.4.1"	NA
## KernSmooth	"Unlimited"	NA
## lattice	"GPL (>= 2)"	NA
## MASS	"GPL-2 GPL-3"	NA
## Matrix	"GPL (>= 2) file LICENCE"	NA
## methods	"Part of R 4.4.1"	NA
## mgcv	"GPL (>= 2)"	NA
## nlme	"GPL (>= 2)"	NA
## nnet	"GPL-2 GPL-3"	NA
## parallel	"Part of R 4.4.1"	NA
## rpart	"GPL-2 GPL-3"	NA
## spatial	"GPL-2 GPL-3"	NA
## splines	"Part of R 4.4.1"	NA
## stats	"Part of R 4.4.1"	NA
## stats4	"Part of R 4.4.1"	NA
## survival	"LGPL (>= 2)"	NA
## tcltk	"Part of R 4.4.1"	NA
## tools	"Part of R 4.4.1"	NA
## translations	"Part of R 4.4.1"	NA
## utils	"Part of R 4.4.1"	NA
##	License_restricts_use OS_type MD5sum NeedsCompilation	
## abind	NA NA NA	"no"
## AnnotationDbi	NA NA NA	"no"
## askpass	NA NA NA	"yes"
## backports	NA NA NA	"yes"
## base64enc	NA NA NA	"yes"
## BH	NA NA NA	"no"
## Biobase	NA NA NA	"yes"
## BiocGenerics	NA NA NA	"no"
## BiocIO	NA NA NA	"no"
## BiocManager	NA NA NA	"no"

## BiocParallel	NA	NA	NA	"yes"
## BiocVersion	NA	NA	NA	"no"
## Biostrings	NA	NA	NA	"yes"
## bit	NA	NA	NA	"yes"
## bit64	NA	NA	NA	"yes"
## bitops	NA	NA	NA	"yes"
## blob	NA	NA	NA	"no"
## brew	NA	NA	NA	"no"
## brio	NA	NA	NA	"yes"
## broom	NA	NA	NA	"no"
## bslib	NA	NA	NA	"no"
## cachem	NA	NA	NA	"yes"
## callr	NA	NA	NA	"no"
## cellranger	NA	NA	NA	"no"
## checkmate	NA	NA	NA	"yes"
## cli	NA	NA	NA	"yes"
## clipr	NA	NA	NA	"no"
## colorspace	NA	NA	NA	"yes"
## commonmark	NA	NA	NA	"yes"
## conflicted	NA	NA	NA	"no"
## cpp11	NA	NA	NA	"no"
## crayon	NA	NA	NA	"no"
## credentials	NA	NA	NA	"no"
## curl	NA	NA	NA	"yes"
## data.table	NA	NA	NA	"yes"
## DBI	NA	NA	NA	"no"
## dbplyr	NA	NA	NA	"no"
## DelayedArray	NA	NA	NA	"yes"
## desc	NA	NA	NA	"no"
## devtools	NA	NA	NA	"no"
## diffobj	NA	NA	NA	"yes"
## digest	NA	NA	NA	"yes"
## downlit	NA	NA	NA	"no"
## dplyr	NA	NA	NA	"yes"
## dtplyr	NA	NA	NA	"no"
## ellipsis	NA	NA	NA	"yes"
## evaluate	NA	NA	NA	"no"
## fansi	NA	NA	NA	"yes"
## farver	NA	NA	NA	"yes"
## fastmap	NA	NA	NA	"yes"
## fontawesome	NA	NA	NA	"no"
## forcats	NA	NA	NA	"no"
## formatR	NA	NA	NA	"no"
## Formula	NA	NA	NA	"no"
## fs	NA	NA	NA	"yes"
## futile.logger	NA	NA	NA	"no"
## futile.options	NA	NA	NA	"no"
## gargle	NA	NA	NA	"no"
## generics	NA	NA	NA	"no"
## GenomeInfoDb	NA	NA	NA	"no"
## GenomeInfoDbData	NA	NA	NA	"no"
## GenomicAlignments	NA	NA	NA	"yes"
## GenomicFeatures	NA	NA	NA	"no"
## GenomicRanges	NA	NA	NA	"yes"

## gert	NA	NA	NA	"yes"
## ggplot2	NA	NA	NA	"no"
## gh	NA	NA	NA	"no"
## gitcreds	NA	NA	NA	"no"
## glue	NA	NA	NA	"yes"
## googledrive	NA	NA	NA	"no"
## googlesheets4	NA	NA	NA	"no"
## gridExtra	NA	NA	NA	"no"
## gtable	NA	NA	NA	"no"
## haven	NA	NA	NA	"yes"
## highr	NA	NA	NA	"no"
## Hmisc	NA	NA	NA	"yes"
## hms	NA	NA	NA	"no"
## htmlTable	NA	NA	NA	"no"
## htmltools	NA	NA	NA	"yes"
## htmlwidgets	NA	NA	NA	"no"
## httpuv	NA	NA	NA	"yes"
## httr	NA	NA	NA	"no"
## httr2	NA	NA	NA	"no"
## ids	NA	NA	NA	"no"
## ini	NA	NA	NA	"no"
## IRanges	NA	NA	NA	"yes"
## isoband	NA	NA	NA	"yes"
## jquerylib	NA	NA	NA	"no"
## jsonlite	NA	NA	NA	"yes"
## KEGGREST	NA	NA	NA	"no"
## KernSmooth	NA	NA	NA	"yes"
## knitr	NA	NA	NA	"no"
## labeling	NA	NA	NA	"no"
## lambda.r	NA	NA	NA	"no"
## later	NA	NA	NA	"yes"
## lifecycle	NA	NA	NA	"no"
## lubridate	NA	NA	NA	"yes"
## magrittr	NA	NA	NA	"yes"
## MatrixGenerics	NA	NA	NA	"no"
## matrixStats	NA	NA	NA	"yes"
## memoise	NA	NA	NA	"no"
## mime	NA	NA	NA	"yes"
## miniUI	NA	NA	NA	"no"
## modelr	NA	NA	NA	"no"
## munsell	NA	NA	NA	"no"
## name	NA	NA	NA	"no"
## openssl	NA	NA	NA	"yes"
## pillar	NA	NA	NA	"no"
## pkgbuild	NA	NA	NA	"no"
## pkgconfig	NA	NA	NA	"no"
## pkgdown	NA	NA	NA	"no"
## pkgload	NA	NA	NA	"no"
## plogr	NA	NA	NA	"no"
## plyr	NA	NA	NA	"yes"
## png	NA	NA	NA	"yes"
## praise	NA	NA	NA	"no"
## prettyunits	NA	NA	NA	"no"
## processx	NA	NA	NA	"yes"

## profvis	NA	NA	NA	"yes"
## progress	NA	NA	NA	"no"
## promises	NA	NA	NA	"yes"
## ps	NA	NA	NA	"yes"
## purrr	NA	NA	NA	"yes"
## R6	NA	NA	NA	"no"
## ragg	NA	NA	NA	"yes"
## rappdirs	NA	NA	NA	"yes"
## rcmdcheck	NA	NA	NA	"no"
## RColorBrewer	NA	NA	NA	"no"
## Rcpp	NA	NA	NA	"yes"
## RCurl	NA	NA	NA	"yes"
## readr	NA	NA	NA	"yes"
## readxl	NA	NA	NA	"yes"
## rematch	NA	NA	NA	"no"
## rematch2	NA	NA	NA	"no"
## remotes	NA	NA	NA	"no"
## reprex	NA	NA	NA	"no"
## reshape2	NA	NA	NA	"yes"
## restfulr	NA	NA	NA	"yes"
## rhdf5	NA	NA	NA	"yes"
## rhdf5filters	NA	NA	NA	"yes"
## Rhdf5lib	NA	NA	NA	"yes"
## Rhtslib	NA	NA	NA	"yes"
## rJava	NA	NA	NA	"yes"
## rjson	NA	NA	NA	"yes"
## rlang	NA	NA	NA	"yes"
## rmarkdown	NA	NA	NA	"no"
## RMySQL	NA	NA	NA	"yes"
## roxygen2	NA	NA	NA	"yes"
## rprojroot	NA	NA	NA	"no"
## Rsamtools	NA	NA	NA	"yes"
## RSQLite	NA	NA	NA	"yes"
## rstudioapi	NA	NA	NA	"no"
## rtracklayer	NA	NA	NA	"yes"
## rversions	NA	NA	NA	"no"
## rvest	NA	NA	NA	"no"
## S4Arrays	NA	NA	NA	"yes"
## S4Vectors	NA	NA	NA	"yes"
## sass	NA	NA	NA	"yes"
## scales	NA	NA	NA	"yes"
## selectr	NA	NA	NA	"no"
## sessioninfo	NA	NA	NA	"no"
## shiny	NA	NA	NA	"no"
## snow	NA	NA	NA	"no"
## sourcetools	NA	NA	NA	"yes"
## SparseArray	NA	NA	NA	"yes"
## stringi	NA	NA	NA	"yes"
## stringr	NA	NA	NA	"no"
## SummarizedExperiment	NA	NA	NA	"no"
## swirl	NA	NA	NA	"no"
## sys	NA	NA	NA	"yes"
## systemfonts	NA	NA	NA	"yes"
## testthat	NA	NA	NA	"yes"

## textshaping	NA	NA	NA	"yes"
## tibble	NA	NA	NA	"yes"
## tidyr	NA	NA	NA	"yes"
## tidyselect	NA	NA	NA	"yes"
## tidyverse	NA	NA	NA	"no"
## timechange	NA	NA	NA	"yes"
## tinytex	NA	NA	NA	"no"
## tzdb	NA	NA	NA	"yes"
## UCSC.utils	NA	NA	NA	"no"
## urlchecker	NA	NA	NA	"no"
## usethis	NA	NA	NA	"no"
## utf8	NA	NA	NA	"yes"
## uuid	NA	NA	NA	"yes"
## vctrs	NA	NA	NA	"yes"
## viridis	NA	NA	NA	"no"
## viridisLite	NA	NA	NA	"no"
## vroom	NA	NA	NA	"yes"
## waldo	NA	NA	NA	"no"
## whisker	NA	NA	NA	"no"
## withr	NA	NA	NA	"no"
## xfun	NA	NA	NA	"yes"
## XLConnect	NA	NA	NA	"no"
## xlsx	NA	NA	NA	"no"
## xlsxjars	NA	NA	NA	"no"
## XML	NA	NA	NA	"yes"
## xml2	NA	NA	NA	"yes"
## xopen	NA	NA	NA	"no"
## xtable	NA	NA	NA	"no"
## XVector	NA	NA	NA	"yes"
## yaml	NA	NA	NA	"yes"
## zip	NA	NA	NA	"yes"
## zlibbioc	NA	NA	NA	"yes"
## base	NA	NA	NA	NA
## boot	NA	NA	NA	"no"
## class	NA	NA	NA	"yes"
## cluster	NA	NA	NA	"yes"
## codetools	NA	NA	NA	"no"
## compiler	NA	NA	NA	NA
## datasets	NA	NA	NA	NA
## foreign	NA	NA	NA	"yes"
## graphics	NA	NA	NA	"yes"
## grDevices	NA	NA	NA	"yes"
## grid	NA	NA	NA	"yes"
## KernSmooth	NA	NA	NA	"yes"
## lattice	NA	NA	NA	"yes"
## MASS	NA	NA	NA	"yes"
## Matrix	NA	NA	NA	"yes"
## methods	NA	NA	NA	"yes"
## mgcv	NA	NA	NA	"yes"
## nlme	NA	NA	NA	"yes"
## nnet	NA	NA	NA	"yes"
## parallel	NA	NA	NA	"yes"
## rpart	NA	NA	NA	"yes"
## spatial	NA	NA	NA	"yes"

## splines	NA	NA	NA	"yes"
## stats	NA	NA	NA	"yes"
## stats4	NA	NA	NA	NA
## survival	NA	NA	NA	"yes"
## tcltk	NA	NA	NA	"yes"
## tools	NA	NA	NA	"yes"
## translations	NA	NA	NA	NA
## utils	NA	NA	NA	"yes"
##	Built			
## abind	"4.4.1"			
## AnnotationDbi	"4.4.1"			
## askpass	"4.4.2"			
## backports	"4.4.0"			
## base64enc	"4.4.0"			
## BH	"4.4.2"			
## Biobase	"4.4.1"			
## BiocGenerics	"4.4.1"			
## BiocIO	"4.4.1"			
## BiocManager	"4.4.2"			
## BiocParallel	"4.4.1"			
## BiocVersion	"4.4.1"			
## Biostrings	"4.4.2"			
## bit	"4.4.2"			
## bit64	"4.4.1"			
## bitops	"4.4.1"			
## blob	"4.4.2"			
## brew	"4.4.1"			
## brio	"4.4.1"			
## broom	"4.4.2"			
## bslib	"4.4.2"			
## cachem	"4.4.1"			
## callr	"4.4.1"			
## cellranger	"4.4.2"			
## checkmate	"4.4.2"			
## cli	"4.4.1"			
## clipr	"4.4.1"			
## colorspace	"4.4.2"			
## commonmark	"4.4.2"			
## conflicted	"4.4.2"			
## cpp11	"4.4.2"			
## crayon	"4.4.1"			
## credentials	"4.4.2"			
## curl	"4.4.2"			
## data.table	"4.4.2"			
## DBI	"4.4.2"			
## dbplyr	"4.4.2"			
## DelayedArray	"4.4.1"			
## desc	"4.4.1"			
## devtools	"4.4.2"			
## diffobj	"4.4.1"			
## digest	"4.4.2"			
## downlit	"4.4.1"			
## dplyr	"4.4.1"			
## dtplyr	"4.4.2"			

## ellipsis	"4.4.1"
## evaluate	"4.4.2"
## fansi	"4.4.1"
## farver	"4.4.1"
## fastmap	"4.4.1"
## fontawesome	"4.4.2"
## forcats	"4.4.2"
## formatR	"4.4.2"
## Formula	"4.4.0"
## fs	"4.4.2"
## futile.logger	"4.4.2"
## futile.options	"4.4.0"
## gargle	"4.4.2"
## generics	"4.4.1"
## GenomeInfoDb	"4.4.2"
## GenomeInfoDbData	"4.4.1"
## GenomicAlignments	"4.4.1"
## GenomicFeatures	"4.4.1"
## GenomicRanges	"4.4.1"
## gert	"4.4.2"
## ggplot2	"4.4.2"
## gh	"4.4.1"
## gitcreds	"4.4.1"
## glue	"4.4.2"
## googledrive	"4.4.2"
## googlesheets4	"4.4.2"
## gridExtra	"4.4.2"
## gtable	"4.4.2"
## haven	"4.4.2"
## highr	"4.4.1"
## Hmisc	"4.4.2"
## hms	"4.4.2"
## htmlTable	"4.4.2"
## htmltools	"4.4.1"
## htmlwidgets	"4.4.1"
## httpuv	"4.4.1"
## httr	"4.4.2"
## httr2	"4.4.1"
## ids	"4.4.2"
## ini	"4.4.1"
## IRanges	"4.4.2"
## isoband	"4.4.1"
## jquerylib	"4.4.1"
## jsonlite	"4.4.2"
## KEGGREST	"4.4.1"
## KernSmooth	"4.4.2"
## knitr	"4.4.2"
## labeling	"4.4.0"
## lambda.r	"4.4.2"
## later	"4.4.2"
## lifecycle	"4.4.1"
## lubridate	"4.4.2"
## magrittr	"4.4.1"
## MatrixGenerics	"4.4.2"

## matrixStats	"4.4.2"
## memoise	"4.4.1"
## mime	"4.4.0"
## miniUI	"4.4.1"
## modelr	"4.4.2"
## munsell	"4.4.1"
## name	"4.4.2"
## openssl	"4.4.2"
## pillar	"4.4.2"
## pkgbuild	"4.4.1"
## pkgconfig	"4.4.1"
## pkgdown	"4.4.2"
## pkgload	"4.4.1"
## plogr	"4.4.2"
## plyr	"4.4.2"
## png	"4.4.0"
## praise	"4.4.1"
## prettyunits	"4.4.1"
## processx	"4.4.2"
## profvis	"4.4.2"
## progress	"4.4.2"
## promises	"4.4.2"
## ps	"4.4.2"
## purrr	"4.4.1"
## R6	"4.4.1"
## ragg	"4.4.2"
## rappdirs	"4.4.1"
## rcmdcheck	"4.4.1"
## RColorBrewer	"4.4.0"
## Rcpp	"4.4.2"
## RCurl	"4.4.2"
## readr	"4.4.2"
## readxl	"4.4.2"
## rematch	"4.4.2"
## rematch2	"4.4.1"
## remotes	"4.4.1"
## reprex	"4.4.2"
## reshape2	"4.4.2"
## restfulr	"4.4.2"
## rhdf5	"4.4.2"
## rhdf5filters	"4.4.1"
## Rhdf5lib	"4.4.1"
## Rhtslib	"4.4.1"
## rJava	"4.4.0"
## rjson	"4.4.1"
## rlang	"4.4.1"
## rmarkdown	"4.4.2"
## RMySQL	"4.4.2"
## roxygen2	"4.4.1"
## rprojroot	"4.4.1"
## Rsamtools	"4.4.1"
## RSQLite	"4.4.2"
## rstudioapi	"4.4.2"
## rtracklayer	"4.4.1"

## rversions	"4.4.1"
## rvest	"4.4.2"
## S4Arrays	"4.4.1"
## S4Vectors	"4.4.1"
## sass	"4.4.1"
## scales	"4.4.1"
## selectr	"4.4.2"
## sessioninfo	"4.4.1"
## shiny	"4.4.2"
## snow	"4.4.0"
## sourcetools	"4.4.1"
## SparseArray	"4.4.1"
## stringi	"4.4.0"
## stringr	"4.4.1"
## SummarizedExperiment	"4.4.1"
## swirl	"4.4.2"
## sys	"4.4.2"
## systemfonts	"4.4.2"
## testthat	"4.4.2"
## textshaping	"4.4.2"
## tibble	"4.4.2"
## tidyr	"4.4.2"
## tidyselect	"4.4.1"
## tidyverse	"4.4.2"
## timechange	"4.4.2"
## tinytex	"4.4.2"
## tzdb	"4.4.2"
## UCSC.utils	"4.4.1"
## urlchecker	"4.4.1"
## usethis	"4.4.2"
## utf8	"4.4.1"
## uuid	"4.4.1"
## vctrs	"4.4.1"
## viridis	"4.4.2"
## viridisLite	"4.4.1"
## vroom	"4.4.2"
## waldo	"4.4.2"
## whisker	"4.4.1"
## withr	"4.4.2"
## xfun	"4.4.2"
## XLConnect	"4.4.2"
## xlsx	"4.4.2"
## xlsxjars	"4.4.0"
## XML	"4.4.2"
## xml2	"4.4.1"
## xopen	"4.4.1"
## xtable	"4.4.1"
## XVector	"4.4.1"
## yaml	"4.4.1"
## zip	"4.4.1"
## zlibbioc	"4.4.1"
## base	"4.4.1"
## boot	"4.4.1"
## class	"4.4.1"


```
## cluster          "4.4.1"
## codetools        "4.4.1"
## compiler         "4.4.1"
## datasets         "4.4.1"
## foreign          "4.4.1"
## graphics         "4.4.1"
## grDevices        "4.4.1"
## grid             "4.4.1"
## KernSmooth       "4.4.1"
## lattice          "4.4.1"
## MASS             "4.4.1"
## Matrix           "4.4.1"
## methods          "4.4.1"
## mgcv             "4.4.1"
## nlme             "4.4.1"
## nnet             "4.4.1"
## parallel         "4.4.1"
## rpart            "4.4.1"
## spatial          "4.4.1"
## splines          "4.4.1"
## stats            "4.4.1"
## stats4           "4.4.1"
## survival         "4.4.1"
## tcltk            "4.4.1"
## tools            "4.4.1"
## translations     "4.4.1"
## utils            "4.4.1"
```

```
library() #alternate
packageVersion("ggplot2")
```

```
## [1] '3.5.1'
```

```
old.packages(repos = "http://cran.us.r-project.org") #check packages to update
```

```
##      Package      LibPath
## curl      "curl"      "C:/Users/Owner/AppData/Local/R/win-library/4.4"
## rlang      "rlang"      "C:/Users/Owner/AppData/Local/R/win-library/4.4"
## xfun       "xfun"       "C:/Users/Owner/AppData/Local/R/win-library/4.4"
## boot       "boot"       "C:/Program Files/R/R-4.4.1/library"
## class      "class"      "C:/Program Files/R/R-4.4.1/library"
## cluster    "cluster"    "C:/Program Files/R/R-4.4.1/library"
## foreign    "foreign"    "C:/Program Files/R/R-4.4.1/library"
## KernSmooth "KernSmooth" "C:/Program Files/R/R-4.4.1/library"
## MASS       "MASS"       "C:/Program Files/R/R-4.4.1/library"
## Matrix     "Matrix"     "C:/Program Files/R/R-4.4.1/library"
## nlme       "nlme"       "C:/Program Files/R/R-4.4.1/library"
## nnet       "nnet"       "C:/Program Files/R/R-4.4.1/library"
## rpart      "rpart"      "C:/Program Files/R/R-4.4.1/library"
## spatial    "spatial"    "C:/Program Files/R/R-4.4.1/library"
## survival   "survival"   "C:/Program Files/R/R-4.4.1/library"
##      Installed Built  ReposVer
## curl      "6.1.0"    "4.4.2" "6.2.0"
```

```
## rlang      "1.1.4"      "4.4.1" "1.1.5"
## xfun       "0.49"       "4.4.2" "0.50"
## boot       "1.3-30"     "4.4.1" "1.3-31"
## class      "7.3-22"     "4.4.1" "7.3-23"
## cluster    "2.1.6"      "4.4.1" "2.1.8"
## foreign    "0.8-86"     "4.4.1" "0.8-88"
## KernSmooth "2.23-24"    "4.4.1" "2.23-26"
## MASS       "7.3-60.2"   "4.4.1" "7.3-64"
## Matrix     "1.7-0"      "4.4.1" "1.7-2"
## nlme       "3.1-164"    "4.4.1" "3.1-167"
## nnet       "7.3-19"     "4.4.1" "7.3-20"
## rpart      "4.1.23"     "4.4.1" "4.1.24"
## spatial    "7.3-17"     "4.4.1" "7.3-18"
## survival   "3.6-4"      "4.4.1" "3.8-3"
##
## Repository
## curl       "http://cran.us.r-project.org/src/contrib"
## rlang      "http://cran.us.r-project.org/src/contrib"
## xfun       "http://cran.us.r-project.org/src/contrib"
## boot       "http://cran.us.r-project.org/src/contrib"
## class      "http://cran.us.r-project.org/src/contrib"
## cluster    "http://cran.us.r-project.org/src/contrib"
## foreign    "http://cran.us.r-project.org/src/contrib"
## KernSmooth "http://cran.us.r-project.org/src/contrib"
## MASS       "http://cran.us.r-project.org/src/contrib"
## Matrix     "http://cran.us.r-project.org/src/contrib"
## nlme       "http://cran.us.r-project.org/src/contrib"
## nnet       "http://cran.us.r-project.org/src/contrib"
## rpart      "http://cran.us.r-project.org/src/contrib"
## spatial    "http://cran.us.r-project.org/src/contrib"
## survival   "http://cran.us.r-project.org/src/contrib"
```

```
# update.packages(repos = "http://cran.us.r-project.org") #update all packages
install.packages("ggplot2") #to update single package
```

```
## Warning: package 'ggplot2' is in use and will not be installed
```

```
detach("package:ggplot2", unload=TRUE) #unload function
# remove.packages("ggtree") #remove package
help(package = "ggplot2") #package info
browseVignettes("ggplot2") #extended help files
```

```
## starting httpd help server ... done
```

R Profiler and Optimization

- Systematic way to examine time spent in various part of the program. Useful to optimize the code.
- DON'T PREMATURELY OPTIMIZE
- Measure, not guess, data on what needs to be optimized.

- User time: computer experienced, may be greater if multiple cores/processors (accessible in multi-threaded BLAS libraries). Elapsed time: wall-clock time, may be greater if other computing tasks.

```
system.time(read.csv("hw1_data.csv")) # returns seconds to execute, if error then seconds to error. Wrap
```

```
##      user  system elapsed
##      0.00    0.00    0.03
```

```
data(mtcars)
```

```
Rprof() # track function call stack at intervals (def = 0.02 sec), time spent in functions.
```

```
fit <- lm(mtcars$mpg ~ mtcars$cyl)
```

```
Rprof(NULL)
```

```
summaryRprof() # makes Rprof readable, tabulates, time in each function
```

```
## $by.self
##               self.time self.pct total.time total.pct
## "lazyLoadDBfetch"    0.02    100      0.02    100
##
## $by.total
##               total.time total.pct self.time self.pct
## "lazyLoadDBfetch"      0.02    100      0.02    100
## "block_exec"           0.02    100      0.00     0
## "call_block"           0.02    100      0.00     0
## "doWithOneRestart"      0.02    100      0.00     0
## "eng_r"                 0.02    100      0.00     0
## "eval"                  0.02    100      0.00     0
## "evaluate"              0.02    100      0.00     0
## "evaluate::evaluate"    0.02    100      0.00     0
## "in_dir"                0.02    100      0.00     0
## "in_input_dir"          0.02    100      0.00     0
## "knitr::knit"           0.02    100      0.00     0
## "lm"                    0.02    100      0.00     0
## "model.frame.default"   0.02    100      0.00     0
## "process_file"          0.02    100      0.00     0
## "process_group"         0.02    100      0.00     0
## "rmarkdown::render"     0.02    100      0.00     0
## "stats::model.frame"    0.02    100      0.00     0
## "with_handlers"         0.02    100      0.00     0
## "withCallingHandlers"   0.02    100      0.00     0
## "withOneRestart"        0.02    100      0.00     0
## "withRestartList"       0.02    100      0.00     0
## "withRestarts"          0.02    100      0.00     0
## "withVisible"           0.02    100      0.00     0
## "xfun::handle_error"    0.02    100      0.00     0
##
## $sample.interval
## [1] 0.02
##
## $sampling.time
## [1] 0.02
```

```
# $by.total - divides time spent per function by total run time  
# $by.self - same as by.total but first subtracts time spent in function above in call stack. Helps tar  
rm(list=ls())
```