

BIOL4800/6220_Fall2022_RTutorial

R Basic

Introduction

R as a calculator

```
1 + 100
```

```
## [1] 101
```

```
2^2
```

```
## [1] 4
```

```
7/2
```

```
## [1] 3.5
```

```
4-1
```

```
## [1] 3
```

```
2*2
```

```
## [1] 4
```

```
3+5*2
```

```
## [1] 13
```

```
(3+5)*2
```

```
## [1] 16
```

```
2e2
```

```
## [1] 200
```

```
2/10000
```

```
## [1] 2e-04
```

```
sin(1)
```

```
## [1] 0.841471
```

```
log(1)
```

```
## [1] 0
```

```
exp(0)
```

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

```
1 == 1
```

```
## [1] TRUE
```

```
1 >= 1
```

```
## [1] TRUE
```

```
1 < 1
```

```
## [1] FALSE
```

```
1 != 2
```

```
## [1] TRUE
```

```
x <- 10
```

```
x
```

```
## [1] 10
```

```
x + x
```

```
## [1] 20
```

```
x - 5
```

```
## [1] 5
```

```
x^2
```

```
## [1] 100
```

```
y <- x + x  
y
```

```
## [1] 20
```

Vectorization

```
1:5
```

```
## [1] 1 2 3 4 5
```

```
2^(1:5)
```

```
## [1] 2 4 8 16 32
```

```
v <- 1:5  
2^v
```

```
## [1] 2 4 8 16 32
```

```
log10(v)
```

```
## [1] 0.0000000 0.3010300 0.4771213 0.6020600 0.6989700
```

Environment

```
ls()
```

```
## [1] "v" "x" "y"
```

```
rm(v)  
ls()
```

```
## [1] "x" "y"
```

Package Management

```
installed.packages()
```

```
##          Package
## ade4      "ade4"
## agricolae "agricolae"
## AICcmodavg "AICcmodavg"
## AlgDesign "AlgDesign"
## ape       "ape"
## Biobase   "Biobase"
## BiocGenerics "BiocGenerics"
## BiocManager "BiocManager"
## BiocVersion "BiocVersion"
## biomformat "biomformat"
## Biostrings "Biostrings"
## broom     "broom"
## bslib     "bslib"
## car       "car"
## carData   "carData"
## checkmate "checkmate"
## cli       "cli"
## combinat  "combinat"
## corrplot  "corrplot"
## cowplot   "cowplot"
## cpp11     "cpp11"
## DataCombine "DataCombine"
## dbstats   "dbstats"
## ecodist   "ecodist"
## effects   "effects"
## ellipsis  "ellipsis"
## emmeans   "emmeans"
## estimability "estimability"
## fastmap   "fastmap"
## foreach   "foreach"
## formatR   "formatR"
## Formula   "Formula"
## futile.logger "futile.logger"
## futile.options "futile.options"
## ggforce    "ggforce"
## ggplot2    "ggplot2"
## ggpubr     "ggpubr"
## ggrepel    "ggrepel"
## ggsci      "ggsci"
## ggsignif    "ggsignif"
## glue       "glue"
## haven      "haven"
## htmlTable  "htmlTable"
## htmltools  "htmltools"
## igraph     "igraph"
## indicpecies "indicspecies"
## insight    "insight"
## IRanges    "IRanges"
```

## iterators	"iterators"
## jpeg	"jpeg"
## jquerylib	"jquerylib"
## klaR	"klaR"
## labdsv	"labdsv"
## labelled	"labelled"
## lambda.r	"lambda.r"
## latticeExtra	"latticeExtra"
## lme4	"lme4"
## lmerTest	"lmerTest"
## magrittr	"magrittr"
## maptools	"maptools"
## MatrixModels	"MatrixModels"
## miniUI	"miniUI"
## minqa	"minqa"
## mitools	"mitools"
## mnormt	"mnormt"
## multcomp	"multcomp"
## multcompView	"multcompView"
## multtest	"multtest"
## MuMIn	"MuMIn"
## mvtnorm	"mvtnorm"
## nloptr	"nloptr"
## nortest	"nortest"
## numDeriv	"numDeriv"
## pbkrtest	"pbkrtest"
## permute	"permute"
## phyloseq	"phyloseq"
## picante	"picante"
## pixmap	"pixmap"
## pls	"pls"
## plsr	"plsr"
## plyr	"plyr"
## polyclip	"polyclip"
## polynom	"polynom"
## psych	"psych"
## quantreg	"quantreg"
## questionr	"questionr"
## R.cache	"R.cache"
## R.methodsS3	"R.methodsS3"
## R.oo	"R.oo"
## R.utils	"R.utils"
## rappdirs	"rappdirs"
## Rcmdr	"Rcmdr"
## RcmdrMisc	"RcmdrMisc"
## RcppArmadillo	"RcppArmadillo"
## RcppEigen	"RcppEigen"
## readstata13	"readstata13"
## relimp	"relimp"
## rematch2	"rematch2"
## reshape	"reshape"
## reshape2	"reshape2"
## rhdf5	"rhdf5"
## rhdf5filters	"rhdf5filters"

## Rhdf5lib	"Rhdf5lib"
## rlang	"rlang"
## rmarkdown	"rmarkdown"
## rstatix	"rstatix"
## Rtsne	"Rtsne"
## S4Vectors	"S4Vectors"
## sandwich	"sandwich"
## sass	"sass"
## SparseM	"SparseM"
## styler	"styler"
## survey	"survey"
## tcltk2	"tcltk2"
## TH.data	"TH.data"
## tinytex	"tinytex"
## tmvnsim	"tmvnsim"
## tweenr	"tweenr"
## unmarked	"unmarked"
## vctr	"vctr"
## vegan	"vegan"
## VennDiagram	"VennDiagram"
## VGAM	"VGAM"
## xfun	"xfun"
## XVector	"XVector"
## zlibbioc	"zlibbioc"
## zoo	"zoo"
## abind	"abind"
## askpass	"askpass"
## assertthat	"assertthat"
## backports	"backports"
## base	"base"
## base64enc	"base64enc"
## BH	"BH"
## blob	"blob"
## boot	"boot"
## broom	"broom"
## callr	"callr"
## cellranger	"cellranger"
## class	"class"
## classInt	"classInt"
## cli	"cli"
## clipr	"clipr"
## cluster	"cluster"
## codetools	"codetools"
## colorspace	"colorspace"
## commonmark	"commonmark"
## compiler	"compiler"
## crayon	"crayon"
## crosstalk	"crosstalk"
## curl	"curl"
## data.table	"data.table"
## datasets	"datasets"
## DBI	"DBI"
## dbplyr	"dbplyr"
## desc	"desc"

## dichromat	"dichromat"
## digest	"digest"
## dplyr	"dplyr"
## e1071	"e1071"
## elevatr	"elevatr"
## ellipsis	"ellipsis"
## evaluate	"evaluate"
## fansi	"fansi"
## farver	"farver"
## fastmap	"fastmap"
## forcats	"forcats"
## foreign	"foreign"
## fs	"fs"
## gapminder	"gapminder"
## generics	"generics"
## ggplot2	"ggplot2"
## glue	"glue"
## graphics	"graphics"
## grDevices	"grDevices"
## grid	"grid"
## gridExtra	"gridExtra"
## gtable	"gtable"
## haven	"haven"
## hexbin	"hexbin"
## highr	"highr"
## hms	"hms"
## htmltools	"htmltools"
## htmlwidgets	"htmlwidgets"
## httpuv	"httpuv"
## httr	"httr"
## isoband	"isoband"
## jsonlite	"jsonlite"
## KernSmooth	"KernSmooth"
## knitr	"knitr"
## labeling	"labeling"
## Lahman	"Lahman"
## later	"later"
## lattice	"lattice"
## lazyeval	"lazyeval"
## leafem	"leafem"
## leaflet	"leaflet"
## leaflet.providers	"leaflet.providers"
## leafsync	"leafsync"
## lifecycle	"lifecycle"
## lubridate	"lubridate"
## lwgeom	"lwgeom"
## magrittr	"magrittr"
## mapdata	"mapdata"
## maps	"maps"
## markdown	"markdown"
## MASS	"MASS"
## Matrix	"Matrix"
## methods	"methods"
## mgcv	"mgcv"

## mime	"mime"
## modelr	"modelr"
## munsell	"munsell"
## nlme	"nlme"
## nnet	"nnet"
## nycflights13	"nycflights13"
## openssl	"openssl"
## packrat	"packrat"
## parallel	"parallel"
## pillar	"pillar"
## pkgbuild	"pkgbuild"
## pkgconfig	"pkgconfig"
## pkgload	"pkgload"
## plotly	"plotly"
## png	"png"
## praise	"praise"
## prettyunits	"prettyunits"
## processx	"processx"
## progress	"progress"
## promises	"promises"
## ps	"ps"
## purrr	"purrr"
## R6	"R6"
## raster	"raster"
## RColorBrewer	"RColorBrewer"
## Rcpp	"Rcpp"
## readr	"readr"
## readxl	"readxl"
## rematch	"rematch"
## reprex	"reprex"
## rgdal	"rgdal"
## rlang	"rlang"
## rmarkdown	"rmarkdown"
## rpart	"rpart"
## rprojroot	"rprojroot"
## rsconnect	"rsconnect"
## rstudioapi	"rstudioapi"
## rvest	"rvest"
## scales	"scales"
## selectr	"selectr"
## sf	"sf"
## shiny	"shiny"
## shinythemes	"shinythemes"
## sourcetools	"sourcetools"
## sp	"sp"
## spatial	"spatial"
## splines	"splines"
## stars	"stars"
## stats	"stats"
## stats4	"stats4"
## stringi	"stringi"
## stringr	"stringr"
## survival	"survival"
## sys	"sys"

## tcltk	"tcltk"
## testthat	"testthat"
## tibble	"tibble"
## tidyr	"tidyr"
## tidyselect	"tidyselect"
## tidyverse	"tidyverse"
## tinytex	"tinytex"
## tmap	"tmap"
## tmaptools	"tmaptools"
## tools	"tools"
## units	"units"
## utf8	"utf8"
## utils	"utils"
## vctrs	"vctrs"
## viridis	"viridis"
## viridisLite	"viridisLite"
## whisker	"whisker"
## widgetframe	"widgetframe"
## withr	"withr"
## xfun	"xfun"
## XML	"XML"
## xml2	"xml2"
## xtable	"xtable"
## yaml	"yaml"
##	LibPath
## ade4	"/Users/colinfinlay/Library/R/4.0/library"
## agricolae	"/Users/colinfinlay/Library/R/4.0/library"
## AICcmodavg	"/Users/colinfinlay/Library/R/4.0/library"
## AlgDesign	"/Users/colinfinlay/Library/R/4.0/library"
## ape	"/Users/colinfinlay/Library/R/4.0/library"
## Biobase	"/Users/colinfinlay/Library/R/4.0/library"
## BiocGenerics	"/Users/colinfinlay/Library/R/4.0/library"
## BiocManager	"/Users/colinfinlay/Library/R/4.0/library"
## BiocVersion	"/Users/colinfinlay/Library/R/4.0/library"
## biomformat	"/Users/colinfinlay/Library/R/4.0/library"
## Biostrings	"/Users/colinfinlay/Library/R/4.0/library"
## broom	"/Users/colinfinlay/Library/R/4.0/library"
## bslib	"/Users/colinfinlay/Library/R/4.0/library"
## car	"/Users/colinfinlay/Library/R/4.0/library"
## carData	"/Users/colinfinlay/Library/R/4.0/library"
## checkmate	"/Users/colinfinlay/Library/R/4.0/library"
## cli	"/Users/colinfinlay/Library/R/4.0/library"
## combinat	"/Users/colinfinlay/Library/R/4.0/library"
## corrplot	"/Users/colinfinlay/Library/R/4.0/library"
## cowplot	"/Users/colinfinlay/Library/R/4.0/library"
## cpp11	"/Users/colinfinlay/Library/R/4.0/library"
## DataCombine	"/Users/colinfinlay/Library/R/4.0/library"
## dbstats	"/Users/colinfinlay/Library/R/4.0/library"
## ecodist	"/Users/colinfinlay/Library/R/4.0/library"
## effects	"/Users/colinfinlay/Library/R/4.0/library"
## ellipsis	"/Users/colinfinlay/Library/R/4.0/library"
## emmeans	"/Users/colinfinlay/Library/R/4.0/library"
## estimability	"/Users/colinfinlay/Library/R/4.0/library"
## fastmap	"/Users/colinfinlay/Library/R/4.0/library"

```

## foreach                "/Users/colinfinlay/Library/R/4.0/library"
## formatR                "/Users/colinfinlay/Library/R/4.0/library"
## Formula                "/Users/colinfinlay/Library/R/4.0/library"
## futile.logger          "/Users/colinfinlay/Library/R/4.0/library"
## futile.options         "/Users/colinfinlay/Library/R/4.0/library"
## ggforce                "/Users/colinfinlay/Library/R/4.0/library"
## ggplot2                "/Users/colinfinlay/Library/R/4.0/library"
## ggpubr                 "/Users/colinfinlay/Library/R/4.0/library"
## ggrepel                "/Users/colinfinlay/Library/R/4.0/library"
## ggsci                  "/Users/colinfinlay/Library/R/4.0/library"
## ggsignif               "/Users/colinfinlay/Library/R/4.0/library"
## glue                   "/Users/colinfinlay/Library/R/4.0/library"
## haven                  "/Users/colinfinlay/Library/R/4.0/library"
## htmlTable              "/Users/colinfinlay/Library/R/4.0/library"
## htmltools              "/Users/colinfinlay/Library/R/4.0/library"
## igraph                 "/Users/colinfinlay/Library/R/4.0/library"
## indicSpecies           "/Users/colinfinlay/Library/R/4.0/library"
## insight                "/Users/colinfinlay/Library/R/4.0/library"
## IRanges                "/Users/colinfinlay/Library/R/4.0/library"
## iterators              "/Users/colinfinlay/Library/R/4.0/library"
## jpeg                   "/Users/colinfinlay/Library/R/4.0/library"
## jquerylib              "/Users/colinfinlay/Library/R/4.0/library"
## kLaR                   "/Users/colinfinlay/Library/R/4.0/library"
## labdsv                 "/Users/colinfinlay/Library/R/4.0/library"
## labelled               "/Users/colinfinlay/Library/R/4.0/library"
## lambda.r               "/Users/colinfinlay/Library/R/4.0/library"
## latticeExtra           "/Users/colinfinlay/Library/R/4.0/library"
## lme4                   "/Users/colinfinlay/Library/R/4.0/library"
## lmerTest               "/Users/colinfinlay/Library/R/4.0/library"
## magrittr               "/Users/colinfinlay/Library/R/4.0/library"
## maptools               "/Users/colinfinlay/Library/R/4.0/library"
## MatrixModels           "/Users/colinfinlay/Library/R/4.0/library"
## miniUI                 "/Users/colinfinlay/Library/R/4.0/library"
## minqa                  "/Users/colinfinlay/Library/R/4.0/library"
## mitools                "/Users/colinfinlay/Library/R/4.0/library"
## mnormt                 "/Users/colinfinlay/Library/R/4.0/library"
## multcomp               "/Users/colinfinlay/Library/R/4.0/library"
## multcompView           "/Users/colinfinlay/Library/R/4.0/library"
## multtest               "/Users/colinfinlay/Library/R/4.0/library"
## MuMIn                  "/Users/colinfinlay/Library/R/4.0/library"
## mvtnorm                "/Users/colinfinlay/Library/R/4.0/library"
## nloptr                 "/Users/colinfinlay/Library/R/4.0/library"
## nortest                "/Users/colinfinlay/Library/R/4.0/library"
## numDeriv               "/Users/colinfinlay/Library/R/4.0/library"
## pbkrtest               "/Users/colinfinlay/Library/R/4.0/library"
## permute                "/Users/colinfinlay/Library/R/4.0/library"
## phyloseq               "/Users/colinfinlay/Library/R/4.0/library"
## picante                "/Users/colinfinlay/Library/R/4.0/library"
## pixmap                 "/Users/colinfinlay/Library/R/4.0/library"
## pls                    "/Users/colinfinlay/Library/R/4.0/library"
## plsR                   "/Users/colinfinlay/Library/R/4.0/library"
## plyr                   "/Users/colinfinlay/Library/R/4.0/library"
## polyclip               "/Users/colinfinlay/Library/R/4.0/library"
## polynom                "/Users/colinfinlay/Library/R/4.0/library"

```

```

## psych "/Users/colinfinlay/Library/R/4.0/library"
## quantreg "/Users/colinfinlay/Library/R/4.0/library"
## questionr "/Users/colinfinlay/Library/R/4.0/library"
## R.cache "/Users/colinfinlay/Library/R/4.0/library"
## R.methodsS3 "/Users/colinfinlay/Library/R/4.0/library"
## R.oo "/Users/colinfinlay/Library/R/4.0/library"
## R.utils "/Users/colinfinlay/Library/R/4.0/library"
## rappdirs "/Users/colinfinlay/Library/R/4.0/library"
## Rcmdr "/Users/colinfinlay/Library/R/4.0/library"
## RcmdrMisc "/Users/colinfinlay/Library/R/4.0/library"
## RcppArmadillo "/Users/colinfinlay/Library/R/4.0/library"
## RcppEigen "/Users/colinfinlay/Library/R/4.0/library"
## readstata13 "/Users/colinfinlay/Library/R/4.0/library"
## relimp "/Users/colinfinlay/Library/R/4.0/library"
## rematch2 "/Users/colinfinlay/Library/R/4.0/library"
## reshape "/Users/colinfinlay/Library/R/4.0/library"
## reshape2 "/Users/colinfinlay/Library/R/4.0/library"
## rhdf5 "/Users/colinfinlay/Library/R/4.0/library"
## rhdf5filters "/Users/colinfinlay/Library/R/4.0/library"
## Rhdf5lib "/Users/colinfinlay/Library/R/4.0/library"
## rlang "/Users/colinfinlay/Library/R/4.0/library"
## rmarkdown "/Users/colinfinlay/Library/R/4.0/library"
## rstatix "/Users/colinfinlay/Library/R/4.0/library"
## Rtsne "/Users/colinfinlay/Library/R/4.0/library"
## S4Vectors "/Users/colinfinlay/Library/R/4.0/library"
## sandwich "/Users/colinfinlay/Library/R/4.0/library"
## sass "/Users/colinfinlay/Library/R/4.0/library"
## SparseM "/Users/colinfinlay/Library/R/4.0/library"
## styler "/Users/colinfinlay/Library/R/4.0/library"
## survey "/Users/colinfinlay/Library/R/4.0/library"
## tcltk2 "/Users/colinfinlay/Library/R/4.0/library"
## TH.data "/Users/colinfinlay/Library/R/4.0/library"
## tinytex "/Users/colinfinlay/Library/R/4.0/library"
## tmvnsim "/Users/colinfinlay/Library/R/4.0/library"
## tweenr "/Users/colinfinlay/Library/R/4.0/library"
## unmarked "/Users/colinfinlay/Library/R/4.0/library"
## vctr "/Users/colinfinlay/Library/R/4.0/library"
## vegan "/Users/colinfinlay/Library/R/4.0/library"
## VennDiagram "/Users/colinfinlay/Library/R/4.0/library"
## VGAM "/Users/colinfinlay/Library/R/4.0/library"
## xfun "/Users/colinfinlay/Library/R/4.0/library"
## XVector "/Users/colinfinlay/Library/R/4.0/library"
## zlibbioc "/Users/colinfinlay/Library/R/4.0/library"
## zoo "/Users/colinfinlay/Library/R/4.0/library"
## abind "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## askpass "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## assertthat "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## backports "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## base "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## base64enc "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## BH "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## blob "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## boot "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## broom "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"

```

```

## callr "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## cellranger "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## class "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## classInt "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## cli "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## clipr "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## cluster "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## codetools "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## colorspace "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## commonmark "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## compiler "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## crayon "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## crosstalk "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## curl "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## data.table "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## datasets "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## DBI "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## dbplyr "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## desc "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## dichromat "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## digest "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## dplyr "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## e1071 "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## elevatr "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## ellipsis "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## evaluate "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## fansi "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## farver "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## fastmap "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## forcats "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## foreign "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## fs "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## gapminder "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## generics "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## ggplot2 "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## glue "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## graphics "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## grDevices "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## grid "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## gridExtra "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## gtable "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## haven "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## hexbin "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## highr "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## hms "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## htmltools "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## htmlwidgets "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## httpuv "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## httr "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## isoband "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## jsonlite "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## KernSmooth "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## knitr "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## labeling "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"

```

```

## Lahman           "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## later            "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## lattice          "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## lazyeval         "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## leafem           "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## leaflet          "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## leaflet.providers "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## leafsync         "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## lifecycle        "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## lubridate        "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## lwgeom           "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## magrittr         "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## mapdata          "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## maps             "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## markdown         "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## MASS             "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## Matrix           "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## methods          "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## mgcv             "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## mime             "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## modelr           "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## munsell          "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## nlme             "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## nnet             "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## nycflights13     "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## openssl          "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## packrat          "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## parallel         "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## pillar           "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## pkgbuild         "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## pkgconfig        "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## pkgload          "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## plotly           "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## png              "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## praise           "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## prettyunits      "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## processx         "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## progress         "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## promises         "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## ps               "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## purrr            "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## R6               "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## raster           "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## RColorBrewer     "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## Rcpp             "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## readr            "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## readxl           "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## rematch          "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## reprex           "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## rgdal            "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## rlang            "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## rmarkdown        "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## rpart            "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## rprojroot        "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"

```

```

## rsconnect      "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## rstudioapi     "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## rvest          "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## scales         "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## selectr        "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## sf              "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## shiny           "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## shinythemes    "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## sourcetools     "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## sp              "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## spatial         "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## splines         "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## stars           "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## stats           "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## stats4          "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## stringi         "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## stringr         "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## survival        "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## sys             "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## tcltk           "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## testthat        "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## tibble          "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## tidyr           "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## tidyselect      "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## tidyverse       "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## tinytex         "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## tmap            "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## tmaptools       "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## tools           "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## units           "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## utf8            "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## utils           "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## vctrs           "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## viridis         "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## viridisLite     "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## whisker         "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## widgetframe     "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## withr           "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## xfun            "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## XML             "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## xml2            "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## xtable          "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
## yaml            "/Library/Frameworks/R.framework/Versions/4.0/Resources/library"
##
## Version      Priority
## ade4          "1.7-18"      NA
## agricolae     "1.3-5"       NA
## AICcmodavg    "2.3-1"       NA
## AlgDesign     "1.2.0"       NA
## ape           "5.5"         NA
## Biobase       "2.50.0"      NA
## BiocGenerics  "0.36.1"      NA
## BiocManager   "1.30.16"     NA
## BiocVersion   "3.12.0"      NA
## biomformat    "1.18.0"      NA

```

## Biostrings	"2.58.0"	NA
## broom	"0.7.12"	NA
## bslib	"0.3.1"	NA
## car	"3.0-12"	NA
## carData	"3.0-5"	NA
## checkmate	"2.1.0"	NA
## cli	"3.2.0"	NA
## combinat	"0.0-8"	NA
## corrplot	"0.92"	NA
## cowplot	"1.1.1"	NA
## cpp11	"0.4.2"	NA
## DataCombine	"0.2.21"	NA
## dbstats	"1.0.5"	NA
## ecodist	"2.0.7"	NA
## effects	"4.2-1"	NA
## ellipsis	"0.3.2"	NA
## emmeans	"1.7.2"	NA
## estimability	"1.3"	NA
## fastmap	"1.1.0"	NA
## foreach	"1.5.1"	NA
## formatR	"1.12"	NA
## Formula	"1.2-4"	NA
## futile.logger	"1.4.3"	NA
## futile.options	"1.0.1"	NA
## ggforce	"0.3.3"	NA
## ggplot2	"3.3.5"	NA
## ggpubr	"0.4.0"	NA
## ggrepel	"0.9.1"	NA
## ggsci	"2.9"	NA
## ggsignif	"0.6.3"	NA
## glue	"1.6.2"	NA
## haven	"2.4.3"	NA
## htmlTable	"2.4.0"	NA
## htmltools	"0.5.2"	NA
## igraph	"1.2.9"	NA
## indicpecies	"1.7.12"	NA
## insight	"0.17.1"	NA
## IRanges	"2.24.1"	NA
## iterators	"1.0.13"	NA
## jpeg	"0.1-9"	NA
## jquerylib	"0.1.4"	NA
## klaR	"1.7-0"	NA
## labdsv	"2.0-1"	NA
## labelled	"2.9.0"	NA
## lambda.r	"1.2.4"	NA
## latticeExtra	"0.6-29"	NA
## lme4	"1.1-27.1"	NA
## lmerTest	"3.1-3"	NA
## magrittr	"2.0.2"	NA
## maptools	"1.1-3"	NA
## MatrixModels	"0.5-0"	NA
## miniUI	"0.1.1.1"	NA
## minqa	"1.2.4"	NA
## mitools	"2.4"	NA

## mnormt	"2.0.2"	NA
## multcomp	"1.4-18"	NA
## multcompView	"0.1-8"	NA
## multtest	"2.46.0"	NA
## MuMIn	"1.46.0"	NA
## mvtnorm	"1.1-3"	NA
## nloptr	"1.2.2.3"	NA
## noritest	"1.0-4"	NA
## numDeriv	"2016.8-1.1"	NA
## pbkrtest	"0.5.1"	NA
## permute	"0.9-5"	NA
## phyloseq	"1.34.0"	NA
## picante	"1.8.2"	NA
## pixmap	"0.4-12"	NA
## pls	"2.8-0"	NA
## plsr	"0.0.1"	NA
## plyr	"1.8.6"	NA
## polyclip	"1.10-0"	NA
## polynom	"1.4-0"	NA
## psych	"2.1.9"	NA
## quantreg	"5.88"	NA
## questionr	"0.7.7"	NA
## R.cache	"0.15.0"	NA
## R.methodsS3	"1.8.1"	NA
## R.oo	"1.24.0"	NA
## R.utils	"2.11.0"	NA
## rappdirs	"0.3.3"	NA
## Rcmdr	"2.7-2"	NA
## RcmdrMisc	"2.7-2"	NA
## RcppArmadillo	"0.10.8.1.0"	NA
## RcppEigen	"0.3.3.9.1"	NA
## readstata13	"0.10.0"	NA
## relimp	"1.0-5"	NA
## rematch2	"2.1.2"	NA
## reshape	"0.8.8"	NA
## reshape2	"1.4.4"	NA
## rhdf5	"2.34.0"	NA
## rhdf5filters	"1.2.1"	NA
## Rhdf5lib	"1.12.1"	NA
## rlang	"1.0.2"	NA
## rmarkdown	"2.14"	NA
## rstatix	"0.7.0"	NA
## Rtsne	"0.15"	NA
## S4Vectors	"0.28.1"	NA
## sandwich	"3.0-1"	NA
## sass	"0.4.1"	NA
## SparseM	"1.81"	NA
## styler	"1.7.0"	NA
## survey	"4.1-1"	NA
## tcltk2	"1.2-11"	NA
## TH.data	"1.1-0"	NA
## tinytex	"0.40"	NA
## tmvnsim	"1.0-2"	NA
## tweenr	"1.0.2"	NA

## unmarked	"1.1.1"	NA
## vctr	"0.3.8"	NA
## vegan	"2.5-7"	NA
## VennDiagram	"1.7.3"	NA
## VGAM	"1.1-6"	NA
## xfun	"0.31"	NA
## XVector	"0.30.0"	NA
## zlibbioc	"1.36.0"	NA
## zoo	"1.8-9"	NA
## abind	"1.4-5"	NA
## askpass	"1.1"	NA
## assertthat	"0.2.1"	NA
## backports	"1.1.8"	NA
## base	"4.0.2"	"base"
## base64enc	"0.1-3"	NA
## BH	"1.72.0-3"	NA
## blob	"1.2.1"	NA
## boot	"1.3-25"	"recommended"
## broom	"0.7.0"	NA
## callr	"3.4.3"	NA
## cellranger	"1.1.0"	NA
## class	"7.3-17"	"recommended"
## classInt	"0.4-3"	NA
## cli	"2.0.2"	NA
## clipr	"0.7.0"	NA
## cluster	"2.1.0"	"recommended"
## codetools	"0.2-16"	"recommended"
## colorspace	"1.4-1"	NA
## commonmark	"1.7"	NA
## compiler	"4.0.2"	"base"
## crayon	"1.3.4"	NA
## crosstalk	"1.1.0.1"	NA
## curl	"4.3"	NA
## data.table	"1.13.2"	NA
## datasets	"4.0.2"	"base"
## DBI	"1.1.0"	NA
## dbplyr	"1.4.4"	NA
## desc	"1.2.0"	NA
## dichromat	"2.0-0"	NA
## digest	"0.6.25"	NA
## dplyr	"1.0.2"	NA
## e1071	"1.7-3"	NA
## elevatr	"0.3.1"	NA
## ellipsis	"0.3.1"	NA
## evaluate	"0.14"	NA
## fansi	"0.4.1"	NA
## farver	"2.0.3"	NA
## fastmap	"1.0.1"	NA
## forcats	"0.5.0"	NA
## foreign	"0.8-80"	"recommended"
## fs	"1.4.2"	NA
## gapminder	"0.3.0"	NA
## generics	"0.0.2"	NA
## ggplot2	"3.3.2"	NA

## glue	"1.4.1"	NA
## graphics	"4.0.2"	"base"
## grDevices	"4.0.2"	"base"
## grid	"4.0.2"	"base"
## gridExtra	"2.3"	NA
## gtable	"0.3.0"	NA
## haven	"2.3.1"	NA
## hexbin	"1.28.1"	NA
## highr	"0.8"	NA
## hms	"0.5.3"	NA
## htmltools	"0.5.0"	NA
## htmlwidgets	"1.5.1"	NA
## httpuv	"1.5.4"	NA
## httr	"1.4.2"	NA
## isoband	"0.2.2"	NA
## jsonlite	"1.7.0"	NA
## KernSmooth	"2.23-17"	"recommended"
## knitr	"1.29"	NA
## labeling	"0.3"	NA
## Lahman	"8.0-0"	NA
## later	"1.1.0.1"	NA
## lattice	"0.20-41"	"recommended"
## lazyeval	"0.2.2"	NA
## leafem	"0.1.3"	NA
## leaflet	"2.0.3"	NA
## leaflet.providers	"1.9.0"	NA
## leafsync	"0.1.0"	NA
## lifecycle	"0.2.0"	NA
## lubridate	"1.7.9"	NA
## lwgeom	"0.2-5"	NA
## magrittr	"1.5"	NA
## mapdata	"2.3.0"	NA
## maps	"3.3.0"	NA
## markdown	"1.1"	NA
## MASS	"7.3-51.6"	"recommended"
## Matrix	"1.2-18"	"recommended"
## methods	"4.0.2"	"base"
## mgcv	"1.8-31"	"recommended"
## mime	"0.9"	NA
## modelr	"0.1.8"	NA
## munsell	"0.5.0"	NA
## nlme	"3.1-148"	"recommended"
## nnet	"7.3-14"	"recommended"
## nycflights13	"1.0.1"	NA
## openssl	"1.4.2"	NA
## packrat	"0.5.0"	NA
## parallel	"4.0.2"	"base"
## pillar	"1.4.6"	NA
## pkgbuild	"1.1.0"	NA
## pkgconfig	"2.0.3"	NA
## pkgload	"1.1.0"	NA
## plotly	"4.9.2.1"	NA
## png	"0.1-7"	NA
## praise	"1.0.0"	NA

## prettyunits	"1.1.1"	NA
## processx	"3.4.3"	NA
## progress	"1.2.2"	NA
## promises	"1.1.1"	NA
## ps	"1.3.3"	NA
## purrr	"0.3.4"	NA
## R6	"2.4.1"	NA
## raster	"3.3-13"	NA
## RColorBrewer	"1.1-2"	NA
## Rcpp	"1.0.5"	NA
## readr	"1.3.1"	NA
## readxl	"1.3.1"	NA
## rematch	"1.0.1"	NA
## reprex	"0.3.0"	NA
## rgdal	"1.5-18"	NA
## rlang	"0.4.7"	NA
## rmarkdown	"2.3"	NA
## rpart	"4.1-15"	"recommended"
## rprojroot	"1.3-2"	NA
## rsconnect	"0.8.16"	NA
## rstudioapi	"0.11"	NA
## rvest	"0.3.6"	NA
## scales	"1.1.1"	NA
## selectr	"0.4-2"	NA
## sf	"0.9-5"	NA
## shiny	"1.5.0"	NA
## shinythemes	"1.1.2"	NA
## sourcetools	"0.1.7"	NA
## sp	"1.4-2"	NA
## spatial	"7.3-12"	"recommended"
## splines	"4.0.2"	"base"
## stars	"0.4-3"	NA
## stats	"4.0.2"	"base"
## stats4	"4.0.2"	"base"
## stringi	"1.4.6"	NA
## stringr	"1.4.0"	NA
## survival	"3.1-12"	"recommended"
## sys	"3.4"	NA
## tcltk	"4.0.2"	"base"
## testthat	"2.3.2"	NA
## tibble	"3.0.3"	NA
## tidyr	"1.1.0"	NA
## tidyselect	"1.1.0"	NA
## tidyverse	"1.3.0"	NA
## tinytex	"0.25"	NA
## tmap	"3.1"	NA
## tmaptools	"3.1"	NA
## tools	"4.0.2"	"base"
## units	"0.6-7"	NA
## utf8	"1.1.4"	NA
## utils	"4.0.2"	"base"
## vctrs	"0.3.2"	NA
## viridis	"0.5.1"	NA
## viridisLite	"0.3.0"	NA

```

## whisker           "0.4"           NA
## widgetframe       "0.3.1"         NA
## withr             "2.2.0"         NA
## xfun              "0.16"          NA
## XML               "3.99-0.5"      NA
## xml2              "1.3.2"         NA
## xtable            "1.8-4"         NA
## yaml              "2.2.1"         NA
## Depends
## ade4              "R (>= 2.10)"
## agricolae         "R (>= 2.10)"
## AICcmodavg        "R (>= 3.2.0)"
## AlgDesign         NA
## ape               "R (>= 3.2.0)"
## Biobase           "R (>= 2.10), BiocGenerics (>= 0.27.1), utils"
## BiocGenerics      "R (>= 4.0.0), methods, utils, graphics, stats, parallel"
## BiocManager       NA
## BiocVersion       "R (>= 4.0.0)"
## biomformat        "R (>= 3.2), methods"
## Biostrings        "R (>= 3.5.0), methods, BiocGenerics (>= 0.31.5), S4Vectors (>= 0.27.12), IRanges"
## broom             "R (>= 3.1)"
## bslib             "R (>= 2.10)"
## car               "R (>= 3.5.0), carData (>= 3.0-0)"
## carData           "R (>= 3.5.0)"
## checkmate         "R (>= 3.0.0)"
## cli               "R (>= 2.10)"
## combinat          NA
## corrplot          NA
## cowplot           "R (>= 3.5.0)"
## cpp11             NA
## DataCombine       "R (>= 3.0.2)"
## dbstats           "R (>= 2.10.0), cluster, pls"
## ecodist           "R (>= 3.0.0)"
## effects           "R (>= 3.5.0), carData"
## ellipsis          "R (>= 3.2)"
## emmeans           "R (>= 3.5.0)"
## estimability      "stats"
## fastmap           NA
## foreach           "R (>= 2.5.0)"
## formatR           "R (>= 3.2.3)"
## Formula           "R (>= 2.0.0), stats"
## futile.logger     "R (>= 3.0.0)"
## futile.options    "R (>= 2.8.0)"
## ggforce           "ggplot2 (>= 3.0.0), R (>= 3.3.0)"
## ggplot2           "R (>= 3.3)"
## ggpubr            "R (>= 3.1.0), ggplot2"
## ggrepel           "R (>= 3.0.0), ggplot2 (>= 2.2.0)"
## ggsci             "R (>= 3.0.2)"
## ggsignif          NA
## glue              "R (>= 3.4)"
## haven             "R (>= 3.2)"
## htmlTable         NA
## htmltools         "R (>= 2.14.1)"
## igraph            "methods"

```

```

## indicpecies      "permute"
## insight          "R (>= 3.4)"
## IRanges          "R (>= 4.0.0), methods, utils, stats, BiocGenerics (>= 0.36.0),\nS4Vectors (>= 0.2
## iterators        "R (>= 2.5.0), utils"
## jpeg             "R (>= 2.9.0)"
## jquerylib        NA
## klaR             "R (>= 2.10.0), MASS"
## labdsv           "R (>= 2.10), mgcv"
## labelled         "R (>= 3.0)"
## lambda.r         "R (>= 3.0.0)"
## latticeExtra     "R (>= 3.6.0), lattice"
## lme4             "R (>= 3.2.0), Matrix (>= 1.2-1), methods, stats"
## lmerTest         "R (>= 3.2.5), lme4 (>= 1.1-10), stats, methods"
## magrittr         NA
## maptools         "R (>= 2.10), sp (>= 1.0-11)"
## MatrixModels     "R (>= 3.0.1)"
## miniUI           NA
## minqa            NA
## mitools          NA
## mnormt           "R (>= 2.2.0)"
## multcomp         "stats, graphics, mvtnorm (>= 1.0-10), survival (>= 2.39-4),\nTH.data (>= 1.0-2)"
## multcompView     NA
## multtest         "R (>= 2.10), methods, BiocGenerics, Biobase"
## MuMIn            "R (>= 3.5.0)"
## mvtnorm          "R(>= 3.5.0)"
## nloptr           NA
## nortest          NA
## numDeriv         "R (>= 2.11.1)"
## pbkrtest         "R (>= 3.5.0), lme4 (>= 1.1.10)"
## permute          "R (>= 2.14.0)"
## phyloseq         "R (>= 3.3.0)"
## picante          "ape, vegan, nlme, methods"
## pixmap           NA
## pls              "R (>= 2.10)"
## plsr             "R (>= 2.10)"
## plyr             "R (>= 3.1.0)"
## polyclip         "R (>= 3.0.0)"
## polynom          NA
## psych            NA
## quantreg         "R (>= 2.6), stats, SparseM"
## questionr        "R (>= 3.5.0)"
## R.cache          "R (>= 2.14.0)"
## R.methodsS3       "R (>= 2.13.0)"
## R.oo             "R (>= 2.13.0), R.methodsS3 (>= 1.8.0)"
## R.utils          "R (>= 2.14.0), R.oo (>= 1.24.0)"
## rappdirs         "R (>= 3.2)"
## Rcmdr            "R (>= 3.5.0), grDevices, graphics, methods, stats, utils,\nSplines, RcmdrMisc (>=
## RcmdrMisc        "R (>= 3.5.0), utils, car (>= 3.0-0), sandwich"
## RcppArmadillo    "R (>= 3.3.0)"
## RcppEigen        NA
## readstata13      NA
## relimp           "R (>= 2.0.0)"
## rematch2         NA
## reshape          "R (>= 2.6.1)"

```

## reshape2	"R (>= 3.1)"
## rhdf5	"R (>= 3.5.0), methods"
## rhdf5filters	NA
## Rhdf5lib	"R (>= 3.3.0)"
## rlang	"R (>= 3.4.0)"
## rmarkdown	"R (>= 3.0)"
## rstatix	"R (>= 3.3.0)"
## Rtsne	NA
## S4Vectors	"R (>= 4.0.0), methods, utils, stats, stats4, BiocGenerics (>=\n0.36.0)"
## sandwich	"R (>= 3.0.0)"
## sass	NA
## SparseM	"R (>= 2.15), methods"
## styler	"R (>= 3.4.0)"
## survey	"R (>= 3.5.0), grid, methods, Matrix, survival"
## tcltk2	"R (>= 2.8.0), tcltk"
## TH.data	"R (>= 3.5.0), survival, MASS"
## tinytex	NA
## tmvnsim	NA
## tweenr	"R (>= 3.2.0)"
## unmarked	"R (>= 2.12.0), methods, lattice"
## vctrs	"R (>= 3.3)"
## vegan	"permute (>= 0.9-0), lattice, R (>= 3.4.0)"
## VennDiagram	"R (>= 3.5.0), grid (>= 2.14.1), futile.logger"
## VGAM	"R (>= 3.5.0), methods, stats, stats4, splines"
## xfun	NA
## XVector	"R (>= 2.8.0), methods, BiocGenerics (>= 0.19.2), S4Vectors (>=\n0.27.12), IRanges"
## zlibbioc	NA
## zoo	"R (>= 3.1.0), stats"
## abind	"R (>= 1.5.0)"
## askpass	NA
## assertthat	NA
## backports	"R (>= 3.0.0)"
## base	NA
## base64enc	"R (>= 2.9.0)"
## BH	NA
## blob	NA
## boot	"R (>= 3.0.0), graphics, stats"
## broom	"R (>= 3.1)"
## callr	NA
## cellranger	"R (>= 3.0.0)"
## class	"R (>= 3.0.0), stats, utils"
## classInt	"R (>= 2.2)"
## cli	"R (>= 2.10)"
## clipr	NA
## cluster	"R (>= 3.3.0)"
## codetools	"R (>= 2.1)"
## colorspace	"R (>= 3.0.0), methods"
## commonmark	NA
## compiler	NA
## crayon	NA
## crosstalk	NA
## curl	"R (>= 3.0.0)"
## data.table	"R (>= 3.1.0)"
## datasets	NA

```

## DBI "methods, R (>= 3.0.0)"
## dbplyr "R (>= 3.1)"
## desc "R (>= 3.1.0)"
## dichromat "R (>= 2.10), stats"
## digest "R (>= 3.1.0)"
## dplyr "R (>= 3.2.0)"
## e1071 NA
## elevatr "R (>= 3.0.0)"
## ellipsis "R (>= 3.2)"
## evaluate "R (>= 3.0.2)"
## fansi "R (>= 3.1.0)"
## farver NA
## fastmap NA
## forcats "R (>= 3.2)"
## foreign "R (>= 4.0.0)"
## fs "R (>= 3.1)"
## gapminder "R (>= 3.1.0)"
## generics "R (>= 3.1)"
## ggplot2 "R (>= 3.2)"
## glue "R (>= 3.1)"
## graphics NA
## grDevices NA
## grid NA
## gridExtra NA
## gtable "R (>= 3.0)"
## haven "R (>= 3.2)"
## hexbin "R (>= 2.0.1), methods"
## highr "R (>= 3.2.3)"
## hms NA
## htmltools "R (>= 2.14.1)"
## htmlwidgets NA
## httpuv "R (>= 2.15.1)"
## httr "R (>= 3.2)"
## isoband NA
## jsonlite "methods"
## KernSmooth "R (>= 2.5.0), stats"
## knitr "R (>= 3.2.3)"
## labeling NA
## Lahman "R (>= 3.5.0)"
## later NA
## lattice "R (>= 3.0.0)"
## lazyeval "R (>= 3.1.0)"
## leafem "R (>= 3.1.0)"
## leaflet "R (>= 3.1.0)"
## leaflet.providers "R (>= 2.10)"
## leafsync "R (>= 3.1.0), methods"
## lifecycle "R (>= 3.2)"
## lubridate "methods, R (>= 3.2)"
## lwgeom "R (>= 3.3.0)"
## magrittr NA
## mapdata "R (>= 2.14.0), maps (>= 2.0-7)"
## maps "R (>= 3.0.0)"
## markdown "R (>= 2.11.1)"
## MASS "R (>= 3.1.0), grDevices, graphics, stats, utils"

```

```

## Matrix                "R (>= 3.2.0)"
## methods              NA
## mgcv                 "R (>= 2.14.0), nlme (>= 3.1-64)"
## mime                 NA
## modelr               "R (>= 3.2)"
## munsell              NA
## nlme                 "R (>= 3.4.0)"
## nnet                 "R (>= 3.0.0), stats, utils"
## nycflights13         "R (>= 3.2)"
## openssl              NA
## packrat              "R (>= 3.0.0)"
## parallel             NA
## pillar               NA
## pkgbuild             "R (>= 3.1)"
## pkgconfig            NA
## pkgload              NA
## plotly               "R (>= 3.2.0), ggplot2 (>= 3.0.0)"
## png                  "R (>= 2.9.0)"
## praise               NA
## prettyunits          NA
## processx             NA
## progress             NA
## promises             NA
## ps                   "R (>= 3.1)"
## purrr                "R (>= 3.2)"
## R6                   "R (>= 3.0)"
## raster               "sp (>= 1.4.1), R (>= 3.5.0)"
## RColorBrewer         "R (>= 2.0.0)"
## Rcpp                 NA
## readr                "R (>= 3.1)"
## readxl               NA
## rematch              NA
## reprex               "R (>= 3.1)"
## rgdal                "R (>= 3.5.0), methods, sp (>= 1.1-0)"
## rlang                "R (>= 3.2.0)"
## rmarkdown            "R (>= 3.0)"
## rpart                "R (>= 2.15.0), graphics, stats, grDevices"
## rprojroot            "R (>= 3.0.0)"
## rsconnect            "R (>= 3.0.0)"
## rstudioapi           NA
## rvest                "R (>= 3.2), xml2"
## scales               "R (>= 3.2)"
## selectr              "R (>= 3.0)"
## sf                   "methods, R (>= 3.3.0)"
## shiny                "R (>= 3.0.2), methods"
## shinythemes          "R (>= 3.0.0)"
## sourcetools          "R (>= 3.0.2)"
## sp                   "R (>= 3.0.0), methods"
## spatial              "R (>= 3.0.0), graphics, stats, utils"
## splines              NA
## stars                "R (>= 3.3.0), abind, sf (>= 0.9-0)"
## stats                NA
## stats4               NA
## stringi              "R (>= 2.14)"

```



```

## stringr      "R (>= 3.1)"
## survival     "R (>= 3.4.0)"
## sys          NA
## tcltk        NA
## testthat     "R (>= 3.1)"
## tibble       "R (>= 3.1.0)"
## tidyr        "R (>= 3.1)"
## tidyselect   "R (>= 3.2)"
## tidyverse    "R (>= 3.2)"
## tinytex      NA
## tmap         "R (>= 3.5.0), methods"
## tmaptools     "R (>= 3.5), methods"
## tools        NA
## units        "R (>= 3.0.2)"
## utf8         "R (>= 2.10)"
## utils        NA
## vctr         "R (>= 3.2)"
## viridis      "R (>= 2.10), viridisLite (>= 0.3.0)"
## viridisLite  "R (>= 2.10)"
## whisker      NA
## widgetframe  "R (>= 3.1.0), htmlwidgets,"
## withr        "R (>= 3.2.0)"
## xfun         NA
## XML          "R (>= 4.0.0), methods, utils"
## xml2         "R (>= 3.1.0)"
## xtable       "R (>= 2.10.0)"
## yaml         NA
##             Imports
## ade4         "graphics, grDevices, methods, stats, utils, MASS, pixmap, sp"
## agricolae    "klaR, MASS, nlme, cluster, AlgDesign, graphics"
## AICcmodavg   "methods, stats, graphics, lattice, MASS, Matrix, nlme, stats4,\nsurvival, unmarked"
## AlgDesign    NA
## ape          "nlme, lattice, graphics, methods, stats, tools, utils,\nparallel, Rcpp (>= 0.12.0)"
## Biobase      "methods"
## BiocGenerics "methods, utils, graphics, stats, parallel"
## BiocManager  "utils"
## BiocVersion  NA
## biomformat   "plyr (>= 1.8), jsonlite (>= 0.9.16), Matrix (>= 1.2), rhdf5"
## Biostrings   "methods, utils, grDevices, graphics, stats, crayon"
## broom        "backports, dplyr (>= 1.0.0), ellipsis, generics (>= 0.0.2),\nnglue, methods, purrr"
## bslib        "grDevices, htmltools (>= 0.5.2), jsonlite, sass (>= 0.4.0),\nnjquerylib (>= 0.1.3)"
## car          "abind, MASS, mgcv, nnet, pbkrtest (>= 0.4-4), quantreg,\ngrDevices, utils, stats,"
## carData      NA
## checkmate    "backports (>= 1.1.0), utils"
## cli          "glue (>= 1.6.0), utils"
## combinat     NA
## corrplot     NA
## cowplot      "ggplot2 (> 2.2.1), grid, gtable, grDevices, methods, rlang,\nnscales"
## cpp11        NA
## DataCombine  "data.table, dplyr (>= 0.4)"
## dbstats      NA
## ecodist      "stats, graphics"
## effects      "lme4, nnet, lattice, grid, colorspace, graphics, grDevices,\nstats, survey, utils"
## ellipsis     "rlang (>= 0.3.0)"

```

```

## emmeans "estimability (>= 1.3), graphics, methods, numDeriv, stats,\nutils, mvtnorm, xtable"
## estimability NA
## fastmap NA
## foreach "codetools, utils, iterators"
## formatR NA
## Formula NA
## futile.logger "utils, lambda.r (>= 1.1.0), futile.options"
## futile.options NA
## ggforce "Rcpp (>= 0.12.2), grid, scales, MASS, tweenr (>= 0.1.5),\ngtable, rlang, polyclip"
## ggplot2 "digest, glue, grDevices, grid, gtable (>= 0.1.1), isoband,\nMASS, mgcv, rlang (>= 0.1.1), ggplot2"
## ggpubr "ggrepel, grid, ggsci, stats, utils, tidyr, purrr, dplyr (>=\n0.7.1), cowplot, ggs"
## ggrepel "grid, Rcpp, rlang (>= 0.3.0), scales (>= 0.5.0)"
## ggsci "grDevices, scales, ggplot2 (>= 2.0.0)"
## ggsignif "ggplot2 (>= 3.3.5)"
## glue "methods"
## haven "forcats (>= 0.2.0), hms, methods, readr (>= 0.1.0), rlang (>=\n0.4.0), tibble, tidyr"
## htmlTable "stringr, knitr (>= 1.6), magrittr (>= 1.5), methods,\ncheckmate, htmlwidgets, htmltools"
## htmltools "utils, digest, grDevices, base64enc, rlang (>= 0.4.10),\nfastmap"
## igraph "graphics, grDevices, magrittr, Matrix, pkgconfig (>= 2.0.0),\nstats, utils"
## indicpecies NA
## insight "methods, stats, utils"
## IRanges "stats4"
## iterators NA
## jpeg NA
## jquerylib "htmltools"
## kLaR "combinat, questionr, grDevices, stats, utils, graphics"
## labdsv "cluster, Rtsne, MASS"
## labelled "haven (>= 2.4.1), dplyr (>= 1.0.0), lifecycle, rlang, vctrs,\nstringr, tidyr"
## lambda.r "formatR"
## latticeExtra "grid, stats, utils, grDevices, png, jpeg, RColorBrewer"
## lme4 "graphics, grid, splines, utils, parallel, MASS, lattice, boot,\nnlme (>= 3.1-123)"
## lmerTest "numDeriv, MASS, ggplot2"
## magrittr NA
## maptools "foreign (>= 0.8), methods, grid, lattice, stats, utils,\ngrDevices"
## MatrixModels "stats, methods, Matrix (>= 1.1-5)"
## miniUI "shiny (>= 0.13), htmltools (>= 0.3), utils"
## minqa "Rcpp (>= 0.9.10)"
## mitools "DBI, methods, stats"
## mnormt "tmvnsim (>= 1.0-2)"
## multcomp "sandwich (>= 2.3-0), codetools"
## multcompView "grid"
## multtest "survival, MASS, stats4"
## MuMIn "graphics, methods, Matrix, stats, stats4, nlme"
## mvtnorm "stats, methods"
## nloptr NA
## nortest "stats"
## numDeriv NA
## pbkrtest "broom, dplyr, magrittr, MASS, Matrix (>= 1.2.3), methods,\nnumDeriv, parallel, knitr"
## permute "stats"
## phyloseq "ade4 (>= 1.7.4), ape (>= 5.0), Biobase (>= 2.36.2),\nBiocGenerics (>= 0.22.0), bi"
## picante NA
## pixmap "methods, graphics, grDevices"
## pls "grDevices, graphics, methods, stats"
## plsR "boot, ggplot2, reshape2, shiny"

```

```

## plyr "Rcpp (>= 0.11.0)"
## polyclip NA
## polynom "stats, graphics"
## psych "mnormt,parallel,stats,graphics,grDevices,methods,lattice,nlme"
## quantreg "methods, graphics, Matrix, MatrixModels"
## questionr "shiny (>= 1.0.5), miniUI, rstudioapi, highr, styler, classInt,\nhtmltools, graphi
## R.cache "utils, R.methodsS3 (>= 1.8.1), R.oo (>= 1.24.0), R.utils (>=\n2.10.1), digest (>=
## R.methodsS3 "utils"
## R.oo "methods, utils"
## R.utils "methods, utils, tools, R.methodsS3 (>= 1.8.1)"
## rappdirs NA
## Rcmdr "tcltk, tcltk2 (>= 1.2-6), abind, relimp (>= 1.0-5), lme4"
## RcmdrMisc "abind, colorspace, Hmisc (>= 4.1-0), MASS, e1071, foreign,\nhaven, readstata13, r
## RcppArmadillo "Rcpp (>= 0.11.0), stats, utils, methods"
## RcppEigen "Matrix (>= 1.1-0), Rcpp (>= 0.11.0), stats, utils"
## readstata13 "Rcpp (>= 0.11.5)"
## relimp "stats, utils"
## rematch2 "tibble"
## reshape "plyr"
## reshape2 "plyr (>= 1.8.1), Rcpp, stringr"
## rhdf5 "Rhdf5lib (>= 1.11.0), rhdf5filters"
## rhdf5filters NA
## Rhdf5lib NA
## rlang "utils"
## rmarkdown "bslib (>= 0.2.5.1), evaluate (>= 0.13), htmltools (>= 0.3.5),\nnjquerylib, jsonlite
## rstatix "stats, utils, tidyr (>= 1.0.0), purrr, broom (>= 0.7.4), rlang\n(>= 0.3.1), tibble
## Rtsne "Rcpp (>= 0.11.0), stats"
## S4Vectors NA
## sandwich "stats, utils, zoo"
## sass "fs, rlang (>= 0.4.10), htmltools (>= 0.5.1), R6, rappdirs"
## SparseM "graphics, stats, utils"
## styler "cli (>= 3.1.1), magrittr (>= 2.0.0), purrr (>= 0.2.3), R.cache\n(>= 0.15.0), rema
## survey "stats, graphics, splines, lattice, minqa, numDeriv, mitools\n(>= 2.4)"
## tcltk2 NA
## TH.data NA
## tinytex "xfun (>= 0.29)"
## tmvnsim NA
## tweenr "Rcpp (>= 0.12.3), grDevices, farver, magrittr, rlang"
## unmarked "graphics, lme4, MASS, Matrix, parallel, plyr, raster, Rcpp (>=\n0.8.0), stats, TM
## vctrs "ellipsis (>= 0.2.0), glue, rlang (>= 0.4.10)"
## vegan "MASS, cluster, mgcv"
## VennDiagram "methods"
## VGAM NA
## xfun "stats, tools"
## XVector "methods, utils, tools, zlibbioc, BiocGenerics, S4Vectors,\nIRanges"
## zlibbioc NA
## zoo "utils, graphics, grDevices, lattice (>= 0.20-27)"
## abind "methods, utils"
## askpass "sys (>= 2.1)"
## assertthat "tools"
## backports "utils"
## base NA
## base64enc NA
## BH NA

```

```

## blob "methods, rlang, vctrs (>= 0.2.1)"
## boot NA
## broom "backports, dplyr, ellipsis, generics (>= 0.0.2), glue,\nmethods, purrr, rlang, st
## callr "processx (>= 3.4.0), R6, utils"
## cellranger "rematch, tibble"
## class "MASS"
## classInt "grDevices, stats, graphics, e1071, class, KernSmooth"
## cli "assertthat, crayon (>= 1.3.4), glue, methods, utils, fansi"
## clipr "utils"
## cluster "graphics, grDevices, stats, utils"
## codetools NA
## colorspace "graphics, grDevices, stats"
## commonmark NA
## compiler NA
## crayon "grDevices, methods, utils"
## crosstalk "htmltools (>= 0.3.6), jsonlite, lazyeval, R6"
## curl NA
## data.table "methods"
## datasets NA
## DBI NA
## dbplyr "assertthat (>= 0.2.0), DBI (>= 1.0.0), dplyr (>= 0.8.0), glue\n(>= 1.2.0), lifecy
## desc "assertthat, utils, R6, crayon, rprojroot"
## dichromat NA
## digest "utils"
## dplyr "ellipsis, generics, glue (>= 1.3.2), lifecycle (>= 0.2.0),\nmagrittr (>= 1.5), me
## e1071 "graphics, grDevices, class, stats, methods, utils"
## elevatr "sp, raster, httr, jsonlite, progress, sf, methods"
## ellipsis "rlang (>= 0.3.0)"
## evaluate "methods"
## fansi NA
## farver NA
## fastmap NA
## forcats "ellipsis, magrittr, rlang, tibble"
## foreign "methods, utils, stats"
## fs "methods"
## gapminder "tibble"
## generics "methods"
## ggplot2 "digest, glue, grDevices, grid, gtable (>= 0.1.1), isoband,\nMASS, mgcv, rlang (>=
## glue "methods"
## graphics "grDevices"
## grDevices NA
## grid "grDevices, utils"
## gridExtra "gtable, grid, grDevices, graphics, utils"
## gtable "grid"
## haven "forcats (>= 0.2.0), hms, methods, Rcpp (>= 0.11.4), readr (>=\n0.1.0), rlang (>=
## hexbin "lattice, grid, graphics, grDevices, stats, utils"
## highr NA
## hms "methods, pkgconfig, rlang, vctrs (>= 0.2.1)"
## htmltools "utils, digest, grDevices, base64enc, rlang"
## htmlwidgets "grDevices, htmltools (>= 0.3), jsonlite (>= 0.9.16), yaml"
## httpuv "Rcpp (>= 0.11.0), utils, R6, promises, later (>= 0.8.0)"
## httr "curl (>= 3.0.0), jsonlite, mime, openssl (>= 0.8), R6"
## isoband "grid, utils"
## jsonlite NA

```

```

## KernSmooth      NA
## knitr            "evaluate (>= 0.10), highr, markdown, stringr (>= 0.6), yaml\n(>= 2.1.19), methods"
## labeling        NA
## Lahman           "dplyr"
## later            "Rcpp (>= 0.12.9), rlang"
## lattice          "grid, grDevices, graphics, stats, utils"
## lazyeval         NA
## leafem           "base64enc, htmltools (>= 0.3), htmlwidgets, leaflet (>= \n2.0.1), raster, sf, png"
## leaflet          "base64enc, crosstalk, htmlwidgets, htmltools, magrittr,\nmarkdown, methods, png, l
## leaflet.providers NA
## leafsync         "htmltools (>= 0.3), htmlwidgets, leaflet (>= 2.0.1)"
## lifecycle        "glue, rlang (>= 0.4.0)"
## lubridate        "generics, Rcpp (>= 0.12.13)"
## lwgeom           "Rcpp, units, sf (>= 0.9-3)"
## magrittr         NA
## mapdata          NA
## maps             "graphics, utils"
## markdown         "utils, xfun, mime (>= 0.3)"
## MASS             "methods"
## Matrix           "methods, graphics, grid, stats, utils, lattice"
## methods          "utils, stats"
## mgcv             "methods, stats, graphics, Matrix, splines, utils"
## mime             "tools"
## modelr           "broom, magrittr, purrr (>= 0.2.2), rlang (>= 0.2.0), tibble,\nntidyr (>= 0.8.0), t
## munsell          "colorspace, methods"
## nlme             "graphics, stats, utils, lattice"
## nnet             NA
## nycflights13     "tibble"
## openssl          "askpass"
## packrat          "tools, utils"
## parallel         "tools, compiler"
## pillar           "cli, crayon (>= 1.3.4), ellipsis, fansi, lifecycle, rlang (>= \n0.3.0), utf8 (>= 1
## pkgbuild         "callr (>= 3.2.0), cli, crayon, desc, prettyunits, R6,\nprojroot, withr (>= 2.1.2
## pkgconfig        "utils"
## pkgload          "cli, crayon, desc, methods, pkgbuild, rlang, rprojroot,\nrstudioapi, utils, withr
## plotly           "tools, scales, httr, jsonlite (>= 1.6), magrittr, digest,\nviridisLite, base64enc
## png             NA
## praise           NA
## prettyunits      NA
## processx         "ps (>= 1.2.0), R6, utils"
## progress         "hms, prettyunits, R6, crayon"
## promises         "R6, Rcpp, later, rlang, stats, magrittr"
## ps              "utils"
## purrr            "magrittr (>= 1.5), rlang (>= 0.3.1)"
## R6              NA
## raster           "Rcpp, methods"
## RColorBrewer     NA
## Rcpp             "methods, utils"
## readr            "Rcpp (>= 0.12.0.5), tibble, hms (>= 0.4.1), R6, clipr, crayon,\nmethods"
## readxl           "cellranger, Rcpp (>= 0.12.18), tibble (>= 1.3.1), utils"
## rematch         NA
## reprex           "callr (>= 2.0.0), clipr (>= 0.4.0), fs, rlang, rmarkdown,\nutils, whisker, withr"
## rgdal            "grDevices, graphics, stats, utils"
## rlang            NA

```

```

## rmarkdown "tools, utils, knitr (>= 1.22), yaml (>= 2.1.19), htmltools (>= 0.3.5), evaluate
## rpart NA
## rprojroot "backports"
## rsconnect "curl, digest, jsonlite, openssl, packrat (>= 0.4.8-1), \nrstudioapi (>= 0.5), yaml
## rstudioapi NA
## rvest "httr (>= 0.5), magrittr, selectr"
## scales "farver (>= 2.0.3), labeling, lifecycle, munsell (>= 0.5), R6, \nRColorBrewer, viri
## selectr "methods, stringr, R6"
## sf "classInt (>= 0.4-1), DBI (>= 0.8), graphics, grDevices, grid, \nmagrittr, Rcpp (>=
## shiny "utils, grDevices, httpuv (>= 1.5.2), mime (>= 0.3), jsonlite\n(>= 0.9.16), xtable
## shinythemes "shiny (>= 0.11)"
## sourcetools NA
## sp "utils, stats, graphics, grDevices, lattice, grid"
## spatial NA
## splines "graphics, stats"
## stars "methods, parallel, classInt (>= 0.4-1), lwgeom, rlang, units"
## stats "utils, grDevices, graphics"
## stats4 "graphics, methods, stats"
## stringi "tools, utils, stats"
## stringr "glue (>= 1.2.0), magrittr, stringi (>= 1.1.7)"
## survival "graphics, Matrix, methods, splines, stats, utils"
## sys NA
## tcltk "utils"
## testthat "cli, crayon (>= 1.3.4), digest, ellipsis, evaluate, magrittr, \nmmethods, pkgload, p
## tibble "cli, crayon (>= 1.3.4), ellipsis (>= 0.2.0), fansi (>= 0.4.0), \nlifecycle (>= 0.2
## tidyr "dplyr (>= 0.8.2), ellipsis (>= 0.1.0), glue, magrittr, purrr, \nRcpp, rlang, string
## tidyselect "ellipsis, glue (>= 1.3.0), purrr (>= 0.3.2), rlang (>= 0.4.6), \nvctrs (>= 0.2.2)"
## tidyverse "broom (>= 0.5.2), cli (>= 1.1.0), crayon (>= 1.3.4), dbplyr\n(>= 1.4.2), dplyr (>
## tinytex "xfun (>= 0.5)"
## tmap "tmapttools (>= 3.1), sf (>= 0.9-3), stars (>= 0.4-2), units (>= 0.6-1), grid, RCo
## tmapttools "sf (>= 0.9.2), lwgeom (>= 0.1-4), stars (>= 0.4-1), units (>= 0.6-1), grid, clas
## tools NA
## units "Rcpp"
## utf8 NA
## utils NA
## vctrs "ellipsis (>= 0.2.0), digest, glue, rlang (>= 0.4.7)"
## viridis "stats, ggplot2 (>= 1.0.1), gridExtra"
## viridisLite NA
## whisker NA
## widgetframe "htmltools, purrr, magrittr, utils, tools"
## withr "graphics, grDevices, stats"
## xfun "stats, tools"
## XML NA
## xml2 "methods"
## xtable "stats, utils"
## yaml NA
## LinkingTo
## ade4 NA
## agricolae NA
## AICcmodavg NA
## AlgDesign NA
## ape "Rcpp"
## Biobase NA
## BiocGenerics NA

```

## BiocManager	NA
## BiocVersion	NA
## biomformat	NA
## Biostrings	"S4Vectors, IRanges, XVector"
## broom	NA
## bslib	NA
## car	NA
## carData	NA
## checkmate	NA
## cli	NA
## combinat	NA
## corrplot	NA
## cowplot	NA
## cpp11	NA
## DataCombine	NA
## dbstats	NA
## ecodist	NA
## effects	NA
## ellipsis	NA
## emmeans	NA
## estimability	NA
## fastmap	NA
## foreach	NA
## formatR	NA
## Formula	NA
## futile.logger	NA
## futile.options	NA
## ggforce	"Rcpp, RcppEigen"
## ggplot2	NA
## ggpubr	NA
## ggrepel	"Rcpp"
## ggsci	NA
## ggsignif	NA
## glue	NA
## haven	"cpp11"
## htmlTable	NA
## htmltools	NA
## igraph	NA
## indicpecies	NA
## insight	NA
## IRanges	"S4Vectors"
## iterators	NA
## jpeg	NA
## jquerylib	NA
## klaR	NA
## labdsv	NA
## labelled	NA
## lambda.r	NA
## latticeExtra	NA
## lme4	"Rcpp (>= 0.10.5), RcppEigen"
## lmerTest	NA
## magrittr	NA
## maptools	NA
## MatrixModels	NA

## miniUI	NA
## minqa	"Rcpp"
## mitools	NA
## mnormt	NA
## multcomp	NA
## multcompView	NA
## multtest	NA
## MuMIn	NA
## mvtnorm	NA
## nloptr	NA
## noritest	NA
## numDeriv	NA
## pbkrtest	NA
## permute	NA
## phyloseq	NA
## picante	NA
## pixmap	NA
## pls	NA
## plsr	NA
## plyr	"Rcpp"
## polyclip	NA
## polynom	NA
## psych	NA
## quantreg	NA
## questionr	NA
## R.cache	NA
## R.methodsS3	NA
## R.oo	NA
## R.utils	NA
## rappdirs	NA
## Rcmdr	NA
## RcmdrMisc	NA
## RcppArmadillo	"Rcpp"
## RcppEigen	"Rcpp"
## readstata13	"Rcpp"
## relimp	NA
## rematch2	NA
## reshape	NA
## reshape2	"Rcpp"
## rhdf5	"Rhdf5lib"
## rhdf5filters	"Rhdf5lib"
## Rhdf5lib	NA
## rlang	NA
## rmarkdown	NA
## rstatix	NA
## Rtsne	"Rcpp"
## S4Vectors	NA
## sandwich	NA
## sass	NA
## SparseM	NA
## styler	NA
## survey	NA
## tcltk2	NA
## TH.data	NA

## tinytex	NA
## tmvnsim	NA
## tweenr	"Rcpp"
## unmarked	"Rcpp, RcppArmadillo, TMB"
## vctr	NA
## vegan	NA
## VennDiagram	NA
## VGAM	NA
## xfun	NA
## XVector	"S4Vectors, IRanges"
## zlibbioc	NA
## zoo	NA
## abind	NA
## askpass	NA
## assertthat	NA
## backports	NA
## base	NA
## base64enc	NA
## BH	NA
## blob	NA
## boot	NA
## broom	NA
## callr	NA
## cellranger	NA
## class	NA
## classInt	NA
## cli	NA
## clipr	NA
## cluster	NA
## codetools	NA
## colorspace	NA
## commonmark	NA
## compiler	NA
## crayon	NA
## crosstalk	NA
## curl	NA
## data.table	NA
## datasets	NA
## DBI	NA
## dbplyr	NA
## desc	NA
## dichromat	NA
## digest	NA
## dplyr	NA
## e1071	NA
## elevatr	NA
## ellipsis	NA
## evaluate	NA
## fansi	NA
## farver	NA
## fastmap	NA
## forcats	NA
## foreign	NA
## fs	NA

## gapminder	NA
## generics	NA
## ggplot2	NA
## glue	NA
## graphics	NA
## grDevices	NA
## grid	NA
## gridExtra	NA
## gtable	NA
## haven	"Rcpp"
## hexbin	NA
## highr	NA
## hms	NA
## htmltools	NA
## htmlwidgets	NA
## httpuv	"Rcpp, BH, later"
## httr	NA
## isoband	"testthat"
## jsonlite	NA
## KernSmooth	NA
## knitr	NA
## labeling	NA
## Lahman	NA
## later	"Rcpp, BH"
## lattice	NA
## lazyeval	NA
## leafem	NA
## leaflet	NA
## leaflet.providers	NA
## leafsync	NA
## lifecycle	NA
## lubridate	"Rcpp"
## lwgeom	"Rcpp, sf (>= 0.6-0)"
## magrittr	NA
## mapdata	NA
## maps	NA
## markdown	NA
## MASS	NA
## Matrix	NA
## methods	NA
## mgcv	NA
## mime	NA
## modelr	NA
## munsell	NA
## nlme	NA
## nnet	NA
## nycflights13	NA
## openssl	NA
## packrat	NA
## parallel	NA
## pillar	NA
## pkgbuild	NA
## pkgconfig	NA
## pkgload	NA

## plotly	NA
## png	NA
## praise	NA
## prettyunits	NA
## processx	NA
## progress	NA
## promises	"later, Rcpp"
## ps	NA
## purrr	NA
## R6	NA
## raster	"Rcpp"
## RColorBrewer	NA
## Rcpp	NA
## readr	"Rcpp, BH"
## readxl	"progress, Rcpp"
## rematch	NA
## reprex	NA
## rgdal	"sp"
## rlang	NA
## rmarkdown	NA
## rpart	NA
## rprojroot	NA
## rsconnect	NA
## rstudioapi	NA
## rvest	NA
## scales	NA
## selectr	NA
## sf	"Rcpp"
## shiny	NA
## shinythemes	NA
## sourcetools	NA
## sp	NA
## spatial	NA
## splines	NA
## stars	NA
## stats	NA
## stats4	NA
## stringi	NA
## stringr	NA
## survival	NA
## sys	NA
## tcltk	NA
## testthat	NA
## tibble	NA
## tidyr	"Rcpp"
## tidyselect	NA
## tidyverse	NA
## tinytex	NA
## tmap	NA
## tmaptools	NA
## tools	NA
## units	"Rcpp (>= 0.12.10)"
## utf8	NA
## utils	NA

```

## vctr      NA
## viridis   NA
## viridisLite NA
## whisker   NA
## widgetframe NA
## withr     NA
## xfun      NA
## XML       NA
## xml2      NA
## xtable    NA
## yaml      NA
##           Suggests
## ade4      "ade4TkGUI, adeggraphics, adephylo, ape, CircStats, deldir,\nlattice, spdep, splanc
## agricolae NA
## AICcmodavg "betareg, coxme, fitdistrplus, glmmTMB, lavaan, lme4, maxlike,\nnnet, ordinal, psc
## AlgDesign NA
## ape       "gee, expm, igraph, phangorn"
## Biobase   "tools, tkWidgets, ALL, RUnit, golubEsets"
## BiocGenerics "Biobase, S4Vectors, IRanges, GenomicRanges, DelayedArray,\nBiostrings, Rsamtools,
## BiocManager "BiocVersion, remotes, rmarkdown, testthat, withr, curl, knitr"
## BiocVersion NA
## biomformat "testthat (>= 0.10), knitr (>= 1.10), BiocStyle (>= 1.6),\nrmmarkdown (>= 0.7)"
## Biostrings "BSgenome (>= 1.13.14), BSgenome.Celegans.UCSC.ce2 (>= \n1.3.11), BSgenome.Dmelanog
## broom      "AER, akima, AUC, bbmle, betareg, biglm, binGroup, boot,\nbtergm, car, caret, clus
## bslib      "shiny (>= 1.6.0), rmarkdown (>= 2.7), thematic, knitr,\ntestthat, withr, rappdirs
## car        "alr4, boot, coxme, effects, knitr, leaps, lmtest, Matrix,\nMatrixModels, rgl (>=
## carData    "car (>= 3.0-0)"
## checkmate  "R6, fastmatch, data.table (>= 1.9.8), devtools, ggplot2,\nknitr, magrittr, microb
## cli        "asciicast, callr, covr, digest, grDevices, htmltools,\nhtmlwidgets, knitr, method
## combinat   NA
## corrplot   "seriation, knitr, RColorBrewer, rmarkdown, magrittr,\nprettydoc, testthat"
## cowplot    "Cairo, covr, dplyr, forcats, gridGraphics (>= 0.4-0), knitr,\nlattice, magick, map
## cpp11      "bench, brio, callr, cli, covr, decor, desc, ggplot2, glue,\nknitr, lobster, mockery
## DataCombine "devtools, testthat"
## dbstats    "proxy"
## ecodist     "knitr, testthat, markdown"
## effects     "pbkrtest (>= 0.4-4), nlme, MASS, polCA, heplots, splines,\nordinal, car, knitr, b
## ellipsis    "covr, testthat"
## emmeans     "bayesplot, bayestestR, biglm, brms, car, coda (>= 0.17),\nggplot2, lattice, logsp
## estimability NA
## fastmap     "testthat (>= 2.1.1)"
## foreach     "randomForest, doMC, doParallel, testthat, knitr, rmarkdown"
## formatR     "rstudioapi, shiny, testit, rmarkdown, knitr"
## Formula     NA
## futile.logger "testthat, jsonlite"
## futile.options NA
## ggforce     "sessioninfo, concaveman, deldir, reshape2, units (>= 0.4-6),\ncovr"
## ggplot2     "covr, ragg, dplyr, ggplot2movies, hexbin, Hmisc, interp,\nknitr, lattice, mapproj
## ggpubr      "grDevices, knitr, RColorBrewer, gtable"
## ggrepel     "knitr, rmarkdown, testthat, gridExtra, devtools, prettydoc,\nggbeeswarm, dplyr, ma
## ggsci       "knitr, rmarkdown, gridExtra, reshape2"
## ggsignif    "knitr, rmarkdown, spelling, testthat, vdiffr (>= 1.0.2)"
## glue        "covr, crayon, DBI, dplyr, forcats, ggplot2, knitr, magrittr,\nmicrobenchmark, R.u
## haven       "cli, covr, crayon, fs, knitr, pillar (>= 1.4.0), rmarkdown,\ntestthat (>= 3.0.0)"

```

```

## htmlTable "testthat, XML, xml2, Hmisc, reshape, rmarkdown, chron,\nlubridate, tibble, purrr,
## htmltools "markdown, testthat, withr, Cairo, ragg, shiny"
## igraph "ape, graph, igraphdata, rgl, scales, stats4, tcltk, testthat,\nwithr, digest"
## indicpecies "sp, rgeos, rmarkdown, knitr"
## insight "AER, afex, aod, BayesFactor, bayestestR, bbmle, bdsmatrix,\nbetareg, bife, biglm,
## IRanges "XVector, GenomicRanges, Rsamtools, GenomicAlignments,\nGenomicFeatures, BSgenome.
## iterators "RUnit, foreach"
## jpeg NA
## jquerylib "testthat"
## klaR "scatterplot3d (>= 0.3-22), som, mlbench, rpart, e1071"
## labdsv "optpart"
## labelled "testthat, knitr, rmarkdown, questionr, snakecase, utf8, covr,\nspelling"
## lambda.r "testit"
## latticeExtra "maps, mapproj, deldir, tripack, quantreg, zoo, MASS, mgcv"
## lme4 "knitr, rmarkdown, PKPDmodels, MEMSS, testthat (>= 0.8.1),\nnggplot2, mlmRev, optim
## lmerTest "pbkrtest (>= 0.4-3), tools"
## magrittr "covr, knitr, rlang, rmarkdown, testthat"
## maptools "rgeos (>= 0.1-8), spatstat.geom (>= 1.65-0), PBSmapping,\nmaps, RColorBrewer, ras
## MatrixModels NA
## miniUI NA
## minqa NA
## mitools "RODBC, foreign"
## mnormt NA
## multcomp "lme4 (>= 0.999375-16), nlme, robustbase, coin, MASS, foreign,\nxttable, lmtest, co
## multcompView "multcomp, pgirmess, MASS"
## multtest "snow"
## MuMIn "lme4 (>= 1.1.0), mgcv (>= 1.7.5), gamm4, MASS, nnet, survival\n(>= 3.1.0), geepack
## mvtnorm NA
## nloptr "testthat (>= 0.8.1), knitr, rmarkdown, inline (>= 0.3.14)"
## noritest NA
## numDeriv NA
## pbkrtest NA
## permute "vegan (>= 2.0-0), testthat (>= 0.5), parallel"
## phyloseq "BiocStyle (>= 2.4), DESeq2 (>= 1.16.1), genefilter (>= 1.58),\nknitr (>= 1.16), m
## picante "brglm, circular, corpcor, quantreg"
## pixmap NA
## pls "MASS, parallel, Rmpi, testthat, RUnit"
## plsr "knitr, rmarkdown"
## plyr "abind, covr, doParallel, foreach, iterators, itertools,\nntcltk, testthat"
## polyclip NA
## polynom "knitr, rmarkdown"
## psych "psychTools, GPArotation, lavaan, lme4, Rcsdp, graph, knitr,\nRgraphviz"
## quantreg "tripack, akima, MASS, survival, rgl, logspline, norlmix,\nFormula, zoo, R.rsp, co
## questionr "testthat, roxygen2, dplyr, ggplot2, tidyr, janitor, forcats,\nknitr, rmarkdown, s
## R.cache NA
## R.methodsS3 "codetools"
## R.oo "tools"
## R.utils "digest (>= 0.6.10)"
## rappdirs "roxygen2, testthat (>= 3.0.0), covr, withr"
## Rcmdr "aplpack, boot, colorspace, e1071, foreign, grid, Hmisc,\nknitr, lattice, leaps, l
## RcmdrMisc "boot, datasets, carData"
## RcppArmadillo "tinytest, Matrix (>= 1.3.0), pkgKitten, reticulate, slam"
## RcppEigen "inline, tinytest, pkgKitten, microbenchmark"
## readstata13 "testthat"

```

```

## relimp "tcltk, nnet, MASS, Rcmdr"
## rematch2 "covr, testthat"
## reshape NA
## reshape2 "covr, lattice, testthat (>= 0.8.0)"
## rhdf5 "bit64, BiocStyle, knitr, rmarkdown, testthat, microbenchmark,\ndplyr, ggplot2"
## rhdf5filters "BiocStyle, knitr, rmarkdown, testthat (>= 2.1.0)"
## Rhdf5lib "BiocStyle, knitr, rmarkdown, tinytest"
## rlang "cli (>= 3.1.0), covr, crayon, fs, glue, knitr, magrittr,\nmethods, pillar, rmarkd
## rmarkdown "digest, dygraphs, fs, rsconnect, downlit (>= 0.4.0), katex\n(>= 1.4.0), sass (>=
## rstatix "knitr, rmarkdown, ggpubr, graphics, emmeans, coin, boot,\ntestthat, spelling"
## Rtsne "irlba, testthat"
## S4Vectors "IRanges, GenomicRanges, SummarizedExperiment, Matrix,\nDelayedArray, ShortRead, g
## sandwich "AER, car, geepack, lattice, lmtest, MASS, multiwayvcov,\nparallel, pcse, plm, psc
## sass "testthat, knitr, rmarkdown, withr, shiny, curl"
## SparseM NA
## styler "data.tree (>= 0.1.6), digest, dplyr, here, knitr, prettycode,\nrmarkdown, roxygen
## survey "foreign, MASS, KernSmooth, hexbin, RSQLite, quantreg,\nparallel, CompQuadForm, DB
## tcltk2 "utils"
## TH.data "dplyr, gdata, plyr, trtf, tram, rms, coin, ATR, multcomp,\ngridExtra, vcd, colors
## tinytex "testit, rstudioapi"
## tmvnsim NA
## tweenr "testthat, covr"
## unmarked NA
## vctrs "bit64, covr, crayon, dplyr (>= 0.8.5), generics, knitr,\npillar (>= 1.4.4), pkgdov
## vegan "parallel, tcltk, knitr, markdown"
## VennDiagram "testthat"
## VGAM "VGAMextra, MASS, mgcv"
## xfun "testit, parallel, codetools, rstudioapi, tinytex (>= 0.30),\nmime, markdown, knit
## XVector "Biostrings, drosophila2probe, RUnit"
## zlibbioc NA
## zoo "AER, coda, chron, fts, ggplot2 (>= 3.0.0), mondate, scales,\nstinepack, strucchan
## abind NA
## askpass "testthat"
## assertthat "testthat, covr"
## backports NA
## base "methods"
## base64enc NA
## BH NA
## blob "covr, crayon, pillar (>= 1.2.1), testthat"
## boot "MASS, survival"
## broom "AER, akima, AUC, bbmle, betareg, biglm, binGroup, boot,\nbtergm, car, caret, clus
## callr "cliapp, covr, crayon, fansi, pingr, ps, rprojroot, spelling,\ntestthat, tibble, w
## cellranger "covr, testthat (>= 1.0.0), knitr, rmarkdown"
## class NA
## classInt "spData (>= 0.2.6.2), units, knitr, rmarkdown"
## cli "callr, covr, htmlwidgets, knitr, mockery, rmarkdown,\nrstudioapi, prettycode (>=
## clipr "covr, knitr, rmarkdown, rstudioapi (>= 0.5), testthat (>= \n2.0.0)"
## cluster "MASS, Matrix"
## codetools NA
## colorspace "datasets, utils, KernSmooth, MASS, kernlab, mvtnorm, vcd,\ntcltk, shiny, shinyjs,
## commonmark "curl, testthat, xml2"
## compiler NA
## crayon "mockery, rstudioapi, testthat, withr"
## crosstalk "shiny, ggplot2, testthat (>= 2.1.0)"

```

```

## curl "spelling, testthat (>= 1.0.0), knitr, jsonlite, rmarkdown,\nmagrittr, httpuv (>= 1.0.0), bit64, curl, R.utils, xts, nanotime, zoo, yaml, knitr,\nrmarkdown"
## data.table "bit64, curl, R.utils, xts, nanotime, zoo, yaml, knitr,\nrmarkdown"
## datasets NA
## DBI "blob, covr, hms, knitr, magrittr, rmarkdown, rprojroot,\nrSQLite (>= 1.1-2), testthat (>= 1.0.0), knitr, rmarkdown"
## dbplyr "bit64, covr, knitr, Lahman, nycflights13, odbc, RMariaDB (>= 1.0.2), rmarkdown, RPostgreSQL (>= 0.4-3), testthat (>= 1.0.0), knitr, rmarkdown"
## desc "covr, testthat, whoami, withr"
## dichromat NA
## digest "tinytest, knitr, rmarkdown"
## dplyr "bench, broom, callr, covr, DBI, dbplyr (>= 1.4.3), knitr,\nLahman, lobster, microbenchmark, rprojroot, rstatix, rtestthat, rvest, tidyr, testthat (>= 1.0.0), knitr, rmarkdown"
## e1071 "cluster, mlbench, nnet, randomForest, rpart, SparseM, xtable,\nMatrix, MASS, slam, testthat (>= 1.0.0), knitr, rmarkdown"
## elevatr "testthat, knitr, rmarkdown, formatR, rgdal"
## ellipsis "covr, testthat"
## evaluate "testthat, lattice, ggplot2"
## fansi "unitizer, knitr, rmarkdown"
## farver "testthat (>= 2.1.0), covr"
## fastmap "testthat (>= 2.1.1)"
## forcats "covr, ggplot2, testthat, readr, knitr, rmarkdown, dplyr"
## foreign NA
## fs "testthat, covr, pillar (>= 1.0.0), tibble (>= 1.1.0), crayon,\nrmarkdown, knitr, rprojroot"
## gapminder "dplyr, ggplot2, testthat"
## generics "covr, pkgload, testthat, tibble"
## ggplot2 "covr, dplyr, ggplot2movies, hexbin, Hmisc, knitr, lattice,\nmapproj, maps, maptools, rprojroot, rstatix, rtestthat, rvest, tidyr, testthat (>= 1.0.0), knitr, rmarkdown"
## glue "testthat, covr, magrittr, crayon, knitr, rmarkdown, DBI,\nrSQLite, R.utils, forcats"
## graphics NA
## grDevices "KernSmooth"
## grid "lattice"
## gridExtra "ggplot2, egg, lattice, knitr, testthat"
## gtable "covr, testthat, knitr, rmarkdown, ggplot2, profvis"
## haven "covr, fs, knitr, rmarkdown, testthat, pillar (>= 1.4.0), cli,\nncrayon"
## hexbin "marray, affy, Biobase, limma, knitr"
## highr "knitr, testit"
## hms "crayon, lubridate, pillar (>= 1.1.0), testthat"
## htmltools "markdown, testthat, withr, Cairo, ragg"
## htmlwidgets "knitr (>= 1.8)"
## httpuv "testthat, callr, curl, websocket"
## httr "covr, httpuv, jpeg, knitr, png, readr, rmarkdown, testthat\n(>= 0.8.0), xml2"
## isoband "covr, ggplot2, knitr, magick, microbenchmark, rmarkdown, sf,\nntestthat"
## jsonlite "httr, curl, plyr, testthat, knitr, rmarkdown, R.rsp, sf, sp"
## KernSmooth "MASS"
## knitr "formatR, testit, digest, rgl (>= 0.95.1201), codetools,\nrmarkdown, htmlwidgets (>= 1.8)"
## labeling NA
## Lahman "lattice, ggplot2, googleVis, data.table, vcd, reshape2,\nntidyr, knitr, rmarkdown"
## later "knitr, rmarkdown, testthat"
## lattice "KernSmooth, MASS, latticeExtra"
## lazyeval "knitr, rmarkdown (>= 0.2.65), testthat, covr"
## leafem "clipr, gdalUtils, leafgl, mapdeck, plainview, stars"
## leaflet "knitr, maps, sf, shiny, rgdal, rgeos, R6, RJSONIO, purrr,\nntestthat"
## leaflet.providers "V8, jsonlite, testthat (>= 2.1.0)"
## leafsync NA
## lifecycle "covr, crayon, knitr, rmarkdown, testthat (>= 2.1.0)"
## lubridate "covr, knitr, testthat (>= 2.1.0), vctrs (>= 0.3.0)"
## lwgeom "covr, sp, geosphere, testthat"
## magrittr "testthat, knitr"
## mapdata NA

```

```

## maps "mapproj (>= 1.2-0), mapdata (>= 2.3.0), sp, maptools,\nrnaturalearth"
## markdown "knitr, RCurl"
## MASS "lattice, nlme, nnet, survival"
## Matrix "expm, MASS"
## methods "codetools"
## mgcv "parallel, survival, MASS"
## mime NA
## modelr "compiler, covr, ggplot2, testthat"
## munsell "ggplot2, testthat"
## nlme "Hmisc, MASS"
## nnet "MASS"
## nycflights13 "dplyr"
## openssl "testthat (>= 2.1.0), digest, knitr, rmarkdown, jsonlite,\njose, sodium"
## packrat "testthat (>= 0.7), devtools, httr, knitr, rmarkdown"
## parallel "methods"
## pillar "bit64, knitr, lubridate, testthat (>= 2.0.0), withr"
## pkgbuild "Rcpp, cpp11, testthat, covr"
## pkgconfig "covr, testthat, disposables (>= 1.0.3)"
## pkgload "bitops, covr, Rcpp, testthat"
## plotly "MASS, maps, ggthemes, GGally, testthat, knitr, devtools,\nshiny (>= 1.1.0), shiny"
## png NA
## praise "testthat"
## prettyunits "codetools, covr, testthat"
## processx "callr (>= 3.2.0), codetools, covr, crayon, curl, debugme,\nparallel, testthat, withr"
## progress "Rcpp, testthat, withr"
## promises "testthat, future, knitr, rmarkdown"
## ps "callr, covr, curl, pingr, processx (>= 3.1.0), R6, rlang,\ntestthat, tibble"
## purrr "covr, crayon, dplyr (>= 0.7.8), knitr, rmarkdown, testthat,\ntibble, tidyselect"
## R6 "knitr, microbenchmark, pryr, testthat, ggplot2, scales"
## raster "rgdal (>= 1.5-8), rgeos (>= 0.3-8), ncdf4, igraph, tcltk,\nparallel, rasterVis, RColorBrewer"
## RColorBrewer NA
## Rcpp "tinytest, inline, rbenchmark, pkgKitten (>= 0.1.2)"
## readr "curl, testthat, knitr, rmarkdown, stringi, covr, spelling"
## readxl "covr, knitr, rmarkdown, rprojroot (>= 1.1), testthat"
## rematch "covr, testthat"
## reprex "covr, devtools, fortunes, knitr, miniUI, rprojroot,\nrstudioapi, shiny, styler (>= 1.4.0)"
## rgdal "knitr, DBI, RSQLite, maptools, mapview, rmarkdown, curl"
## rlang "cli, covr, crayon, glue, magrittr, methods, pillar,\nrmarkdown, testthat (>= 2.3.0)"
## rmarkdown "shiny (>= 0.11), tufte, testthat, digest, dygraphs, tibble,\nfs, pkgdown, rsconnect"
## rpart "survival"
## rprojroot "testthat, mockr, knitr, withr, rmarkdown"
## rsconnect "RCurl, callr, httpuv, knitr, plumber (>= 0.3.2), reticulate,\nrmarkdown (>= 1.1), rstudioapi"
## rstudioapi "testthat, knitr, rmarkdown, clipr"
## rvest "covr, knitr, png, rmarkdown, spelling, stringi (>= 0.3.1),\ntestthat"
## scales "bit64, covr, dichromat, ggplot2, hms (>= 0.5.0), testthat (>= \n2.1.0)"
## selectr "testthat, XML, xml2"
## sf "blob, covr, dplyr (>= 0.8-3), ggplot2, knitr, lwgeom (>= \n0.2-1), maps, mapview, r"
## shiny "datasets, Cairo (>= 1.5-5), testthat (>= 2.1.1), knitr (>= \n1.6), markdown, rmarkdown"
## shinythemes NA
## sourcetools "testthat"
## sp "RColorBrewer, rgdal (>= 1.2-3), rgeos (>= 0.3-13), gstat,\nmaptools, deldir"
## spatial "MASS"
## splines "Matrix, methods"
## stars "PCICt, RNetCDF (>= 1.8-2), covr, cubelyr, digest, dplyr (>= \n0.7-0), exactextractr"

```



```

## stats "MASS, Matrix, SuppDists, methods, stats4"
## stats4 NA
## stringi NA
## stringr "covr, htmltools, htmlwidgets, knitr, rmarkdown, testthat"
## survival NA
## sys "unix (>= 1.4), spelling, testthat"
## tcltk NA
## testthat "covr, curl (>= 0.9.5), devtools, knitr, rmarkdown, usethis,\nvctrs (>= 0.1.0), xm
## tibble "bench, bit64, blob, covr, dplyr, evaluate, formattable, hms,\nhtmltools, import, l
## tidyr "covr, jsonlite, knitr, repurrrsive (>= 1.0.0), rmarkdown,\nreadr, testthat (>= 2.
## tidyselect "covr, crayon, dplyr, knitr, magrittr, rmarkdown, testthat (>= \n2.3.0), tibble (>=
## tidyverse "covr, feather, glue, knitr, rmarkdown, testthat"
## tinytex "testit, rstudioapi"
## tmap "rmapshaper, rmarkdown, knitr, png, cartogram, osmdata,\nggplot2, dplyr, tidyr, sh
## tmaptools "tmap (>= 3.0), rmapshaper, osmdata, OpenStreetMap, raster,\npng, shiny, shinyjs"
## tools "codetools, methods, xml2, curl, commonmark"
## units "udunits2, NISTunits, measurements, xml2, magrittr, pillar (>= \n1.3.0), dplyr (>=
## utf8 "knitr, rmarkdown, testthat"
## utils "methods, xml2, commonmark"
## vctrs "bit64, covr, crayon, dplyr (>= 0.8.5), generics, knitr,\npillar (>= 1.4.4), pkgdov
## viridis "hexbin (>= 1.27.0), scales, MASS, knitr, dichromat,\ncolorspace, rasterVis, httr,
## viridisLite "hexbin (>= 1.27.0), ggplot2 (>= 1.0.1), testthat, covr"
## whisker "markdown"
## widgetframe "knitr, rmarkdown"
## withr "covr, DBI, knitr, lattice, methods, rmarkdown, RSQLite,\ntestthat (>= 2.1.0)"
## xfun "testit, parallel, codetools, rstudioapi, tinytex, mime,\nmarkdown, knitr, htmltoo
## XML "bitops, RCurl"
## xml2 "covr, curl, httr, knitr, magrittr, mockery, rmarkdown,\ntestthat (>= 2.1.0)"
## xtable "knitr, plm, zoo, survival"
## yaml "RUnit"
## Enhances
## ade4 NA
## agricolae NA
## AICcmodavg NA
## AlgDesign NA
## ape NA
## Biobase NA
## BiocGenerics NA
## BiocManager NA
## BiocVersion NA
## biomformat NA
## Biostrings "Rmpi"
## broom NA
## bslib NA
## car NA
## carData NA
## checkmate NA
## cli NA
## combinat NA
## corrplot NA
## cowplot NA
## cpp11 NA
## DataCombine NA
## dbstats NA

```

```

## ecodist          NA
## effects          NA
## ellipsis         NA
## emmeans          "CARBayes, coxme, gee, geepack, MCMCglmm, MCMCpack, mice,\nnnet, pscl, rstanarm, s
## estimability     NA
## fastmap          NA
## foreach          NA
## formatR          NA
## Formula          NA
## futile.logger    NA
## futile.options   NA
## ggforce          NA
## ggplot2          "sp"
## ggpubr           NA
## ggrepel          NA
## ggsci            NA
## ggsignif         NA
## glue             NA
## haven            NA
## htmlTable        NA
## htmltools        "knitr"
## igraph           NA
## indicpecies      NA
## insight          NA
## IRanges          NA
## iterators        NA
## jpeg             NA
## jquerylib        NA
## klaR             "clustMixType, randomForest, ClustVarLV"
## labdsv           "vegan"
## labelled         "memisc"
## lambda.r         NA
## latticeExtra     NA
## lme4             NA
## lmerTest         NA
## magrittr         NA
## maptools         "gpclib"
## MatrixModels     NA
## miniUI           NA
## minqa            NA
## mitools          NA
## mnormt           NA
## multcomp         NA
## multcompView     NA
## multtest         NA
## MuMIn            "aod, aods3, betareg, caper, coxme, cplm, gee, glmmML,\nlogistf, MCMCglmm, ordinal
## mvtnorm          NA
## nloptr           NA
## nortest          NA
## numDeriv         NA
## pbkrtest         NA
## permute          NA
## phyloseq         "doParallel (>= 1.0.10)"
## picante          NA

```

## pixmap	NA
## pls	NA
## plsr	NA
## plyr	NA
## polyclip	NA
## polynom	NA
## psych	NA
## quantreg	NA
## questionr	NA
## R.cache	NA
## R.methodsS3	NA
## R.oo	NA
## R.utils	NA
## rappdirs	NA
## Rcmdr	NA
## RcmdrMisc	NA
## RcppArmadillo	NA
## RcppEigen	NA
## readstata13	NA
## relimp	NA
## rematch2	NA
## reshape	NA
## reshape2	NA
## rhdf5	NA
## rhdf5filters	NA
## Rhdf5lib	NA
## rlang	"winch"
## rmarkdown	NA
## rstatix	NA
## Rtsne	NA
## S4Vectors	NA
## sandwich	NA
## sass	NA
## SparseM	NA
## styler	NA
## survey	NA
## tcltk2	NA
## TH.data	NA
## tinytex	NA
## tmvnsim	NA
## tweenr	NA
## unmarked	NA
## vctrs	NA
## vegan	NA
## VennDiagram	NA
## VGAM	"VGAMdata"
## xfun	NA
## XVector	NA
## zlibbioc	NA
## zoo	NA
## abind	NA
## askpass	NA
## assertthat	NA
## backports	NA

## base	NA
## base64enc	"png"
## BH	NA
## blob	NA
## boot	NA
## broom	NA
## callr	NA
## cellranger	NA
## class	NA
## classInt	NA
## cli	NA
## clipr	NA
## cluster	NA
## codetools	NA
## colorspace	NA
## commonmark	NA
## compiler	NA
## crayon	NA
## crosstalk	NA
## curl	NA
## data.table	NA
## datasets	NA
## DBI	NA
## dbplyr	NA
## desc	NA
## dichromat	NA
## digest	NA
## dplyr	NA
## e1071	NA
## elevatr	NA
## ellipsis	NA
## evaluate	NA
## fansi	NA
## farver	NA
## fastmap	NA
## forcats	NA
## foreign	NA
## fs	NA
## gapminder	NA
## generics	NA
## ggplot2	"sp"
## glue	NA
## graphics	NA
## grDevices	NA
## grid	NA
## gridExtra	NA
## gtable	NA
## haven	NA
## hexbin	NA
## highr	NA
## hms	NA
## htmltools	"knitr"
## htmlwidgets	"shiny (>= 1.1)"
## httpuv	NA

```

## httr                NA
## isoband              NA
## jsonlite            NA
## KernSmooth          NA
## knitr               NA
## labeling            NA
## Lahman              NA
## later              NA
## lattice             "chron"
## lazyeval            NA
## leafem              NA
## leaflet             NA
## leaflet.providers NA
## leafsync            NA
## lifecycle           NA
## lubridate           "chron, timeDate, tis, zoo"
## lwgeom              NA
## magrittr            NA
## mapdata             NA
## maps               NA
## markdown            NA
## MASS                NA
## Matrix              "MatrixModels, graph, SparseM, sfsmisc"
## methods            NA
## mgcv                NA
## mime                NA
## modelr              NA
## munsell             NA
## nlme                NA
## nnet                NA
## nycflights13        NA
## openssl             NA
## packrat             NA
## parallel            "snow, nws, Rmpi"
## pillar              NA
## pkgbuild            NA
## pkgconfig           NA
## pkgload             NA
## plotly              NA
## png                 NA
## praise              NA
## prettyunits         NA
## processx            NA
## progress            NA
## promises            NA
## ps                  NA
## purrr               NA
## R6                  NA
## raster              NA
## RColorBrewer        NA
## Rcpp                NA
## readr               NA
## readxl              NA
## rematch             NA

```

## reprex	NA	
## rgdal	NA	
## rlang	NA	
## rmarkdown	NA	
## rpart	NA	
## rprojroot	NA	
## rsconnect	NA	
## rstudioapi	NA	
## rvest	NA	
## scales	NA	
## selectr	NA	
## sf	NA	
## shiny	NA	
## shinythemes	NA	
## sourcetools	NA	
## sp	NA	
## spatial	NA	
## splines	NA	
## stars	NA	
## stats	NA	
## stats4	NA	
## stringi	NA	
## stringr	NA	
## survival	NA	
## sys	NA	
## tcltk	NA	
## testthat	NA	
## tibble	NA	
## tidyr	NA	
## tidyselect	NA	
## tidyverse	NA	
## tinytex	NA	
## tmap	NA	
## tmaptools	NA	
## tools	NA	
## units	NA	
## utf8	NA	
## utils	NA	
## vctrs	NA	
## viridis	NA	
## viridisLite	NA	
## whisker	NA	
## widgetframe	NA	
## withr	NA	
## xfun	NA	
## XML	NA	
## xml2	NA	
## xtable	NA	
## yaml	NA	
##	License	License_is_FOSS
## ade4	"GPL (>= 2)"	NA
## agricolae	"GPL"	NA
## AICcmodavg	"GPL (>= 2)"	NA
## AlgDesign	"GPL (>= 2)"	NA

## ape	"GPL-2 GPL-3"	NA
## Biobase	"Artistic-2.0"	NA
## BiocGenerics	"Artistic-2.0"	NA
## BiocManager	"Artistic-2.0"	NA
## BiocVersion	"Artistic-2.0"	NA
## biomformat	"GPL-2"	NA
## Biostrings	"Artistic-2.0"	NA
## broom	"MIT + file LICENSE"	NA
## bslib	"MIT + file LICENSE"	NA
## car	"GPL (>= 2)"	NA
## carData	"GPL (>= 2)"	NA
## checkmate	"BSD_3_clause + file LICENSE"	NA
## cli	"MIT + file LICENSE"	NA
## combinat	"GPL-2"	NA
## corrplot	"MIT + file LICENSE"	NA
## cowplot	"GPL-2"	NA
## cpp11	"MIT + file LICENSE"	NA
## DataCombine	"GPL (>= 3)"	NA
## dbstats	"GPL-2"	NA
## ecodist	"GPL (>= 2)"	NA
## effects	"GPL (>= 2)"	NA
## ellipsis	"MIT + file LICENSE"	NA
## emmeans	"GPL-2 GPL-3"	NA
## estimability	"GPL (>= 3)"	NA
## fastmap	"MIT + file LICENSE"	NA
## foreach	"Apache License (== 2.0)"	NA
## formatR	"GPL"	NA
## Formula	"GPL-2 GPL-3"	NA
## futile.logger	"LGPL-3"	NA
## futile.options	"LGPL-3"	NA
## ggforce	"MIT + file LICENSE"	NA
## ggplot2	"MIT + file LICENSE"	NA
## ggpubr	"GPL-2"	NA
## ggrepel	"GPL-3 file LICENSE"	NA
## ggsci	"GPL-3 file LICENSE"	NA
## ggsignif	"GPL-3 file LICENSE"	NA
## glue	"MIT + file LICENSE"	NA
## haven	"MIT + file LICENSE"	NA
## htmlTable	"GPL (>= 3)"	NA
## htmltools	"GPL (>= 2)"	NA
## igraph	"GPL (>= 2)"	NA
## indicpecies	"GPL (>= 2)"	NA
## insight	"GPL-3"	NA
## IRanges	"Artistic-2.0"	NA
## iterators	"Apache License (== 2.0)"	NA
## jpeg	"GPL-2 GPL-3"	NA
## jquerylib	"MIT + file LICENSE"	NA
## klaR	"GPL-2 GPL-3"	NA
## labdsv	"GPL (>= 2)"	NA
## labelled	"GPL-3"	NA
## lambda.r	"LGPL-3"	NA
## latticeExtra	"GPL (>= 2)"	NA
## lme4	"GPL (>= 2)"	NA
## lmerTest	"GPL (>= 2)"	NA

## magrittr	"MIT + file LICENSE"	NA
## maptools	"GPL (>= 2)"	NA
## MatrixModels	"GPL (>= 2)"	NA
## miniUI	"GPL-3"	NA
## minqa	"GPL-2"	NA
## mitools	"GPL-2"	NA
## mnormt	"GPL-2 GPL-3"	NA
## multcomp	"GPL-2"	NA
## multcompView	"GPL"	NA
## multtest	"LGPL"	NA
## MuMIn	"GPL-2"	NA
## mvtnorm	"GPL-2"	NA
## nloptr	"LGPL-3"	NA
## nortest	"GPL (>= 2)"	NA
## numDeriv	"GPL-2"	NA
## pbkrtest	"GPL (>= 2)"	NA
## permute	"GPL-2"	NA
## phyloseq	"AGPL-3"	NA
## picante	"GPL-2"	NA
## pixmap	"GPL-2"	NA
## pls	"GPL-2"	NA
## plsr	"GPL-3"	NA
## plyr	"MIT + file LICENSE"	NA
## polyclip	"BSL"	NA
## polynom	"GPL-2"	NA
## psych	"GPL (>= 2)"	NA
## quantreg	"GPL (>= 2)"	NA
## questionr	"GPL (>= 2)"	NA
## R.cache	"LGPL (>= 2.1)"	NA
## R.methodsS3	"LGPL (>= 2.1)"	NA
## R.oo	"LGPL (>= 2.1)"	NA
## R.utils	"LGPL (>= 2.1)"	NA
## rappdirs	"MIT + file LICENSE"	NA
## Rcmdr	"GPL (>= 2)"	NA
## RcmdrMisc	"GPL (>= 2)"	NA
## RcppArmadillo	"GPL (>= 2)"	NA
## RcppEigen	"GPL (>= 2) file LICENSE"	NA
## readstata13	"GPL-2 file LICENSE"	NA
## relimp	"GPL (>= 2)"	NA
## rematch2	"MIT + file LICENSE"	NA
## reshape	"MIT + file LICENSE"	NA
## reshape2	"MIT + file LICENSE"	NA
## rhdf5	"Artistic-2.0"	NA
## rhdf5filters	"BSD_2_clause + file LICENSE"	NA
## Rhdf5lib	"Artistic-2.0"	NA
## rlang	"MIT + file LICENSE"	NA
## rmarkdown	"GPL-3"	NA
## rstatix	"GPL-2"	NA
## Rtsne	"file LICENSE"	"yes"
## S4Vectors	"Artistic-2.0"	NA
## sandwich	"GPL-2 GPL-3"	NA
## sass	"MIT + file LICENSE"	NA
## SparseM	"GPL (>= 2)"	NA
## styler	"MIT + file LICENSE"	NA

## survey	"GPL-2 GPL-3"	NA
## tcltk2	"LGPL-3 + file LICENSE"	NA
## TH.data	"GPL-3"	NA
## tinytex	"MIT + file LICENSE"	NA
## tmvnsim	"GPL-2"	NA
## tweenr	"MIT + file LICENSE"	NA
## unmarked	"GPL (>= 3)"	NA
## vctr	"MIT + file LICENSE"	NA
## vegan	"GPL-2"	NA
## VennDiagram	"GPL-2"	NA
## VGAM	"GPL-3"	NA
## xfun	"MIT + file LICENSE"	NA
## XVector	"Artistic-2.0"	NA
## zlibbioc	"Artistic-2.0 + file LICENSE"	NA
## zoo	"GPL-2 GPL-3"	NA
## abind	"LGPL (>= 2)"	NA
## askpass	"MIT + file LICENSE"	NA
## assertthat	"GPL-3"	NA
## backports	"GPL-2 GPL-3"	NA
## base	"Part of R 4.0.2"	NA
## base64enc	"GPL-2 GPL-3"	NA
## BH	"BSL-1.0"	NA
## blob	"GPL-3"	NA
## boot	"Unlimited"	NA
## broom	"MIT + file LICENSE"	NA
## callr	"MIT + file LICENSE"	NA
## cellranger	"MIT + file LICENSE"	NA
## class	"GPL-2 GPL-3"	NA
## classInt	"GPL (>= 2)"	NA
## cli	"MIT + file LICENSE"	NA
## clipr	"GPL-3"	NA
## cluster	"GPL (>= 2)"	NA
## codetools	"GPL"	NA
## colorspace	"BSD_3_clause + file LICENSE"	NA
## commonmark	"BSD_2_clause + file LICENSE"	NA
## compiler	"Part of R 4.0.2"	NA
## crayon	"MIT + file LICENSE"	NA
## crosstalk	"MIT + file LICENSE"	NA
## curl	"MIT + file LICENSE"	NA
## data.table	"MPL-2.0 file LICENSE"	NA
## datasets	"Part of R 4.0.2"	NA
## DBI	"LGPL (>= 2.1)"	NA
## dbplyr	"MIT + file LICENSE"	NA
## desc	"MIT + file LICENSE"	NA
## dichromat	"GPL-2"	NA
## digest	"GPL (>= 2)"	NA
## dplyr	"MIT + file LICENSE"	NA
## e1071	"GPL-2 GPL-3"	NA
## elevatr	"CC0"	NA
## ellipsis	"GPL-3"	NA
## evaluate	"MIT + file LICENSE"	NA
## fansi	"GPL (>= 2)"	NA
## farver	"MIT + file LICENSE"	NA
## fastmap	"MIT + file LICENSE"	NA

## forcats	"GPL-3"	NA
## foreign	"GPL (>= 2)"	NA
## fs	"GPL-3"	NA
## gapminder	"CC0"	NA
## generics	"GPL-2"	NA
## ggplot2	"GPL-2 file LICENSE"	NA
## glue	"MIT + file LICENSE"	NA
## graphics	"Part of R 4.0.2"	NA
## grDevices	"Part of R 4.0.2"	NA
## grid	"Part of R 4.0.2"	NA
## gridExtra	"GPL (>= 2)"	NA
## gtable	"GPL-2"	NA
## haven	"MIT + file LICENSE"	NA
## hexbin	"GPL-2"	NA
## highr	"GPL"	NA
## hms	"GPL-3"	NA
## htmltools	"GPL (>= 2)"	NA
## htmlwidgets	"MIT + file LICENSE"	NA
## httpuv	"GPL (>= 2) file LICENSE"	NA
## httr	"MIT + file LICENSE"	NA
## isoband	"MIT + file LICENSE"	NA
## jsonlite	"MIT + file LICENSE"	NA
## KernSmooth	"Unlimited"	NA
## knitr	"GPL"	NA
## labeling	"MIT + file LICENSE Unlimited"	NA
## Lahman	"GPL"	NA
## later	"GPL (>= 2)"	NA
## lattice	"GPL (>= 2)"	NA
## lazyeval	"GPL-3"	NA
## leafem	"MIT + file LICENSE"	NA
## leaflet	"GPL-3"	NA
## leaflet.providers	"BSD_2_clause + file LICENSE"	NA
## leafsync	"MIT + file LICENSE"	NA
## lifecycle	"GPL-3"	NA
## lubridate	"GPL (>= 2)"	NA
## lwgeom	"GPL-2"	NA
## magrittr	"MIT + file LICENSE"	NA
## mapdata	"GPL-2"	NA
## maps	"GPL-2"	NA
## markdown	"GPL-2"	NA
## MASS	"GPL-2 GPL-3"	NA
## Matrix	"GPL (>= 2) file LICENSE"	NA
## methods	"Part of R 4.0.2"	NA
## mgcv	"GPL (>= 2)"	NA
## mime	"GPL"	NA
## modelr	"GPL-3"	NA
## munsell	"MIT + file LICENSE"	NA
## nlme	"GPL (>= 2) file LICENSE"	NA
## nnet	"GPL-2 GPL-3"	NA
## nycflights13	"CC0"	NA
## openssl	"MIT + file LICENSE"	NA
## packrat	"GPL-2"	NA
## parallel	"Part of R 4.0.2"	NA
## pillar	"GPL-3"	NA

## pkgbuild	"GPL-3"	NA
## pkgconfig	"MIT + file LICENSE"	NA
## pkgload	"GPL-3"	NA
## plotly	"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
## progress	"MIT + file LICENSE"	NA
## promises	"MIT + file LICENSE"	NA
## ps	"BSD_3_clause + file LICENSE"	NA
## purrr	"GPL-3 file LICENSE"	NA
## R6	"MIT + file LICENSE"	NA
## raster	"GPL (>= 3)"	NA
## RColorBrewer	"Apache License 2.0"	NA
## Rcpp	"GPL (>= 2)"	NA
## readr	"GPL (>= 2) file LICENSE"	NA
## readxl	"GPL-3"	NA
## rematch	"MIT + file LICENSE"	NA
## reprex	"MIT + file LICENSE"	NA
## rgdal	"GPL (>= 2)"	NA
## rlang	"GPL-3"	NA
## rmarkdown	"GPL-3"	NA
## rpart	"GPL-2 GPL-3"	NA
## rprojroot	"GPL-3"	NA
## rsconnect	"GPL-2"	NA
## rstudioapi	"MIT + file LICENSE"	NA
## rvest	"GPL-3"	NA
## scales	"MIT + file LICENSE"	NA
## selectr	"BSD_3_clause + file LICENSE"	NA
## sf	"GPL-2 MIT + file LICENSE"	NA
## shiny	"GPL-3 file LICENSE"	NA
## shinythemes	"GPL-3 file LICENSE"	NA
## sourcetools	"MIT + file LICENSE"	NA
## sp	"GPL (>= 2)"	NA
## spatial	"GPL-2 GPL-3"	NA
## splines	"Part of R 4.0.2"	NA
## stars	"Apache License"	NA
## stats	"Part of R 4.0.2"	NA
## stats4	"Part of R 4.0.2"	NA
## stringi	"file LICENSE"	"yes"
## stringr	"GPL-2 file LICENSE"	NA
## survival	"LGPL (>= 2)"	NA
## sys	"MIT + file LICENSE"	NA
## tcltk	"Part of R 4.0.2"	NA
## testthat	"MIT + file LICENSE"	NA
## tibble	"MIT + file LICENSE"	NA
## tidyr	"MIT + file LICENSE"	NA
## tidyselect	"GPL-3"	NA
## tidyverse	"GPL-3 file LICENSE"	NA
## tinytex	"MIT + file LICENSE"	NA
## tmap	"GPL-3"	NA
## tmaptools	"GPL-3"	NA
## tools	"Part of R 4.0.2"	NA

## units	"GPL-2"			NA	
## utf8	"Apache License (== 2.0) file LICENSE"			NA	
## utils	"Part of R 4.0.2"			NA	
## vctrs	"GPL-3"			NA	
## viridis	"MIT + file LICENSE"			NA	
## viridisLite	"MIT + file LICENSE"			NA	
## whisker	"GPL-3"			NA	
## widgetframe	"MIT + file LICENSE"			NA	
## withr	"GPL (>= 2)"			NA	
## xfun	"MIT + file LICENSE"			NA	
## XML	"BSD_3_clause + file LICENSE"			NA	
## xml2	"GPL (>= 2)"			NA	
## xtable	"GPL (>= 2)"			NA	
## yaml	"BSD_3_clause + file LICENSE"			NA	
##	License_restricts_use	OS_type	MD5sum	NeedsCompilation	Built
## ade4	NA	NA	NA	"yes"	"4.0.2"
## agricolae	NA	NA	NA	"no"	"4.0.2"
## AICcmodavg	NA	NA	NA	"no"	"4.0.2"
## AlgDesign	NA	NA	NA	"yes"	"4.0.2"
## ape	NA	NA	NA	"yes"	"4.0.2"
## Biobase	NA	NA	NA	"yes"	"4.0.3"
## BiocGenerics	NA	NA	NA	"no"	"4.0.5"
## BiocManager	NA	NA	NA	"no"	"4.0.2"
## BiocVersion	NA	NA	NA	"no"	"4.0.0"
## biomformat	NA	NA	NA	"no"	"4.0.3"
## Biostrings	NA	NA	NA	"yes"	"4.0.3"
## broom	NA	NA	NA	"no"	"4.0.5"
## bslib	NA	NA	NA	"no"	"4.0.2"
## car	NA	NA	NA	"no"	"4.0.2"
## carData	NA	NA	NA	"no"	"4.0.5"
## checkmate	NA	NA	NA	"yes"	"4.0.2"
## cli	NA	NA	NA	"yes"	"4.0.5"
## combinat	NA	NA	NA	NA	"4.0.2"
## corrplot	NA	NA	NA	"no"	"4.0.2"
## cowplot	NA	NA	NA	"no"	"4.0.2"
## cpp11	NA	NA	NA	"no"	"4.0.2"
## DataCombine	NA	NA	NA	"no"	"4.0.2"
## dbstats	NA	NA	NA	"no"	"4.0.2"
## ecodist	NA	NA	NA	"yes"	"4.0.2"
## effects	NA	NA	NA	"no"	"4.0.5"
## ellipsis	NA	NA	NA	"yes"	"4.0.2"
## emmeans	NA	NA	NA	"no"	"4.0.5"
## estimability	NA	NA	NA	"no"	"4.0.2"
## fastmap	NA	NA	NA	"yes"	"4.0.2"
## foreach	NA	NA	NA	"no"	"4.0.2"
## formatR	NA	NA	NA	"no"	"4.0.5"
## Formula	NA	NA	NA	"no"	"4.0.2"
## futile.logger	NA	NA	NA	"no"	"4.0.2"
## futile.options	NA	NA	NA	"no"	"4.0.2"
## ggforce	NA	NA	NA	"yes"	"4.0.2"
## ggplot2	NA	NA	NA	"no"	"4.0.2"
## ggpubr	NA	NA	NA	"no"	"4.0.2"
## ggrepel	NA	NA	NA	"yes"	"4.0.2"
## ggsci	NA	NA	NA	"no"	"4.0.2"

## ggsignif	NA	NA	NA	"no"	"4.0.2"
## glue	NA	NA	NA	"yes"	"4.0.5"
## haven	NA	NA	NA	"yes"	"4.0.2"
## htmlTable	NA	NA	NA	"no"	"4.0.5"
## htmltools	NA	NA	NA	"yes"	"4.0.2"
## igraph	NA	NA	NA	"yes"	"4.0.2"
## indicpecies	NA	NA	NA	"no"	"4.0.5"
## insight	NA	NA	NA	"no"	"4.0.2"
## IRanges	NA	NA	NA	"yes"	"4.0.3"
## iterators	NA	NA	NA	"no"	"4.0.2"
## jpeg	NA	NA	NA	"yes"	"4.0.2"
## jquerylib	NA	NA	NA	"no"	"4.0.2"
## klaR	NA	NA	NA	"no"	"4.0.5"
## labdsv	NA	NA	NA	"yes"	"4.0.2"
## labelled	NA	NA	NA	"no"	"4.0.2"
## lambda.r	NA	NA	NA	"no"	"4.0.2"
## latticeExtra	NA	NA	NA	"no"	"4.0.2"
## lme4	NA	NA	NA	"yes"	"4.0.2"
## lmerTest	NA	NA	NA	"no"	"4.0.2"
## magrittr	NA	NA	NA	"yes"	"4.0.5"
## maptools	NA	NA	NA	"yes"	"4.0.5"
## MatrixModels	NA	NA	NA	"no"	"4.0.2"
## miniUI	NA	NA	NA	"no"	"4.0.2"
## minqa	NA	NA	NA	"yes"	"4.0.2"
## mitools	NA	NA	NA	"no"	"4.0.2"
## mnormt	NA	NA	NA	"yes"	"4.0.2"
## multcomp	NA	NA	NA	"no"	"4.0.5"
## multcompView	NA	NA	NA	"no"	"4.0.2"
## multtest	NA	NA	NA	"yes"	"4.0.3"
## MuMIn	NA	NA	NA	"no"	"4.0.5"
## mvtnorm	NA	NA	NA	"yes"	"4.0.2"
## nloptr	NA	NA	NA	"yes"	"4.0.2"
## nortest	NA	NA	NA	"no"	"4.0.2"
## numDeriv	NA	NA	NA	"no"	"4.0.2"
## pbkrtest	NA	NA	NA	"no"	"4.0.2"
## permute	NA	NA	NA	"no"	"4.0.2"
## phyloseq	NA	NA	NA	"no"	"4.0.3"
## picante	NA	NA	NA	"yes"	"4.0.2"
## pixmap	NA	NA	NA	"no"	"4.0.2"
## pls	NA	NA	NA	"no"	"4.0.2"
## plsr	NA	NA	NA	"no"	"4.0.2"
## plyr	NA	NA	NA	"yes"	"4.0.2"
## polyclip	NA	NA	NA	"yes"	"4.0.2"
## polynom	NA	NA	NA	"no"	"4.0.2"
## psych	NA	NA	NA	"no"	"4.0.2"
## quantreg	NA	NA	NA	"yes"	"4.0.5"
## questionr	NA	NA	NA	"no"	"4.0.5"
## R.cache	NA	NA	NA	"no"	"4.0.2"
## R.methodsS3	NA	NA	NA	"no"	"4.0.2"
## R.oo	NA	NA	NA	"no"	"4.0.2"
## R.utils	NA	NA	NA	"no"	"4.0.2"
## rappdirs	NA	NA	NA	"yes"	"4.0.2"
## Rcmdr	NA	NA	NA	"no"	"4.0.5"
## RcmdrMisc	NA	NA	NA	"no"	"4.0.5"

## RcppArmadillo	NA	NA	NA	"yes"	"4.0.5"
## RcppEigen	NA	NA	NA	"yes"	"4.0.2"
## readstata13	NA	NA	NA	"yes"	"4.0.2"
## relimp	NA	NA	NA	"no"	"4.0.2"
## rematch2	NA	NA	NA	"no"	"4.0.2"
## reshape	NA	NA	NA	"yes"	"4.0.2"
## reshape2	NA	NA	NA	"yes"	"4.0.2"
## rhdf5	NA	NA	NA	"yes"	"4.0.3"
## rhdf5filters	NA	NA	NA	"yes"	"4.0.5"
## Rhdf5lib	NA	NA	NA	"yes"	"4.0.3"
## rlang	NA	NA	NA	"yes"	"4.0.5"
## rmarkdown	NA	NA	NA	"no"	"4.0.2"
## rstatix	NA	NA	NA	"no"	"4.0.2"
## Rtsne	NA	NA	NA	"yes"	"4.0.2"
## S4Vectors	NA	NA	NA	"yes"	"4.0.3"
## sandwich	NA	NA	NA	"no"	"4.0.2"
## sass	NA	NA	NA	"yes"	"4.0.5"
## SparseM	NA	NA	NA	"yes"	"4.0.2"
## styler	NA	NA	NA	"no"	"4.0.5"
## survey	NA	NA	NA	"no"	"4.0.2"
## tcltk2	NA	NA	NA	"no"	"4.0.2"
## TH.data	NA	NA	NA	"no"	"4.0.2"
## tinytex	NA	NA	NA	"no"	"4.0.2"
## tmvnsim	NA	NA	NA	"yes"	"4.0.2"
## tweenr	NA	NA	NA	"yes"	"4.0.2"
## unmarked	NA	NA	NA	"yes"	"4.0.2"
## vctrs	NA	NA	NA	"yes"	"4.0.2"
## vegan	NA	NA	NA	"yes"	"4.0.2"
## VennDiagram	NA	NA	NA	"no"	"4.0.2"
## VGAM	NA	NA	NA	"yes"	"4.0.5"
## xfun	NA	NA	NA	"yes"	"4.0.2"
## XVector	NA	NA	NA	"yes"	"4.0.3"
## zlibbioc	NA	NA	NA	"yes"	"4.0.3"
## zoo	NA	NA	NA	"yes"	"4.0.2"
## abind	NA	NA	NA	"no"	"4.0.2"
## askpass	NA	NA	NA	"yes"	"4.0.2"
## assertthat	NA	NA	NA	"no"	"4.0.2"
## backports	NA	NA	NA	"yes"	"4.0.2"
## base	NA	NA	NA	NA	"4.0.2"
## base64enc	NA	NA	NA	"yes"	"4.0.2"
## BH	NA	NA	NA	"no"	"4.0.2"
## blob	NA	NA	NA	"no"	"4.0.2"
## boot	NA	NA	NA	"no"	"4.0.2"
## broom	NA	NA	NA	"no"	"4.0.2"
## callr	NA	NA	NA	"no"	"4.0.2"
## cellranger	NA	NA	NA	"no"	"4.0.2"
## class	NA	NA	NA	"yes"	"4.0.2"
## classInt	NA	NA	NA	"yes"	"4.0.2"
## cli	NA	NA	NA	"no"	"4.0.2"
## clipr	NA	NA	NA	"no"	"4.0.2"
## cluster	NA	NA	NA	"yes"	"4.0.2"
## codetools	NA	NA	NA	"no"	"4.0.2"
## colorspace	NA	NA	NA	"yes"	"4.0.2"
## commonmark	NA	NA	NA	"yes"	"4.0.2"

## compiler	NA	NA	NA	NA	"4.0.2"
## crayon	NA	NA	NA	"no"	"4.0.2"
## crosstalk	NA	NA	NA	"no"	"4.0.2"
## curl	NA	NA	NA	"yes"	"4.0.1"
## data.table	NA	NA	NA	"yes"	"4.0.2"
## datasets	NA	NA	NA	NA	"4.0.2"
## DBI	NA	NA	NA	"no"	"4.0.2"
## dbplyr	NA	NA	NA	"no"	"4.0.2"
## desc	NA	NA	NA	"no"	"4.0.2"
## dichromat	NA	NA	NA	NA	"4.0.2"
## digest	NA	NA	NA	"yes"	"4.0.2"
## dplyr	NA	NA	NA	"yes"	"4.0.2"
## e1071	NA	NA	NA	"yes"	"4.0.2"
## elevatr	NA	NA	NA	"no"	"4.0.2"
## ellipsis	NA	NA	NA	"yes"	"4.0.2"
## evaluate	NA	NA	NA	"no"	"4.0.1"
## fansi	NA	NA	NA	"yes"	"4.0.2"
## farver	NA	NA	NA	"yes"	"4.0.2"
## fastmap	NA	NA	NA	"yes"	"4.0.2"
## forcats	NA	NA	NA	"no"	"4.0.2"
## foreign	NA	NA	NA	"yes"	"4.0.2"
## fs	NA	NA	NA	"yes"	"4.0.2"
## gapminder	NA	NA	NA	"no"	"4.0.2"
## generics	NA	NA	NA	"no"	"4.0.2"
## ggplot2	NA	NA	NA	"no"	"4.0.2"
## glue	NA	NA	NA	"yes"	"4.0.2"
## graphics	NA	NA	NA	"yes"	"4.0.2"
## grDevices	NA	NA	NA	"yes"	"4.0.2"
## grid	NA	NA	NA	"yes"	"4.0.2"
## gridExtra	NA	NA	NA	"no"	"4.0.2"
## gtable	NA	NA	NA	"no"	"4.0.2"
## haven	NA	NA	NA	"yes"	"4.0.2"
## hexbin	NA	NA	NA	"yes"	"4.0.2"
## highr	NA	NA	NA	"no"	"4.0.2"
## hms	NA	NA	NA	"no"	"4.0.2"
## htmltools	NA	NA	NA	"yes"	"4.0.2"
## htmlwidgets	NA	NA	NA	"no"	"4.0.2"
## httpuv	NA	NA	NA	"yes"	"4.0.2"
## httr	NA	NA	NA	"no"	"4.0.2"
## isoband	NA	NA	NA	"yes"	"4.0.2"
## jsonlite	NA	NA	NA	"yes"	"4.0.2"
## KernSmooth	NA	NA	NA	"yes"	"4.0.2"
## knitr	NA	NA	NA	"no"	"4.0.2"
## labeling	NA	NA	NA	"no"	"4.0.2"
## Lahman	NA	NA	NA	"no"	"4.0.2"
## later	NA	NA	NA	"yes"	"4.0.2"
## lattice	NA	NA	NA	"yes"	"4.0.2"
## lazyeval	NA	NA	NA	"yes"	"4.0.2"
## leafem	NA	NA	NA	"no"	"4.0.2"
## leaflet	NA	NA	NA	"no"	"4.0.2"
## leaflet.providers	NA	NA	NA	"no"	"4.0.2"
## leafsync	NA	NA	NA	"no"	"4.0.2"
## lifecycle	NA	NA	NA	"no"	"4.0.2"
## lubridate	NA	NA	NA	"yes"	"4.0.2"

## lwgeom	NA	NA	NA	"yes"	"4.0.2"
## magrittr	NA	NA	NA	"no"	"4.0.2"
## mapdata	NA	NA	NA	"yes"	"4.0.2"
## maps	NA	NA	NA	"yes"	"4.0.2"
## markdown	NA	NA	NA	"yes"	"4.0.2"
## MASS	NA	NA	NA	"yes"	"4.0.2"
## Matrix	NA	NA	NA	"yes"	"4.0.2"
## methods	NA	NA	NA	"yes"	"4.0.2"
## mgcv	NA	NA	NA	"yes"	"4.0.2"
## mime	NA	NA	NA	"yes"	"4.0.2"
## modelr	NA	NA	NA	"no"	"4.0.2"
## munsell	NA	NA	NA	"no"	"4.0.2"
## nlme	NA	NA	NA	"yes"	"4.0.2"
## nnet	NA	NA	NA	"yes"	"4.0.2"
## nycflights13	NA	NA	NA	"no"	"4.0.2"
## openssl	NA	NA	NA	"yes"	"4.0.1"
## packrat	NA	NA	NA	"no"	"4.0.2"
## parallel	NA	NA	NA	"yes"	"4.0.2"
## pillar	NA	NA	NA	"no"	"4.0.2"
## pkgbuild	NA	NA	NA	"no"	"4.0.2"
## pkgconfig	NA	NA	NA	"no"	"4.0.2"
## pkgload	NA	NA	NA	"yes"	"4.0.2"
## plotly	NA	NA	NA	"no"	"4.0.2"
## png	NA	NA	NA	"yes"	"4.0.2"
## praise	NA	NA	NA	"no"	"4.0.2"
## prettyunits	NA	NA	NA	"no"	"4.0.2"
## processx	NA	NA	NA	"yes"	"4.0.2"
## progress	NA	NA	NA	"no"	"4.0.2"
## promises	NA	NA	NA	"yes"	"4.0.2"
## ps	NA	NA	NA	"yes"	"4.0.2"
## purrr	NA	NA	NA	"yes"	"4.0.2"
## R6	NA	NA	NA	"no"	"4.0.2"
## raster	NA	NA	NA	"yes"	"4.0.2"
## RColorBrewer	NA	NA	NA	"no"	"4.0.2"
## Rcpp	NA	NA	NA	"yes"	"4.0.2"
## readr	NA	NA	NA	"yes"	"4.0.2"
## readxl	NA	NA	NA	"yes"	"4.0.2"
## rematch	NA	NA	NA	"no"	"4.0.2"
## reprex	NA	NA	NA	"no"	"4.0.2"
## rgdal	NA	NA	NA	"yes"	"4.0.2"
## rlang	NA	NA	NA	"yes"	"4.0.2"
## rmarkdown	NA	NA	NA	"no"	"4.0.2"
## rpart	NA	NA	NA	"yes"	"4.0.2"
## rprojroot	NA	NA	NA	"no"	"4.0.2"
## rsconnect	NA	NA	NA	"no"	"4.0.2"
## rstudioapi	NA	NA	NA	"no"	"4.0.2"
## rvest	NA	NA	NA	"no"	"4.0.2"
## scales	NA	NA	NA	"no"	"4.0.2"
## selectr	NA	NA	NA	"no"	"4.0.2"
## sf	NA	NA	NA	"yes"	"4.0.2"
## shiny	NA	NA	NA	"no"	"4.0.2"
## shinythemes	NA	NA	NA	"no"	"4.0.2"
## sourcetools	NA	NA	NA	"yes"	"4.0.2"
## sp	NA	NA	NA	"yes"	"4.0.2"

## spatial	NA	NA	NA	"yes"	"4.0.2"
## splines	NA	NA	NA	"yes"	"4.0.2"
## stars	NA	NA	NA	"no"	"4.0.2"
## stats	NA	NA	NA	"yes"	"4.0.2"
## stats4	NA	NA	NA	NA	"4.0.2"
## stringi	NA	NA	NA	"yes"	"4.0.2"
## stringr	NA	NA	NA	"no"	"4.0.2"
## survival	NA	NA	NA	"yes"	"4.0.2"
## sys	NA	NA	NA	"yes"	"4.0.2"
## tcltk	NA	NA	NA	"yes"	"4.0.2"
## testthat	NA	NA	NA	"yes"	"4.0.2"
## tibble	NA	NA	NA	"yes"	"4.0.2"
## tidyr	NA	NA	NA	"yes"	"4.0.2"
## tidyselect	NA	NA	NA	"yes"	"4.0.2"
## tidyverse	NA	NA	NA	"no"	"4.0.2"
## tinytex	NA	NA	NA	"no"	"4.0.2"
## tmap	NA	NA	NA	"no"	"4.0.2"
## tmaptools	NA	NA	NA	"no"	"4.0.2"
## tools	NA	NA	NA	"yes"	"4.0.2"
## units	NA	NA	NA	"yes"	"4.0.2"
## utf8	NA	NA	NA	"yes"	"4.0.2"
## utils	NA	NA	NA	"yes"	"4.0.2"
## vctrs	NA	NA	NA	"yes"	"4.0.2"
## viridis	NA	NA	NA	"no"	"4.0.2"
## viridisLite	NA	NA	NA	"no"	"4.0.1"
## whisker	NA	NA	NA	"no"	"4.0.2"
## widgetframe	NA	NA	NA	"no"	"4.0.2"
## withr	NA	NA	NA	"no"	"4.0.2"
## xfun	NA	NA	NA	"yes"	"4.0.2"
## XML	NA	NA	NA	"yes"	"4.0.2"
## xml2	NA	NA	NA	"yes"	"4.0.2"
## xtable	NA	NA	NA	"no"	"4.0.2"
## yaml	NA	NA	NA	"yes"	"4.0.2"

```
#install.packages("vegan", dependencies = TRUE) #Already installed
```

```
library(vegan)
```

```
## Loading required package: permute
```

```
## Loading required package: lattice
```

```
## This is vegan 2.5-7
```

```
#remove.packages()
```