

## A.10: R packages

This page describes basic steps for **package installation** from a **CRAN mirror site** and how to update installed packages following installation of a new version of R. See at the end of this page for a list of packages described in Mike's Biostatistics Book.

### Adding packages to base R installation

Installing R packages is straightforward, assuming the package is part of CRAN. Select a CRAN mirror site, e.g., **0-Cloud**, RStudio's mirror site.

```
chooseCRANmirror()
```

To find out what CRAN mirror was set for the current session use

```
findCRANmirror()
```

A list of mirror sites is stored on your computer once R is installed, see `CRAN_mirrors.csv` in the doc folder, e.g., `~/R-4.3.1/doc`.

Once the CRAN mirror is selected, and assuming you have the name of the package, e.g., `package.name`, then

```
install.packages("package.name")
```

will work.

Useful additional command options include

```
install.packages("package.name", dependencies=TRUE)
```

which will also download and install any additional packages required, and

```
install.packages("package.name", quiet=TRUE)
```

cuts down on the amount of screen output during installation.

If you receive the following **warning message**,

```
Warning: package 'package.name' is not available (for R version 4.3.2)
```

it may be possible that the package has not yet become available, but first double-check for typos.

Another warning message may be that a **binary version** is available, but a more recent **source version** is available, prompted by the question, *Do you want to install from sources the package which needs compilation?* In most cases, the answer is no. R will install a previous binary version. In order to install from source, **RTools** must be installed.

### Update R packages after installing new R version

After updating to new version of R you'll need to download and update the user installed packages again. If you are running RStudio, see [instructions here](#). For Win11 users you can download and run a package called `installr`, for macOS users download and install `updateR`, which will assist you to update R packages.

I prefer to run a script, modified from [R-Bloggers.com](https://www.r-bloggers.com/). This script works on any operating system, but updates only CRAN packages (e.g., not github or Bioconductor).

Before installing the new version of base R, start up your current R installation and set your working directory, `setwd()`. Enter the following script to gather and save all installed R packages. Select CRAN mirror when prompted.

```
tmp <- installed.packages()
installedpkgs <- as.vector(tmp[is.na(tmp[, "Priority"]), 1])
save(installedpkgs, file="installed_old.rda")
```

Shutdown R, then install and start the new version of R (see [Install R](#) for help).

In the new version of R, set your working directory as above. Enter the following script

```
load(file="installed_old.rda")
tmp <- installed.packages()
installedpkgs.new <- as.vector(tmp[is.na(tmp[, "Priority"]), 1])
missing <- setdiff(installedpkgs, installedpkgs.new)
install.packages(missing)
update.packages(ask=FALSE)
```

Should be good to go. You can remove old R version installation.

#### Note:

To check installed packages, just view the object `installedpkgs` created earlier.

## R packages used in Mike's Biostatistics Book

list updated 12 August 2024

package	chapter
agRee	<a href="#">16.5 – Instrument reliability and validity</a>
ape	<a href="#">20.11 - Plot a Newick tree</a>
baseline	<a href="#">20.3 - Baseline correction</a>
BiocManager	<a href="#">20.11 - Plot a Newick tree</a>
Bioconductor	<a href="#">20.11 - Plot a Newick tree</a>
BiodiversityR	<a href="#">5.6 - Sampling from Populations</a>
boot	<a href="#">19.2 - Bootstrap sampling</a>
bootstrap	<a href="#">19.1 - Jackknife sampling</a>
BSDA	<a href="#">11.4 - Two-sample effect size</a>
cairoDevice	<a href="#">13.3 - Test assumption of normality</a>
car	<a href="#">4.3 - Box plots</a>
carData	<a href="#">4.1 - Bar (column) charts</a>
cholera	<a href="#">2.3 - A brief history of (bio)statistics</a>
clipr	<a href="#">4 - How to report statistics</a>
combinat	<a href="#">6.3 - Combinations and permutations</a>
confintr	<a href="#">19.2 - Bootstrap sampling</a>
contingencytables	<a href="#">9.6 - McNemar's test</a>
correlation	<a href="#">16.6 - Similarity and Distance</a>

package	chapter
cranlogs	<a href="#">2.2 - Why do we use R Software?</a>
datasets	<a href="#">4.5 - Scatter plots</a>
digitize	<a href="#">12.3 - Fixed effects, random effects, and ICC</a>
drc	<a href="#">20.10 - Growth equations and dose response calculations</a>
effectsize	<a href="#">12.5 – Effect size for ANOVA</a>
effsize	<a href="#">11.4 - Two-sample effect size</a>
epiR	<a href="#">5.4 - Clinical trials</a>
epitools	<a href="#">7.4 – Epidemiology: Relative risk and absolute risk, explained</a>
exact2x2	<a href="#">9.6 – McNemar’s test</a>
factoextra	<a href="#">20.6 – Dimensional analysis</a>
findpeaks	<a href="#">20.2 - Peak detection</a>
forecast	<a href="#">20.5 - Time series</a>
geepack	<a href="#">20.1 - Area under the curve</a>
geeM	<a href="#">20.1 - Area under the curve</a>
geodist	<a href="#">16.6 - Similarity and Distance</a>
ggplot2	<a href="#">4.1 - Bar (column) charts</a>
ggtree	<a href="#">20.11 - Plot a Newick tree</a>
gplots	<a href="#">4.1 - Bar (column) charts</a>
gtools	<a href="#">6.3 - Combinations and permutations</a>
GrapheR	<a href="#">4.10 - Graph software</a>
HH	<a href="#">12.4 - ANOVA from "sufficient statistics"</a>
HistData	<a href="#">3.2 - Measures of Central Tendency</a>
lattice	<a href="#">4.10 - Graph software</a>
lmboot	<a href="#">19.1 - Jackknife sampling</a>
irr	<a href="#">12.3 - Fixed effects, random effects, and ICC</a>
MASS	<a href="#">12.4 - ANOVA from "sufficient statistics"</a>
Matrix	<a href="#">20.1 - Area under the curve</a>
mcp	<a href="#">12.6 - ANOVA post-hoc tests</a>
MESS	<a href="#">20.1 - Area under the curve</a>
mlr3misc	<a href="#">8.2 – The controversy over proper hypothesis testing</a>
modeest	<a href="#">3.2 - Measures of Central Tendency</a>
multcomp	<a href="#">12.6 - ANOVA posthoc tests</a>
NCStats	<a href="#">3.3 - Measures of dispersion</a>
nlopt	<a href="#">20.10 - Growth equations and dose response calculations</a>

package	chapter
nortest	<a href="#">13.3 – Test assumption of normality</a>
PairedData	<a href="#">10.3 – Paired t-test</a>
peakDetection	<a href="#">20.2 - Peak detection</a>
Phylotools	<a href="#">20.11 - Plot a Newick tree</a>
Phytools	<a href="#">20.11 - Plot a Newick tree</a>
plotly	<a href="#">4.10 - Graph software</a>
plyr	<a href="#">4.1 - Bar (column) charts</a>
polychor	<a href="#">16.4 – Spearman and other correlations</a>
propCIs	<a href="#">7.6 - Confidence intervals</a>
psa	<a href="#">20.6 – Dimensional analysis</a>
psy	<a href="#">12.3 - Fixed effects, random effects, and ICC</a>
psych	<a href="#">3.2 - Measures of Central Tendency</a>
pwr	<a href="#">11.5 - Power analysis in R</a>
random	<a href="#">6.6 - Continuous distributions</a>
rattle	<a href="#">13.3 - Test assumption of normality</a>
Rcmdr	<a href="#">1.1 - A quick look at R and R Commander</a>
RcmdrMisc	<a href="#">1.1 - A quick look at R and R Commander</a>
RcmdrPlugin.EBM	<a href="#">4.4 - Mosaic plots</a>
RcmdrPlugin.EZR	<a href="#">11.5 - Power analysis in R</a>
RcmdrPlugin.HH	<a href="#">12.4 - ANOVA from "sufficient statistics"</a>
RcmdrPlugin.KMggplot2	<a href="#">4.1 - Bar (column) charts</a>
RcmdrPlugin.mosaic	<a href="#">4.4 - Mosaic plots</a>
RcmdrPlugin.survival	<a href="#">20.9 - Survival analysis</a>
Rcolorbrewer	<a href="#">4.4 - Mosaic plots</a>
reshape2	<a href="#">4.6 - Adding a second Y axis</a>
rgl	<a href="#">18.1 - Multiple Linear Regression</a>
Rmisc	<a href="#">3.5 - Statistics of error</a>
ROCR	<a href="#">20.1 - Area under the curve</a>
rptR	<a href="#">12.3 - Fixed effects, random effects, and ICC</a>
RGtk2	<a href="#">13.3 - Test assumption of normality</a>
season	<a href="#">20.5 – Time series</a>
shotGroups	<a href="#">3.5 - Statistics of error</a>
stats	<a href="#">4 – How to report statistics</a>
survival	<a href="#">3.1 - Data types</a>

package	chapter
tangle	<a href="#">20.11 - Plot a Newick tree</a>
Ternary	<a href="#">4.8 - Ternary plots</a>
testequavar	<a href="#">13.4 - Tests for Equal Variances</a>
tidyverse	<a href="#">4.3 - Box plot</a>
tigerstats	<a href="#">8.4 - Tails of a test</a>
timeseries	<a href="#">20.5 - Time series</a>
TOSTER	<a href="#">16.1 - Product-moment correlation</a>
vegan	<a href="#">20.8 - Diversity indexes</a>
WRS2	<a href="#">3.3 - Measures of dispersion</a>

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