

# Useful things

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A personal collection of useful R packages and more.

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This chapter is a collection of things I wish I had known earlier in my years using R and that I hope can be of use to you. Sections are named after R packages or whatever applies and sorted alphabetically.

## 1 {broom}

In R, results from statistical tests, models etc. are often formatted in a way that may not be optimal for further processing steps. Luckily, `{broom}` will format the results of [the most common functions](#) into [tidy data structures](#).

```
# Correlation Analysis for built-in example data "mtcars"
mycor <- cor.test(mtcars$mpg, mtcars$disp)
mycor
```

```
Pearson's product-moment correlation
```

```
data: mtcars$mpg and mtcars$disp
t = -8.7472, df = 30, p-value = 9.38e-10
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.9233594 -0.7081376
sample estimates:
      cor
-0.8475514
```

```
library(broom)
tidy(mycor)
```

```
# A tibble: 1 x 8
  estimate statistic p.value parameter conf.low conf.high method alternative
  <dbl>      <dbl>   <dbl>    <int>    <dbl>    <dbl> <chr>      <chr>
1  -0.848      -8.75 9.38e-10      30  -0.923    -0.708 Pearson'~ two.sided
```

## 2 {conflicted}

Sometimes, different packages have different functions with identical names. A famous example is the function `filter()`, which exists in `{stats}` and `{dplyr}`. If both of these packages are loaded, it is not clear which of the two functions should be used. This is called a function conflict and it is especially tricky here since `{stats}` is always loaded. By default, R will simply pick the package that was loaded later - which is obviously not optimal.

One way of dealing with function conflicts is by using the `packagename::functionname()` method, because when writing `dplyr::filter()` instead of `filter()` it is no longer ambiguous which function you are referring to.

Another way of dealing with function conflicts more explicitly is by loading the `{conflicted}` package. Once it is loaded, function conflicts will lead to an **Error** that forces you to deal with the issue:

```
library(conflicted)
library(dplyr)

PlantGrowth %>% filter(weight > 6)
```

Error:

```
! [conflicted] filter found in 2 packages.
Either pick the one you want with `::`:
* dplyr::filter
* stats::filter
Or declare a preference with `conflicts_prefer()``
* `conflicts_prefer(dplyr::filter)`
* `conflicts_prefer(stats::filter)`
```

As you can see, it first suggests using the `packagename::functionname()` method mentioned above, but also points to the `conflict_prefer()` function. By running this function once in the beginning of the script, R will always use the function from the package that you declared the “winner”:

```
library(conflicted)
library(dplyr)

conflicts_prefer(dplyr::filter)

PlantGrowth %>% filter(weight > 6)
```

```

  weight group
1   6.11  ctrl
2   6.03  trt1
3   6.31  trt2
4   6.15  trt2

```

### 3 {desplot}

`{desplot}` makes it easy to plot experimental designs of field trials in agriculture. However, you do need two columns that provide the x and y coordinates of the individual plots on your field.

TO DO

### 4 {dlookr}

When providing descriptive statistics tables, one may find the number of relevant measures become annoyingly large so that even with the `{tidyverse}`, several lines of code are necessary. Here are just five measures, and they are not even including the `na.rm = TRUE` argument, which is necessary for data with missing values.

```

library(tidyverse)

PlantGrowth %>%
  group_by(group) %>%
  summarise(
    mean = mean(weight),
    stddev = sd(weight),
    median = median(weight),
    min = min(weight),
    max = max(weight)
  )

```

```

# A tibble: 3 x 6
  group mean stddev median  min  max
<fct> <dbl>  <dbl>  <dbl> <dbl> <dbl>
1 ctrl   5.03   0.583   5.15  4.17  6.11
2 trt1   4.66   0.794   4.55  3.59  6.03
3 trt2   5.53   0.443   5.44  4.92  6.31

```

Obviously, there are multiple packages who try to address just that. The one I've been using for some time now is `{dlookr}` with its `describe()` function. It actually provides more measures than I usually need<sup>1</sup>, but it has everything I want and I disregard the rest (via `select()`).

```
PlantGrowth %>%
  group_by(group) %>%
  dlookr::describe(weight)

# A tibble: 3 x 27
  described_variables group      n    na mean    sd se_mean  IQR skewness
  <chr>                <fct> <int> <int> <dbl> <dbl>   <dbl> <dbl>   <dbl>
1 weight              ctrl    10     0  5.03  0.583   0.184  0.743   0.321
2 weight              trt1     10     0  4.66  0.794   0.251  0.662   0.659
3 weight              trt2     10     0  5.53  0.443   0.140  0.467   0.673
# i 18 more variables: kurtosis <dbl>, p00 <dbl>, p01 <dbl>, p05 <dbl>,
#   p10 <dbl>, p20 <dbl>, p25 <dbl>, p30 <dbl>, p40 <dbl>, p50 <dbl>,
#   p60 <dbl>, p70 <dbl>, p75 <dbl>, p80 <dbl>, p90 <dbl>, p95 <dbl>,
#   p99 <dbl>, p100 <dbl>
```

#### **i** Note

It is intentional that I did not actually load the `{dlookr}` package, but instead used its `describe()` function via the `package::functionname()` method. This is because of a minor bug in the `{dlookr}` package described [here](#), which is only relevant if you are using the package with knitr/Rmarkdown/quarto. I am using quarto to generate this website and thus I avoid loading the package. This is fine for me, since I usually only need this one function one time during an analysis. It is also fine for you, since the code works the same way in a standard R script.

## 5 {ggtext}

Adding long text to plots created via `{ggplot2}` is problematic, since you have to insert line breaks yourself. However, `{ggtext}`'s `geom_textbox()` for data labels and `element_textbox_simple()` for title, caption etc. will automatically add line breaks:

```
longtext <- "Lorem ipsum dolor sit amet, consetetur sadipscing elitr, sed diam nonumy eirm"
```

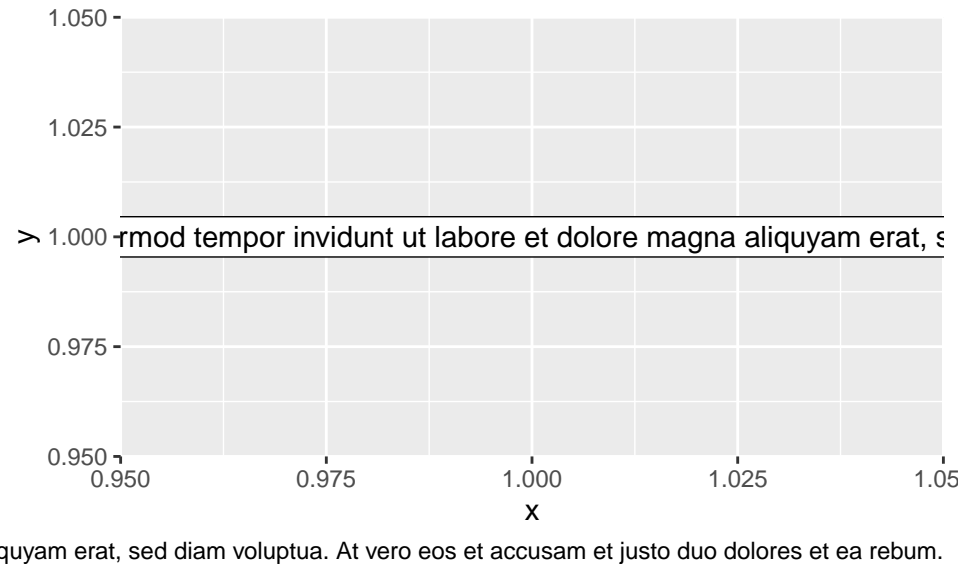
---

<sup>1</sup>Keep in mind that `p00` is the 0th percentile and thus the minimum. Analogously, `p50` is the median and `p100` the maximum.

```
library(ggplot2)
```

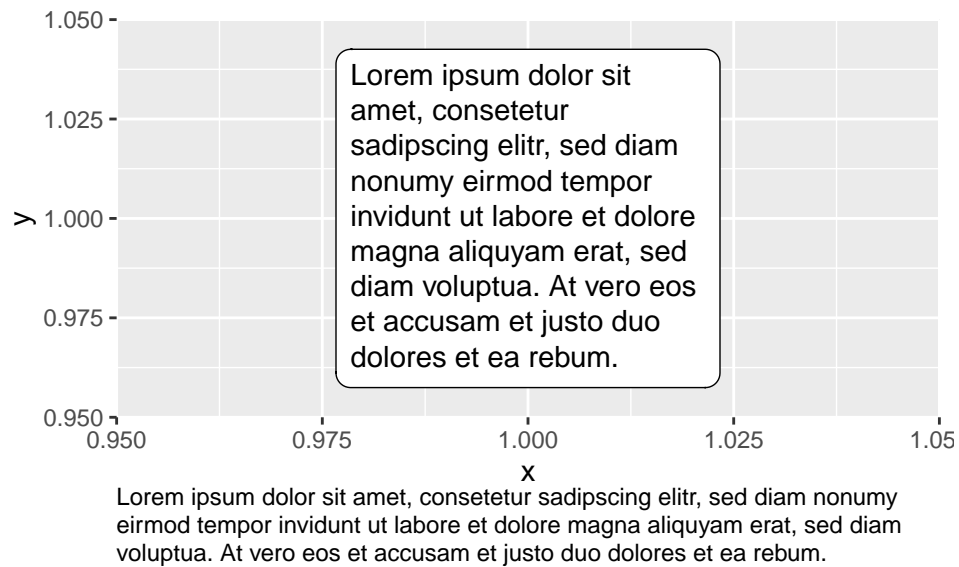
```
ggplot() +
```

```
  aes(y = 1, x = 1, label = longtext) +  
  geom_label() +  
  labs(caption = longtext)
```



```
library(ggtext)
```

```
ggplot() +  
  theme(plot.caption =  
    element_textbox_simple()) +  
  aes(y = 1, x = 1, label = longtext) +  
  geom_textbox() +  
  labs(caption = longtext)
```



## 6 {here}

TO DO

## 7 {insight}

TO DO

## 8 {janitor}

TO DO

## 9 Keyboard shortcuts

Here are shortcuts I actually use regularly in RStudio:

Shortcut	Description
CTRL+ENTER	Run selected lines of code
CTRL+C	Convert all selected lines to comment
CTRL+SHIFT+M	Insert %>%

Shortcut	Description
CTRL+SHIFT+R	Insert code section header
CTRL+LEFT/RIGHT	Jump to Word
CTRL+SHIFT+LEFT/RIGHT	Select Word
ALT+LEFT/RIGHT	Jump to Line Start/End
ALT+SHIFT+LEFT/RIGHT	Select to Line Start/End
CTRL+A	Highlight everything (to run the entire code)
CTRL+Z	Undo

Keyboard shortcuts can be customized in RStudio as described [here](#).

## 10 {modelbased}

TO DO

## 11 {openxlsx}

TO DO

## 12 {pacman}

You now know how to install and load R packages the standard way. However, over the years I switched to using the function `p_load()` from the `{pacman}` package instead of `library()` and `install.packages()`. The reason is simple: Usually R-scripts start with multiple lines of `library()` statements that load the necessary packages. However, when this code is run on a different computer, the user may not have all these packages installed and will therefore get an error message. This can be avoided by using the `p_load()`, because it

- loads all packages that are installed and
- installs and loads all packages that are not installed.

Obviously, `{pacman}` itself must first be installed (the standard way). Moreover, you may now think that in order to use `p_load()` we do need a single `library(pacman)` first. However, we can avoid this by writing `pacman::p_load()` instead. Simply put, writing `package_name::function_name()` [makes sure](#) that this explicit function from this explicit package is being used. Additionally, R actually lets you use this function without loading the corresponding package. Thus, we now arrived at the way I handle packages at the beginning of all my R-scripts:



```
pacman::p_load(  
  package_name_1,  
  package_name_2,  
  package_name_3  
)
```

## 13 {patchwork}

TO DO

## 14 {performance}

TO DO

## 15 {readxl}

TO DO

## 16 {reprex}

TO DO

## 17 {scales}

TO DO

## 18 %in% and %not\_in%

R has the built-in function `%in%` which checks whether something is present in a vector.

```
treatments <- c("Ctrl", "A", "B")
```

Not only can we check which treatments are present in our `treatment` vector (left), but we can also easily keep only those that are (right).

```
c("A", "D") %in% treatments
```

```
[1] TRUE FALSE
```

```
c("A", "D") %>% .[, %in% treatments]
```

```
[1] "A"
```

Not built-in, for some reason, is the opposite of that function - checking whether something is **not** present. Yet, we can quickly build our own function that does exactly that:

```
`%not_in%` <- Negate(`%in%`)
```

```
c("A", "D") %not_in% treatments
```

```
[1] FALSE TRUE
```

```
c("A", "D") %>% .[, %not_in% treatments]
```

```
[1] "D"
```

**19** `system('open "file.png"')`

TO DO