Useful things

true

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A personal collection of useful R packages and more.

Table of contents

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        alter~1
     <dbl>     <dbl>    <dbl>     <int>    <dbl>     <dbl> <chr>         <chr>
1   -0.848     -8.75 9.38e-10        30   -0.923    -0.708 Pearson's pr~ two.si~
```

```
# ... with abbreviated variable name 1: alternative
```

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 `conflict_prefer()`
* conflict_prefer("filter", "dplyr")
* conflict_prefer("filter", "stats")
```

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)
```

```r
conflict_prefer("filter", "dplyr")

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.

```r
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[1], 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_~1 group     n    na  mean    sd se_mean   IQR skewn~2 kurto~3   p00
  <chr>        <fct> <int> <int> <dbl> <dbl>   <dbl> <dbl>   <dbl>   <dbl> <dbl>
1 weight       ctrl     10     0  5.03 0.583   0.184 0.743   0.321  -0.229  4.17
2 weight       trt1     10     0  4.66 0.794   0.251 0.662   0.659  -0.203  3.59
3 weight       trt2     10     0  5.53 0.443   0.140 0.467   0.673  -0.324  4.92
# ... with 16 more variables: 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>, and
#   abbreviated variable names 1: described_variables, 2: skewness, 3: kurtosis
```

Note

It is intentional that I did not actually load the {dlookr} package, but instead used its `describe()` function via the packagename::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.

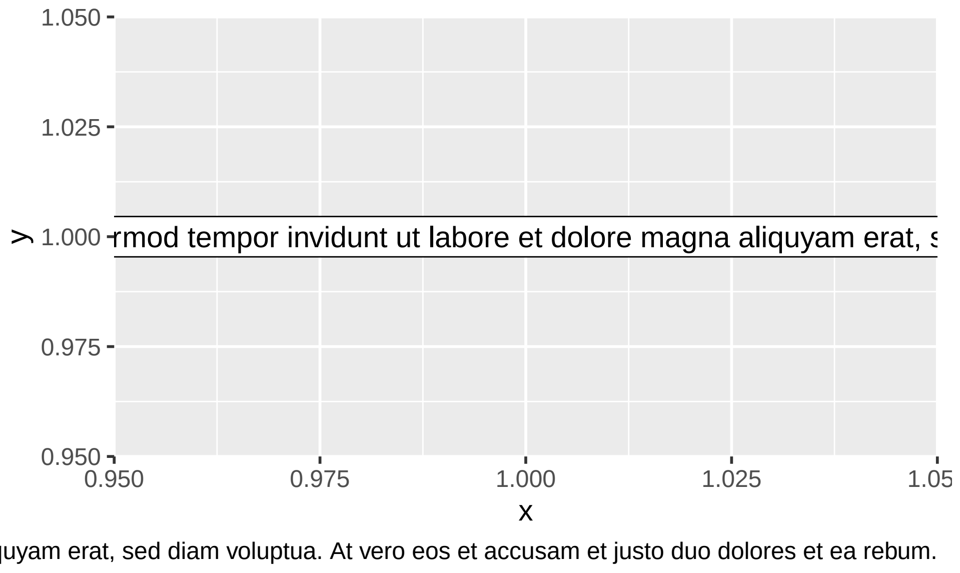
[1] Keep in mind that `p00` is the 0th percentile and thus the minimum. Analogously, `p50` is the median and `p100` the maximum.

5 {ggtext}

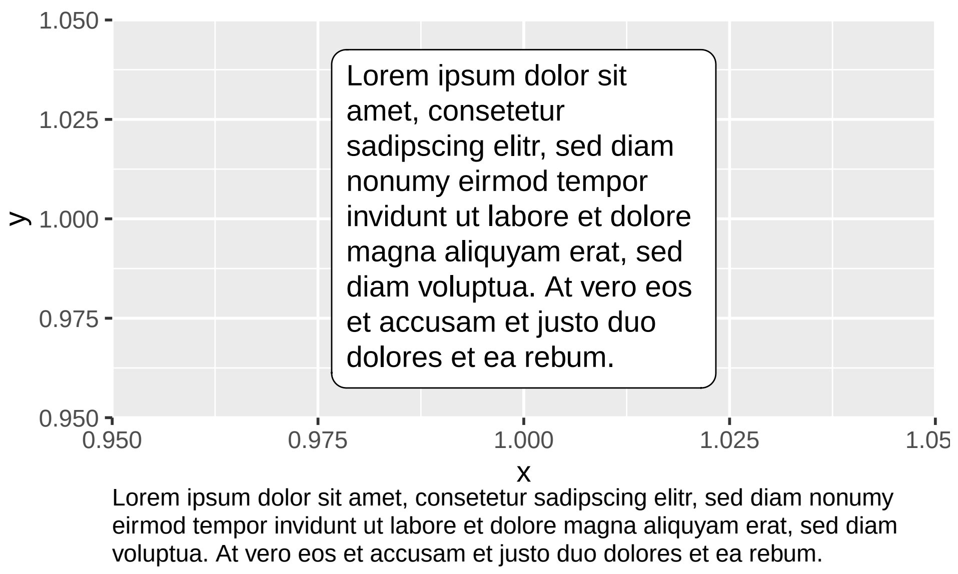
Adding long text to plots created via {ggplot2} is problematic, since you have to insert line breaks yourself. However, {ggext}'s `geom_textbox()` for data labels and `element_textbox_simple()` for title, caption etc. will automatically add line breaks:

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

```
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 `%>%`
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 checke 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 built 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