Useful things

true

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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 {dlookr} - descriptive statistics

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[1], but it has everything I want and I disregard the rest (via `select()`).

```
library(dlookr)

PlantGrowth %>%
  group_by(group) %>%
  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
```

2 {forcats} - factor level handling

In my experience, R beginners really only care about the difference between `factor` and `character` variables once the factor level order is not as they want it to be - typically on the x-axis of a plot. Luckily, {forcats} can deal with this.

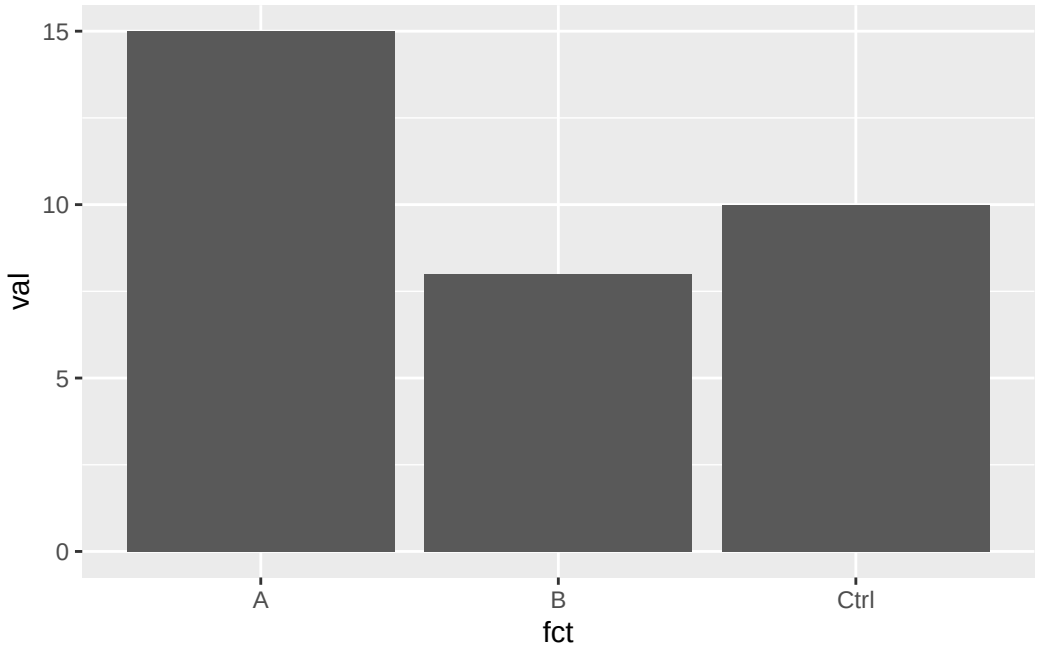
[1] Keep in mind that `p00` is the 0th percentile and thus the minimum. Analogously, `p50` is the median and `p100` the maximum.

In the following example, we create a column `fct` that is a copy of the column `chr`, except that they are formatted as `factor` and `character`, respectively.

```
library(tidyverse)

dat <- tribble(
     ~val,   ~chr,
       10, "Ctrl",
       15,    "A",
        8,    "B"
) %>%
  mutate(fct = as.factor(chr))

ggplot(dat) +
  aes(y = val, x = fct) +
  geom_col()
```



Even though the data is sorted so that Ctrl is first, then A, then B, the x-Axis is sorted differently[2]. This is because factor levels are always sorted alphabetically by default. We can reorder them via different functions in {forcats}:

[2]It does not make a difference here, whether we put `x = chr` or `x = fct` in the ggplot statement.

```r
dat <- dat %>%
  mutate(
    fct2 = fct_relevel(fct, c("Ctrl", "A", "B")),
    fct3 = fct_reorder(fct, val, mean)
    )

str(dat)
```

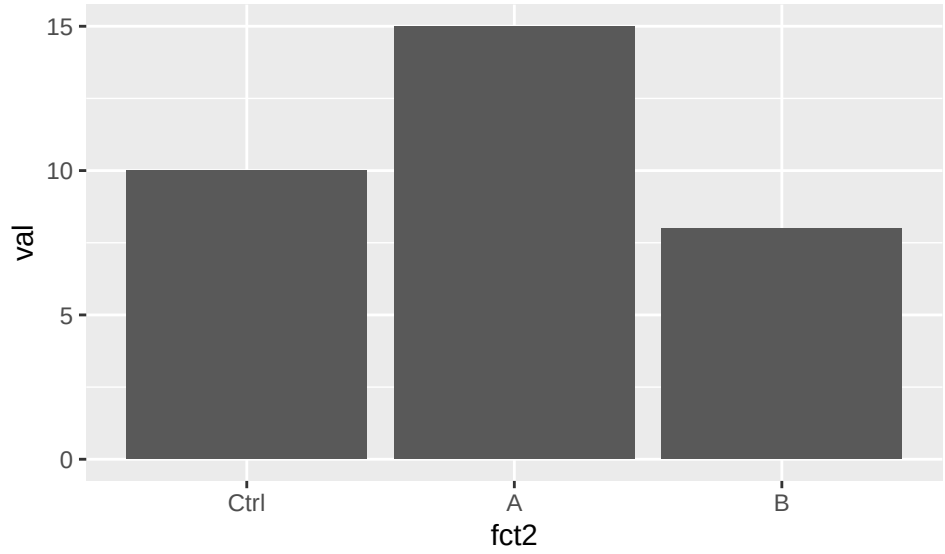
```
tibble [3 x 5] (S3: tbl_df/tbl/data.frame)
 $ val : num [1:3] 10 15 8
 $ chr : chr [1:3] "Ctrl" "A" "B"
 $ fct : Factor w/ 3 levels "A","B","Ctrl": 3 1 2
 $ fct2: Factor w/ 3 levels "Ctrl","A","B": 1 2 3
 $ fct3: Factor w/ 3 levels "B","Ctrl","A": 2 3 1
```

Above are just two popular examples for sorting factor levels: `fct_relevel` sorts the levels manually by providing a vector with the level names in the order they should appear, while `fct_reorder` here sorts the levels according to their respective group mean[3] of the values in the `val` column.

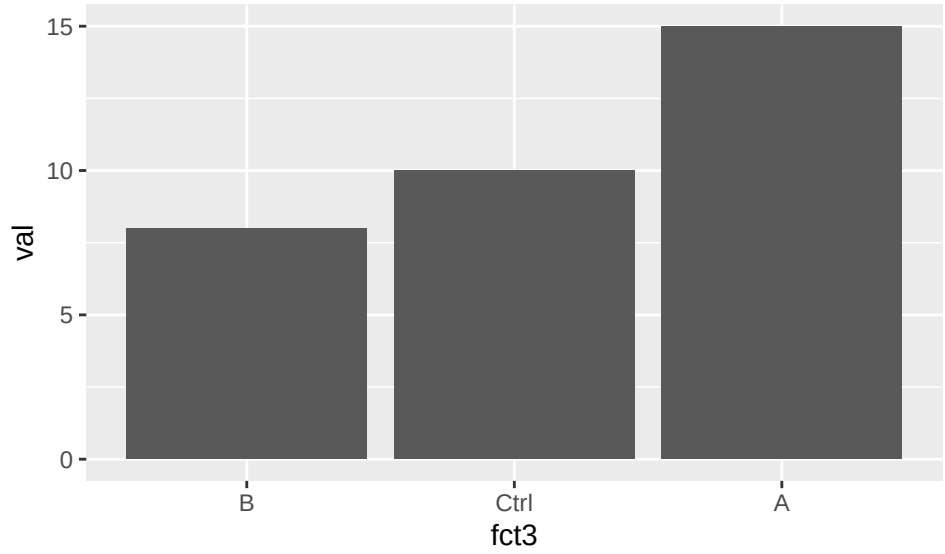
You can see that it worked in the output of `str(dat)` above and in the plots below.

```r
ggplot(dat) +
  aes(y = val, x = fct2) +
  geom_col()
```

[3] Yes, the mean in this example is not really a mean, since there is only one number per group.




```
ggplot(dat) +
  aes(y = val, x = fct3) +
  geom_col()
```



3 {ggtext} - automatic word wrapping

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:

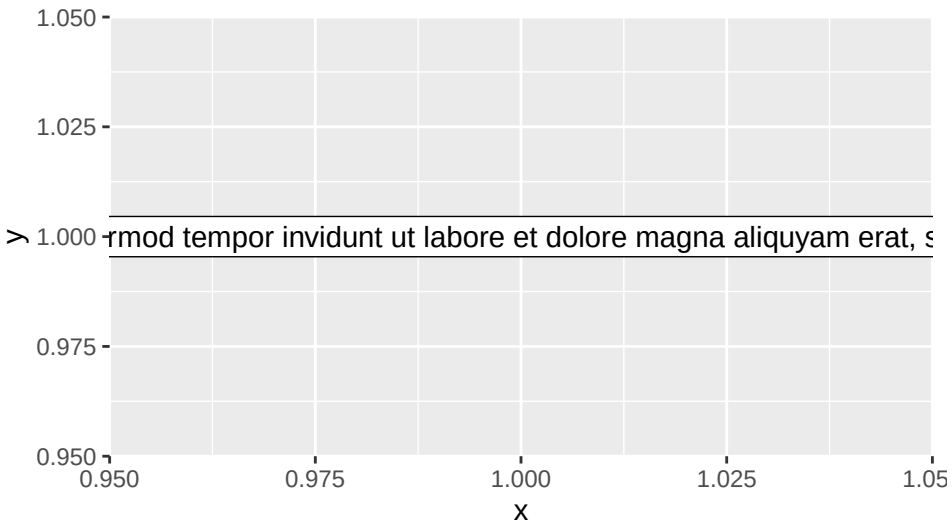
```
longtext <- "Lorem ipsum dolor sit amet, consetetur sadipscing elitr, sed diam nonumy eirm
```

```
library(ggplot2)

ggplot() +



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



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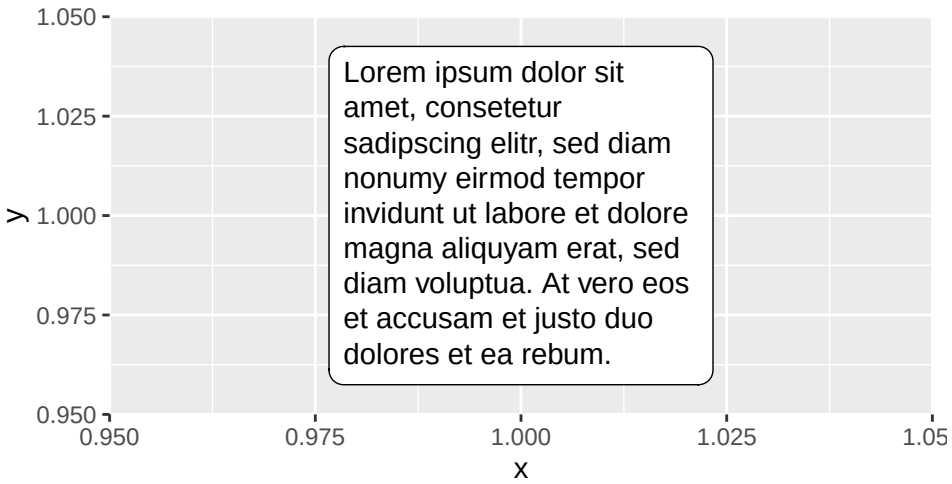
```
library(ggtext)

ggplot() +
  theme(plot.caption =
          element_textbox_simple()
```

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



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4 %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"
```