

RStatsbook

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Invalid Date

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Preface

This booklet is meant as companion to my R / statistics seminars. It is NOT a complete guide to either R or statistical data analysis.

1 Introduction

There are plenty of books available, check out e.g.

[R for Data Science](#)

[Modern Statistics for Modern Biology](#)

[Modern R with the tidyverse](#)

[ggplot2: Elegant Graphics for Data Analysis](#)

Chapters will follow my usual schedule, starting from R basics, introducing ggplot, data import, data preparation and cleaning, descriptive statistics, simple test statistics, then progression to linear models (regression/ANOVA), generalized linear models with logistic regression as example, linear mixed effect models, and machine learning.

2 *Syntax rules / basic things to know about R*

This is going to be the boring technical stuff... We'll get to the more interesting topics in the next chapters.

2.1 *Script preparation / basic setup*

At the beginning of (almost) every script we define packages to be used. This could be done by either

- *checking if packages needed are installed and otherwise do so, followed by function library(packagename)*

OR

- *simplifying this using function p_load() from package pacman; if you want to create fool-proof scripts, check for pacman and install if needed.*

```
# ↑ this is the head of a code chunk
Sys.setenv(LANG="en_EN.UTF-8") # to get errors/warnings in English
if(!requireNamespace("pacman", quietly = TRUE)){
  install.packages("pacman")
}
pacman::p_load(
  conflicted, # tests/solutions for name conflicts
  tidyverse, # metapackage
  wrappedtools, # my own tools package
  randomNames # used to create pseudo names
)
conflict_scout()
```

2 conflicts

```
* `filter()`': dplyr and stats
* `lag()`': dplyr and stats
```

```
conflicts_prefer(dplyr::filter,  
                  stats::lag)
```

[conflicted] Will prefer dplyr::filter over any other package.

[conflicted] Will prefer stats::lag over any other package.

2.2 Numeric operations

```
### simple calculations ####  
2+5
```

[1] 7

```
3*5
```

[1] 15

```
15/3 #not 15:3!!, would create vector 15,14,13 ... 3
```

[1] 5

```
3^2
```

[1] 9

```
9^0.5
```

[1] 3

```
10%%3 #modulo
```

[1] 1

2.3 Variables

2.3.1 Variable names

Naming things is harder than you may expect. Try to be verbose and consistent in language and style. Commonly used are `snake_case_style` and `CamelCaseStyle`.

Decide about computer-friendly (syntactical) or human-friendly names, illegal names can be used inside backticks: ‘measure [unit]’. My preference is syntactical for script variables and humane for data variables, e.g. column names, print labels etc.

There are rules for valid syntactical names:

- `UPPERCASE` and lowercase are distinguished
- start with letter or symbols as `.__`, but not with a number
- no mathematical symbols or brackets allowed

To store some value into a variable, use the assignment operator `<-` ; while it possible to use `=` or `->` , this is rather unusual. Assignments are silent, so either a call of the variable, or `print()` / `cat()` function are needed to inspect. Alternatively, put brackets around assignment: `(varname <- content)`.

```
### Variable names #####
test <- 1
test1 <- 1
# 1test <- 2 # wrong, would result in error
`1test` <- 2 # this would be possible
test_1 <- 5
test.1 <- 2
`test-1` <- 6
`test(1)` <- 5
Test <- "bla"
HereAreFilteredData <- "" #CamelCase
here_are_filtered_data <- "test" #snake_case
`Weight [kg]` <- 67
```

2.3.2 Basic classes of data

`R` is ‘guessing’ the suitable type of data from input. This should be checked after e.g. importing data! If elements of different classes are found, the more inclusive is used. There are functions to change / force a type if needed.

The `class()` function returns the class of an object, which determines how it behaves with respect to functions like `print()`. The class of an object can be changed by using generic functions and methods.

The `typeof()` function returns the basic data type of an object, which determines how it is stored in memory. The basic data type of an object cannot be changed.

The `str()` function shows class and examples of an object.

2.3.2.1 Guessed classes

```
float_num <- 123.456  
class(float_num)
```

```
[1] "numeric"
```

```
typeof(float_num)
```

```
[1] "double"
```

```
str(float_num)
```

```
num 123
```

```
int_num <- 123L # L specifies integer, guessing requires more values  
class(int_num)
```

```
[1] "integer"
```

```
typeof(int_num)
```

```
[1] "integer"
```

```
integer(length = 3)
```

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

```
result<-9^(1/2)  
result
```

```
[1] 3
```

```
print(result)
```

```
[1] 3
```

```
cat(result)
```

```
3
```

```
char_var <- "some words"  
class(char_var)
```

```
[1] "character"
```

```
typeof(char_var)
```

```
[1] "character"
```

```
character(length = 5)
```

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

```
logical_var <- TRUE # can be abbreviated to T  
logical_var2 <- FALSE # or F, seen as bad style  
class(logical_var)
```

```
[1] "logical"
```

```
typeof(logical_var)
```

```
[1] "logical"
```

```
logical(length = 3)
```

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

```
# logicals usually are defined by conditions:  
int_num < float_num
```

```
[1] TRUE
```

```
# all numbers are true but 0  
as.logical(c(0,1,5,-7.45678)) # c() combines values into a vector
```

```
[1] FALSE TRUE TRUE TRUE
```

*Factor: categorical variables with limited set of distinct values, internally stored as integers.
Everything intended to group subjects or representing categories should be stored as factor.
Package forcats provides nice tools for factors!*

```
factor_var <- factor(c("m","m","f","m","f","f","?"))  
factor_var
```

```
[1] m m f m f f ?  
Levels: ? f m
```

```
class(factor_var)
```

```
[1] "factor"
```

```
typeof(factor_var) # that is why factors can be called enumerated type
```

```
[1] "integer"
```

```
# factor definition can reorder, rename, and drop levels:  
factor_var2 <- factor(c("m","m","f","m","f","f","?"),  
                        levels=c("m","f"),  
                        labels=c("male","female"))  
factor_var2
```

```
[1] male male female male female female <NA>  
Levels: male female
```

Dates / Time:

```
(date_var <- Sys.Date())
```

```
[1] "2024-01-27"
```

```
class(date_var)
```

```
[1] "Date"
```

```
typeof(date_var)
```

```
[1] "double"
```

```
class(Sys.time())
```

```
[1] "POSIXct" "POSIXt"
```

Mixed classes:

```
test2 <- c(1,2,"a","b")
class(test2)
```

```
[1] "character"
```

```
test2
```

```
[1] "1" "2" "a" "b"
```

2.3.2.2 *Forcing / casting classes*

Casting functions usually start with `as.` , when creating variables filled with NA, use casting functions or specific variants of NA to force type!

```
(test <- c(1,2,3,"a","b","c"))
```

```
[1] "1" "2" "3" "a" "b" "c"
```

```
(test_n <- as.numeric(test))
```

Warning: NAs introduced by coercion

```
[1] 1 2 3 NA NA NA
```

```
as.numeric(factor_var)
```

```
[1] 3 3 2 3 2 2 1
```

```
as.character(10:19)
```

```
[1] "10" "11" "12" "13" "14" "15" "16" "17" "18" "19"
```

```
# NAs  
(test_NA1 <- rep(NA,10))
```

```
[1] NA NA NA NA NA NA NA NA NA NA
```

```
class((test_NA1))
```

```
[1] "logical"
```

```
class(NA_real_)
```

```
[1] "numeric"
```

```
(test_NA2 <- rep(NA_real_,10))
```

```
[1] NA NA NA NA NA NA NA NA NA NA
```

```
class((test_NA2))
```

```
[1] "numeric"
```

```

class(NA_integer_)

[1] "integer"

class(NA_character_)

[1] "character"

class(NA_Date_) # from package lubridate

[1] "Date"

# test_NA_factor <-
#   factor(rep(NA,10),
#         levels=c("WT","Mutation1", "Mutation2"))
# class(test_NA_factor)

```

2.3.3 Indexing variables

The most general kind of indexing is by position, starting with 1. Negative numbers result in exclusion of position(s). Position indices are provided within square brackets. The index can (and usually will) be a variable instead of hard coded numbers.

```

(numbers1<-c(5,3,6,8,2,1))

[1] 5 3 6 8 2 1

numbers1[1]

[1] 5

numbers1[1:3]

[1] 5 3 6

```

```
numbers1[-c(1,3)]
```

```
[1] 3 8 2 1
```

```
numbers2 <- 1:3  
numbers1[numbers2]
```

```
[1] 5 3 6
```

```
# numbers1[1,2] #Error: incorrect number of dimensions
```

To get first or last entries, `head()` and `tail()` can be used. By default 6 entries are returned.

```
tail(x=numbers1, n = 1)
```

```
[1] 1
```

```
head(x = numbers1, n = 3)
```

```
[1] 5 3 6
```

```
nth(x = numbers1, n=-2) # 2nd to last
```

```
[1] 2
```

2.3.4 Usage of variables

Variables are like placeholders for their content, so that you don't have to remember where you left things. Operations on variables are operations on their content. Changing the content of a variable does not automatically save those changes back to the variable, this needs to be done explicitly!

```
numbers1 + 100 # not stored anywhere, just printed
```

```
[1] 105 103 106 108 102 101
```

```
numbers1 + numbers2 # why does this even work?
```

```
[1] 6 5 9 9 4 4
```

When combining variables of different length, the short one is recycled, so the numbers2 is added to the first 3 elements of numbers2, then is reused and added to the remaining 3 elements. If the length of the longer is not a multiple of the shorter, there will be a warning.

```
c(2,4,6,8) + 1
```

```
[1] 3 5 7 9
```

```
c(2,4,6,8) + c(1,2)
```

```
[1] 3 6 7 10
```

```
c(2,4,6,8) + c(1,2,3)
```

Warning in c(2, 4, 6, 8) + c(1, 2, 3): longer object length is not a multiple of shorter object length

```
[1] 3 6 9 9
```

2.4 Functions

2.4.1 Function usage

Functions have the same naming rules as variables, but the name is always followed by opening/closing round brackets, within those brackets function parameters/arguments can be specified to provide input or control behavior:

FunctionName(parameter1=x1,parameter2=x2,x3,...)

Most functions have named arguments, those argument names may be omitted as long as parameter values are supplied in the defined order. Arguments may have predefined default values, see *help!* Some functions like *c()* use unnamed arguments.

```
c("my", "name") # unnamed
```

```
[1] "my"    "name"
```

```
# ?mean  
mean(x = c(3,5,7,NA)) #using default parameters
```

```
[1] NA
```

```
mean(x = c(3,5,7,NA),na.rm = TRUE) #overriding default parameter
```

```
[1] 5
```

```
mean(na.rm = TRUE, x=c(3,5,7,NA)) # changed order of arguments
```

```
[1] 5
```

```
mean(c(3,5,7,NA), na.rm = TRUE) # name of 1st argument omitted
```

```
[1] 5
```

```
sd(c(3,5,7,NA), na.rm = TRUE)
```

```
[1] 2
```

```
# same logic as mean, partially the same arguments  
median(1:100, TRUE)
```

```
[1] 50.5
```

```
# omitting arguments influences readability of a function, careful!  
t <- c(1:10,100)  
quantile(t,probs = c(.2,.8))
```

```
20% 80%  
3     9
```

```
# putting text elements together  
paste("some text", 1:3)
```

```
[1] "some text 1" "some text 2" "some text 3"
```

```
paste0("some text", 1:3)
```

```
[1] "some text1" "some text2" "some text3"
```

```
paste("some text", 1:3, sep = ": ")
```

```
[1] "some text: 1" "some text: 2" "some text: 3"
```

```
paste("some text", 1:3,sep = ": ", collapse = "; ")
```

```
[1] "some text: 1; some text: 2; some text: 3"
```

```
paste("some text", 1:3,sep = ": ", collapse = "\n") |> cat()
```

```
some text: 1  
some text: 2  
some text: 3
```

```
paste("mean", "SD", sep = " \u00b1 ")
```

```
[1] "mean ± SD"
```

2.4.2 Functions combined

Functions often just solve one problem or task, so usually we need to combine them. This can be done by nesting or piping. Piping makes reading/understanding scripts easier, as it shows order of functions:

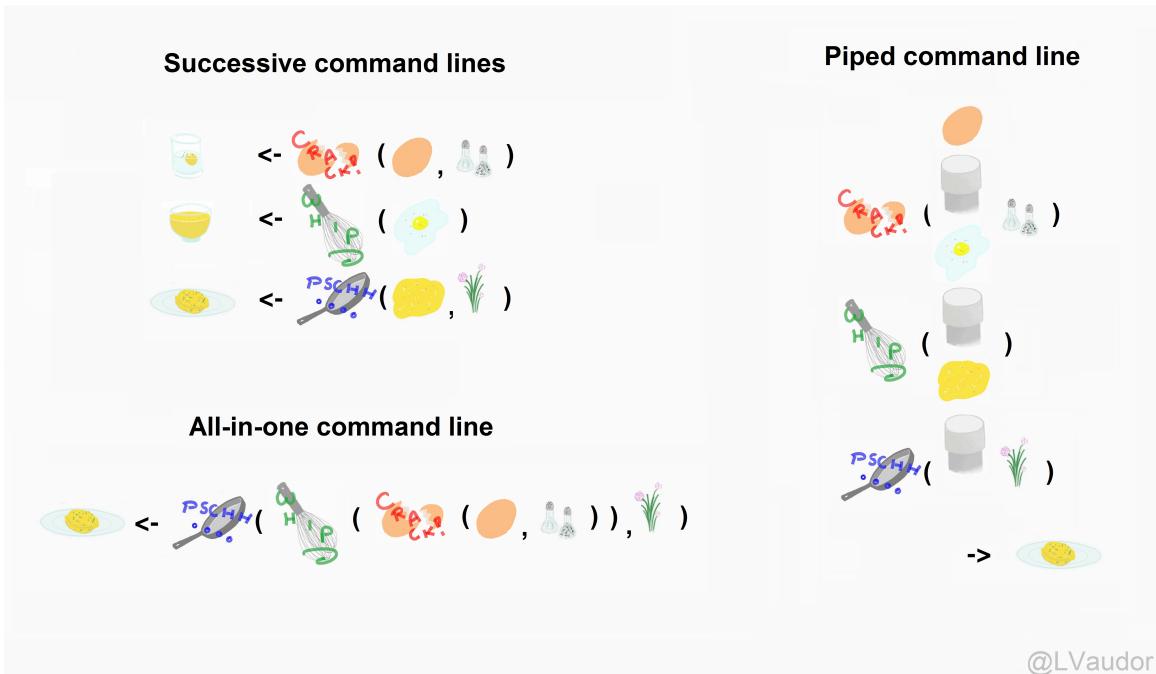


Figure 2.1: *Piping functions*

```
# functions may be nested:
floor(
  as.numeric(
    Sys.Date() -
    as.Date("1985/12/10"))/
  365.25)
```

[1] 38

```
# or (usually better) piped:
mtcars |> # inbuild example data, use F1!
  mutate(am=factor(am,
    levels=c(0,1),
    labels=c("automatic",
      "manual"))) |> #change into better class
  filter(vs==1) |> #filter out V-shaped
  group_by(am) |> # ask for grouped analysis
  summarize(across(.cols = c(wt, mpg, qsec, disp),
    .fns = meansd)) |>
  pivot_longer(cols = -am, names_to = "Measure") |> # put variables in rows
  pivot_wider(id_cols = Measure, names_from = am, #put groups in cols
    values_from = value)
```

```
# A tibble: 4 x 3
  Measure automatic manual
  <chr>    <chr>     <chr>
1 wt       3.2 ± 0.3 2.0 ± 0.4
2 mpg      21 ± 2    28 ± 5
3 qsec     20 ± 1    19 ± 1
4 disp     175 ± 49   90 ± 19
```

If a sequence of functions is used often, combining them into a new function is advisable, e.g. this combination of descriptive and test statistics:

```
# can be combined into higher order functions:
compare2numvars(data = mtcars,
                  dep_vars = c("mpg", "wt", "qsec"),
                  indep_var = "am",
                  add_n = TRUE,
                  gaussian = TRUE)
```

```
# A tibble: 3 x 5
  Variable desc_all          `am 0`          `am 1`          p
  <fct>    <chr>            <chr>            <chr>            <chr>
1 mpg       20 ± 6 [n=32]    17 ± 4 [n=19]    24 ± 6 [n=13]  0.001
2 wt        3.2 ± 1.0 [n=32] 3.8 ± 0.8 [n=19]  2.4 ± 0.6 [n=13] 0.001
3 qsec      18 ± 2 [n=32]   18 ± 2 [n=19]   17 ± 2 [n=13]  0.206
```

2.4.3 Writing functions

```
#FunctionName<-function(parameters...){definition}
division <- function(x, y){
  return(x/y)
}
(Sys.Date()-as.Date("1958/12/10")) |>
  as.numeric() |>
  division(y = 365.25, x=_) |>
  floor()
```

```
[1] 65
```

```
Mymean<-function(values)
{
  return(base::mean(values, na.rm=TRUE))
}
```

```

mark_sign<-function(SignIn) {
  SignIn <- as.numeric(SignIn)
  if(is.na(SignIn)){
    SignOut<-"wrong input, stupido!"
  } else {
    # if (!is.na(SignIn)) {
    SignOut<-"n.s."
    if(SignIn<=0.1) {SignOut<-"+"}
    if(SignIn<=0.05) {SignOut<-"*"}
    if(SignIn<=0.01) {SignOut<-"**"}
    if(SignIn<=0.001) {SignOut<-"***"}
    }
    return(SignOut)
  }
}

mark_sign(SignIn=0.035)

```

[1] "*"

```
mark_sign(SignIn="0.35")
```

[1] "n.s."

```
mark_sign(SignIn = "p=3,5%")  #wrong input
```

Warning in mark_sign(SignIn = "p=3,5%"): NAs introduced by coercion

[1] "wrong input, stupido!"

different implementation

```

markSign0 <- function(SignIn, plabel = c("n.s.", "+", "*", "**", "***")) {
  SignIn <- suppressWarnings(
    as.numeric(SignIn))
  SignOut <- cut(SignIn,
                  breaks = c(-Inf, .001, .01, .05, .1, 1),
                  labels = rev(plabel))
}
return(SignOut)

```

```
}
```

```
markSign0(SignIn=c(0.035, 0.00002, .234))
```

```
[1] *      ***  n.s.  
Levels: *** ** * + n.s.
```

```
markSign0(SignIn="0.35")
```

```
[1] n.s.  
Levels: *** ** * + n.s.
```

```
markSign0(SignIn = "p=3,5%")    #wrong input
```

```
[1] <NA>  
Levels: *** ** * + n.s.
```

```
#source("F:/Aktenschrank/Analysen/R/myfunctions.R")
```

2.5 More complex data types, created by functions

2.5.1 Matrix

A matrix is a 2-dimensional data structure, where all elements are of the same class.

2.5.1.1 Creation

```
my1.Matrix<-  
  matrix(data=1:12,  
         # nrow=4, # this is not needed, can be derived from data  
         ncol=3,  
         byrow=TRUE, # date are put into row 1 first  
         dimnames=list(paste0("row", 1:4),  
                       paste0("col", 1:3)))  
print(my1.Matrix)
```

```

    col1 col2 col3
row1    1    2    3
row2    4    5    6
row3    7    8    9
row4   10   11   12

```

```

data <- seq(from = 1, to = 100, by = 1) #1:100
nrow <- 10
matrix(data=data,
       nrow=nrow,
       byrow=FALSE, # data are put into column 1 first
       dimnames=list(paste0("row",1:nrow),
                     paste0("col",1:(length(data)/nrow)))) |>
head()

```

```

    col1 col2 col3 col4 col5 col6 col7 col8 col9 col10
row1    1   11   21   31   41   51   61   71   81   91
row2    2   12   22   32   42   52   62   72   82   92
row3    3   13   23   33   43   53   63   73   83   93
row4    4   14   24   34   44   54   64   74   84   94
row5    5   15   25   35   45   55   65   75   85   95
row6    6   16   26   36   46   56   66   76   86   96

```

```

my2.Matrix <- matrix(c(1,2,3, 11,12,13),
                      nrow = 2, ncol=3) #byrow=FALSE, specified but default
my2.Matrix

```

```

[,1] [,2] [,3]
[1,]    1    3   12
[2,]    2   11   13

```

2.5.1.2 Indexing

Addressing a matrix is done with [row_index, column_index]

```
my1.Matrix[2, 3] # Index:[row,column]
```

```
[1] 6
```

```
my1.Matrix[2,] # all columns
```

```
col1 col2 col3  
4      5      6
```

```
my1.Matrix[, 2] # all rows
```

```
row1 row2 row3 row4  
2      5      8      11
```

```
my1.Matrix[c(1, 3), -2] # exclude column 2
```

```
col1 col3  
row1    1    3  
row3    7    9
```

```
my1.Matrix[1,1] <- NA # Index can be used for writing as well
```

2.5.2 Data frame

A data frame has 2 dimensions, it can handle various data types (1 per columns). This structure is rather superseded by tibbles (see below).

2.5.2.1 Creation

Data frames are defined by creating and filling columns, functions can be used (and piped) to create content.

```
patientN<-15  
(myTable<-data.frame(  
  patientCode=paste0("pat",1:patientN),  
  Var1 = 1, # gets recycled  
  Var2 = NA_Date_)) |> head()
```

```
patientCode Var1 Var2  
1          pat1    1 <NA>  
2          pat2    1 <NA>  
3          pat3    1 <NA>  
4          pat4    1 <NA>  
5          pat5    1 <NA>  
6          pat6    1 <NA>
```

```
str(myTable)
```

```
'data.frame': 15 obs. of 3 variables:  
$ patientCode: chr "pat1" "pat2" "pat3" "pat4" ...  
$ Var1       : num 1 1 1 1 1 1 1 1 1 1 ...  
$ Var2       : Date, format: NA NA ...
```

```
set.seed(101)  
myTable<-data.frame(  
  patientCode=paste0("pat",1:patientN),  
  Age=runif(n=patientN,min=18,max=65) |> floor(),  
  Sex=factor(rep(x=NA,times=patientN),  
             levels=c("m","f")),  
  `sysRR (mmHg)`=round(rnorm(n=patientN,mean=140,sd=10)),  
  check.names = FALSE)  
head(myTable)
```

	patientCode	Age	Sex	sysRR (mmHg)
1	pat1	35	<NA>	142
2	pat2	20	<NA>	132
3	pat3	51	<NA>	122
4	pat4	48	<NA>	157
5	pat5	29	<NA>	144
6	pat6	32	<NA>	148

2.5.2.2 Indexing

Beside the numeric index, columns can be addressed by name. This can be done by either `dfname$colname` (for the content of a single column) or `dfname[, "colname"]` for 1 or more columns.

```
myTable[1:5,1]
```

```
[1] "pat1" "pat2" "pat3" "pat4" "pat5"
```

```
myTable$patientCode[1:5]
```

```
[1] "pat1" "pat2" "pat3" "pat4" "pat5"
```

```
myTable[1:5,"patientCode"]
```

```
[1] "pat1" "pat2" "pat3" "pat4" "pat5"
```

```
# returns vector of values for a single column, data.frame otherwise  
myTable["patientCode"] # returns df
```

```
patientCode  
1      pat1  
2      pat2  
3      pat3  
4      pat4  
5      pat5  
6      pat6  
7      pat7  
8      pat8  
9      pat9  
10     pat10  
11     pat11  
12     pat12  
13     pat13  
14     pat14  
15     pat15
```

```
columns<-c("Sex", "Age")  
myTable[1:5, columns]
```

```
Sex Age  
1 <NA> 35  
2 <NA> 20  
3 <NA> 51  
4 <NA> 48  
5 <NA> 29
```

```
myTable[1:5, c("patientCode", "Age")]
```

```
patientCode Age  
1      pat1 35  
2      pat2 20  
3      pat3 51  
4      pat4 48  
5      pat5 29
```

```
myTable[,1] <- paste0("Code", 1:patientN)
```

2.5.3 Tibble

Tibbles are a modern and efficient data structure that extends data frames, providing enhanced features and performance for data manipulation and analysis.

2.5.3.1 Creation

```
patientN <- 25
rawdata <- tibble(
  PatID=paste("P",1:patientN), # as in data.frame
  Sex=sample(x = c("male","female"), # random generator
             size = patientN,replace = TRUE,
             prob = c(.7,.3)),
  Ethnicity=sample(x = 1:6,
                   size = patientN,
                   replace = TRUE,
                   prob = c(.01,.01,.05,.03,.75,.15)),
  # random assignments
  `Given name`=randomNames(n = patientN,
                            gender = Sex,
                            # this is a reference to column Sex
                            ethnicity = Ethnicity,
                            which.names = "first"),
  `Family name`=randomNames(n = patientN,
                            ethnicity = Ethnicity,
                            which.names = "last"),
  Treatment=sample(x = c("Placebo","Verum"),
                    size = patientN,
                    replace = TRUE),
  `sysRR (mmHg)`=round(rnorm(n=patientN,mean=140,sd=10))-
    (Treatment=="Verum")*15,
  `diaRR (mmHg)`=round(rnorm(n=patientN,mean=80,sd=10))-
    (Treatment=="Verum")*10,
  HR=round(rnorm(n=patientN,mean=90,sd=7)))
rawdata
```

```
# A tibble: 25 x 9
  PatID Sex   Ethnicity `Given name` `Family name` Treatment `sysRR (mmHg)` `diaRR (mmHg)`
  <chr> <chr>     <int> <chr>       <chr>       <chr>           <dbl>
1 P 1   male      5 Ian        Roy      Placebo        128
```

```

2 P 2   male      3 Dametrious    Martin      Placebo      116
3 P 3   female     5 Alyxandra    Fisher      Verum       120
4 P 4   female     6 Musfira      el-Karimi    Verum       130
5 P 5   male       6 Saleel       al-Bey      Placebo      135
6 P 6   male       5 Kahner       Melott      Verum       148
7 P 7   male       5 Skylar       Burgess     Verum       137
8 P 8   male       5 Michael      Harper      Placebo      139
9 P 9   female     5 Julia        Tovrea     Placebo      154
10 P 10  male      4 Eric         Barreras    Verum       113
# i 15 more rows
# i 2 more variables: `diaRR (mmHg)` <dbl>, HR <dbl>

```

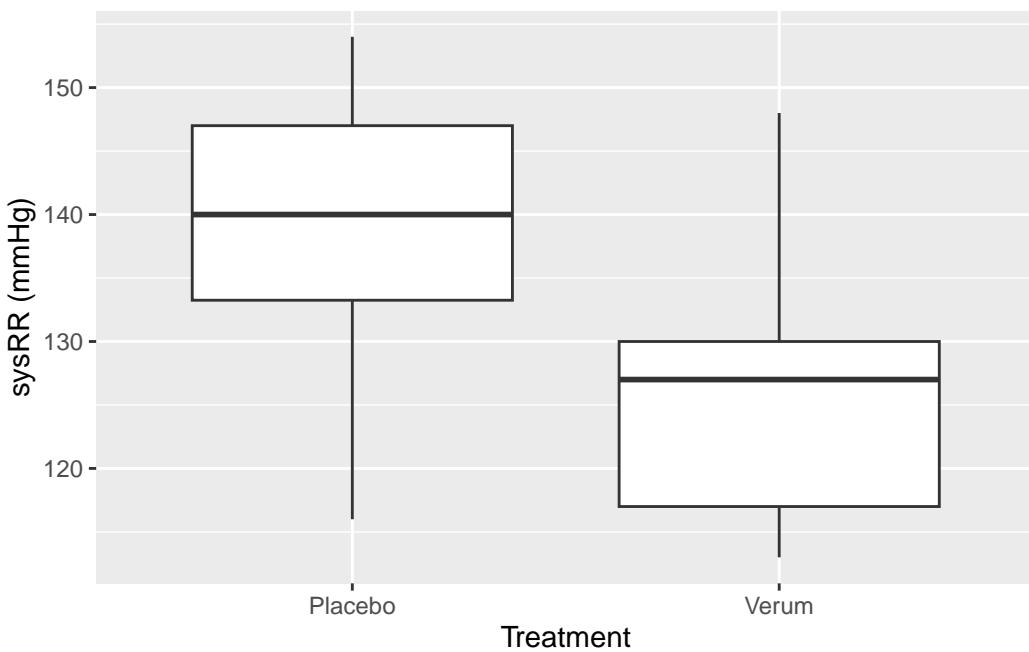
```
colnames(rawdata)
```

```
[1] "PatID"          "Sex"           "Ethnicity"      "Given name"    "Family name"
[6] "Treatment"     "sysRR (mmHg)"  "diaRR (mmHg)"  "HR"
```

```
cn() # shortcut from wrappedtools
```

```
[1] "PatID"          "Sex"           "Ethnicity"      "Given name"    "Family name"
[6] "Treatment"     "sysRR (mmHg)"  "diaRR (mmHg)"  "HR"
```

```
# example of data management for a tibble, recoding ethnicity:
rawdata <- rawdata |>
  mutate(Ethnicity=factor(
    Ethnicity, levels = 1:6,
    labels= c(
      "American Indian or Native Alaskan",
      "Asian or Pacific Islander",
      "Black (not Hispanic)",
      "Hispanic",
      "White (not Hispanic)",
      "Middle-Eastern, Arabic")))
# quick visual inspection
ggplot(rawdata,aes(x = Treatment,y = `sysRR (mmHg)`))+
  geom_boxplot()
```



2.5.3.2 Indexing

The same rules as for the data frame, but more consistent behavior.

```
rawdata[1:5,1:2]
```

```
# A tibble: 5 x 2
  PatID Sex
  <chr> <chr>
1 P 1   male
2 P 2   male
3 P 3   female
4 P 4   female
5 P 5   male
```

```
rawdata[,6]
```

```
# A tibble: 25 x 1
  Treatment
  <chr>
1 Placebo
2 Placebo
3 Verum
```

```
4 Verum
5 Placebo
6 Verum
7 Verum
8 Placebo
9 Placebo
10 Verum
# i 15 more rows
```

```
rawdata[6]
```

```
# A tibble: 25 x 1
  Treatment
  <chr>
1 Placebo
2 Placebo
3 Verum
4 Verum
5 Placebo
6 Verum
7 Verum
8 Placebo
9 Placebo
10 Verum
# i 15 more rows
```

```
rawdata[[6]]
```

```
[1] "Placebo" "Placebo" "Verum"    "Verum"    "Placebo" "Verum"    "Verum"
[8] "Placebo" "Placebo" "Verum"    "Verum"    "Verum"   "Verum"    "Placebo"
[15] "Verum"   "Verum"   "Verum"    "Placebo"  "Placebo"  "Verum"    "Placebo"
[22] "Placebo" "Placebo" "Placebo"  "Verum"
```

```
rawdata$`Family name`
```

```
[1] "Roy"          "Martin"        "Fisher"        "el-Karimi"
[5] "al-Bey"       "Melott"        "Burgess"       "Harper"
[9] "Tovrea"      "Barreras"     "Klamerus"     "al-Satter"
[13] "al-Sultana"  "Yi"           "Helm"         "Molina-Peinado"
[17] "Spilsted"    "Egan"         "Thompson"     "Schauss"
[21] "Owens"        "Vick"         "Reeves"        "Chesney"
[25] "Minnillo"
```

Differences in addressing data frames and tibbles:

- *tibble and [always returns tibble*
- *tibble and [[always returns vector*
- *data.frame and [may return data.frame (if >1 column) or vector*
- *data.frame and [[always returns vector*

```
rawdata_df <- as.data.frame(rawdata)
rawdata[2] #returns Tibble with 1 column
```

```
# A tibble: 25 x 1
  Sex
  <chr>
 1 male
 2 male
 3 female
 4 female
 5 male
 6 male
 7 male
 8 male
 9 female
10 male
# i 15 more rows
```

```
rawdata[[2]] #returns vector
```

```
[1] "male"    "male"    "female"   "female"   "male"    "male"    "male"    "male"
[9] "female"   "male"    "female"   "male"     "male"    "male"    "male"    "female"
[17] "female"   "male"    "female"   "female"   "male"    "male"    "male"    "female"
[25] "female"
```

```
rawdata[,2] #returns Tibble with 1 column
```

```
# A tibble: 25 x 1
  Sex
  <chr>
 1 male
 2 male
 3 female
 4 female
```

```
5 male
6 male
7 male
8 male
9 female
10 male
# i 15 more rows
```

```
rawdata[,2:3] #returns tibble with 2 columns
```

```
# A tibble: 25 x 2
  Sex    Ethnicity
  <chr>  <fct>
1 male   White (not Hispanic)
2 male   Black (not Hispanic)
3 female White (not Hispanic)
4 female Middle-Eastern, Arabic
5 male   Middle-Eastern, Arabic
6 male   White (not Hispanic)
7 male   White (not Hispanic)
8 male   White (not Hispanic)
9 female White (not Hispanic)
10 male  Hispanic
# i 15 more rows
```

```
rawdata_df[2] #returns DF with 1 column
```

```
Sex
1 male
2 male
3 female
4 female
5 male
6 male
7 male
8 male
9 female
10 male
11 female
12 male
13 male
14 male
15 male
```

```

16 female
17 female
18 male
19 female
20 female
21 female
22 male
23 male
24 female
25 female

rawdata_df[[2]] #returns vector

[1] "male"    "male"    "female"  "female"  "male"    "male"    "male"    "male"
[9] "female"  "male"    "female"  "male"    "male"    "male"    "male"    "female"
[17] "female"  "male"    "female"  "female"  "female"  "male"    "male"    "female"
[25] "female"

rawdata_df[,2] #returns vector

[1] "male"    "male"    "female"  "female"  "male"    "male"    "male"    "male"
[9] "female"  "male"    "female"  "male"    "male"    "male"    "male"    "female"
[17] "female"  "male"    "female"  "female"  "female"  "male"    "male"    "female"
[25] "female"

rawdata_df[,2:3] #returns DF with 2 columns

      Sex           Ethnicity
1   male     White (not Hispanic)
2   male     Black (not Hispanic)
3 female    White (not Hispanic)
4 female Middle-Eastern, Arabic
5   male     Middle-Eastern, Arabic
6   male     White (not Hispanic)
7   male     White (not Hispanic)
8   male     White (not Hispanic)
9 female    White (not Hispanic)
10  male          Hispanic
11 female   White (not Hispanic)
12  male Middle-Eastern, Arabic
13  male Middle-Eastern, Arabic
14  male Asian or Pacific Islander

```

```

15 male      White (not Hispanic)
16 female    Hispanic
17 female    White (not Hispanic)
18 male      White (not Hispanic)
19 female    White (not Hispanic)
20 female    White (not Hispanic)
21 female    White (not Hispanic)
22 male      Black (not Hispanic)
23 male      White (not Hispanic)
24 female    White (not Hispanic)
25 female    White (not Hispanic)

```

There are specific functions for picking columns or rows, especially useful in pipes.

```
rawdata |> select(PatID:Ethnicity, `sysRR (mmHg)` :HR)
```

```

# A tibble: 25 x 6
  PatID Sex   Ethnicity `sysRR (mmHg)` `diaRR (mmHg)`   HR
  <chr> <chr> <fct>        <dbl>        <dbl> <dbl>
1 P 1   male  White (not Hispanic)     128          87    88
2 P 2   male  Black (not Hispanic)    116          72    82
3 P 3   female White (not Hispanic)   120          60    93
4 P 4   female Middle-Eastern, Arabic 130          76    82
5 P 5   male  Middle-Eastern, Arabic  135          60   100
6 P 6   male  White (not Hispanic)    148          85    85
7 P 7   male  White (not Hispanic)    137          54    98
8 P 8   male  White (not Hispanic)    139          95    94
9 P 9   female White (not Hispanic)   154          71    83
10 P 10  male  Hispanic                113          74    82
# i 15 more rows

```

```
rawdata |> select(PatID:Ethnicity, `sysRR (mmHg)` :HR) |> slice(1:5)
```

```

# A tibble: 5 x 6
  PatID Sex   Ethnicity `sysRR (mmHg)` `diaRR (mmHg)`   HR
  <chr> <chr> <fct>        <dbl>        <dbl> <dbl>
1 P 1   male  White (not Hispanic)     128          87    88
2 P 2   male  Black (not Hispanic)    116          72    82
3 P 3   female White (not Hispanic)   120          60    93
4 P 4   female Middle-Eastern, Arabic 130          76    82
5 P 5   male  Middle-Eastern, Arabic  135          60   100

```

```
rawdata |> select(contains("RR", ignore.case = F))
```

```
# A tibble: 25 x 2
`sysRR (mmHg)` `diaRR (mmHg)`
<dbl>          <dbl>
1      128          87
2      116          72
3      120          60
4      130          76
5      135          60
6      148          85
7      137          54
8      139          95
9      154          71
10     113          74
# i 15 more rows
```

```
rawdata |> select(ends_with("r"))
```

```
# A tibble: 25 x 1
HR
<dbl>
1 88
2 82
3 93
4 82
5 100
6 85
7 98
8 94
9 83
10 82
# i 15 more rows
```

```
rawdata |> select(-contains("name"))
```

```
# A tibble: 25 x 7
  PatID Sex   Ethnicity Treatment `sysRR (mmHg)` `diaRR (mmHg)` HR
  <chr> <chr>  <fct>    <chr>          <dbl>          <dbl> <dbl>
1 P 1   male   White (not Hispan~ Placebo          128          87  88
2 P 2   male   Black (not Hispan~ Placebo          116          72  82
3 P 3   female White (not Hispan~ Verum           120          60  93
```

```

4 P 4   female Middle-Eastern, A~ Verum           130      76     82
5 P 5   male   Middle-Eastern, A~ Placebo        135      60     100
6 P 6   male   White (not Hispan~ Verum         148      85     85
7 P 7   male   White (not Hispan~ Verum         137      54     98
8 P 8   male   White (not Hispan~ Placebo        139      95     94
9 P 9   female White (not Hispan~ Placebo        154      71     83
10 P 10 male   Hispanic             Verum       113      74     82
# i 15 more rows

```

```
rawdata |> select(`sysRR (mmHg)`)
```

```

# A tibble: 25 x 1
`sysRR (mmHg)`
<dbl>
1      128
2      116
3      120
4      130
5      135
6      148
7      137
8      139
9      154
10     113
# i 15 more rows

```

```
rawdata |> select(contains("r"), -contains("rr"))
```

```

# A tibble: 25 x 2
Treatment    HR
<chr>      <dbl>
1 Placebo     88
2 Placebo     82
3 Verum       93
4 Verum       82
5 Placebo    100
6 Verum       85
7 Verum       98
8 Placebo     94
9 Placebo     83
10 Verum      82
# i 15 more rows

```

```
rawdata |> pull(`sysRR (mmHg)`)
```

```
[1] 128 116 120 130 135 148 137 139 154 113 118 117 117 127 143 117 135 117 147 127  
[20] 130 136 141 150 147 130
```

Exercise: Think of a cruet_stand / Gewürzmenage

- define `n_elements <- 5*10^3`
- create a tibble “menage” with columns `saltshaker`, `peppercaster` and `n_elements` each for `saltgrain` and `pepperflake`
- print `saltshaker`
- print `salt`
- print 100 `saltgrains`



2.5.4 List

While `matrix`, `data.frames`, and `tibbles` always have the same number of rows for each column, sometimes different lengths are required. A list can handle all kinds of data with different number of elements for each sublist. This is a typical output format for statistical functions and is useful for collecting e.g. result tables or figures. Package `rlist` provides useful tools.

2.5.4.1 Creation

```
shopping<-list(beverages=c("beer","water",
                             "gin(not Gordons!!)","tonic"),
                 snacks=c("chips","pretzels"),
                 nonfood=c("DVDs","Akku"),
                 mengen=1:10,
                 volumen=rnorm(50,100,2))
shopping
```

```
$beverages
[1] "beer"          "water"         "gin(not Gordons!!)"
[4] "tonic"

$snacks
[1] "chips"        "pretzels"

$nonfood
[1] "DVDs" "Akku"

$mengen
[1] 1 2 3 4 5 6 7 8 9 10

$volumen
 [1] 101.98092 99.72118 101.25978 99.50115 99.88413 103.65050 100.35412
 [8] 103.72203 97.45847 98.51527 98.86176 100.25617 99.18075 101.11364
[15] 99.49699 99.67630 99.17729 100.27251 100.64437 98.00664 99.25581
[22] 100.43009 100.20727 100.25817 98.48912 96.71237 96.46227 101.04724
[29] 96.47107 100.85070 97.64126 100.82651 102.66924 98.58853 99.72314
[36] 100.51849 98.90033 101.05662 100.26360 97.92360 100.89800 98.84879
[43] 101.56033 98.08456 100.80067 101.36969 94.41230 100.80553 99.60254
[50] 100.62478
```

```
shopping$snacks
```

```
[1] "chips"      "pretzels"
```

2.5.4.2 Indexing

```
shopping[1]    #returns a list
```

```
$beverages
[1] "beer"           "water"          "gin(not Gordons!!)"
[4] "tonic"
```

```
shopping[[1]] #returns a vector
```

```
[1] "beer"           "water"          "gin(not Gordons!!)"
[4] "tonic"
```

```
str(shopping[1])
```

```
List of 1
$ beverages: chr [1:4] "beer" "water" "gin(not Gordons!!)" "tonic"
```

```
str(shopping[[1]])
```

```
chr [1:4] "beer" "water" "gin(not Gordons!!)" "tonic"
```

```
str(shopping$beverages)
```

```
chr [1:4] "beer" "water" "gin(not Gordons!!)" "tonic"
```

```
shopping[1][2]
```

```
$<NA>
NULL
```

```
shopping[[1]][2]
```

```
[1] "water"
```

```
shopping$beverages[2]
```

```
[1] "water"
```

```
t_out <- t.test(x = rnorm(n = 20, mean = 10, sd = 1),  
                 y = rnorm(20, 12, 1))  
str(t_out)
```

```
List of 10  
$ statistic : Named num -5.74  
..- attr(*, "names")= chr "t"  
$ parameter : Named num 36.1  
..- attr(*, "names")= chr "df"  
$ p.value   : num 1.52e-06  
$ conf.int  : num [1:2] -2.35 -1.12  
..- attr(*, "conf.level")= num 0.95  
$ estimate  : Named num [1:2] 10.2 11.9  
..- attr(*, "names")= chr [1:2] "mean of x" "mean of y"  
$ null.value: Named num 0  
..- attr(*, "names")= chr "difference in means"  
$ stderr    : num 0.302  
$ alternative: chr "two.sided"  
$ method    : chr "Welch Two Sample t-test"  
$ data.name  : chr "rnorm(n = 20, mean = 10, sd = 1) and rnorm(20, 12, 1)"  
- attr(*, "class")= chr "htest"
```

```
t_out$p.value
```

```
[1] 1.523729e-06
```

```
t_out |> pluck("p.value")
```

```
[1] 1.523729e-06
```

2.6 Control structures

2.6.1 Loops

Repetitive tasks like computation of descriptive statistics over many variables or repeated simulations of data can be declared inside of a loop. There are functions (like `summarize(across(...))`) that create those repetitions internally, but often doing this explicitly improves readability or helps solving various tasks like describing AND plotting data.

2.6.1.1 *for-loop*

In a *for-loop*, we can define the number of runs in advance, e.g. by the number of variables to describe. There are 2 ways/styles, how to define this number:

1. by creating an index variable with an integer vector 1,2,3, ... number of runs/variables
2. by creating an index containing e.g. colnames

```
# integer index
print("### Game of Loops ###")
```

```
[1] "### Game of Loops ###"
```

```
for(season_i in 1:3) {
  cat(paste("GoL Season",season_i,"\n"))
  for(episode_i in 1:5) {
    cat(paste0("  GoL S.",season_i,
               " Episode ",episode_i,"\n"))
  }
  cat("\n")
}
```

```
GoL Season 1
GoL S.1 Episode 1
GoL S.1 Episode 2
GoL S.1 Episode 3
GoL S.1 Episode 4
GoL S.1 Episode 5
```

```
GoL Season 2
GoL S.2 Episode 1
GoL S.2 Episode 2
GoL S.2 Episode 3
GoL S.2 Episode 4
GoL S.2 Episode 5
```

```
GoL Season 3
GoL S.3 Episode 1
GoL S.3 Episode 2
GoL S.3 Episode 3
GoL S.3 Episode 4
GoL S.3 Episode 5
```

```

# content index
## names of elements
for(col_i in colnames(rawdata)){
  print(col_i)
}

```

```

[1] "PatID"
[1] "Sex"
[1] "Ethnicity"
[1] "Given name"
[1] "Family name"
[1] "Treatment"
[1] "sysRR (mmHg)"
[1] "diaRR (mmHg)"
[1] "HR"

```

```

## content of elements
for(col_i in shopping){
  print(col_i)
}

```

```

[1] "beer"           "water"          "gin(not Gordons!!)"
[4] "tonic"
[1] "chips"         "pretzels"
[1] "DVDs"          "Akku"
[1] 1 2 3 4 5 6 7 8 9 10
[1] 101.98092 99.72118 101.25978 99.50115 99.88413 103.65050 100.35412
[8] 103.72203 97.45847 98.51527 98.86176 100.25617 99.18075 101.11364
[15] 99.49699 99.67630 99.17729 100.27251 100.64437 98.00664 99.25581
[22] 100.43009 100.20727 100.25817 98.48912 96.71237 96.46227 101.04724
[29] 96.47107 100.85070 97.64126 100.82651 102.66924 98.58853 99.72314
[36] 100.51849 98.90033 101.05662 100.26360 97.92360 100.89800 98.84879
[43] 101.56033 98.08456 100.80067 101.36969 94.41230 100.80553 99.60254
[50] 100.62478

```

```

# automatic creation of integer index from elements
#for(col_i in 1:ncol(rawdata)){
  for(col_i in seq_along(colnames(rawdata))){
    print(colnames(rawdata)[col_i])
  }
}

```

```

[1] "PatID"

```

```
[1] "Sex"  
[1] "Ethnicity"  
[1] "Given name"  
[1] "Family name"  
[1] "Treatment"  
[1] "sysRR (mmHg)"  
[1] "diaRR (mmHg)"  
[1] "HR"
```

```
# edge-case of 0 elements -> 0 runs  
for(col_i in seq_len(0)){  
  print(colnames(rawdata)[col_i])  
}
```

2.6.1.2 *while-loops*

If not number of repetitions is know, but a condition.

```
test <- 0  
while(test<10){  
  print(test)  
  test <- test + 1  
}
```

```
[1] 0  
[1] 1  
[1] 2  
[1] 3  
[1] 4  
[1] 5  
[1] 6  
[1] 7  
[1] 8  
[1] 9
```

2.6.2 *Conditions*

2.6.2.1 *if else*

We can run code if condition(s) are true:

```
sex<-"female"
if(sex=="male") {
  print("Male")
} else {
  print("Female")
}
```

```
[1] "Female"
```

```
if(sex=="male") {
  print("Male")
}

if(sex!="male"){
  print("Female")
}
```

```
[1] "Female"
```

```
testvar <- 4
if(testvar %in% c(1,3,5)){
  print("uneven")
} else {
  print("probably even")
}
```

```
[1] "probably even"
```

```
TRUE & FALSE # AND
```

```
[1] FALSE
```

```
all(TRUE, FALSE)
```

```
[1] FALSE
```

```
(1<10) & (sex=="male")
```

```
[1] FALSE
```

```
all(1<10,sex=="male")
```

```
[1] FALSE
```

```
TRUE | FALSE # OR
```

```
[1] TRUE
```

```
any(TRUE, FALSE)
```

```
[1] TRUE
```

```
(1>10) | (1<5)
```

```
[1] TRUE
```

```
age <- 5  
(sex=="female" & age<=12) | (sex=="male" & age <= 14)
```

```
[1] TRUE
```

```
any(all(sex=="female",age<=12),  
    all(sex=="male", age <= 14))
```

```
[1] TRUE
```

2.6.2.2 *ifelse*

We can get text conditionally:

```
print(ifelse(test = sex=="male",  
            yes = "is male",  
            no = "is female"))
```

```
[1] "is female"
```

```

p <- .012
paste0("That is ",
       ifelse(test = p<=.05, yes = "", no = "not "),
       "significant")

```

```
[1] "That is significant"
```

```

if(p>=.05){
  sign_out <- "not "
} else {
  sign_out <- ""
}
paste0("That is ",
       sign_out,
       "significant")

```

```
[1] "That is significant"
```

2.6.2.3 `case_when` / `case_match`

When there are many tests to do, `case_when` or `case_match` are nice replacements for `ifelse`. While `case_when` allows complex conditions, `case_match` is used for for simple comparisons:

```

rawdata <- mutate(.data = rawdata,
  Hypertension=case_when(
    `sysRR (mmHg)`<120 & `diaRR (mmHg)`<70 ~ "normotensive",
    `sysRR (mmHg)`<160 & `diaRR (mmHg)`<=80 ~ "borderline",
    .default = "hypertensive"),
  `prescribe something?` = case_match(
    Hypertension,
    "hypertensive" ~ "yes",
    "borderline" ~ "possibly",
    "normotensive" ~ "no"))
rawdata |>
  select(contains("RR"),Hypertension, contains("pres"))

```

```

# A tibble: 25 x 4
`sysRR (mmHg)` `diaRR (mmHg)` Hypertension `prescribe something?`
<dbl>          <dbl> <chr>           <chr>
1            128             87 hypertensive yes

```

```
2      116    72 borderline  possibly
3      120    60 borderline  possibly
4      130    76 borderline  possibly
5      135    60 borderline  possibly
6      148    85 hypertensive yes
7      137    54 borderline  possibly
8      139    95 hypertensive yes
9      154    71 borderline  possibly
10     113    74 borderline  possibly
# i 15 more rows
```

3 Importing data

```
pacman::p_load(conflicted,tidyverse, wrappedtools, readxl)
```

3.1 Import from text files (.txt, .csv)

3.2 Import from Excel

3.2.1 Tidy Excel files

```
rawdata <- read_excel(path = "data/Medtest_e.xlsx") |>
  rename_with(.fn = ~str_replace_all(.x,pattern="_",replacement=" ")) |>
  rename_with(.fn=str_to_title,
              .cols = !contains(c("BP","BMI","NY"))) |>
  rename(~`Size (cm)`=Size, #newname=oldname
        ~`Weight (kg)`=Weight) |>
  select(-`Sex M`)
  saveRDS(rawdata,file = "data/rawdata.rds")
```

3.2.2 Excel file with units row

1. Import names section and data section separately
2. Loop over all columns
 1. test for existence of unit, if not NA
 2. paste 1st row, ” [“, 2nd row,”]”
3. Use 1st row as colnames for data

```
cn_temp <- read_excel(path = "data/Medtest_e.xlsx",
                      range = "A1:Y2",col_names = FALSE,
                      sheet = 2)
```

```

New names:
* `` -> `...1`
* `` -> `...2`
* `` -> `...3`
* `` -> `...4`
* `` -> `...5`
* `` -> `...6`
* `` -> `...7`
* `` -> `...8`
* `` -> `...9`
* `` -> `...10`
* `` -> `...11`
* `` -> `...12`
* `` -> `...13`
* `` -> `...14`
* `` -> `...15`
* `` -> `...16`
* `` -> `...17`
* `` -> `...18`
* `` -> `...19`
* `` -> `...20`
* `` -> `...21`
* `` -> `...22`
* `` -> `...23`
* `` -> `...24`
* `` -> `...25`

```

```

for(col_i in colnames(cn_temp)){
  if(!is.na(cn_temp |> slice(2) |> pull(col_i))){
    cn_temp[1,col_i] <-
      paste0(cn_temp[1,col_i], " [", cn_temp[2,col_i], "]")
  }
}

rawdata <- read_excel(path = "data/Medtest_e.xlsx",
                      skip = 2, col_names = FALSE,
                      sheet = 2)

```

```

New names:
* `` -> `...1`
* `` -> `...2`
* `` -> `...3`
* `` -> `...4`
* `` -> `...5`
* `` -> `...6`

```

```
* `` -> `...7`  
* `` -> `...8`  
* `` -> `...9`  
* `` -> `...10`  
* `` -> `...11`  
* `` -> `...12`  
* `` -> `...13`  
* `` -> `...14`  
* `` -> `...15`  
* `` -> `...16`  
* `` -> `...17`  
* `` -> `...18`  
* `` -> `...19`  
* `` -> `...20`  
* `` -> `...21`  
* `` -> `...22`  
* `` -> `...23`  
* `` -> `...24`  
* `` -> `...25`
```

```
colnames(rawdata) <- cn_temp[1,]
```

3.3 Import from SPSS

3.4 Import from SAS

4 Changing structure wide <-> long

When working with repeated measures (e.g. follow-ups or changes over shorter periods of time) there are two typical formats:

1. wide data:

ID	Var1Time1	Var1Time2	Var2Time1	Var2Time2
P1				
P2				
P3				

2. long data

ID	Time	Var1	Var2
P1	1		
P1	2		
P2	1		
P2	2		
P3	1		
P3	2		

While long data can be seen as the tidier version and is necessary for many statistical procedures, the wide format makes computation of differences and procedures as the t-test for dependent samples easier. Package `tidyverse` provides the functions `pivot_wider` and `pivot_longer` for conversations between those forms. Another use-case is the plotting of several variables into ggplot facets, which can be achieved by combining those variables into a single column. Summarizing several variables and grouped data may result in a wide table with groups as rows and variables as columns, contrary to the common opposite form, another use-case.

There are many examples and explanations in the vignette:

<https://tidyverse.org/articles/pivot.html>

```
pacman::p_load(conflicted,tidyverse, wrappedtools)
```

Example 1: single repeated measure

```

n <- 3
wide_data <- tibble(ID = paste("P", 1:n),
                      Var1 = LETTERS[1:n],
                      Var2Time1 = rnorm(n = n, mean = 100, sd = 15),
                      Var2Time2 = Var2Time1 + rnorm(n, 10, 5))
wide_data

```

```

# A tibble: 3 x 4
  ID    Var1  Var2Time1  Var2Time2
  <chr> <chr>     <dbl>      <dbl>
1 P 1    A        87.2       94.1
2 P 2    B        91.7      105.
3 P 3    C        78.8       86.8

```

```

long_data <- pivot_longer(
  data = wide_data,
  cols = contains("Time")
)
long_data

```

```

# A tibble: 6 x 4
  ID    Var1   name     value
  <chr> <chr> <chr>     <dbl>
1 P 1    A     Var2Time1  87.2
2 P 1    A     Var2Time2  94.1
3 P 2    B     Var2Time1  91.7
4 P 2    B     Var2Time2 105.
5 P 3    C     Var2Time1  78.8
6 P 3    C     Var2Time2  86.8

```

Example 2: several repeated measures

```

wide_data <- tibble(ID = paste("P", 1:n),
                      Var1Time1 = rnorm(n = n, mean = 100, sd = 15),
                      Var1Time2 = Var1Time1 + rnorm(n, 10, 5),
                      Var2Time1 = rnorm(n = n, mean = 10, sd = 2),
                      Var2Time2 = Var2Time1 + rnorm(n, 0, 1),
                      Var3 = LETTERS[1:n])
wide_data

```

```

# A tibble: 3 x 6
  ID    Var1Time1  Var1Time2  Var2Time1  Var2Time2  Var3
  <chr>     <dbl>      <dbl>     <dbl>      <dbl> <chr>
1 P 1    100.0      110.0     100.0      102.0 A
2 P 2    100.0      110.0     100.0      102.0 B
3 P 3    100.0      110.0     100.0      102.0 C

```

	<chr>	<dbl>	<dbl>	<dbl>	<dbl> <chr>
1	P 1	96.7	111.	8.50	8.39 A
2	P 2	106.	111.	7.65	5.72 B
3	P 3	98.3	109.	12.0	13.3 C

```
# version with intermediate step:
very_long_data <- pivot_longer(
  data = wide_data,
  cols = contains("Time"),
  names_to = c("Variable", "Time"),
  names_pattern = "(Var\\d+)(Time[12])",
  values_to = "Value"
)
very_long_data
```

```
# A tibble: 12 x 5
  ID    Var3 Variable Time   Value
  <chr> <chr> <chr>   <chr> <dbl>
1 P 1   A     Var1    Time1  96.7
2 P 1   A     Var1    Time2  111.
3 P 1   A     Var2    Time1  8.50
4 P 1   A     Var2    Time2  8.39
5 P 2   B     Var1    Time1  106.
6 P 2   B     Var1    Time2  111.
7 P 2   B     Var2    Time1  7.65
8 P 2   B     Var2    Time2  5.72
9 P 3   C     Var1    Time1  98.3
10 P 3  C     Var1    Time2  109.
11 P 3  C     Var2    Time1  12.0
12 P 3  C     Var2    Time2  13.3
```

```
long_data <- pivot_wider(very_long_data,
                         names_from = Variable,
                         values_from = Value)
long_data
```

```
# A tibble: 6 x 5
  ID    Var3 Time   Var1  Var2
  <chr> <chr> <chr> <dbl> <dbl>
1 P 1   A     Time1  96.7  8.50
2 P 1   A     Time2  111.  8.39
3 P 2   B     Time1  106.  7.65
4 P 2   B     Time2  111.  5.72
```

```
5 P 3    C      Time1  98.3 12.0
6 P 3    C      Time2 109.  13.3
```

```
# alternatively in 1 step:
long_data <- pivot_longer(
  data=wide_data,
  cols=contains("Time"),
  names_to = c(".value","Time"), # .value will be replace dynamically
  names_pattern = "(Var\\d+)(Time[12])"
)
```

Example 3: long to wide

```
wide_again_data <- pivot_wider(
  data = long_data,
  names_from = Time,
  values_from = Var1:Var2,
  names_glue = "{.value}_{Time}"
)
```

5 Grouping of variables by type / distribution / use

```
pacman::p_load(conflicted,wrappedtools,tidyverse)
conflicts_prefer(dplyr::filter)
```

[conflicted] Will prefer dplyr::filter over any other package.

```
rawdata <- readRDS('data/rawdata.rds')
```

5.1 Test for Normal distribution

5.1.1 Testing a single variable

Before computing some test-statistics, a graphical exploration should be done by e.g. density plots.

There are a number of tests for Normal distribution, all testing the Null hypothesis of data coming from a population with Normal distribution. So small p-values lead to rejection of the Null and indicate deviation from normality. Kolmogorov-Smirnov-test (for larger sample sizes) and Shapiro-Wilk-test (for smaller samples) will be used as examples.

```
ks.test(x = rawdata$`Size (cm)`,
        "pnorm",
        mean=mean(rawdata$`Size (cm)`),
        na.rm = TRUE),
        sd=sd(rawdata$`Size (cm)`),
        na.rm = TRUE))
```

Warning in ks.test.default(x = rawdata\$`Size (cm)` , "pnorm", mean =
mean(rawdata\$`Size (cm)` , : für den Komogorov-Smirnov-Test sollten keine
Bindungen vorhanden sein

Asymptotic one-sample Kolmogorov-Smirnov test

```
data: rawdata$`Size (cm)`  
D = 0.13284, p-value = 0.7064  
alternative hypothesis: two-sided
```

```
ksnormal(rawdata$`Size (cm)`)
```

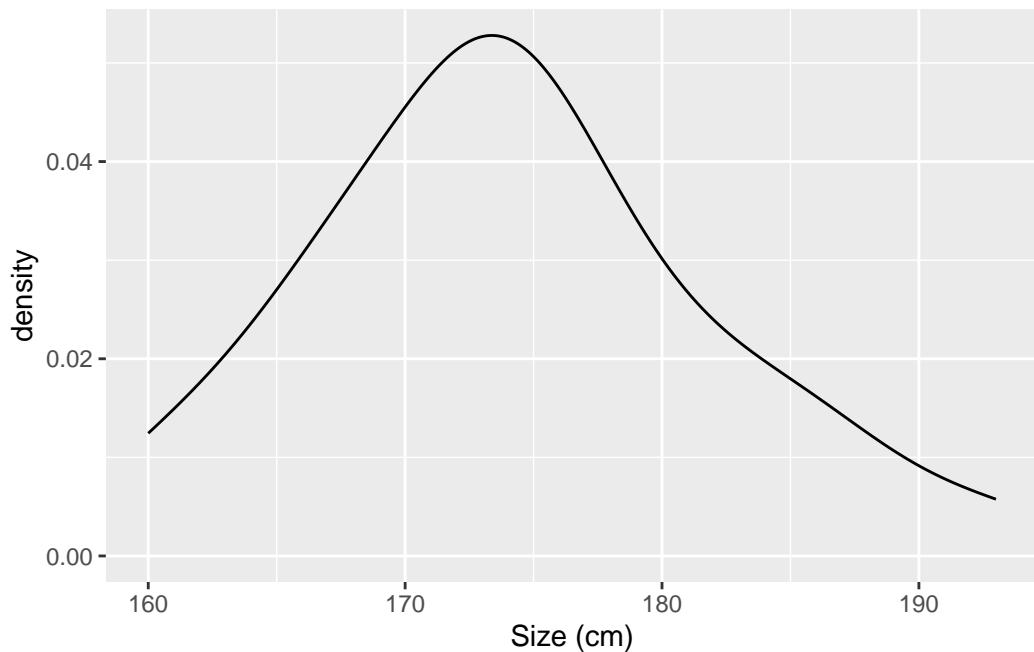
```
[1] 0.7063825
```

```
shapiro.test(rawdata$`Size (cm)`)
```

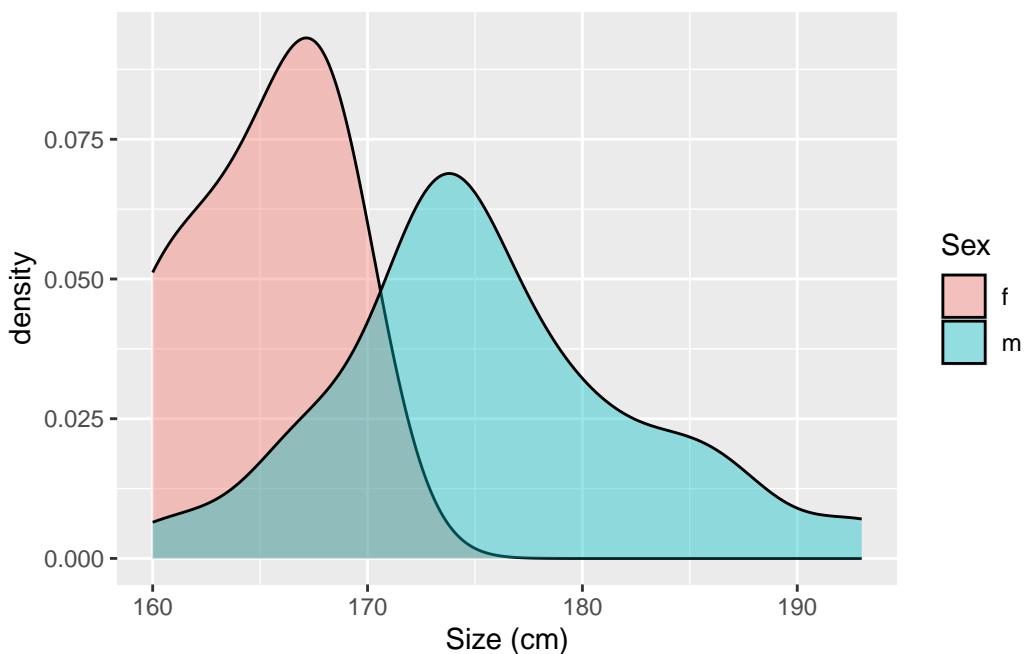
Shapiro-Wilk normality test

```
data: rawdata$`Size (cm)`  
W = 0.9766, p-value = 0.7627
```

```
ggplot(rawdata,aes(x = `Size (cm)`))+  
  geom_density()
```



```
ggplot(rawdata,aes(x = `Size (cm)`,fill=Sex))+  
  geom_density(alpha=.4)
```



If severe group difference can be expected (case/control, sex ...), exploration and analyses should be done in subgroups.

```
rawdata |> filter(Sex=="m") |>  
  pull(`Size (cm)`)|>  
  ksnormal()
```

```
[1] 0.5748486
```

```
rawdata |>  
  group_by(Sex) |>  
  summarize(p_KS = ksnormal(`Size (cm)`),  
            `pGauss (Shapiro)` = shapiro.test(`Size (cm)`)$p.value)
```

```
# A tibble: 2 x 3  
  Sex     p_KS `pGauss (Shapiro)`  
  <chr>   <dbl>          <dbl>  
1 f       0.905          0.272  
2 m       0.575          0.638
```

5.1.2 Testing several variables

To explore larger data sets, it may be useful to test all numerical variables for normality, this can be done in a loop or with the across-function. As a start for the loop-solution we can get the names and positions for all (or selected) numerical variables with the ColSeeker-function from wrappedtools.

```
numvars <- ColSeeker(varclass = "numeric")
numvars$index

[1] 1 2 3 4 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24

head(numvars$names)

[1] "Randomcode"      "Included"       "Finalized"       "Testmedication"
[5] "Size (cm)"       "Weight (kg)"

numvars$count

[1] 23
```

Loops can be created with either a numeric counter-like index or content-based index.

Loop Version 1:

```
## result table v1, pre-filled
resulttable1 <- tibble(
  Variables=numvars$names,
  pKS=NA_real_,
  pSh=NA_real_
)
## loop version 1
for(var_i in seq_len(numvars$count)){
  resulttable1$pKS[var_i] <-
    ksnormal(rawdata[[numvars$names[var_i]]])
  resulttable1$pSh[var_i] <-
    shapiro.test(rawdata |>
      pull(numvars$names[var_i]))$p.value
}
head(resulttable1)
```

```
# A tibble: 6 x 3
Variables          pKS      pSh
<chr>            <dbl>    <dbl>
1 Randomcode      0.999    3.10e- 1
2 Included        0.000000170 2.25e-11
3 Finalized       0.000000800 1.86e- 9
4 Testmedication  0.00347   4.31e- 7
5 Size (cm)       0.706    7.63e- 1
6 Weight (kg)     0.760    8.96e- 2
```

Loop Version 2:

```
## result table v2, just structure
resulttable2 <- tibble(Variables=NA_character_,
                      pKS_Placebo=NA_character_,
                      pKS_Verum=NA_character_,
                      .rows = 0)
for(var_i in numvars$names){
  ks_tmp <- by(data = rawdata[[var_i]],
                INDICES=rawdata$Testmedication,
                FUN=ksnormal)
  resulttable2 <-add_row(resulttable2,
                          Variables=var_i,
                          pKS_Placebo=ks_tmp[[1]] |>
                            formatP(), # added rounding/formatting
                          pKS_Verum=ks_tmp[[2]] |>
                            formatP())
}
head(resulttable2)
```

```
# A tibble: 6 x 3
Variables      pKS_Placebo pKS_Verum
<chr>        <chr>       <chr>
1 Randomcode   0.994      0.996
2 Included     0.001      0.001
3 Finalized    0.003      0.001
4 Testmedication 0.001    0.001
5 Size (cm)    0.955      0.964
6 Weight (kg)  0.553      0.793
```

across() - Version:

```
resulttable1a <-
  rawdata |>
```

```

summarize(across(all_of(numvars$names[-(2:4)]),
  .fns = list(
    pKS=~ksnormal(.x) |>
      formatP(mark = TRUE),
    pSh=~shapiro.test(.x) |>
      pluck("p.value") |>
      formatP(mark = TRUE)))) |>
pivot_longer(everything(),
  names_to=c("Variable","test"),
  names_sep = "_") |>
pivot_wider(names_from=test, values_from=value)
head(resulttable1a)

```

```

# A tibble: 6 x 3
  Variable     pKS      pSh
  <chr>       <chr>    <chr>
1 Randomcode  0.999 n.s.  0.310 n.s.
2 Size (cm)   0.706 n.s.  0.763 n.s.
3 Weight (kg) 0.760 n.s.  0.090 +
4 sysBP V0    0.864 n.s.  0.256 n.s.
5 diaBP V0    0.571 n.s.  0.095 +
6 Lv Edv Mri  0.736 n.s.  0.167 n.s.

```

```
head(resulttable1)
```

```

# A tibble: 6 x 3
  Variables          pKS      pSh
  <chr>            <dbl>    <dbl>
1 Randomcode        0.999    3.10e- 1
2 Included         0.000000170 2.25e-11
3 Finalized        0.000000800 1.86e- 9
4 Testmedication   0.00347   4.31e- 7
5 Size (cm)        0.706    7.63e- 1
6 Weight (kg)      0.760    8.96e- 2

```

```

resulttable2a <-
  rawdata |>
  group_by(Testmedication) |>
  summarize(across(all_of(numvars$names[-(2:4)]),
    .fns = ~ksnormal(.x) |>
      formatP(mark = TRUE))) |>
pivot_longer(-Testmedication,
  names_to="Variable") |>

```

```

pivot_wider(names_from=Testmedication,
            values_from=value)
head(resulttable2a)

```

```

# A tibble: 6 x 3
  Variable     `0`     `1`
  <chr>       <chr>    <chr>
1 Randomcode  0.994 n.s. 0.996 n.s.
2 Size (cm)   0.955 n.s. 0.964 n.s.
3 Weight (kg) 0.553 n.s. 0.793 n.s.
4 sysBP V0    0.555 n.s. 0.774 n.s.
5 diaBP V0    0.647 n.s. 0.942 n.s.
6 Lv Edv Mri  1.000 n.s. 0.880 n.s.

```

```

head(resulttable2)

```

```

# A tibble: 6 x 3
  Variables      pKS_Placebo pKS_Verum
  <chr>          <chr>        <chr>
1 Randomcode    0.994        0.996
2 Included      0.001        0.001
3 Finalized    0.003        0.001
4 Testmedication 0.001        0.001
5 Size (cm)    0.955        0.964
6 Weight (kg)   0.553        0.793

```

```

resulttable3 <-
  rawdata |>
  group_by(Testmedication) |>
  summarize(across(all_of(numvars$names[-(2:4)]),
    .fns = list(
      Mean=~mean(.x, na.rm=TRUE) |>
        roundR(5),
      Median=~median(.x, na.rm=TRUE) |>
        roundR(5),
      pKS=~ksnormal(.x) |>
        formatP(mark = TRUE),
      pSh=~shapiro.test(.x) |>
        pluck("p.value") |>
        formatP(mark = TRUE)))) |>
  pivot_longer(-Testmedication,
              names_to=c("Variable","test"),

```

```

    names_sep = "_") |>
pivot_wider(names_from=test, values_from=value) |>
arrange(Variable)
head(resulttable3)

```

```

# A tibble: 6 x 6
  Testmedication Variable     Mean   Median pKS      pSh
  <dbl> <chr>       <chr>  <chr>   <chr>    <chr>
1          0 Age        60.429 64.000 0.489 n.s.  0.425 n.s.
2          1 Age        60.429 60.000 0.935 n.s.  0.282 n.s.
3          0 BMI        30.244 29.246 0.956 n.s.  0.430 n.s.
4          1 BMI        28.016 27.484 0.992 n.s.  0.862 n.s.
5          0 Ferritin Lab 258.21 220.00 0.595 n.s.  0.176 n.s.
6          1 Ferritin Lab 305.23 222.00 0.139 n.s.  0.003 **

```

5.2 Picking column names and positions

Based on data inspection, testing, and background knowledge, variables can be sorted into scale levels:

```

gaussvars <- ColSeeker(
  namepattern = c("si","we","BMI","BP","mri"),
  casesensitive = FALSE)

ordvars <- ColSeeker(namepattern = c("Age","Lab"))

factvars <- ColSeeker(namepattern = c("Sex","med","NYHA"),
                      returnclass = TRUE)

rawdata <- mutate(rawdata,
                  across(all_of(factvars$names),
                         ~factor(.x)))
save(rawdata,list = ls(pattern = "vars"),
     file = "data/bookdata1.RData")

```

6 Visualize data with ggplot

While there are various packages providing visualizations, here we are focusing on `ggplot2` (grammar of graphics) as a very flexible and versatile approach with many extensions implemented in additional packages. See e.g. <https://exts.ggplot2.tidyverse.org/>.

```
pacman::p_load(conflicted, tidyverse,
  grid,gridExtra,car,
  ggsci,ggsignif, ggthemes, ggridges,
  # gganimate,
  ggforce,
  ggbeeswarm,
  wrappedtools,
  emojiifont,
  patchwork)
conflicts_prefer(dplyr::filter) # solves name conflict
```

[conflicted] Will prefer `dplyr::filter` over any other package.

6.1 Example data

The typical examples use either diamonds from `ggplot2` or mtcars from `datasets`. There are help files for both.

```
head(diamonds)

# A tibble: 6 x 10
  carat cut      color clarity depth table price     x     y     z
  <dbl> <ord>    <ord> <ord>   <dbl> <dbl> <int> <dbl> <dbl> <dbl>
1 0.23 Ideal    E      SI2     61.5    55    326  3.95  3.98  2.43
2 0.21 Premium  E      SI1     59.8    61    326  3.89  3.84  2.31
3 0.23 Good     E      VS1     56.9    65    327  4.05  4.07  2.31
4 0.29 Premium  I      VS2     62.4    58    334  4.2    4.23  2.63
5 0.31 Good     J      SI2     63.3    58    335  4.34  4.35  2.75
6 0.24 Very Good J      VVS2    62.8    57    336  3.94  3.96  2.48
```

```
head(mtcars)
```

	mpg	cyl	disp	hp	drat	wt	qsec	vs	am	gear	carb
Mazda RX4	21.0	6	160	110	3.90	2.620	16.46	0	1	4	4
Mazda RX4 Wag	21.0	6	160	110	3.90	2.875	17.02	0	1	4	4
Datsun 710	22.8	4	108	93	3.85	2.320	18.61	1	1	4	1
Hornet 4 Drive	21.4	6	258	110	3.08	3.215	19.44	1	0	3	1
Hornet Sportabout	18.7	8	360	175	3.15	3.440	17.02	0	0	3	2
Valiant	18.1	6	225	105	2.76	3.460	20.22	1	0	3	1

6.2 Basic structure of a ggplot call

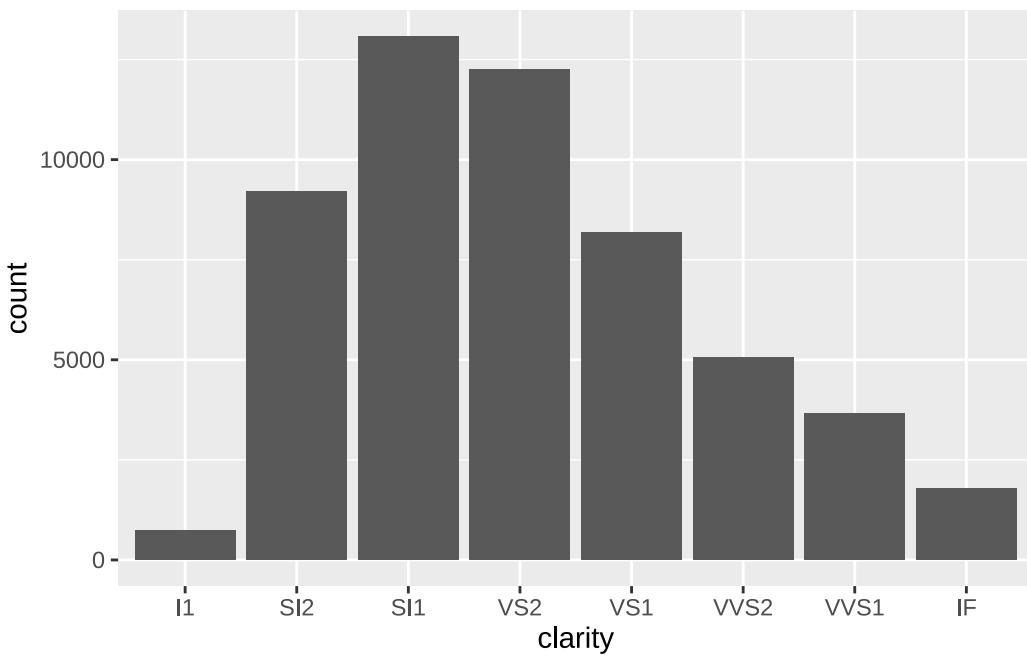
To create a figure, we at least use 2 function calls:

1. `ggplot(data = my_data, mapping = aes(x=..., y=..., color=..., shape=...))` to define data and inside `aes()` some global defaults for aesthetic mappings, this (sort of) creates the canvas to draw on
2. `geom_xxx()` to define the geometry to be used to show the data, e.g. bar, boxplot, point

When mapping data to aesthetics, the class of data matters: Numerical data are interpreted as continuous, so a color heatmap is mapped rather than discrete colors, grouping of data requires factors / characters.

Minimal example:

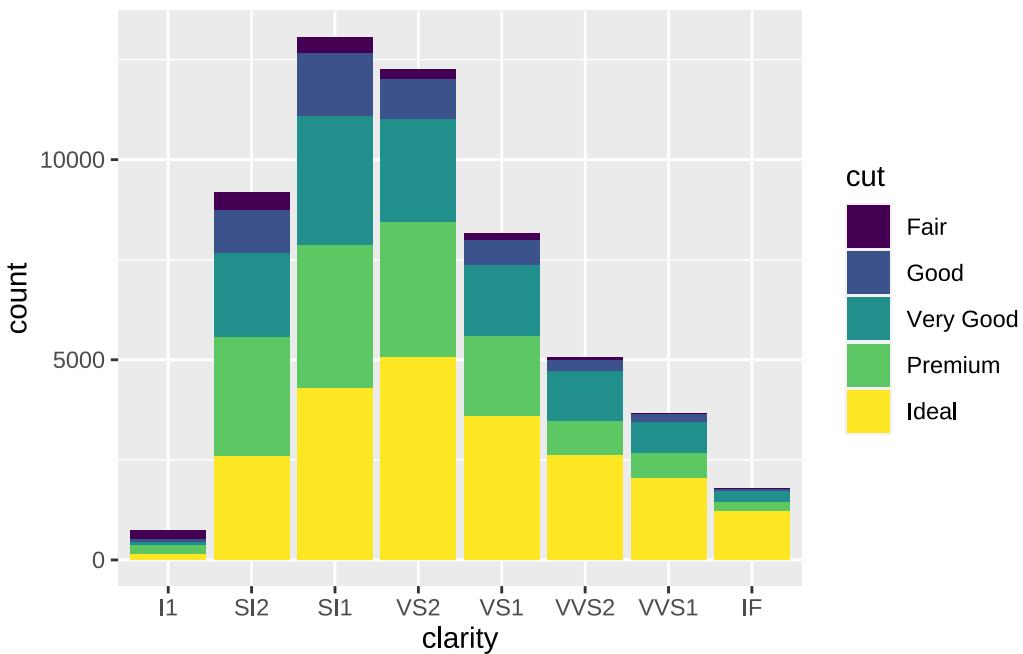
```
ggplot(data=diamonds,mapping = aes(x=clarity))+  
  geom_bar()
```



`geom_bar()` inherits the global aesthetic `x` (*build a x-axis based on values in column clarity*) and does not need a y-axis definition, as it uses some in-build statistics (“count”) and defines `y`.

We can add additional aesthetic parameters like `fill=`. This automatically creates sub-groups for counting:

```
ggplot(data=diamonds,aes(x=clarity,fill=cut))+  
  geom_bar()
```



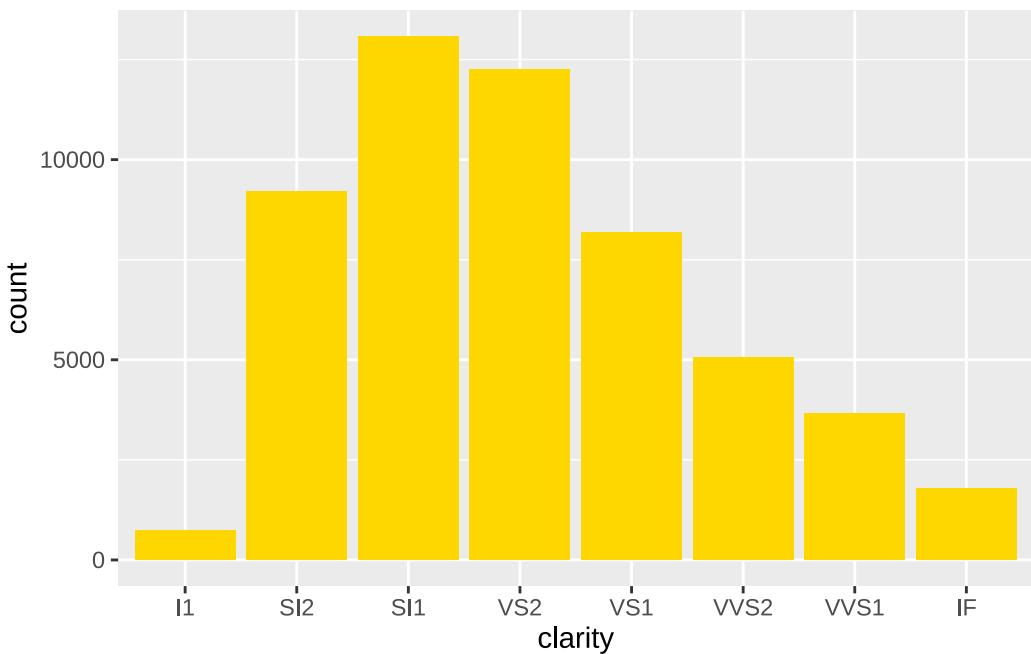
This graph represents this count table:

```
diamonds |>
  group_by(clarity,cut) |>
  count() |>
  pivot_wider(names_from = clarity,values_from=n)
```

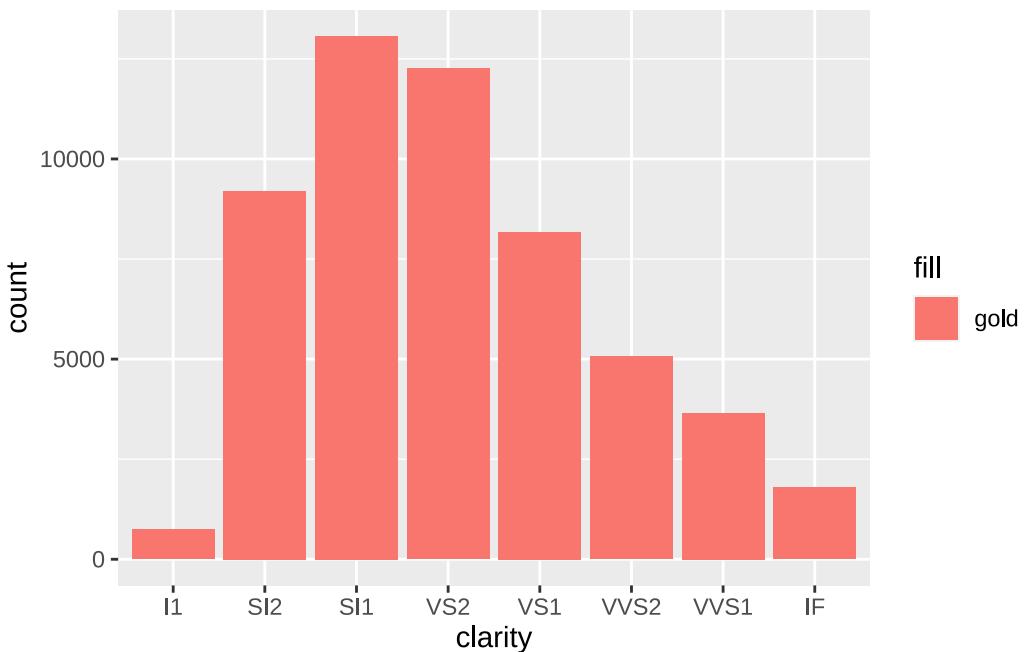
```
# A tibble: 5 x 9
# Groups:   cut [5]
  cut      I1    SI2    SI1    VS2    VS1    VVS2   VVS1    IF
  <ord>  <int> <int> <int> <int> <int> <int> <int>
1 Fair     210    466   408   261   170    69     17     9
2 Good     96    1081  1560   978   648   286    186    71
3 Very Good  84    2100  3240  2591  1775  1235   789   268
4 Premium   205   2949  3575  3357  1989   870   616   230
5 Ideal     146   2598  4282  5071  3589  2606  2047  1212
```

Aesthetic parameters can represent data / have some meaning (as cut quality), but they can be defined to reflect your taste rather than data. In that case, you define them outside of `aes()`. Careful, as this may lead to confusion:

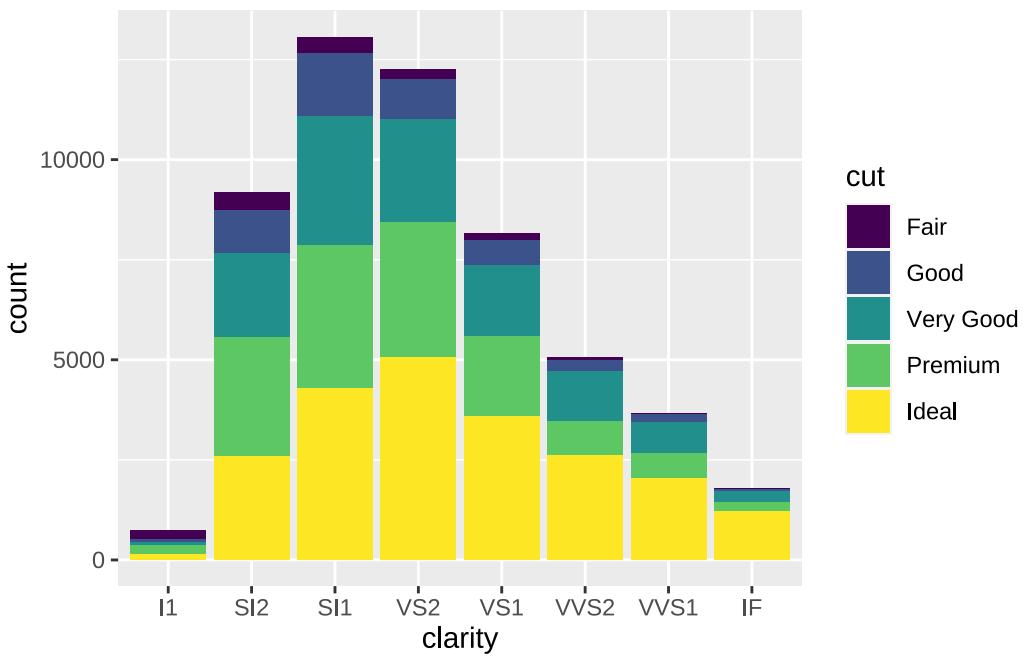
```
#aesthetics outside aes
ggplot(data=diamonds,aes(x=clarity))+  
  geom_bar(fill="gold")
```



```
ggplot(data=diamonds,aes(x=clarity))+  
  geom_bar(aes(fill="gold")) #should be outside aes!
```



```
ggplot(data=diamonds,aes(x=clarity))+  
  geom_bar(aes(fill=cut)) # may be defined locally as well globally
```



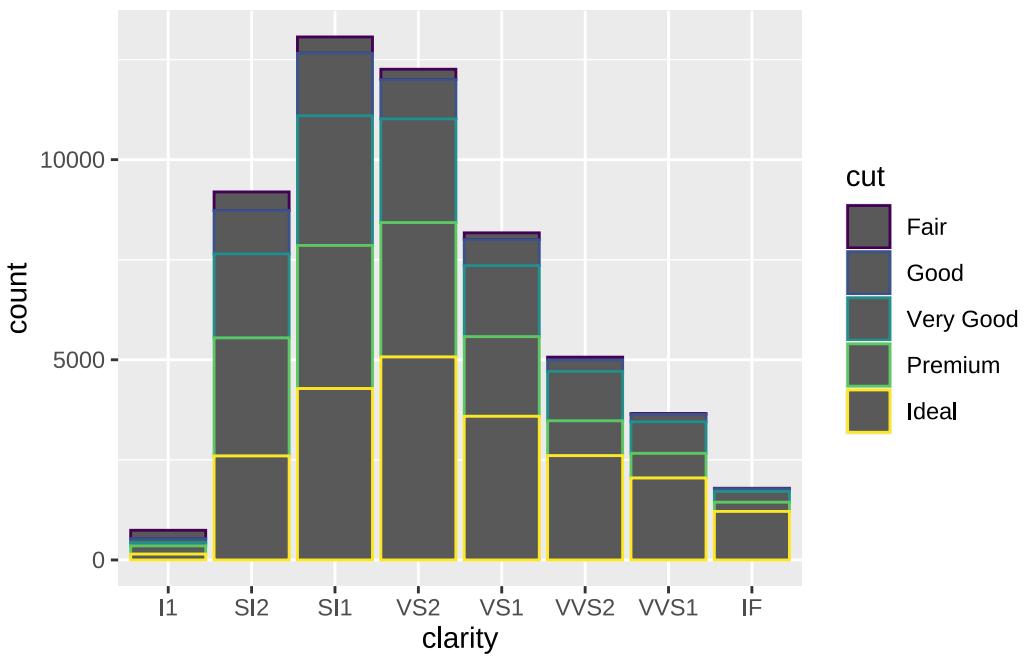
6.3 fill vs. color

Some elements (as e.g. the bar or boxplot) know 2 color elements:

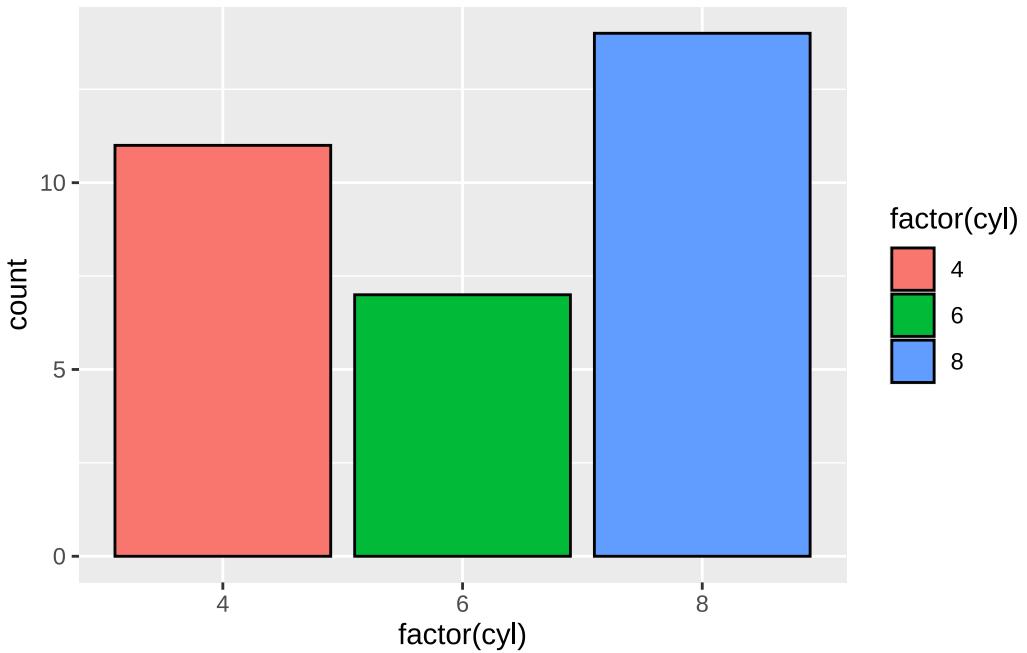
- inner color, defined by `fill`
- outer frame color, defined by `color`

Other elements (as e.g. the line) only have a single color definition, specified by `color`. And for some elements (as e.g. dots), it depends. See help for points for examples.

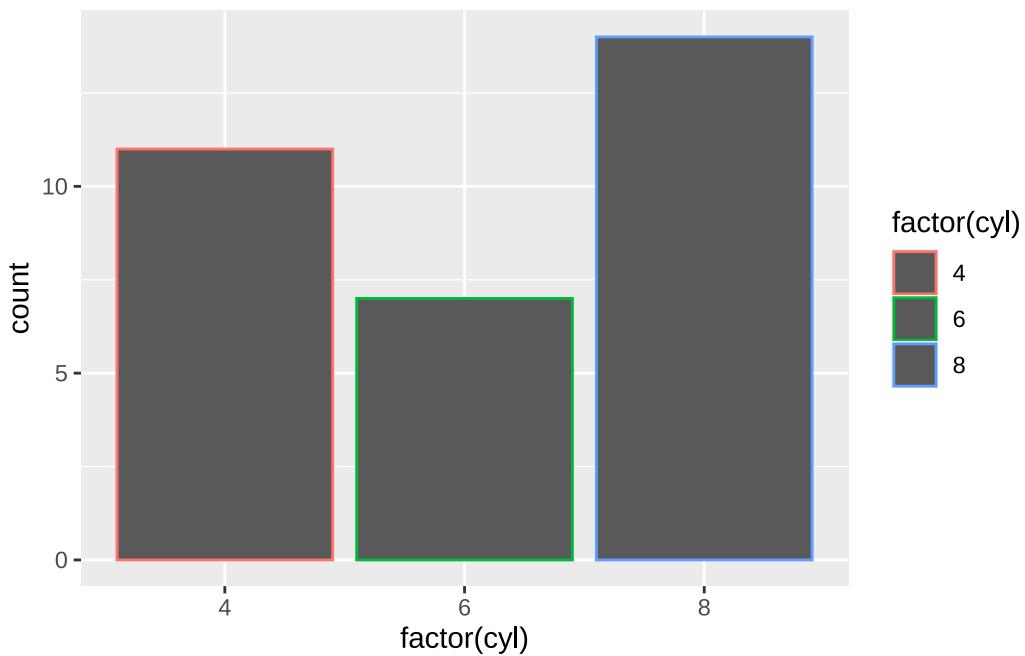
```
ggplot(data=diamonds,aes(x=clarity,color=cut))+  
  geom_bar()
```



```
ggplot(data=mtcars,aes(factor(cyl),fill=factor(cyl)))+
  geom_bar(color="black")
```



```
ggplot(data=mtcars,aes(factor(cyl),color=factor(cyl)))+
  geom_bar()
```

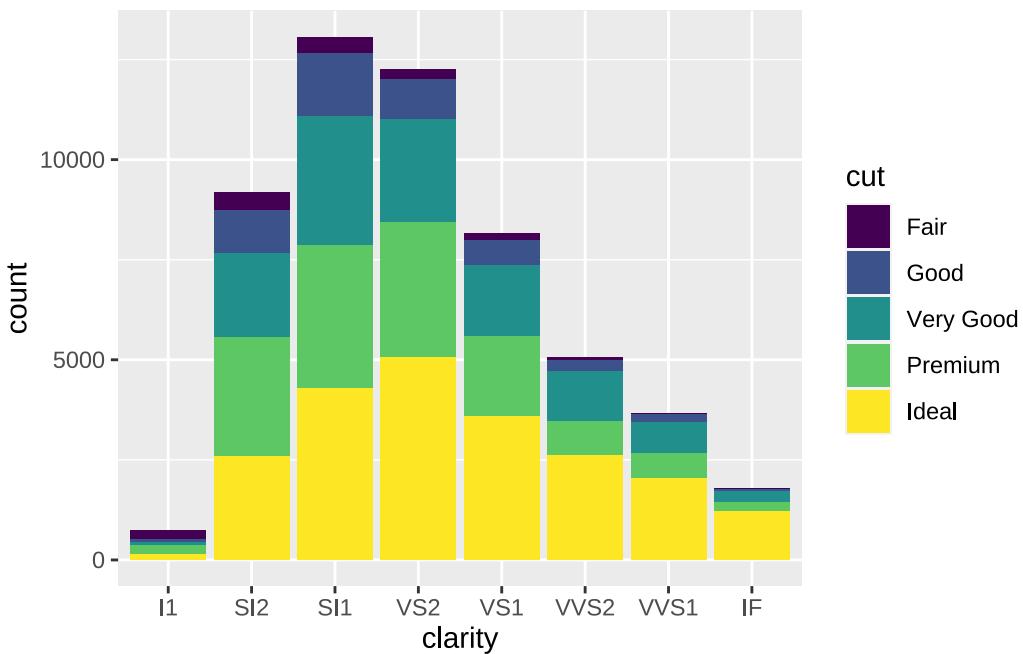


6.4 Color systems

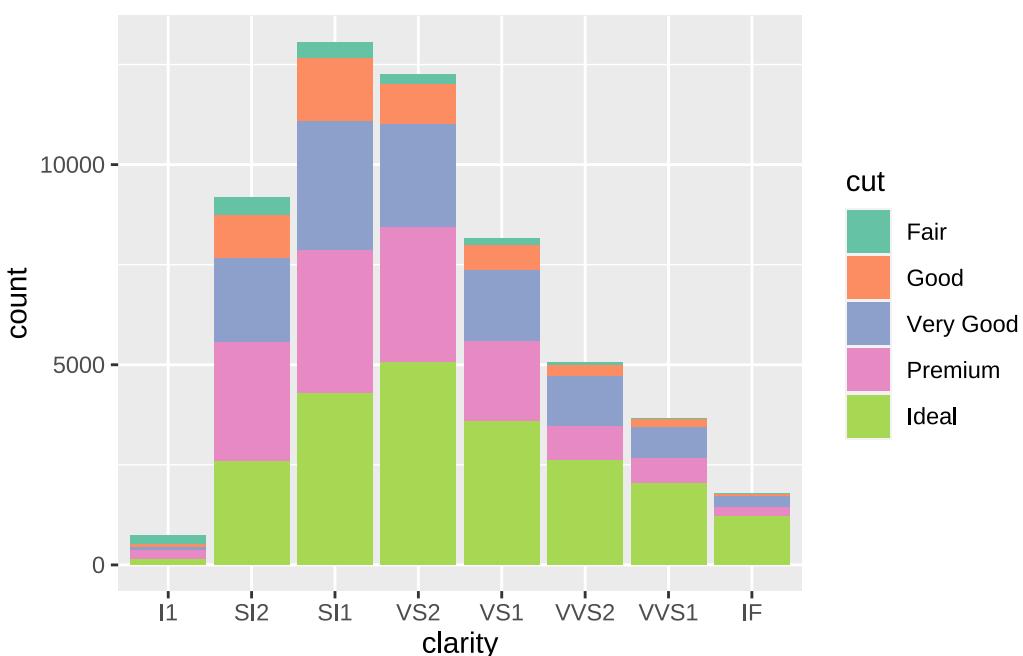
ggplot2 comes with various color definitions, many external packages extend that. Manual definition of colors is possible as well. Redefining the mapping between data and aesthetics can be done with `scale_...` functions

For the demonstration, I store a plot into a variable, this includes all data and plot definitions, nothing like jpg!

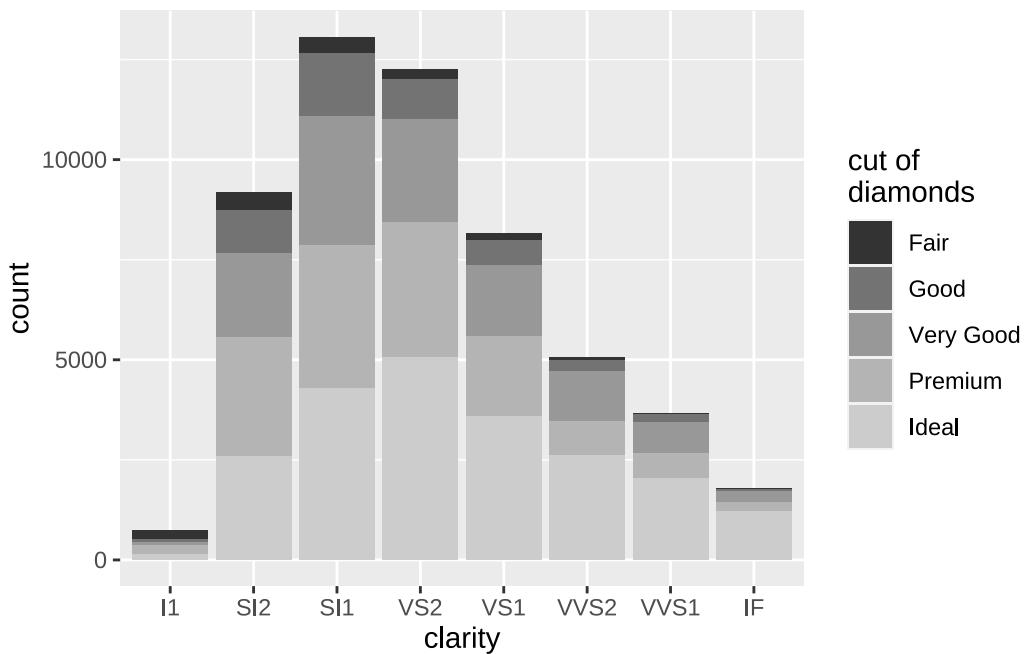
```
(plottemp <- ggplot(data=diamonds, aes(x=clarity, fill=cut))+
  geom_bar())
```



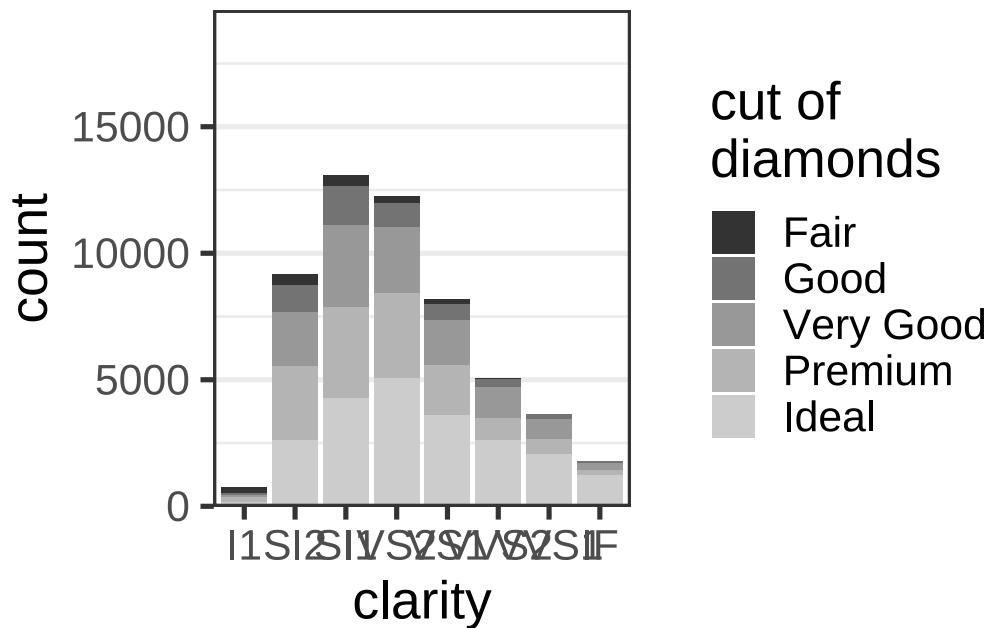
```
plottemp + scale_fill_brewer(palette="Set2") #in-built "scale" for fill
```



```
plottemp + scale_fill_grey(name = "cut of\ndiamonds")
```

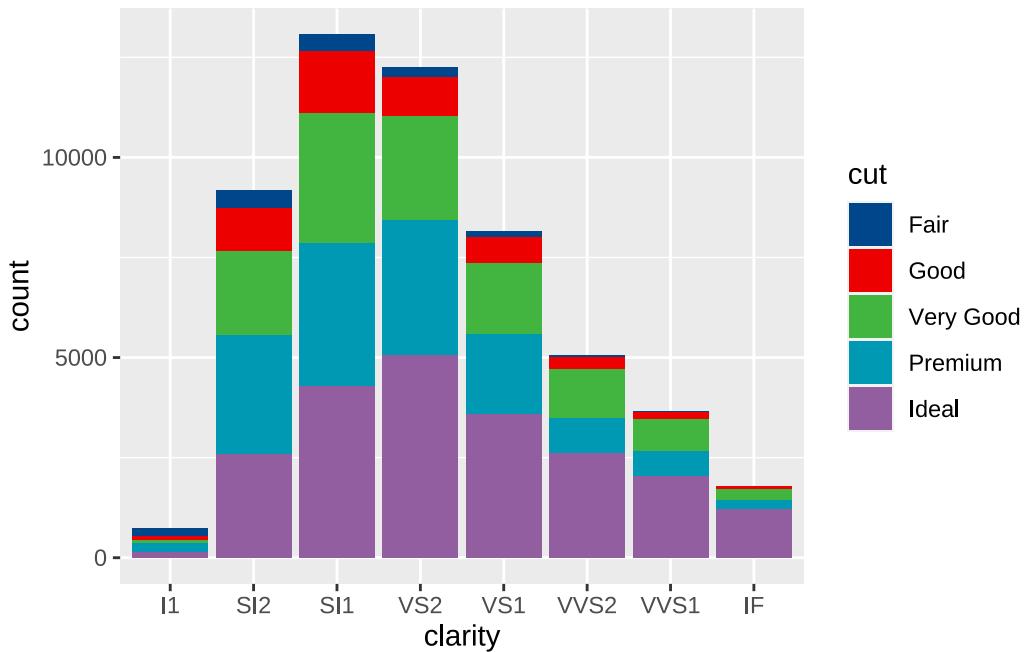


```
plottemp + scale_fill_grey(name = "cut of diamonds") +
  scale_y_continuous(expand = expansion(mult = c(0,.5)))+ # rescaling y
  theme_bw(base_size = 20) +
  theme(panel.grid.major.x = element_blank())
```

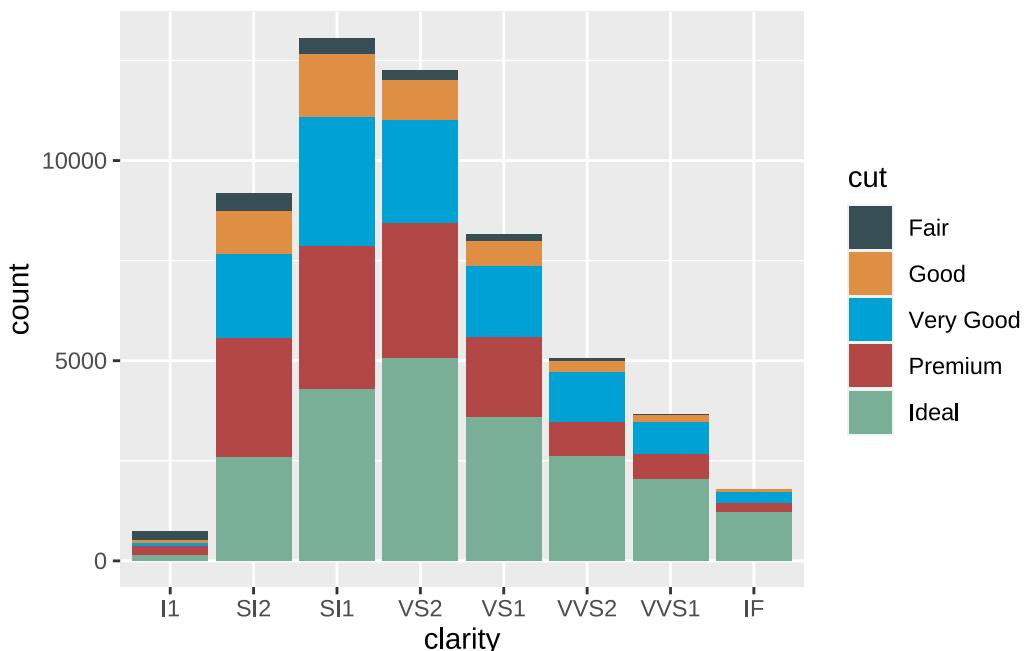


6.4.1 External color definitions from ggsci

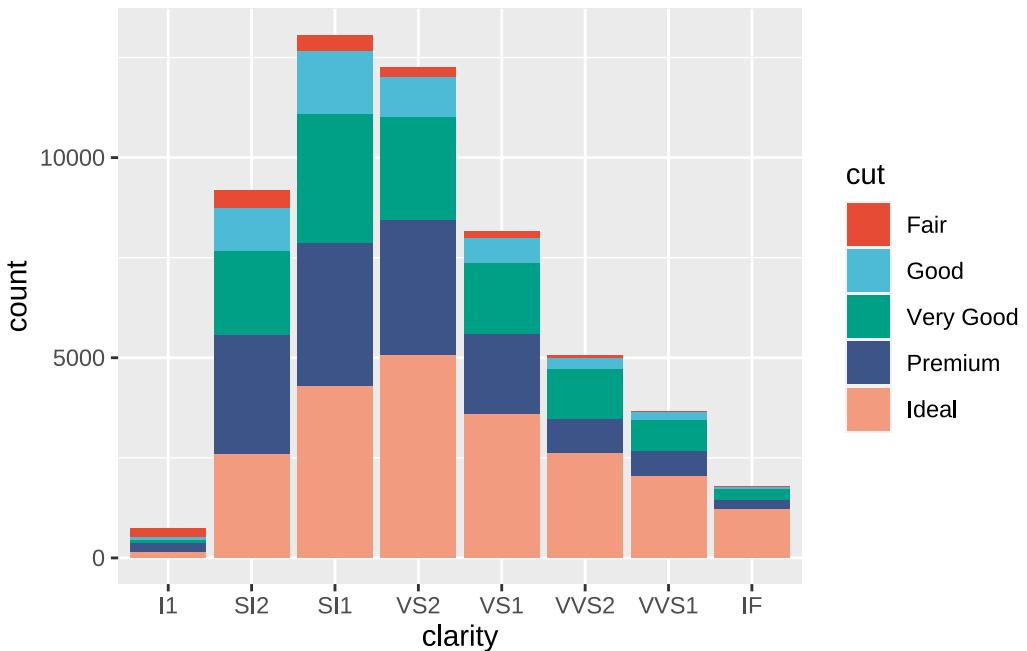
```
plottemp+scale_fill_lancet()
```



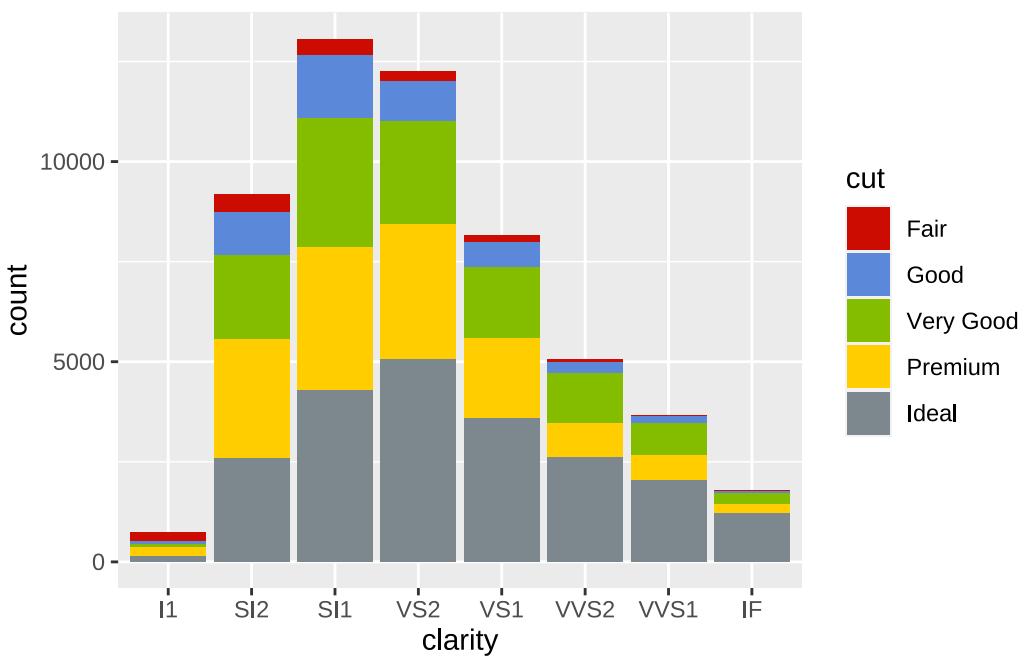
```
plottemp+scale_fill_jama()
```



```
plottemp+scale_fill_npg()
```



```
(printplot <- plottemp+scale_fill_startrek())
```



6.5 Exporting ggplots

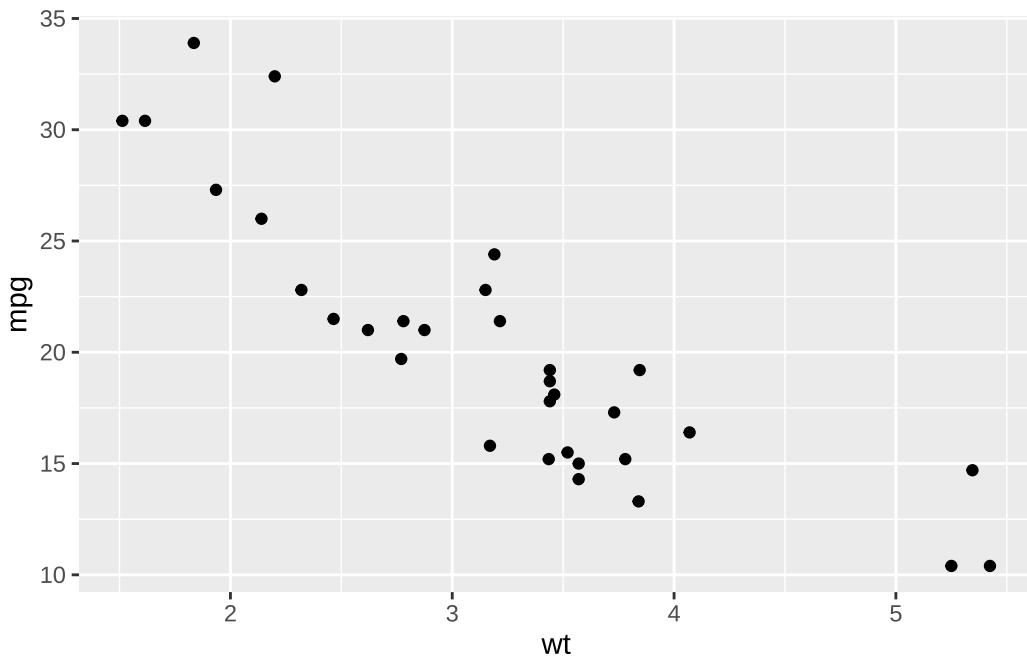
There are two distinct ways, using `ggsave()` or more generally creating an external graphic device with e.g. `png()` / `tiff()` / `pdf()`:

```
ggsave(filename = "Graphs/ggtestplot.png",
        plot = printplot,
        width=20,height=20,
        units="cm",dpi=150)
ggsave(filename = "Graphs/ggtestplot.tiff",
        plot = printplot,
        width=20,height=20,
        units="cm",dpi=600)
ggsave(filename = "Graphs/ggtestplot_c.tiff",
        plot = printplot,
        width=20,height=20, compression="lzw",
        units="cm",dpi=600)
# alternative:
png(filename = "Graphs/ggtestplot2.png",
     width = 20,height = 20,units = "cm",res = 150)
plottemp
dev.off()
```

6.6 Other geoms

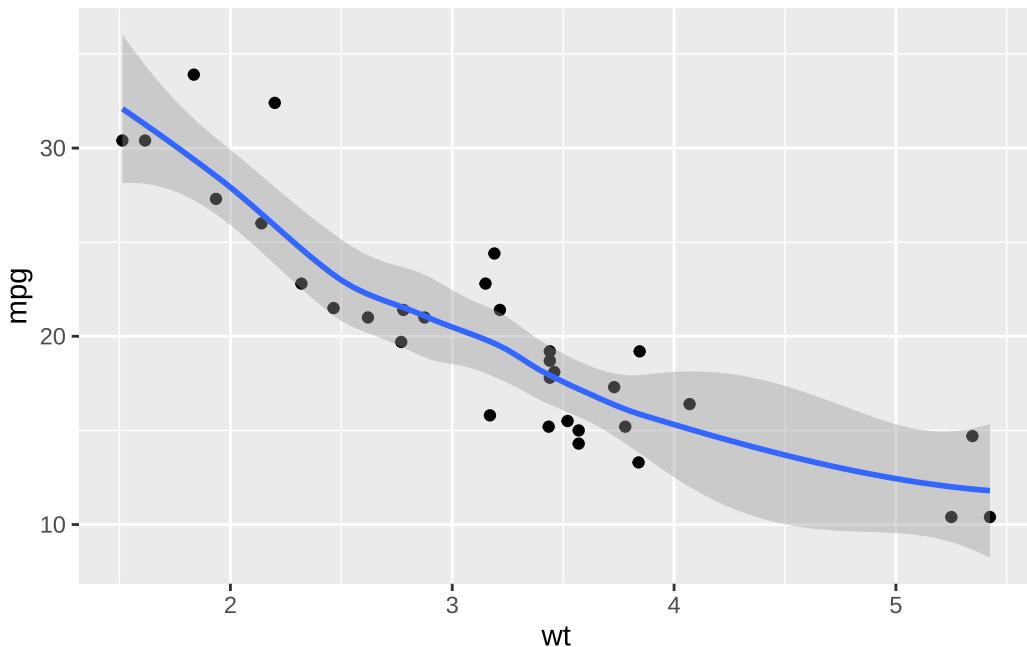
Common forms of plots are barplots, boxplots, scatterplots (possibly with regression line), and density-plots. For plotting dots for groups, there are various options to avoid overplotting of repeated data, with the `beeswarm` as my preference.

```
ggplot(data=mtcars,aes(x = wt,y = mpg))+  
  geom_point()
```



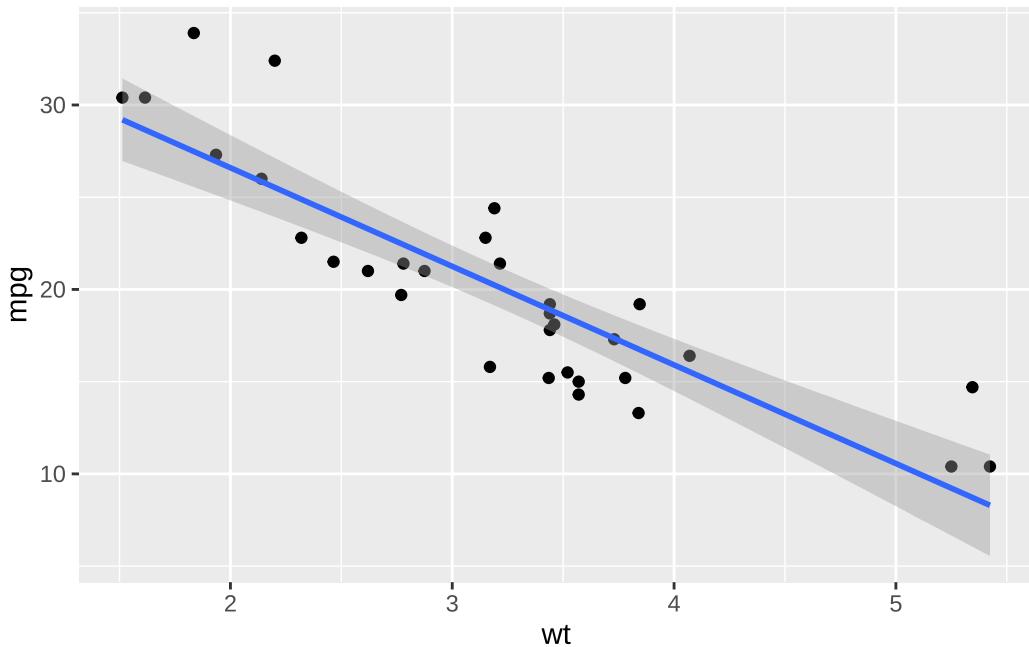
```
ggplot(data=mtcars,aes(x = wt,y = mpg))+  
  geom_point() +  
  geom_smooth()
```

```
`geom_smooth()` using method = 'loess' and formula = 'y ~ x'
```

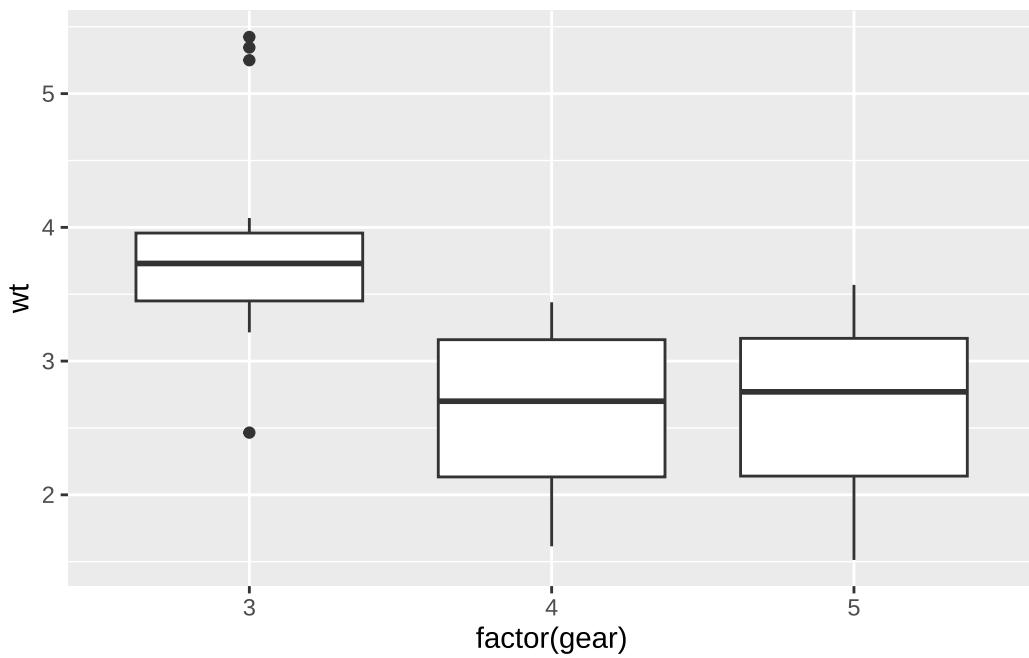


```
ggplot(data=mtcars,aes(x = wt,y = mpg))+  
  geom_point() +  
  geom_smooth(method="lm")
```

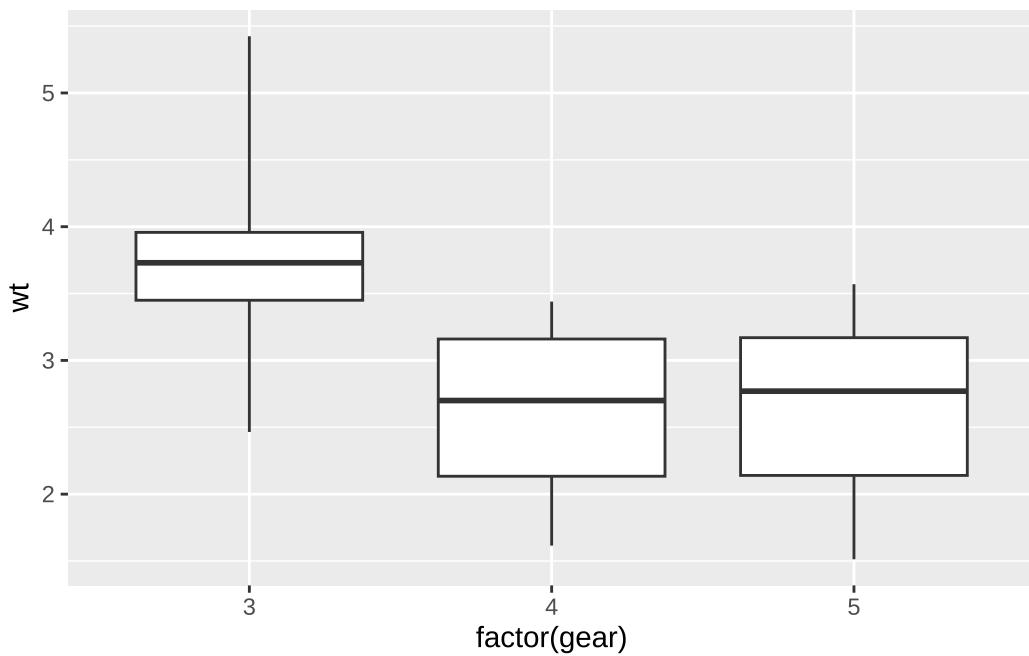
`geom_smooth()` using formula = 'y ~ x'



```
ggplot(mtcars,aes(x = factor(gear),y = wt))+  
  geom_boxplot() #default 1.5 IQR
```

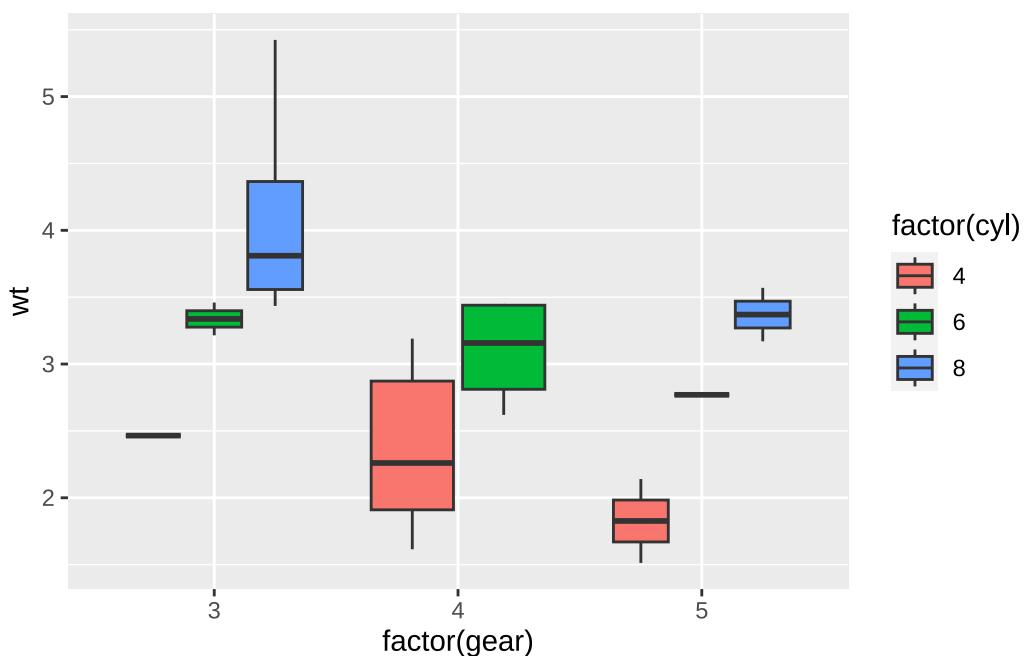


```
ggplot(mtcars,aes(x = factor(gear),y = wt))+  
  geom_boxplot(coef=3) # this extends range of expected values
```

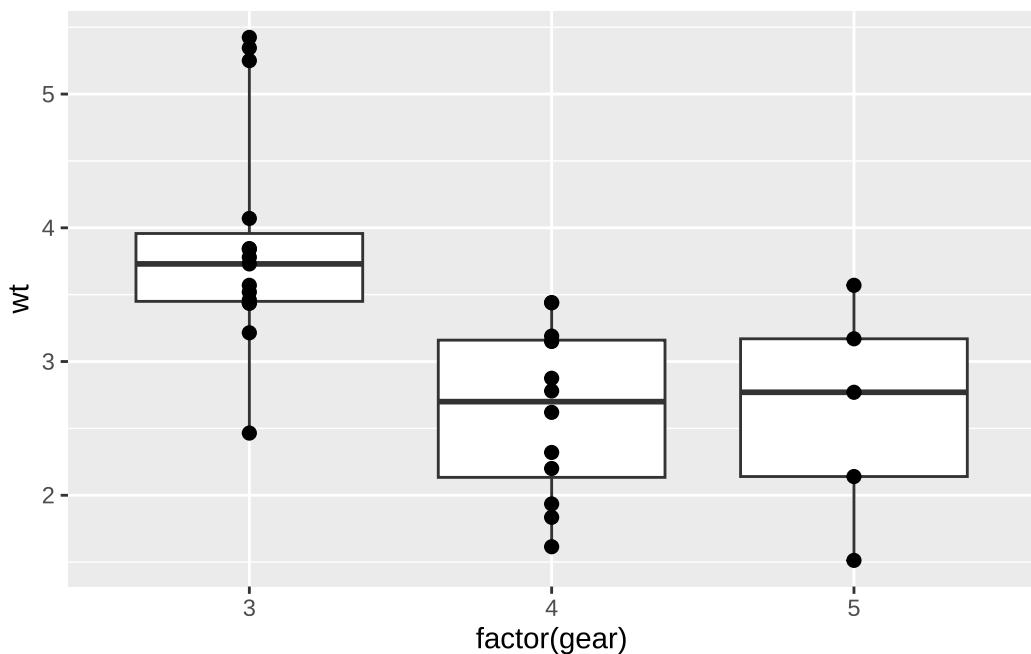


```
ggplot(mtcars,aes(x = factor(gear),y = wt,  
  fill=factor(cyl)))+
```

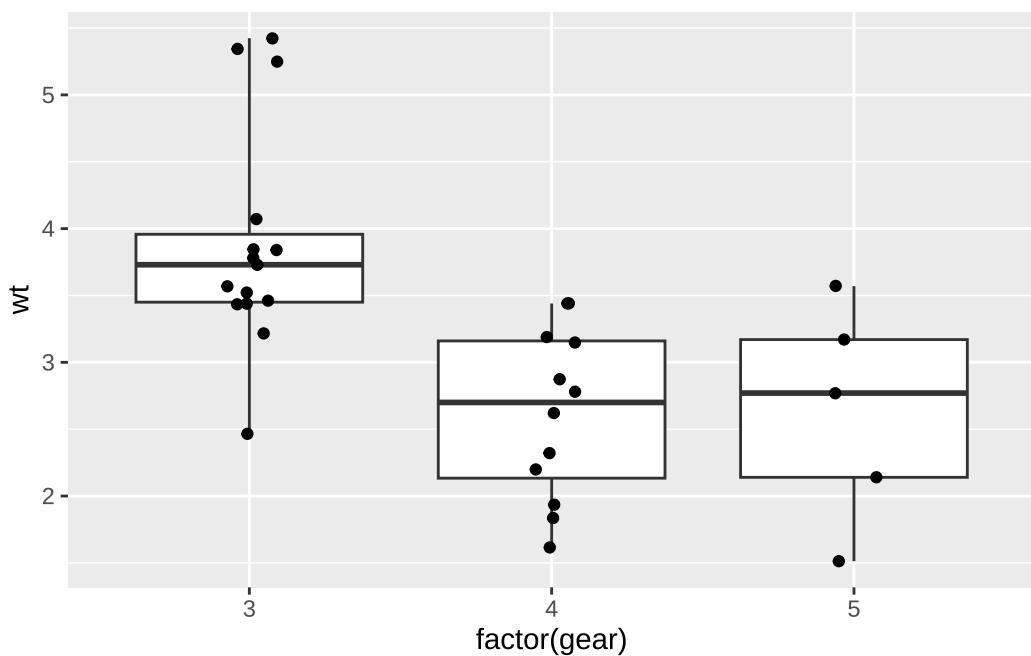
```
geom_boxplot(coef=3) # group by cyl, as it is mapped to fill
```



```
ggplot(mtcars,aes(x = factor(gear),y = wt))+  
  geom_boxplot(coef=3)+  
  geom_point(size=2) # may contain overlapping points
```

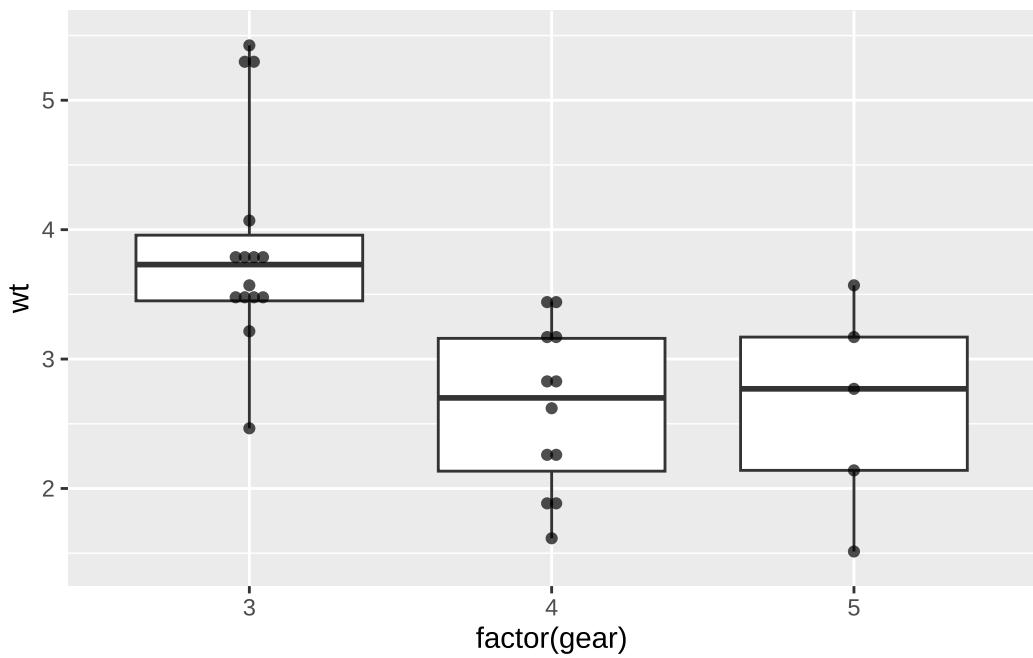


```
ggplot(mtcars,aes(x = factor(gear),y = wt))+  
  geom_boxplot(coef=3)+  
  geom_point(position = position_jitter(width = .1))
```

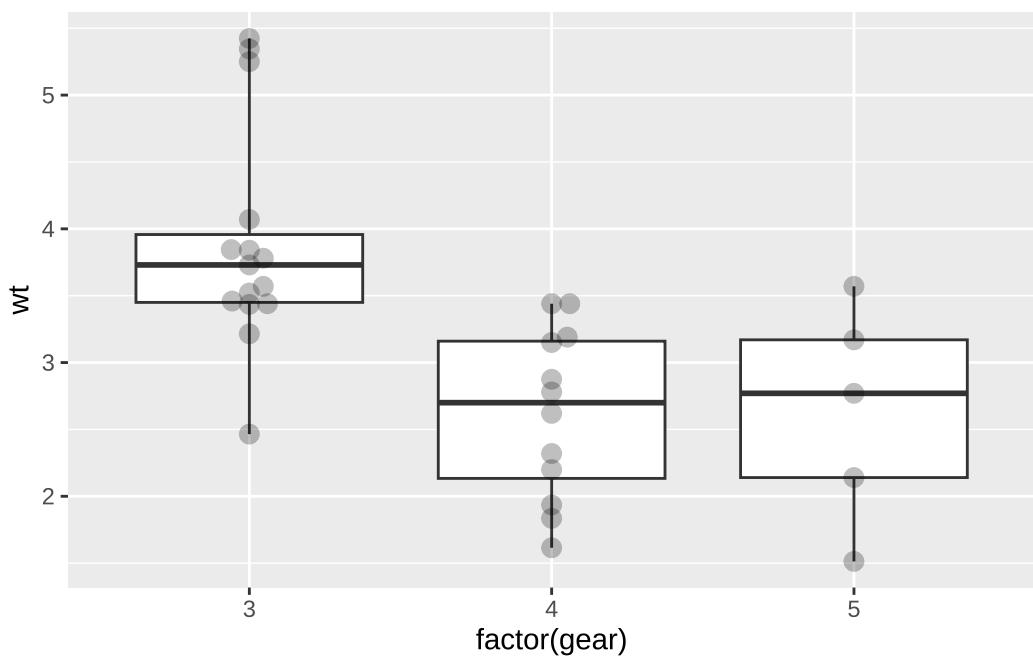


```
ggplot(mtcars,aes(x = factor(gear),y = wt))+  
  geom_boxplot(coef=3)+  
  geom_dotplot(alpha=.7, # group similar(ish) data on a line  
               binaxis = "y",stackdir = "center",  
               stackratio = .9,dotsize = .6)
```

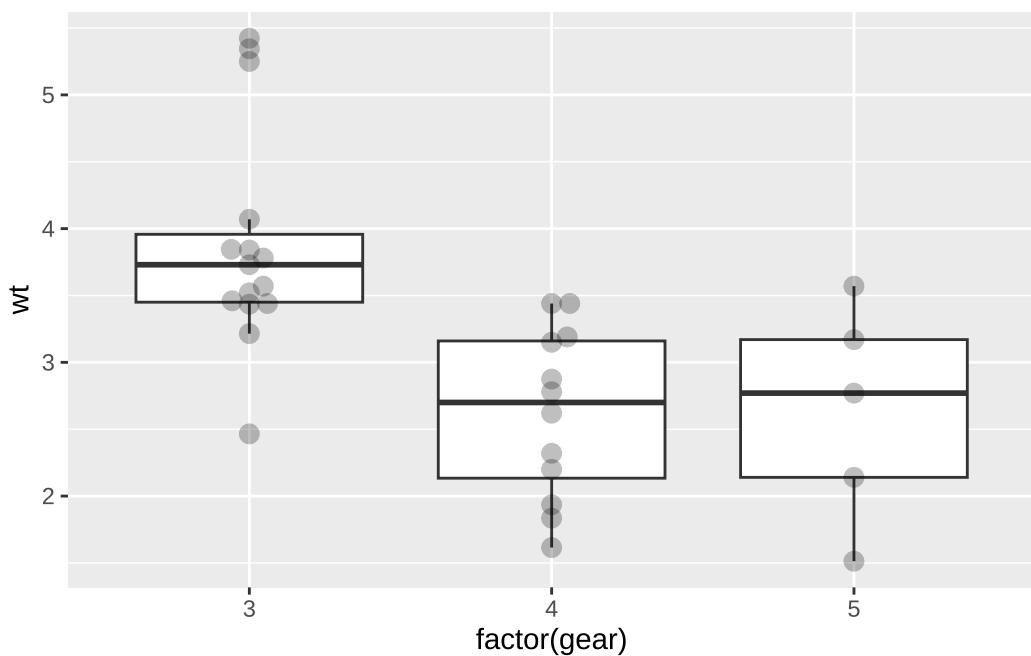
Bin width defaults to 1/30 of the range of the data. Pick better value with `binwidth`.



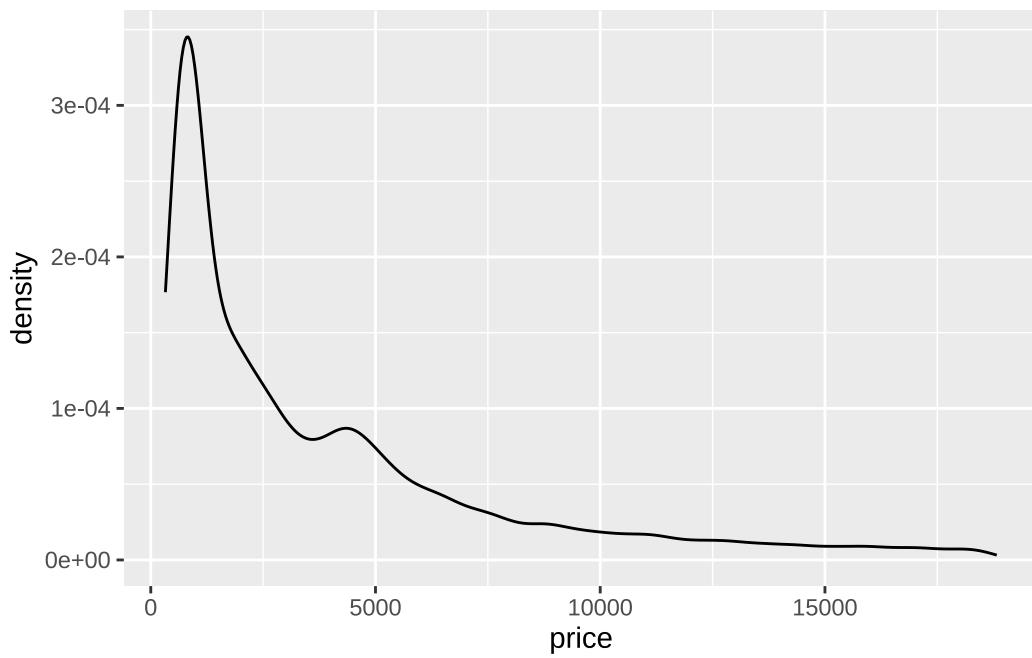
```
ggplot(mtcars,aes(x = factor(gear),y = wt))+  
  geom_boxplot(coef=3)+  
  ggbeeswarm::geom_beeswarm(cex = 2,size=3,alpha=.25)
```



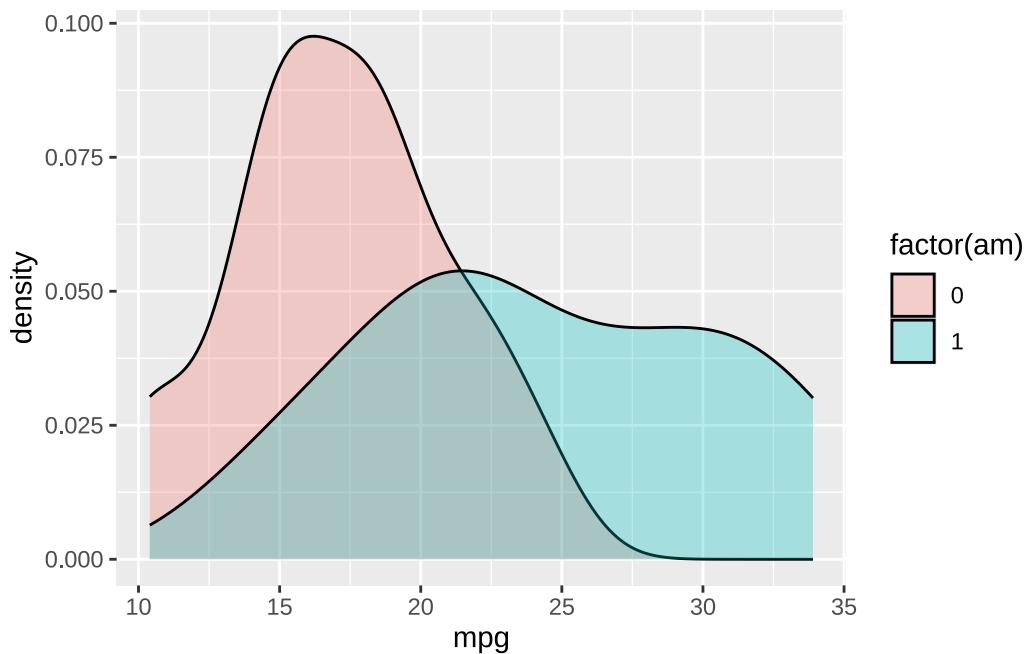
```
ggplot(mtcars,aes(x = factor(gear),y = wt))+  
  geom_boxplot(outlier.alpha = 0)+ # to avoid plotting outliers twice  
  geom_beeswarm(cex = 2,size=3,alpha=.25)
```



```
#density plot  
ggplot(diamonds,aes(price))+  
  geom_density()
```

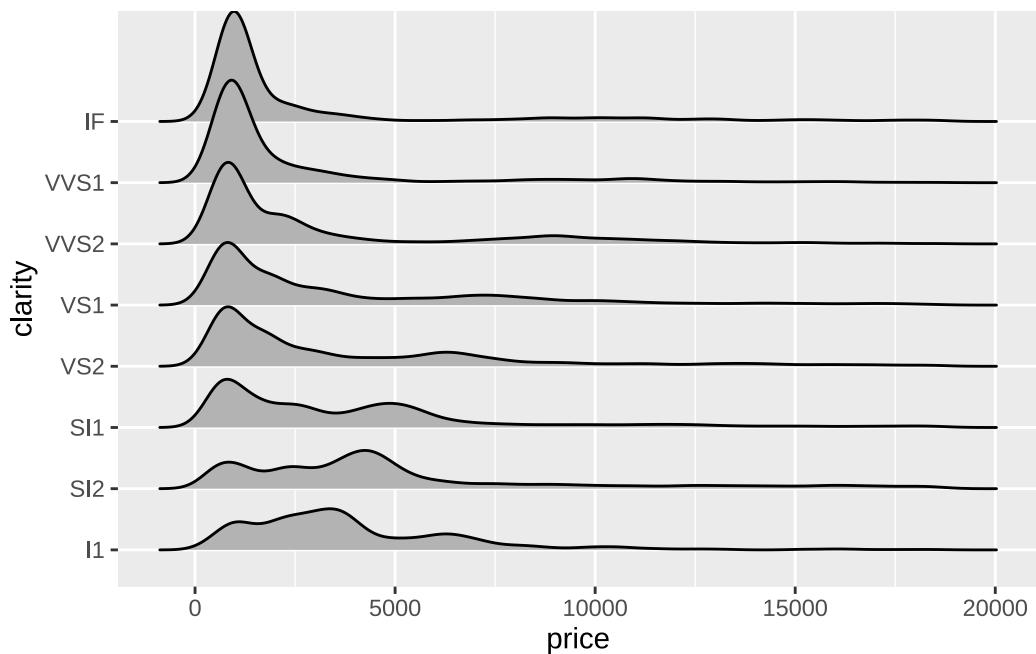


```
ggplot(mtcars,aes(mpg, fill=factor(am)))+  
  geom_density(alpha=.3)
```



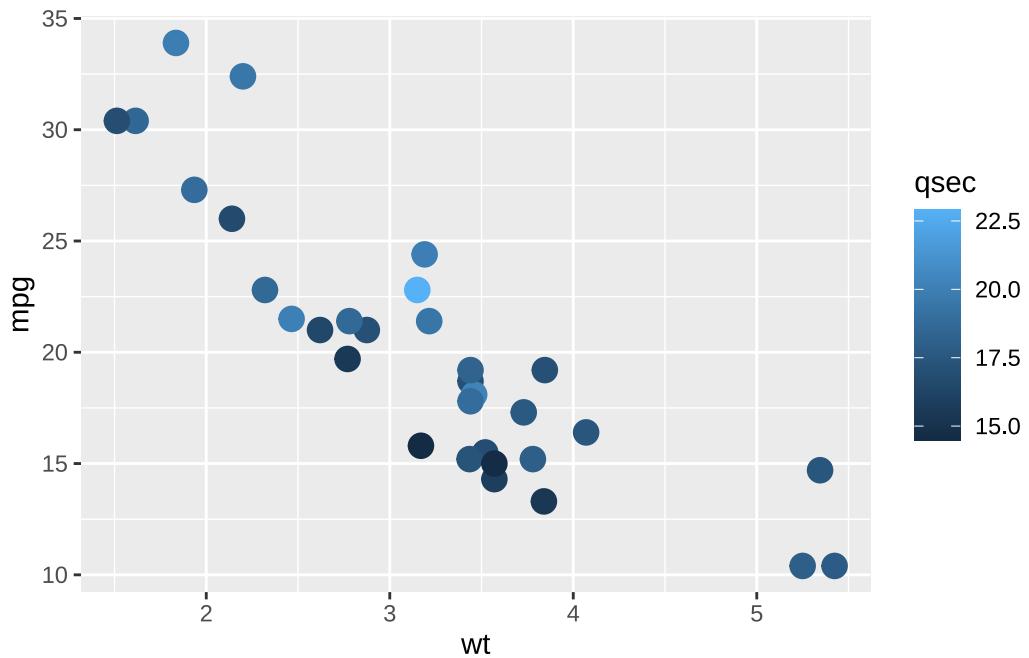
```
ggplot(diamonds,aes(price,y=clarity))+  
  geom_density_ridges()
```

Picking joint bandwidth of 403

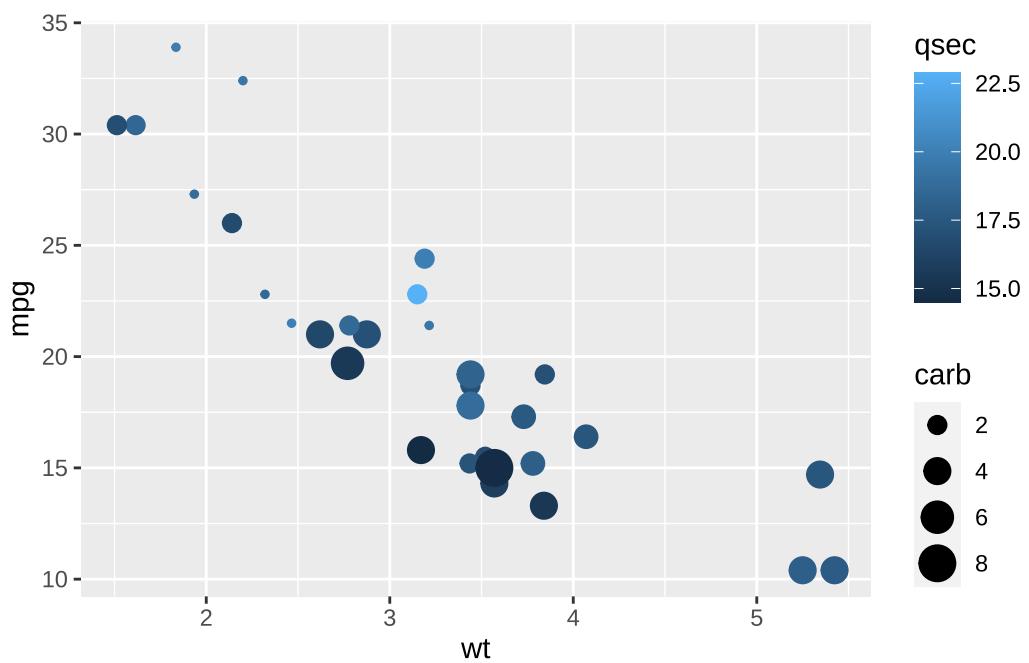


6.7 Combining and finetuning aesthetics

```
ggplot(data=mtcars,aes(wt, mpg,color=qsec))+  
  geom_point(size=4) #outside aes!
```

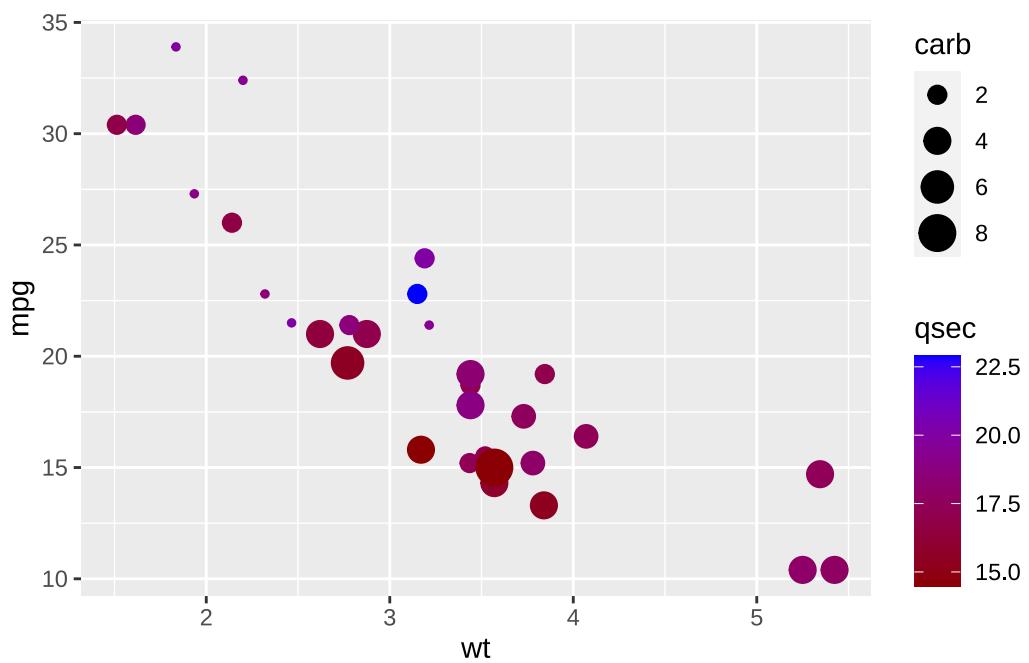


```
ggplot(data=mtcars,aes(wt, mpg,color=qsec, size=carb))+  
  geom_point()
```

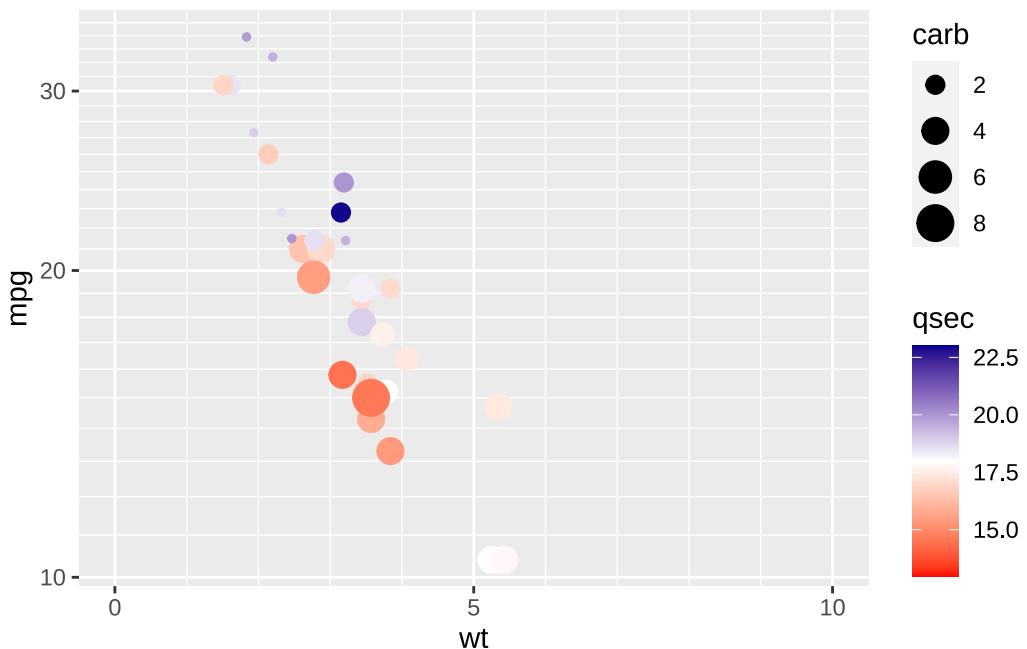


```
ggplot(data=mtcars,aes(wt, mpg,color=qsec, size=carb))+  
  scale_color_gradient(low="darkred",high="blue")+
```

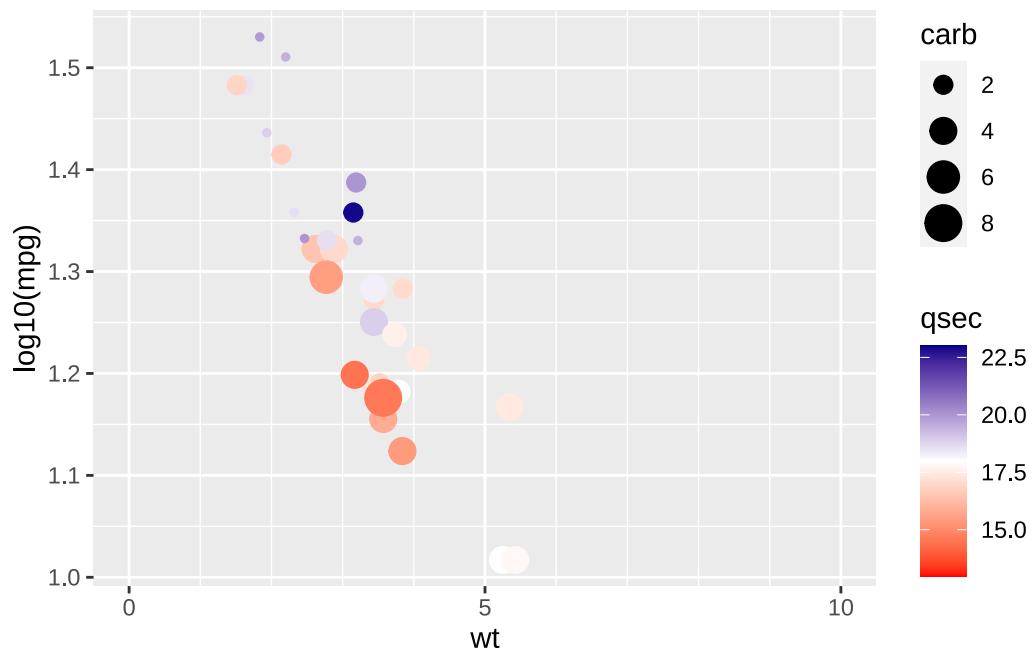
```
geom_point()
```



```
ggplot(data=mtcars,aes(wt, mpg,color=qsec, size=carb))+  
  scale_color_gradient2(low="red",high="darkblue",  
                        mid="white",  
                        limits=c(13,23),midpoint=18)+  
  geom_point()+  
  scale_x_continuous(breaks = seq(0,100,5),  
                     minor_breaks=seq(0,100,1),  
                     limits = c(0,10))+  
  scale_y_log10(minor_breaks=seq(0,100,1))
```

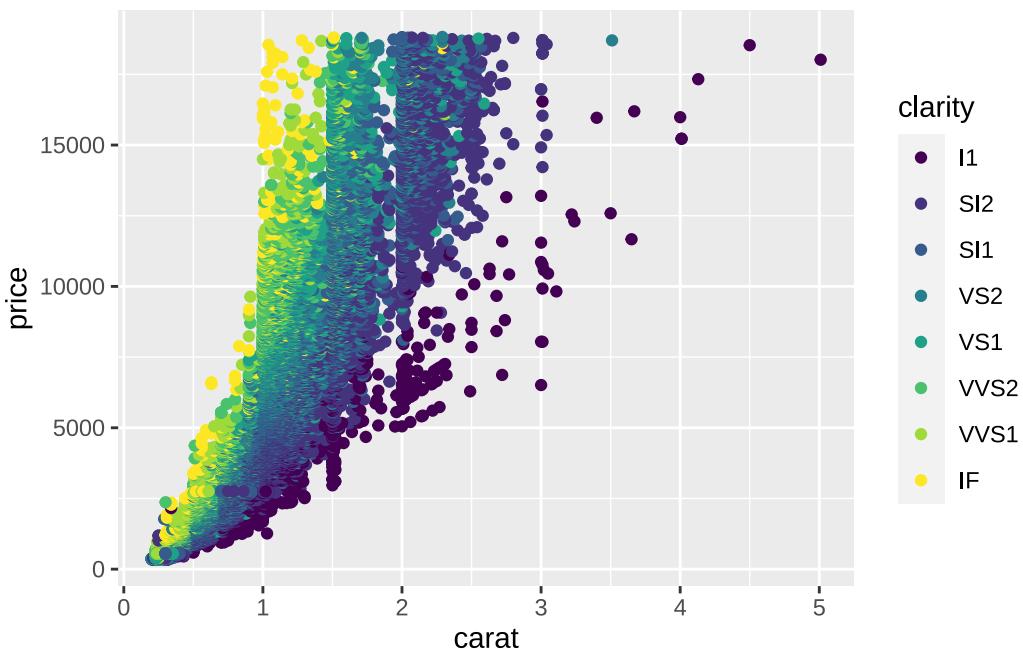


```
ggplot(data=mtcars,aes(wt, log10(mpg),color=qsec, size=carb))+  
  scale_color_gradient2(low="red",high="darkblue",  
    mid="white",  
    limits=c(13,23),midpoint=18)+  
  geom_point() +  
  scale_x_continuous(breaks = seq(0,100,5),  
    minor_breaks=seq(0,100,1),  
    limits = c(0,10))#+
```

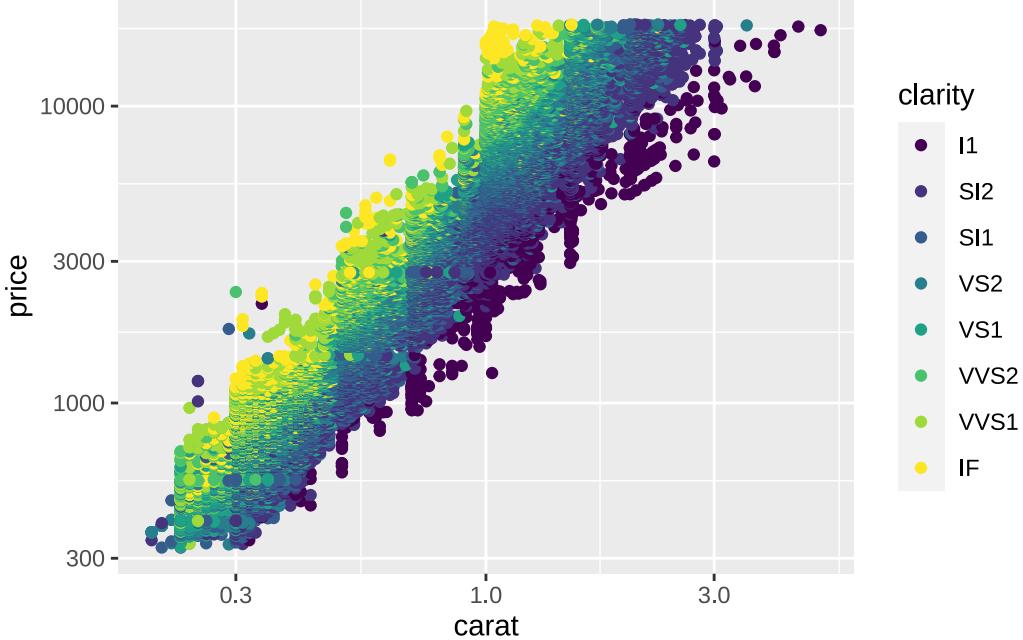


```
# scale_y_log10(minor_breaks=seq(0,100,1))

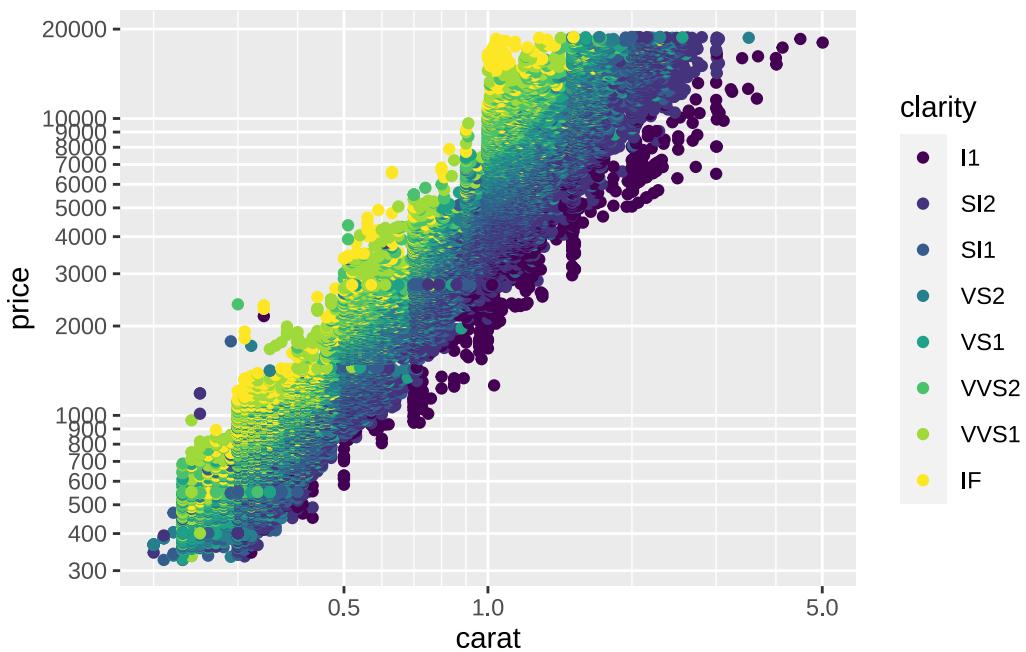
ggplot(diamonds,aes(carat,price,color=clarity))+
  geom_point()
```



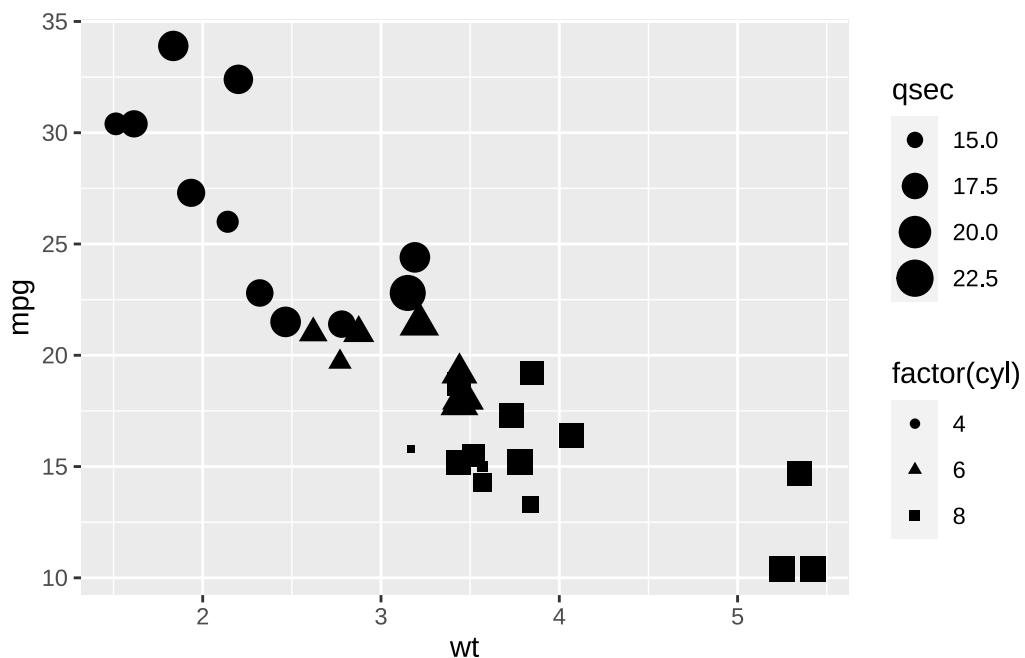
```
ggplot(diamonds,aes(carat,price,color=clarity))+  
  geom_point() +  
  scale_x_log10() +  
  scale_y_log10()
```



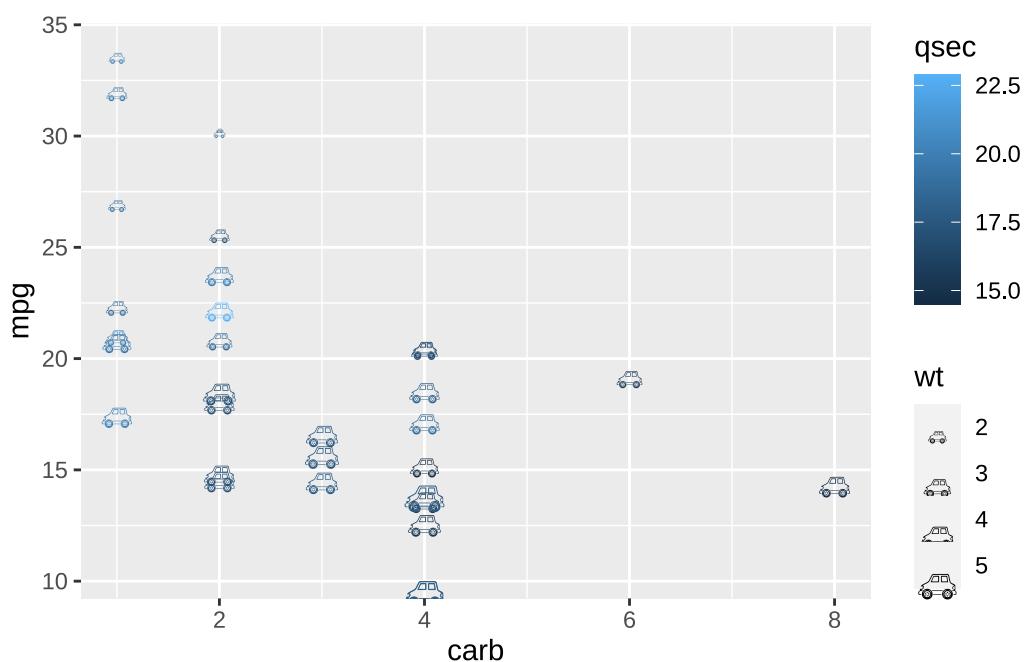
```
ggplot(diamonds,aes(carat,price,color=clarity))+  
  geom_point() +  
  scale_x_log10(  
    breaks=logrange_15,  
    minor_breaks=logrange_123456789) +  
  scale_y_log10(  
    breaks=logrange_123456789,  
    minor_breaks=logrange_123456789)
```



```
# use different aesthetic mappings  
ggplot(data=mtcars,  
        aes(wt, mpg, size=qsec, shape=factor(cyl)))+  
  geom_point()
```



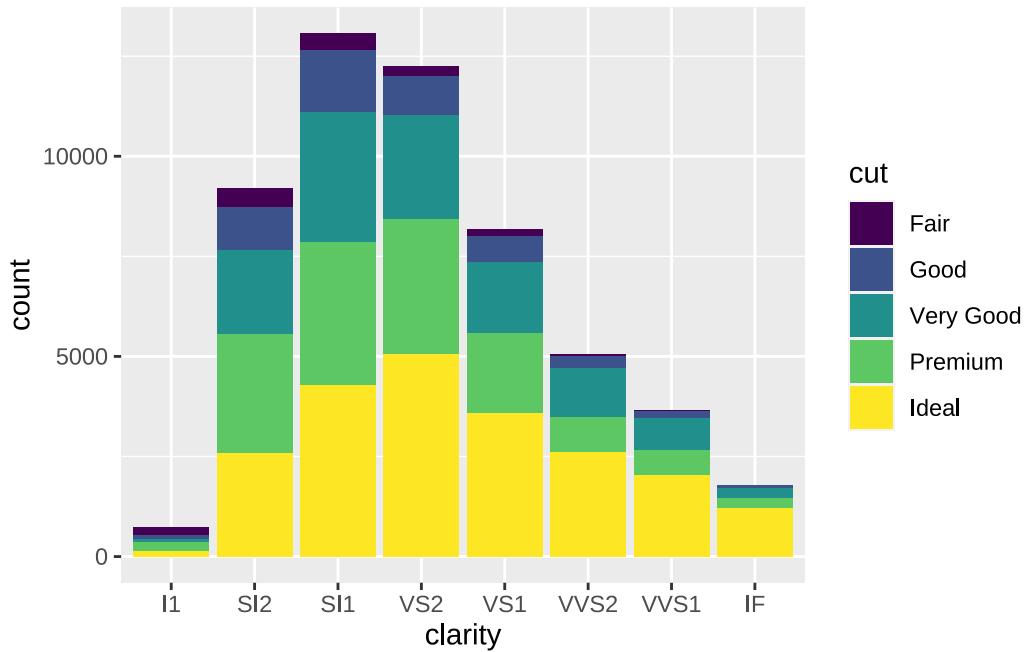
```
ggplot(data=mtcars,aes(carb, mpg,color=qsec, size=wt))+  
  geom_text(family="EmojiOne",label="\U1F697")
```



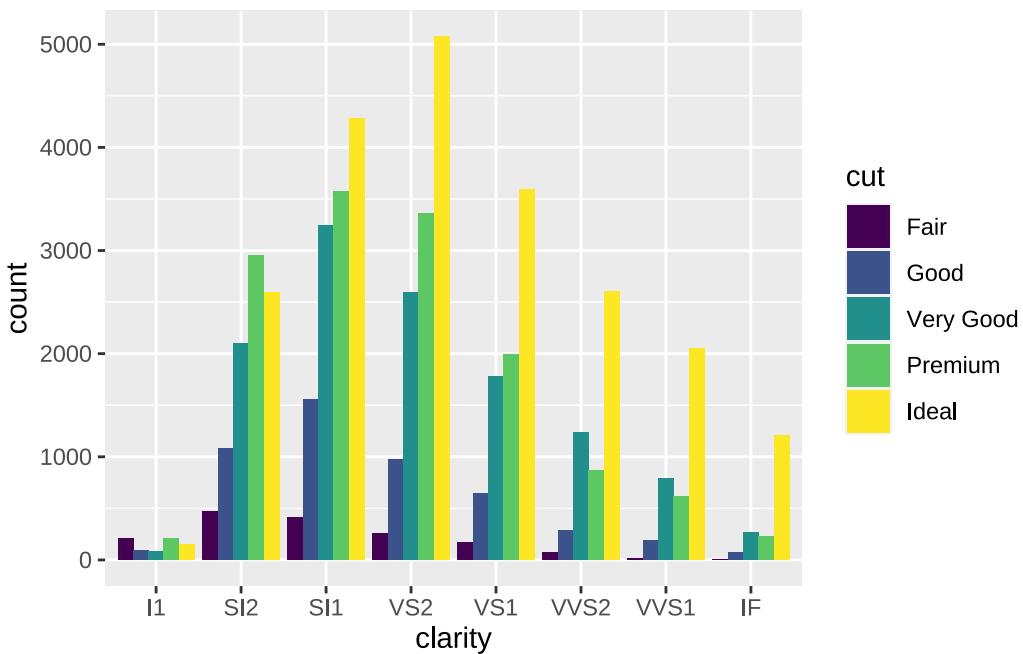
6.8 Positioning elements

The position arguments allows stacking, dodging, jittering and exact positioning of elements. Positioning is an essential part of storytelling, the same data can be presented with different focus.

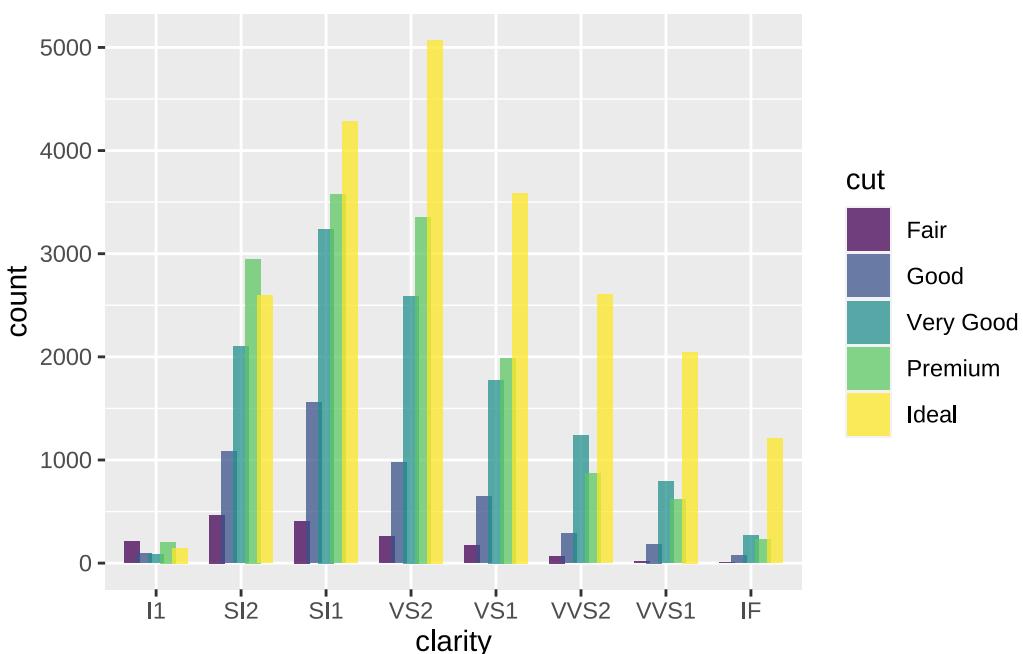
```
p<-ggplot(data=diamonds,aes(clarity,fill=cut))  
p+geom_bar(position="stack") # default for bar
```



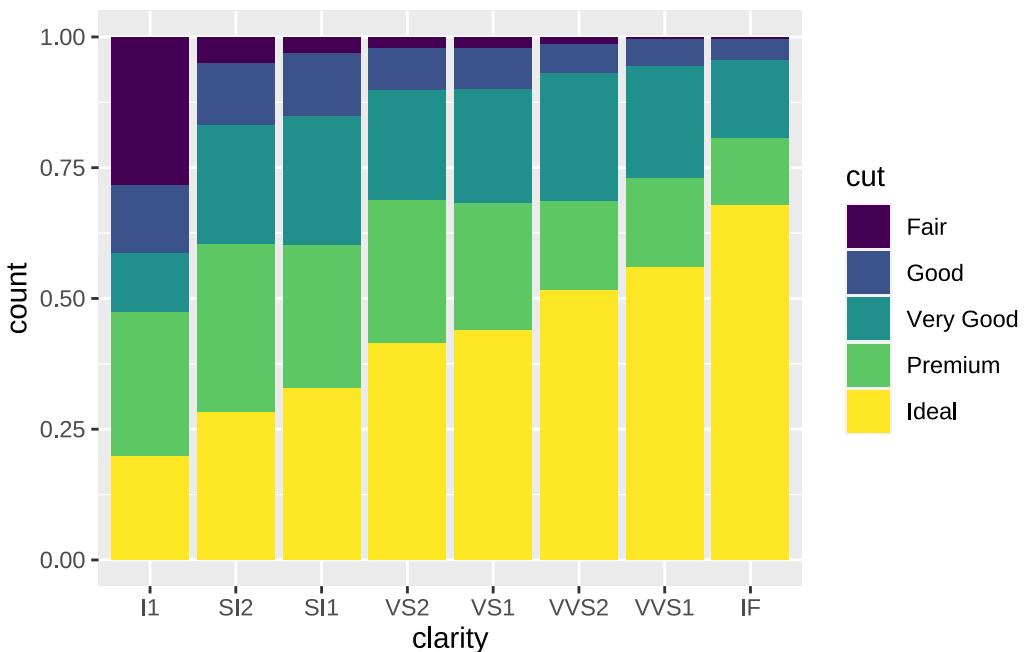
```
p+geom_bar(position="dodge")
```



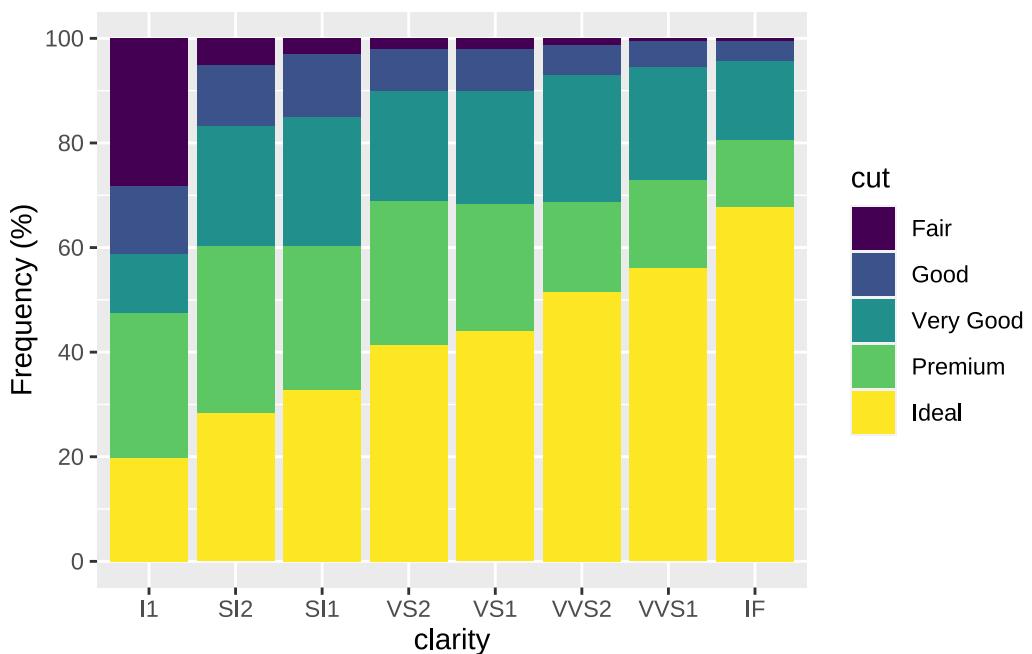
```
p+geom_bar(position=position_dodge(width = 0.7), alpha=.75)
```



```
p+geom_bar(position="fill") #y-axis labeling needs tuning
```



```
p+geom_bar(position="fill")+
  scale_y_continuous(name = "Frequency (%)",
                     breaks=seq(0,1,.2), #steps
                     labels=seq(0,100,20))
```

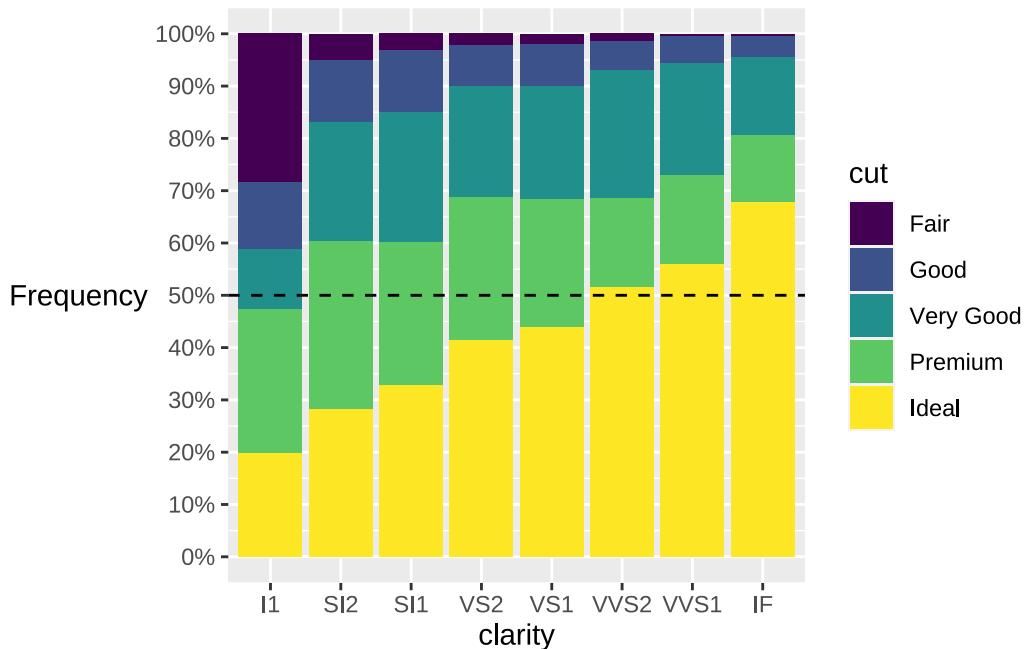


```

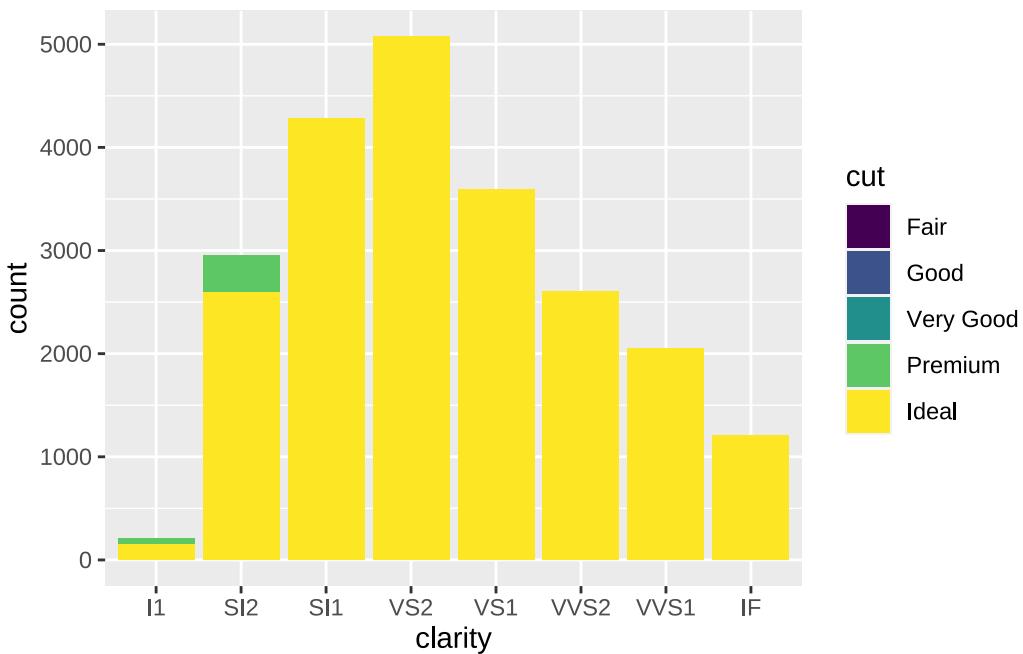
p+geom_bar(position="fill")+
  scale_y_continuous("Frequency",
                     breaks=seq(0,1,.1),
                     labels=scales::percent)+
  theme(axis.title.y = element_text(angle = 0,
                                    vjust = .5))+  

  geom_hline(yintercept = .5, linetype=2) # e.g. for reference lines

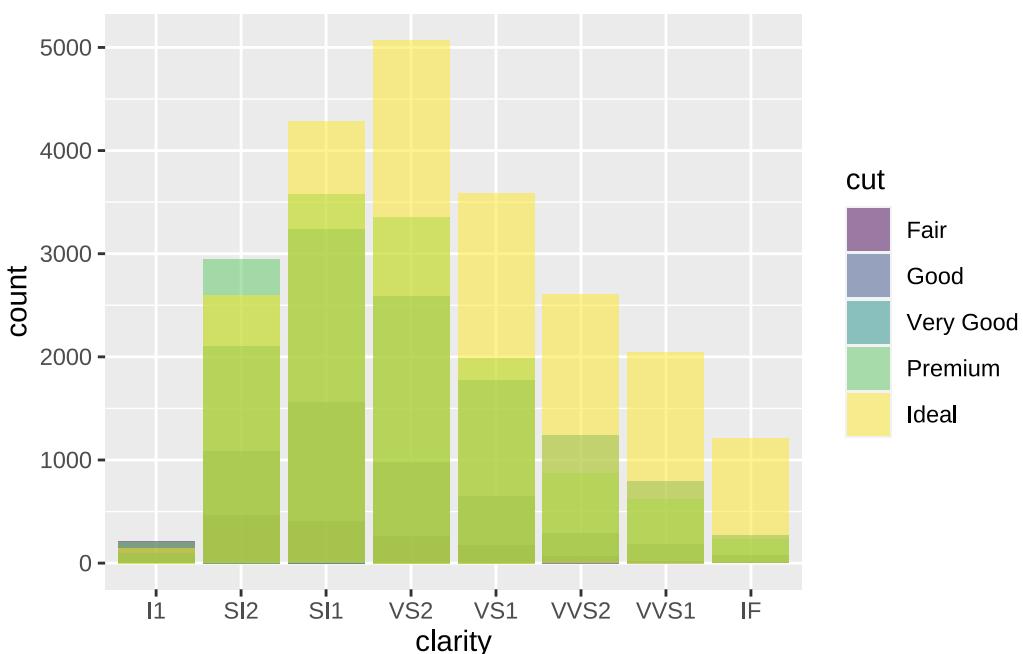
```



```
p+geom_bar(position="identity") # bad idea!
```

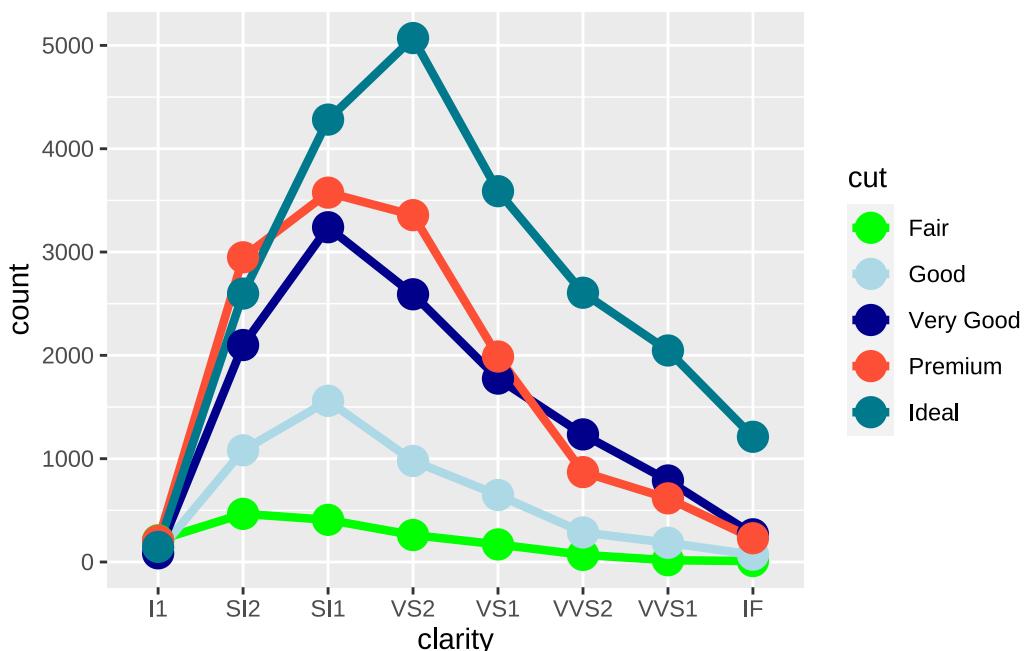


```
p+geom_bar(position="identity",alpha=.5) # even worse!!
```



```
ggplot(data=diamonds,aes(clarity,color=cut, group=cut))+  
  geom_freqpoly(stat="count",position="identity",lwd=1.5)+  
  geom_point(stat="count",size=5)+
```

```
scale_color_manual(values = c("green","lightblue",
                             "darkblue",
                             "rgb(253,79,54,maxColorValue = 255),
                             "#00798d"))
```



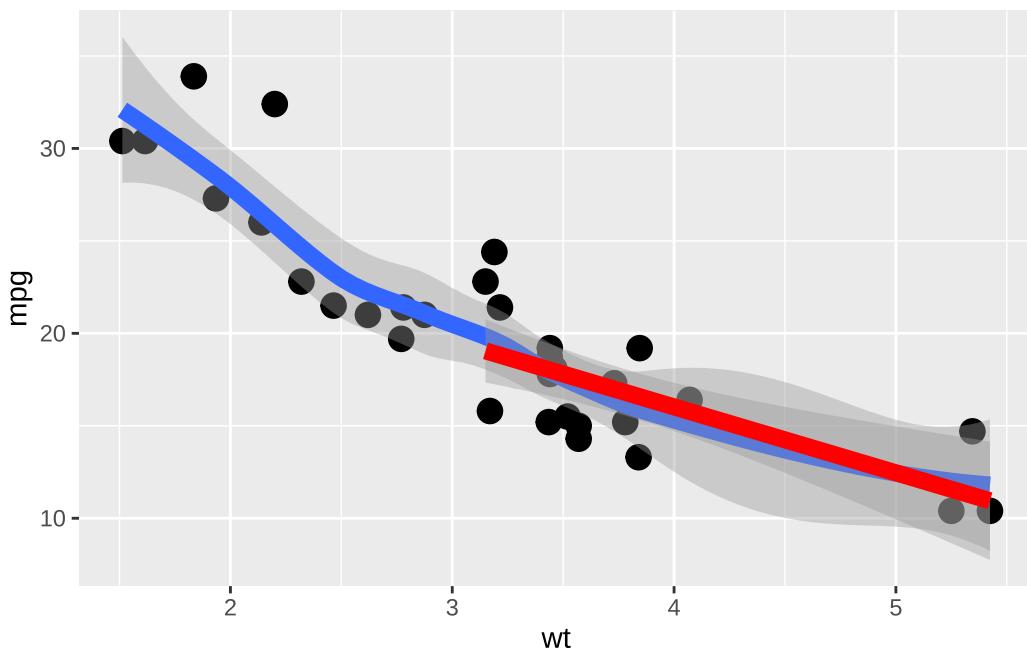
6.9 Order of layers

When combining various geoms, the order is important, as elements are not transparent by default.

```
ggplot(data=mtcars,aes(wt, mpg))+  
  geom_point(size=4)+  
  geom_smooth(size=3)+ # line overlaps points  
  geom_smooth(data=mtcars |> filter(wt>3), #picks a sub-sample  
              method="lm", linewidth=3, color="red")
```

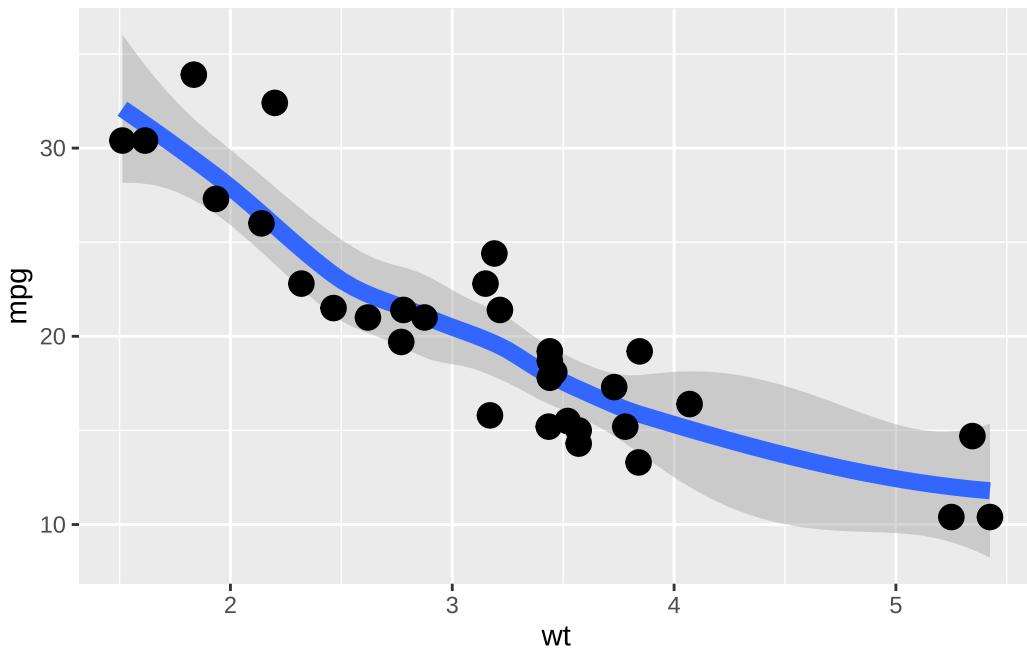
Warning: Using `size` aesthetic for lines was deprecated in ggplot2 3.4.0.
i Please use `linewidth` instead.

`geom_smooth()` using method = 'loess' and formula = 'y ~ x'
`geom_smooth()` using formula = 'y ~ x'



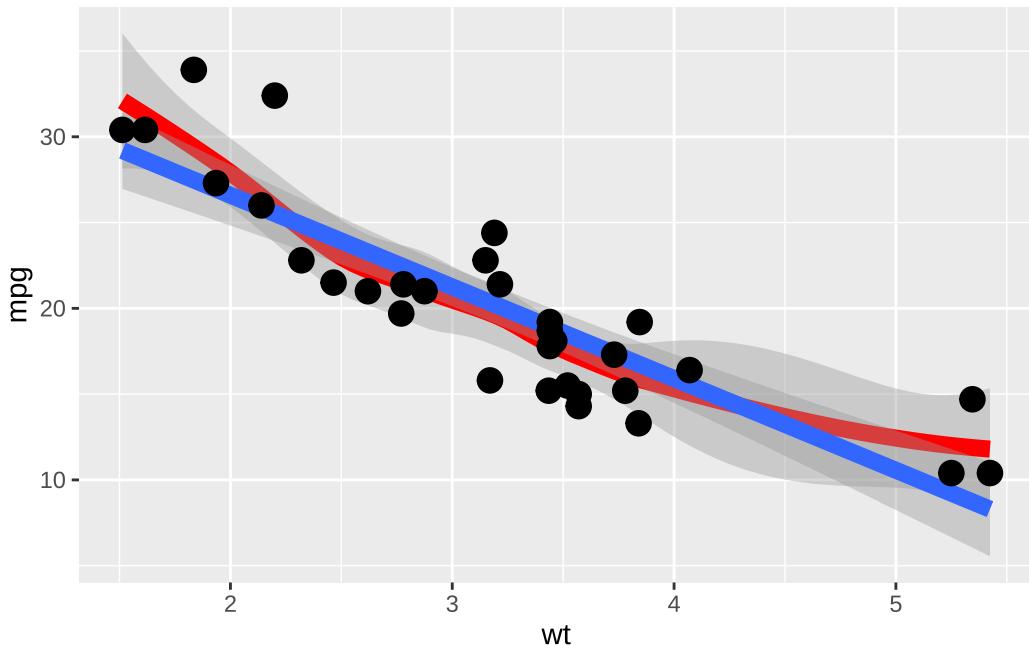
```
ggplot(data=mtcars,aes(wt, mpg))+  
  geom_smooth(linewidth=3)+  
  geom_point(size=4)
```

```
`geom_smooth()` using method = 'loess' and formula = 'y ~ x'
```



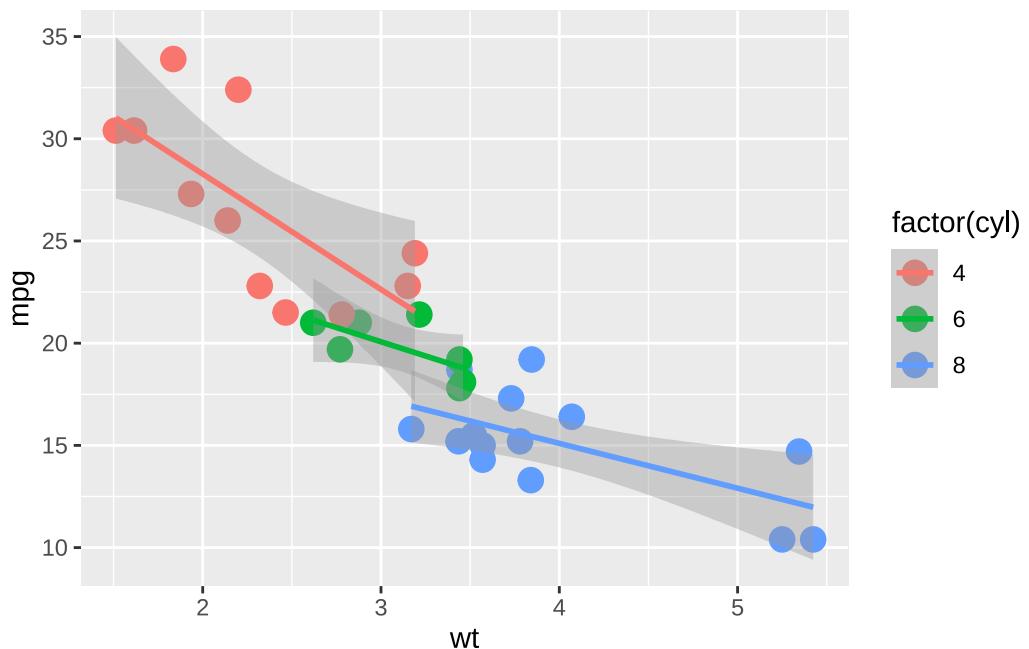
```
ggplot(data=mtcars,aes(wt, mpg))+  
  geom_smooth(linewidth=3,color="red") +  
  geom_smooth(method="lm", linewidth=3) +  
  geom_point(size=4)
```

```
`geom_smooth()` using method = 'loess' and formula = 'y ~ x'  
`geom_smooth()` using formula = 'y ~ x'
```

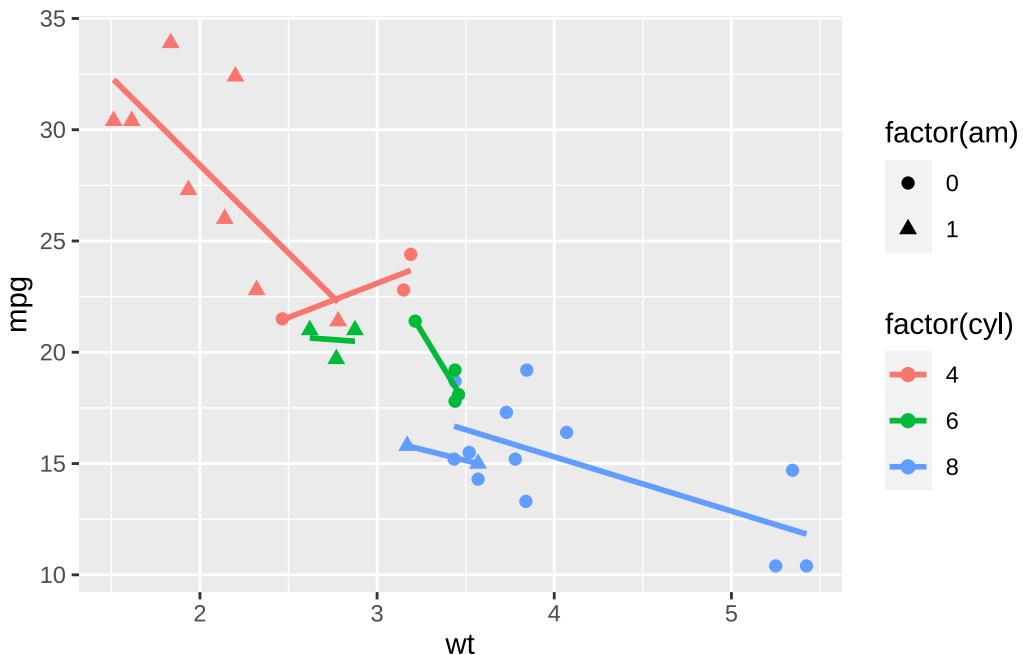


```
ggplot(data=mtcars,aes(wt, mpg,  
                      color=factor(cyl)))+  
  geom_point(size=4)+  
  geom_smooth(method="lm", linewidth=1)
```

```
`geom_smooth()` using formula = 'y ~ x'
```



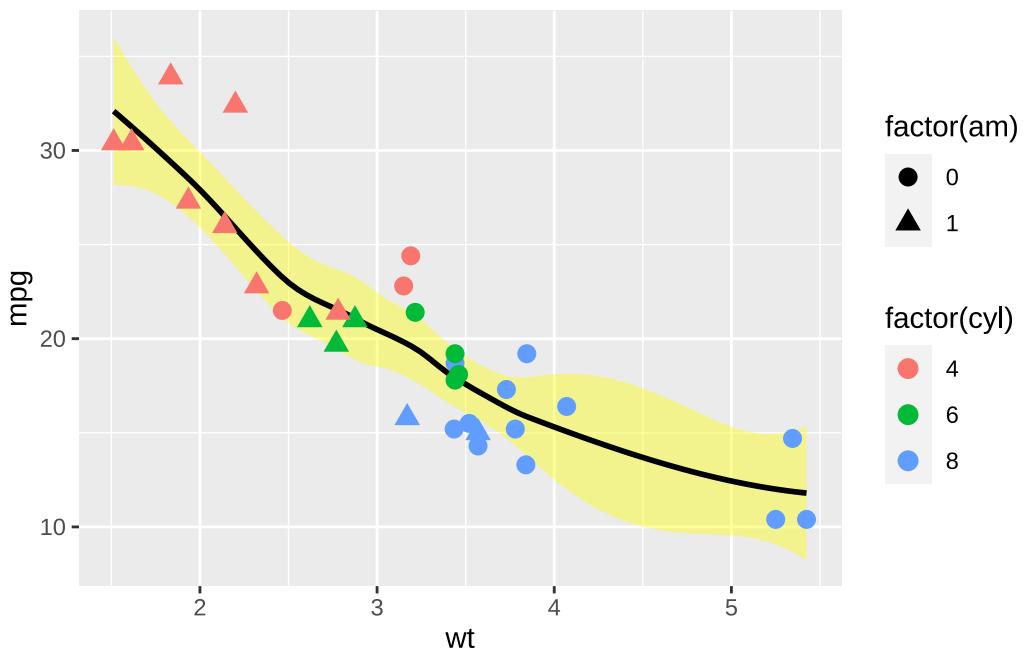
```
ggplot(data=mtcars,aes(wt, mpg,
                        color=factor(cyl),
                        shape=factor(am)))+
  geom_point(size=2)+
  geom_smooth(method="lm", linewidth=1, se=FALSE)
`geom_smooth()` using formula = 'y ~ x'
```



6.10 Local aesthetics for layers

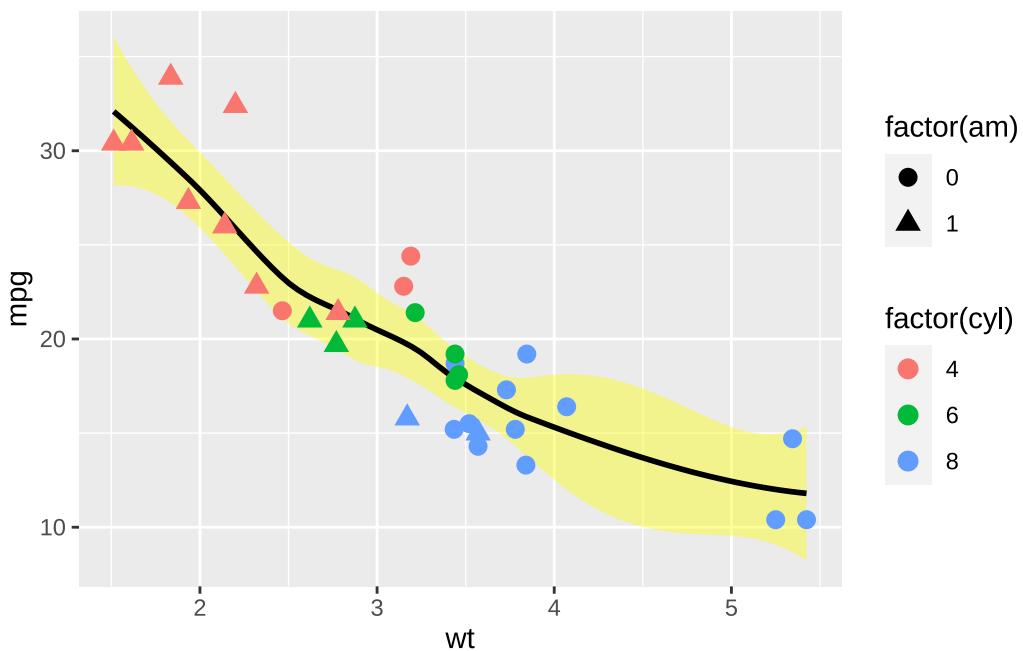
```
#? lm for all?
ggplot(data=mtcars,aes(wt, mpg))+
  geom_smooth(size=1,color="black",fill="yellow")+
  geom_point(size=3,aes(color=factor(cyl),shape=factor(am))) #aes for geom only

`geom_smooth()` using method = 'loess' and formula = 'y ~ x'
```



```
ggplot(data=mtcars, aes(wt, mpg, color=factor(cyl)))+
  geom_smooth(size=1, color="black", fill="yellow")+ # global color overwritten
  geom_point(size=3, aes(shape=factor(am)))
```

`geom_smooth()` using method = 'loess' and formula = 'y ~ x'



6.11 Faceting (splitting) plots

Visualizing many groups can lead to confusing / too-busy plots, splitting is often an alternative. Visualizing many variables at the same time can be achieved with facets as well (after pivot_longer).

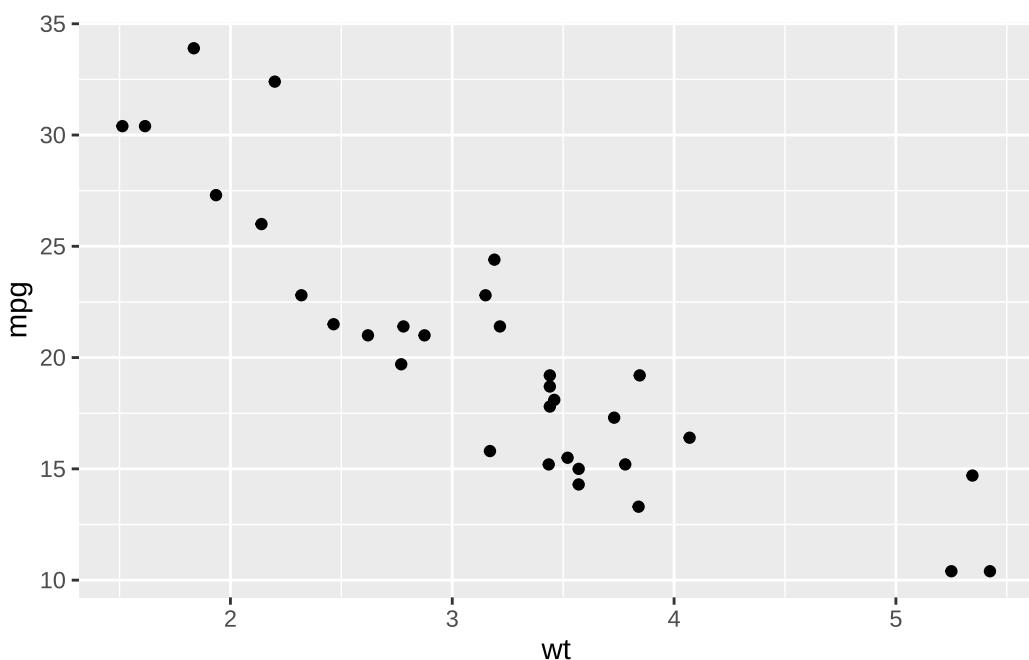
6.11.1 facet_grid

Grids are specified by defining variables for rows and/or columns, empty combinations still are shown.

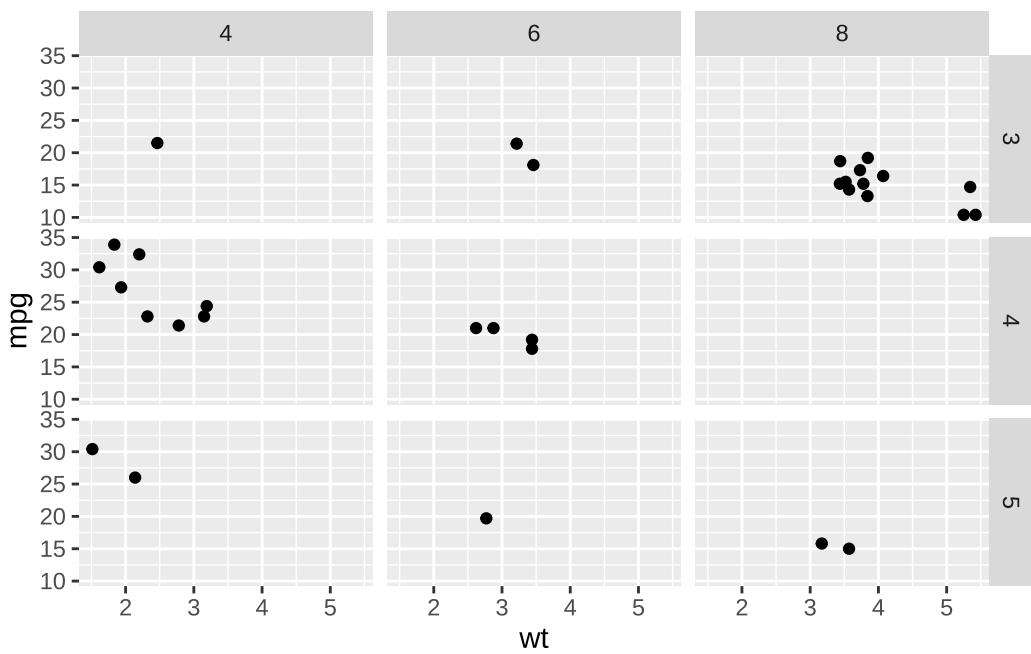
Labeling of facets often requires name and content to be informative.

Margins (taking all elements together) can be shown for rows and/or columns.

```
(p.tmp <- ggplot(mtcars, aes(wt, mpg)) +  
  geom_point())
```



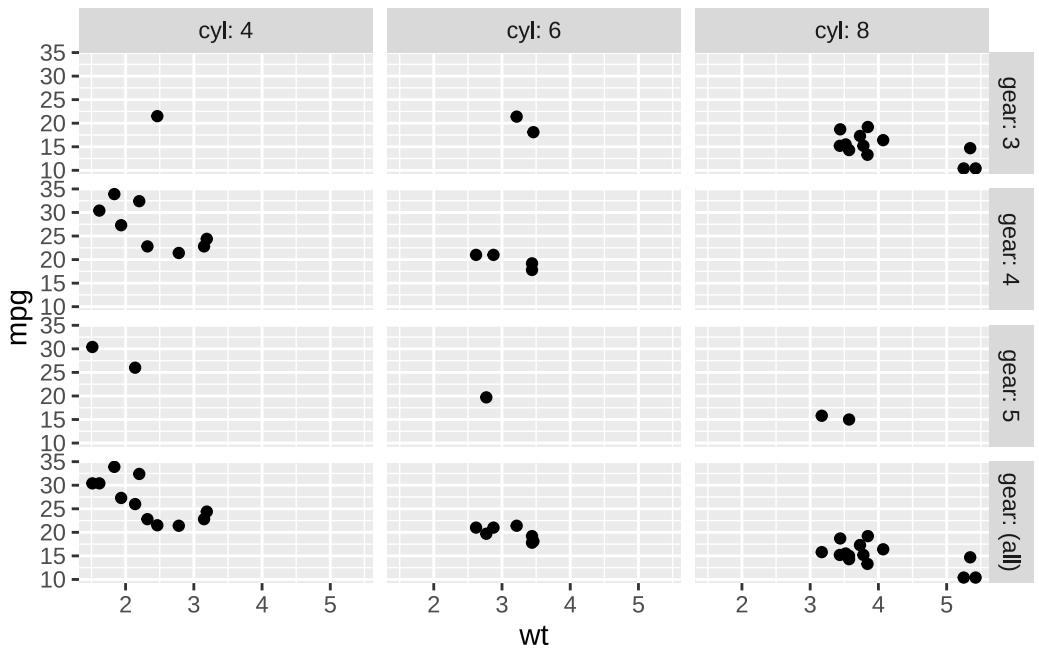
```
p.tmp + facet_grid(rows = vars(gear),  
                    cols = vars(cyl))
```



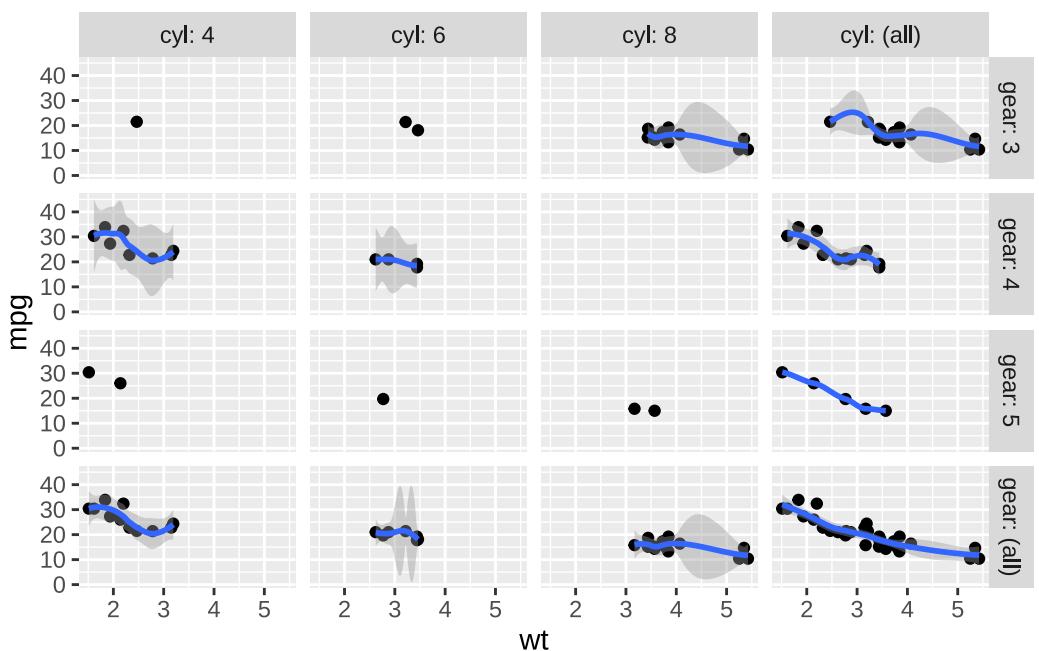
```
cat("facet labeling improved:\n")
```

facet labeling improved:

```
p.tmp + facet_grid(rows = vars(gear),  
                    cols = vars(cyl),  
                    labeller=label_both,margins="gear")
```



```
# options(warn=-1)
p + geom_smooth() +
  facet_grid(rows = vars(gear),
             cols = vars(cyl),
             labeller=label_both, margins=TRUE)
```

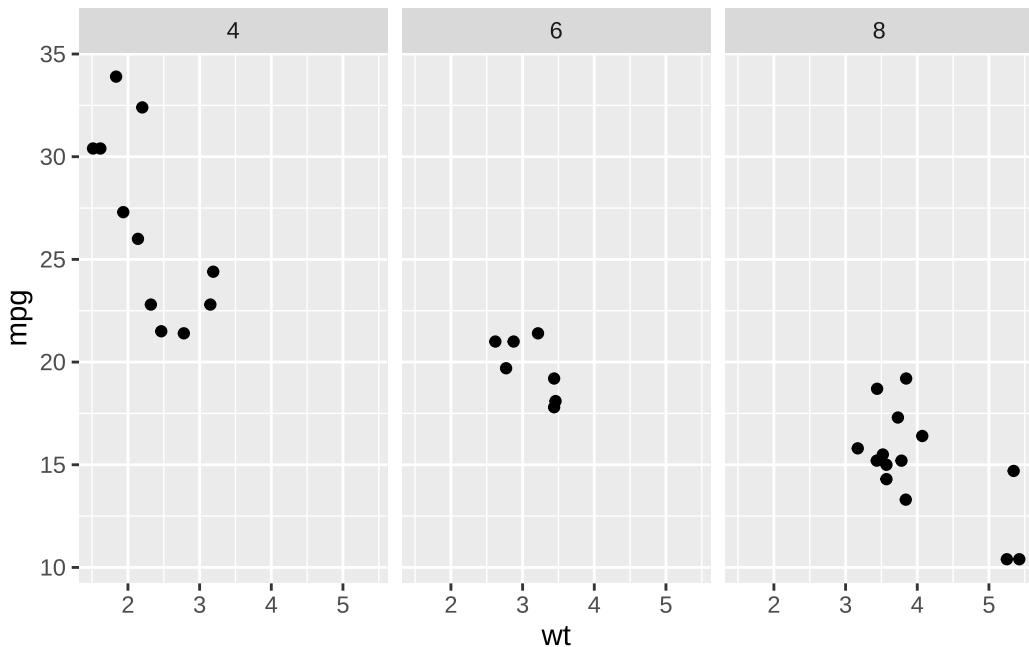


```
# options(warn=0)
```

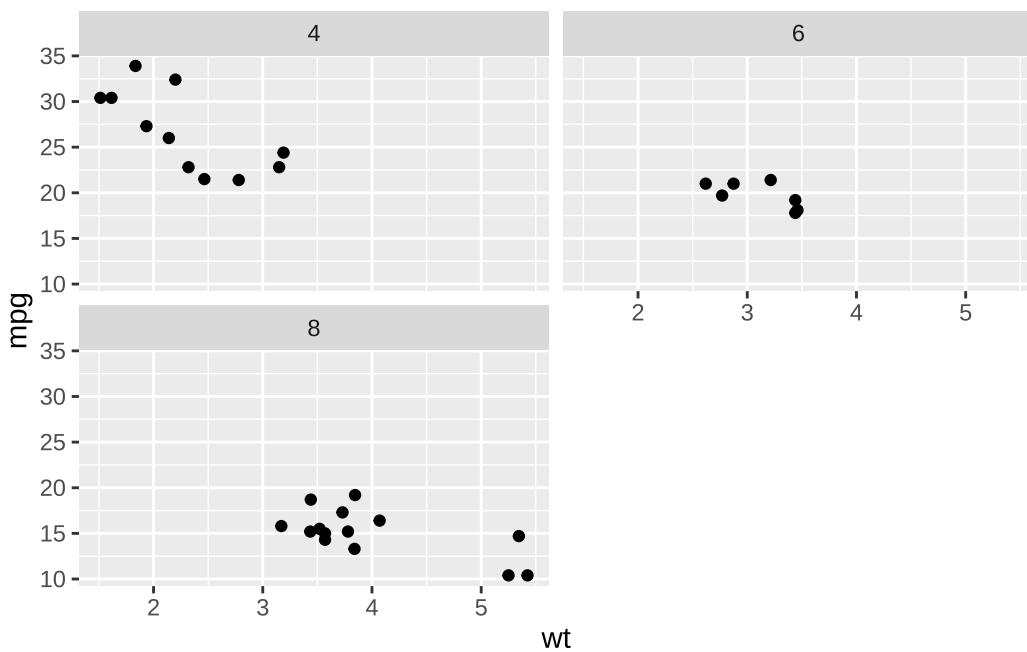
6.11.2 facet_wrap

When showing many facets, wrapping around after some is useful, less systematic than grid.

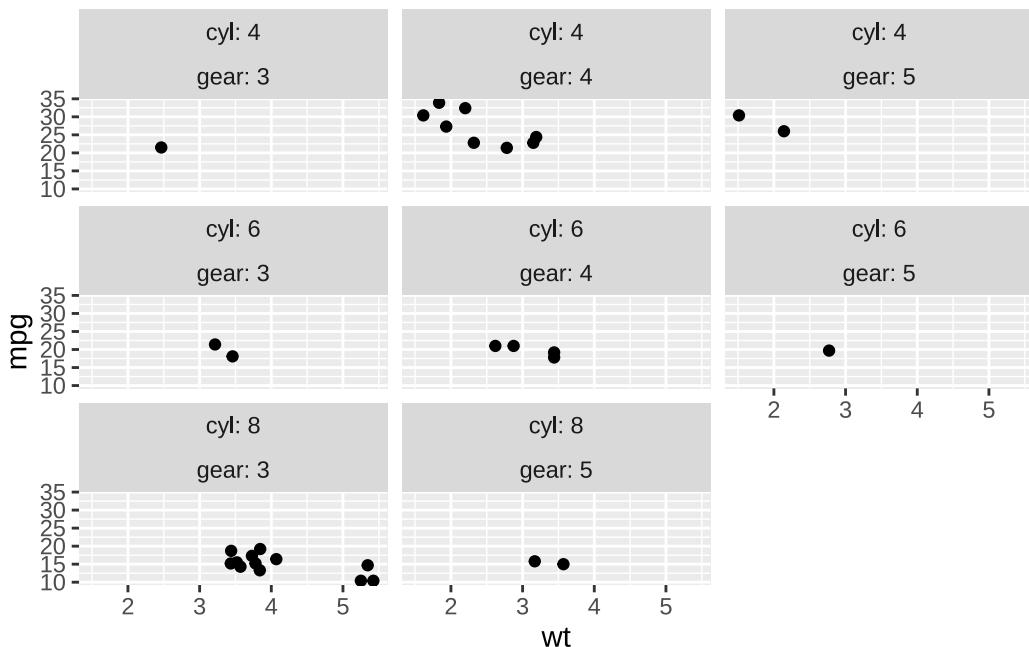
```
p.tmp + facet_wrap(facets = vars(cyl))
```



```
p.tmp + facet_wrap(facets = vars(cyl), ncol=2)
```



```
# empty combination is dropped
p.tmp + facet_wrap(facets=vars(cyl,gear), labeller=label_both)
```



```
#combining variables
mtcars |>
```

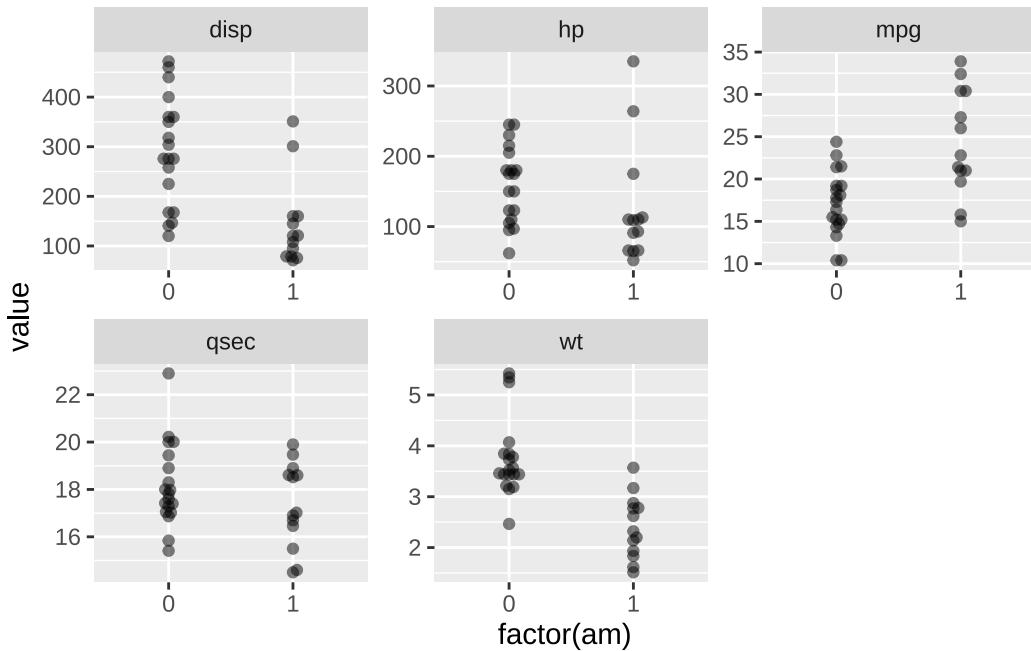
```

pivot_longer(cols = c(wt, mpg, hp, disp, qsec)) |>
ggplot(aes(x=factor(am), y=value))+  

geom_beeswarm(alpha=.5, cex=2)+  

facet_wrap(facets = vars(name), scales="free")

```

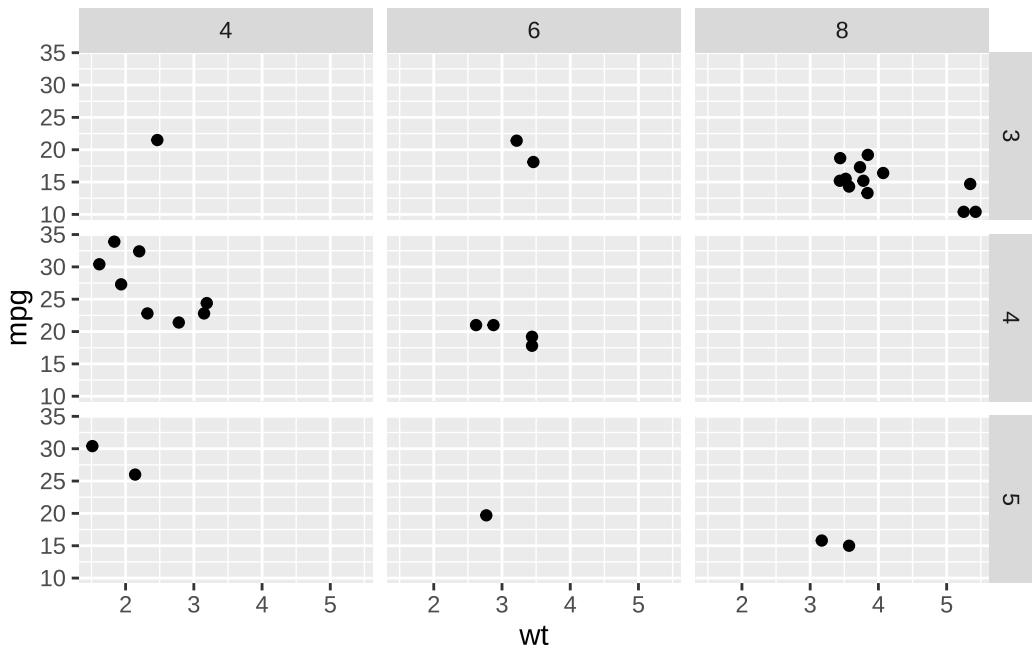


6.11.3 Controlling scales in facets (default: scales="fixed")

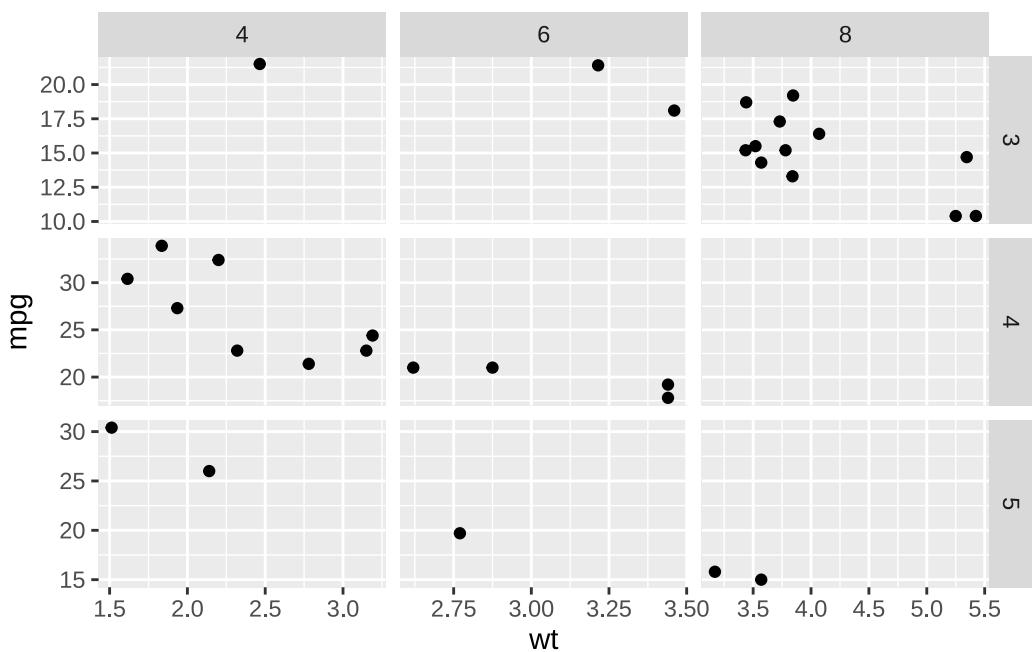
```

p.tmp + facet_grid(gear~cyl, scales="fixed")

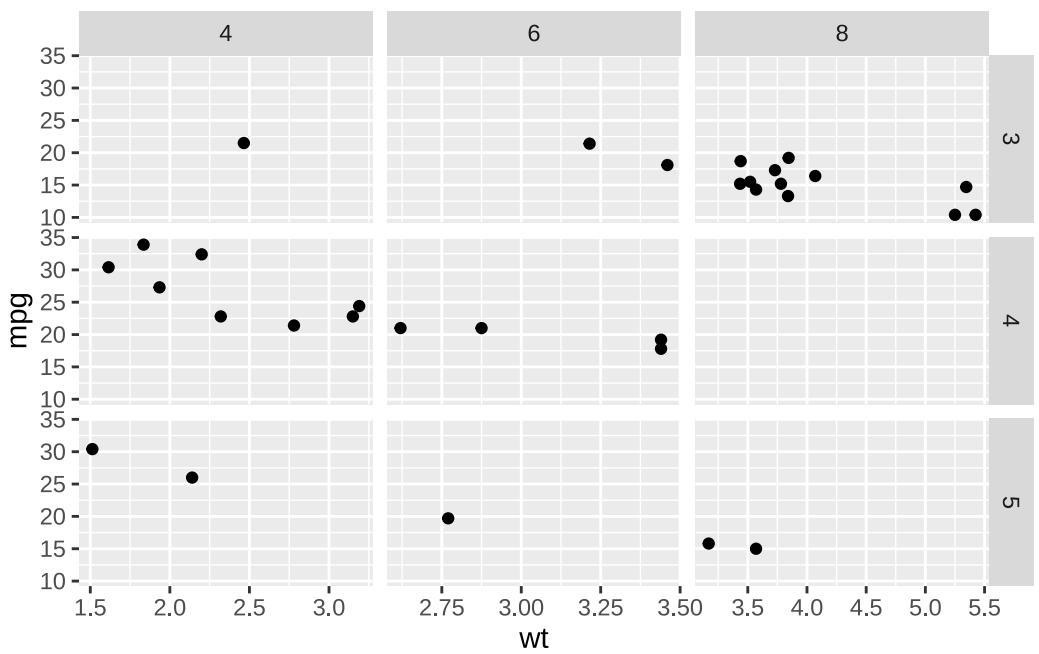
```



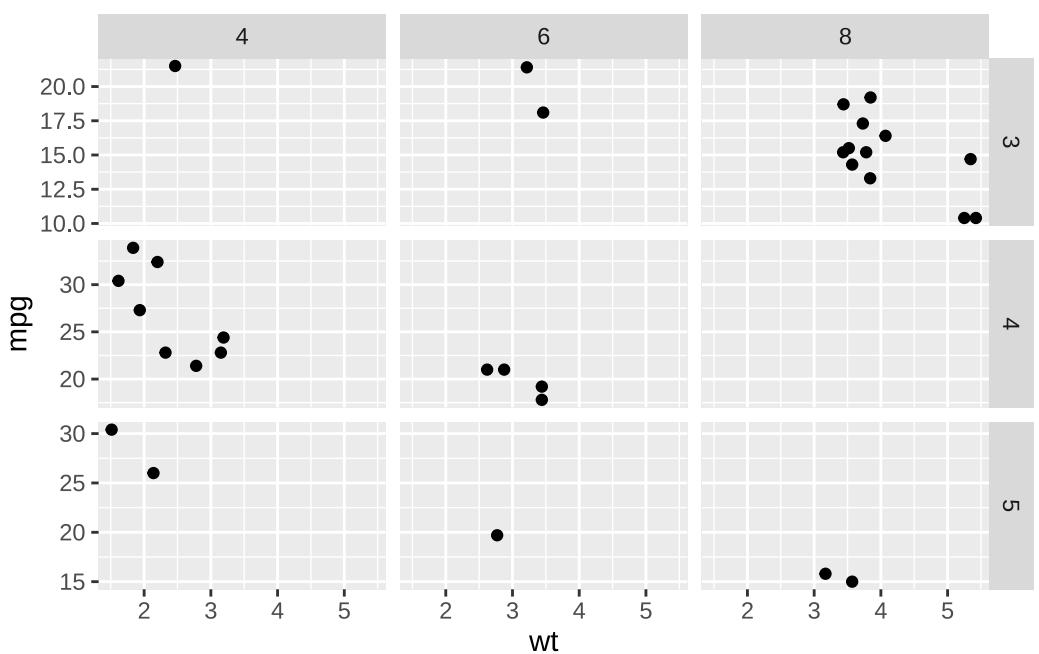
```
p.tmp + facet_grid(gear~cyl, scales="free")
```



```
p.tmp + facet_grid(gear~cyl, scales="free_x")
```



```
p.tmp + facet_grid(gear~cyl, scales="free_y")
```

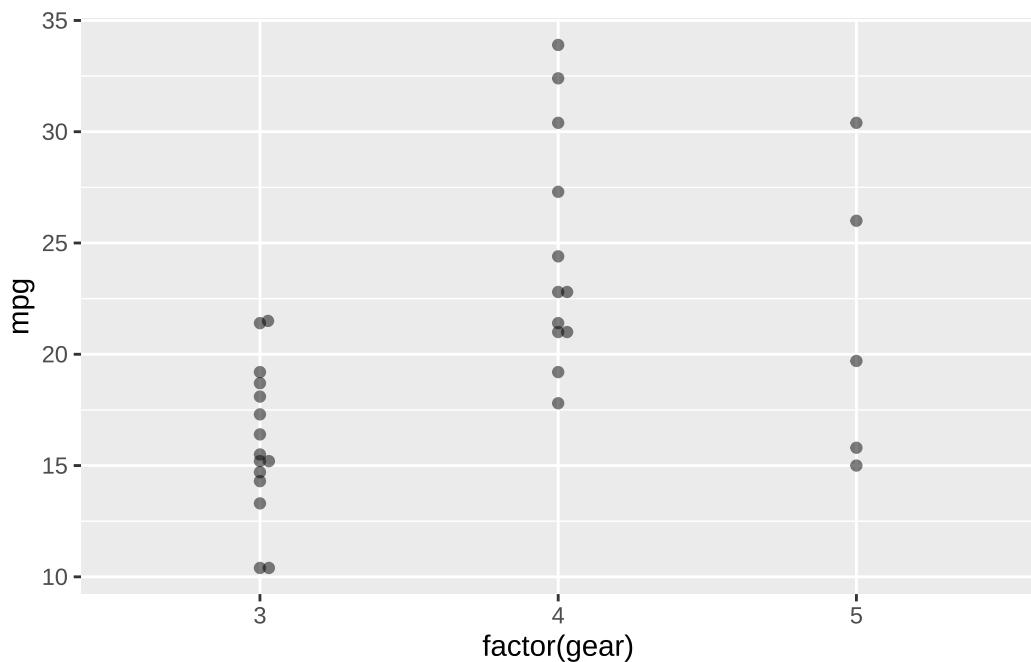


6.12 Showing summaries

While plotting underlying rawdata is pretty informative, adding summary statistics guides the viewer. Error bars help to evaluate differences visible, but need to be labelled!!

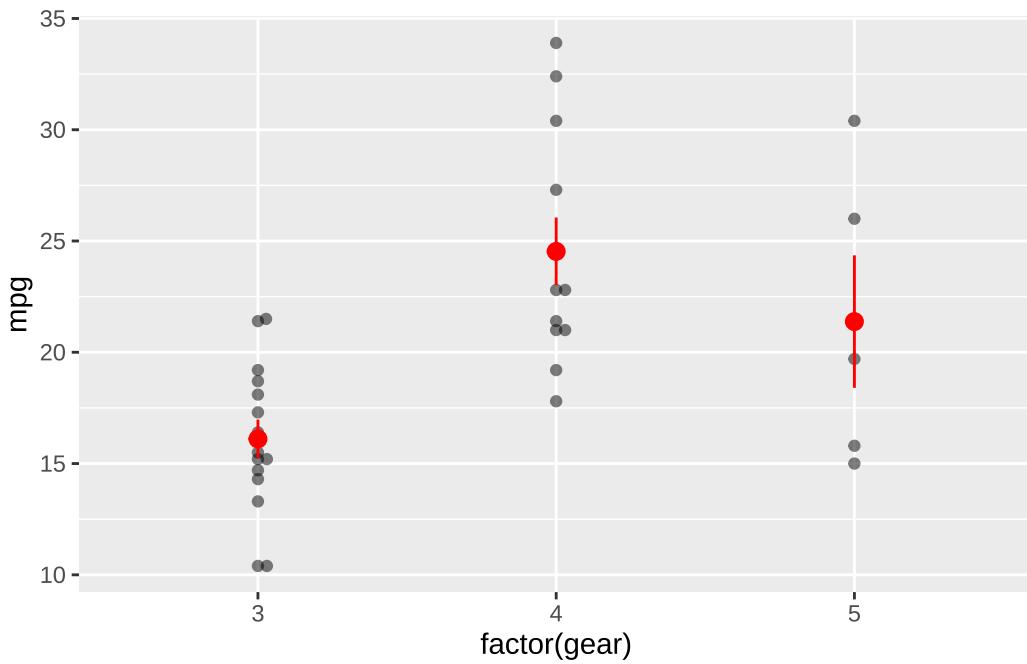
Functions for summary statistics (mean_se, mean_cl_normal, mean_cl_boot etc.) are build on top of Hmisc functions. So this package is needed but not automatically installed with ggplot2.

```
(plottemp <- ggplot(mtcars,aes(factor(gear),mpg))+  
  geom_beeswarm(alpha=.5))
```

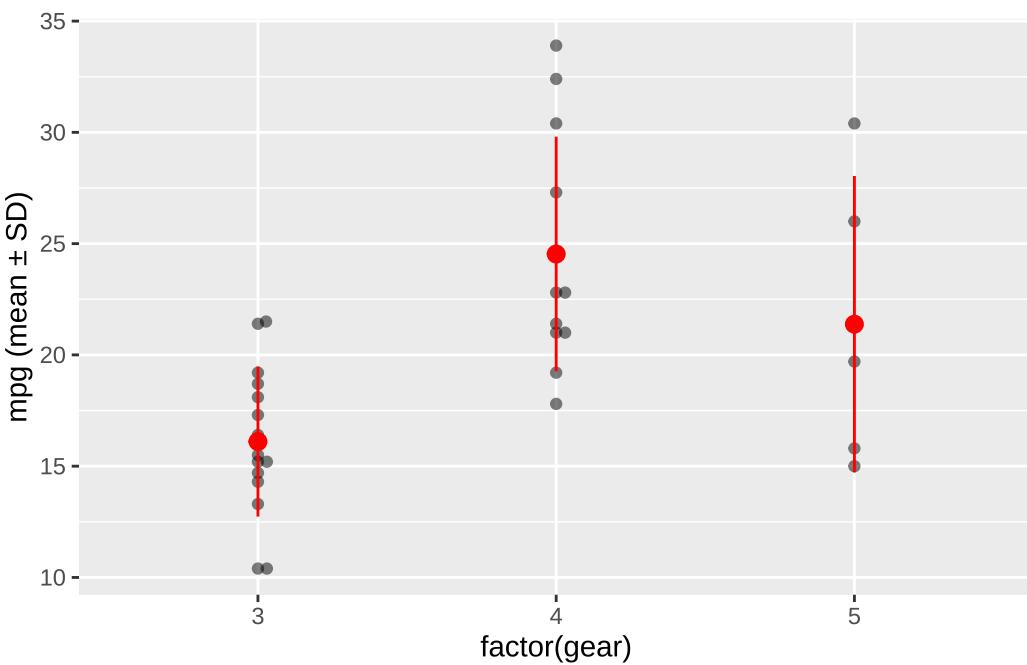


```
plottemp+stat_summary(color="red")
```

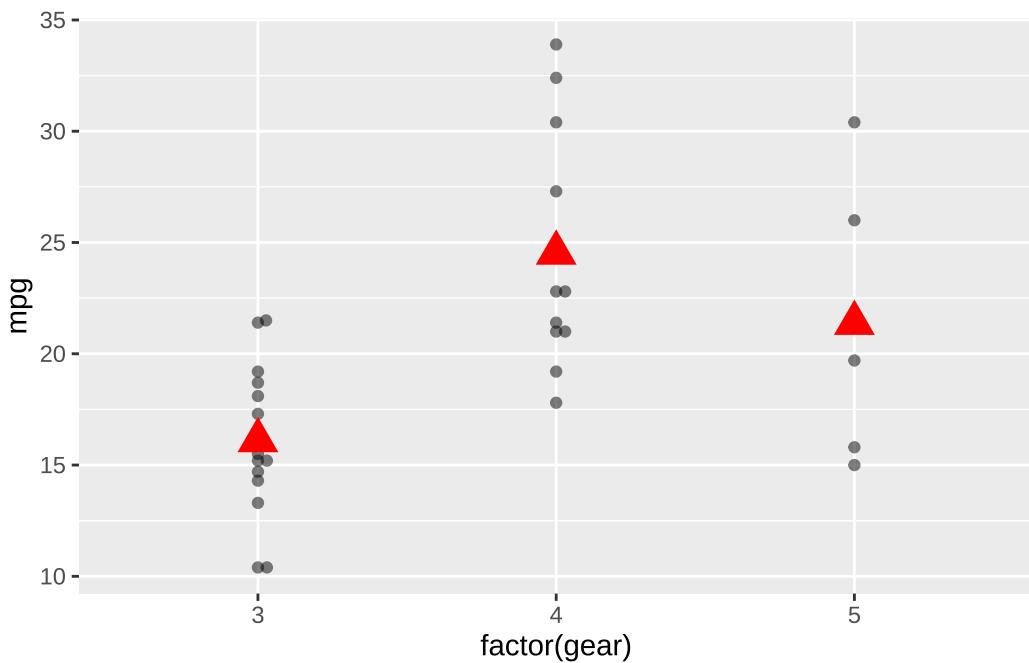
```
No summary function supplied, defaulting to `mean_se()`
```



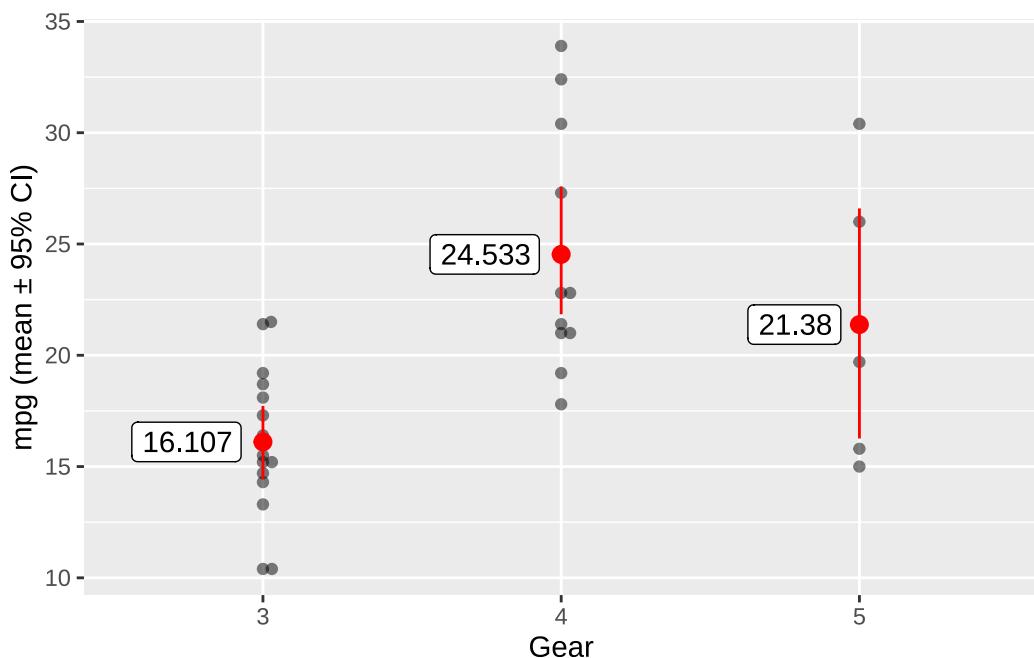
```
plottemp+stat_summary(fun.data="mean_sdl",
                      fun.args=list(mult=1),
                      color="red")+
  ylab("mpg (mean \u00b1 SD)")
```



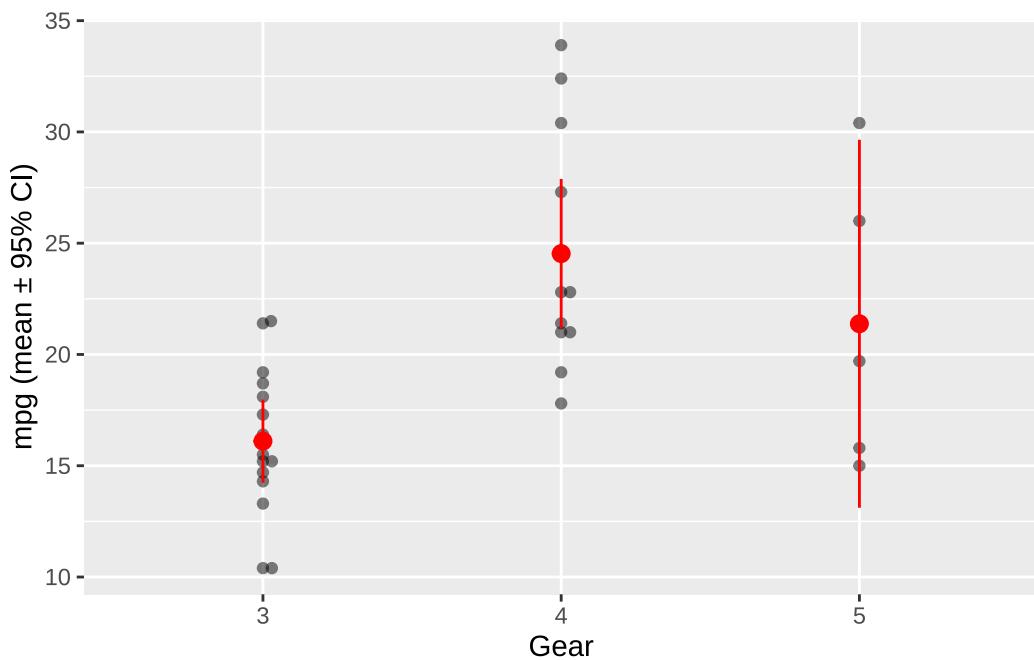
```
plottemp+stat_summary(geom = "point", shape=17, size=5,
                      fun = "mean", color="red")
```



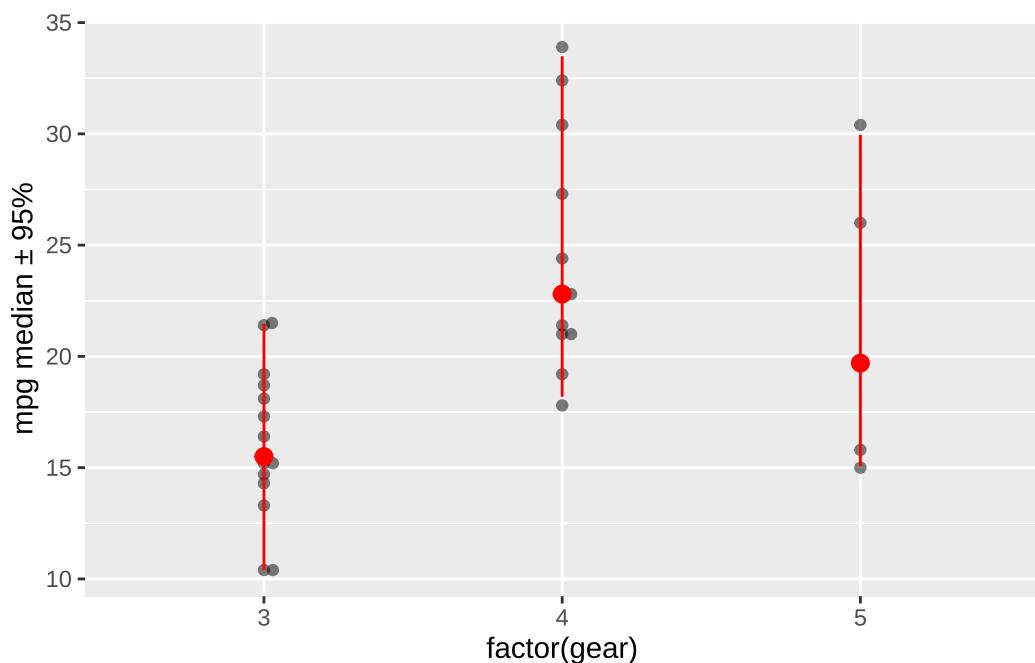
```
means <- mtcars |>
  group_by(gear) |>
  summarise(mean=round(mean(mpg),3),sd=sd(mpg))
plottemp+stat_summary(fun.data="mean_cl_boot",
                      fun.args=list(B=10^4),
                      color="red")+
  geom_label(data=means,
             aes(factor(gear),mean,label=mean),
             hjust=1.2)+
  ylab("mpg (mean \u00b1 95% CI)")+
  xlab("Gear")
```



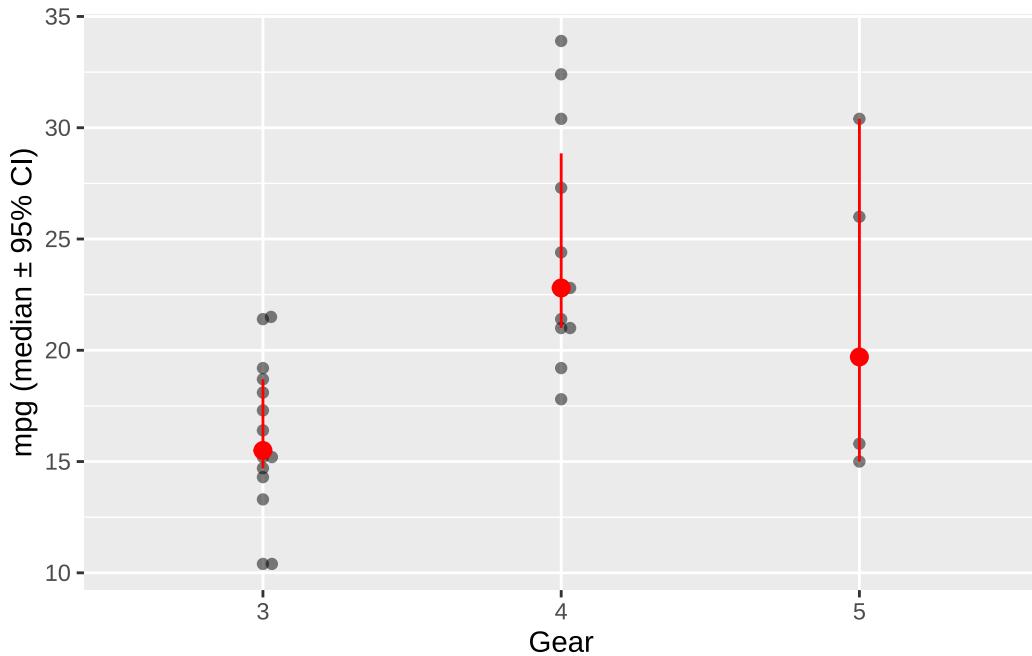
```
plottemp+stat_summary(fun.data="mean_cl_normal",color="red")+
  ylab("mpg (mean \u00b1 95% CI)")+
  xlab("Gear")
```



```
plottemp+stat_summary(fun.data="median_hilow",color="red")+
  ylab("mpg median \u00b1 95%")
```



```
# geom_pointrange()
plottemp+stat_summary(fun.data="median_cl_boot_gg",color="red")+
  ylab("mpg (median \u00b1 95% CI)")+
  xlab("Gear")
```



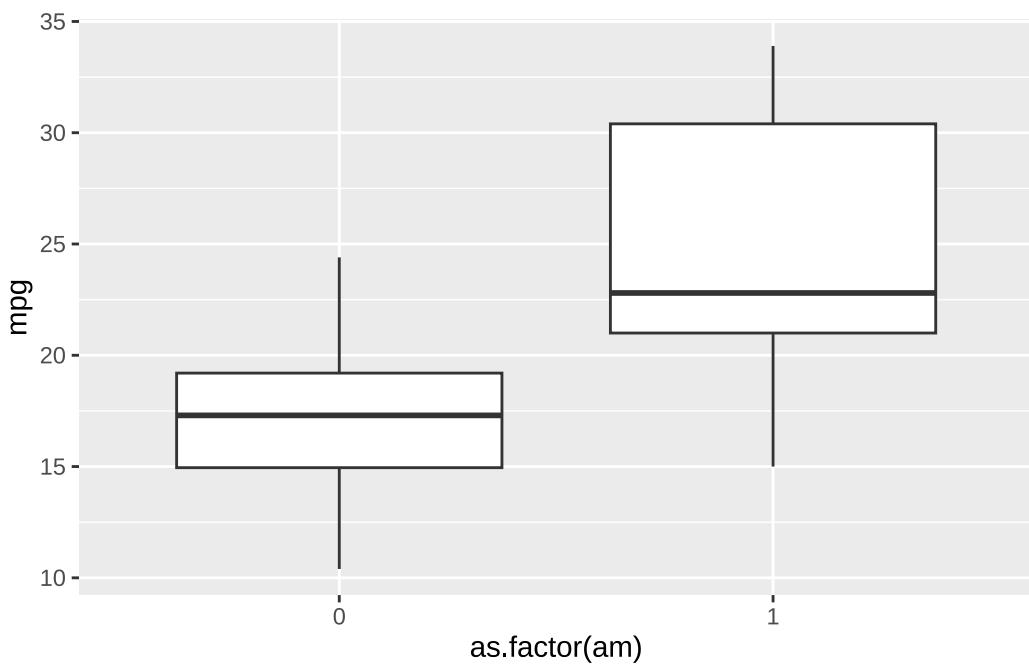
6.13 Indicating significances

Package ggsign makes it easier to add significance brackets (no more photoshopping), it either computes p-values or takes them from your testing (and this is what you should always be doing!).

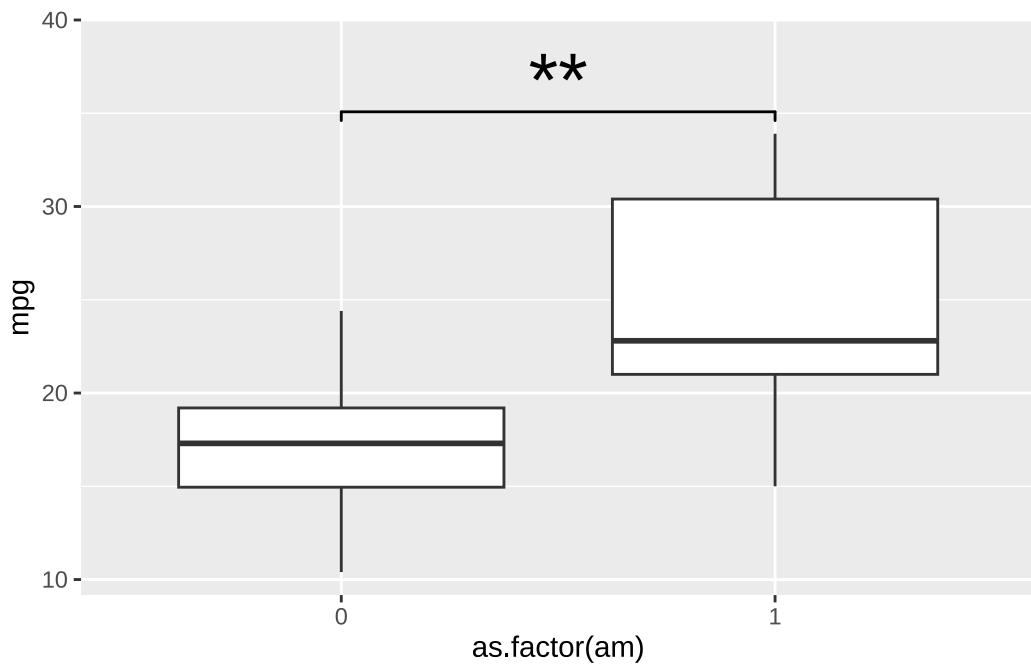
```
# ggsign ####
p <- round(wilcox.test(mtcars$mpg~mtcars$am)$p.value,5)
```

Warning in wilcox.test.default(x = DATA[[1L]], y = DATA[[2L]], ...): kann bei Bindungen keinen exakten p-Wert Berechnen

```
(plottemp <- ggplot(mtcars,aes(as.factor(am),mpg))+  
  geom_boxplot())
```

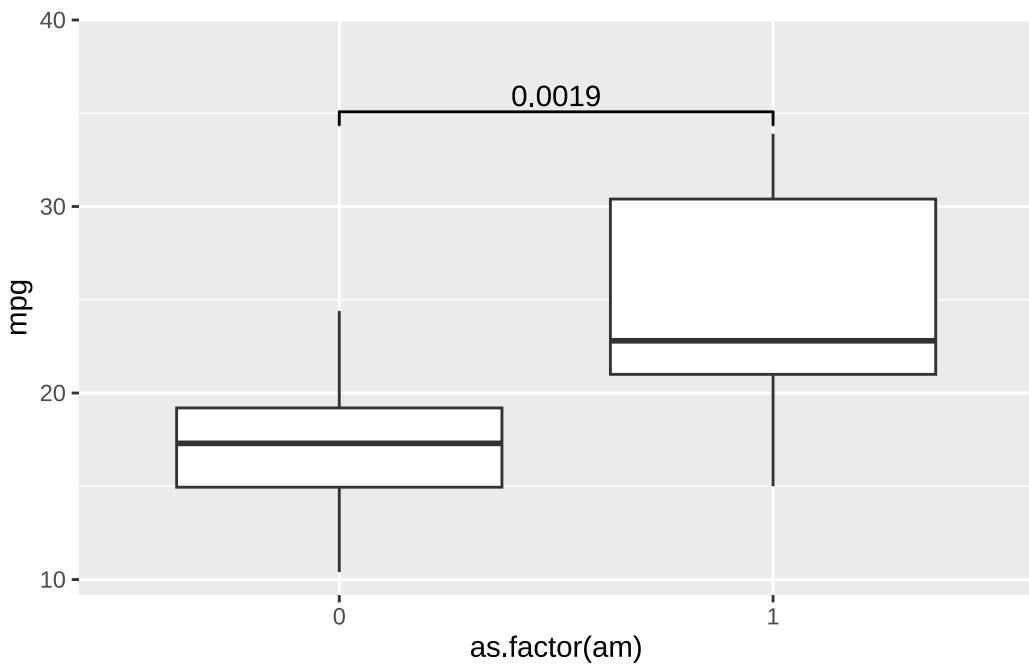


```
plottemp+geom_signif(  
  comparisons=list(c(1,2)),  
  # aes(y=0),  
  textsize = rel(10), vjust = .0,  
  #y_position=max(mtcars$mpg)+3,  
  # annotations=paste0("p = ", p),  
  annotations=markSign(p),  
  # annotations=p,  
  tip_length=.02)+  
  scale_y_continuous(expand = expansion(mult=c(0.05,.2)))
```

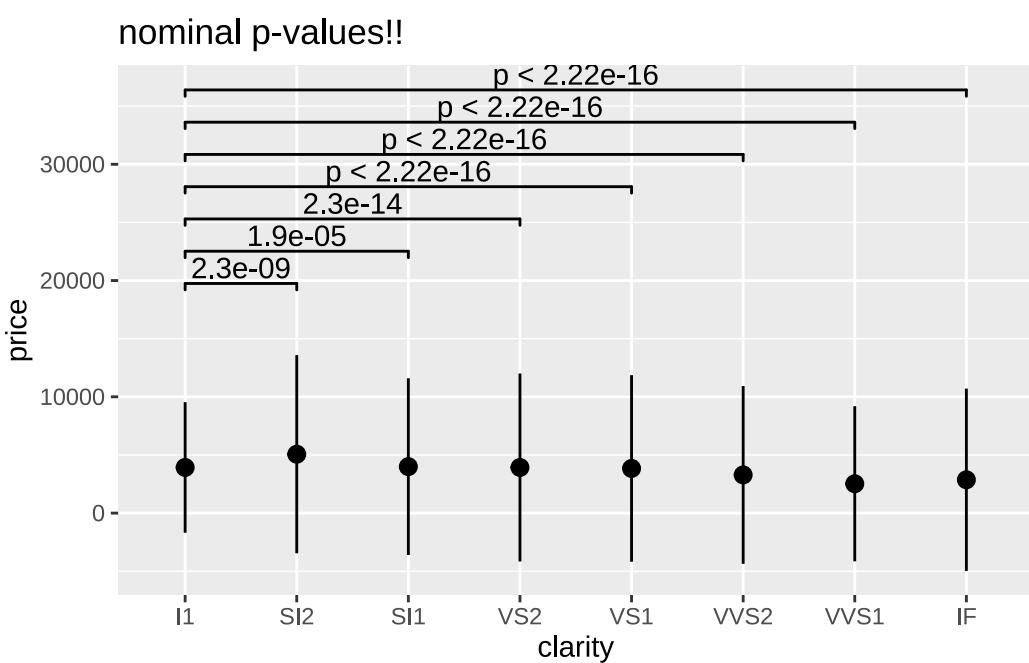


```
plottemp + geom_signif(  
  comparisons=list(1:2))+  
  scale_y_continuous(expand = expansion(mult=c(0.05,.2)))
```

Warning in wilcox.test.default(c(21.4, 18.7, 18.1, 14.3, 24.4, 22.8, 19.2, :
kann bei Bindungen keinen exakten p-Wert Berechnen



```
ggplot(diamonds,aes(clarity, price))+
  stat_summary(fun.data=mean_sdl)+
  geom_signif(comparisons=list(c(1,2),c(1,3),c(1,4),c(1,5),
                                c(1,6),c(1,7),c(1,8)),
               step_increase = 0.15)+
  ggtitle("nominal p-values!!")
```



```

ggplot(diamonds,aes(clarity, price))+  

  stat_summary(fun.data=mean_sdl)+  

  geom_signif(comparisons=list(c(1,2),c(2,3),c(3,4),c(4,5),  

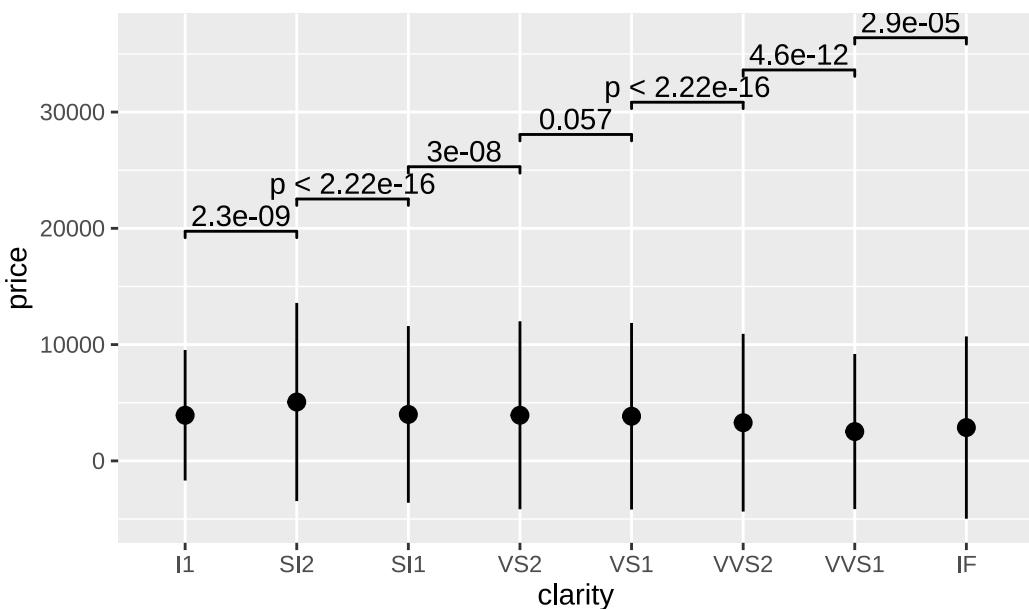
                               c(5,6),c(6,7),c(7,8)),  

              step_increase = 0.15)+  

  ggtitle("nominal p-values!!")

```

nominal p-values!!



```

ggplot(diamonds,aes(clarity, price))+  

  stat_summary(fun.data=mean_sdl)+  

  geom_signif(comparisons=list(c(1,2),c(2,3),c(3,4),c(4,5),  

                               c(5,6),c(6,7),c(7,8)),  

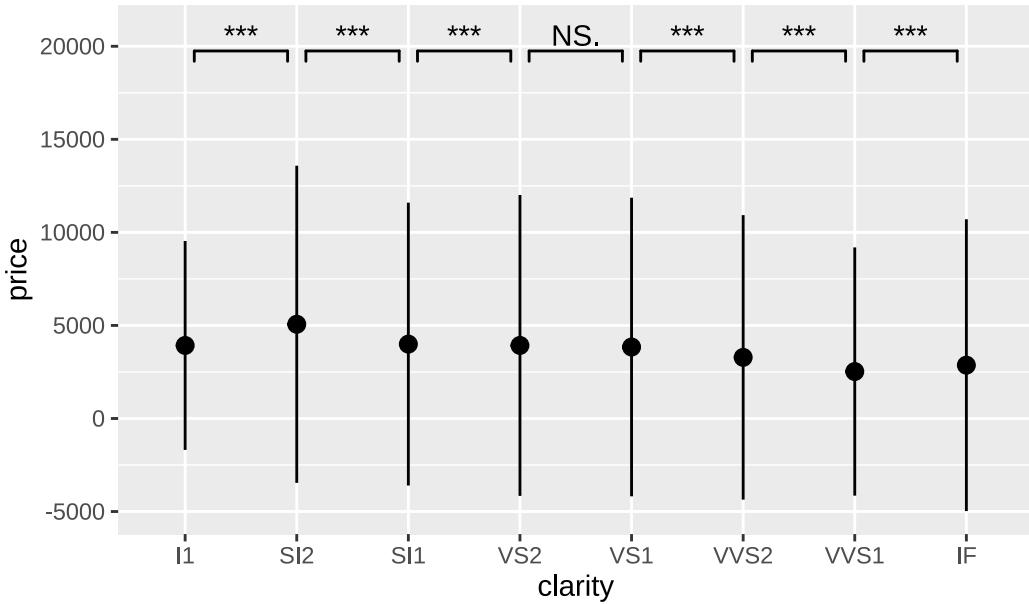
              map_signif_level = TRUE,  

              extend_line = -.01)+  

  ggtitle("nominal p-values!!")+
  scale_y_continuous(expand = expansion(mult=c(0.05,.1)))

```

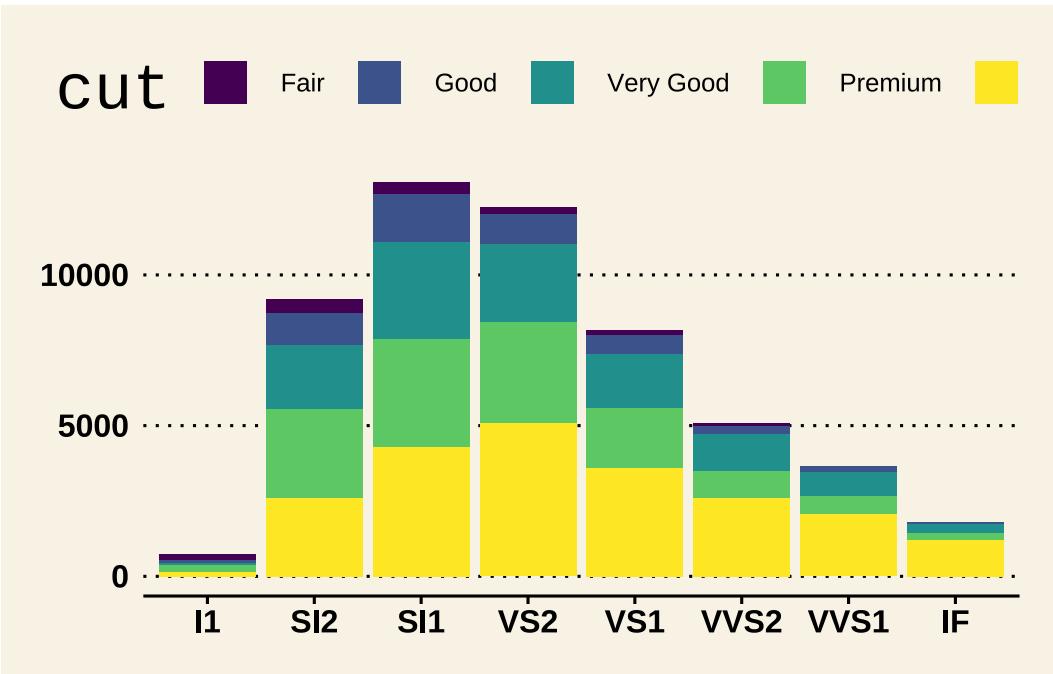
nominal p-values!!



6.14 Theme definitions / changes

Themes define everything not-data-related in your figures, like margins, fonts, background color etc. There are many predefined themes, and all can be customized. You can change a theme for all plots to come (`theme_update()`) or just a single plot (`+theme()`)

```
old <- theme_set(theme_wsj())
ggplot(data=diamonds,aes(x=clarity,fill=cut))+  
  geom_bar()
```

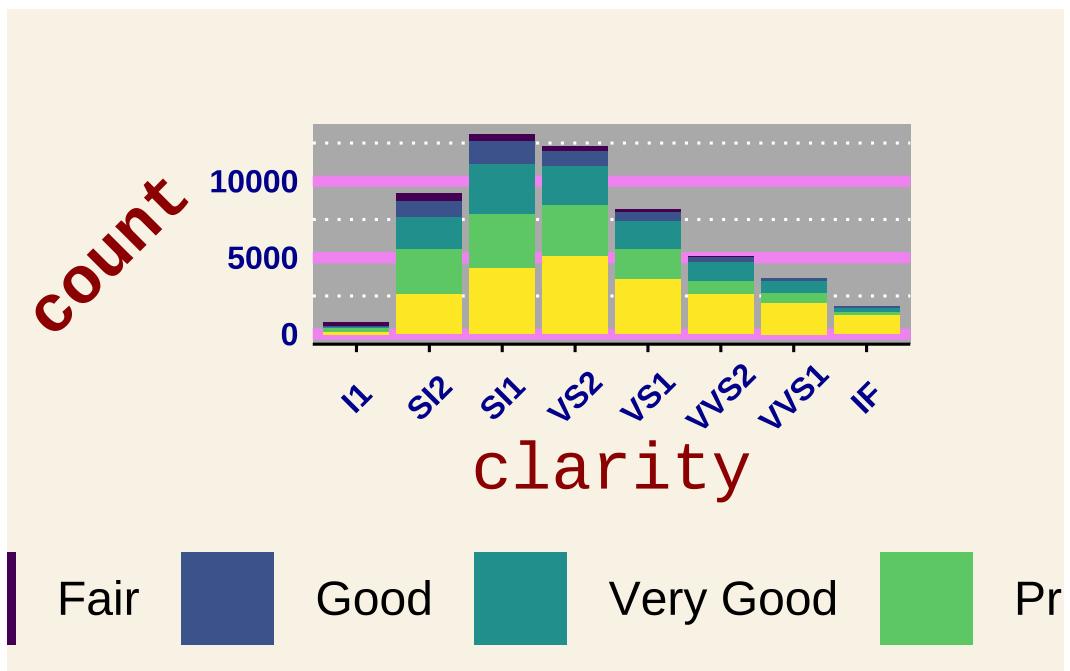


```

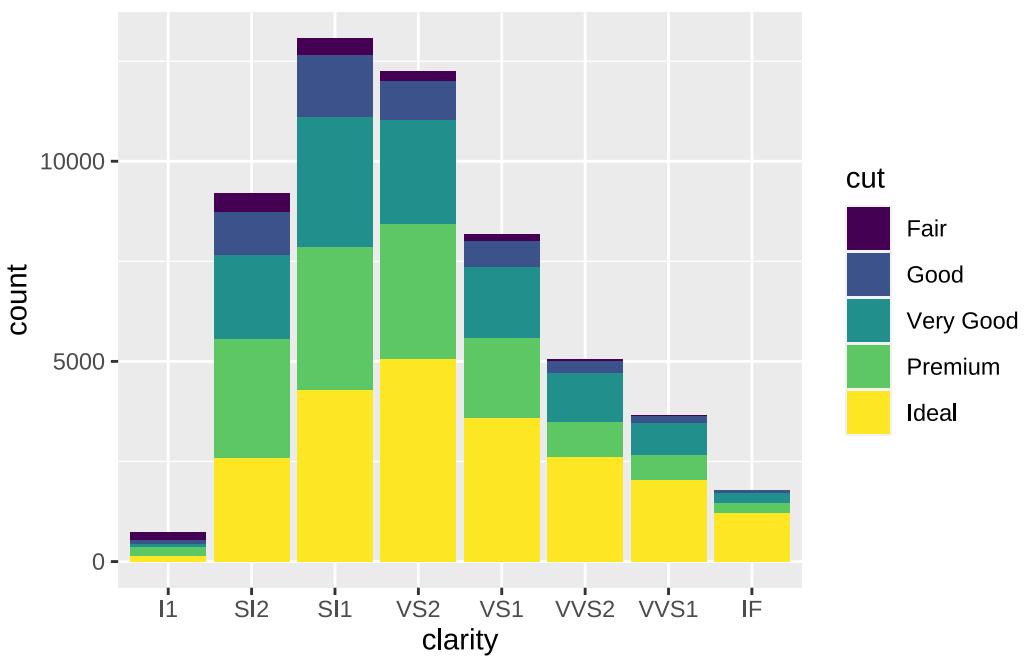
theme_update(legend.position="bottom",
             axis.text=element_text(colour = "darkblue",
                                    size=12),
             axis.text.x=element_text(vjust=0.5,angle=45,
                                      family="sans",
                                      face = "bold"),
             axis.title=element_text(size=25,
                                    color="darkred"),
             plot.margin=unit(c(3,4,.5,.3),"lines"),      #N,E,S,W
             axis.title.y=element_text(vjust=0.4,angle=45,
                                       face="bold"),
             legend.key.size=unit(2.5, "lines"),
             panel.background=element_rect(fill="darkgrey"),
             panel.grid.minor = element_line(colour="white"),
             panel.grid.major = element_line(
               linetype=1,
               color="violet", linewidth = 2),
             legend.text = element_text(size = 18),
             legend.title=element_text(size=30, color="pink"))

ggplot(data=diamonds,aes(x=clarity,fill=cut))+
  geom_bar()

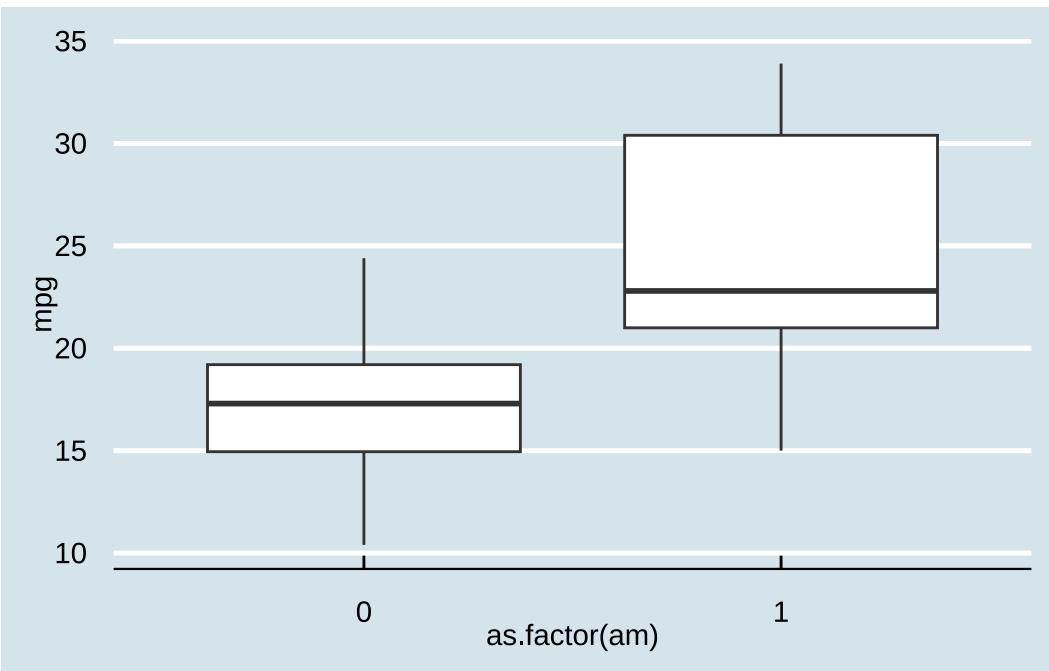
```



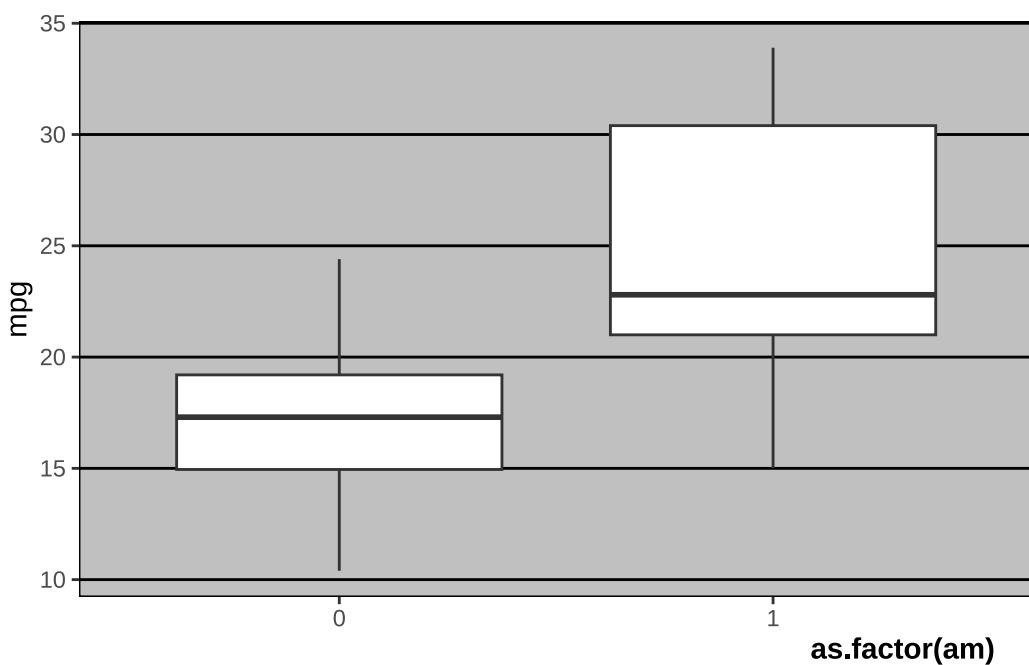
```
theme_set(theme_grey())
#theme_set(old)
ggplot(data=diamonds,aes(x=clarity,fill=cut))+  
  geom_bar()
```



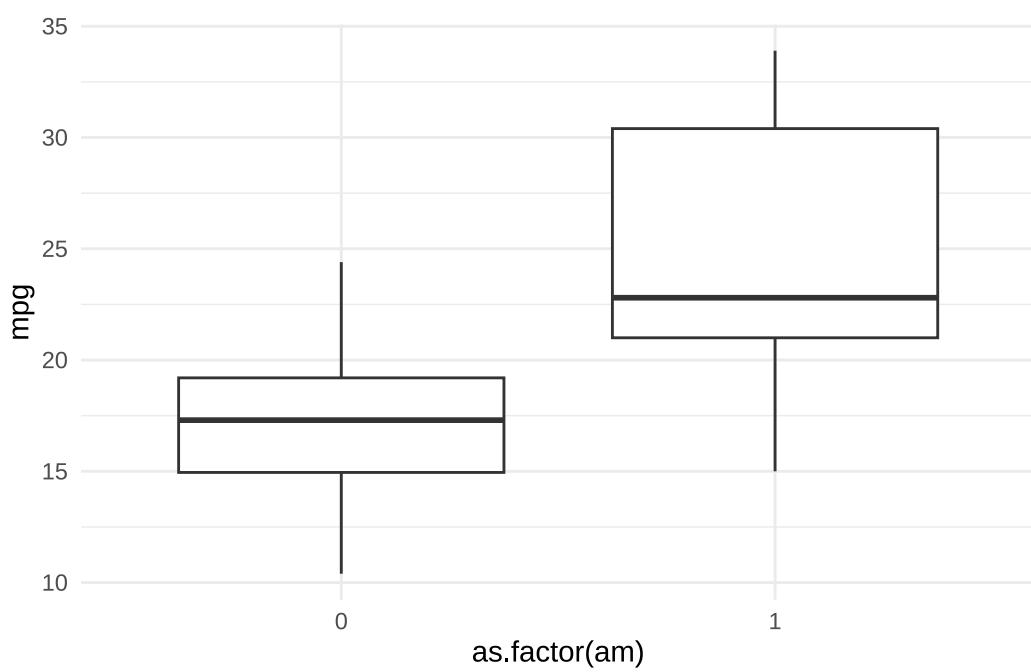
```
# ggthemes #####
plottemp+theme_economist()
```



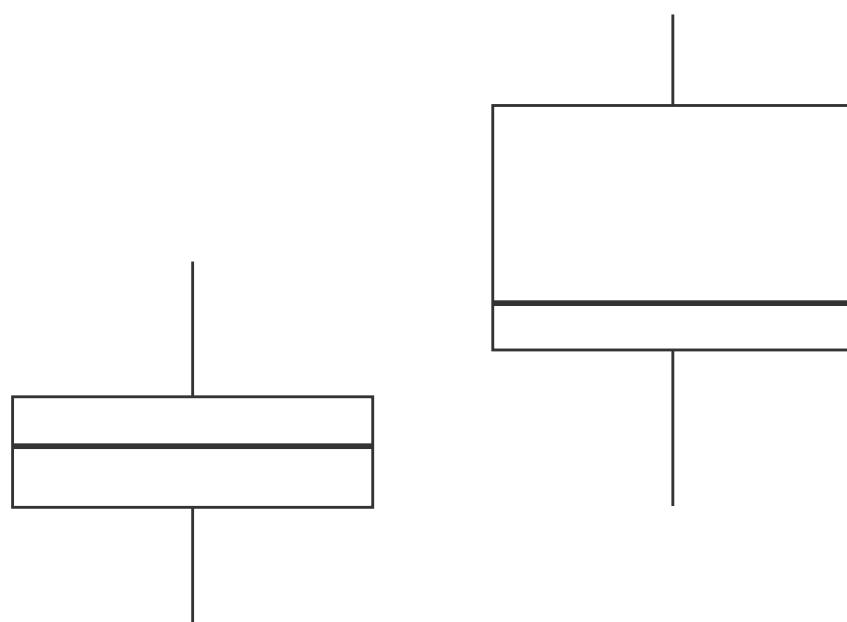
```
plottemp+theme_excel()+
  theme(axis.title.x = element_text(face="bold", hjust=0.95))
```



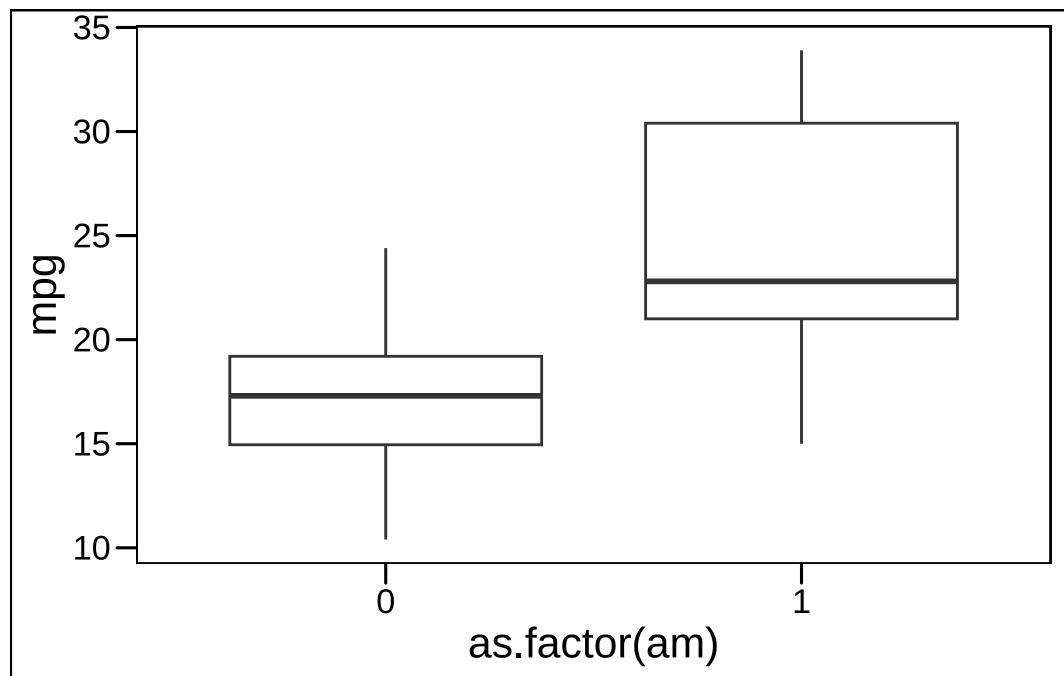
```
plottemp+theme_minimal()
```



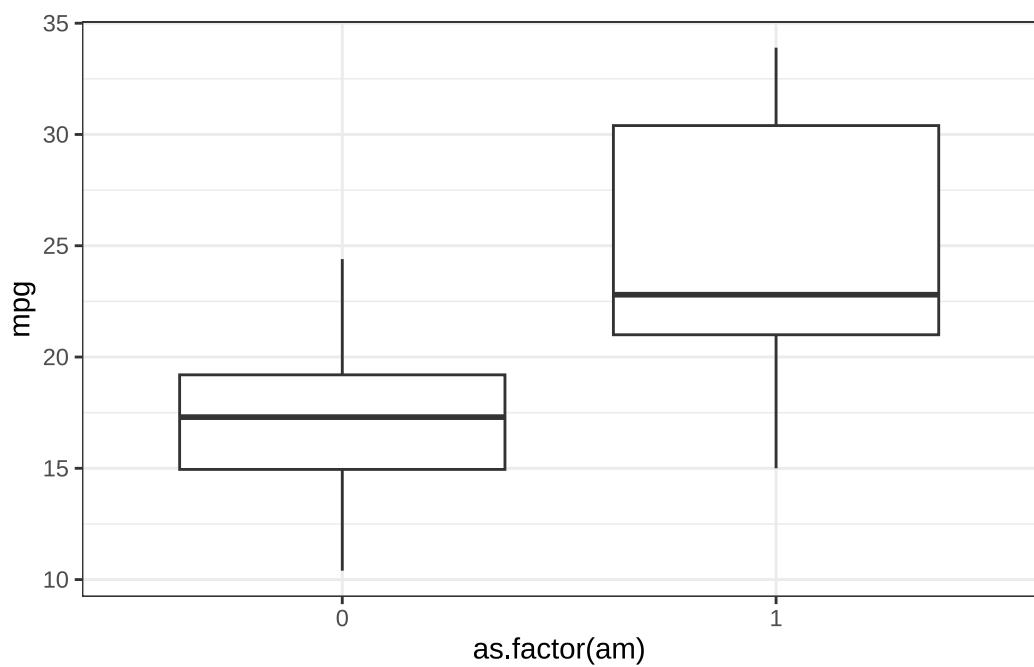
```
plottemp+theme_void()
```



```
plottemp+theme_base()
```



```
plottemp+theme_bw()
```

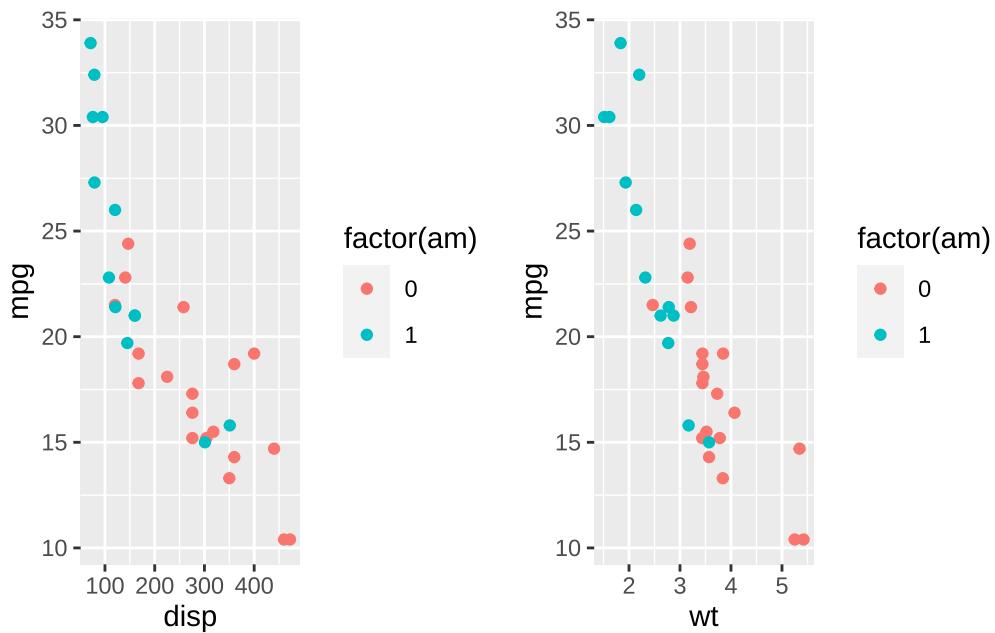


```
# https://www.data-imaginist.com/2019/a-flurry-of-facets/  
# https://github.com/thomasp85/gganimate
```

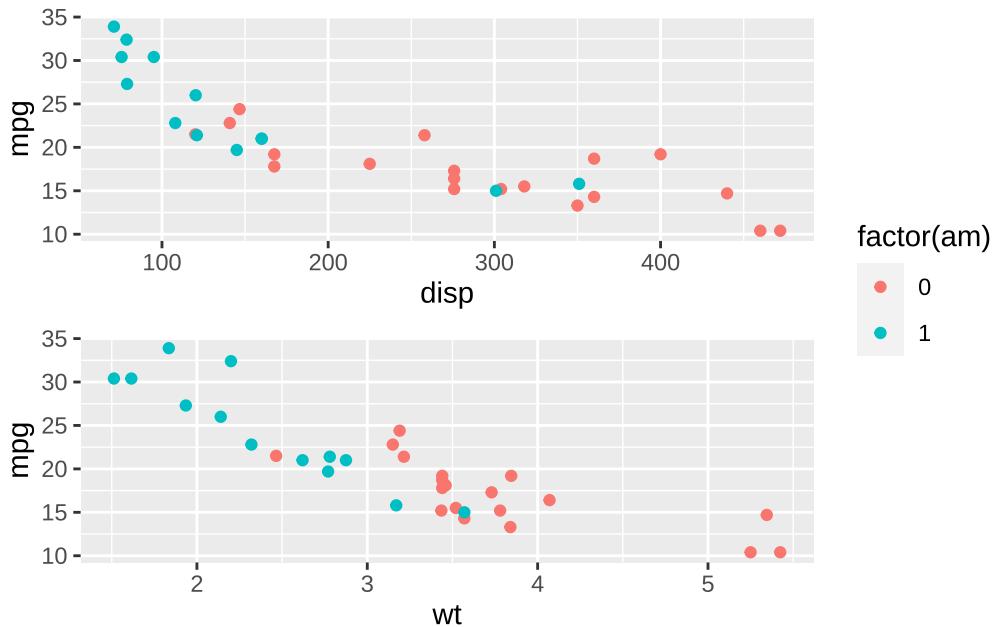
6.15 Combining figures with patchwork

More details on [github](#)

```
p1 <- ggplot(mtcars) +  
  geom_point(aes(disp, mpg, color=factor(am)))  
p2 <- ggplot(mtcars) +  
  geom_point(aes(wt, mpg, color=factor(am)))  
p1 | p2
```



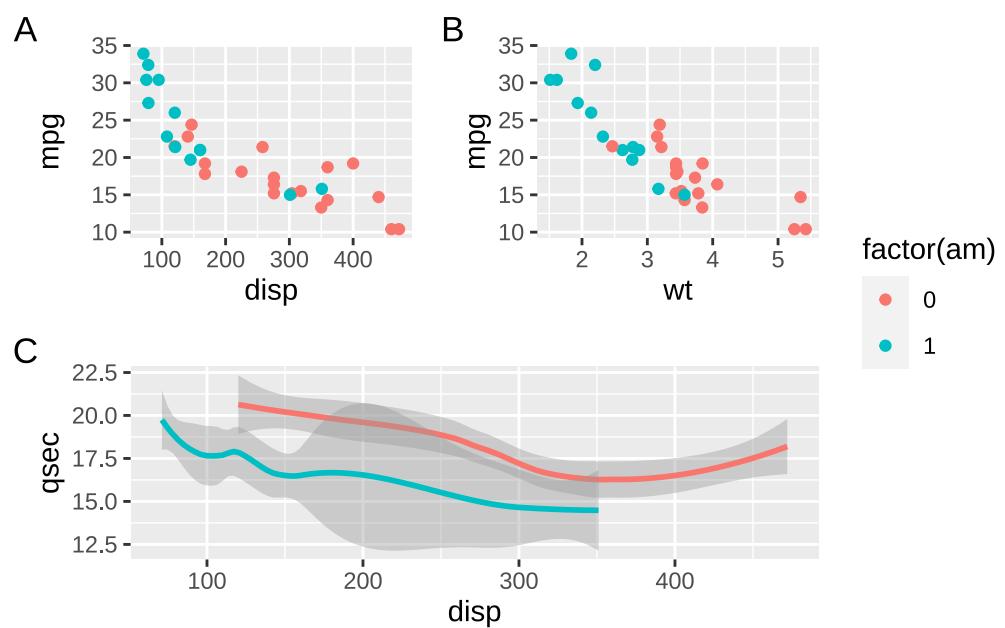
```
(p1 / p2) +  
  plot_layout(guides = "collect")
```



```
p3 <- ggplot(mtcars) +
  geom_smooth(aes(disp, qsec, color=factor(am)))
# p4 <- ggplot(mtcars) +
#   geom_bar(aes(factor(carb)), fill=factor(am))

(p1 | p2) /
  (p3 + guides(color = "none")) +
  plot_annotation(tag_levels = "A") +
  plot_layout(guides = "collect")
```

```
`geom_smooth()` using method = 'loess' and formula = 'y ~ x'
```



[more facets...](#)

[animations...](#)

7 Descriptive statistics

```
pacman::p_load(conflicted,tidyverse,wrappedtools,
                flextable)
#dir("Data/")
load("data/bookdata1.RData")

ggplot(rawdata,aes(`sysBP V0`, `diaBP V0`))+
  geom_point()+
  geom_smooth(se=F)+
  geom_smooth(method="lm",color="red",
              fill="gold", alpha=.15)
```

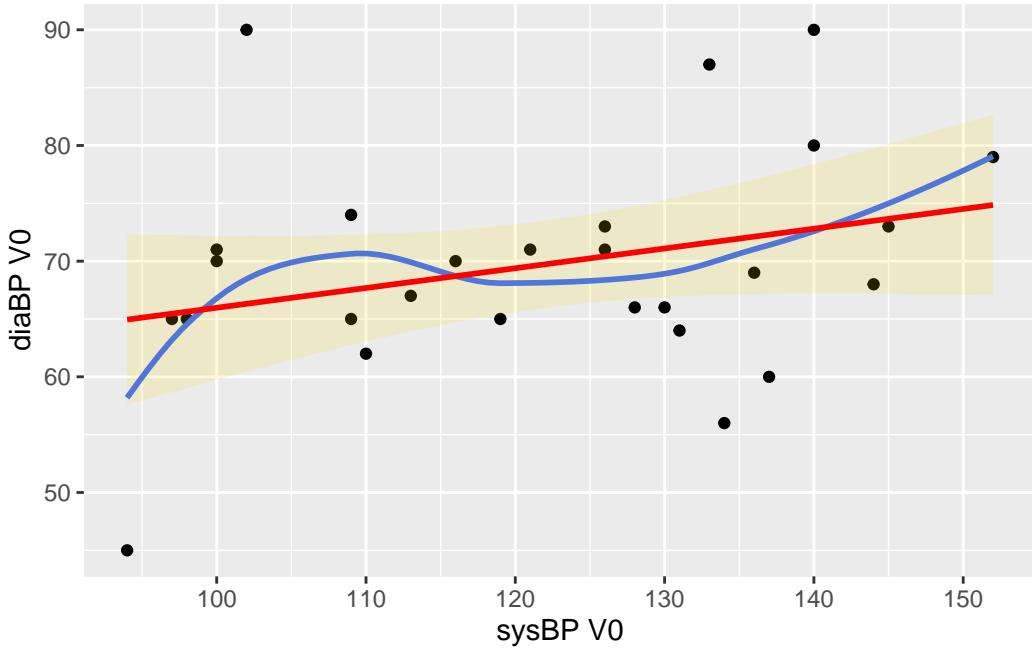
```
`geom_smooth()` using method = 'loess' and formula = 'y ~ x'
```

```
Warning: Removed 1 rows containing non-finite values (`stat_smooth()`).
```

```
`geom_smooth()` using formula = 'y ~ x'
```

```
Warning: Removed 1 rows containing non-finite values (`stat_smooth()`).
```

```
Warning: Removed 1 rows containing missing values (`geom_point()`).
```



```
# descriptives #####
mean_size <- mean(rawdata$`Size (cm)`)
```

```
sd_size <- sd(rawdata$`Size (cm)`)
```

```
min(rawdata$`Size (cm)`)
```

```
[1] 160
```

```
round(mean_size,digits = 2)
```

```
[1] 174.11
```

```
roundR(mean_size,level = 2)
```

```
[1] "174"
```

```
meansd(rawdata$`Size (cm)`, roundDig = 4,
       range = TRUE,add_n = TRUE)
```

```
[1] "174.1 ± 7.8 [160.0 -> 193.0] [n=28]"
```

```
meansd(rawdata$`sysBP VO`, roundDig = 4,  
       range = TRUE,  
       add_n = TRUE,.german = TRUE)
```

```
[1] "121,9 ± 16,9 [94,0 -> 152,0] [n=27]"
```

```
SEM(rawdata$`Size (cm)`)
```

```
[1] 1.468667
```

```
meanse(rawdata$`Size (cm)`, roundDig = 4)
```

```
[1] "174.1±1.5"
```

```
median(rawdata$`Size (cm)`)
```

```
[1] 173.5
```

```
quantile(rawdata$`Size (cm)`,probs = c(.25,.75))
```

```
25%      75%  
168.00 178.25
```

```
median_quart(rawdata$`Size (cm)`)
```

```
[1] "174 (168/179)"
```

```
median_quart(rawdata$Age,range = T)
```

```
[1] "62 (53/67) [43 -> 74]"
```

```
table(rawdata$Sex, useNA = "a")
```

```
f      m <NA>  
4     24     0
```

```
sex_count <- table(rawdata$Sex, useNA = "ifany")
table(rawdata$`NYHA V2`,useNA = "always")
```

```
0      1      2      3 <NA>
1      6      2      2     17
```

```
table(rawdata$`NYHA V2`,useNA = "i")
```

```
0      1      2      3 <NA>
1      6      2      2     17
```

```
table(rawdata$`NYHA V2`,useNA = "no")
```

```
0 1 2 3
1 6 2 2
```

```
randomize <- table(rawdata$Sex, rawdata$Testmedication)
prop.table(sex_count)
```

```
f           m
0.1428571 0.8571429
```

```
prop.table(randomize,margin = 2)*100
```

```
          0          1
f 14.28571 14.28571
m 85.71429 85.71429
```

```
cat_desc_stats(rawdata$`NYHA V2`)
```

```

$level
# A tibble: 4 x 1
  value
  <chr>
1 0
2 1
3 2
4 3

$freq
# A tibble: 4 x 1
  desc
  <chr>
1 1 (9%)
2 6 (55%)
3 2 (18%)
4 2 (18%)

```

```
cat_desc_stats(rawdata$Sex, singleline = TRUE)
```

```

$level
[1] "f m"

$freq
# A tibble: 1 x 1
  desc
  <glue>
1 4 (14%) 24 (86%)

```

```

cat_desc_table(data = rawdata,
               desc_vars = factvars$names) |>
  rename(`n (%)` = desc_all) |>
  flextable() |>
  align(i = `~n (%)` != " ", j = 1, align = "right") |>
  width(j = c(1, 2), width = c(3, 4), unit = "cm") |>
  flex2rmd()

```

```

```{=latex}
\global\setlength{\Oldarrayrulewidth}{\arrayrulewidth}

\global\setlength{\Oldtabcolsep}{\tabcolsep}

```

```
\setlength{\tabcolsep}{0pt}

\renewcommand*\arraystretch{1.5}

\providecommand{\ascline}[3]{\noalign{\global\arrayrulewidth #1}\arrayrulecolor[HTML]{#2}{}}

\begin{longtable}[c]{|p{1.18in}|p{1.57in}|}

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\ascline{1.5pt}{666666}{1-2}\endfirsthead

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\ascline{1.5pt}{666666}{1-2}\endhead

\multicolumn{1}{>{\raggedright}m{\dimexpr 1.18in+0\tabcolsep}}{\textcolor[HTML]{000000}{\f...}}\\

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```

\multicolumn{1}{>{\raggedleft}m{\dimexpr 1.18in+0\tabcolsep}}{\textcolor[HTML]{000000}{\footnotesize \#1}}

\multicolumn{1}{>{\raggedleft}m{\dimexpr 1.18in+0\tabcolsep}}{\textcolor[HTML]{000000}{\footnotesize \#2}}

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\multicolumn{1}{>{\raggedleft}m{\dimexpr 1.18in+0\tabcolsep}}{\textcolor[HTML]{000000}{\footnotesize \#8}}

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\multicolumn{1}{>{\raggedleft}m{\dimexpr 1.18in+0\tabcolsep}}{\textcolor[HTML]{000000}{\footnotesize \#10}}

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```

\multicolumn{1}{>{\raggedleft}\dimexpr 1.18in+0\tabcolsep}{\textcolor{HTML}{000000}{\footnotesize \fontfamily{cmtt}\tiny \multicolumn{1}{l}{\arrayrulecolor{HTML}000000}\arrayrulewidth{1.5pt}\arrayrulecolor{HTML}666666}{1-2}}\\
\end{longtable}

\arrayrulecolor{HTML}000000\\
\global\setlength{\arrayrulewidth}{\Oldarrayrulewidth}\\
\global\setlength{\tabcolsep}{\Oldtabcolsep}\\
\renewcommand*\arraystretch{1}\\
\\

rawdata |>
 group_by(Testmedication, Sex) |>
 summarise(WeightSummary=meansd(`Weight (kg)`),
 .groups="drop")\\

A tibble: 4 x 3
 Testmedication Sex WeightSummary
 <fct> <fct> <chr>
1 0 f 86 ± 9
2 0 m 91 ± 14
3 1 f 66 ± 3
4 1 m 90 ± 14

rawdata |>
 group_by(Sex) |>
 summarize(across(gaussvars$names,
 .fns=~meansd(.x, range=T))) |>
 pivot_longer(cols=-Sex,
 names_to="Variable") |>
 pivot_wider(names_from=Sex)\\

A tibble: 11 x 3

```

Variable	f	m
<chr>	<chr>	<chr>
1 Size (cm)	165 ± 4 [160 -> 168]	176 ± 7 [161 -> 193]
2 Weight (kg)	76 ± 13 [64 -> 93]	90 ± 14 [74 -> 120]
3 sysBP V0	118 ± 14 [102 -> 130]	123 ± 18 [94 -> 152]
4 diaBP V0	71 ± 13 [62 -> 90]	69 ± 9 [45 -> 90]
5 Lv Edv Mri	235 ± 72 [184 -> 286]	203 ± 71 [118 -> 379]
6 Lv Esv Mri	158 ± 56 [119 -> 198]	105 ± 71 [50 -> 294]
7 Lv Ef Mri	33 ± 3 [31 -> 35]	52 ± 15 [17 -> 74]
8 Lv Ef Biplan Mri	26 ± 11 [19 -> 34]	51 ± 13 [21 -> 69]
9 sysBP V2	114 ± 18 [96 -> 132]	120 ± 12 [100 -> 145]
10 diaBP V2	58 ± 12 [51 -> 72]	67 ± 8 [55 -> 80]
11 BMI	28 ± 5 [24 -> 35]	29 ± 4 [23 -> 41]

```
rawdata |>
 group_by(Sex) |>
 summarize(across(gaussvars$names,
 .fns=list(Mean=~mean(.x,na.rm=TRUE),
 SD=~sd(.x,na.rm=TRUE)))) |>
 pivot_longer(cols=-Sex,
 names_to=c("Variable","stat"),
 names_sep="_") |>
 pivot_wider(names_from=c(stat,Sex),
 # names_sep=" ",
 names_glue="{stat} ({Sex})",
 values_from=value)
```

Variable	`Mean (f)`	`SD (f)`	`Mean (m)`	`SD (m)`
<chr>	<dbl>	<dbl>	<dbl>	<dbl>
1 Size (cm)	165	3.83	176.	7.22
2 Weight (kg)	76.2	13.1	90.4	14.1
3 sysBP V0	118.	13.7	123.	17.5
4 diaBP V0	71	12.8	69.5	9.47
5 Lv Edv Mri	235	72.1	203.	71.4
6 Lv Esv Mri	158.	55.9	105.	70.9
7 Lv Ef Mri	33	2.83	51.6	14.6
8 Lv Ef Biplan Mri	26.5	10.6	51	12.9
9 sysBP V2	114	18	120.	12.1
10 diaBP V2	58.3	11.8	67.2	7.83
11 BMI	28.0	4.75	29.3	4.36

```
compare2numvars(rawdata,
 dep_vars = c("Size (cm)", "Weight (kg)",
 "sysBP V0", "diaBP V0"),
 indep_var = "Sex",
 gaussian = TRUE)

A tibble: 4 x 5
 Variable desc_all `Sex f` `Sex m` p
 <fct> <chr> <chr> <chr>
1 Size (cm) 174 ± 8 165 ± 4 176 ± 7 0.009
2 Weight (kg) 88 ± 15 76 ± 13 90 ± 14 0.072
3 sysBP V0 122 ± 17 118 ± 14 123 ± 18 0.587
4 diaBP V0 70 ± 10 71 ± 13 69 ± 9 0.780
```

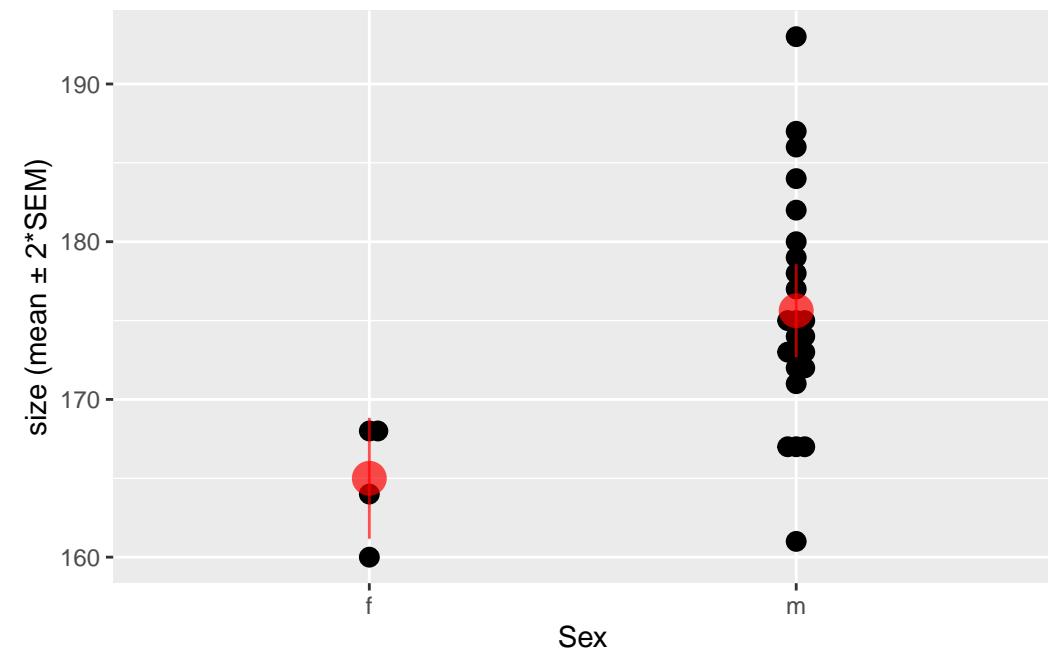
## **8 Better tables with `flextable`**

# 9 Simple test statistics

```
pacman::p_load(conflicted, plotrix, tidyverse, wrappedtools,
 coin, ggsignif, patchwork, ggbeeswarm,
 flextable)
#conflicted)
conflict_prefer("filter", "dplyr")
load("data/bookdata1.RData")
```

## 9.1 Quantitative measures with Gaussian distribution

```
ggplot(rawdata, aes(x=Sex, y=`Size (cm)`))+
 geom_beeswarm(size=3)+
 stat_summary(color="red", size=1.2, alpha=.7,
 fun.data="mean_se", fun.args=list(mult=2))+
```



```

by(data = rawdata$`Size (cm)`, INDICES = rawdata$Sex,
 FUN = meanse)

rawdata$Sex: f
[1] "165±2"

rawdata$Sex: m
[1] "176±1"

t.test(x = rawdata$`Size (cm)`[which(rawdata$Sex=="f")],
 y = rawdata$`Size (cm)`[which(rawdata$Sex=="m")])

```

Welch Two Sample t-test

```

data: rawdata$`Size (cm)`[which(rawdata$Sex == "f")] and rawdata$`Size (cm)`[which(rawdat
t = -4.3967, df = 7.2767, p-value = 0.002887
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
-16.295575 -4.954425
sample estimates:
mean of x mean of y
165.000 175.625

```

```
(tOut<-t.test(rawdata$`Size (cm)`~rawdata$Sex))
```

Welch Two Sample t-test

```

data: rawdata$`Size (cm)` by rawdata$Sex
t = -4.3967, df = 7.2767, p-value = 0.002887
alternative hypothesis: true difference in means between group f and group m is not equal
95 percent confidence interval:
-16.295575 -4.954425
sample estimates:
mean in group f mean in group m
165.000 175.625

```

```
tOut$p.value
```

```
[1] 0.00288704
```

```
equal variances assumption?
(vartestOut<-var.test(rawdata$`Size (cm)`~rawdata$Sex))
```

F test to compare two variances

```
data: rawdata$`Size (cm)` by rawdata$Sex
F = 0.2812, num df = 3, denom df = 23, p-value = 0.3232
alternative hypothesis: true ratio of variances is not equal to 1
95 percent confidence interval:
 0.07497668 3.97434769
sample estimates:
ratio of variances
 0.281199
```

```
(t0Out<-t.test(rawdata$`Size (cm)`~rawdata$Sex,
 var.equal = vartestOut$p.value>.05))
```

Two Sample t-test

```
data: rawdata$`Size (cm)` by rawdata$Sex
t = -2.8446, df = 26, p-value = 0.008552
alternative hypothesis: true difference in means between group f and group m is not equal
95 percent confidence interval:
 -18.302594 -2.947406
sample estimates:
mean in group f mean in group m
 165.000 175.625
```

```
(t0Out<=
 t.test(rawdata$`Size (cm)`~rawdata$Sex,
 var.equal=var.test(
 rawdata$`Size (cm)`~rawdata$Sex)$p.value>.05))
```

Two Sample t-test

```
data: rawdata$`Size (cm)` by rawdata$Sex
t = -2.8446, df = 26, p-value = 0.008552
alternative hypothesis: true difference in means between group f and group m is not equal
95 percent confidence interval:
```

```
-18.302594 -2.947406
sample estimates:
mean in group f mean in group m
165.000 175.625
```

```
t_var_test(data = rawdata,
 formula = " `Size (cm)` ~ Sex",
 cutoff = .1)
```

### Two Sample t-test

```
data: Size (cm) by Sex
t = -2.8446, df = 26, p-value = 0.008552
alternative hypothesis: true difference in means between group f and group m is not equal
95 percent confidence interval:
-18.302594 -2.947406
sample estimates:
mean in group f mean in group m
165.000 175.625
```

```
print(c(mean(rawdata$`sysBP V0`,na.rm=T),
 mean(rawdata$`sysBP V2`,na.rm=T)))
```

```
[1] 121.8519 119.4583
```

```
t.test(rawdata$`sysBP V0`,
 rawdata$`sysBP V2`,
 alternative="greater", # x>y
 paired=TRUE) #pairwise t-test, within subject
```

### Paired t-test

```
data: rawdata$`sysBP V0` and rawdata$`sysBP V2`
t = 0.88151, df = 23, p-value = 0.1936
alternative hypothesis: true mean difference is greater than 0
95 percent confidence interval:
-2.793386 Inf
sample estimates:
mean difference
2.958333
```

```
t.test(rawdata$`sysBP V0`,
 rawdata$`sysBP V2`,
 # alternative="greater", # x>y
 paired=T)$p.value/2 #pairwise t-test, within subject
```

[1] 0.1935805

```
t.test(rawdata$`Size (cm)`,mu = 173)
```

One Sample t-test

```
data: rawdata$`Size (cm)`
t = 0.75384, df = 27, p-value = 0.4575
alternative hypothesis: true mean is not equal to 173
95 percent confidence interval:
171.0937 177.1206
sample estimates:
mean of x
174.1071
```

```
groupvars <- ColSeeker(namepattern = c("Sex","Test"))

compare2numvars(data = rawdata,dep_vars = gaussvars$names,
 indep_var = "Sex",gaussian = T) |>
 flextable() |>
 flex2rmd()
```

```
```{=latex}
\global\setlength{\Oldarrayrulewidth}{\arrayrulewidth}

\global\setlength{\Oldtabcolsep}{\tabcolsep}

\setlength{\tabcolsep}{0pt}

\renewcommand*\arraystretch{1.5}
```

```
\providecommand{\ascline}[3]{\noalign{\global\arrayrulewidth #1}\arrayrulecolor[HTML]{#2}\vrule width #1 height #2}
```

```
\begin{longtable}[c]{|p{0.75in}|p{0.75in}|p{0.75in}|p{0.75in}|p{0.75in}|}
```



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```
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\ascline{1.5pt}{666666}{1-5}\endhead
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```



```
\global\setlength{\tabcolsep}{\Oldtabcolsep}

\renewcommand*\arraystretch{1}
```

compare2numvars(data = rawdata,dep_vars = gaussvars$names,
 indep_var = "Testmedication",gaussian = T) |>
 flextable() |>
 flex2rmd()

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\setlength{\tabcolsep}{0pt}

\renewcommand*\arraystretch{1.5}

\providetcommand{\ascline}[3]{\noalign{\global\arrayrulewidth #1}\arrayrulecolor[HTML]{#2}\
\begin{longtable}{c|p{0.75in}|p{0.75in}|p{0.75in}|p{0.75in}|p{0.75in}}\\

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\ascline{1.5pt}{666666}{1-5}\endfirsthead

\ascline{1.5pt}{666666}{1-5}

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\end{longtable}

\arrayrulecolor{HTML}{000000}
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\global\setlength{\tabcolsep}{\Oldtabcolsep}
\renewcommand*\arraystretch{1}
```

for(group_i in seq_len(groupvars$count)){
 resulttmp <- compare2numvars(data = rawdata, dep_vars = gaussvars$names,
 indep_var = groupvars$names[group_i], gaussian = T)
 # print(resulttmp)
 flextable(resulttmp) |>
 flextable_to_rmd()
 cat(" \\n\\n")
}

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\global\setlength{\Oldtabcolsep}{\tabcolsep}

```



```

\end{longtable}

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\renewcommand*\arraystretch{1}
```


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\renewcommand*\arraystretch{1.5}

\providetcommand{\ascline}[3]{\noalign{\global\arrayrulewidth #1}\arrayrulecolor [HTML]{#2}{}}

\begin{longtable}{c}{|p{0.75in}|p{0.75in}|p{0.75in}|p{0.75in}|p{0.75in}|p{0.75in}|}

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\ascline{1.5pt}{666666}{1-5}\endfirsthead

\ascline{1.5pt}{666666}{1-5}

\multicolumn{1}{>{\raggedright}\m{\dimexpr 0.75in+0\tabcolsep}}{\textcolor [HTML]{000000}{\f{f}}}

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```



```
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\end{longtable}

\arrayrulecolor[HTML]{000000}

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\renewcommand*\arraystretch{1}
```

```

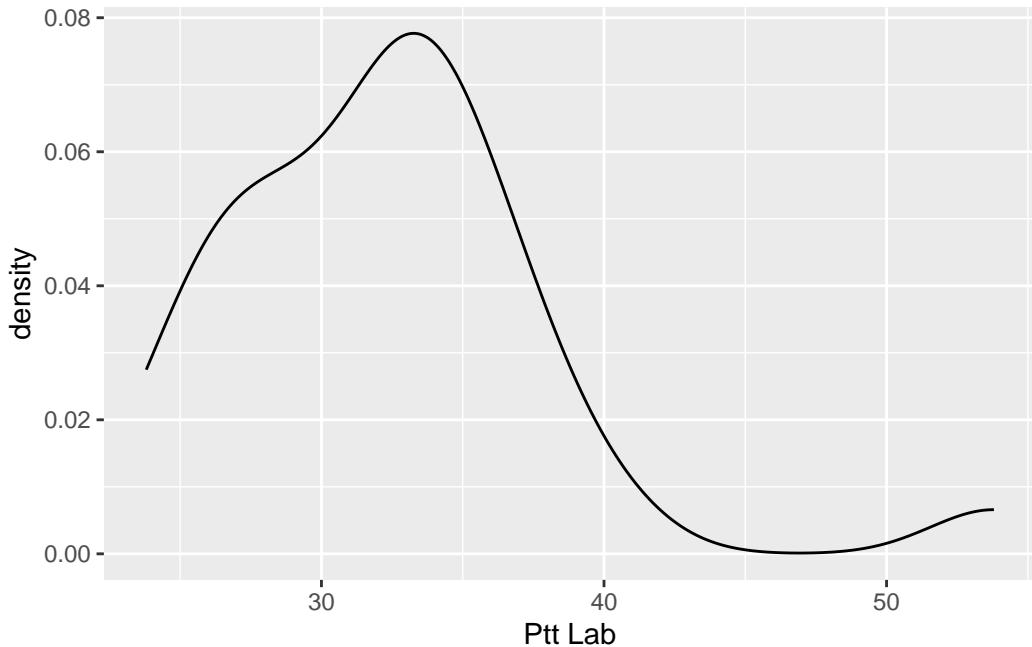
## 9.2 Ordinal data

ordvars\$names

```
[1] "Ptt Lab" "Ferritin Lab" "Iron Lab" "Transferrin Lab"
[5] "Age"
```

```
ggplot(rawdata, aes(`Ptt Lab`))+
 geom_density()
```

```
Warning: Removed 1 rows containing non-finite values (`stat_density()`).
```



```
by(data = rawdata[[ordvars$index[1]]],
 INDICES = rawdata$Sex, FUN = median_quart)
```

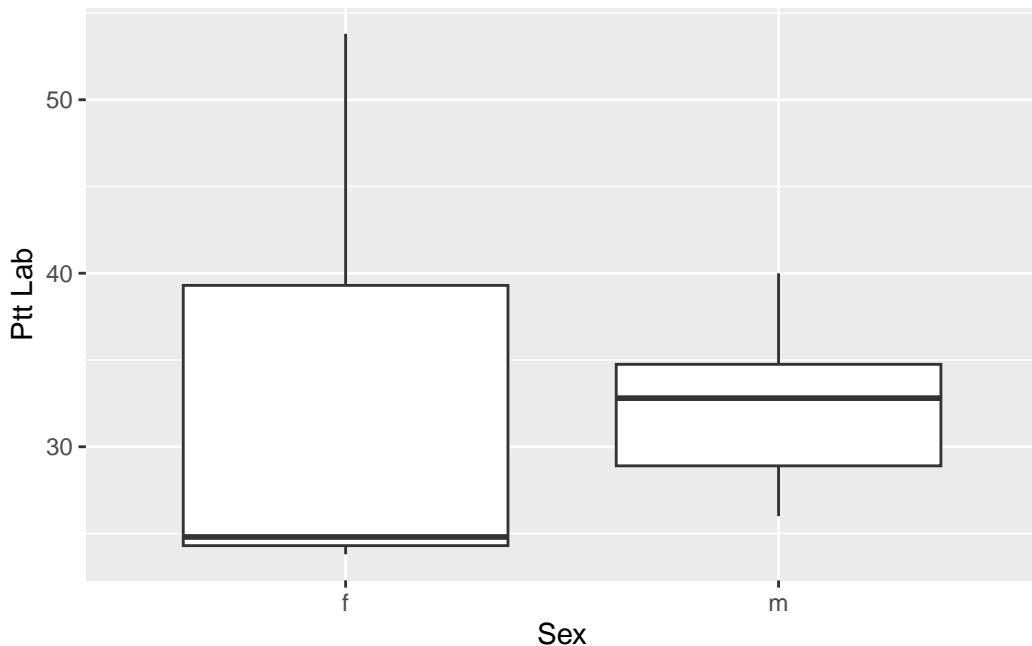
```
rawdata$Sex: f
[1] "25 (24/49)"
```

```

rawdata$Sex: m
[1] "33 (29/35)"
```

```
ggplot(rawdata, aes(Sex, `Ptt Lab`)) +
 geom_boxplot()
```

```
Warning: Removed 1 rows containing non-finite values (`stat_boxplot()`).
```



```
(u0Out<-wilcox.test(
 rawdata[[ordvars$index[3]]] ~ rawdata$Sex, exact=F))
```

Wilcoxon rank sum test with continuity correction

```
data: rawdata[[ordvars$index[3]]] by rawdata$Sex
W = 54.5, p-value = 0.1648
alternative hypothesis: true location shift is not equal to 0
```

```
u0Out$p.value
```

```
[1] 0.1647858
```

```
coin::wilcox_test
(u0Out2<-wilcox_test(`Ptt Lab`~as.factor(Sex),
 data=rawdata))
```

Asymptotic Wilcoxon-Mann-Whitney Test

```
data: Ptt Lab by as.factor(Sex) (f, m)
Z = -0.9261, p-value = 0.3544
alternative hypothesis: true mu is not equal to 0
```

```
pvalue(uOut2) #no list-object, but methods to extract infos like p
```

```
[1] 0.3543925
```

```
wilcox.test(`Ptt Lab`~Sex,exact=F,correct=F,
 data=rawdata)
```

```
Wilcoxon rank sum test
```

```
data: Ptt Lab by Sex
W = 24, p-value = 0.3544
alternative hypothesis: true location shift is not equal to 0
```

```
wilcox.test(x=rawdata$`sysBP V0`,y=rawdata$`sysBP V2`,
 exact=FALSE,
 correct=TRUE,paired=TRUE)
```

```
Wilcoxon signed rank test with continuity correction
```

```
data: rawdata$`sysBP V0` and rawdata$`sysBP V2`
V = 143, p-value = 0.3478
alternative hypothesis: true location shift is not equal to 0
```

```
compare2numvars(data = rawdata,dep_vars = ordvars$names,
 indep_var = "Sex",gaussian = F) |>
flextable() |>
flex2rmd()
```

```
```{=latex}  
\global\setlength{\Oldarrayrulewidth}{\arrayrulewidth}  
  
\global\setlength{\Oldtabcolsep}{\tabcolsep}  
  
\setlength{\tabcolsep}{0pt}  
  
\renewcommand*\arraystretch{1.5}
```

```
\providecommand{\ascline}[3]{\noalign{\global\arrayrulewidth #1}\arrayrulecolor[HTML]{#2}{}}

\begin{longtable}{c|p{0.75in}|p{0.75in}|p{0.75in}|p{0.75in}|p{0.75in}}


\ascline{1.5pt}{666666}{1-5}

\multicolumn{1}{>{\raggedright}m{\dimexpr 0.75in+0\tabcolsep}}{\textcolor[HTML]{000000}{\f

\ascline{1.5pt}{666666}{1-5}\endfirsthead

\ascline{1.5pt}{666666}{1-5}

\multicolumn{1}{>{\raggedright}m{\dimexpr 0.75in+0\tabcolsep}}{\textcolor[HTML]{000000}{\f

\ascline{1.5pt}{666666}{1-5}\endhead

\multicolumn{1}{>{\raggedright}m{\dimexpr 0.75in+0\tabcolsep}}{\textcolor[HTML]{000000}{\f

\multicolumn{1}{>{\raggedright}m{\dimexpr 0.75in+0\tabcolsep}}{\textcolor[HTML]{000000}{\f

\multicolumn{1}{>{\raggedright}m{\dimexpr 0.75in+0\tabcolsep}}{\textcolor[HTML]{000000}{\f

\multicolumn{1}{>{\raggedright}m{\dimexpr 0.75in+0\tabcolsep}}{\textcolor[HTML]{000000}{\f
```

```

\multicolumn{1}{>{\raggedright}m{\dimexpr 0.75in+0\tabcolsep}}{\textcolor{HTML}{000000}{\f
\ascline{1.5pt}{666666}{1-5}

\end{longtable}

\arrayrulecolor{HTML}{000000}

\global\setlength{\arrayrulewidth}{\Oldarrayrulewidth}
\global\setlength{\tabcolsep}{\Oldtabcolsep}
\renewcommand*\arraystretch{1}
```

```

### 9.3 Categorial data

```
factvars$names
```

```
[1] "Testmedication" "Sex" "NYHA V1" "NYHA V2"
[5] "NYHA V3"
```

```
(crosstab<-table(rawdata$Sex,rawdata$Testmedication))
```

```
0 1
f 2 2
m 12 12
```

```
chisq.test(crosstab,simulate.p.value=T,B=10^5) #empirical p-value
```

```
Pearson's Chi-squared test with simulated p-value (based on 1e+05
replicates)
```

```
data: crosstab
X-squared = 0, df = NA, p-value = 1
```

```
chisq.test(table(rawdata$Sex, rawdata$`NYHA V1`)) #based on table
```

Warning in chisq.test(table(rawdata\$Sex, rawdata\$`NYHA V1`)): Chi-Quadrat-Approximation kann inkorrekt sein

Pearson's Chi-squared test

```
data: table(rawdata$Sex, rawdata$`NYHA V1`)
X-squared = 4.3849, df = 3, p-value = 0.2228
```

```
chisq.test(x=rawdata$Sex, y=rawdata$`NYHA V1`,
simulate.p.value=T, B=10^5) #based on rawdata
```

Pearson's Chi-squared test with simulated p-value (based on 1e+05 replicates)

```
data: rawdata$Sex and rawdata$`NYHA V1`
X-squared = 4.3849, df = NA, p-value = 0.1754
```

```
fisher_out <- fisher.test(
 table(rawdata$Sex, rawdata$`NYHA V1`))
fisher_out$p.value
```

[1] 0.09558824

```
(crosstab1<-table(rawdata$Sex,
 rawdata$`Weight (kg)`<=
 median(rawdata$`Weight (kg)`)))
```

|   | FALSE | TRUE |
|---|-------|------|
| f | 1     | 3    |
| m | 13    | 11   |

```
(tabletestOut<-chisq.test(crosstab1, simulate.p.value=T,
 B=10^5))
```

```
Pearson's Chi-squared test with simulated p-value (based on 1e+05
replicates)
```

```
data: crosstab1
X-squared = 1.1667, df = NA, p-value = 0.5952
```

```
tabletestOut$p.value
```

```
[1] 0.595234
```

```
tabletestOut$expected
```

|   | FALSE | TRUE |
|---|-------|------|
| f | 2     | 2    |
| m | 12    | 12   |

```
tabletestOut$observed
```

|   | FALSE | TRUE |
|---|-------|------|
| f | 1     | 3    |
| m | 13    | 11   |

```
tabletestOut$statistic
```

```
X-squared
1.166667
```

```
if minimum(expected<5) then Fishers exact test
if(min(tabletestOut$expected)<5) {
 tabletestOut<-fisher.test(crosstab1)
}
tabletestOut$p.value
```

```
[1] 0.5955556
```

```

report_cat
groupvar <- "Testmedication"

compare2qualvars(rawdata,dep_vars = factvars$names[-1],
 indep_var = groupvar,spacer = " ") |>
 flextable() |>
 flex2rmd()

```

```

```{=latex}
\global\setlength{\Oldarrayrulewidth}{\arrayrulewidth}
\global\setlength{\Oldtabcolsep}{\tabcolsep}
\setlength{\tabcolsep}{0pt}
\renewcommand*\arraystretch{1.5}

\providecommand{\ascline}[3]{\noalign{\global\arrayrulewidth #1}\arrayrulecolor[HTML]{#2}\
\begin{longtable}{c|p{0.75in}|p{0.75in}|p{0.75in}|p{0.75in}|p{0.75in}}}

\ascline{1.5pt}{666666}{1-5}

\multicolumn{1}{>{\raggedright}\dimexpr 0.75in+0\tabcolsep}{\textcolor[HTML]{000000}{\f
\ascline{1.5pt}{666666}{1-5}\endfirsthead

\ascline{1.5pt}{666666}{1-5}

\multicolumn{1}{>{\raggedright}\dimexpr 0.75in+0\tabcolsep}{\textcolor[HTML]{000000}{\f
\ascline{1.5pt}{666666}{1-5}\endhead

\multicolumn{1}{>{\raggedright}\dimexpr 0.75in+0\tabcolsep}{\textcolor[HTML]{000000}{\f

```


\multicolumn{1}{>{\raggedright}m{\dimexpr 0.75in+0\tabcolsep}}{\textcolor{[HTML]{000000}}{\ff{f}{\textbf{f}}}}

```
\ascline{1.5pt}{666666}{1-5}

\end{longtable}

\arrayrulecolor[HTML]{000000}

\global\setlength{\arrayrulewidth}{\Oldarrayrulewidth}
\global\setlength{\tabcolsep}{\Oldtabcolsep}
\renewcommand*\arraystretch{1}
...
```

10 Intro to lm

In this chapter, linear models (including linear regression and ANOVA) will be introduced. Output is not optimized for print, but rather for interactive use.

10.1 Setup

All packages necessary will be invoked by `p_load`. Packages with only a single function call or potential for name conflicts can be unloaded, this way we still checked for their existence and installed them if need be.

```
pacman::p_load(conflicted,wrappedtools,car,nlme,broom,
                 multcomp,tidyverse,foreign,DescTools, ez,
                 ggbeeswarm,
                 lme4, nlme,merTools,
                 easystats, patchwork,here)#conflicted,
# rayshader,av)
# pacman::p_unload(DescTools, foreign)
# conflict_scout()
conflicts_prefer(dplyr::select,
                  dplyr::filter,
                  modelbased::standardize)
```

```
[conflicted] Will prefer dplyr::select over any other package.
[conflicted] Will prefer dplyr::filter over any other package.
[conflicted] Will prefer modelbased::standardize over any other package.
```

```
base_dir <- here::here()
```

10.2 Import / Preparation

Data are read from an SPSS file. Numeric column Passage is mutated into a factor as `Passage_F`, this is necessary for group comparisons in ANOVA. The call to `here()` expands the path to a file from the project directory to the full system path.

```

rawdata<-foreign::read.spss(file=here('Data/Zellbeads.sav'),
                             use.value.labels=T,to.data.frame=T) |>
  as_tibble() |>
  dplyr::select(-ZahlZellen) |>
  rename(Growth=Wachstum,Treatment=Bedingung) |>
  mutate(Passage_F=factor(Passage),
         Treatment=fct_recode(Treatment,
                               Control="Kontrolle"))

```

re-encoding from CP1252

10.3 Graphical exploration

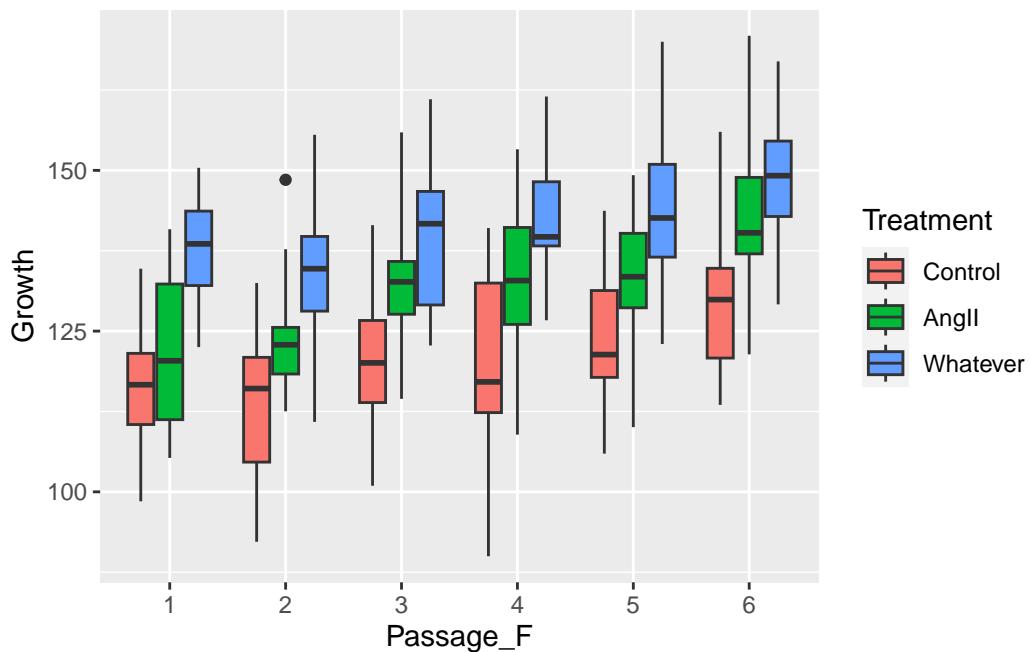
First impression of the data will be attempted by grouped boxplot, followed by interaction plots, both as basic and ggplot with variations.

```

ggplot(rawdata,aes(Passage_F,Growth, fill=Treatment))+  

  geom_boxplot(coef=3)

```



```

with(rawdata, interaction.plot(  

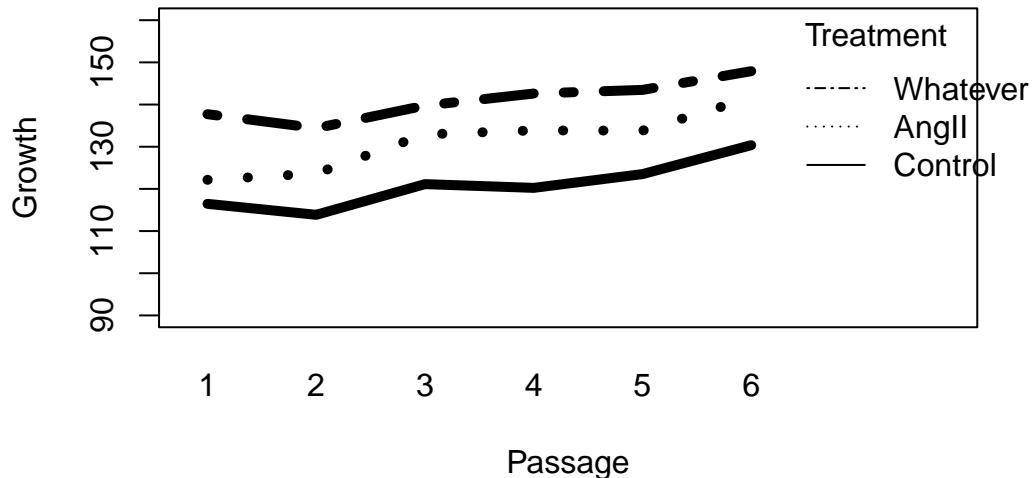
  x.factor=Passage, trace.factor=Treatment, response=Growth,  

  ylim = c(90, 160), lty = c(1,3,12), lwd = 5,  

  ylab = "Growth", xlab = "Passage",

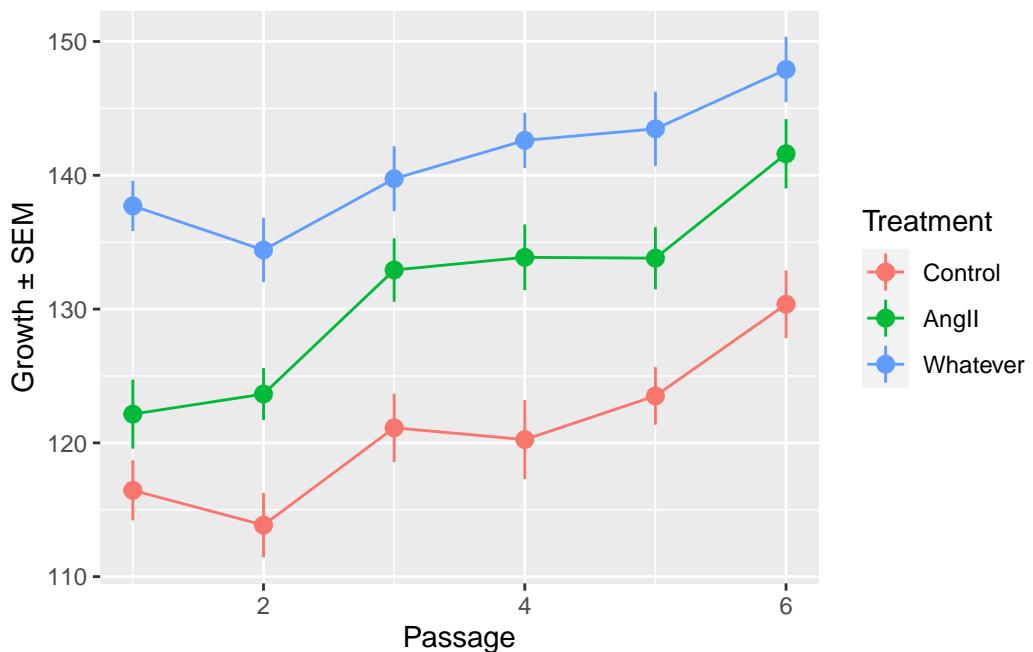
```

```
trace.label = "Treatment"))
```



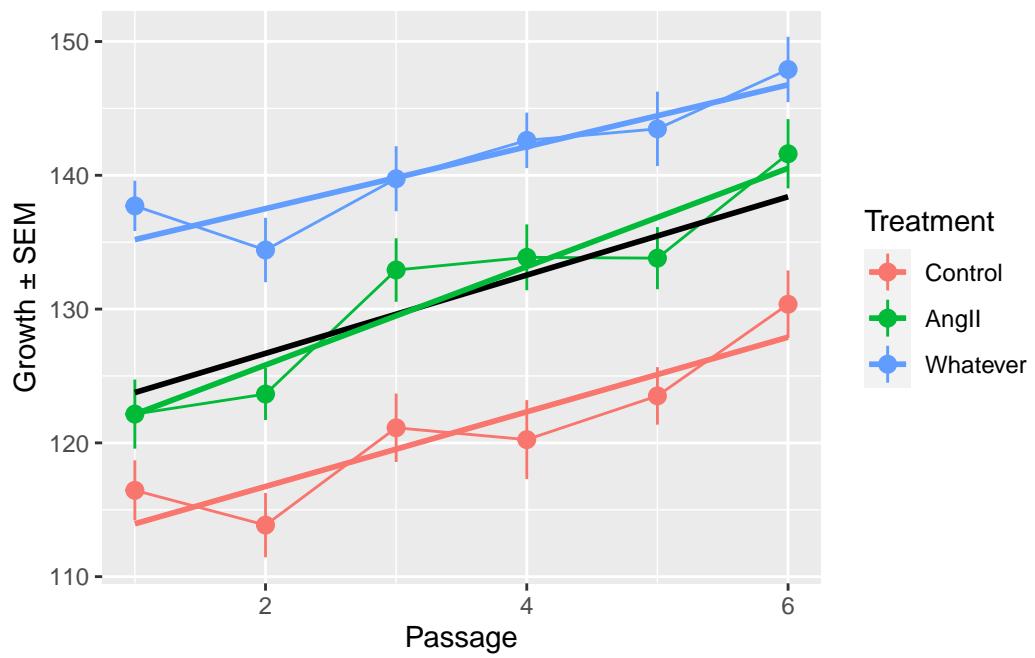
```
# p1<-ggplot(rawdata,aes(x=Passage,y=Growth))+  
#   stat_summary(geom='line',fun='mean',aes(color=Treatment))+  
#   stat_summary(geom='line',fun='mean')  
p1<-ggplot(rawdata,aes(x=Passage,y=Growth))+  
  stat_summary(geom='line',fun='mean',aes(color=Treatment))+  
  stat_summary(aes(color=Treatment))+  
  ylab('Growth \u00b1 SEM')  
p1
```

```
No summary function supplied, defaulting to `mean_se()`
```



```
p1+geom_smooth(method='lm',color='black',se=F)+  
  geom_smooth(method='lm',aes(color=Treatment),se=F)
```

```
No summary function supplied, defaulting to `mean_se()`  
`geom_smooth()` using formula = 'y ~ x'  
`geom_smooth()` using formula = 'y ~ x'
```



```

ggplot(rawdata,aes(x=Passage,y=Growth))+  

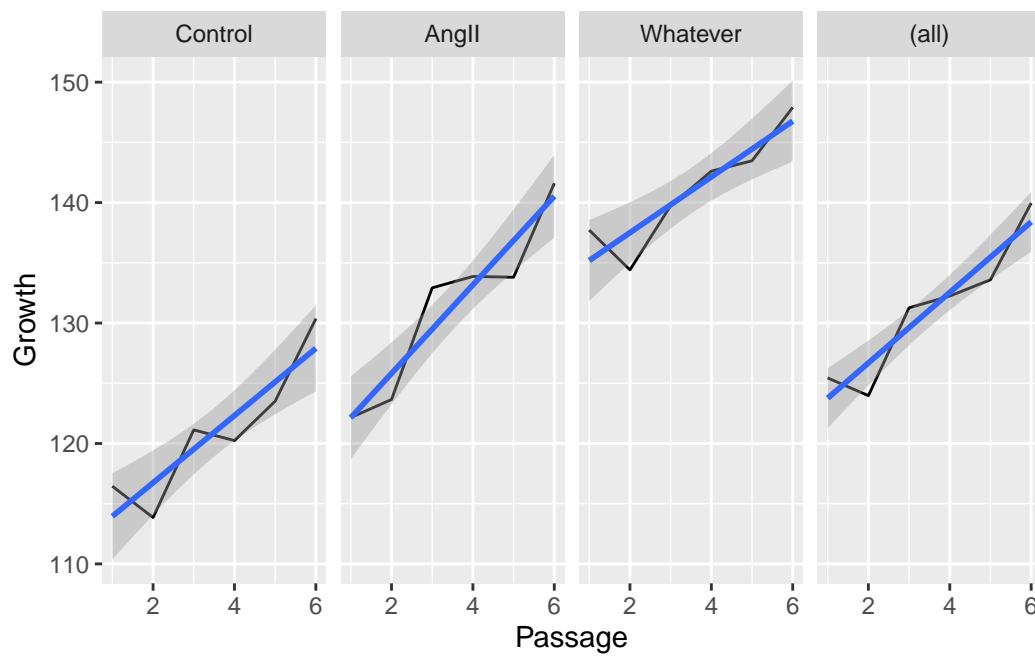
  stat_summary(geom='line',fun='mean')+  

  geom_smooth(method='lm')+  

  facet_grid(cols = vars(Treatment), margins=T)  

`geom_smooth()` using formula = 'y ~ x'

```



10.4 Linear Models

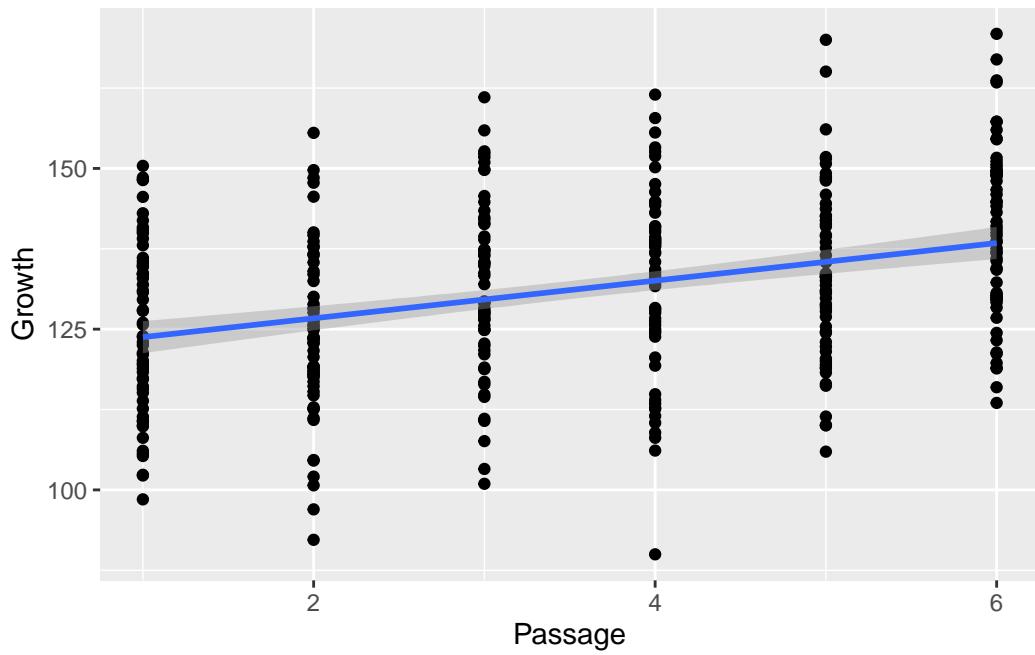
10.4.1 Linear regression

We will analyse the relation between independent variable (IV) Passage and dependent variable (DV) Growth.

10.4.1.1 Graphical exploration

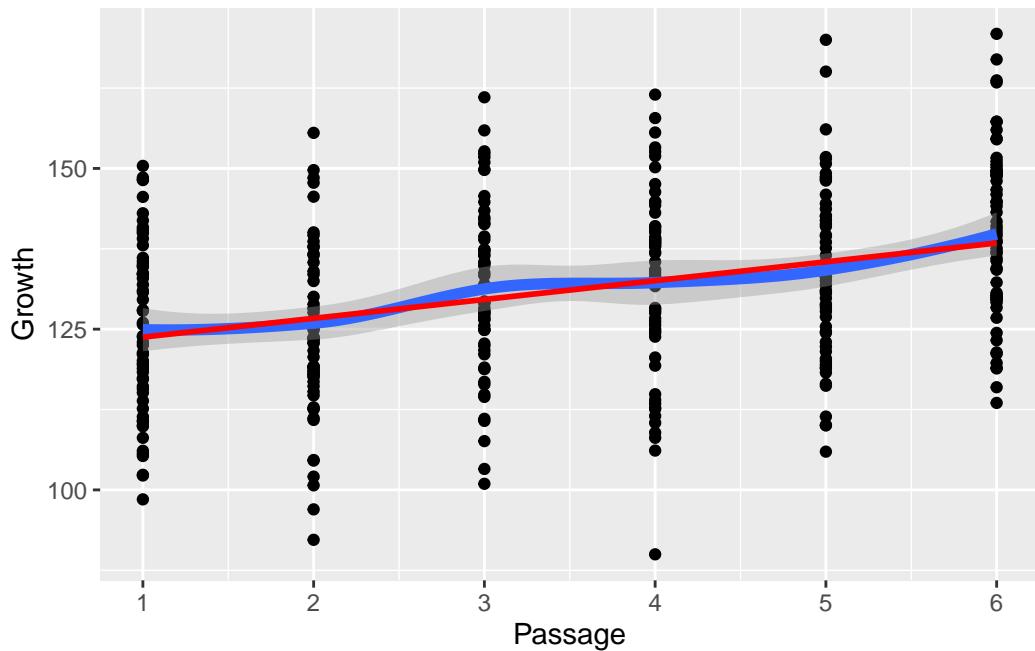
```
ggplot(rawdata,aes(Passage,Growth))+  
  geom_point() +  
  geom_smooth(method=lm)
```

```
`geom_smooth()` using formula = 'y ~ x'
```



```
ggplot(rawdata,aes(Passage,Growth))+  
  geom_point() +  
  scale_x_continuous(breaks=seq(0,10,1)) +  
  geom_smooth(lineWidth=2) +  
  geom_smooth(method=lm,se=F,color='red')
```

```
`geom_smooth()` using method = 'loess' and formula = 'y ~ x'  
`geom_smooth()` using formula = 'y ~ x'
```



10.4.1.2 Modelling

This takes 2 steps, building the model and computing p-values.

```
# model
(regressionOut<-lm(Growth~Passage,data=rawdata))
```

```
Call:
lm(formula = Growth ~ Passage, data = rawdata)
```

```
Coefficients:
(Intercept)      Passage
 120.834        2.927
```

```
# model and p.value for slope, not recommended
tidy(regressionOut)
```

```
# A tibble: 2 x 5
  term       estimate std.error statistic   p.value
  <chr>     <dbl>     <dbl>     <dbl>    <dbl>
1 (Intercept) 121.      1.63      74.2 1.77e-219
2 Passage      2.93      0.418     7.00 1.26e- 11
```

```
# computation of SSQs and p-values, use this!
(anova_out<-anova(regressionOut))
```

Analysis of Variance Table

```
Response: Growth
          Df Sum Sq Mean Sq F value    Pr(>F)
Passage     1   8996   8996.2  49.022 1.257e-11 ***
Residuals 358  65698    183.5
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
anova_out$`Pr(>F)` #|> na.omit()
```

```
[1] 1.257266e-11           NA
```

```
tidy(anova_out)
```

```
# A tibble: 2 x 6
  term      df  sumsq meansq statistic  p.value
  <chr>    <int> <dbl>  <dbl>     <dbl>    <dbl>
1 Passage     1   8996.   8996.     49.0    1.26e-11
2 Residuals  358  65698.   184.      NA      NA
```

```
# summary(regressionOut)
# str(regressionOut)
```

10.4.1.3 Adjusting

To take out the variance due to Passage effects, we can use the residuals and shift them to the original mean:

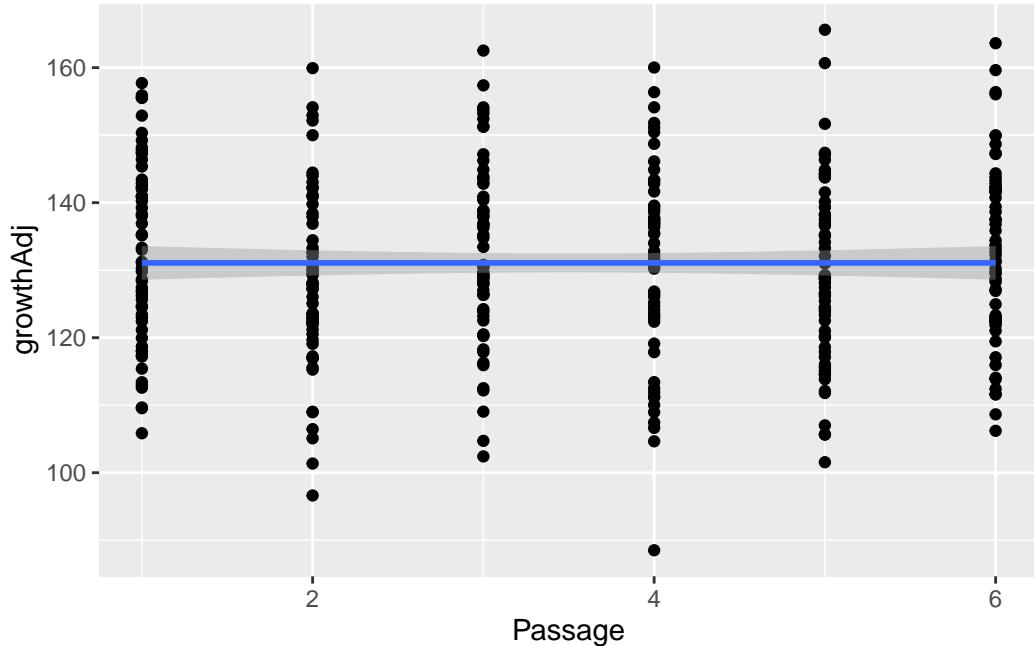
```
rawdata <-
  mutate(rawdata,
        growthAdj = regressionOut$residuals+mean(Growth))

  summarise(rawdata,
            across(contains('growth'),
                   ~meansd(.x,roundDig =4)))
```

```
# A tibble: 1 x 2
  Growth      growthAdj
  <chr>       <chr>
1 131.1 ± 14.4 131.1 ± 13.5
```

```
ggplot(rawdata,aes(Passage,growthAdj))+
  geom_point()+
  geom_smooth(method = 'lm')
```

```
`geom_smooth()` using formula = 'y ~ x'
```



```
lm(growthAdj~Passage,data=rawdata) |> tidy()
```

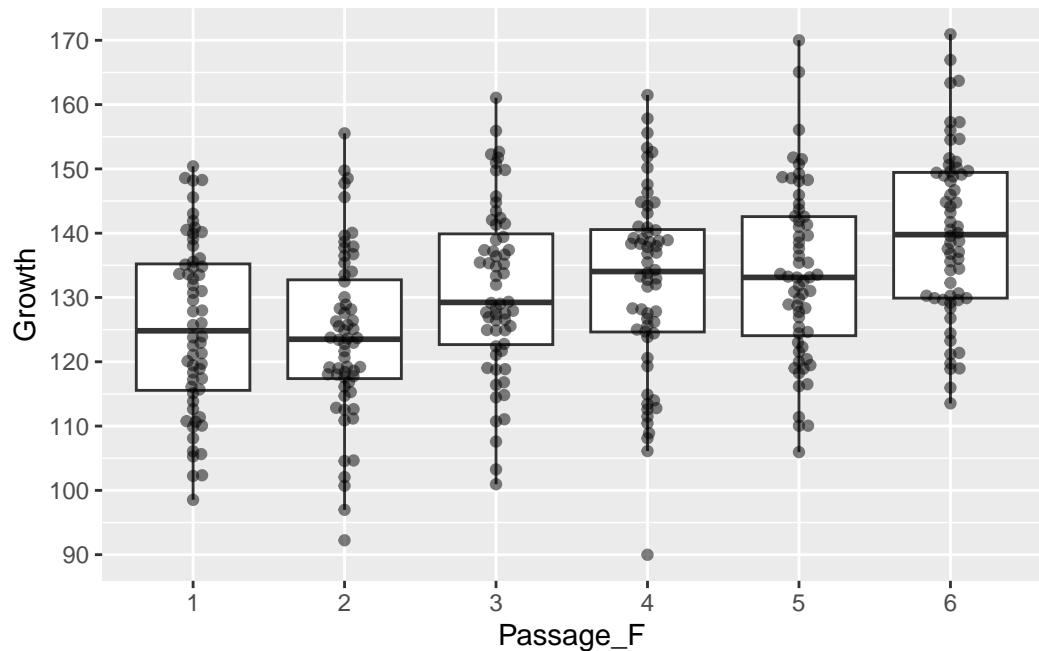
```
# A tibble: 2 x 5
  term      estimate std.error statistic   p.value
  <chr>        <dbl>     <dbl>      <dbl>    <dbl>
1 (Intercept) 1.31e+ 2      1.63     8.05e+ 1 2.04e-231
2 Passage      6.80e-15     0.418    1.63e-14 1.00e+ 0
```

10.4.2 ANOVA

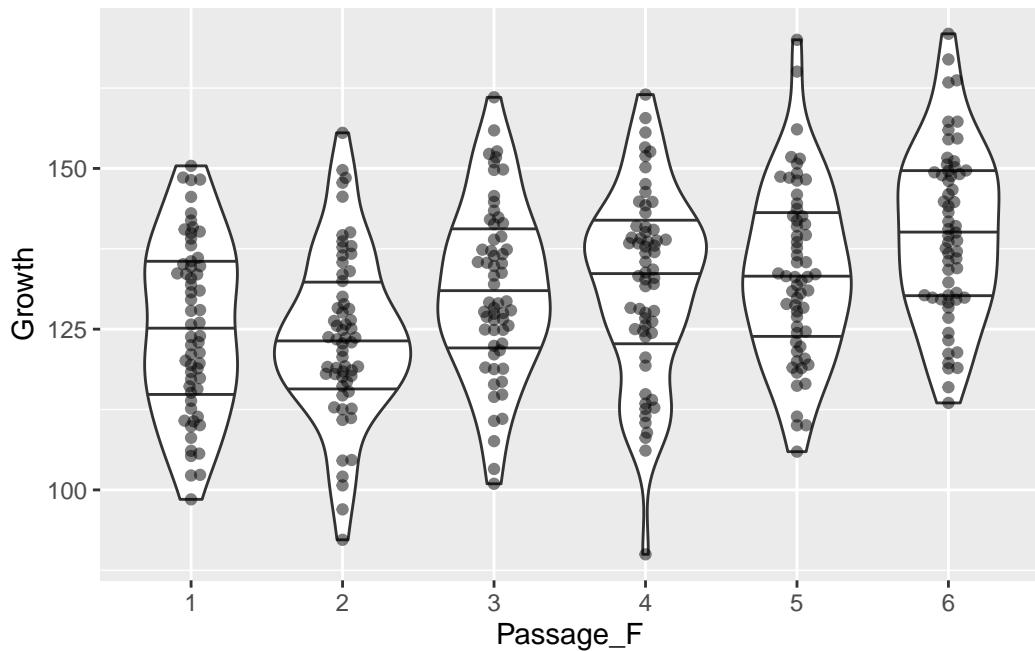
In the linear regression, we had Passage as a continuous IV, estimating a global ‘universal’ effect supposed to be constant. Now we look at Passage_F and model a discrete IV, allowing for specific effects, and thereby comparing means between groups.

10.4.2.1 Graphical exploration

```
ggplot(rawdata,aes(x = Passage_F, y = Growth))+  
  geom_boxplot(outlier.alpha = 0)+  
  geom_beeswarm(alpha=.5)+  
  scale_y_continuous(breaks=seq(0,1000,10))
```



```
ggplot(rawdata,aes(x = Passage_F, y = Growth))+  
  geom_violin(draw_quantiles = c(.25,.5,.75))+  
  geom_beeswarm(alpha=.5)
```



10.4.2.2 Modelling

```
(AnovaOut<-lm(Growth~Passage_F, data=rawdata))
```

Call:
`lm(formula = Growth ~ Passage_F, data = rawdata)`

Coefficients:

	(Intercept)	Passage_F2	Passage_F3	Passage_F4	Passage_F5	Passage_F6
	125.440	-1.467	5.824	6.801	8.156	14.520

```
tidy(AnovaOut)
```

```
# A tibble: 6 x 5
  term      estimate std.error statistic p.value
  <chr>      <dbl>    <dbl>     <dbl>   <dbl>
1 (Intercept) 125.       1.74     71.9  2.20e-213
2 Passage_F2  -1.47     2.47    -0.595 5.52e- 1
3 Passage_F3   5.82     2.47     2.36  1.87e- 2
4 Passage_F4   6.80     2.47     2.76  6.11e- 3
5 Passage_F5   8.16     2.47     3.31  1.04e- 3
6 Passage_F6  14.5      2.47     5.89  9.03e- 9
```

```
# summary(AnovaOut)
(t <- anova(AnovaOut))
```

Analysis of Variance Table

Response: Growth

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Passage_F	5	10134	2026.71	11.113	5.852e-10 ***
Residuals	354	64561	182.38		

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```
t$`Pr(>F)`
```

```
[1] 5.851856e-10           NA
```

```
tidy(t)
```

```
# A tibble: 2 x 6
  term      df    sumsq   meansq statistic   p.value
  <chr>     <int>  <dbl>    <dbl>     <dbl>      <dbl>
1 Passage_F     5 10134.  2027.     11.1  5.85e-10
2 Residuals    354 64561. 182.      NA     NA
```

10.4.2.3 Post-hoc analyses

The p-value from our model only tests the global Null hypothesis of no differences between any group (all means are the same / all groups come from the same population). Post-hoc tests are used to figure out which groups are different. Those tests need to take multiple testing into account. Try to limit selection of tests!

```
# possible in a loop, but nominal p
t.test(rawdata$Growth[which(rawdata$Passage==1)],
       rawdata$Growth[which(rawdata$Passage==2)],
       var.equal = T)
```

Two Sample t-test

```
data: rawdata$Growth[which(rawdata$Passage == 1)] and rawdata$Growth[which(rawdata$Passag
```

```

t = 0.60679, df = 118, p-value = 0.5452
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
-3.321297  6.255936
sample estimates:
mean of x mean of y
125.4396 123.9723

```

```

# all pairwise group combinations
pt_out<-pairwise.t.test(x=rawdata$Growth,
                         g=rawdata$Passage_F,
                         p.adjust.method='none')
pt_out

```

Pairwise comparisons using t tests with pooled SD

```

data: rawdata$Growth and rawdata$Passage_F

      1       2       3       4       5
2 0.55215 -       -       -       -
3 0.01871 0.00331 -       -       -
4 0.00611 0.00088 0.69214 -       -
5 0.00104 0.00011 0.34487 0.58296 -
6 9e-09   3e-10   0.00048 0.00189 0.01025

P value adjustment method: none

```

```

pairwise.t.test(x=rawdata$Growth,g=rawdata$Passage,
                 p.adjust.method='fdr')

```

Pairwise comparisons using t tests with pooled SD

```

data: rawdata$Growth and rawdata$Passage

      1       2       3       4       5
2 0.62460 -       -       -       -
3 0.02552 0.00621 -       -       -
4 0.01018 0.00259 0.69214 -       -
5 0.00259 0.00057 0.43109 0.62460 -
6 6.8e-08 4.5e-09 0.00178 0.00405 0.01538

P value adjustment method: fdr

```

```
pairwise.t.test(x=rawdata$Growth,g=rawdata$Passage,
                 p.adjust.method='bonferroni')
```

Pairwise comparisons using t tests with pooled SD

```
data: rawdata$Growth and rawdata$Passage
```

	1	2	3	4	5
2	1.0000	-	-	-	-
3	0.2807	0.0497	-	-	-
4	0.0917	0.0133	1.0000	-	-
5	0.0155	0.0017	1.0000	1.0000	-
6	1.4e-07	4.5e-09	0.0071	0.0283	0.1538

P value adjustment method: bonferroni

```
# comparison against reference group 1
pt_out$p.value[,1]
```

	2	3	4	5	6
5	5.521460e-01	1.871115e-02	6.110172e-03	1.036173e-03	9.031123e-09

```
# comparison against reference group 6
pt_out$p.value[5,]
```

	1	2	3	4	5
9	0.031123e-09	3.001066e-10	4.757018e-04	1.889098e-03	1.025037e-02

```
# comparison for selection
c(pt_out$p.value[1,1],pt_out$p.value[3,2],
  pt_out$p.value[5,1])
```

[1] 5.521460e-01 8.842382e-04 9.031123e-09

```
# comparison against next level
diag(pt_out$p.value)
```

[1] 0.55214600 0.00331248 0.69214393 0.58295615 0.01025037

```
# adjusting for multiple testing for selected comparisons  
p.adjust(diag(pt_out$p.value),method='fdr')
```

```
[1] 0.69214393 0.01656240 0.69214393 0.69214393 0.02562592
```

```
formatP(p.adjust(pt_out$p.value[,1],method='fdr'))
```

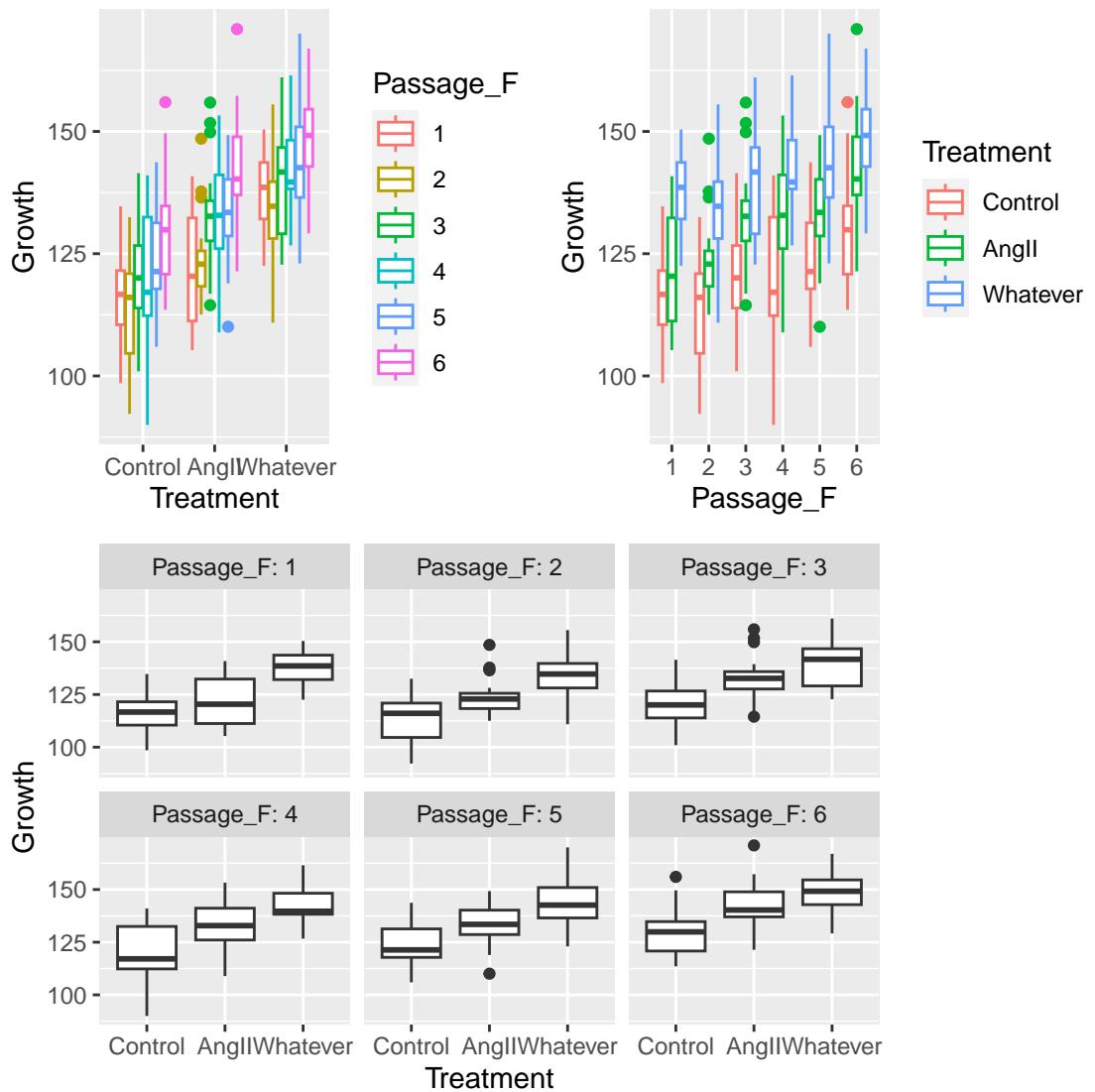
```
[1] "0.552" "0.023" "0.010" "0.003" "0.001"
```

10.4.3 LM with continuous AND categorical IV

Traditionally you may think of *regression OR ANOVA*, but they are no different and can be combined. This is called a general linear model. Multivariable models may contain interactions between independent variables V $IV1*IV2$.

10.4.3.1 Graphical exploration

```
p0 <- ggplot(rawdata,aes(Treatment,Growth))+  
  geom_boxplot()  
p1 <- ggplot(rawdata,aes(Treatment,Growth, color=Passage_F))+  
  geom_boxplot()  
p2 <- ggplot(rawdata,aes(color=Treatment,Growth, x=Passage_F))+  
  geom_boxplot()  
p3 <- ggplot(rawdata,aes(Treatment,Growth))+  
  geom_boxplot()  
  facet_wrap(facets = vars(Passage_F), labeller='label_both')  
# from patchwork  
(p1+p2)/p3
```



10.4.3.2 Modelling

Models with (*) and without (+) interaction are build and tested.

```
lmOut_interaction<-lm(Growth~Passage*Treatment,data=rawdata)
Anova(lmOut_interaction,type = 3)
```

Anova Table (Type III tests)

Response: Growth

	Sum Sq	Df	F value	Pr(>F)
--	--------	----	---------	--------

```

(Intercept) 285160   1 2448.5613 < 2.2e-16 ***
Passage       2723    1   23.3855 1.981e-06 ***
Treatment     5635    2   24.1924 1.419e-10 ***
Passage:Treatment 335    2    1.4376    0.2389
Residuals      41227  354
---
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

```

#
lmOut_additive<-lm(Growth~Passage+Treatment,data=rawdata)
Anova_out <- Anova(lmOut_additive,type=2)
Anova_out$`Pr(>F)`
```

```
[1] 7.051564e-17 4.006053e-36 NA
```

```
tidy(Anova_out)
```

```
# A tibble: 3 x 5
  term      sumsq    df statistic p.value
  <chr>     <dbl> <dbl>     <dbl>     <dbl>
1 Passage    8996.     1      77.1  7.05e-17
2 Treatment  24137.    2      103.   4.01e-36
3 Residuals  41562.   356     NA     NA
```

```

# for comparison, here is the univariable model
lmOut_uni<-lm(Growth~Treatment,data=rawdata)
aOut<-Anova(lmOut_uni,type=3)
a_uni <- anova(lmOut_uni)
a_uni$`Pr(>F)`
```

```
[1] 5.549803e-31 NA
```

10.4.3.3 Post-hoc analyses

For multivariable models, pairwise.t.test() is not appropriate, Dunnet or Tukey tests (depending on hypothesis) are typical solutions.

```

glht_out <-
  summary(glht(model=lmOut_additive,
               linfct=mcp(Treatment='Dunnett'))))
glht_out$test$pvalues
```

```
[1] 1.316836e-12 5.551115e-16  
attr(,"error")  
[1] 1e-15
```

```
summary(glht(model=lmOut_additive,  
            linfct=mcp(Treatment='Tukey')))
```

Simultaneous Tests for General Linear Hypotheses

Multiple Comparisons of Means: Tukey Contrasts

Fit: lm(formula = Growth ~ Passage + Treatment, data = rawdata)

Linear Hypotheses:

	Estimate	Std. Error	t value	Pr(> t)
AngII - Control == 0	10.409	1.395	7.462	<1e-10 ***
Whatever - Control == 0	20.052	1.395	14.375	<1e-10 ***
Whatever - AngII == 0	9.643	1.395	6.913	<1e-10 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
(Adjusted p values reported -- single-step method)

```
DescTools:::DunnettTest(Growth~Passage_F,data=rawdata)
```

Dunnett's test for comparing several treatments with a control :
95% family-wise confidence level

```
$`1`  
    diff      lwr.ci      upr.ci      pval  
2-1 -1.467320 -7.6899251  4.755285  0.9648  
3-1  5.824059 -0.3985468 12.046664  0.0752 .  
4-1  6.801105  0.5784996 13.023710  0.0262 *  
5-1  8.156143  1.9335375 14.378748  0.0048 **  
6-1 14.520106  8.2975011 20.742712 2.6e-08 ***  
  
---  
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
DescTools:::DunnettTest(Growth~Treatment,data=rawdata)
```

```
Dunnett's test for comparing several treatments with a control :  
95% family-wise confidence level
```

```
$Control
```

	diff	lwr.ci	upr.ci	pval
AngII-Control	10.40895	6.996811	13.82109	1e-10 ***
Whatever-Control	20.05199	16.639849	23.46413	<2e-16 ***

```
---
```

```
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
pairwise.t.test(rawdata$Growth, rawdata$Treatment, p.adjust.method = 'n')
```

```
Pairwise comparisons using t tests with pooled SD
```

```
data: rawdata$Growth and rawdata$Treatment
```

	Control	AngII
AngII	5.1e-11	-
Whatever	< 2e-16	1.0e-09

```
P value adjustment method: none
```

```
# mean(rawdata$Growth[which(rawdata$Passage==1 &  
# rawdata$Treatment=='Control')])  
anova_out$'Pr(>F)'
```

```
[1] 1.257266e-11 NA
```

```
#aOut$`Sum Sq`  
summary(lmOut_additive)
```

```
Call:
```

```
lm(formula = Growth ~ Passage + Treatment, data = rawdata)
```

```
Residuals:
```

Min	1Q	Median	3Q	Max
-32.407	-7.793	-0.281	7.255	32.283

```

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) 110.6802    1.5280  72.432 < 2e-16 ***
Passage      2.9271    0.3334   8.778 < 2e-16 ***
TreatmentAngII 10.4089    1.3949   7.462 6.59e-13 ***
TreatmentWhatever 20.0520    1.3949  14.375 < 2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

Residual standard error: 10.8 on 356 degrees of freedom
Multiple R-squared: 0.4436, Adjusted R-squared: 0.4389
F-statistic: 94.6 on 3 and 356 DF, p-value: < 2.2e-16

```
(result<-tibble(predictor=rownames(aOut),
                 p=formatP(aOut$'Pr(>F)',ndigits=5)))
```

```
# A tibble: 3 x 2
  predictor     p
  <chr>       <chr>
1 (Intercept) "0.00001"
2 Treatment    "0.00001"
3 Residuals    "     NA"
```

```
broom::tidy(aOut)
```

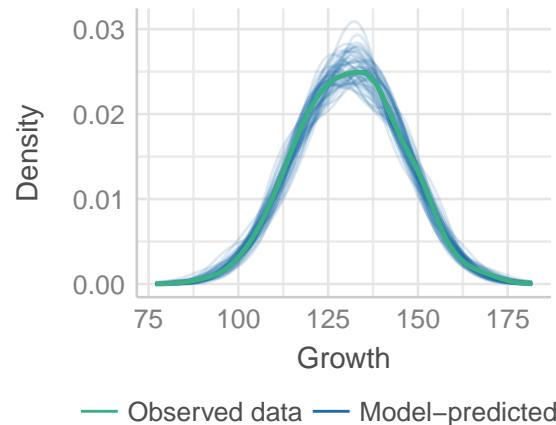
```
# A tibble: 3 x 5
  term        sumsq    df statistic  p.value
  <chr>      <dbl> <dbl>      <dbl>      <dbl>
1 (Intercept) 1754743.     1    12391.  2.91e-279
2 Treatment    24137.      2      85.2  5.55e- 31
3 Residuals    50558.     357      NA      NA
```

10.4.4 Model exploration with package performance

```
# x11() #interactive only!  
  
# from package performance  
check_model(lm0ut_additive)
```

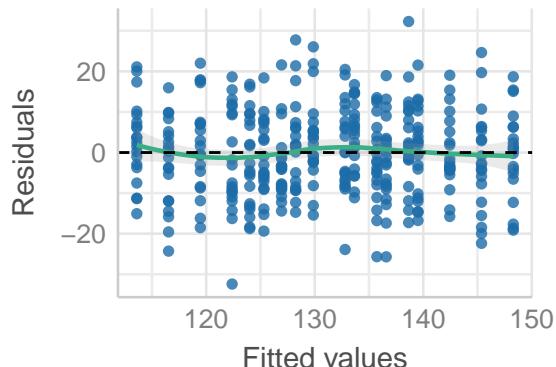
Posterior Predictive Check

Model-predicted lines should resemble observed



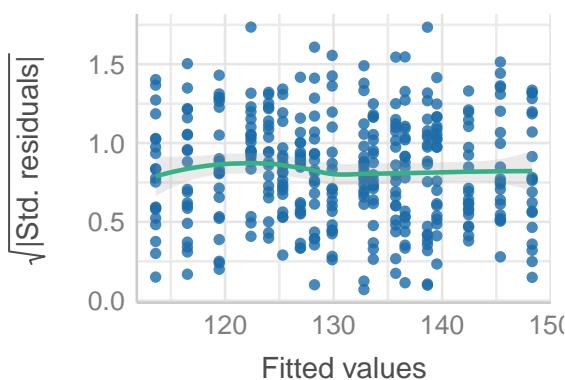
Linearity

Reference line should be flat and horizontal



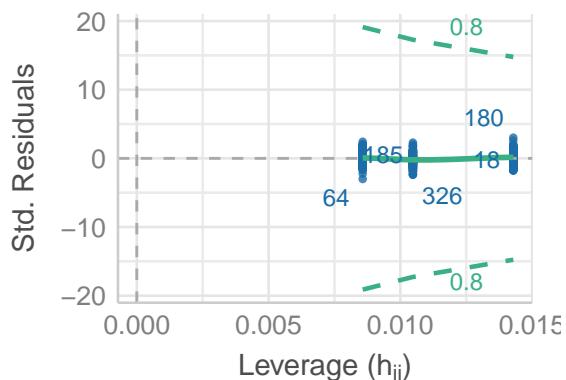
Homogeneity of Variance

Reference line should be flat and horizontal



Influential Observations

Points should be inside the contour lines



Collinearity

High collinearity (VIF) may inflate parameter uncertainty



● Low (< 5)

Normality of Residuals

Dots should fall along the line

