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.

Chapter 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.

Chapter 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 usualy 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:

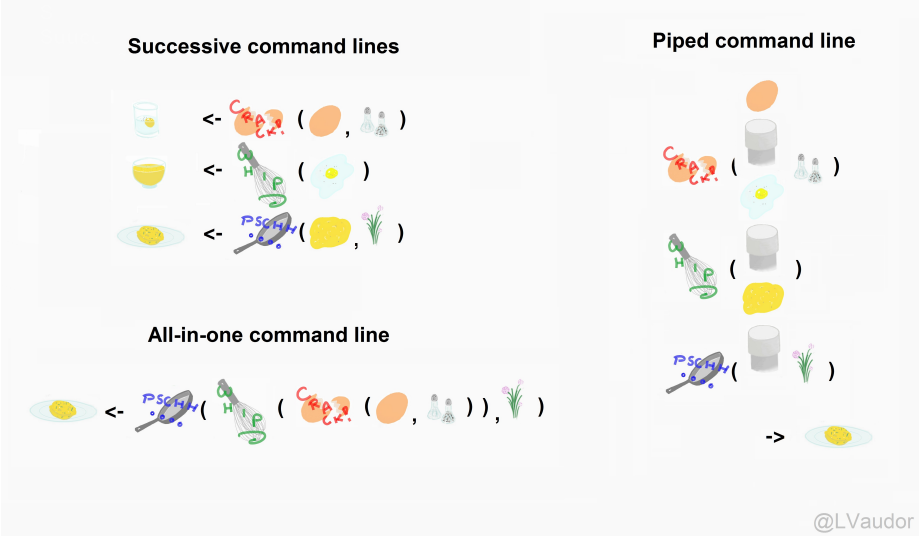


Figure 2.1: *Piping functions*

```
# 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)`
   <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>
```

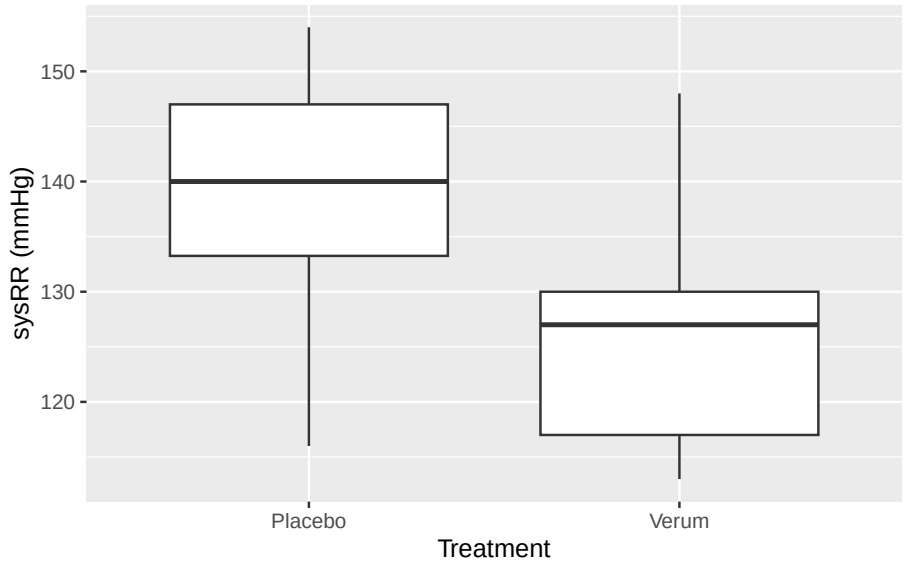
```
colnames(rawdata)
```

```
[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" "female" "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] 128 116 120 130 135 148 137 139 154 113 118 117 127 143 117 135 117 147 127
[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
```

Chapter 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

Chapter 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 tidyr 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://tidyr.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          69.6      78.7
2 P 2   B         115.      126.
3 P 3   C          95.0     109.
```

```
  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  69.6
2 P 1   A     Var2Time2  78.7
3 P 2   B     Var2Time1 115.
4 P 2   B     Var2Time2 126.
5 P 3   C     Var2Time1  95.0
6 P 3   C     Var2Time2 109.
```

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       123.      142.       8.55      8.72 A
2 P 2        88.1      98.7      9.10      7.61 B
3 P 3        88.3     110.       9.48      7.89 C
```

```
#intermediate:
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 123.
 2 P 1   A     Var1     Time2 142.
 3 P 1   A     Var2     Time1   8.55
 4 P 1   A     Var2     Time2   8.72
 5 P 2   B     Var1     Time1  88.1
 6 P 2   B     Var1     Time2  98.7
 7 P 2   B     Var2     Time1   9.10
 8 P 2   B     Var2     Time2   7.61
 9 P 3   C     Var1     Time1  88.3
10 P 3   C     Var1     Time2 110.
11 P 3   C     Var2     Time1   9.48
12 P 3   C     Var2     Time2   7.89
```

```
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 123.   8.55
2 P 1   A     Time2 142.   8.72
3 P 2   B     Time1  88.1  9.10
4 P 2   B     Time2  98.7  7.61
5 P 3   C     Time1  88.3  9.48
6 P 3   C     Time2 110.   7.89
```

Chapter 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
```

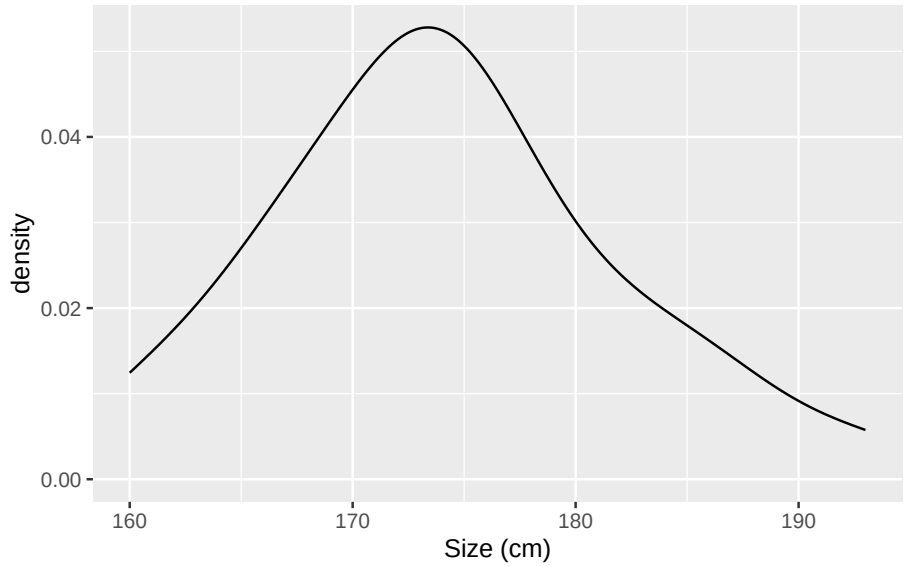
```
ksnormal(rawdata$`Size (cm)`)
```

```
[1] 0.7063825
```

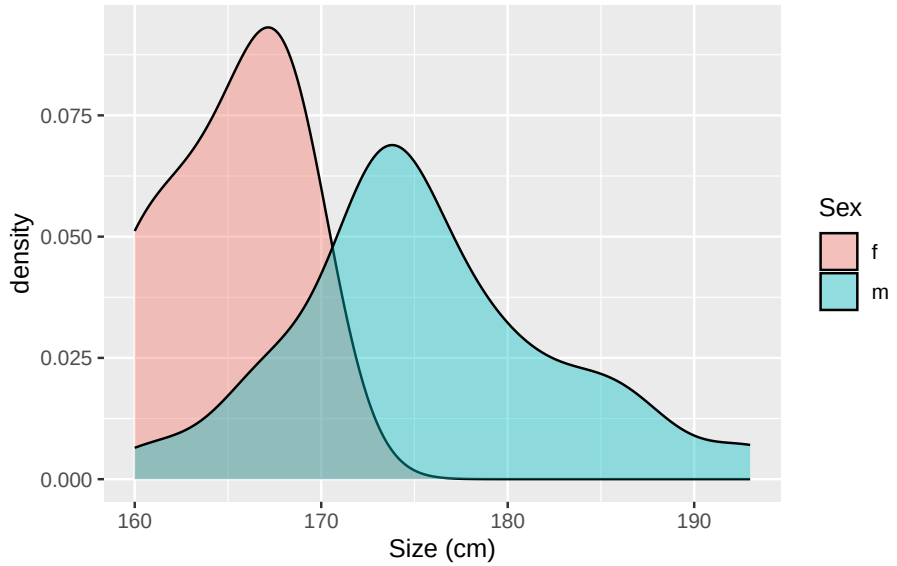
```
shapiro.test(rawdata$`Size (cm)`)
```

```
    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(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")
```

Chapter 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,
                 emojifont,
                 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:

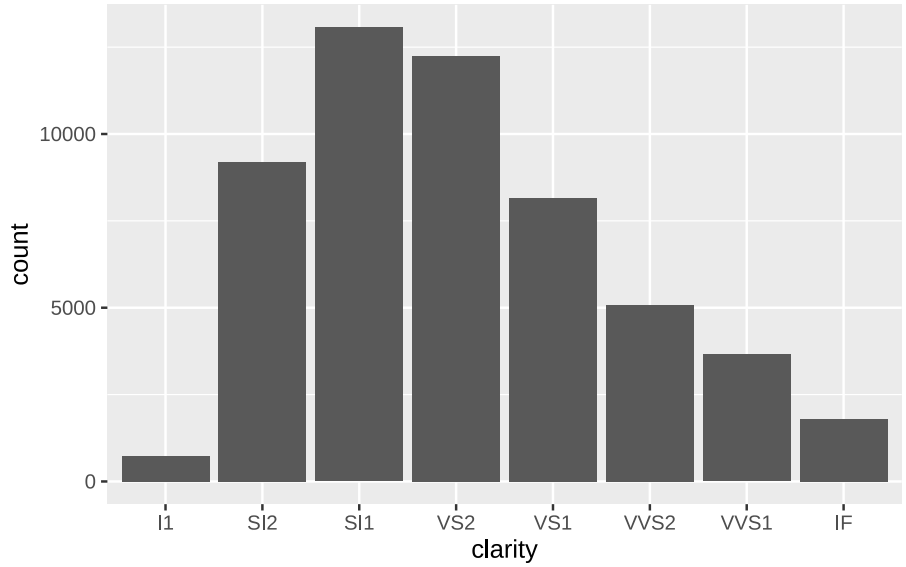
1. ggplot(data = my_data, mapping = aes(x=..., y=..., color=..., shape=...)) to define data and inside aes() some global defaults for aesthetic mappings, this (sort of) creates the canvas to draw on

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:

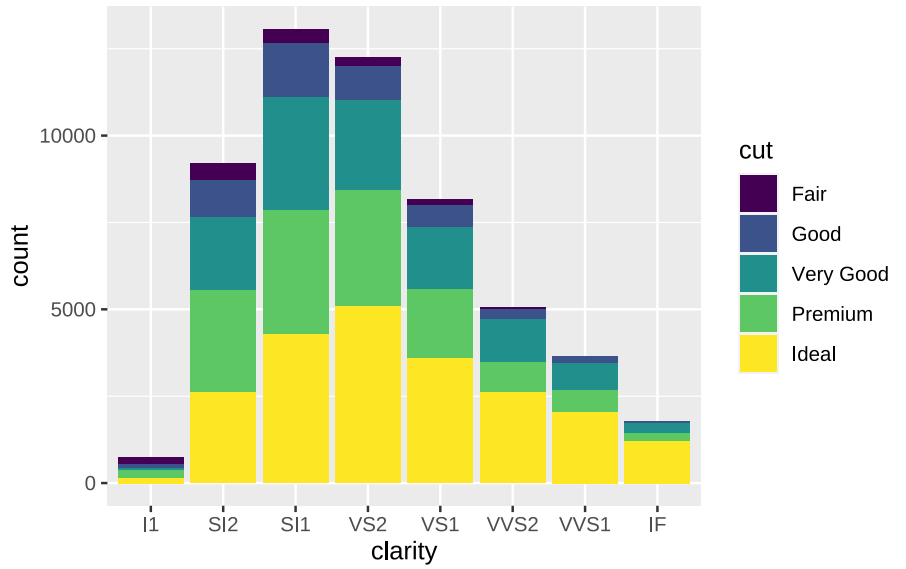
```
ggplot(data=diamonds,mapping = aes(x=clarity))+
  geom_bar()
```



geom_bar() inherits the global aestetic 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-color. This automatically creates sub-groups for counting:

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



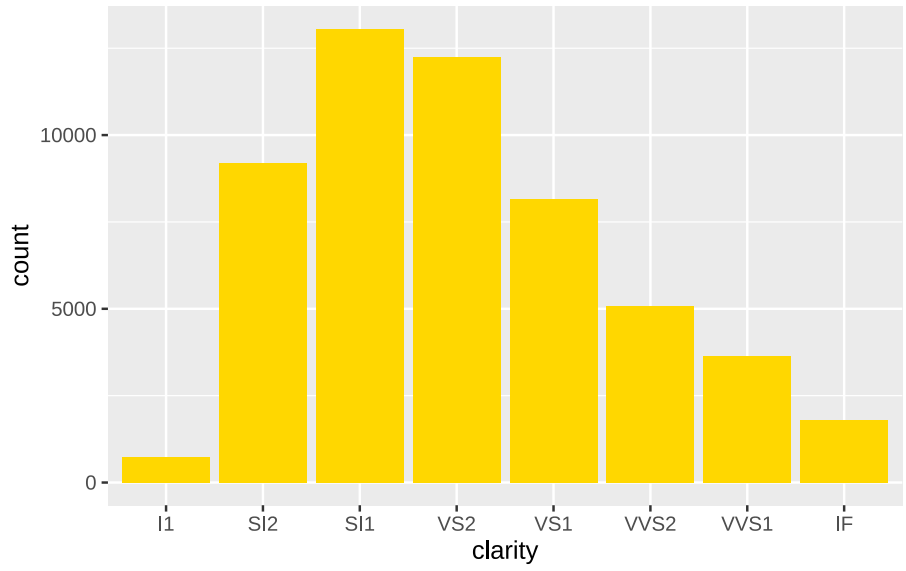
This graph represents this count table:

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

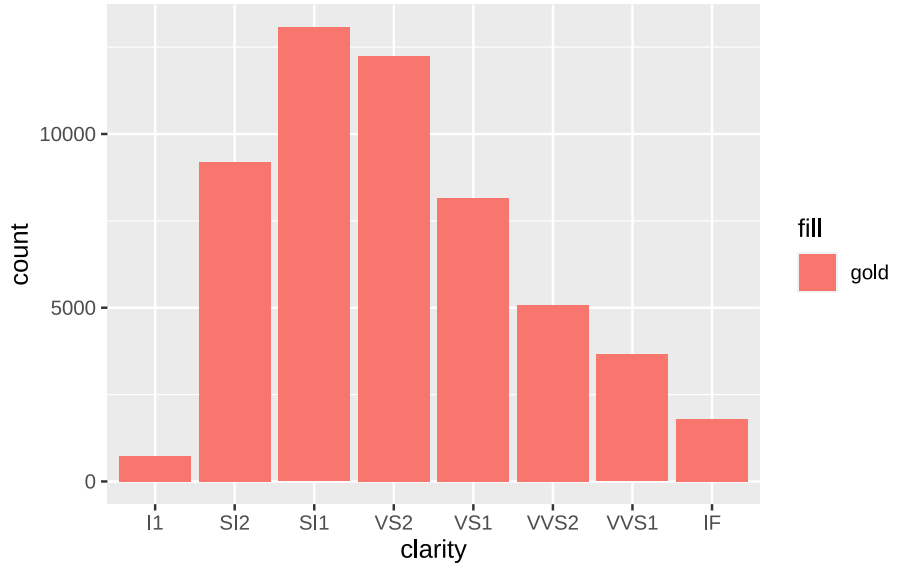
```
# A tibble: 5 x 9
# Groups:   cut [5]
  cut          I1   SI2   SI1   VS2   VS1  VVS2  VVS1    IF
  <ord>     <int> <int> <int> <int> <int> <int> <int> <int>
1 Fair        210   466   408   261   170    69    17     9
2 Good         96  1081  1560   978   648   286   186    71
3 Very Good    84  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:

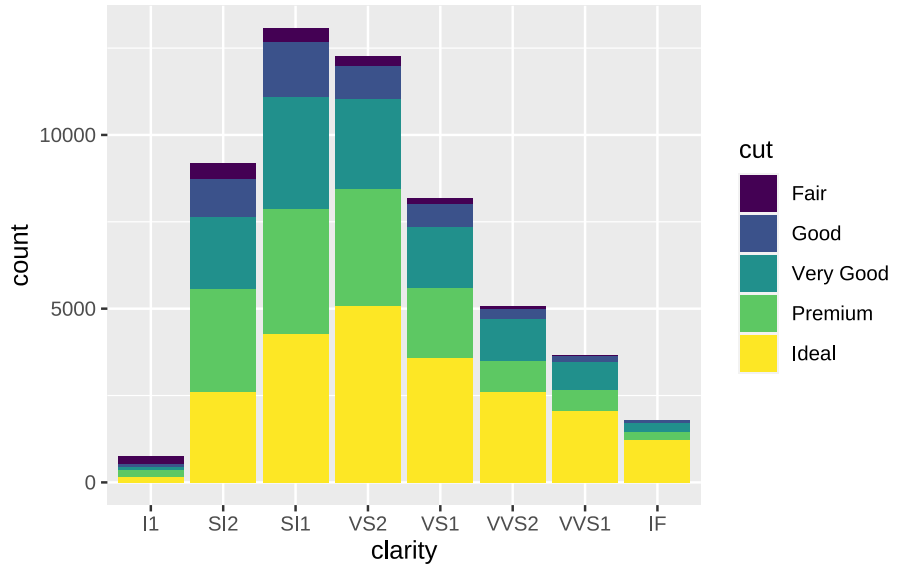
```
#aesthetics outside aes
ggplot(data=diamonds,aes(x=clarity))+
  geom_bar(fill="gold")
```




```
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
```



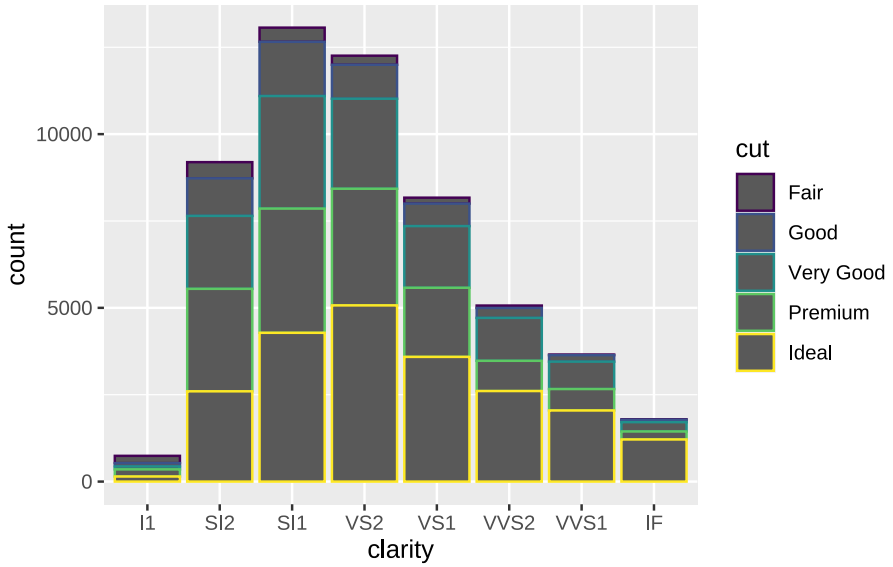
6.3 fill vs. color

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

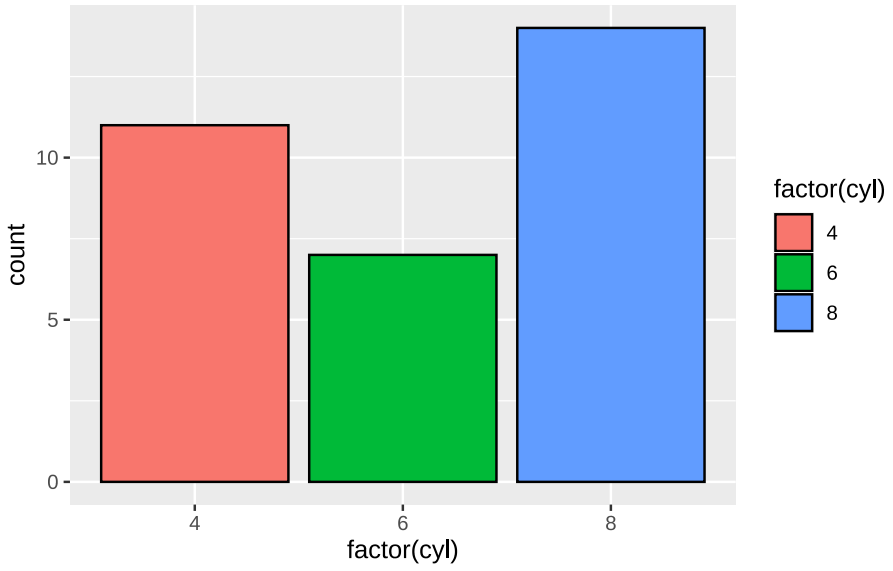
- inner color, defined by `fill`
- outer frame color, defined by `color`

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.

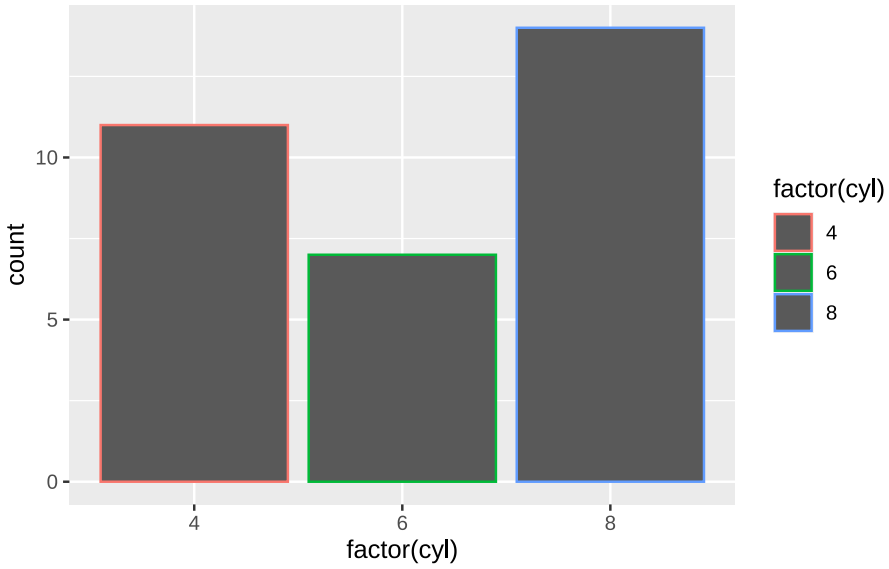
```
ggplot(data=diamonds,aes(x=clarity,color=cut))+
  geom_bar()
```




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



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

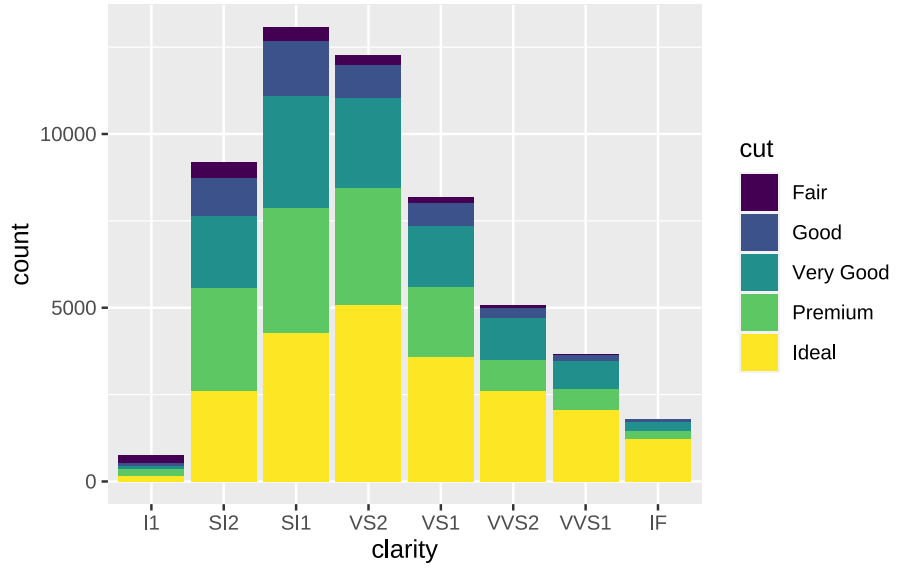


6.4 Color systems

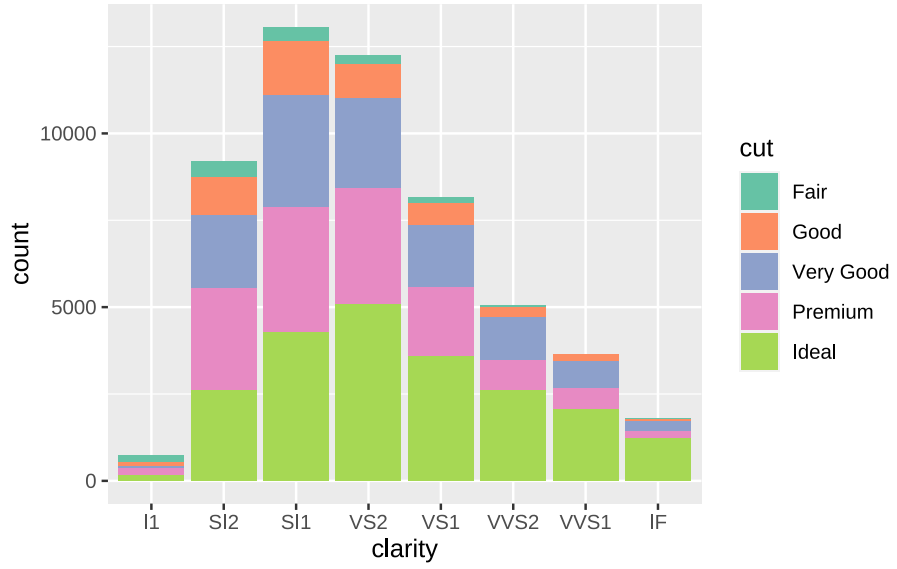
ggplot2 comes with various color definitions, many external packages extend that. Manual definition of colors is possible as well. Redefining the mapping between data and aesthetics can be done with scale_... functions

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

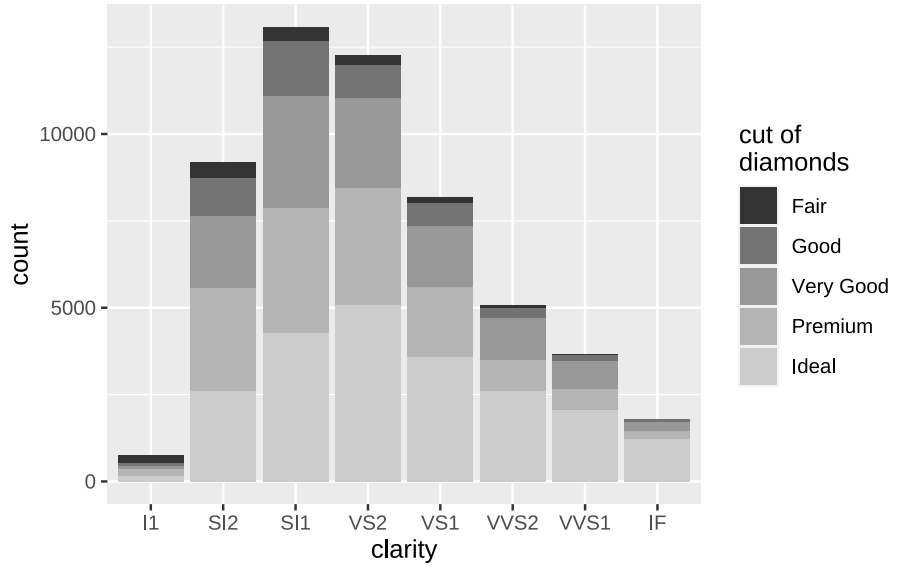
```
(plottemp <- ggplot(data=diamonds,aes(x=clarity,fill=cut))+
    geom_bar())
```



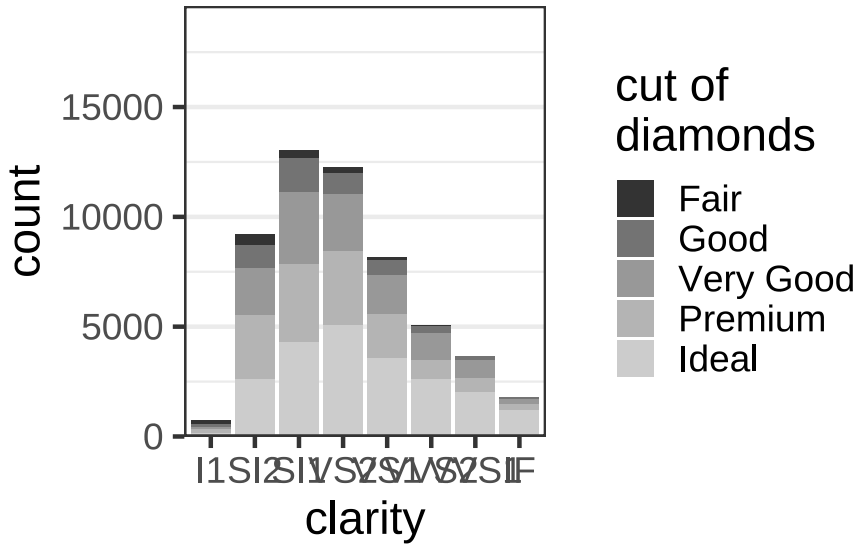

```
plottemp + scale_fill_brewer(palette="Set2") #in-built "scale" for fill
```




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

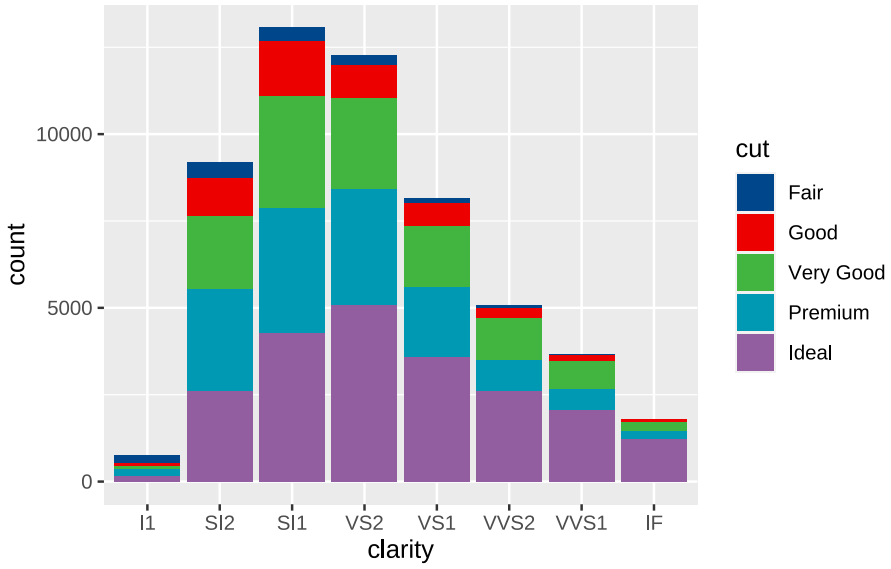



```
plottemp + scale_fill_grey(name = "cut of\ndiamonds") +
  scale_y_continuous(expand = expansion(mult = c(0,.5)))+ # rescaling y
  theme_bw(base_size = 20)+
  theme(panel.grid.major.x = element_blank())
```

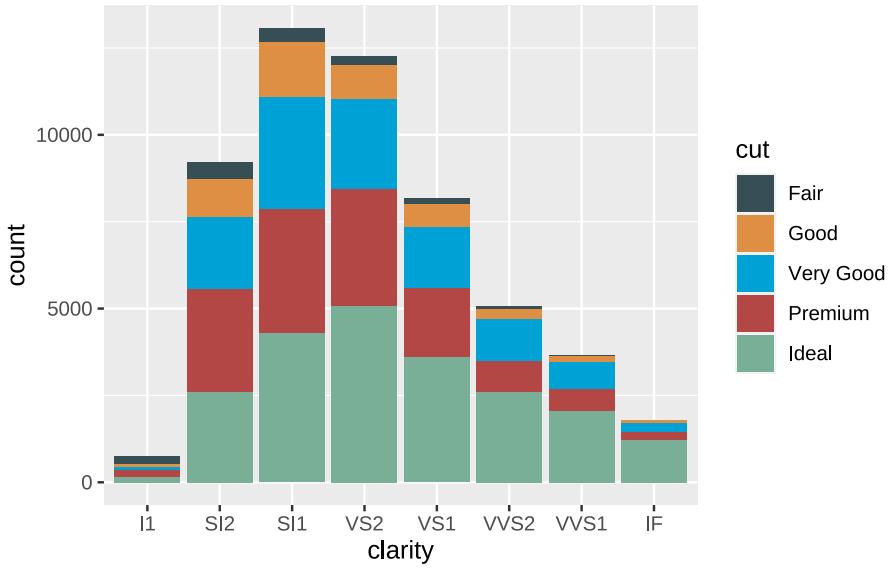


6.4.1 External color definitions from ggsci

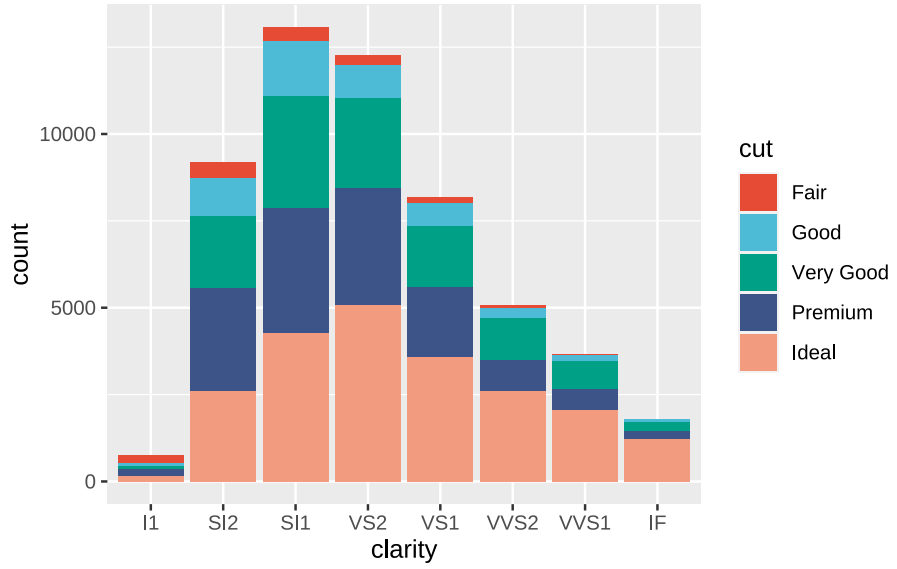
```
plottemp+scale_fill_lancet()
```



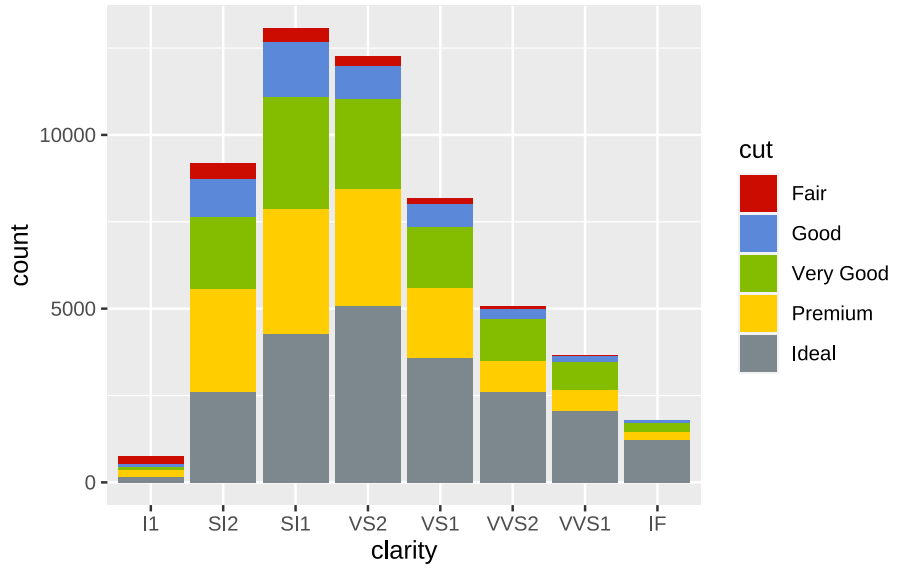

```
plottemp+scale_fill_jama()
```




```
plottemp+scale_fill_npg()
```




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



6.5 Exporting ggplots

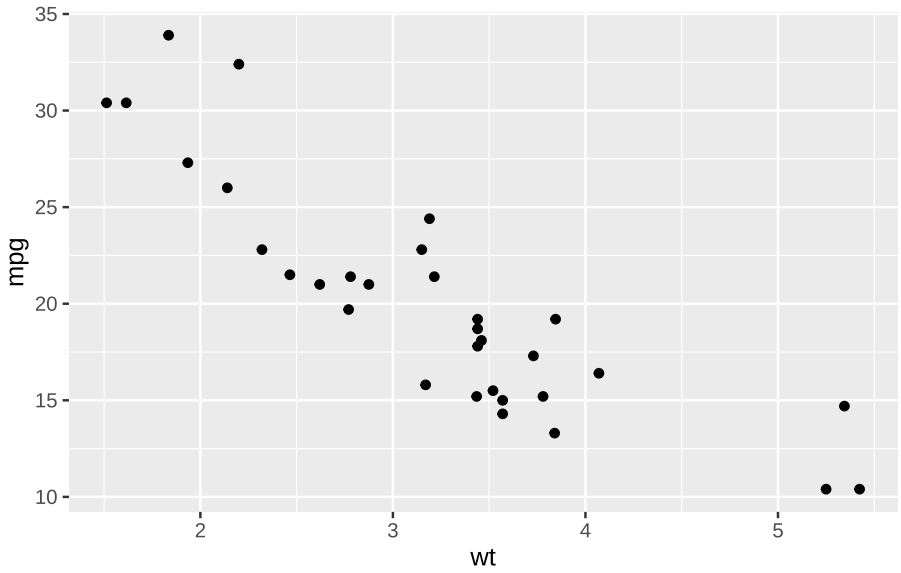
There are two distinct ways, using ggsave() or more generally creating an external graphic device with e.g. png() / tiff() / pdf():

```
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

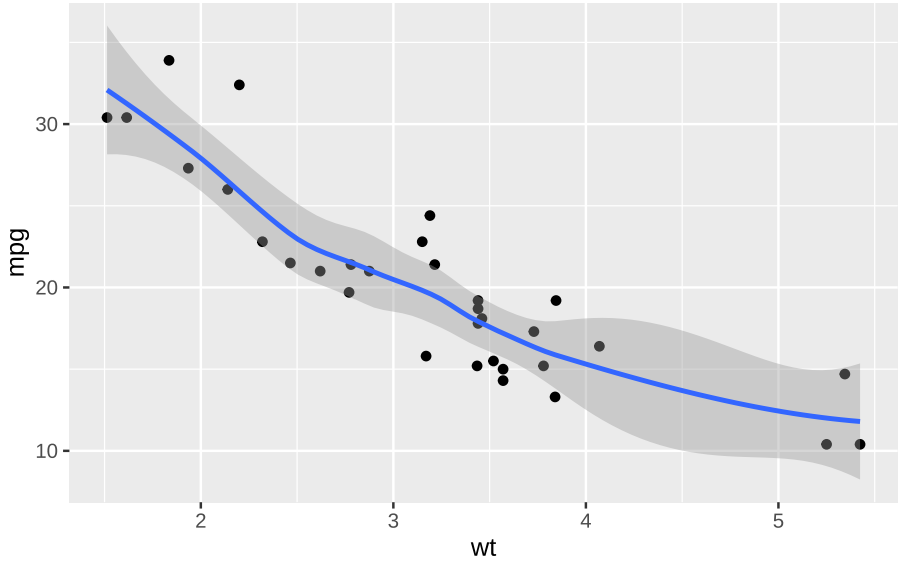
Common forms of plots are barplots, boxplots, scatterplots (possibly with regression line), and density-plots. For plotting dots for groups, there are various options to avoid over-plotting of repeated data, with the beeswarm as my preference.

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



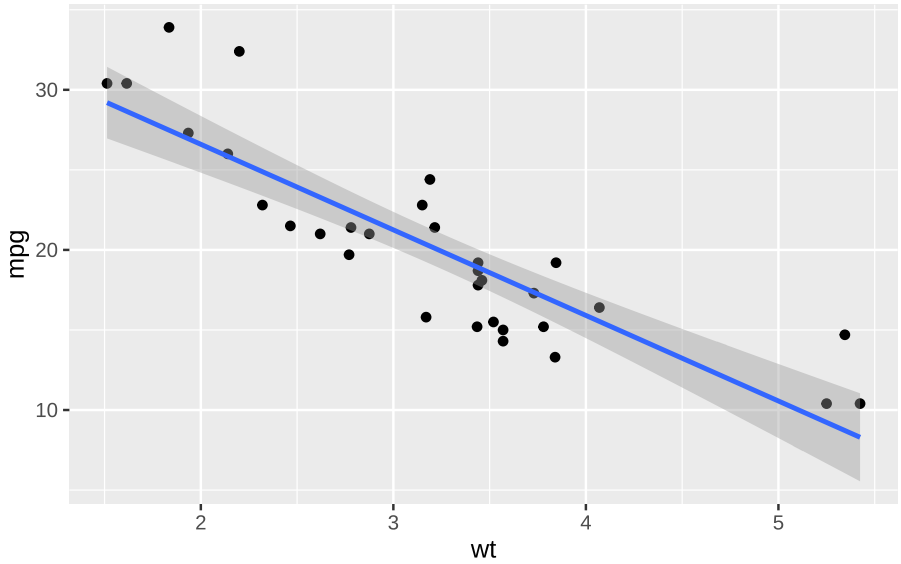
```
ggplot(data=mtcars,aes(x = wt,y = mpg))+
  geom_point()+
  geom_smooth()
```

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

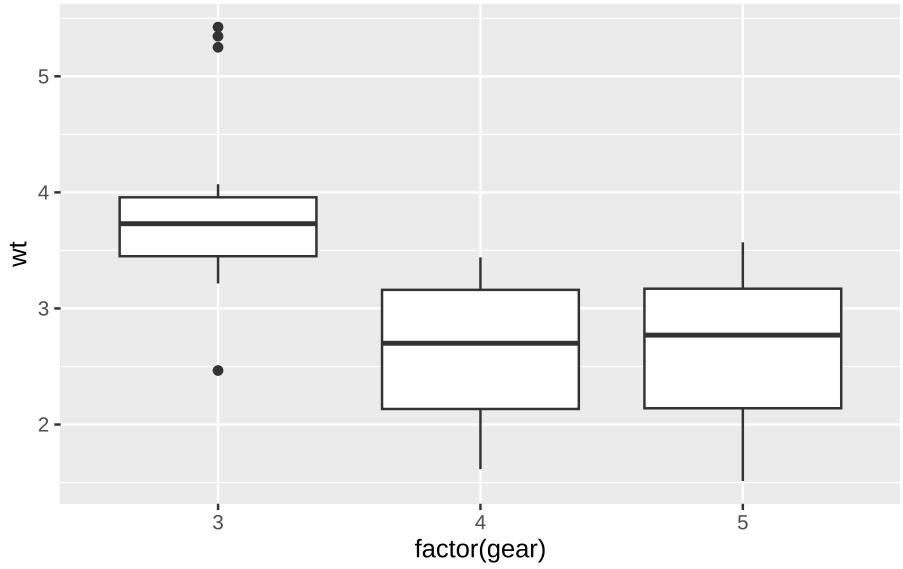



```
ggplot(data=mtcars,aes(x = wt,y = mpg))+
  geom_point()+
  geom_smooth(method="lm")
```

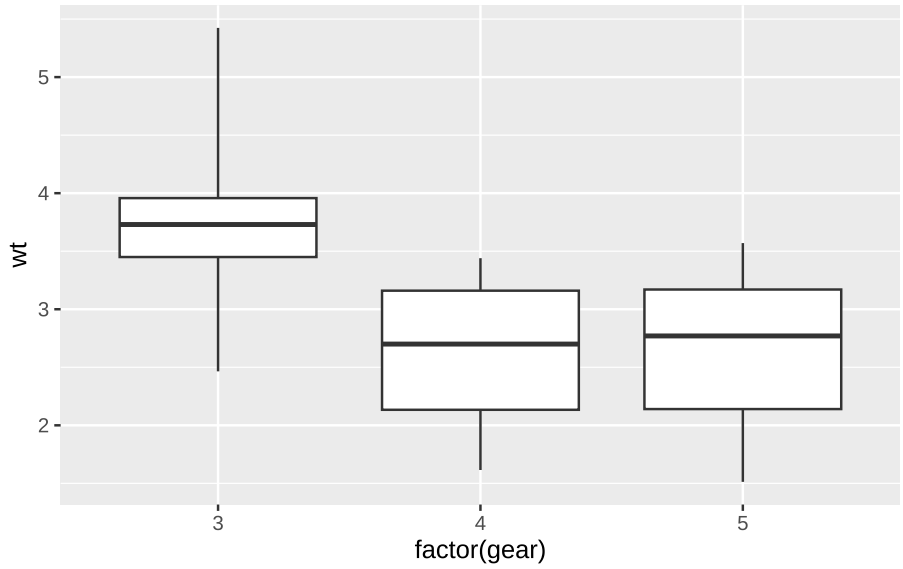
```
`geom_smooth()` using formula = 'y ~ x'
```



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

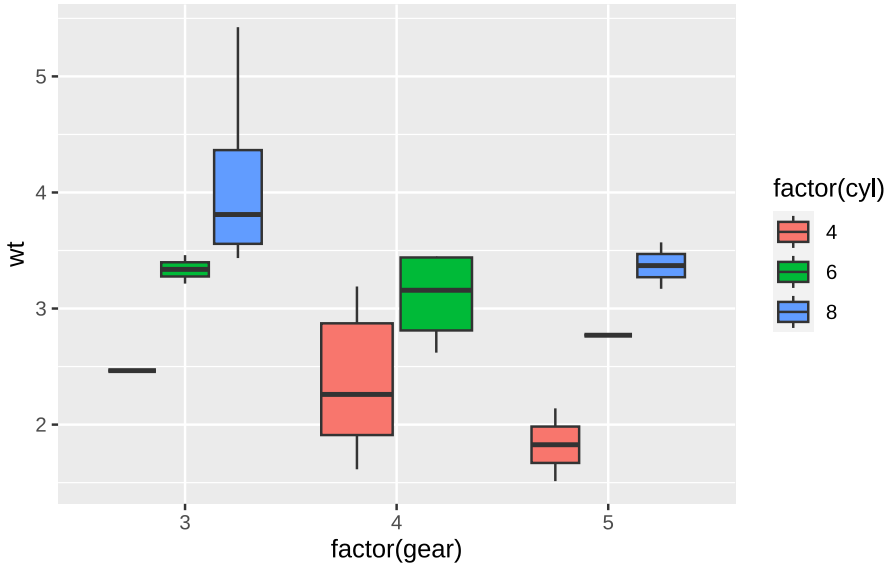



```
ggplot(mtcars,aes(x = factor(gear),y = wt))+
  geom_boxplot(coef=3) # this extends range of expected values
```

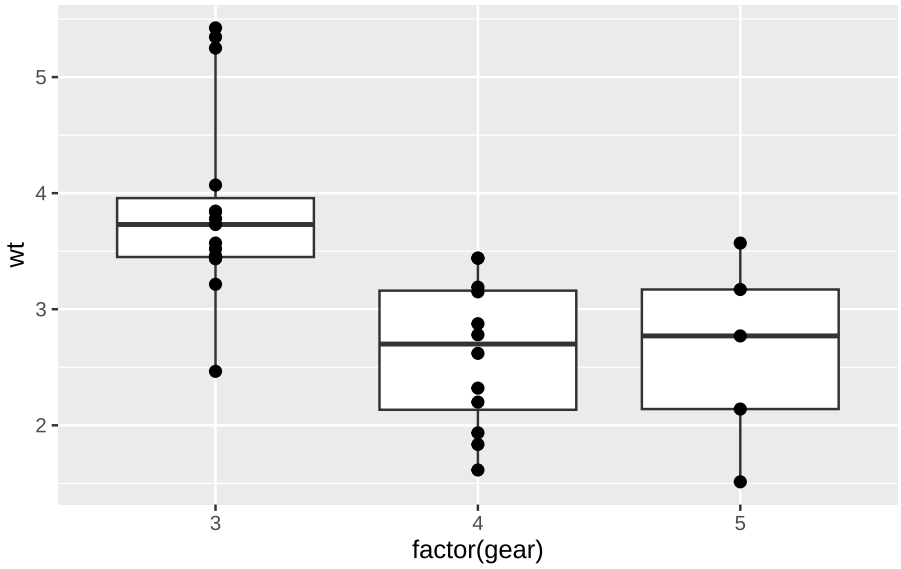



```
ggplot(mtcars,aes(x = factor(gear),y = wt,
                  fill=factor(cyl)))+
```

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

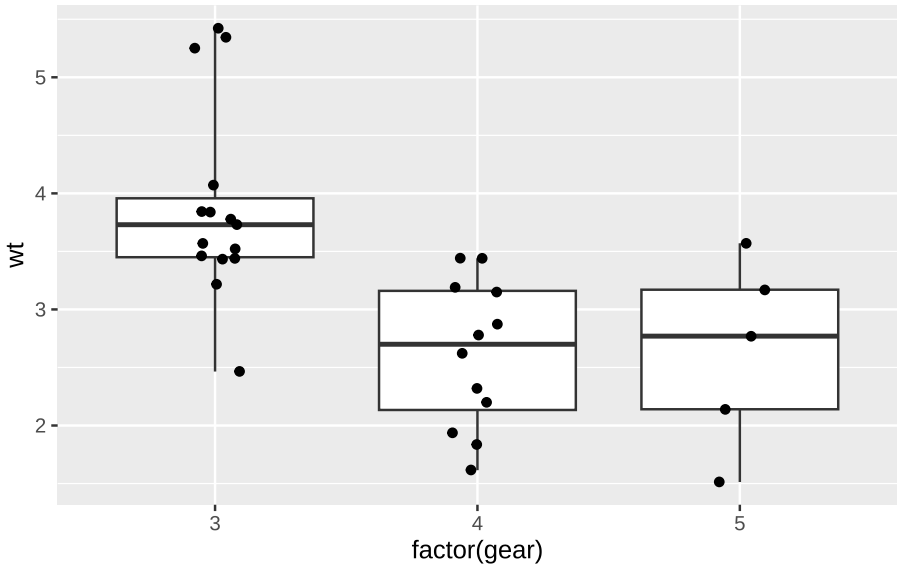



```
ggplot(mtcars,aes(x = factor(gear),y = wt))+
  geom_boxplot(coef=3)+
  geom_point(size=2) # may contain overlapping points
```



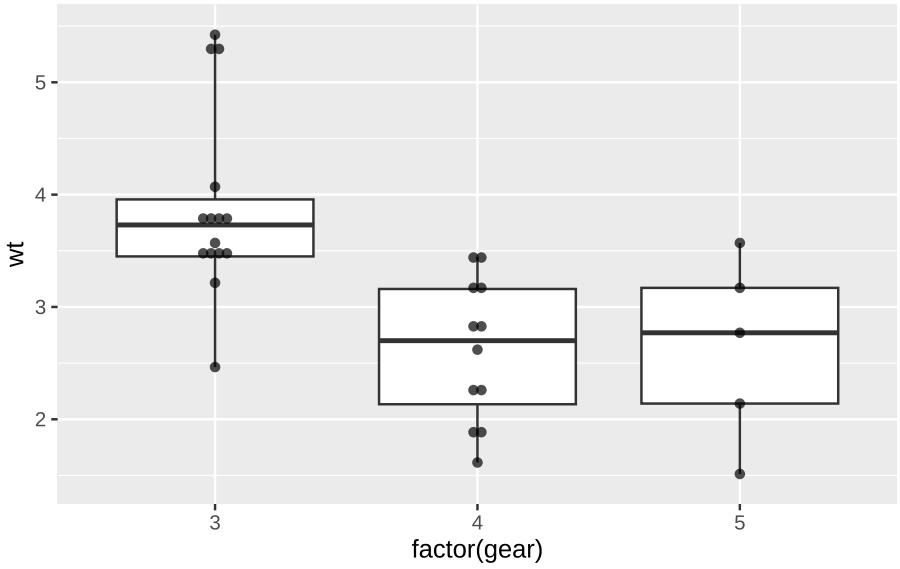

```
ggplot(mtcars,aes(x = factor(gear),y = wt))+
  geom_boxplot(coef=3)+
```

```
    geom_point(position = position_jitter(width = .1))
```

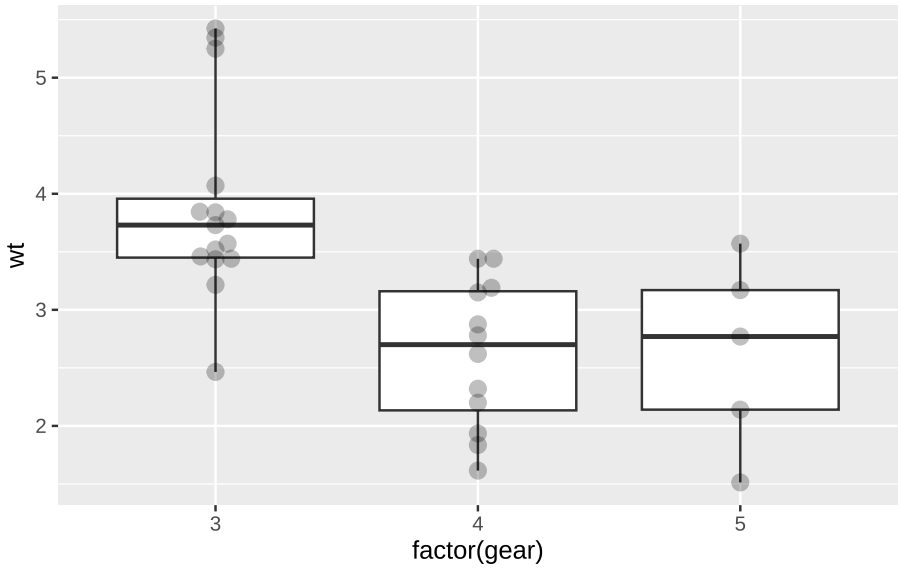



```
ggplot(mtcars,aes(x = factor(gear),y = wt))+
  geom_boxplot(coef=3)+
  geom_dotplot(alpha=.7, # group similar(ish) data on a line
               binaxis = "y",stackdir = "center",
               stackratio = .9,dotsize = .6)
```

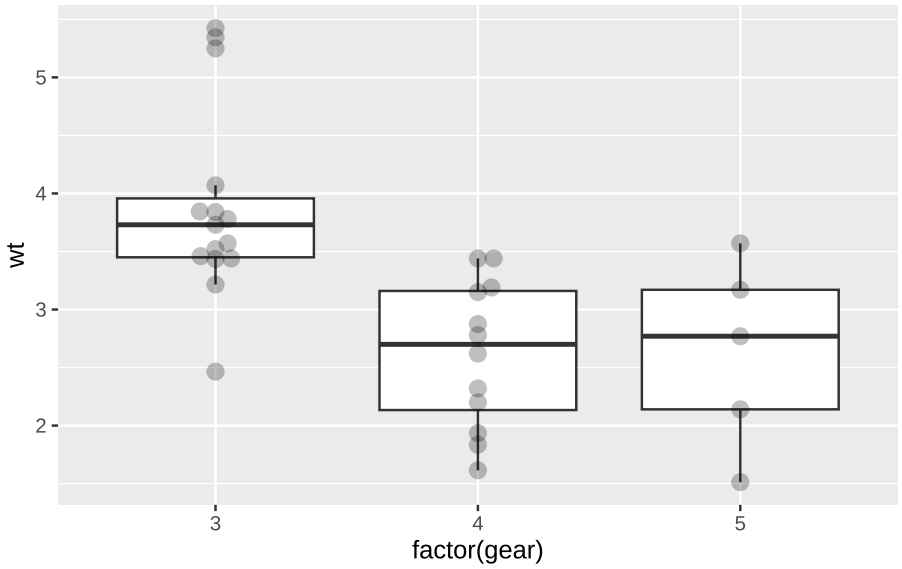
```
Bin width defaults to 1/30 of the range of the data. Pick better value with
`binwidth`.
```



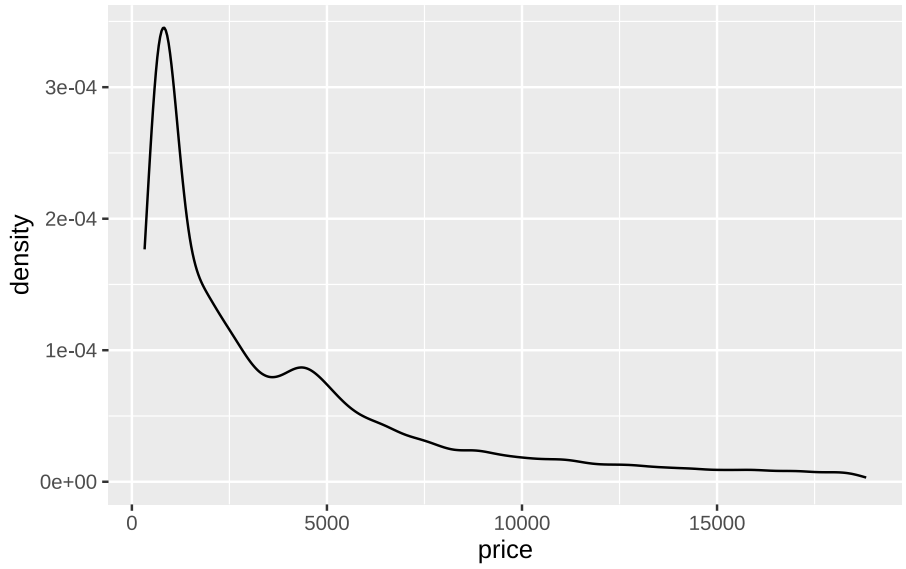
```
ggplot(mtcars,aes(x = factor(gear),y = wt))+
  geom_boxplot(coef=3)+
  ggbeeswarm::geom_beeswarm(cex = 2,size=3,alpha=.25)
```



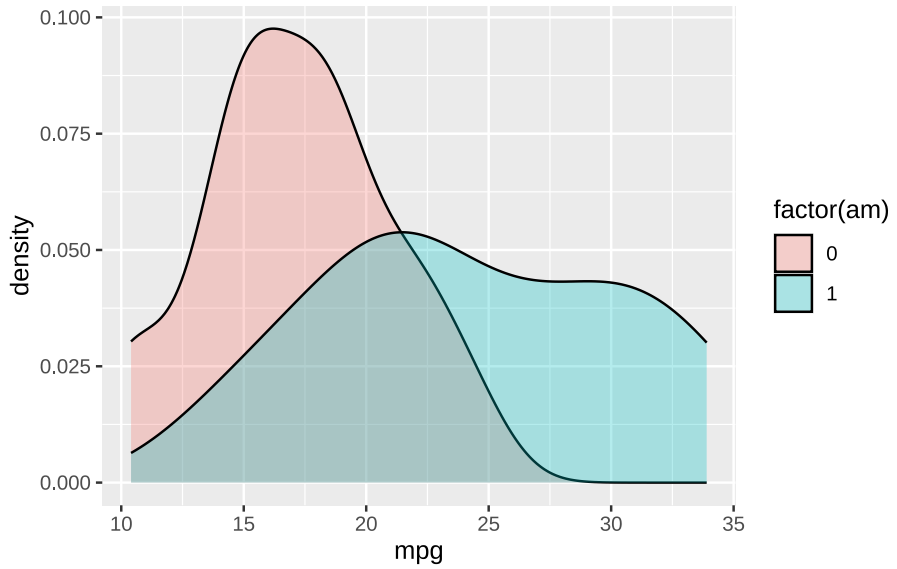

```
ggplot(mtcars,aes(x = factor(gear),y = wt))+
  geom_boxplot(outlier.alpha = 0)+ # to avoid plotting outliers twice
  geom_beeswarm(cex = 2,size=3,alpha=.25)
```



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

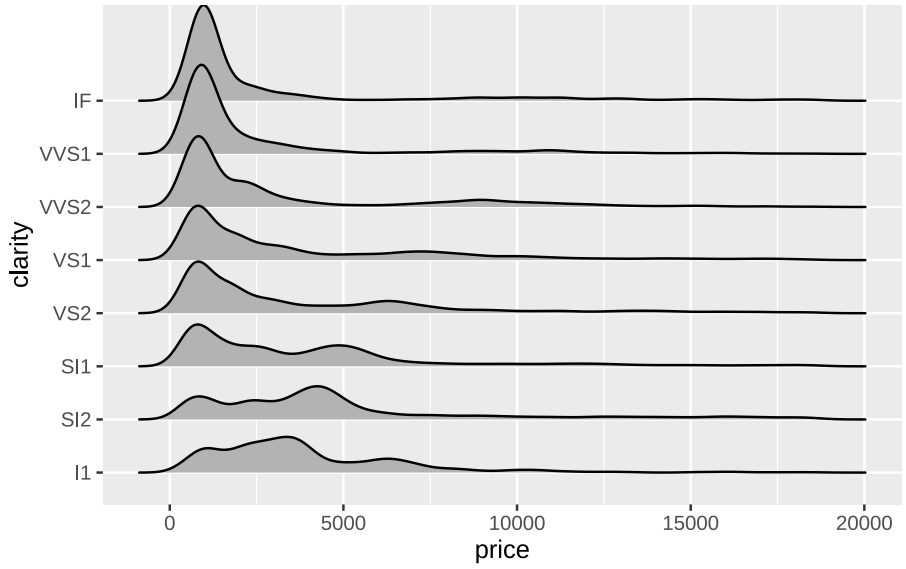



```
ggplot(mtcars,aes(mpg, fill=factor(am)))+
  geom_density(alpha=.3)
```



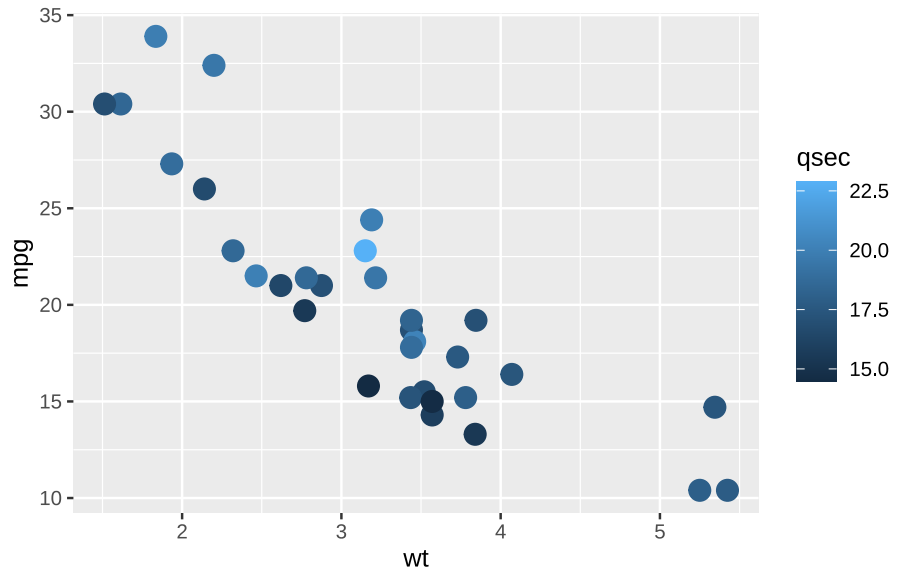
```
ggplot(diamonds,aes(price,y=clarity))+
  geom_density_ridges()
```

```
Picking joint bandwidth of 403
```

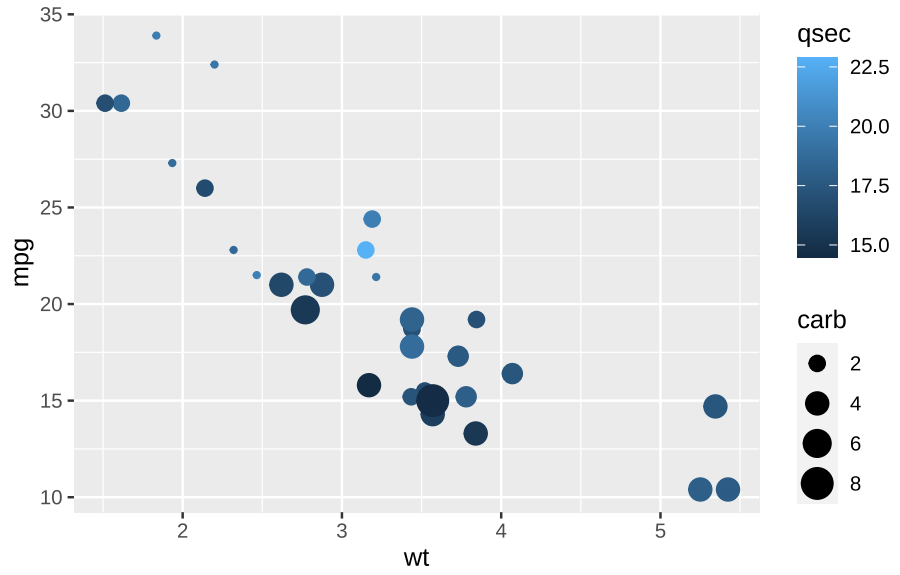


6.7 Combining and finetuning aesthetics

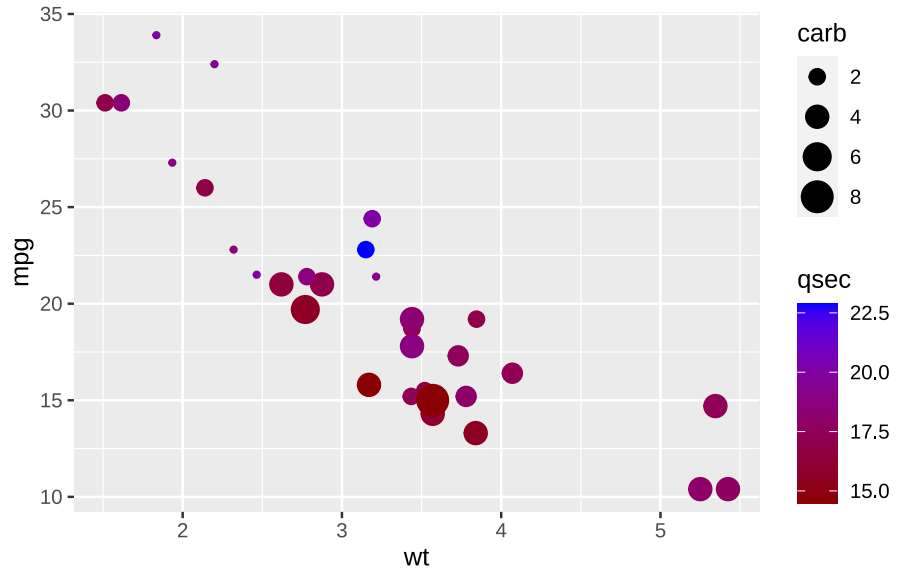
```
ggplot(data=mtcars,aes(wt, mpg,color=qsec))+
  geom_point(size=4) #outside aes!
```



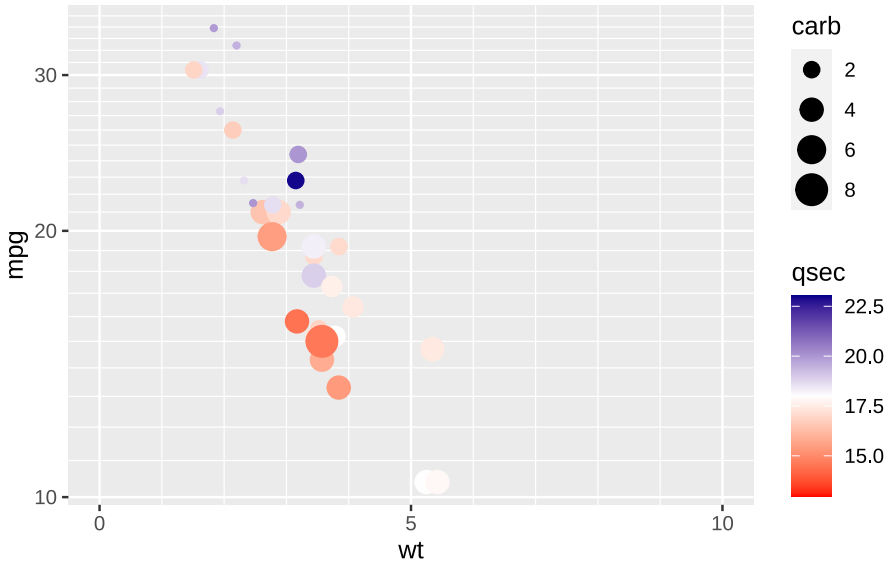
```
ggplot(data=mtcars,aes(wt, mpg,color=qsec, size=carb))+
  geom_point()
```



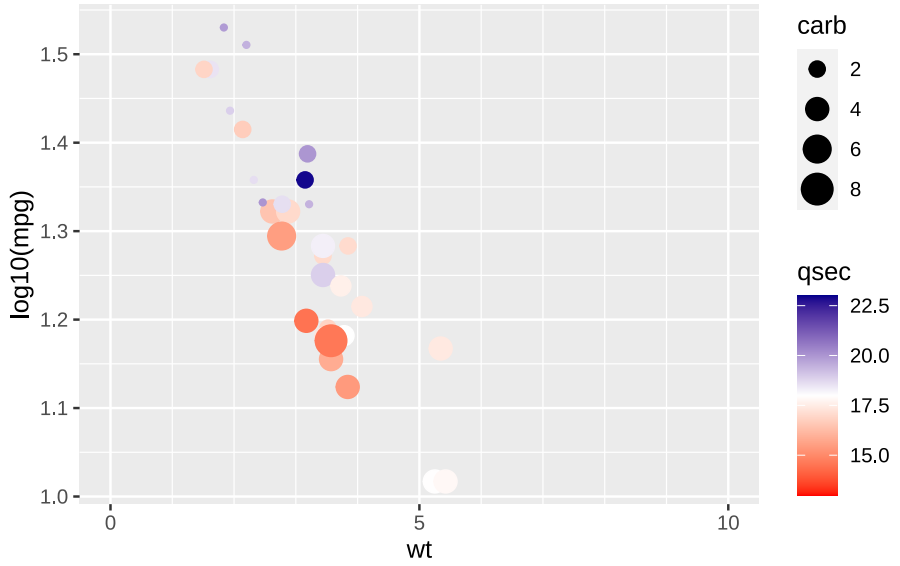

```
ggplot(data=mtcars,aes(wt, mpg,color=qsec, size=carb))+
  scale_color_gradient(low="darkred",high="blue")+
  geom_point()
```



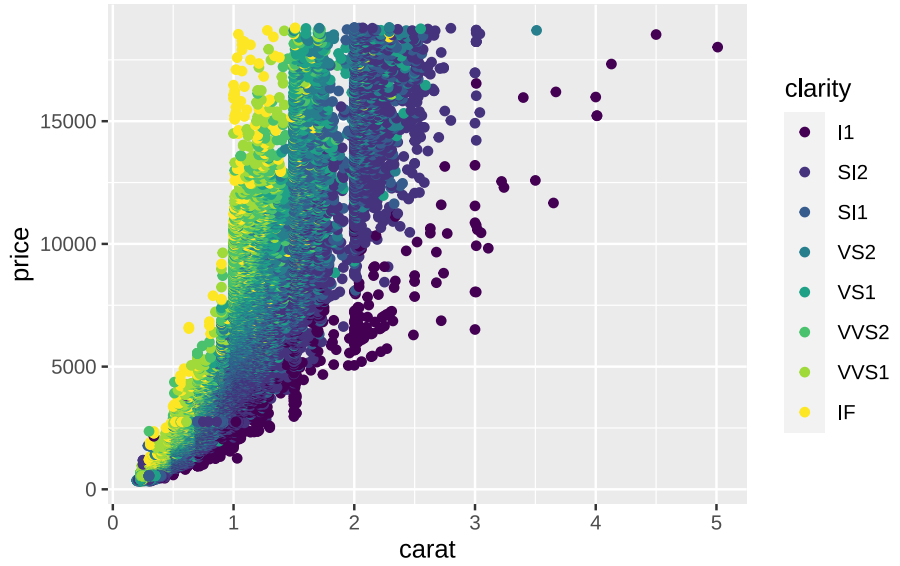
```
ggplot(data=mtcars,aes(wt, mpg,color=qsec, size=carb))+
  scale_color_gradient2(low="red",high="darkblue",
                        mid="white",
                        limits=c(13,23),midpoint=18)+
  geom_point()+
  scale_x_continuous(breaks = seq(0,100,5),
                     minor_breaks=seq(0,100,1),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



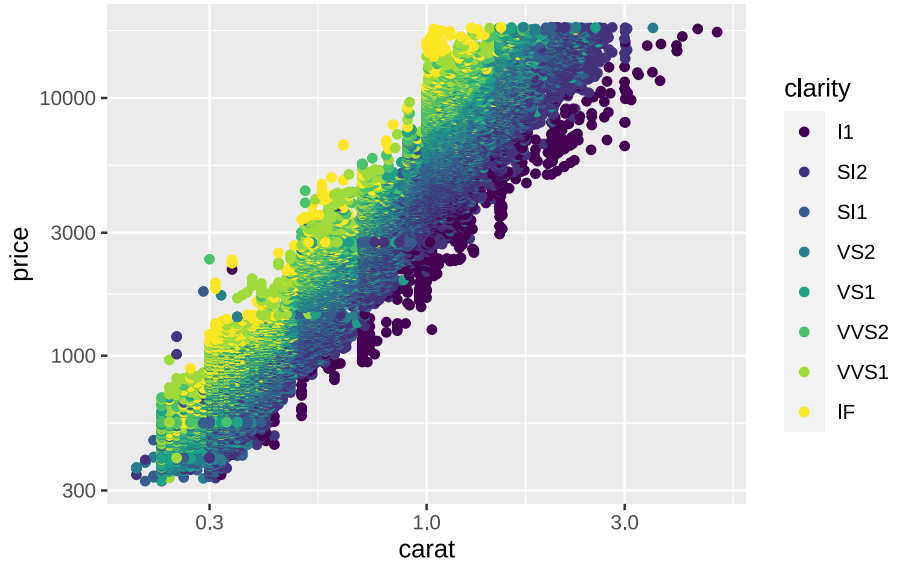

```
ggplot(data=mtcars,aes(wt, log10(mpg),color=qsec, size=carb))+
  scale_color_gradient2(low="red",high="darkblue",
                        mid="white",
                        limits=c(13,23),midpoint=18)+
  geom_point()+
  scale_x_continuous(breaks = seq(0,100,5),
                     minor_breaks=seq(0,100,1),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



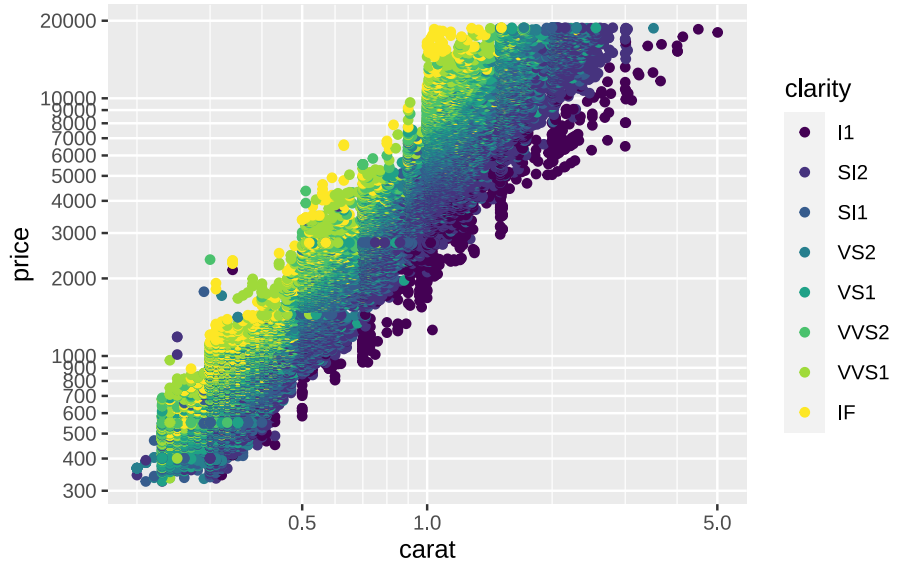

```
  # scale_y_log10(minor_breaks=seq(0,100,1))



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



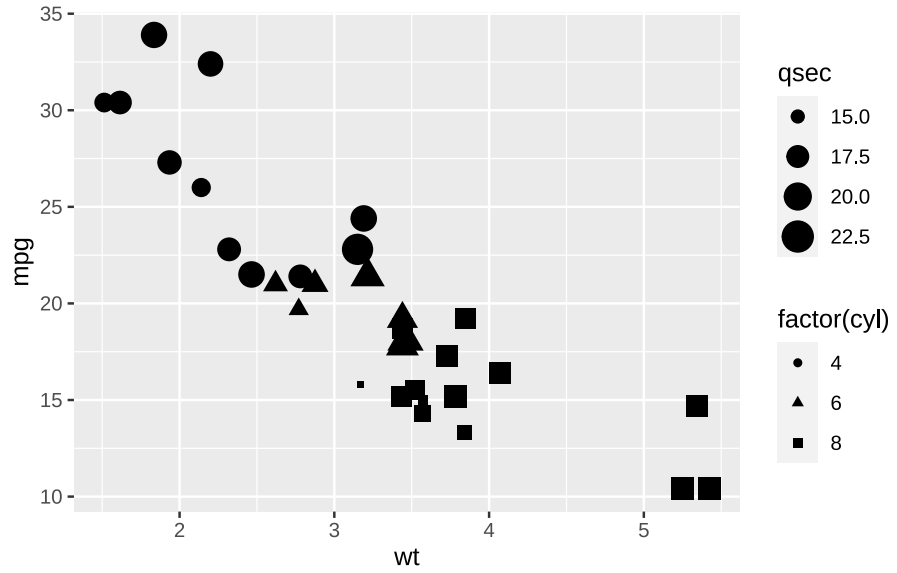
```
ggplot(diamonds,aes(carat,price,color=clarity))+
  geom_point()+
  scale_x_log10()+
  scale_y_log10()
```



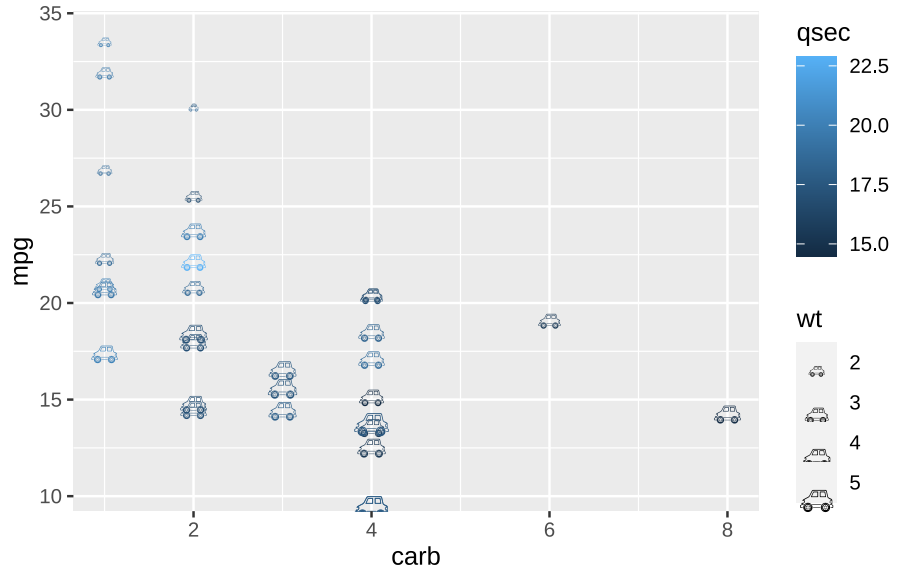

```
ggplot(diamonds,aes(carat,price,color=clarity))+
  geom_point()+
  scale_x_log10(
    breaks=lograngе_15,
    minor_breaks=lograngе_123456789)+
  scale_y_log10(
    breaks=lograngе_123456789,
    minor_breaks=lograngе_123456789)
```




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



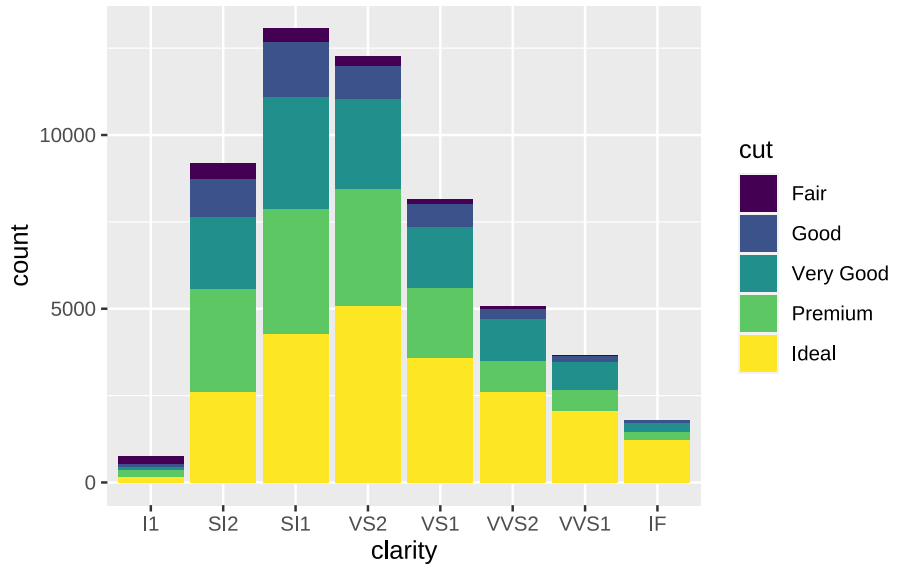

```
ggplot(data=mtcars,aes(carb, mpg,color=qsec, size=wt))+
  geom_text(family="EmojiOne",label="\U1F697")
```



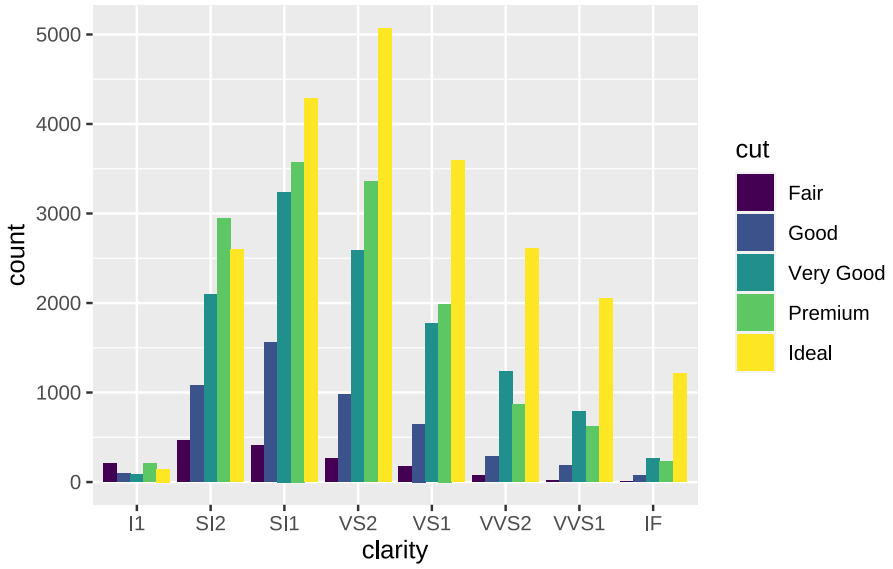
6.8 Positioning elements

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.

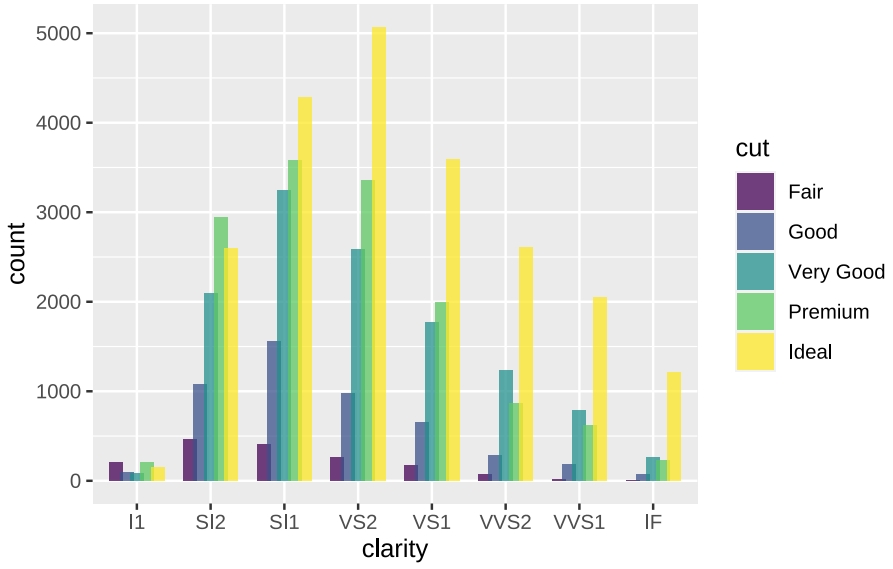
```
p<-ggplot(data=diamonds,aes(clarity,fill=cut))
p+geom_bar(position="stack") # default for bar
```



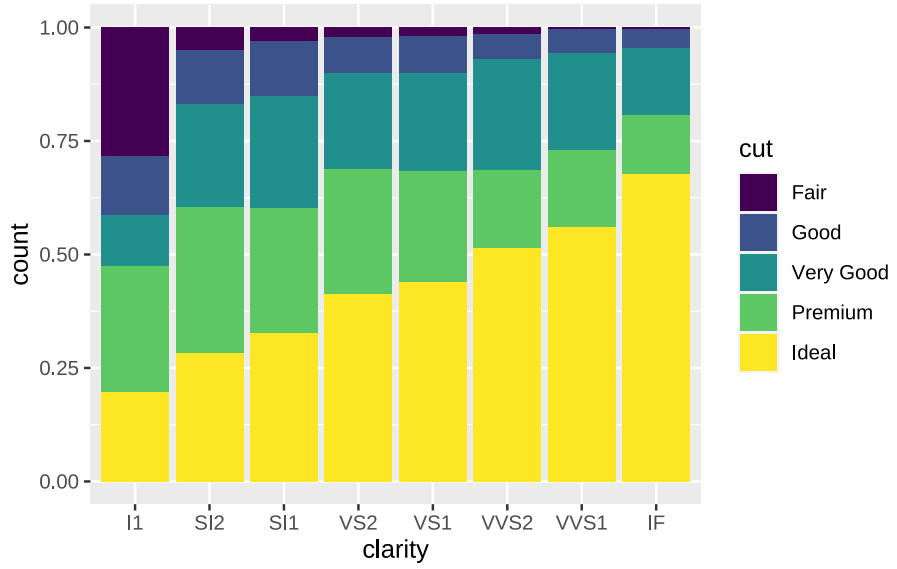
```
p+geom_bar(position="dodge")
```



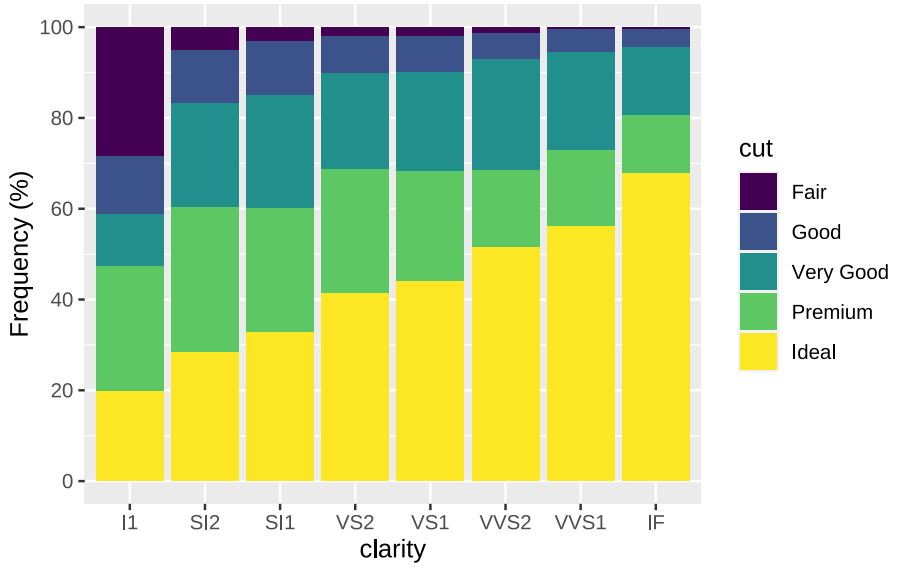

```
p+geom_bar(position=position_dodge(width = 0.7), alpha=.75)
```




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

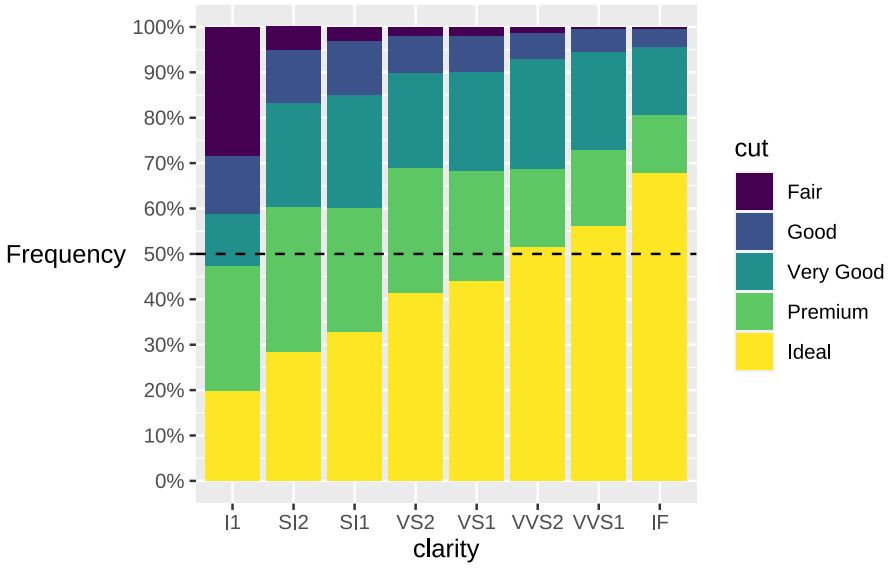



```
p+geom_bar(position="fill")+
  scale_y_continuous(name = "Frequency (%)",
                     breaks=seq(0,1,.2), #steps
                     labels=seq(0,100,20))
```

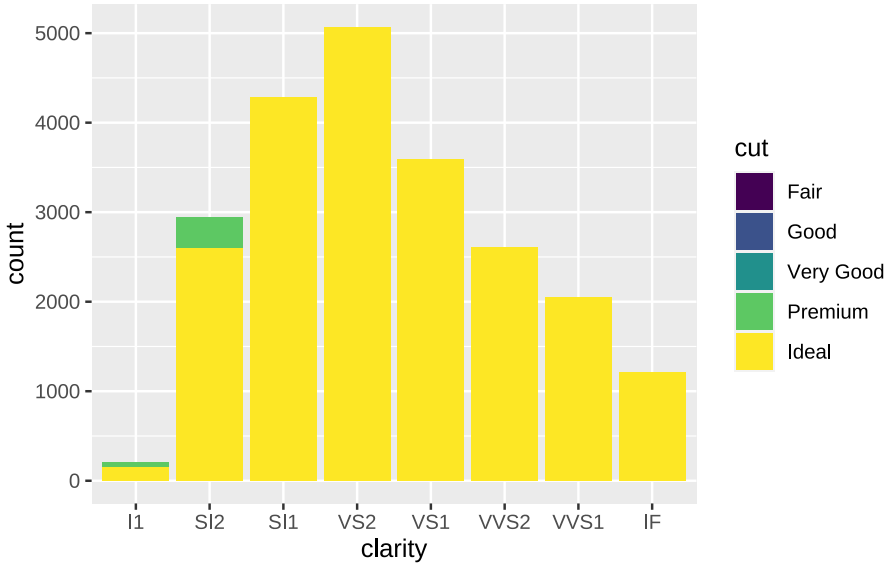



```
p+geom_bar(position="fill")+
  scale_y_continuous("Frequency",
                     breaks=seq(0,1,.1),
                     labels=scales::percent)+
```

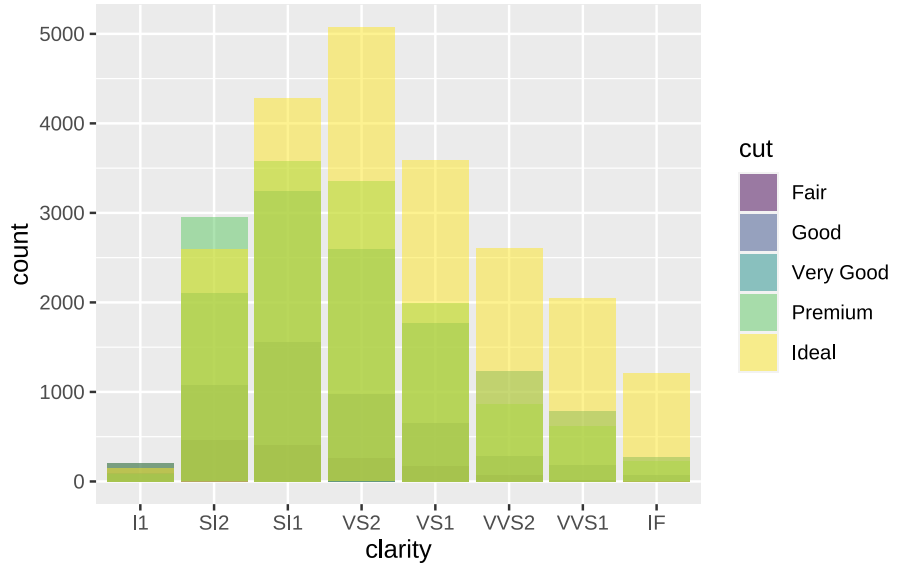
```
    theme(axis.title.y = element_text(angle = 0,
                                      vjust = .5))+
    geom_hline(yintercept = .5, linetype=2) # e.g. for reference lines
```



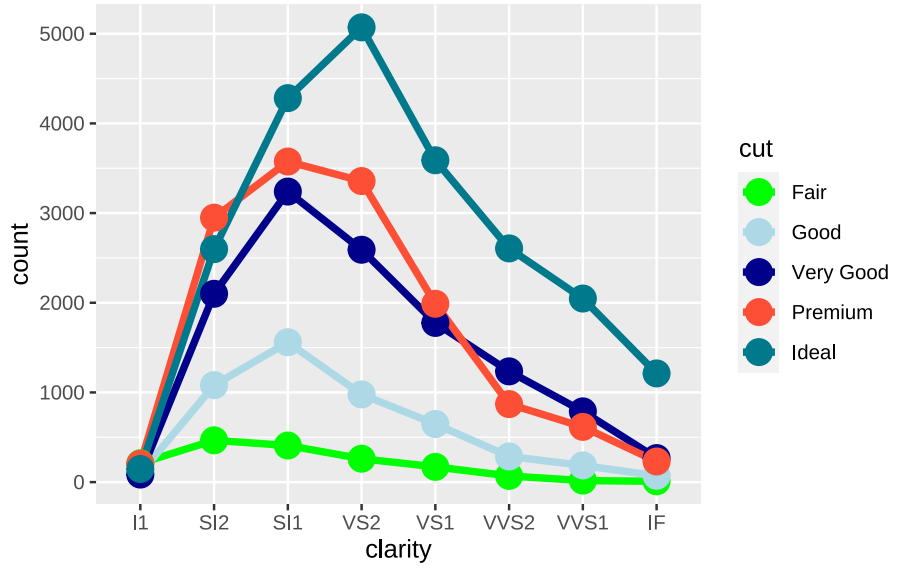

```
p+geom_bar(position="identity") # bad idea!
```




```
p+geom_bar(position="identity",alpha=.5)
```




```
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"))
```



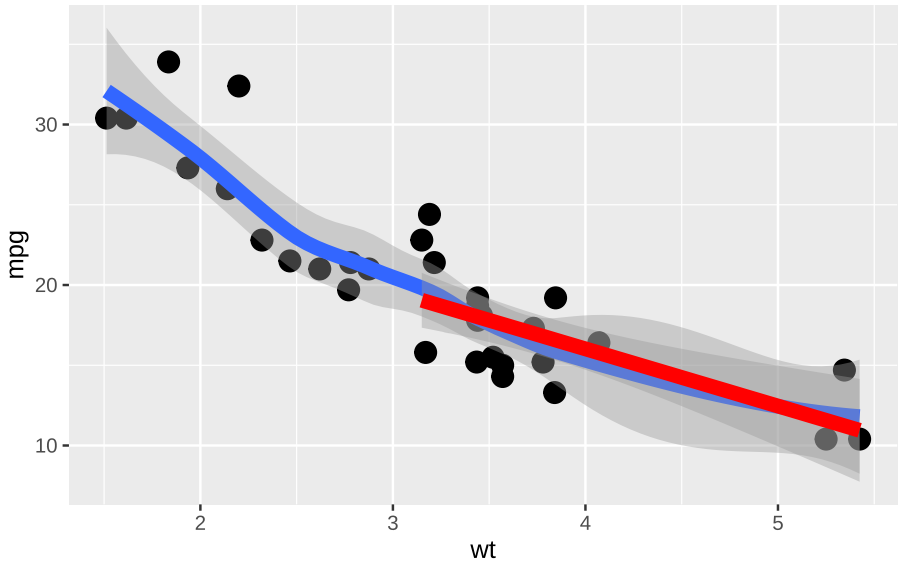
6.9 Order of layers

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")
```

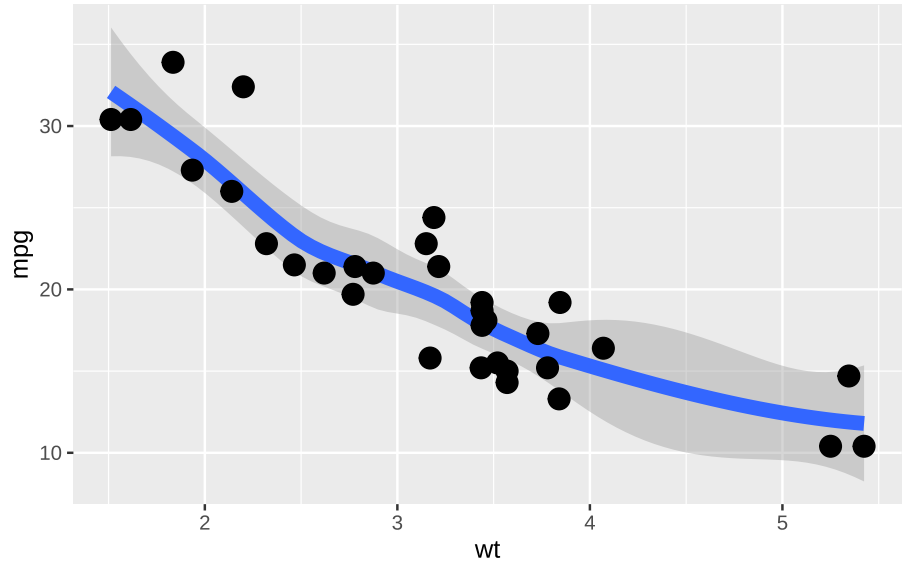
```
Warning: Using `size` aesthetic for lines was deprecated in ggplot2 3.4.0.
i Please use `linewidth` instead.
```

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



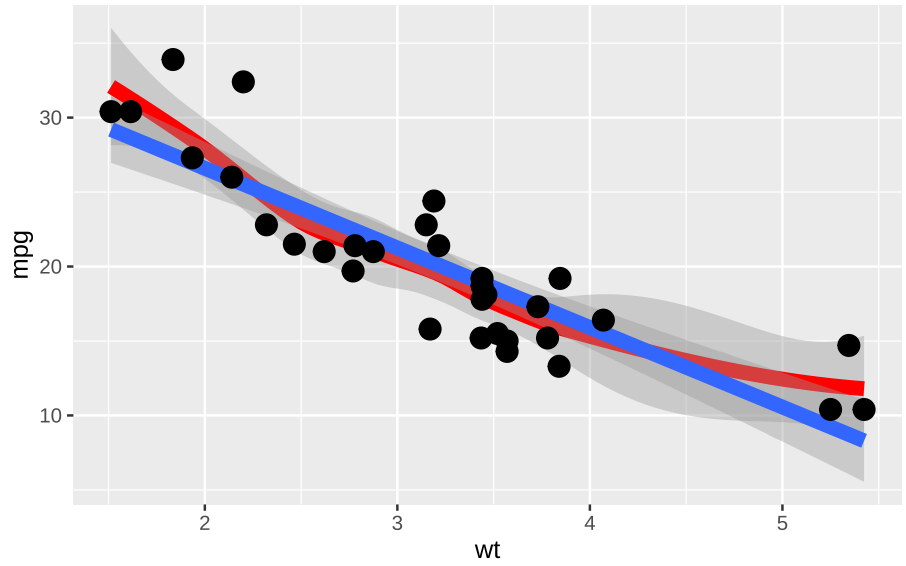

```
ggplot(data=mtcars,aes(wt, mpg))+
  geom_smooth(linewidth=3)+
  geom_point(size=4)
```

```
`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)
```

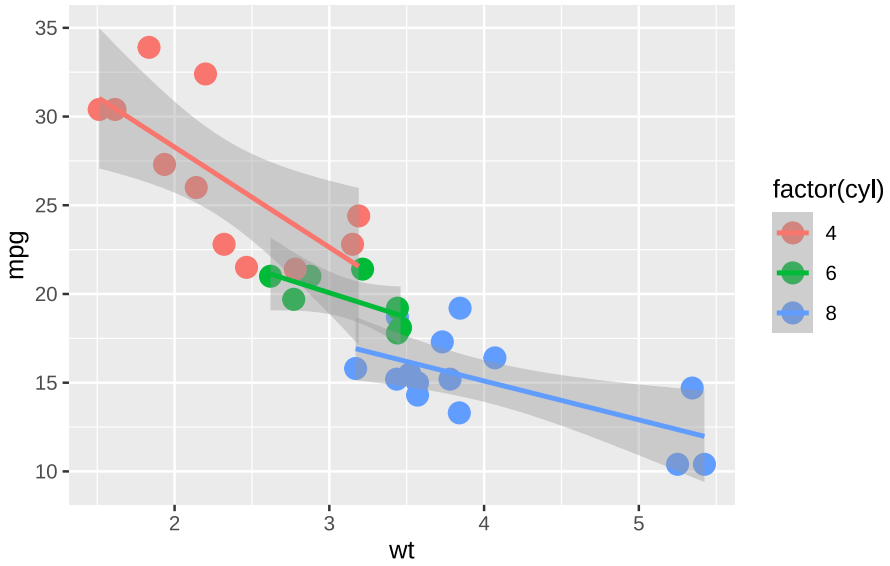
```
`geom_smooth()` using method = 'loess' and formula = 'y ~ x'
`geom_smooth()` using formula = 'y ~ x'
```




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

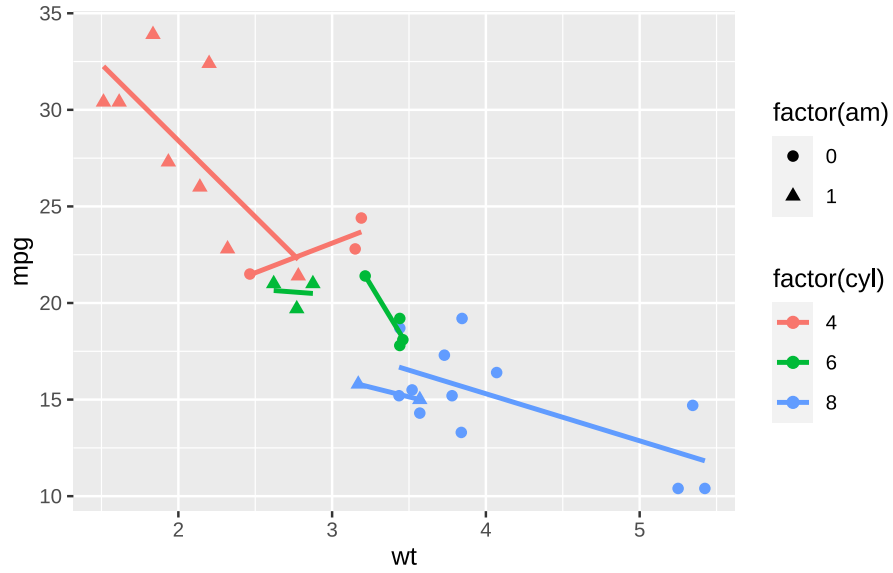
```
    geom_point(size=4)+
    geom_smooth(method="lm",linewidth=1)
```

```
`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)
```

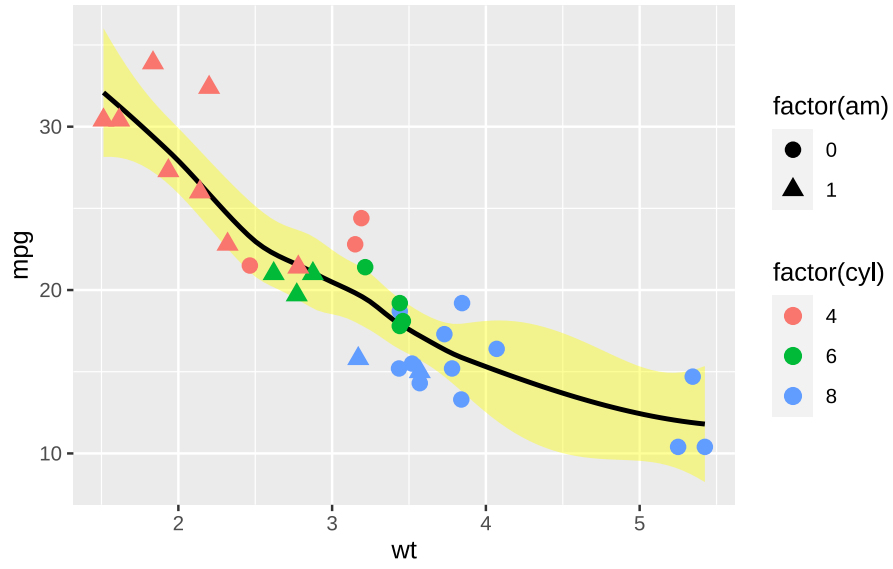
```
`geom_smooth()` using formula = 'y ~ x'
```



6.10 Local aesthetics for layers

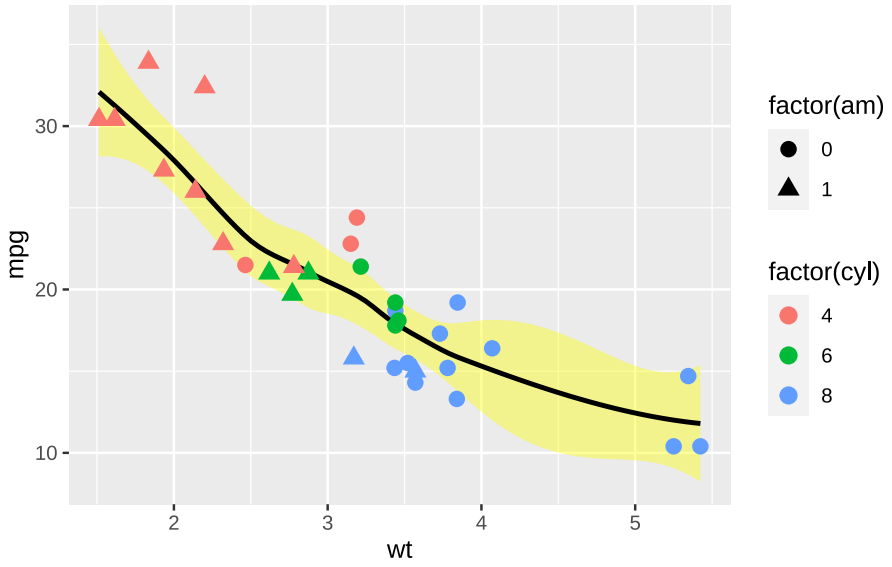
```
#? lm for all?
ggplot(data=mtcars,aes(wt, mpg))+
  geom_smooth(size=1,color="black",fill="yellow")+
  geom_point(size=3,aes(color=factor(cyl),shape=factor(am))) #aes for geom only
```

```
`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).

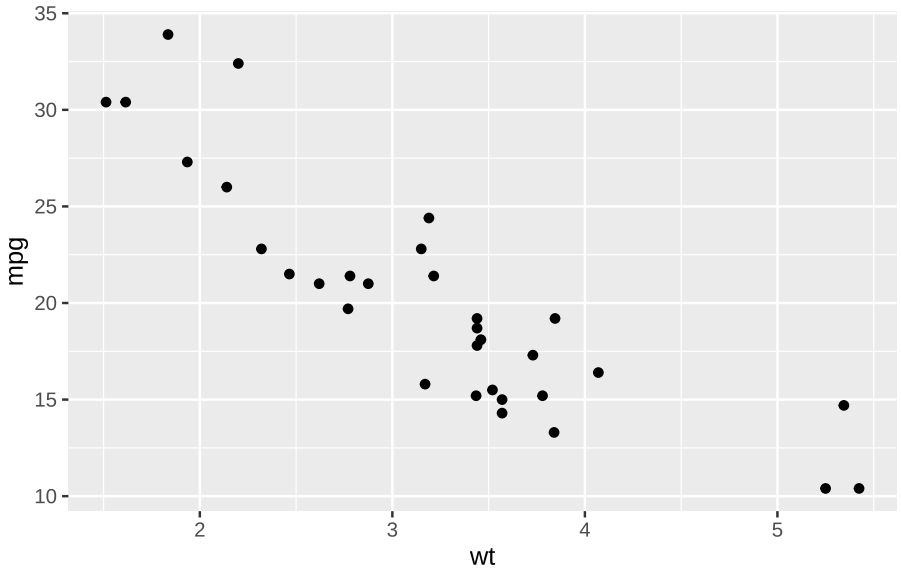
6.11.1 facet_grid

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

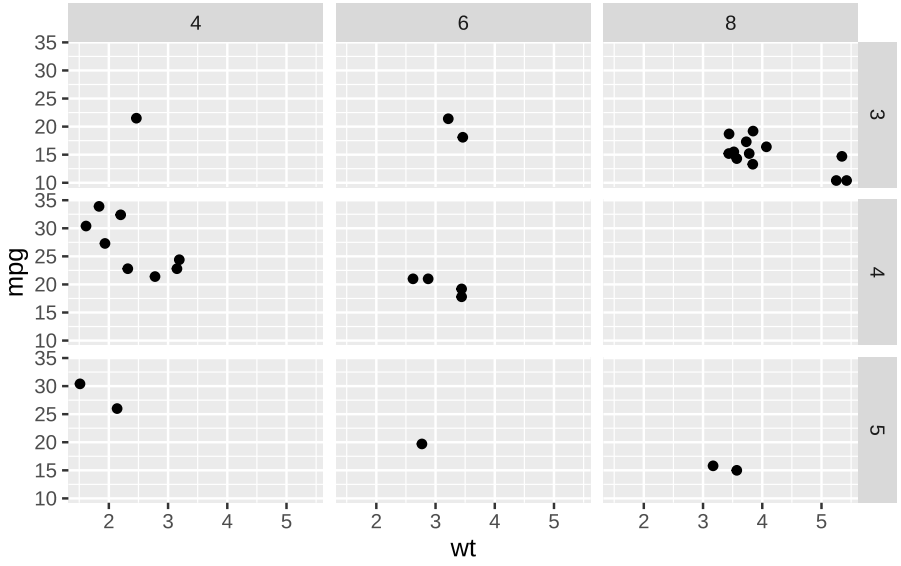
Labeling of facets often requires name and content to be informative.

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))
```

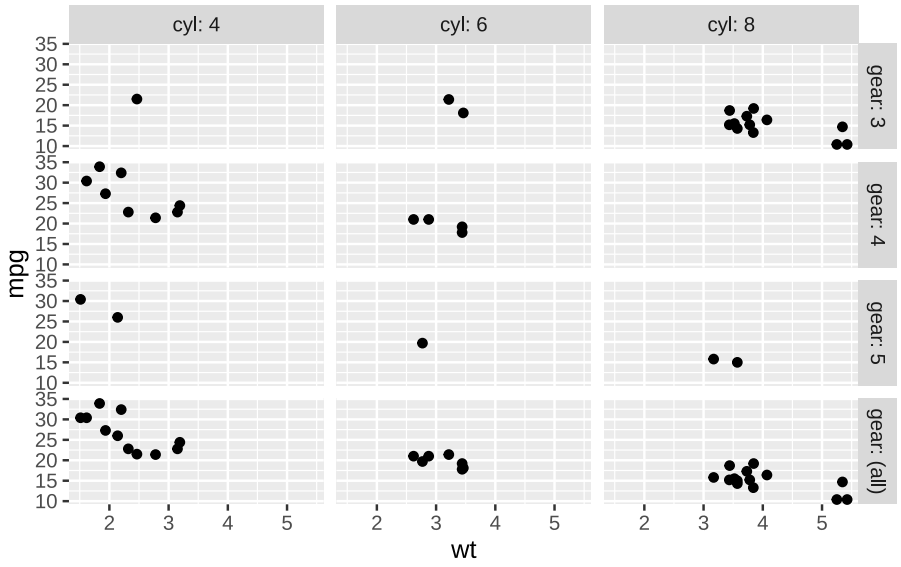



```
cat("facet labeling improved:\n")
```

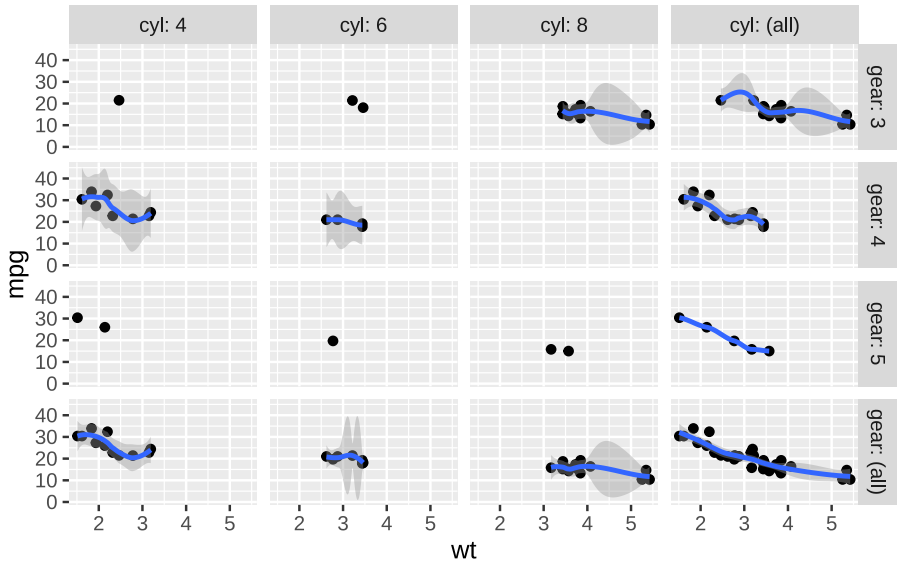
```
facet labeling improved:
```

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

```
                    labeller=label_both,margins="gear")
```




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

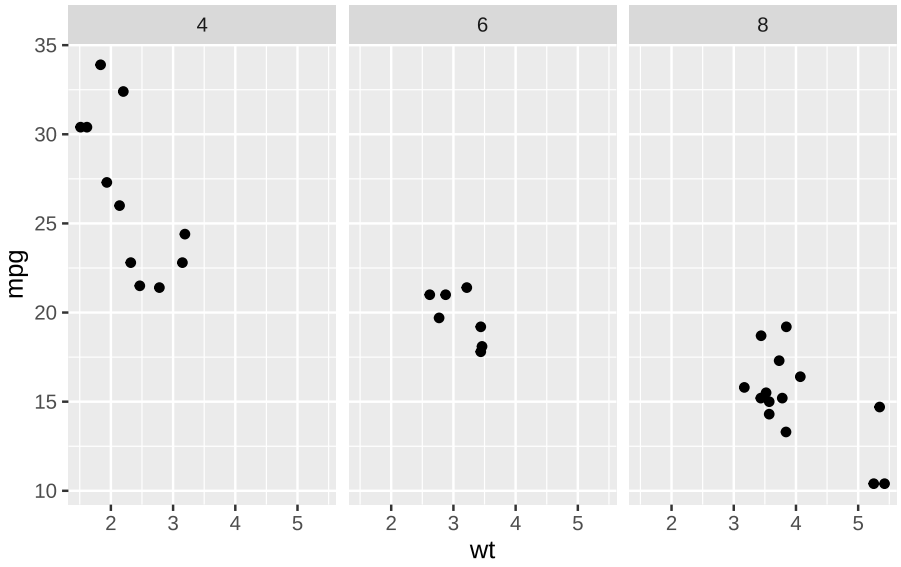


```
# options(warn=0)
```

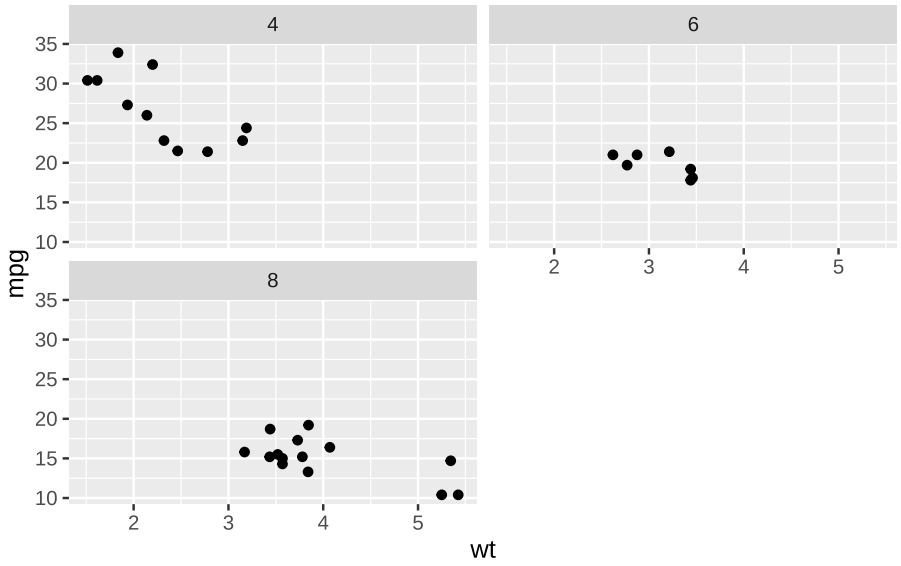
6.11.2 facet_wrap

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

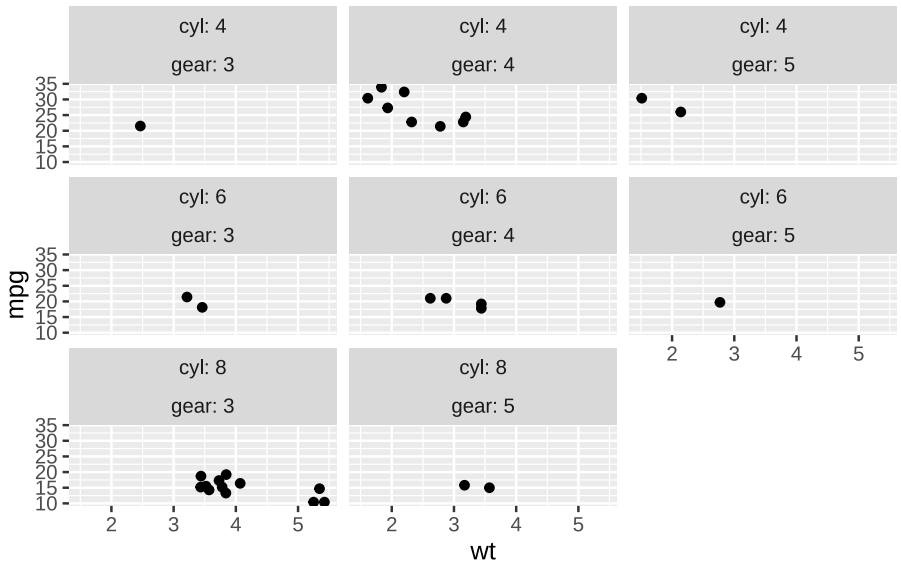
```
p.tmp + facet_wrap(facets = vars(cyl))
```



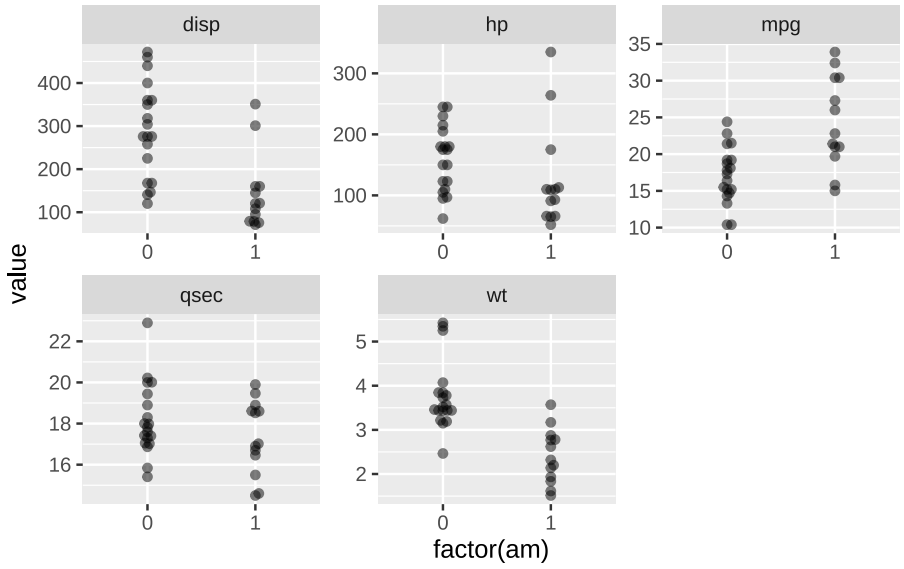

```
p.tmp + facet_wrap(facets = vars(cyl), ncol=2)
```




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

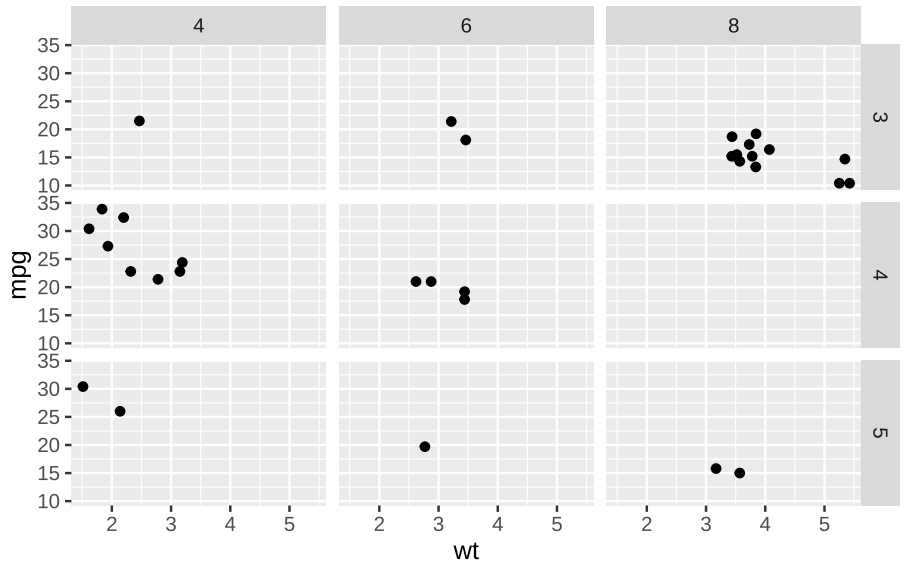



```
#combining variables
mtcars |>
  pivot_longer(cols = c(wt, mpg, hp, disp, qsec)) |>
  ggplot(aes(x=factor(am), y=value))+
  geom_beeswarm(alpha=.5, cex=2)+
  facet_wrap(facets = vars(name), scales="free")
```

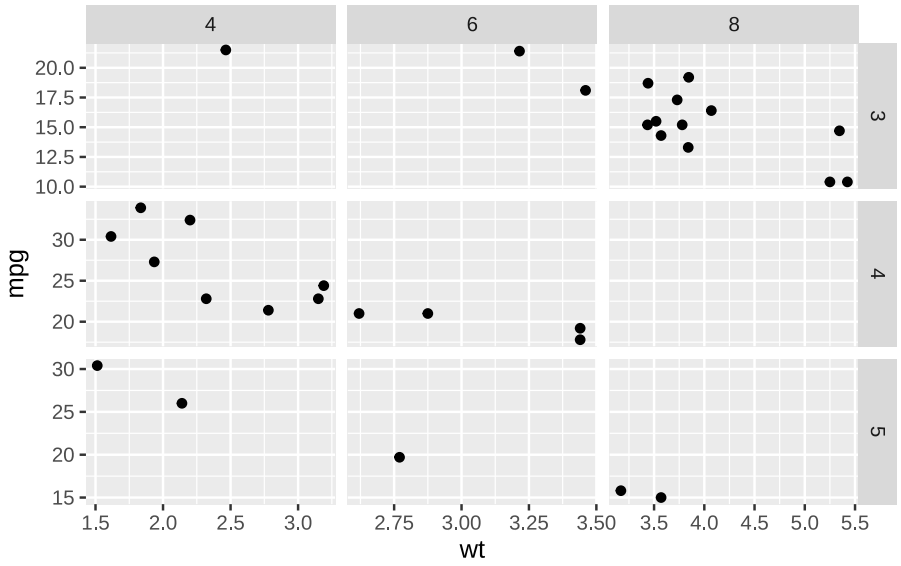


6.11.3 Controlling scales in facets (default: scales="fixed")

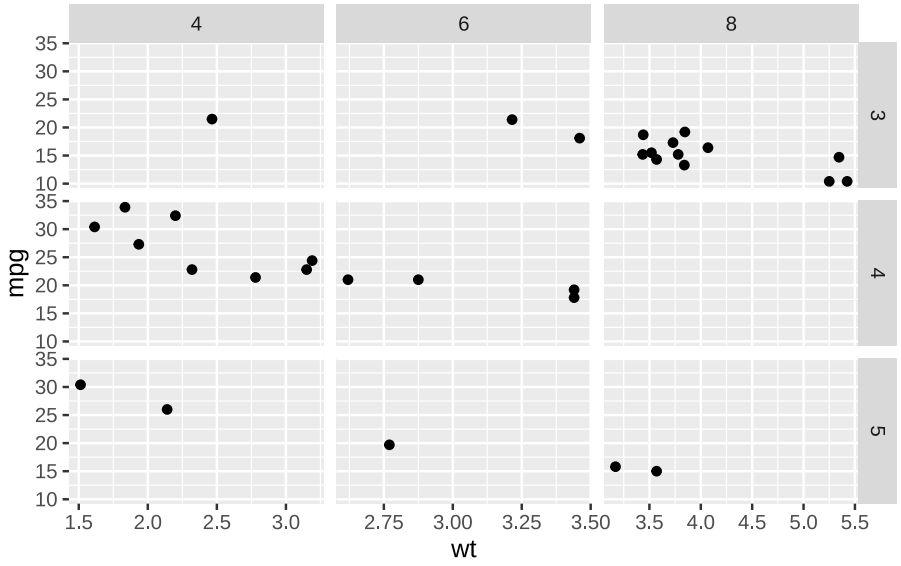
```
p.tmp + facet_grid(gear~cyl, scales="fixed")
```



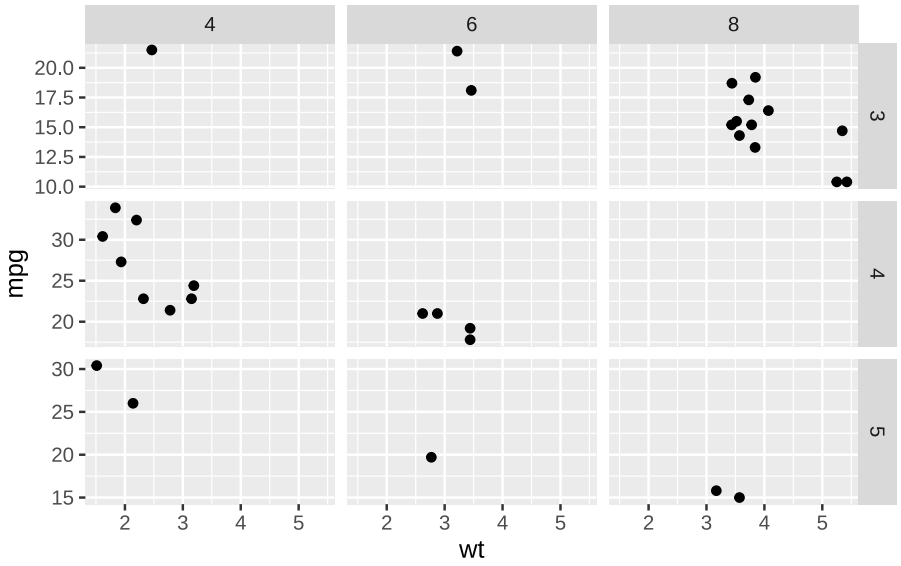

```
p.tmp + facet_grid(gear~cyl, scales="free")
```




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




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

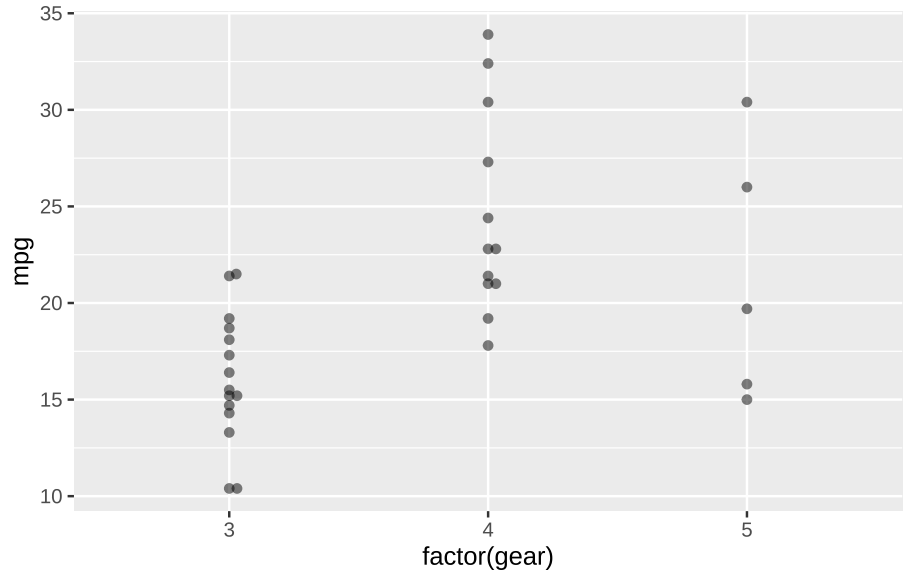


6.12 Showing summaries

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!!

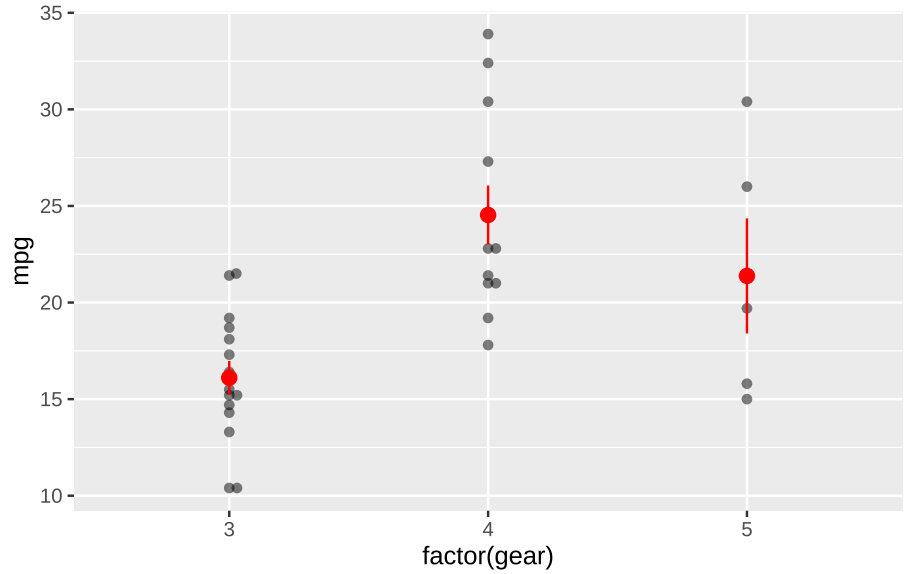
Functions for summary statistics (mean_se, mean_cl_normal, mean_cl_boot etc.) are build on top of Hmisc functions. So this package is needed but not automatically installed with ggplot2.

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

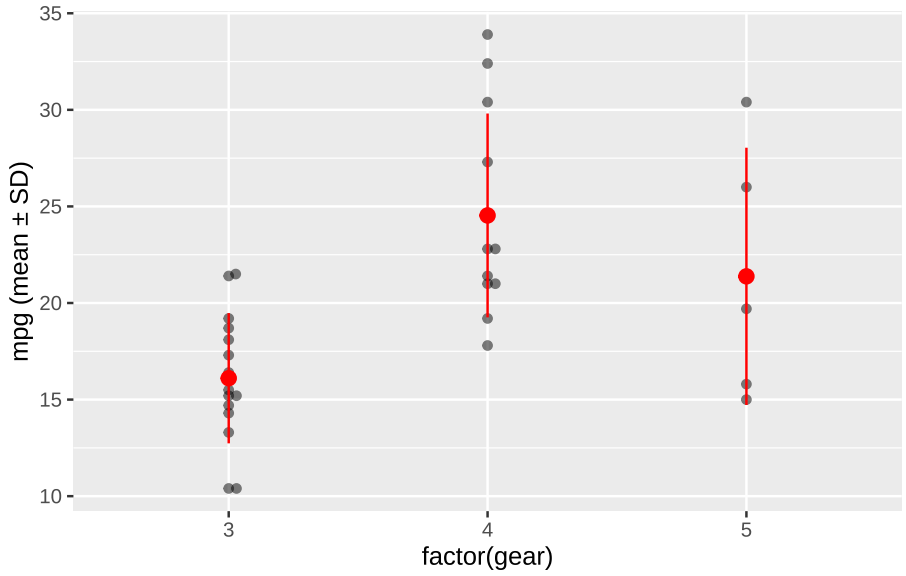



```
plottemp+stat_summary(color="red")
```

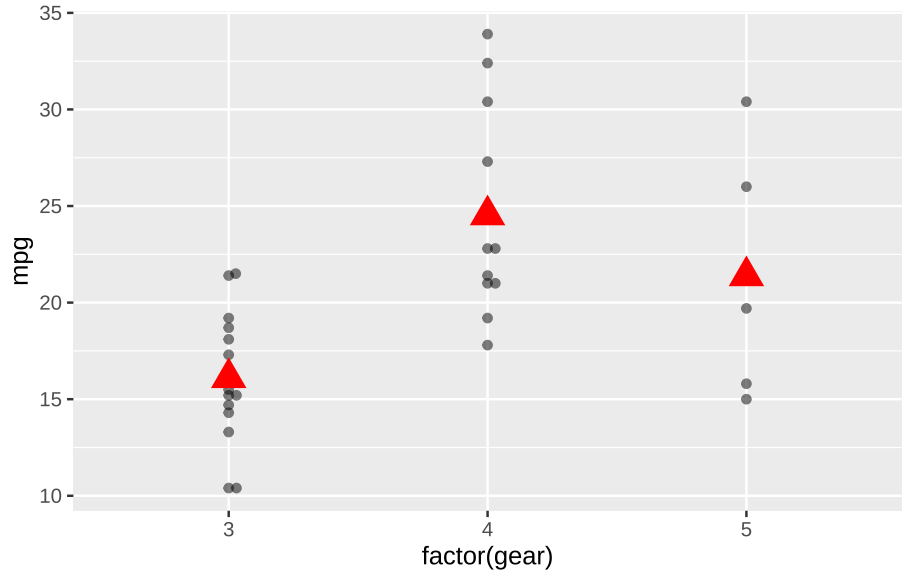
```
No summary function supplied, defaulting to `mean_se()`
```




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

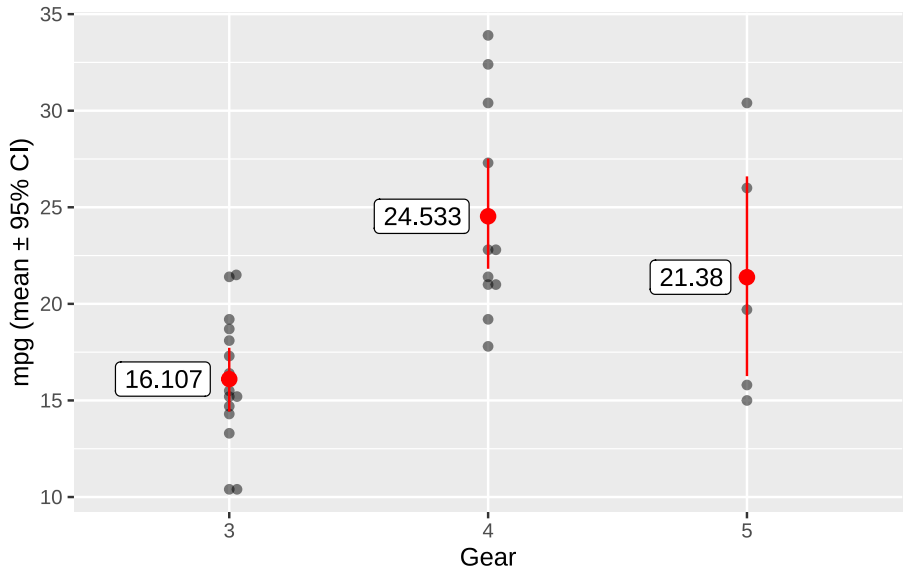



```
plottemp+stat_summary(geom = "point", shape=17,size=5,
                      fun = "mean",color="red")
```

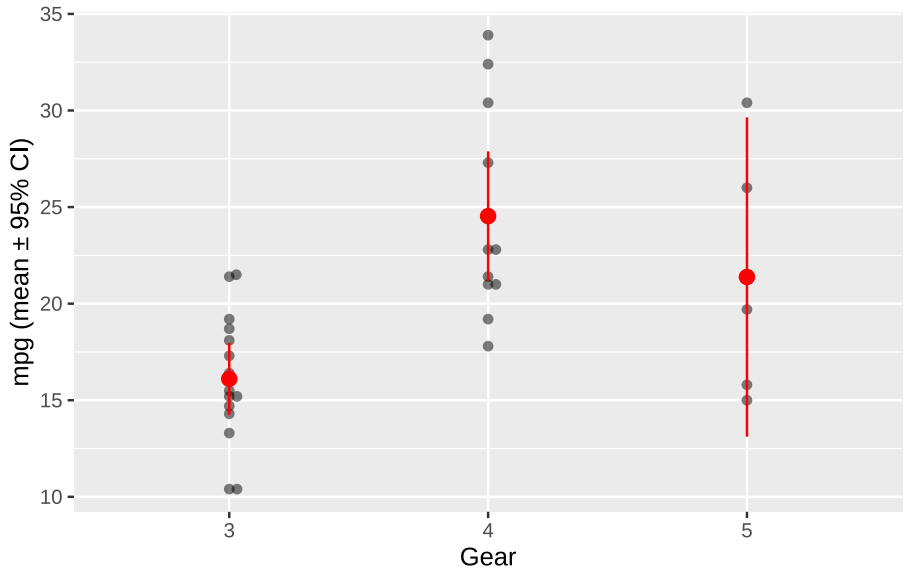



```
means <- mtcars |>
  group_by(gear) |>
  summarise(mean=round(mean(mpg),3),sd=sd(mpg))
plottemp+stat_summary(fun.data="mean_cl_boot",
                      fun.args=list(B=10^4),
                      color="red")+
```

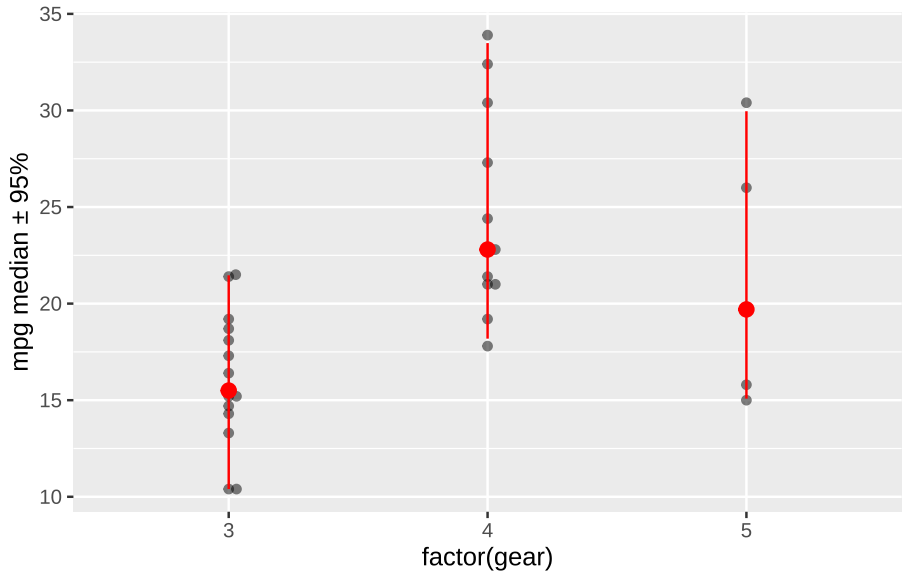
```
  geom_label(data=means,
             aes(factor(gear),mean,label=mean),
             hjust=1.2)+
  ylab("mpg (mean \u00b1 95% CI)")+
  xlab("Gear")
```




```
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()
```

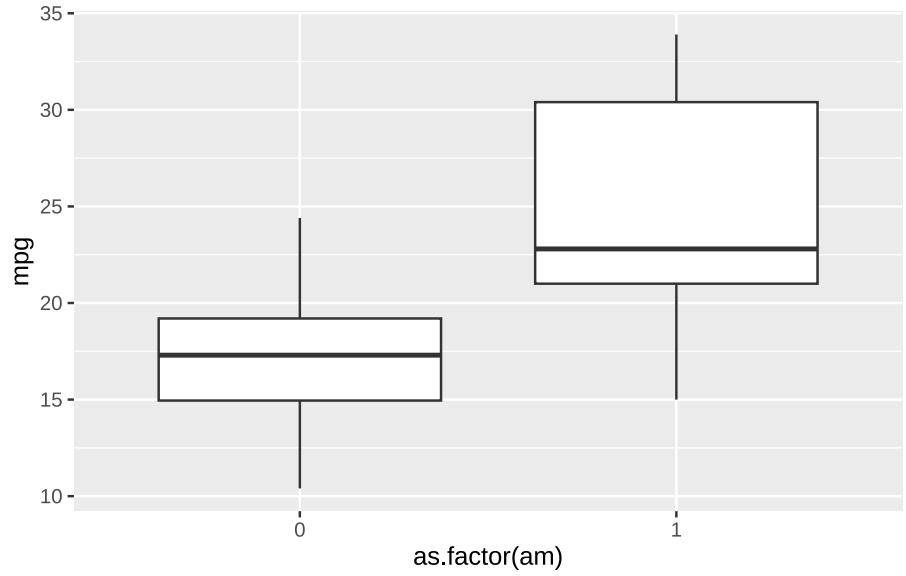
6.13 Indicating significances

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!).

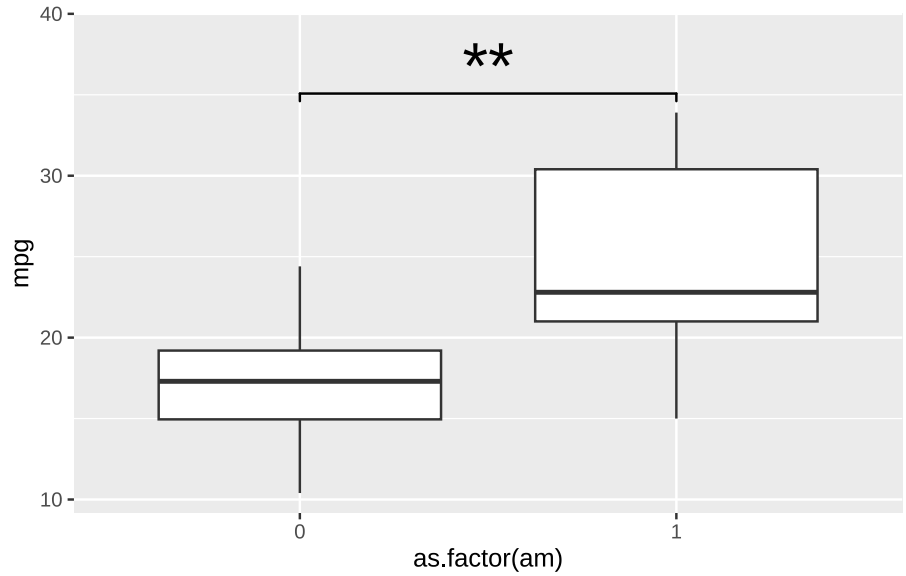
```
# ggsign ####
p <- round(wilcox.test(mtcars$mpg~mtcars$am)$p.value,5)
```

```
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())
```

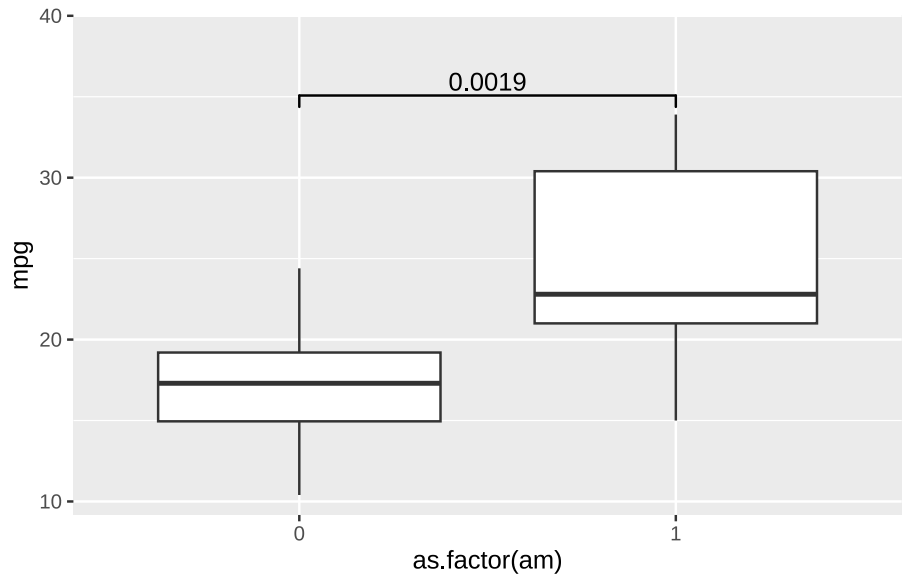



```
plottemp+geom_signif(
  comparisons=list(c(1,2)),
  # aes(y=0),
  textsize = rel(10), vjust = .0,
  #y_position=max(mtcars$mpg+3),
  # annotations=paste0("p = ", p),
  annotations=markSign(p),
  # annotations=p,
  tip_length=.02)+
  scale_y_continuous(expand = expansion(mult=c(0.05,.2)))
```

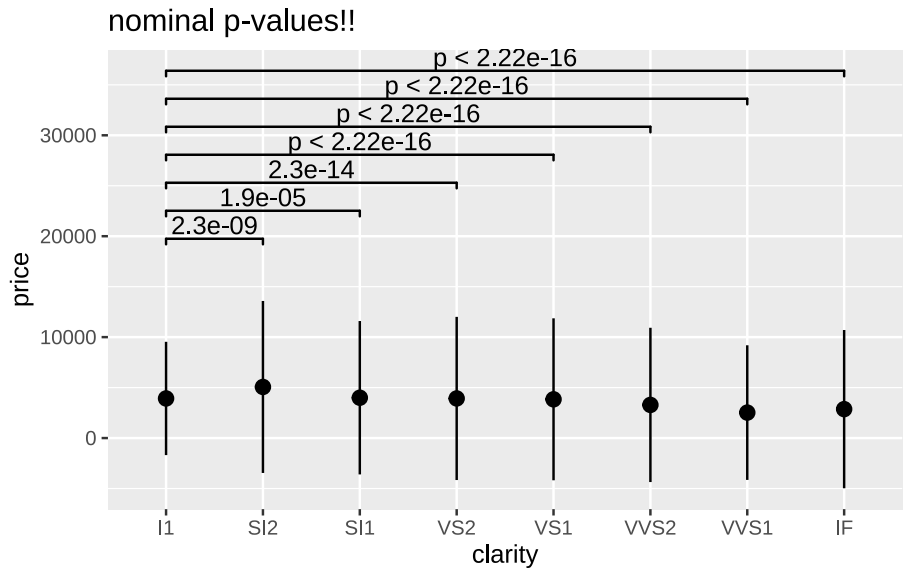


```
plottemp + geom_signif(
  comparisons=list(1:2))+
  scale_y_continuous(expand = expansion(mult=c(0.05,.2)))
```

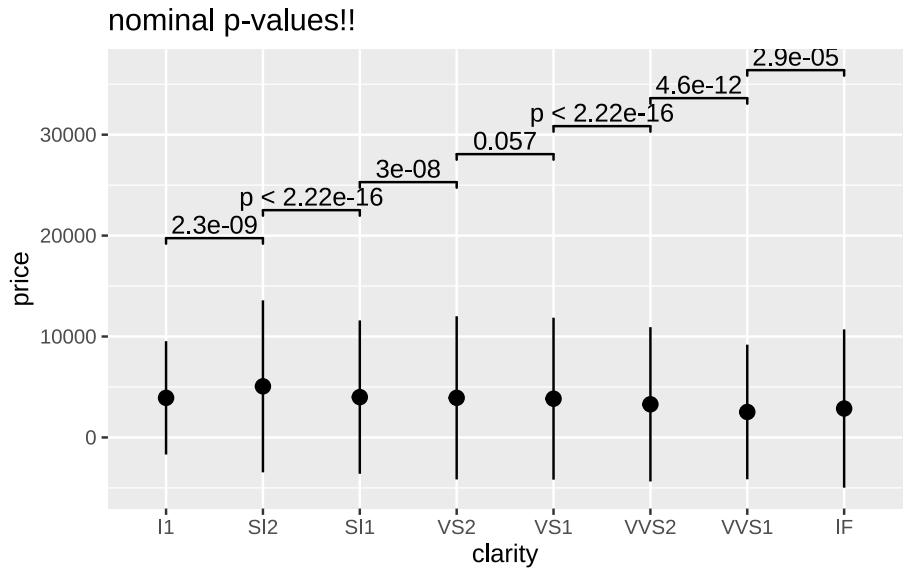
```
Warning in wilcox.test.default(c(21.4, 18.7, 18.1, 14.3, 24.4, 22.8, 19.2, :
kann bei Bindungen keinen exakten p-Wert Berechnen
```




```
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!!")
```

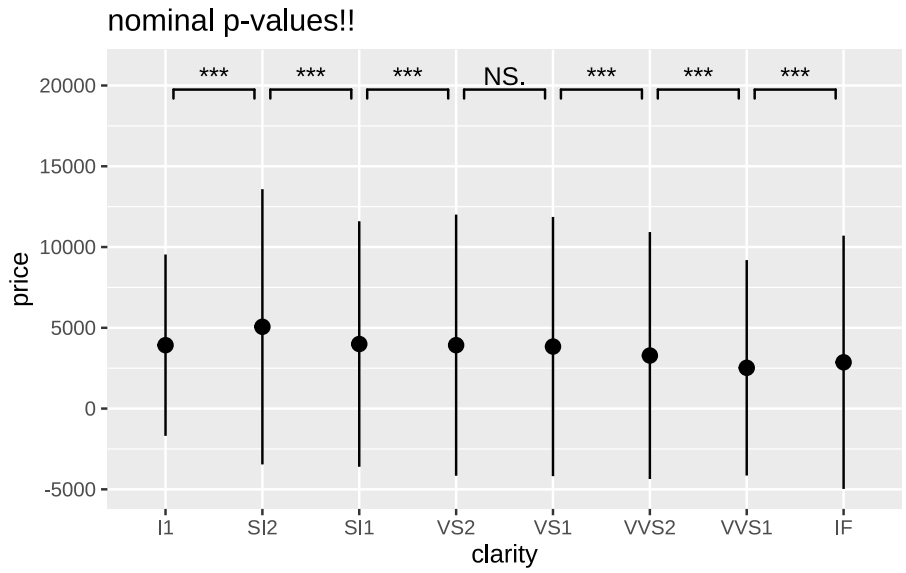



```
ggplot(diamonds,aes(clarity, price))+
  stat_summary(fun.data=mean_sdl)+
  geom_signif(comparisons=list(c(1,2),c(2,3),c(3,4),c(4,5),
                               c(5,6),c(6,7),c(7,8)),
              step_increase = 0.15)+
  ggtitle("nominal p-values!!")
```




```
ggplot(diamonds,aes(clarity, price))+
  stat_summary(fun.data=mean_sdl)+
```

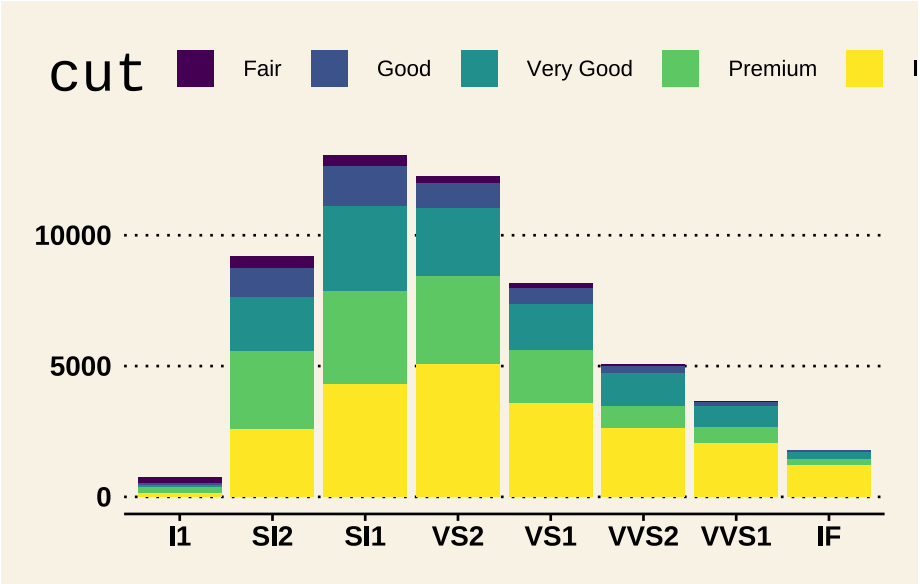
```
  geom_signif(comparisons=list(c(1,2),c(2,3),c(3,4),c(4,5),
                               c(5,6),c(6,7),c(7,8)),
              map_signif_level = TRUE,
              extend_line = -.01)+
  ggtitle("nominal p-values!!")+
  scale_y_continuous(expand = expansion(mult=c(0.05,.1)))
```



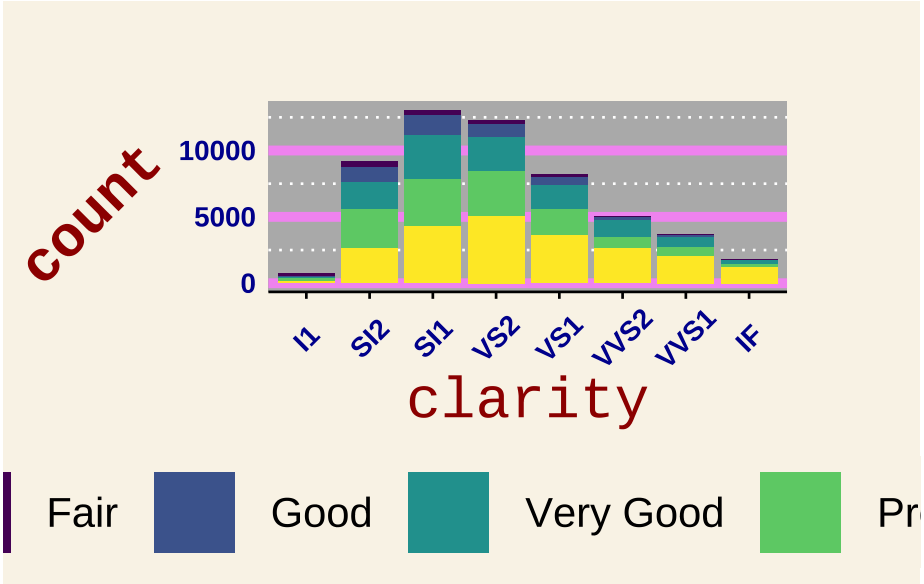
6.14 Theme definitions / changes

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

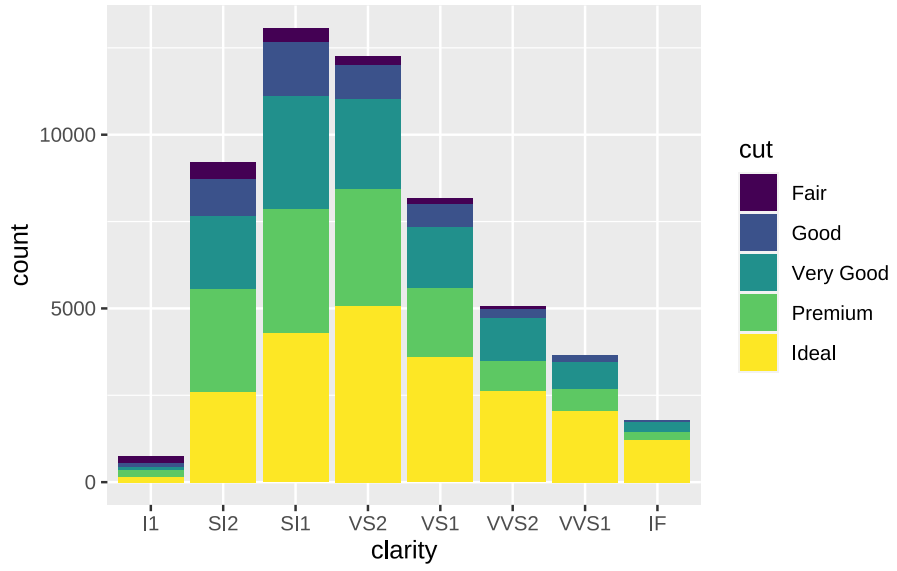
```
old <- theme_set(theme_wsj())
ggplot(data=diamonds,aes(x=clarity,fill=cut))+
  geom_bar()
```



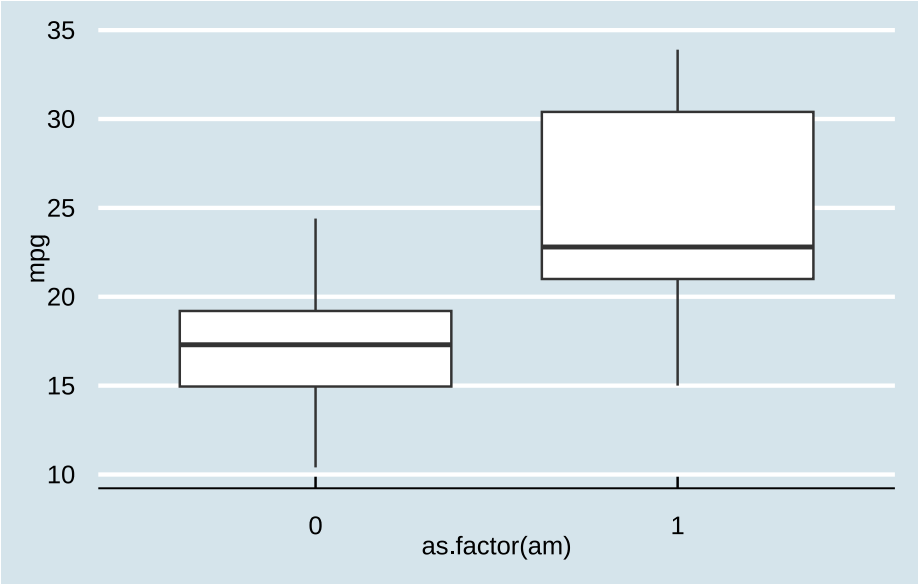

```
theme_update(legend.position="bottom",
             axis.text=element_text(colour = "darkblue",
                                    size=12),
             axis.text.x=element_text(vjust=0.5,angle=45,
                                      family="sans",
                                      face = "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()
```



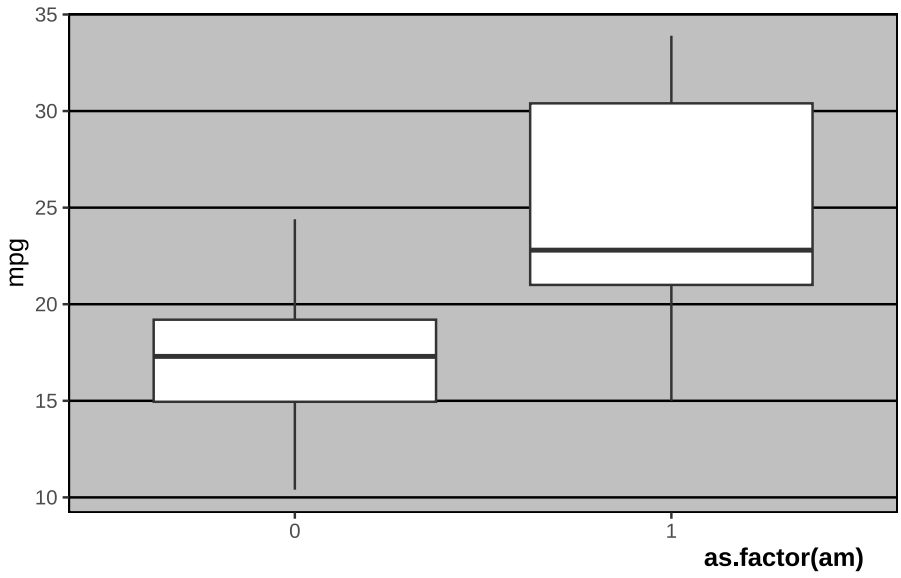

```
theme_set(theme_grey())
#theme_set(old)
ggplot(data=diamonds,aes(x=clarity,fill=cut))+
  geom_bar()
```



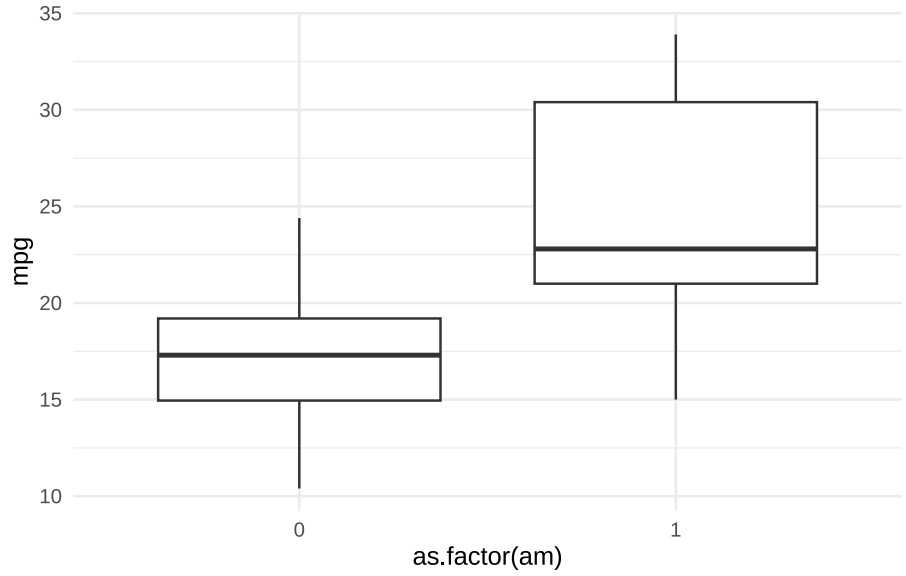

```
# ggthemes ####
plottemp+theme_economist()
```



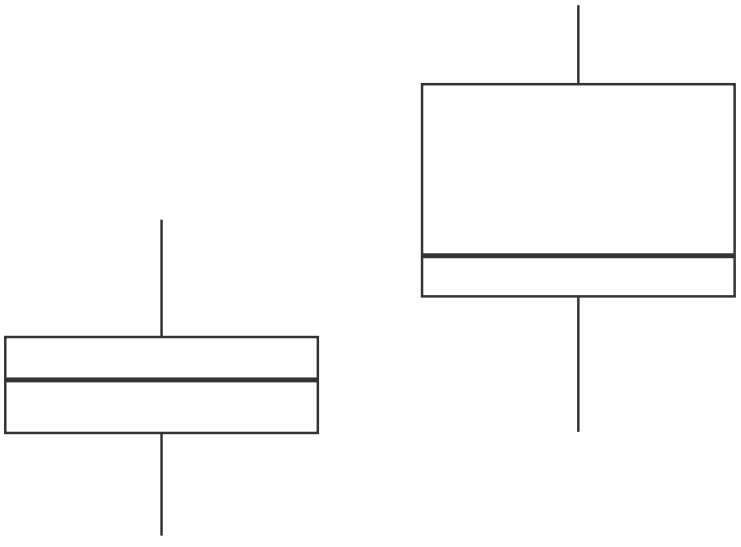

```
plottemp+theme_excel()+
  theme(axis.title.x =  element_text(face="bold", hjust=0.95))
```



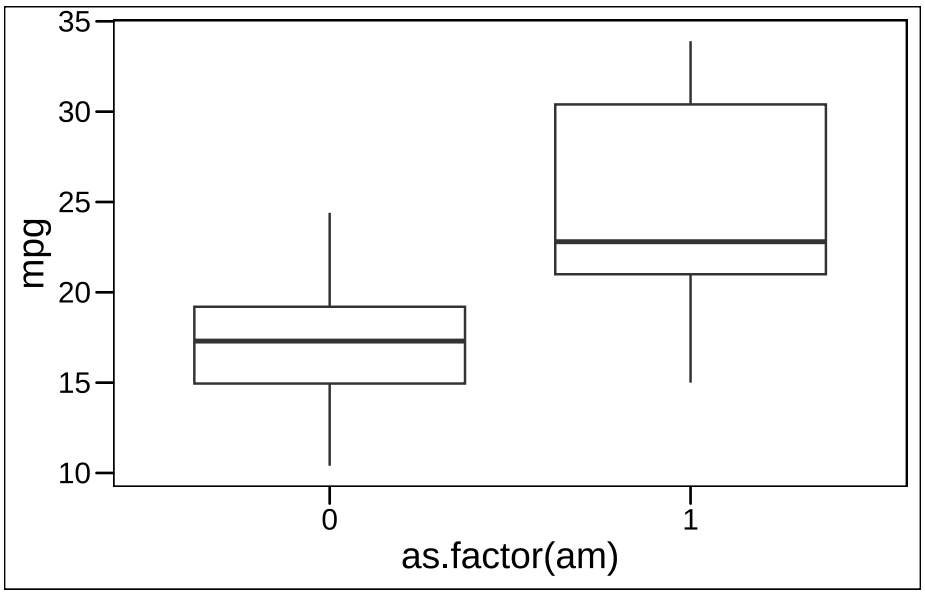

```
plottemp+theme_minimal()
```



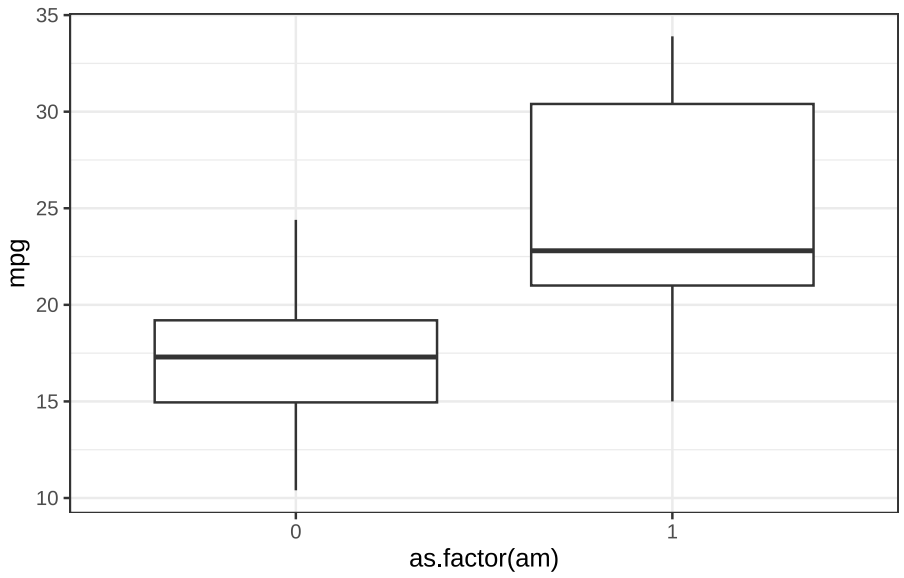

```
plottemp+theme_void()
```



```
plottemp+theme_base()
```




```
plottemp+theme_bw()
```

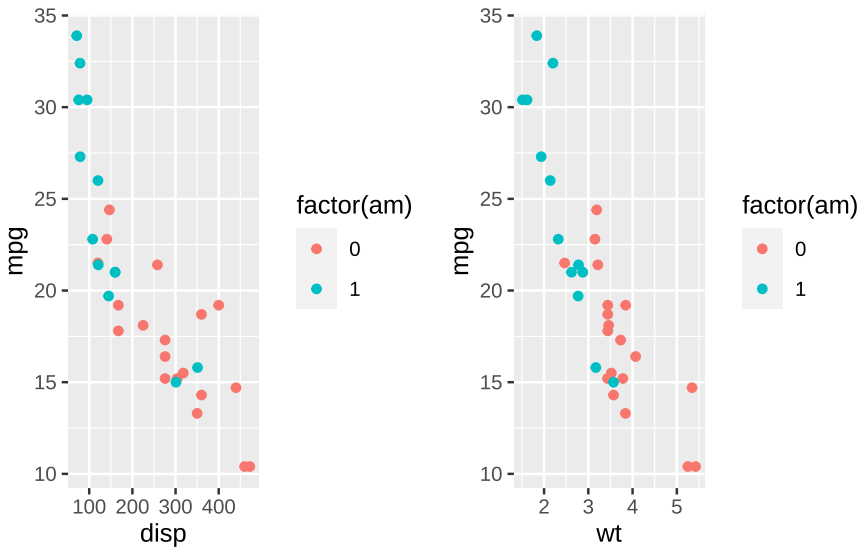



```
# https://github.com/thomasp85/patchwork


# https://www.data-imaginist.com/2019/a-flurry-of-facets/

# https://github.com/thomasp85/gganimate
```

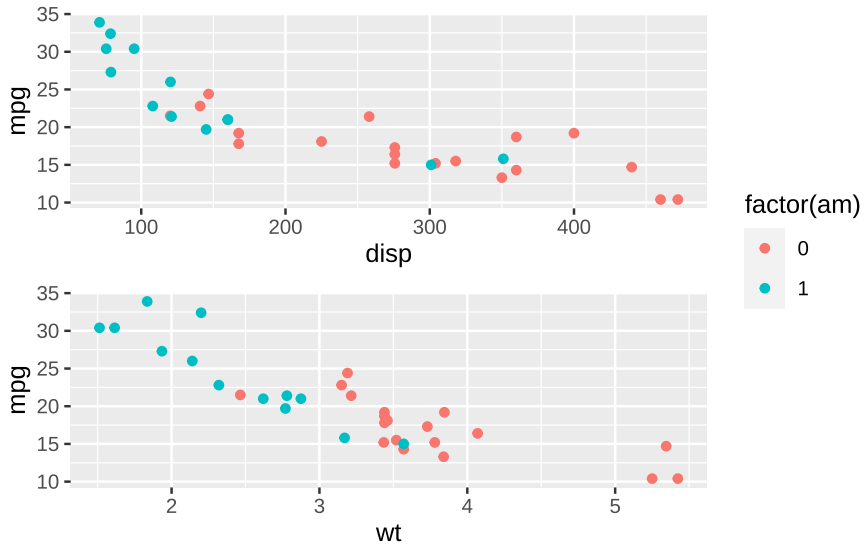
6.15 Combining figures with patchwork

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
```

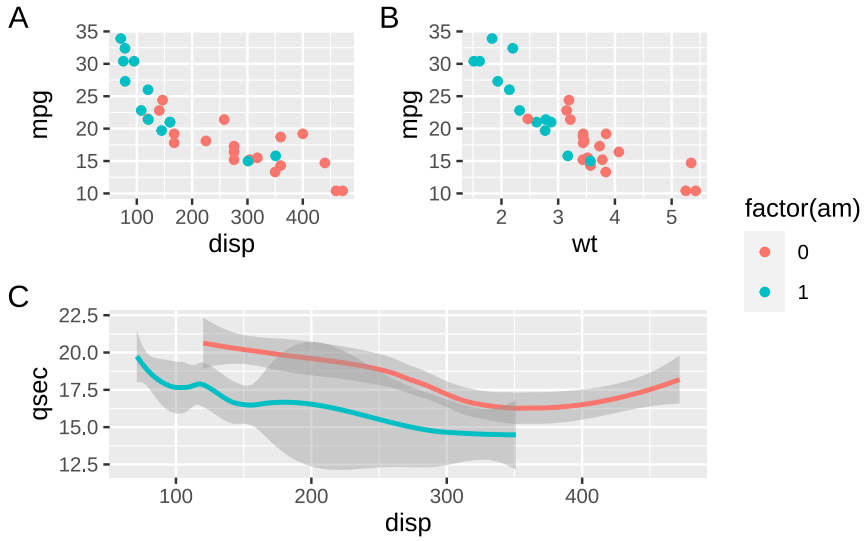



```
(p1 / p2) +
  plot_layout(guides = "collect")
```




```
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'
```



Chapter 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)
```

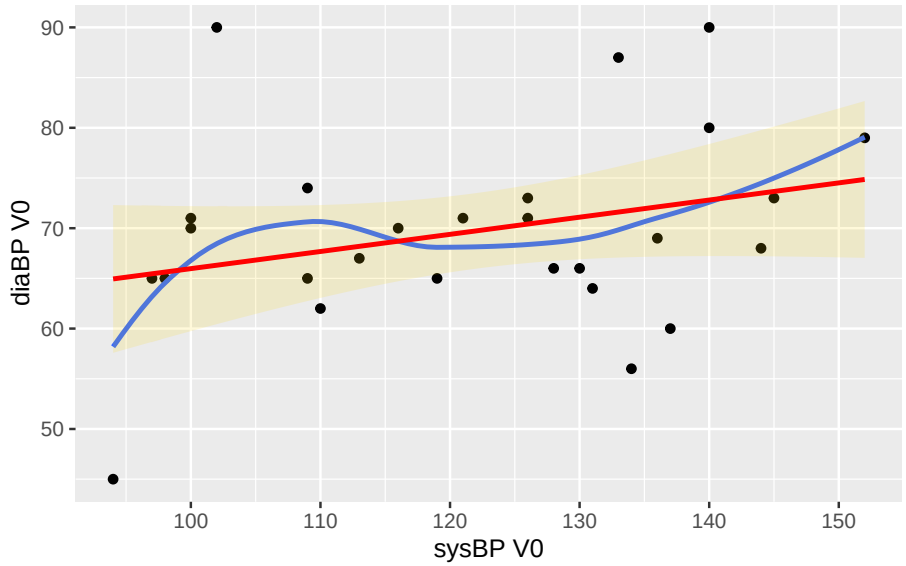
```
`geom_smooth()` using method = 'loess' and formula = 'y ~ x'
```

```
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 V0`, 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}\cline

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


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

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

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

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

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

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


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



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

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

\multicolumn{1}{>{\raggedright}m{\dimexpr 1.18in+0\tabcolsep}}{\textcolor[HTML]{00000

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

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

\multicolumn{1}{>{\raggedright}m{\dimexpr 1.18in+0\tabcolsep}}{\textcolor[HTML]{00000

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

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```

```
rawdata |>
  group_by(Sex,Testmedication) |>
  summarise(WeightSummary=meansd(`Weight (kg)`))
```

```
`summarise()` has grouped output by 'Sex'. You can override using the `.groups`
argument.
```

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

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

```
# A tibble: 4 x 5
  Variable    desc_all      `Sex f`       `Sex m`       p
  <fct>       <chr>         <chr>         <chr>         <chr>
1 Size (cm)   174 (168/179) 166 (162/168) 174 (172/180) 0.011
```

2	Weight (kg)	84 (77/96)	74 (66/88)	86 (80/104)	0.107
3	sysBP V0	126 (109/136)	119 (105/129)	126 (109/137)	0.609
4	diaBP V0	69 (65/73)	66 (64/80)	70 (65/73)	0.784

Chapter 8

Better tables with flextable

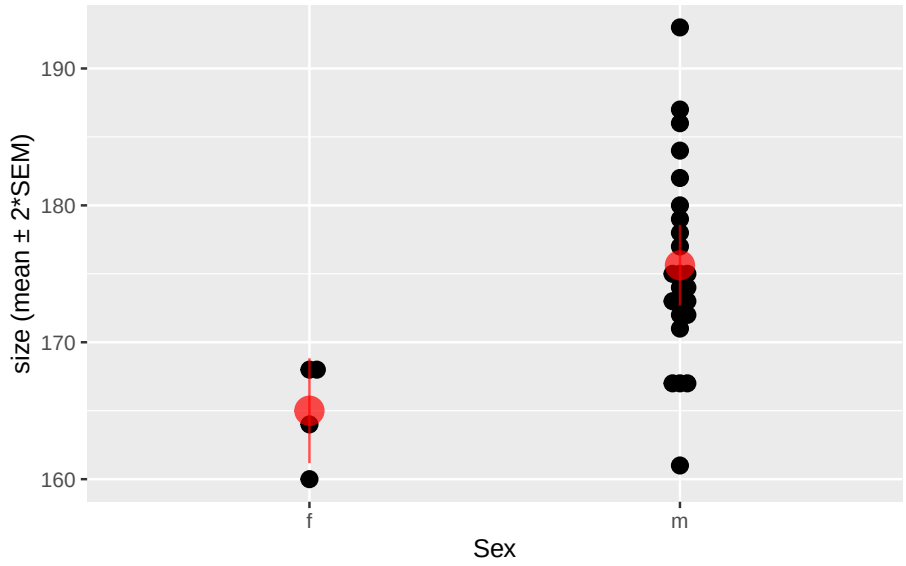
Chapter 9

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))+
  ylab("size (mean \u00B1 2*SEM)")
```




```
  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(r
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 to 0
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
```

```
(tOut<-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 to 0
95 percent confidence interval:
 -18.302594  -2.947406
sample estimates:
mean in group f mean in group m
        165.000         175.625
```

```
(tOut<-
    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 e
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 e
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()
```

```
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```

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

```
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```

```
  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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```

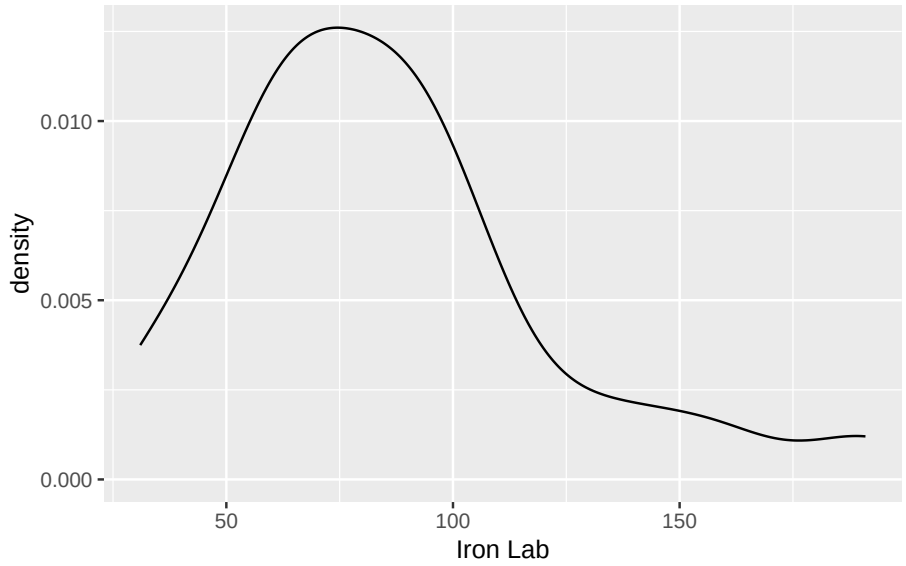

9.2 Ordinal data

```
ordvars$names
```

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

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

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

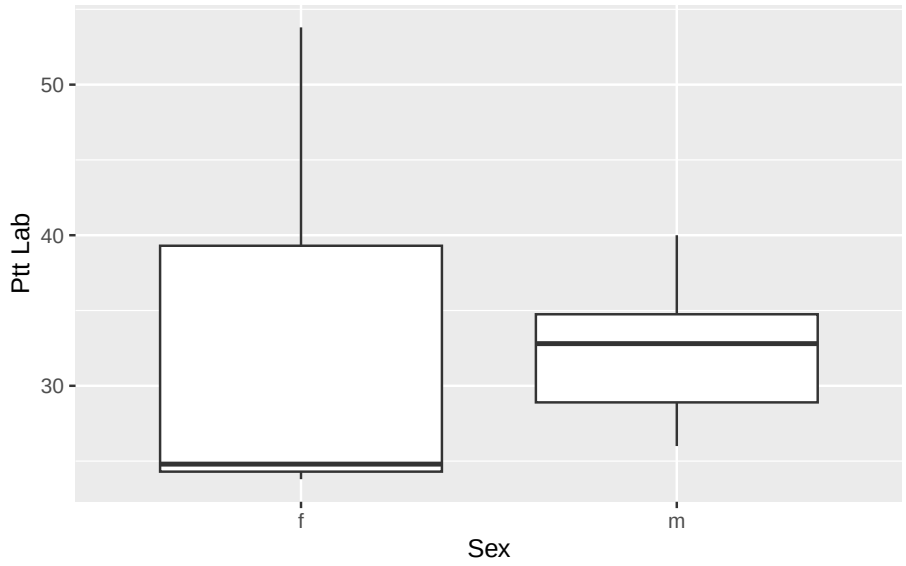



```
by(data = rawdata[[ordvars$index[1]]],
   INDICES = rawdata$Sex,FUN = median_quart)
```

```
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()`).
```




```
  (uOut<-wilcox.test(
    rawdata[[ordvars$index[1]]]~rawdata$Sex,exact=F))
```

```
    Wilcoxon rank sum test with continuity correction

data:  rawdata[[ordvars$index[1]]] by rawdata$Sex
W = 24, p-value = 0.3748
alternative hypothesis: true location shift is not equal to 0
```

```
  uOut$p.value
```

```
[1] 0.3748016
```

```
  #  coin::wilcox_test
  (uOut2<-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()
```

```
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\end{longtable}


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```

```

## 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 = 0.1772
```
```

```
  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 = 0.5944
```

```
  tabletestOut$p.value
```

```
[1] 0.5943941
```

```
  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()
```

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

```
\end{longtable}


\arrayrulecolor[HTML]{000000}

\global\setlength{\arrayrulewidth}{\Oldarrayrulewidth}

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

\renewcommand*{\arraystretch}{1}
```

Chapter 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.

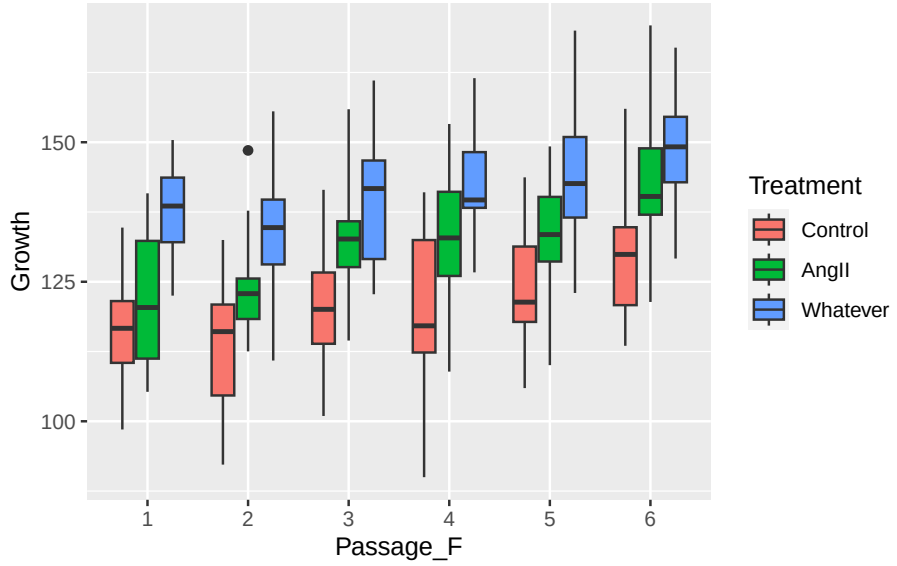
```
rawdata<-foreign::read.spss(file=here('Data/Zellbeads.sav'),
                            use.value.labels=T,to.data.frame=T) |>
  as_tibble() |>
  dplyr::select(-ZahlZellen) |>
  rename(Growth=Wachstum,Treatment=Bedingung) |>
  mutate(Passage_F=factor(Passage),
         Treatment=fct_recode(Treatment,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

```
re-encoding from CP1252
```

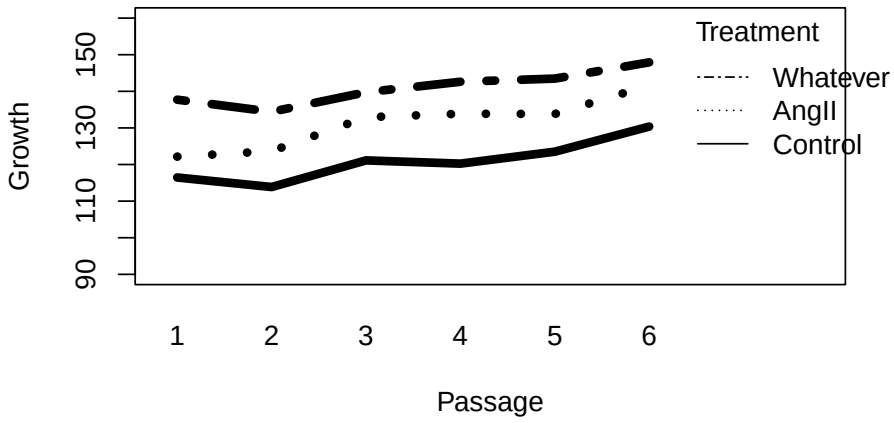
10.3 Graphical exploration

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)
```

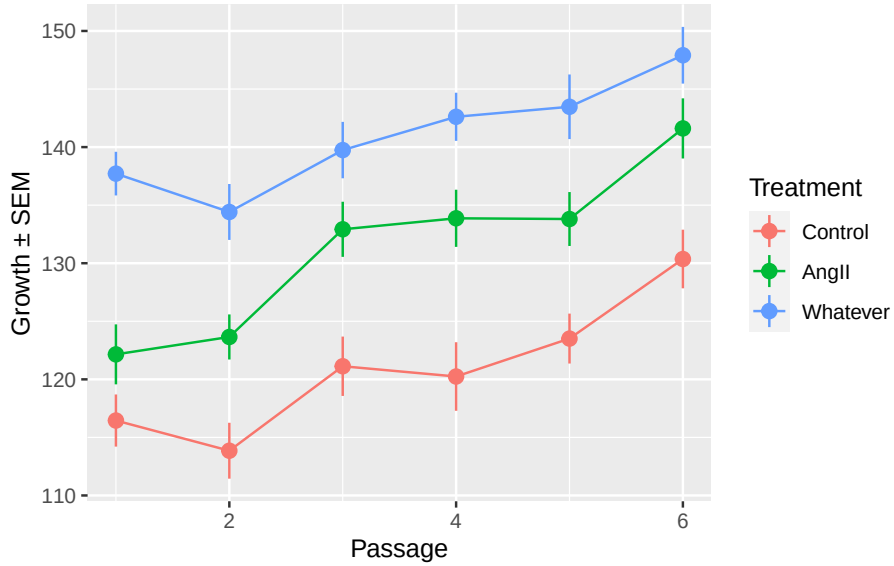



```
with(rawdata, interaction.plot(
  x.factor=Passage, trace.factor=Treatment, response=Growth,
  ylim = c(90, 160), lty = c(1,3,12), lwd = 5,
  ylab = "Growth", xlab = "Passage",
  trace.label = "Treatment"))
```



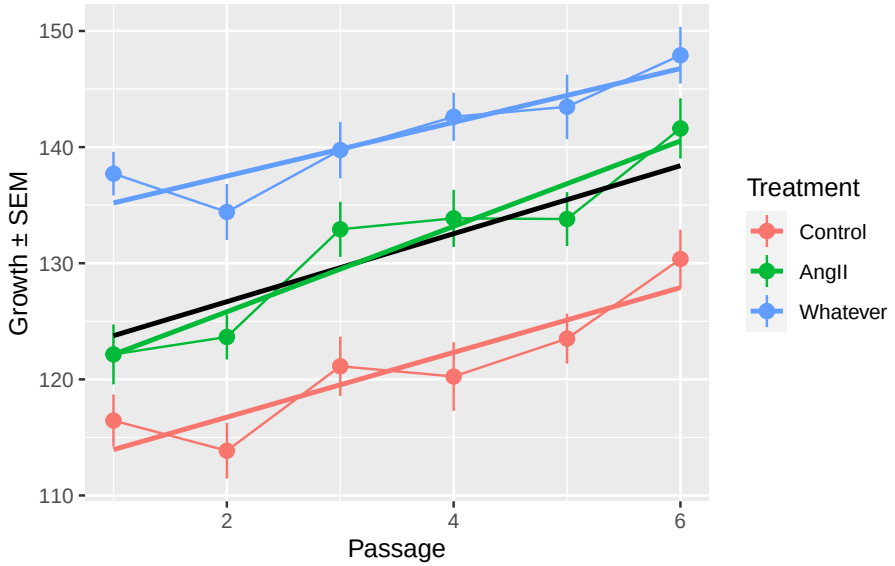

```
# p1<-ggplot(rawdata,aes(x=Passage,y=Growth))+
#    stat_summary(geom='line',fun='mean',aes(color=Treatment))+
#    stat_summary(geom='line',fun='mean')
p1<-ggplot(rawdata,aes(x=Passage,y=Growth))+
  stat_summary(geom='line',fun='mean',aes(color=Treatment))+
  stat_summary(aes(color=Treatment))+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

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



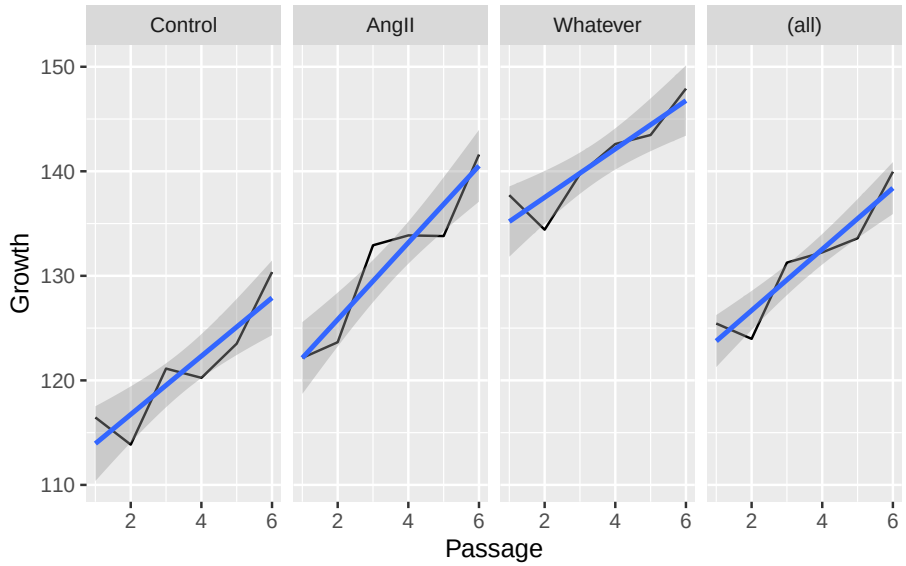
```
p1+geom_smooth(method='lm',color='black',se=F)+
  geom_smooth(method='lm',aes(color=Treatment),se=F)
```

```
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

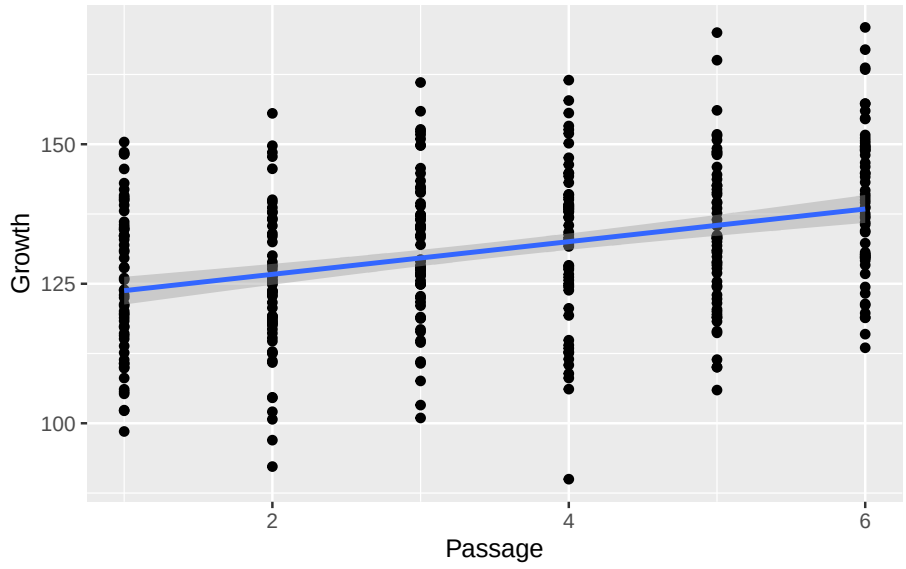
10.4.1 Linear regression

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

10.4.1.1 Graphical exploration

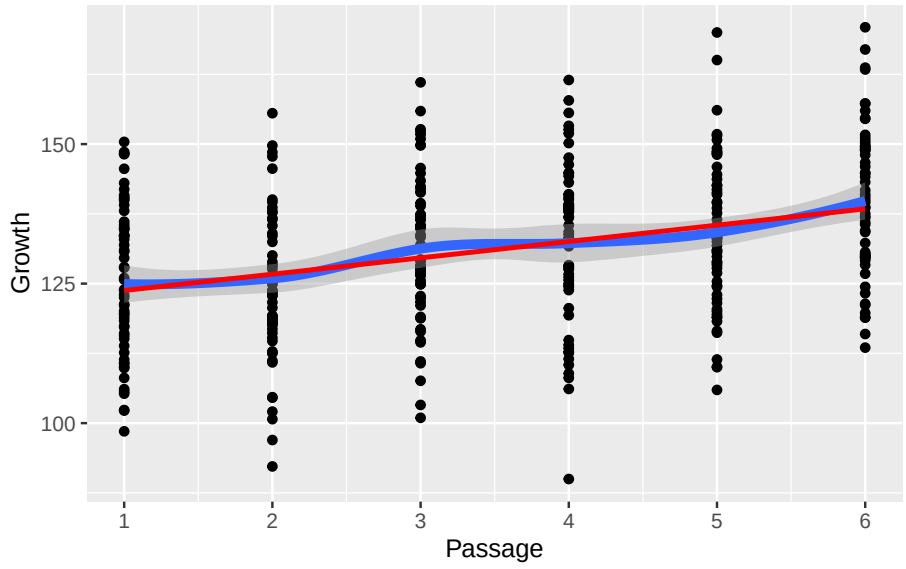
```
ggplot(rawdata,aes(Passage,Growth))+
  geom_point()+
  geom_smooth(method=lm)
```

```
`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:

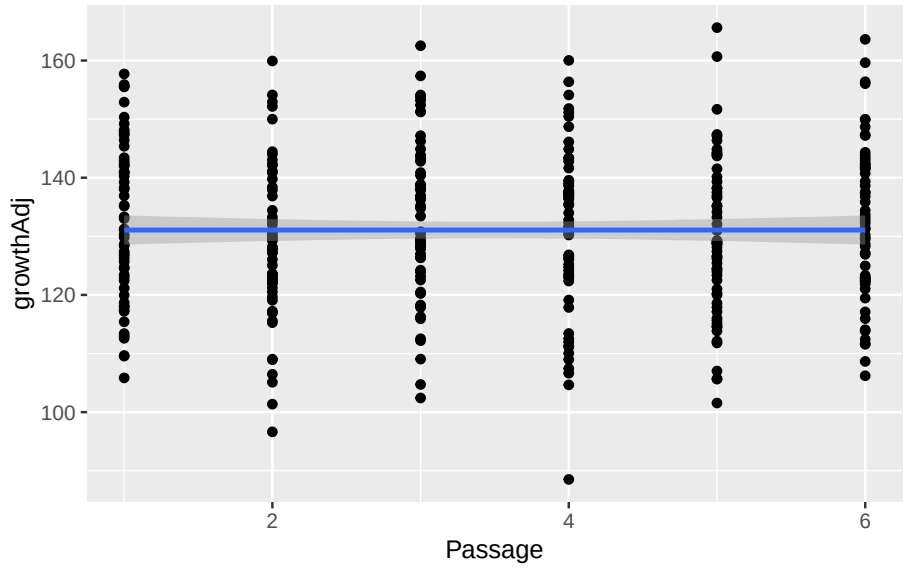
```
rawdata <-
  mutate(rawdata,
         growthAdj = regressionOut$residuals+mean(Growth))

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()
```

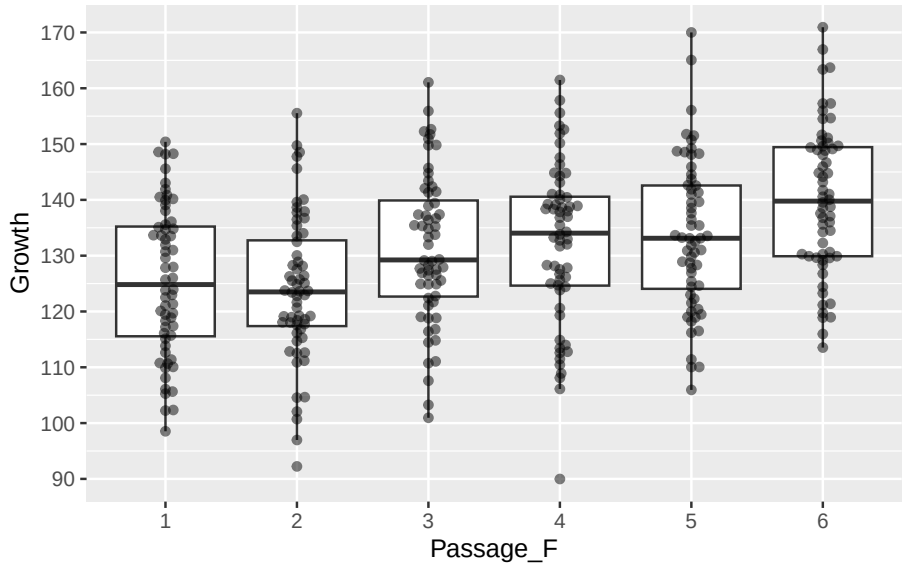
```
# A tibble: 2 x 5
  term        estimate std.error statistic   p.value
  <chr>          <dbl>     <dbl>     <dbl>     <dbl>
1 (Intercept) 1.31e+ 2     1.63   8.05e+ 1 2.04e-231
2 Passage     6.80e-15     0.418  1.63e-14 1.00e+  0
```

10.4.2 ANOVA

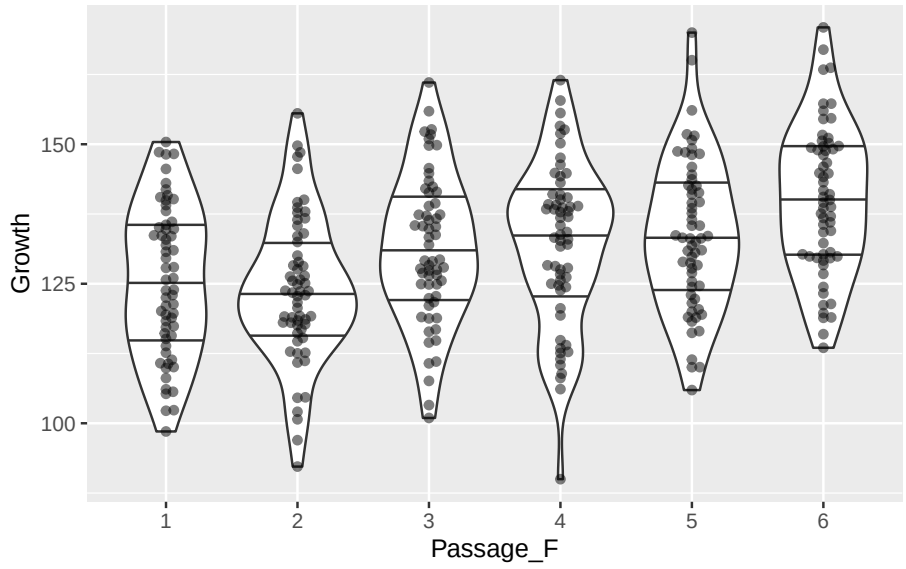
In the linear regression, we had Passage as a continuous IV, estimating a global 'universal' effect supposed to be constant. Now we look at Passage_F and model a discrete IV, allowing for specific effects, and thereby comparing means between groups.

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$Growth[which(rawdata$Passage ==
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
5.521460e-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
9.031123e-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"
```

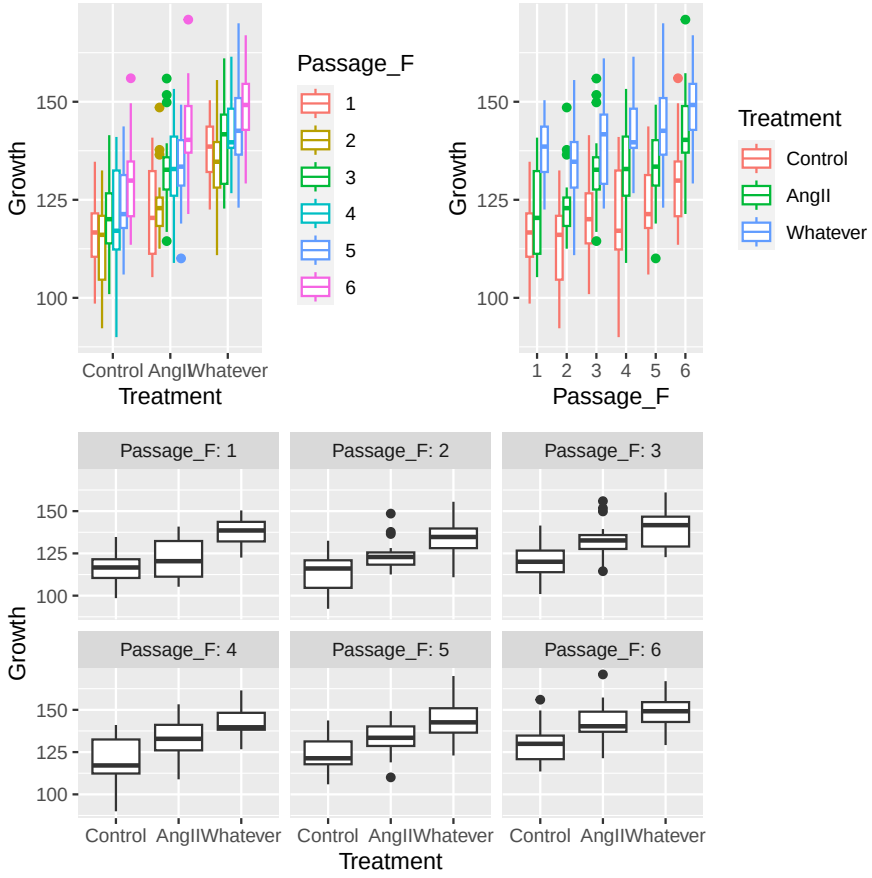
10.4.3 LM with continuous AND categorical IV

Traditionally you may thing 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  0.0264 *
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
```

```
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(lmOut_additive)
```