RStatsbook

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Preface

This is a Quarto book.

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...

1 Introduction

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

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

R for Data Science

Modern Statistics for Modern Biology

Modern R with the tidyverse

ggplot2: Elegant Graphics for Data Analysis

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

2 Syntax rules / basic things to know about R

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

```
if(!require(pacman,quietly = TRUE)){
  install.packages('pacman')
}
pacman::p_load(
  tidyverse, # metapackage
  wrappedtools # my own tools package
  )
```

2.2 Numeric operations

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

```
[1] 7
```

```
3*5
```

```
[1] 15
```

```
15/3 #not 15:3!!
```

```
[1] 5
```

```
3^2
```

```
[1] 9
```

```
9^0.5
```

```
[1] 3
```

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

```
[1] 1
```

2.3 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).

```r
### 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
`Gewicht [kg]` <- 67
```

2.4 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.

2.4.1 Guessed classes

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

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

```r
typeof(float_num)
```

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

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

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

```
typeof(int_num)
```

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

```
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"
```

```r
logical_var <- TRUE
class(logical_var)
```

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

```r
typeof(logical_var)
```

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

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

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

```r
# logicals usualy are defined by conditions:
int_num < float_num
```

```
[1] TRUE
```

```r
# 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
```

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

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

```r
class(factor_var)
```

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

```
typeof(factor_var)
```

```
[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
```

```
# everything intended to group subjects or representing categories should be stored as fac
# package forcats provides nice tools for factors

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

```
[1] "2023-07-05"
```

```
class(date_var)
```

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

```
typeof(date_var)
```

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

```
# mixed classes
test2 <- c(1,2,'a','b')
class(test2)
```

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

2.4.2 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 durch Umwandlung erzeugt
```

```
[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
class(NA_real_)
```

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

```
class(NA_integer_)
```

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

```
  class(NA_character_)
```

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

```
  class(NA_Date_)
```

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

2.4.3 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 be 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[-1]
```

```
[1] 3 6 8 2 1
```

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

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

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
```

```
 #outer() creates immediate output
numbers1+numbers2 #not stored anywhere
```

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

```
c(2,4,6,8)+1 # R (usually) recycles  arguments!
```

```
[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): Länge des längeren Objektes
     ist kein Vielfaches der Länge des kürzeren Objektes
```

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

```r
test_na<-is.na(test_n)
str(test_na)   #Structure of a variable
```

```
 logi [1:6] FALSE FALSE FALSE TRUE TRUE TRUE
```

```r
as.numeric(test_na)
```

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

```r
cat(a <- 6)
```

```
6
```

```r
print(a <- 6)
```

```
[1] 6
```

```r
### functions -----
# FunctionName(parameter1=x1,parameter2=x2,x3,...)
c('my','name')
```

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

```r
mean(x = c(3,5,7,NA),na.rm=TRUE)
```

```
[1] 5
```

```r
mean(na.rm=T,x=c(3,5,7,NA))
```

```
[1] 5
```

```
?mean
```

starte den http Server für die Hilfe fertig

```
mean(c(3,5,7,NA),na.rm=T)
```

```
[1] 5
```

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

```
[1] 2
```

```
median(x = 1:100,na.rm = T)
```

```
[1] 50.5
```

```
# will become more and more complex in future lessons
# functions may be nested:
floor(as.numeric(as.Date(Sys.Date())-
                   as.Date('1985/12/10'))/
        365.25)
```

```
[1] 37
```

```
# or (usually better) piped:
results <- mtcars |>
  dplyr::mutate(am=factor(am))  |>
  dplyr::filter(vs==1) |>
  group_by(am) |>
  summarize(across(c(wt, mpg, qsec, disp),
                   mean))  |>
  pivot_longer(cols = -am,names_to = 'Measure')  |>
  pivot_wider(id_cols = Measure, names_from = am,
```

```
              values_from = value)

# 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
```

```
### More complex data types, created by functions -----
# Matrix: 2 dimensions, 1 data type
my1.Matrix<-
  matrix(data=1:12,
         # nrow=4,
         ncol=3,
         byrow=T,
         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 <- 1:100
nrow <- 20
matrix(data=data,
       nrow=nrow,
       byrow=T,
       dimnames=list(paste0('row',1:nrow),
```

```
                    paste0('col',1:(length(data)/nrow))))
```

```
      col1 col2 col3 col4 col5
row1     1    2    3    4    5
row2     6    7    8    9   10
row3    11   12   13   14   15
row4    16   17   18   19   20
row5    21   22   23   24   25
row6    26   27   28   29   30
row7    31   32   33   34   35
row8    36   37   38   39   40
row9    41   42   43   44   45
row10   46   47   48   49   50
row11   51   52   53   54   55
row12   56   57   58   59   60
row13   61   62   63   64   65
row14   66   67   68   69   70
row15   71   72   73   74   75
row16   76   77   78   79   80
row17   81   82   83   84   85
row18   86   87   88   89   90
row19   91   92   93   94   95
row20   96   97   98   99  100
```

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

```
[1] 6
```

```
  my1.Matrix[2,]
```

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

```
  my1.Matrix[,2]
```

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

```r
my1.Matrix[c(1,3),-2]
```

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

```r
my1.Matrix[1,1]<-NA
mdat <- matrix(c(1,2,3, 11,12,13),
               nrow = 2, ncol=3) #byrow=TRUE,
mdat
```

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

```r
# Data frame: 2 dimensions, various data types (1 per columns)
patientN<-15
#options(stringsAsFactors =F)
(myTable<-data.frame(
  patientCode=paste0('pat',1:patientN),
  Var1=1,
  Var2=NA_Date_))
```

```
   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>
7         pat7    1 <NA>
8         pat8    1 <NA>
9         pat9    1 <NA>
10       pat10    1 <NA>
11       pat11    1 <NA>
12       pat12    1 <NA>
13       pat13    1 <NA>
14       pat14    1 <NA>
15       pat15    1 <NA>
```

```r
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 ...
```

```r
set.seed(501)
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=round(rnorm(n=patientN,mean=140,sd=10)))

head(myTable)
```

```
  patientCode Age  Sex sysRR
1        pat1  51 <NA>   142
2        pat2  31 <NA>   137
3        pat3  52 <NA>   128
4        pat4  31 <NA>   147
5        pat5  49 <NA>   156
6        pat6  38 <NA>   132
```

```r
myTable[,1]
```

```
 [1] "pat1"  "pat2"  "pat3"  "pat4"  "pat5"  "pat6"  "pat7"  "pat8"  "pat9"
[10] "pat10" "pat11" "pat12" "pat13" "pat14" "pat15"
```

```r
myTable$patientCode
```

```
 [1] "pat1"  "pat2"  "pat3"  "pat4"  "pat5"  "pat6"  "pat7"  "pat8"  "pat9"
[10] "pat10" "pat11" "pat12" "pat13" "pat14" "pat15"
```

```
myTable[,"patientCode"]
```

```
 [1] "pat1"  "pat2"  "pat3"  "pat4"  "pat5"  "pat6"  "pat7"  "pat8"  "pat9"
[10] "pat10" "pat11" "pat12" "pat13" "pat14" "pat15"
```

```
spalten<-c('Sex',"Age")
myTable[,spalten]
```

```
    Sex Age
1  <NA>  51
2  <NA>  31
3  <NA>  52
4  <NA>  31
5  <NA>  49
6  <NA>  38
7  <NA>  45
8  <NA>  63
9  <NA>  27
10 <NA>  63
11 <NA>  21
12 <NA>  22
13 <NA>  20
14 <NA>  32
15 <NA>  42
```

```
myTable[,c('patientCode','Age')]
```

```
   patientCode Age
1         pat1  51
2         pat2  31
3         pat3  52
4         pat4  31
5         pat5  49
6         pat6  38
7         pat7  45
8         pat8  63
9         pat9  27
```

```
10        pat10  63
11        pat11  21
12        pat12  22
13        pat13  20
14        pat14  32
15        pat15  42
```

```
myTable$Sex[]<-sample(x=c('m','f',NA),
                      size=patientN,
                      prob = c(.4,.4,.2),
                      replace=T)
str(myTable)
```

```
'data.frame':   15 obs. of  4 variables:
 $ patientCode: chr  "pat1" "pat2" "pat3" "pat4" ...
 $ Age        : num  51 31 52 31 49 38 45 63 27 63 ...
 $ Sex        : Factor w/ 2 levels "m","f": NA 1 1 2 2 2 1 NA 2 2 ...
 $ sysRR      : num  142 137 128 147 156 132 146 131 151 146 ...
```

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

str(myTable)
```

```
'data.frame':   15 obs. of  4 variables:
 $ patientCode: chr  "Code1" "Code2" "Code3" "Code4" ...
 $ Age        : num  51 31 52 31 49 38 45 63 27 63 ...
 $ Sex        : Factor w/ 2 levels "m","f": NA 1 1 2 2 2 1 NA 2 2 ...
 $ sysRR      : num  142 137 128 147 156 132 146 131 151 146 ...
```

```
myTable[c(1,3,4),c(1,4)]
```

```
  patientCode sysRR
1       Code1   142
3       Code3   128
4       Code4   147
```

```r
#lists
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] 101.24498 100.99285 101.09999 101.61369 102.98353 101.03886  99.45161
 [8] 100.01835  99.21011  99.69732  98.62364 100.72063 102.18361 101.03190
[15] 100.82017 104.20466 102.23494 101.30330  97.56465 105.26693 103.41743
[22]  95.74379  99.40701 102.37993  98.13016  98.32520 100.17701  96.45507
[29] 105.83716  98.36719  98.09867 103.31457 101.72139 101.91318 103.57645
[36]  98.75810 100.27766 100.88864 102.97018 103.19208 101.93671  99.05340
[43] 100.19505  99.80348 100.35903 103.65700  99.19059  96.47964  98.77878
[50]  99.98729
```

```r
shopping$snacks
```

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

```r
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 -6.32
  ..- attr(*, "names")= chr "t"
 $ parameter  : Named num 36.1
  ..- attr(*, "names")= chr "df"
 $ p.value    : num 2.53e-07
 $ conf.int   : num [1:2] -2.32 -1.2
  ..- 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 0.278
 $ 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] 2.530727e-07
```

```
  #package rlist

  # tibble ####
  pacman::p_load(wrappedtools, randomNames)
  patientN <- 200
  rawdata <- tibble(
    PatID=paste('P',1:patientN), #wie bei data.frame
```

```
  Sex=sample(x = c('male','female'),
             size = patientN,replace = T,
             prob = c(.7,.3)),
  Ethnicity=sample(1:6,patientN,T,c(.01,.01,.05,.03,.75,.15)),
  `Given name`=randomNames(n = patientN,
                           gender = Sex,
                           ethnicity = Ethnicity,
                           which.names = 'first'),
  `Family name`=randomNames(n = patientN,
                            ethnicity = Ethnicity,
                            which.names = 'last'),
  Treatment=sample(c('Placebo','Verum'),patientN,T),
  `sysRR (mmHg)`=round(rnorm(n=patientN,mean=140,sd=10))-
    (Treatment=='Verum')*15,
  diaRR=round(rnorm(n=patientN,mean=80,sd=10))-
    (Treatment=='Verum')*10,
  HR=round(rnorm(n=patientN,mean=90,sd=7)))
rawdata
```

```
# A tibble: 200 x 9
   PatID Sex    Ethnicity `Given name` `Family name` Treatment `sysRR (mmHg)`
   <chr> <chr>      <int> <chr>        <chr>         <chr>                <dbl>
 1 P 1   male           5 Kevin        Dahlin        Verum                  122
 2 P 2   male           5 Connor       Burns         Verum                  118
 3 P 3   male           6 Nawfal       el-Neman      Verum                  107
 4 P 4   male           5 Peter        Williams      Placebo                135
 5 P 5   male           1 Keenan       Kuck          Verum                  138
 6 P 6   male           5 Chase        Bowen         Verum                  142
 7 P 7   female         5 Sarah        Kuhn          Verum                  103
 8 P 8   male           4 Fzelle       Landa         Placebo                138
 9 P 9   female         6 Layaali      el-Gaber      Verum                  129
10 P 10  male           5 Mitchell     Carlone       Verum                  134
# i 190 more rows
# i 2 more variables: diaRR <dbl>, HR <dbl>
```

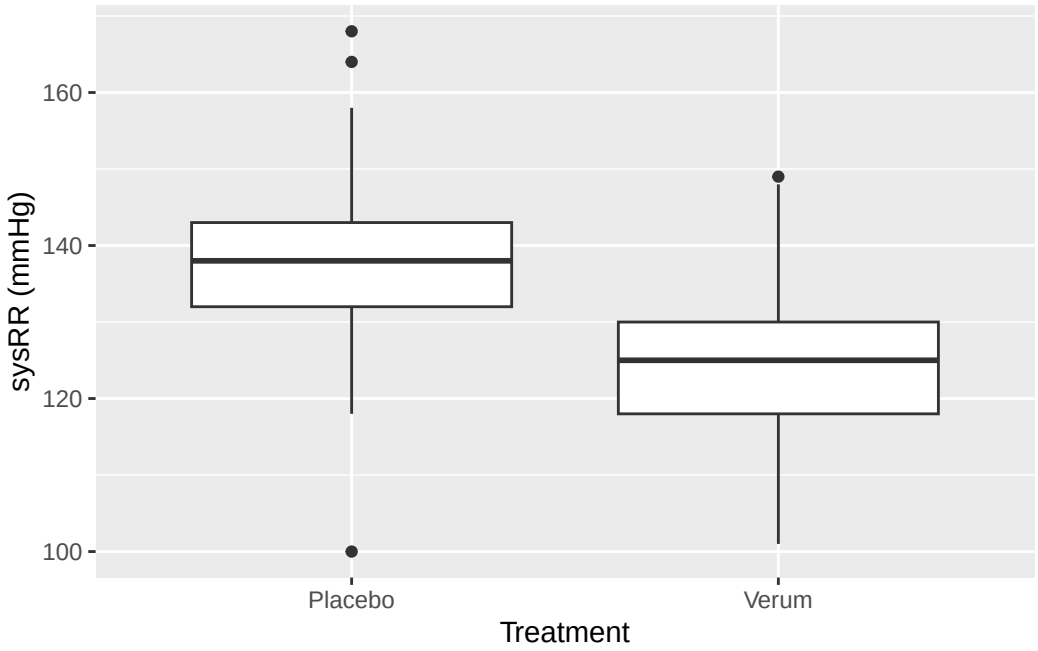
```
colnames(rawdata)
```

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

```
cn()
```

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

```
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')))
ggplot(rawdata,aes(x = Treatment,y = `sysRR (mmHg)`))+
  geom_boxplot()
```




```
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   male
4 P 4   male
5 P 5   male
```

```
rawdata[,6]
```

```
# A tibble: 200 x 1
   Treatment
   <chr>
 1 Verum
 2 Verum
 3 Verum
 4 Placebo
 5 Verum
 6 Verum
 7 Verum
 8 Placebo
 9 Verum
10 Verum
# i 190 more rows
```

```
rawdata[6]
```

```
# A tibble: 200 x 1
   Treatment
   <chr>
 1 Verum
 2 Verum
 3 Verum
 4 Placebo
 5 Verum
 6 Verum
 7 Verum
 8 Placebo
```

```
 9 Verum
10 Verum
# i 190 more rows
```

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

```
  [1] "Verum"   "Verum"   "Verum"   "Placebo" "Verum"   "Verum"   "Verum"
  [8] "Placebo" "Verum"   "Verum"   "Verum"   "Verum"   "Verum"   "Verum"
 [15] "Placebo" "Placebo" "Placebo" "Placebo" "Placebo" "Placebo" "Verum"
 [22] "Placebo" "Placebo" "Placebo" "Placebo" "Placebo" "Verum"   "Verum"
 [29] "Verum"   "Placebo" "Placebo" "Verum"   "Placebo" "Verum"   "Placebo"
 [36] "Verum"   "Verum"   "Verum"   "Verum"   "Verum"   "Verum"   "Verum"
 [43] "Verum"   "Placebo" "Verum"   "Verum"   "Verum"   "Verum"   "Placebo"
 [50] "Verum"   "Verum"   "Verum"   "Placebo" "Placebo" "Verum"   "Placebo"
 [57] "Verum"   "Placebo" "Verum"   "Placebo" "Verum"   "Verum"   "Placebo"
 [64] "Placebo" "Placebo" "Verum"   "Placebo" "Placebo" "Placebo" "Placebo"
 [71] "Placebo" "Placebo" "Verum"   "Placebo" "Placebo" "Verum"   "Placebo"
 [78] "Verum"   "Verum"   "Verum"   "Placebo" "Verum"   "Placebo" "Verum"
 [85] "Verum"   "Verum"   "Verum"   "Placebo" "Verum"   "Verum"   "Placebo"
 [92] "Placebo" "Placebo" "Verum"   "Verum"   "Placebo" "Verum"   "Placebo"
 [99] "Verum"   "Placebo" "Placebo" "Verum"   "Verum"   "Verum"   "Verum"
[106] "Placebo" "Placebo" "Verum"   "Verum"   "Placebo" "Placebo" "Verum"
[113] "Placebo" "Verum"   "Placebo" "Placebo" "Verum"   "Verum"   "Placebo"
[120] "Placebo" "Verum"   "Placebo" "Placebo" "Placebo" "Placebo" "Verum"
[127] "Verum"   "Verum"   "Placebo" "Placebo" "Verum"   "Verum"   "Placebo"
[134] "Placebo" "Placebo" "Verum"   "Verum"   "Verum"   "Verum"   "Verum"
[141] "Verum"   "Verum"   "Verum"   "Verum"   "Verum"   "Placebo" "Verum"
[148] "Placebo" "Placebo" "Verum"   "Placebo" "Placebo" "Placebo" "Placebo"
[155] "Verum"   "Placebo" "Verum"   "Placebo" "Placebo" "Verum"   "Placebo"
[162] "Verum"   "Placebo" "Verum"   "Placebo" "Placebo" "Placebo" "Placebo"
[169] "Placebo" "Verum"   "Verum"   "Placebo" "Placebo" "Placebo" "Placebo"
[176] "Verum"   "Placebo" "Placebo" "Verum"   "Placebo" "Verum"   "Verum"
[183] "Verum"   "Verum"   "Placebo" "Verum"   "Placebo" "Verum"   "Placebo"
[190] "Verum"   "Verum"   "Verum"   "Placebo" "Verum"   "Placebo" "Verum"
[197] "Placebo" "Placebo" "Verum"   "Verum"
```

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

```
[1] "Dahlin"              "Burns"               "el-Neman"
```

```
  [4] "Williams"           "Kuck"                 "Bowen"
  [7] "Kuhn"               "Landa"                "el-Gaber"
 [10] "Carlone"            "Lacy"                 "Malman"
 [13] "Curtis"             "Harbert"              "Zbylski"
 [16] "Conder"             "Deeds"                "al-Barakat"
 [19] "Campbell"           "Mottram"              "Dzenanovic"
 [22] "Masel"              "Duncan"               "Leterneau"
 [25] "Whyte"              "Popescu"              "Kudrna"
 [28] "Dehaan"             "Huffman"              "el-El-Sayed"
 [31] "Smith"              "Venegas"              "Tregay"
 [34] "el-Othman"          "Thomassen"            "Mcphate"
 [37] "al-Azzam"           "Walsh"                "Ueda"
 [40] "el-Yousuf"          "Clark"                "el-Basha"
 [43] "Stevens"            "Booth"                "Rock"
 [46] "Lujan"              "Dehaven"              "Matthews"
 [49] "Axelson"            "Knowles"              "Brown"
 [52] "Bell"               "Ward"                 "al-Hamad"
 [55] "Harold"             "Wiker"                "Wagner"
 [58] "Merkle"             "Glassburner"          "el-Fayad"
 [61] "Wright"             "Carpenter"            "al-Amen"
 [64] "Hogan"              "Roberts"              "Acker"
 [67] "Fassold"            "al-Zaki"              "Allen"
 [70] "Brown"              "Sandoval"             "Harris"
 [73] "Debloois"           "Tedrow"               "Mayer"
 [76] "el-Yasin"           "Thomas"               "el-Abbas"
 [79] "al-Siddiqui"        "Bennett"              "Brinegar"
 [82] "O'Brien"            "al-Emami"             "Lish"
 [85] "Iwan"               "Vangsnes"             "Scott"
 [88] "Howard"             "Day"                  "Faulkner"
 [91] "Sagrillo"           "el-Shahan"            "Hansen"
 [94] "Wadsworth"          "Mcavenia"             "el-Baddour"
 [97] "Adams"              "Abby"                 "Schorzman"
[100] "Eis"                "Barthel"              "el-Javid"
[103] "Williams"           "Welch"                "Linkous"
[106] "Hostetter"          "el-Shabazz"           "al-Shahin"
[109] "Nielsen"            "Bowman"               "Miskines"
[112] "Holt"               "al-Allam"             "Phillips"
[115] "Barber"             "Westbrook"            "Muench"
[118] "Jones"              "Smith"                "el-Salek"
[121] "Kassa"              "Crampton"             "Goble"
[124] "Hoffstetter"        "Nicely"               "al-Pour"
[127] "Osler"              "Holt"                 "Moline"
[130] "al-Dajani"          "Gutierrez-Hernandez"  "Jones"
```

```
[133] "Bain"              "Jacquot"           "Munn"
[136] "Bouchard"          "Dunn"              "Rivera"
[139] "Mcgee"             "Fleharty"          "Lee"
[142] "Carroll"           "King"              "Mantilla"
[145] "Karp"              "Hodson"            "al-Dajani"
[148] "Wilson"            "el-Yasin"          "Cruz Jr"
[151] "Gray"              "Johnson"           "Jagiello"
[154] "Prottsman"         "al-Abraham"        "el-Karim"
[157] "Christoph"         "Spence-Caffrey"    "Coder"
[160] "Cuckler"           "Branz"             "el-Kamara"
[163] "Miles"             "Harwig"            "Lincoln"
[166] "Lemke"             "Farra"             "Shelburne"
[169] "Theodore"          "Schreibvogel"      "Becker"
[172] "Malcolm"           "Lucero"            "Liming"
[175] "Trouskie"          "Nelson"            "Ragatz"
[178] "el-Sayed"          "Brackett"          "Stuber"
[181] "Wisda"             "Bandy"             "Hanna"
[184] "Geisick"           "Camann"            "Orton"
[187] "Tefertiller"       "Weathers"          "Lindsey"
[190] "Scheideler"        "Frye"              "Atkinson"
[193] "Johnson"           "Bayer"             "Heusser"
[196] "Griffin"           "el-Doud"           "Guerra"
[199] "al-Atallah"        "Miller III"
```

```r
#tibble and [ always returns tibble
#tibble and [[ always returns vector
#data.frame and [ may return data.frame or vector
#data.frame and [[ always returns vector
rawdata_df <- as.data.frame(rawdata)
rawdata[2] #returns Tibble with 1 column
```

```
# A tibble: 200 x 1
   Sex
   <chr>
 1 male
 2 male
 3 male
 4 male
 5 male
 6 male
 7 female
```

```
 8 male
 9 female
10 male
# i 190 more rows
```

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

```
  [1] "male"   "male"   "male"   "male"   "male"   "male"   "female" "male"
  [9] "female" "male"   "male"   "male"   "female" "female" "male"   "male"
 [17] "male"   "female" "male"   "male"   "male"   "male"   "male"   "female"
 [25] "female" "male"   "male"   "male"   "male"   "male"   "male"   "male"
 [33] "male"   "male"   "male"   "male"   "male"   "female" "female" "male"
 [41] "female" "female" "female" "male"   "male"   "male"   "male"   "male"
 [49] "male"   "male"   "female" "male"   "male"   "female" "male"   "female"
 [57] "female" "male"   "male"   "male"   "male"   "male"   "female" "female"
 [65] "female" "female" "female" "male"   "male"   "male"   "male"   "male"
 [73] "female" "male"   "male"   "male"   "female" "male"   "female" "male"
 [81] "female" "male"   "female" "female" "female" "male"   "male"   "male"
 [89] "male"   "male"   "female" "male"   "female" "female" "female" "male"
 [97] "male"   "male"   "female" "female" "male"   "female" "male"   "male"
[105] "male"   "female" "female" "male"   "female" "male"   "female" "male"
[113] "male"   "male"   "male"   "female" "female" "female" "female" "male"
[121] "male"   "female" "male"   "male"   "male"   "male"   "male"   "male"
[129] "female" "male"   "female" "male"   "male"   "female" "male"   "male"
[137] "male"   "female" "male"   "male"   "female" "male"   "male"   "male"
[145] "male"   "male"   "male"   "male"   "male"   "female" "female" "male"
[153] "male"   "male"   "male"   "male"   "female" "male"   "male"   "male"
[161] "male"   "female" "male"   "male"   "male"   "female" "male"   "female"
[169] "male"   "female" "female" "male"   "male"   "male"   "male"   "female"
[177] "male"   "male"   "male"   "male"   "female" "male"   "female" "male"
[185] "female" "male"   "male"   "male"   "female" "male"   "male"   "male"
[193] "male"   "male"   "male"   "male"   "male"   "male"   "male"   "male"
```

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

```
# A tibble: 200 x 1
   Sex
   <chr>
 1 male
```

```
 2 male
 3 male
 4 male
 5 male
 6 male
 7 female
 8 male
 9 female
10 male
# i 190 more rows
```

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

```
# A tibble: 200 x 2
   Sex    Ethnicity
   <chr>  <fct>
 1 male   White (not Hispanic)
 2 male   White (not Hispanic)
 3 male   Middle-Eastern, Arabic
 4 male   White (not Hispanic)
 5 male   American Indian or Native Alaskan
 6 male   White (not Hispanic)
 7 female White (not Hispanic)
 8 male   Hispanic
 9 female Middle-Eastern, Arabic
10 male   White (not Hispanic)
# i 190 more rows
```

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

```
       Sex
1     male
2     male
3     male
4     male
5     male
6     male
7   female
8     male
```

```
9   female
10    male
11    male
12    male
13  female
14  female
15    male
16    male
17    male
18  female
19    male
20    male
21    male
22    male
23    male
24  female
25  female
26    male
27    male
28    male
29    male
30    male
31    male
32    male
33    male
34    male
35    male
36    male
37    male
38  female
39  female
40    male
41  female
42  female
43  female
44    male
45    male
46    male
47    male
48    male
49    male
50    male
51  female
```

```
52    male
53    male
54  female
55    male
56  female
57  female
58    male
59    male
60    male
61    male
62    male
63  female
64  female
65  female
66  female
67  female
68    male
69    male
70    male
71    male
72    male
73  female
74    male
75    male
76    male
77  female
78    male
79  female
80    male
81  female
82    male
83  female
84  female
85  female
86    male
87    male
88    male
89    male
90    male
91  female
92    male
93  female
94  female
```

```
95  female
96    male
97    male
98    male
99  female
100 female
101   male
102 female
103   male
104   male
105   male
106 female
107 female
108   male
109 female
110   male
111 female
112   male
113   male
114   male
115   male
116 female
117 female
118 female
119 female
120   male
121   male
122 female
123   male
124   male
125   male
126   male
127   male
128   male
129 female
130   male
131 female
132   male
133   male
134 female
135   male
136   male
137   male
```

```
138 female
139   male
140   male
141 female
142   male
143   male
144   male
145   male
146   male
147   male
148   male
149   male
150 female
151 female
152   male
153   male
154   male
155   male
156   male
157 female
158   male
159   male
160   male
161   male
162 female
163   male
164   male
165   male
166 female
167   male
168 female
169   male
170 female
171 female
172   male
173   male
174   male
175   male
176 female
177   male
178   male
179   male
180   male
```

```
181 female
182   male
183 female
184   male
185 female
186   male
187   male
188   male
189 female
190   male
191   male
192   male
193   male
194   male
195   male
196   male
197   male
198   male
199   male
200   male
```

```
rawdata_df[[2]] #returns vector
```

```
  [1] "male"   "male"   "male"   "male"   "male"   "male"   "female" "male"
  [9] "female" "male"   "male"   "male"   "female" "female" "male"   "male"
 [17] "male"   "female" "male"   "male"   "male"   "male"   "male"   "female"
 [25] "female" "male"   "male"   "male"   "male"   "male"   "male"   "male"
 [33] "male"   "male"   "male"   "male"   "male"   "female" "female" "male"
 [41] "female" "female" "female" "male"   "male"   "male"   "male"   "male"
 [49] "male"   "male"   "female" "male"   "male"   "female" "male"   "female"
 [57] "female" "male"   "male"   "male"   "male"   "male"   "female" "female"
 [65] "female" "female" "female" "male"   "male"   "male"   "male"   "male"
 [73] "female" "male"   "male"   "male"   "female" "male"   "female" "male"
 [81] "female" "male"   "female" "female" "female" "male"   "male"   "male"
 [89] "male"   "male"   "female" "male"   "female" "female" "female" "male"
 [97] "male"   "male"   "female" "female" "male"   "female" "male"   "male"
[105] "male"   "female" "female" "male"   "female" "male"   "female" "male"
[113] "male"   "male"   "male"   "female" "female" "female" "female" "male"
[121] "male"   "female" "male"   "male"   "male"   "male"   "male"   "male"
[129] "female" "male"   "female" "male"   "male"   "female" "male"   "male"
[137] "male"   "female" "male"   "male"   "female" "male"   "male"   "male"
```

```
[145] "male"   "male"   "male"   "male"   "male"   "female" "female" "male"
[153] "male"   "male"   "male"   "male"   "female" "male"   "male"   "male"
[161] "male"   "female" "male"   "male"   "male"   "female" "male"   "female"
[169] "male"   "female" "female" "male"   "male"   "male"   "male"   "female"
[177] "male"   "male"   "male"   "male"   "female" "male"   "female" "male"
[185] "female" "male"   "male"   "male"   "female" "male"   "male"   "male"
[193] "male"   "male"   "male"   "male"   "male"   "male"   "male"   "male"
```

```
rawdata_df[,2] #returns vector
```

```
  [1] "male"   "male"   "male"   "male"   "male"   "male"   "female" "male"
  [9] "female" "male"   "male"   "male"   "female" "female" "male"   "male"
 [17] "male"   "female" "male"   "male"   "male"   "male"   "male"   "female"
 [25] "female" "male"   "male"   "male"   "male"   "male"   "male"   "male"
 [33] "male"   "male"   "male"   "male"   "male"   "female" "female" "male"
 [41] "female" "female" "female" "male"   "male"   "male"   "male"   "male"
 [49] "male"   "male"   "female" "male"   "male"   "female" "male"   "female"
 [57] "female" "male"   "male"   "male"   "male"   "male"   "female" "female"
 [65] "female" "female" "female" "male"   "male"   "male"   "male"   "male"
 [73] "female" "male"   "male"   "male"   "female" "male"   "female" "male"
 [81] "female" "male"   "female" "female" "female" "male"   "male"   "male"
 [89] "male"   "male"   "female" "male"   "female" "female" "female" "male"
 [97] "male"   "male"   "female" "female" "male"   "female" "male"   "male"
[105] "male"   "female" "female" "male"   "female" "male"   "female" "male"
[113] "male"   "male"   "male"   "female" "female" "female" "female" "male"
[121] "male"   "female" "male"   "male"   "male"   "male"   "male"   "male"
[129] "female" "male"   "female" "male"   "male"   "female" "male"   "male"
[137] "male"   "female" "male"   "male"   "female" "male"   "male"   "male"
[145] "male"   "male"   "male"   "male"   "male"   "female" "female" "male"
[153] "male"   "male"   "male"   "male"   "female" "male"   "male"   "male"
[161] "male"   "female" "male"   "male"   "male"   "female" "male"   "female"
[169] "male"   "female" "female" "male"   "male"   "male"   "male"   "female"
[177] "male"   "male"   "male"   "male"   "female" "male"   "female" "male"
[185] "female" "male"   "male"   "male"   "female" "male"   "male"   "male"
[193] "male"   "male"   "male"   "male"   "male"   "male"   "male"   "male"
```

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

```
     Sex                          Ethnicity
```

```
1     male              White (not Hispanic)
2     male              White (not Hispanic)
3     male           Middle-Eastern, Arabic
4     male              White (not Hispanic)
5     male American Indian or Native Alaskan
6     male              White (not Hispanic)
7   female              White (not Hispanic)
8     male                           Hispanic
9   female           Middle-Eastern, Arabic
10    male              White (not Hispanic)
11    male              White (not Hispanic)
12    male              White (not Hispanic)
13  female              White (not Hispanic)
14  female              White (not Hispanic)
15    male              White (not Hispanic)
16    male              White (not Hispanic)
17    male              White (not Hispanic)
18  female           Middle-Eastern, Arabic
19    male              White (not Hispanic)
20    male              White (not Hispanic)
21    male              White (not Hispanic)
22    male              White (not Hispanic)
23    male              White (not Hispanic)
24  female              White (not Hispanic)
25  female              White (not Hispanic)
26    male              White (not Hispanic)
27    male              White (not Hispanic)
28    male              White (not Hispanic)
29    male              White (not Hispanic)
30    male           Middle-Eastern, Arabic
31    male              White (not Hispanic)
32    male                           Hispanic
33    male              White (not Hispanic)
34    male           Middle-Eastern, Arabic
35    male              White (not Hispanic)
36    male              Black (not Hispanic)
37    male           Middle-Eastern, Arabic
38  female              White (not Hispanic)
39  female              White (not Hispanic)
40    male           Middle-Eastern, Arabic
41  female              White (not Hispanic)
42  female           Middle-Eastern, Arabic
43  female              White (not Hispanic)
```

```
44    male              White (not Hispanic)
45    male              White (not Hispanic)
46    male              White (not Hispanic)
47    male              White (not Hispanic)
48    male              White (not Hispanic)
49    male              White (not Hispanic)
50    male              Black (not Hispanic)
51  female American Indian or Native Alaskan
52    male              White (not Hispanic)
53    male              White (not Hispanic)
54  female            Middle-Eastern, Arabic
55    male              White (not Hispanic)
56  female              White (not Hispanic)
57  female              White (not Hispanic)
58    male              White (not Hispanic)
59    male              White (not Hispanic)
60    male            Middle-Eastern, Arabic
61    male              White (not Hispanic)
62    male              White (not Hispanic)
63  female            Middle-Eastern, Arabic
64  female              White (not Hispanic)
65  female              White (not Hispanic)
66  female              White (not Hispanic)
67  female              White (not Hispanic)
68    male            Middle-Eastern, Arabic
69    male              White (not Hispanic)
70    male              Black (not Hispanic)
71    male              White (not Hispanic)
72    male              White (not Hispanic)
73  female              White (not Hispanic)
74    male              White (not Hispanic)
75    male              White (not Hispanic)
76    male            Middle-Eastern, Arabic
77  female              White (not Hispanic)
78    male            Middle-Eastern, Arabic
79  female            Middle-Eastern, Arabic
80    male              White (not Hispanic)
81  female              White (not Hispanic)
82    male              White (not Hispanic)
83  female            Middle-Eastern, Arabic
84  female              White (not Hispanic)
85  female              White (not Hispanic)
86    male              White (not Hispanic)
```

```
87    male              White (not Hispanic)
88    male              Black (not Hispanic)
89    male              White (not Hispanic)
90    male              White (not Hispanic)
91  female              White (not Hispanic)
92    male            Middle-Eastern, Arabic
93  female              White (not Hispanic)
94  female              Black (not Hispanic)
95  female              White (not Hispanic)
96    male            Middle-Eastern, Arabic
97    male              White (not Hispanic)
98    male              Black (not Hispanic)
99  female              White (not Hispanic)
100 female              White (not Hispanic)
101   male              White (not Hispanic)
102 female            Middle-Eastern, Arabic
103   male              White (not Hispanic)
104   male              White (not Hispanic)
105   male              White (not Hispanic)
106 female              White (not Hispanic)
107 female            Middle-Eastern, Arabic
108   male            Middle-Eastern, Arabic
109 female              White (not Hispanic)
110   male              White (not Hispanic)
111 female              White (not Hispanic)
112   male              White (not Hispanic)
113   male            Middle-Eastern, Arabic
114   male              White (not Hispanic)
115   male              Black (not Hispanic)
116 female American Indian or Native Alaskan
117 female              White (not Hispanic)
118 female              White (not Hispanic)
119 female              White (not Hispanic)
120   male            Middle-Eastern, Arabic
121   male              Black (not Hispanic)
122 female              White (not Hispanic)
123   male              White (not Hispanic)
124   male              White (not Hispanic)
125   male              White (not Hispanic)
126   male            Middle-Eastern, Arabic
127   male              Black (not Hispanic)
128   male              White (not Hispanic)
129 female              White (not Hispanic)
```

```
130   male            Middle-Eastern, Arabic
131 female                         Hispanic
132   male              White (not Hispanic)
133   male              White (not Hispanic)
134 female              White (not Hispanic)
135   male              White (not Hispanic)
136   male              White (not Hispanic)
137   male              White (not Hispanic)
138 female              White (not Hispanic)
139   male              White (not Hispanic)
140   male              White (not Hispanic)
141 female         Asian or Pacific Islander
142   male              White (not Hispanic)
143   male              White (not Hispanic)
144   male              White (not Hispanic)
145   male              White (not Hispanic)
146   male              White (not Hispanic)
147   male            Middle-Eastern, Arabic
148   male              White (not Hispanic)
149   male            Middle-Eastern, Arabic
150 female              White (not Hispanic)
151 female              White (not Hispanic)
152   male              White (not Hispanic)
153   male              White (not Hispanic)
154   male              White (not Hispanic)
155   male            Middle-Eastern, Arabic
156   male            Middle-Eastern, Arabic
157 female              White (not Hispanic)
158   male              White (not Hispanic)
159   male              White (not Hispanic)
160   male              White (not Hispanic)
161   male              White (not Hispanic)
162 female            Middle-Eastern, Arabic
163   male              Black (not Hispanic)
164   male              White (not Hispanic)
165   male              White (not Hispanic)
166 female              White (not Hispanic)
167   male              White (not Hispanic)
168 female              White (not Hispanic)
169   male              White (not Hispanic)
170 female              White (not Hispanic)
171 female              White (not Hispanic)
172   male              White (not Hispanic)
```

```
173   male                          Hispanic
174   male              White (not Hispanic)
175   male              White (not Hispanic)
176 female              White (not Hispanic)
177   male              White (not Hispanic)
178   male            Middle-Eastern, Arabic
179   male              White (not Hispanic)
180   male              White (not Hispanic)
181 female              White (not Hispanic)
182   male              White (not Hispanic)
183 female              White (not Hispanic)
184   male              White (not Hispanic)
185 female              White (not Hispanic)
186   male              White (not Hispanic)
187   male              White (not Hispanic)
188   male              White (not Hispanic)
189 female              White (not Hispanic)
190   male              White (not Hispanic)
191   male              White (not Hispanic)
192   male              White (not Hispanic)
193   male              Black (not Hispanic)
194   male              White (not Hispanic)
195   male              White (not Hispanic)
196   male              White (not Hispanic)
197   male            Middle-Eastern, Arabic
198   male                          Hispanic
199   male            Middle-Eastern, Arabic
200   male              White (not Hispanic)
```

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

```
# A tibble: 200 x 6
   PatID Sex    Ethnicity                          `sysRR (mmHg)` diaRR    HR
   <chr> <chr>  <fct>                                       <dbl> <dbl> <dbl>
 1 P 1   male   White (not Hispanic)                           122    52    93
 2 P 2   male   White (not Hispanic)                           118    75   103
 3 P 3   male   Middle-Eastern, Arabic                         107    79    83
 4 P 4   male   White (not Hispanic)                           135    81    87
 5 P 5   male   American Indian or Native Alaskan              138    69   105
 6 P 6   male   White (not Hispanic)                           142    56    90
 7 P 7   female White (not Hispanic)                           103    72    89
```

```
 8 P 8   male   Hispanic                                  138    81    88
 9 P 9   female Middle-Eastern, Arabic                    129    78    92
10 P 10  male   White (not Hispanic)                      134    54    97
# i 190 more rows
```

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

```
# A tibble: 5 x 6
  PatID Sex   Ethnicity                          `sysRR (mmHg)` diaRR    HR
  <chr> <chr> <fct>                                       <dbl> <dbl> <dbl>
1 P 1   male  White (not Hispanic)                         122    52    93
2 P 2   male  White (not Hispanic)                         118    75   103
3 P 3   male  Middle-Eastern, Arabic                      107    79    83
4 P 4   male  White (not Hispanic)                         135    81    87
5 P 5   male  American Indian or Native Alaskan           138    69   105
```

```
rawdata %>% select(contains('RR',ignore.case = F))
```

```
# A tibble: 200 x 2
   `sysRR (mmHg)` diaRR
            <dbl> <dbl>
 1            122    52
 2            118    75
 3            107    79
 4            135    81
 5            138    69
 6            142    56
 7            103    72
 8            138    81
 9            129    78
10            134    54
# i 190 more rows
```

```
rawdata %>% select(ends_with('r'))
```

```
# A tibble: 200 x 2
   diaRR    HR
```

```
   <dbl> <dbl>
 1    52    93
 2    75   103
 3    79    83
 4    81    87
 5    69   105
 6    56    90
 7    72    89
 8    81    88
 9    78    92
10    54    97
# i 190 more rows
```

```
rawdata %>% select(-contains('name'))
```

```
# A tibble: 200 x 7
   PatID Sex    Ethnicity                  Treatment `sysRR (mmHg)` diaRR    HR
   <chr> <chr>  <fct>                      <chr>              <dbl> <dbl> <dbl>
 1 P 1   male   White (not Hispanic)       Verum                122    52    93
 2 P 2   male   White (not Hispanic)       Verum                118    75   103
 3 P 3   male   Middle-Eastern, Arabic     Verum                107    79    83
 4 P 4   male   White (not Hispanic)       Placebo              135    81    87
 5 P 5   male   American Indian or Native ~ Verum                138    69   105
 6 P 6   male   White (not Hispanic)       Verum                142    56    90
 7 P 7   female White (not Hispanic)       Verum                103    72    89
 8 P 8   male   Hispanic                   Placebo              138    81    88
 9 P 9   female Middle-Eastern, Arabic     Verum                129    78    92
10 P 10  male   White (not Hispanic)       Verum                134    54    97
# i 190 more rows
```

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

```
# A tibble: 200 x 1
   `sysRR (mmHg)`
            <dbl>
 1            122
 2            118
 3            107
 4            135
```

```
 5            138
 6            142
 7            103
 8            138
 9            129
10            134
# i 190 more rows
```

```
rawdata %>% select(contains('r'),-contains('rr'))
```

```
# A tibble: 200 x 2
   Treatment    HR
   <chr>     <dbl>
 1 Verum        93
 2 Verum       103
 3 Verum        83
 4 Placebo      87
 5 Verum       105
 6 Verum        90
 7 Verum        89
 8 Placebo      88
 9 Verum        92
10 Verum        97
# i 190 more rows
```

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

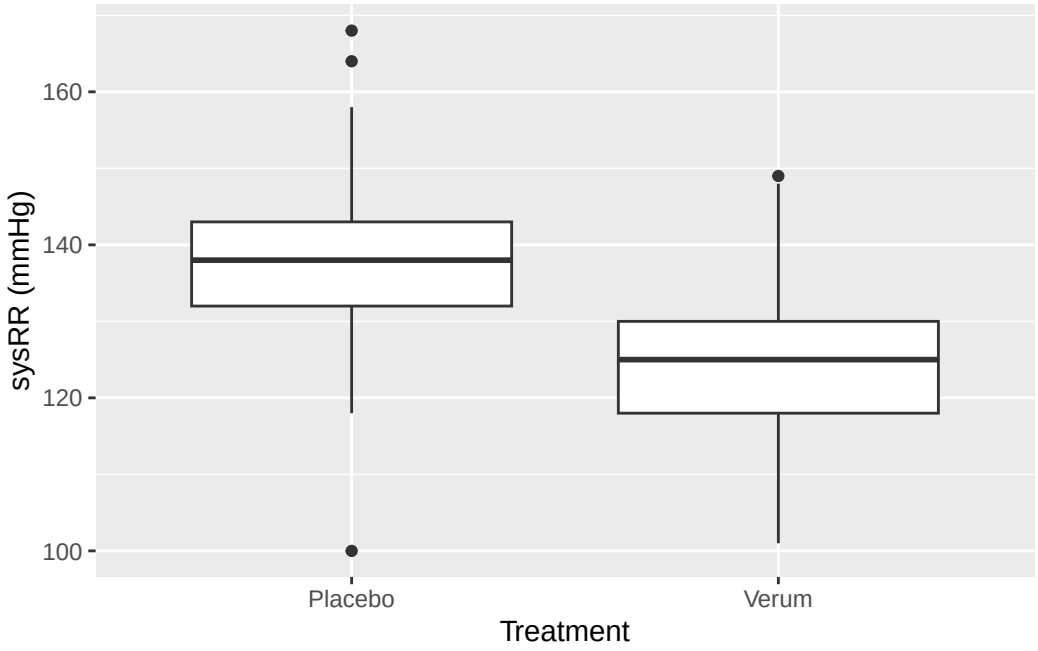
```
  [1] 122 118 107 135 138 142 103 138 129 134 128 122 115 118 143 135 137 142
 [19] 145 137 127 130 141 135 133 154 144 107 116 142 130 118 129 129 119 142
 [37] 126 139 121 118 117 139 122 144 114 137 115 140 132 133 117 114 132 142
 [55] 123 149 125 151 113 158 118 130 132 142 133 129 139 147 143 153 126 150
 [73] 122 137 135 129 133 121 109 122 128 133 131 122 126 122 117 148 126 110
 [91] 135 132 129 118 133 141 125 128 125 125 131 101 121 124 126 140 138 142
[109] 130 146 137 114 134 118 148 131 122 140 149 147 128 129 143 147 136 141
[127] 129 124 138 100 119 119 131 138 136 118 125 119 114 135 130 118 121 127
[145] 139 140 149 141 148 127 145 168 164 131 112 138 146 142 132 135 137 117
[163] 146 128 134 118 142 139 136 125 131 138 125 156 138 126 121 142 127 138
[181] 148 117 131 122 128 130 120 125 143 120 130 111 138 118 124 107 142 135
[199] 142 147
```

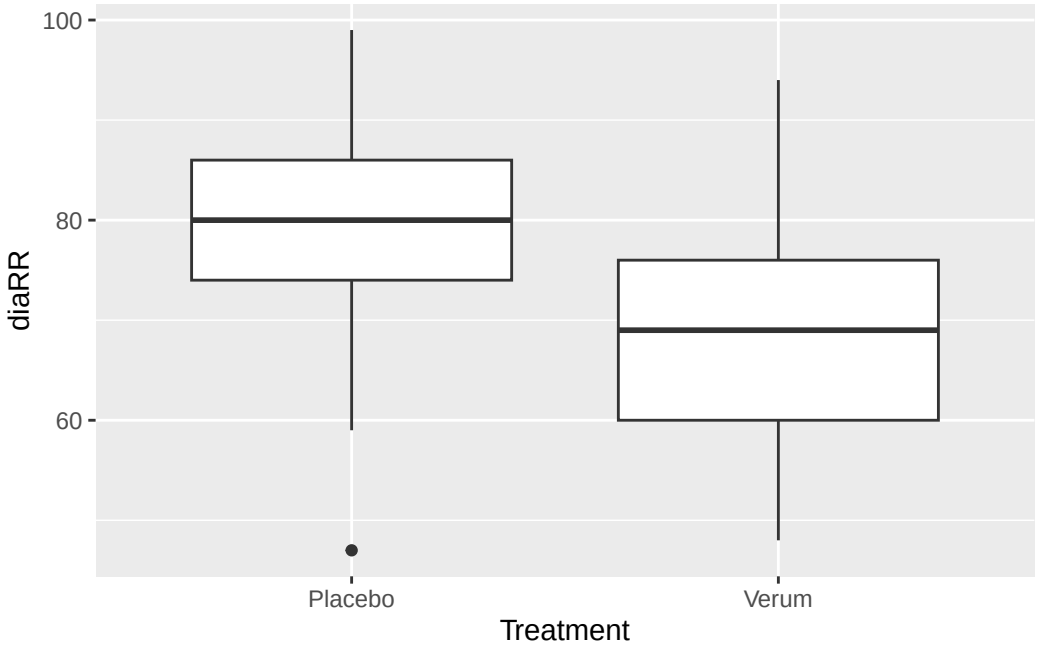
```
  testvars <- FindVars(varnames = c('Eth','Sex','R'))
  rawdata %>% select(testvars$index)
```

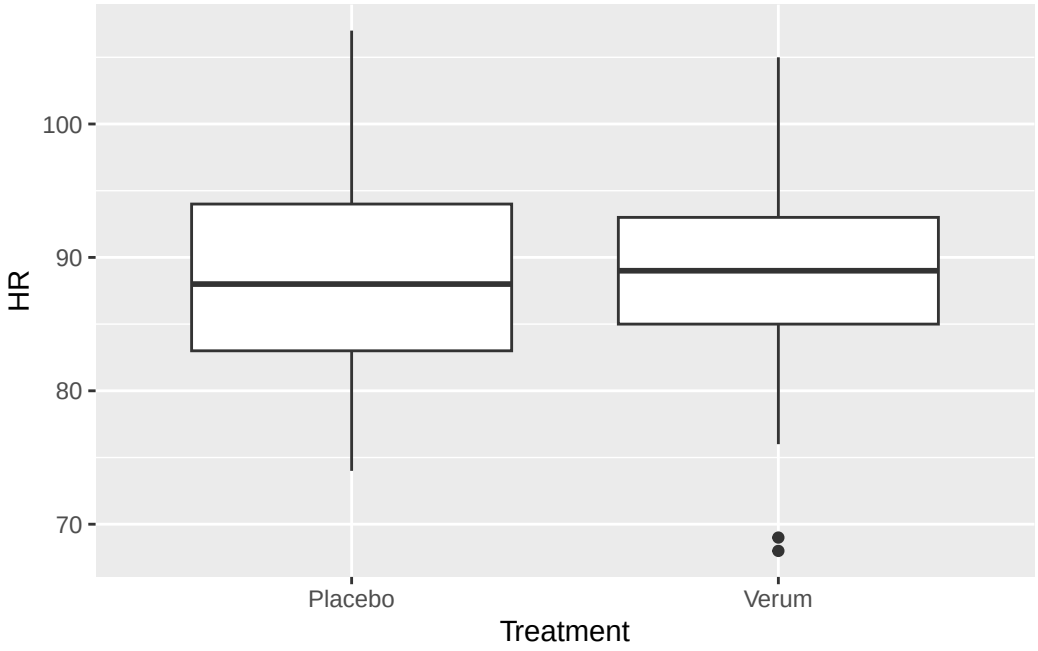
```
# A tibble: 200 x 5
   Sex    Ethnicity                          `sysRR (mmHg)` diaRR    HR
   <chr>  <fct>                                       <dbl> <dbl> <dbl>
 1 male   White (not Hispanic)                          122    52    93
 2 male   White (not Hispanic)                          118    75   103
 3 male   Middle-Eastern, Arabic                       107    79    83
 4 male   White (not Hispanic)                          135    81    87
 5 male   American Indian or Native Alaskan             138    69   105
 6 male   White (not Hispanic)                          142    56    90
 7 female White (not Hispanic)                          103    72    89
 8 male   Hispanic                                      138    81    88
 9 female Middle-Eastern, Arabic                       129    78    92
10 male   White (not Hispanic)                          134    54    97
# i 190 more rows
```

```
  normvars <- FindVars(varnames = c('R'))
  for(var_i in 3:5){
    print(ggplot(rawdata,aes_string(x = 'Treatment',
                                    y = testvars$bticked[var_i]))+
            geom_boxplot())
  }
```

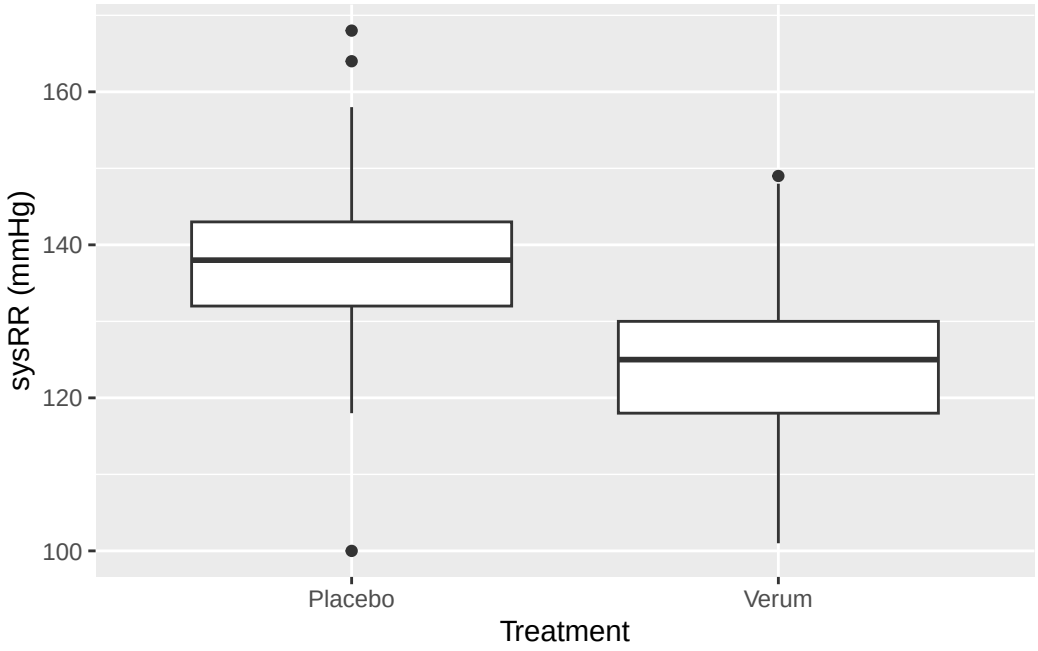
```
Warning: `aes_string()` was deprecated in ggplot2 3.0.0.
i Please use tidy evaluation idioms with `aes()`.
i See also `vignette("ggplot2-in-packages")` for more information.
```

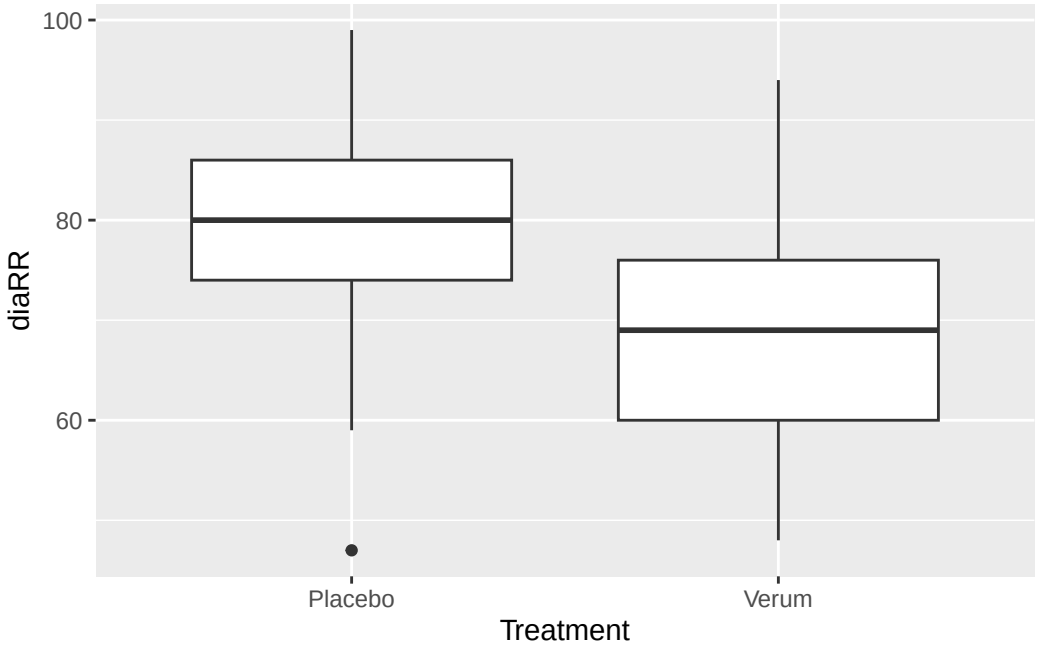

160
140
120
100
sysRR (mmHg)
Placebo
Verum
Treatment

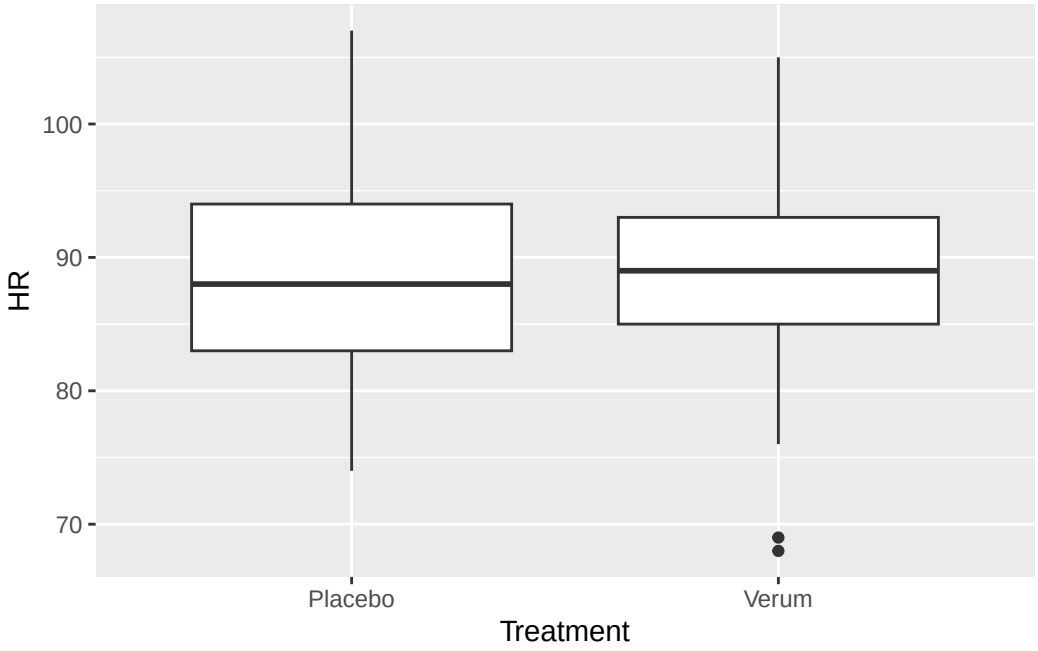

100
80
60
diaRR
Placebo
Verum
Treatment




```
for(var_i in testvars$bticked[3:5]){
  print(ggplot(rawdata,aes_string(x = 'Treatment',
                                  y = var_i))+
          geom_boxplot())
}
```


160
140
120
100
sysRR (mmHg)
Placebo
Verum
Treatment


100
80
60
diaRR
Placebo
Verum
Treatment




```
# Example cruet_stand / Gewürzmenage
n_elements <- 5*10^3
# tibble menage with columns saltshaker, peppercaster and n_elements each
# saltgrain and pepperflake
# print saltshaker
# print salt
# print 100 saltgrain




### functions ####
#FunctionName<-function(parameters...){definition}
markSign<-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)
}

markSign(SignIn=0.035)
```

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

```
markSign(SignIn="0.35")
```

```
[1] "n.s."
```

```
markSign(SignIn = 'p=3,5%')   #wrong parameter
```

```
Warning in markSign(SignIn = "p=3,5%"): NAs durch Umwandlung erzeugt
```

```
[1] "wrong input, stupido!"
```

```
Mymean<-function(werte)
{
  return(base::mean(werte,na.rm=T))
}
# source('myfunctions.R')
### loops ####
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
```

```
  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"
```

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

```
  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] 101.24498 100.99285 101.09999 101.61369 102.98353 101.03886  99.45161
 [8] 100.01835  99.21011  99.69732  98.62364 100.72063 102.18361 101.03190
[15] 100.82017 104.20466 102.23494 101.30330  97.56465 105.26693 103.41743
[22]  95.74379  99.40701 102.37993  98.13016  98.32520 100.17701  96.45507
[29] 105.83716  98.36719  98.09867 103.31457 101.72139 101.91318 103.57645
[36]  98.75810 100.27766 100.88864 102.97018 103.19208 101.93671  99.05340
[43] 100.19505  99.80348 100.35903 103.65700  99.19059  96.47964  98.77878
[50]  99.98729
```

```
  for(col_i in 1:length(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"
[1] "HR"
```

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

```r
for(col_i in seq_len(0)){
  print(colnames(rawdata)[col_i])
}


test <- 0
while(test<100){
  print(test)
  test   <- test + 1 #test <- test+1
}
```

```
[1] 0
[1] 1
[1] 2
[1] 3
[1] 4
[1] 5
[1] 6
[1] 7
[1] 8
[1] 9
[1] 10
[1] 11
[1] 12
[1] 13
[1] 14
[1] 15
[1] 16
[1] 17
[1] 18
[1] 19
```

```
[1] 20
[1] 21
[1] 22
[1] 23
[1] 24
[1] 25
[1] 26
[1] 27
[1] 28
[1] 29
[1] 30
[1] 31
[1] 32
[1] 33
[1] 34
[1] 35
[1] 36
[1] 37
[1] 38
[1] 39
[1] 40
[1] 41
[1] 42
[1] 43
[1] 44
[1] 45
[1] 46
[1] 47
[1] 48
[1] 49
[1] 50
[1] 51
[1] 52
[1] 53
[1] 54
[1] 55
[1] 56
[1] 57
[1] 58
[1] 59
[1] 60
[1] 61
[1] 62
```

```
[1] 63
[1] 64
[1] 65
[1] 66
[1] 67
[1] 68
[1] 69
[1] 70
[1] 71
[1] 72
[1] 73
[1] 74
[1] 75
[1] 76
[1] 77
[1] 78
[1] 79
[1] 80
[1] 81
[1] 82
[1] 83
[1] 84
[1] 85
[1] 86
[1] 87
[1] 88
[1] 89
[1] 90
[1] 91
[1] 92
[1] 93
[1] 94
[1] 95
[1] 96
[1] 97
[1] 98
[1] 99
```

```r
### conditions -----
sex<-'male'
if (sex=='male')  {
```

```
  print('Male')
} else {
  print('Female')
}
```

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

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

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

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

```
if (sex!='male') {
  print('not male')
} else {
  print('male')
}
```

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

```
if (!sex=='male') {
  print('not male')
} else {
  print('male')
}
```

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

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

```
[1] "is male"
```

```
p <- .0012
paste0('That is ',
       ifelse(test = p<=.05,yes = '',no = 'not '),
       'significant')
```

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

```
testvar <- 3
if(testvar %in% c(1,3,5)){
  print('uneven')
}
```

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

```
TRUE&FALSE
```

```
[1] FALSE
```

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

```
[1] FALSE
```

```
TRUE|FALSE
```

```
[1] TRUE
```

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

```
[1] TRUE
```

```
#case_when

### useful tools -----
?any
?'%in%'
2%in%1:5
```

```
[1] TRUE
```

```
2%in%c(1,3,4,5)
```

```
[1] FALSE
```

3 Importing data

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

3.2 Import from Excel

3.2.1 Tidy Excel files

3.2.2 Dirty Excel files

3.3 Import from SPSS

3.4 Import from SAS

4 Grouping of variables by type / distribution / use

```
pacman::p_load(wrappedtools)
```

```
load('data/testdata.RData')
quantvars <- ColSeeker(data = rawdata,
                       varclass = "numeric",
                       exclude = "code")
gaussvars <- ColSeeker(namepattern = c("si","we","BMI","BP","mri"))

ordvars <- ColSeeker(namepattern = c("age","lab"))

factvars <- ColSeeker(namepattern = c("sex","med","NYHA"),
                      returnclass = TRUE)
save(rawdata,list = ls(pattern = "vars"),file = "data/testdata.RData")
```

5 Visualize data with ggplot

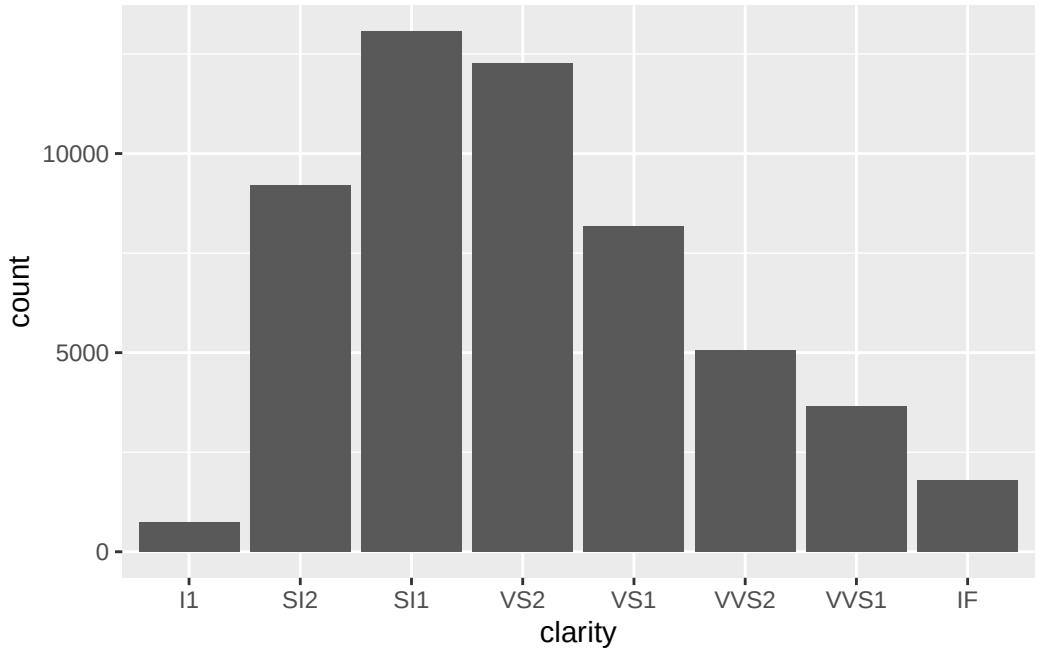
```
pacman::p_load(tidyverse,#plotrix,
               grid,gridExtra,car,
               ggsci,ggsignif, ggthemes, ggridges,
               gganimate,ggforce,
               # survival, survminer,
               ggdendro, ggbeeswarm,
               rpart,rpart.plot,
               gapminder,
               wrappedtools)

#sample data
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
```

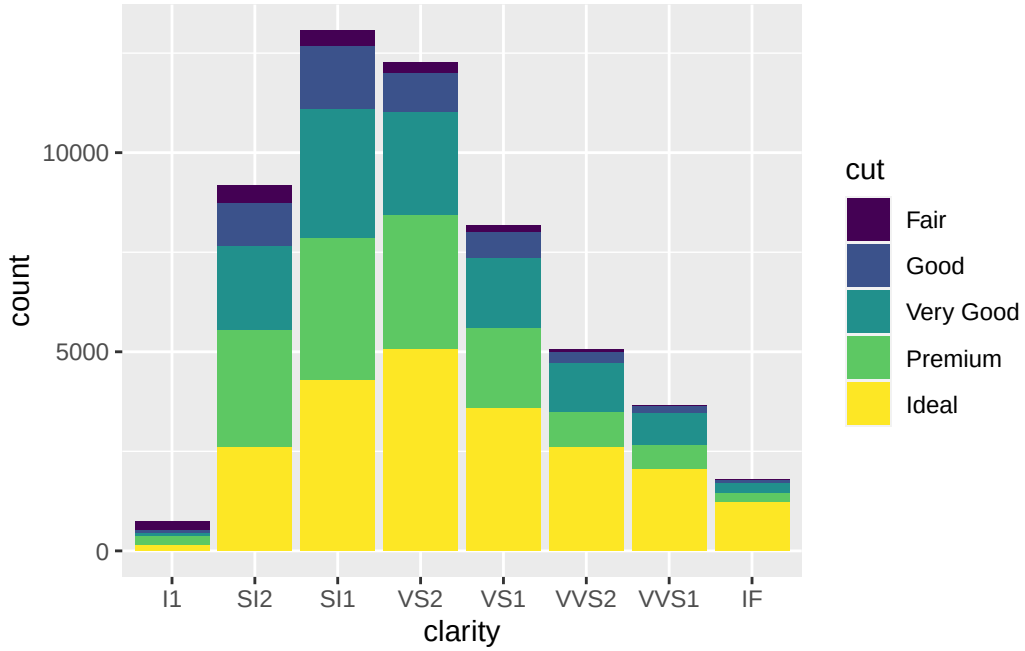
```
head(mtcars)
```

```
                   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
```

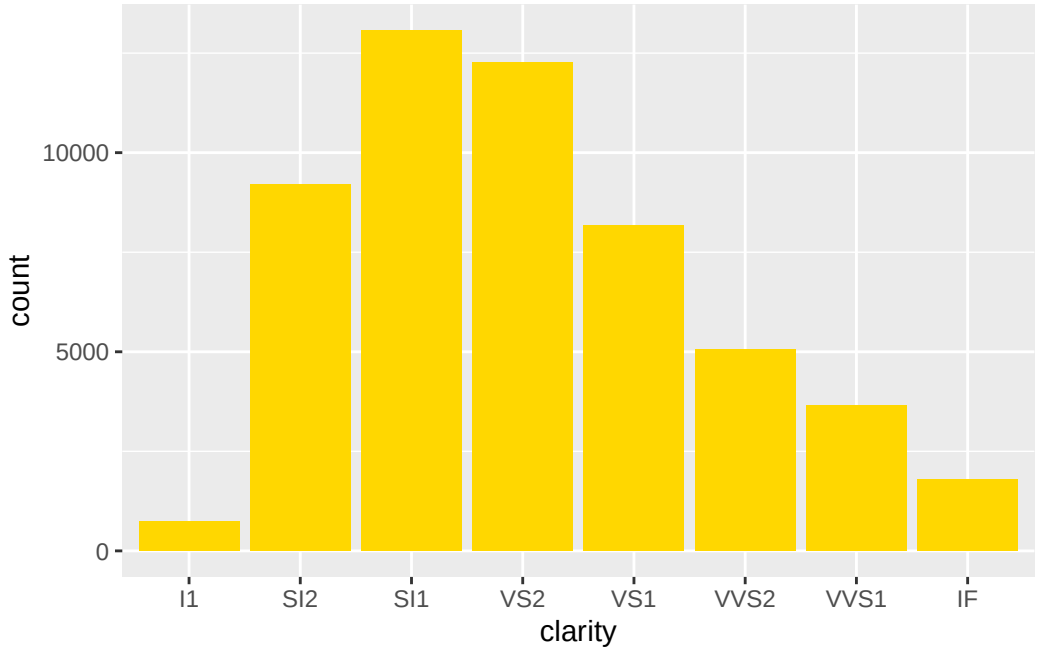
```r
ggplot(data=diamonds,mapping = aes(x=clarity))+
  geom_bar()
```



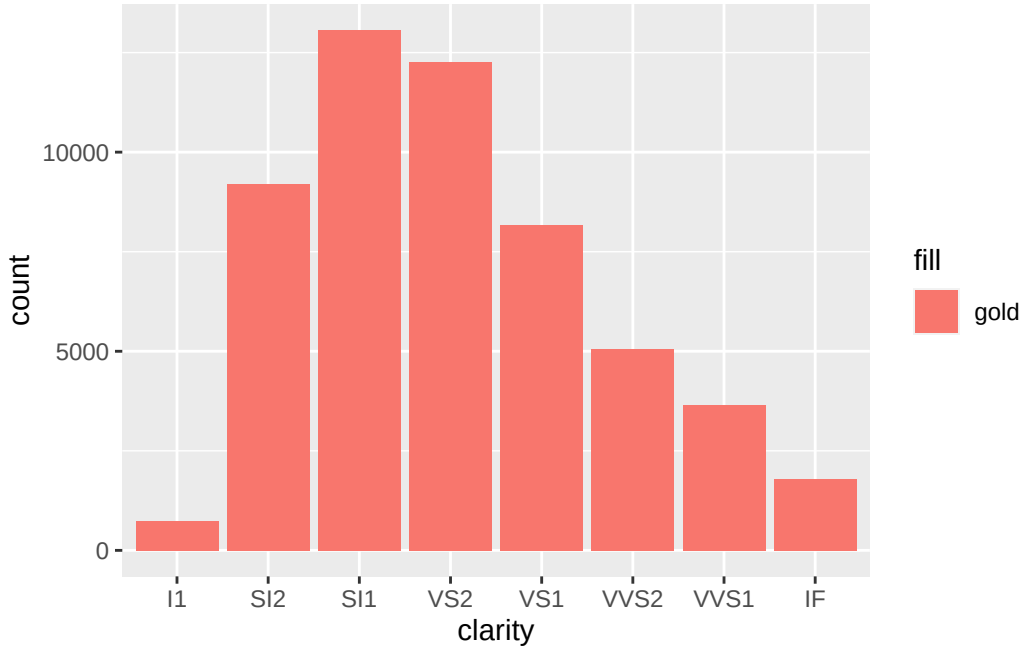

```r
#define aesthetics
ggplot(data=diamonds,aes(x=clarity,fill=cut))+
  geom_bar()
```



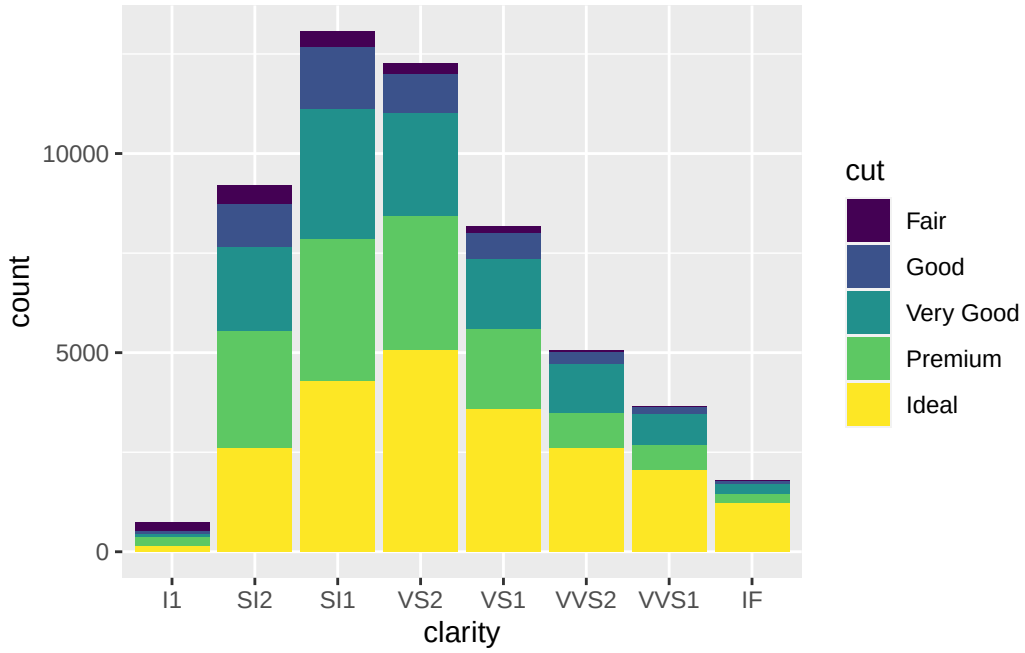

```
#aesthetics outside aes
ggplot(data=diamonds,aes(x=clarity))+
  geom_bar(fill='gold')
```



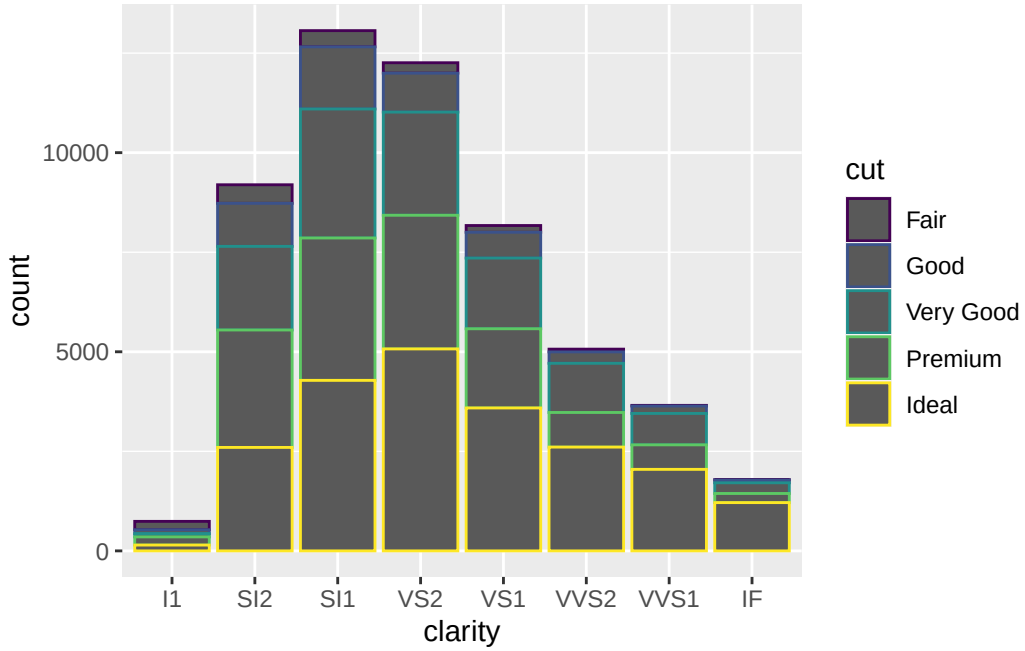

```
ggplot(data=diamonds,aes(x=clarity))+
  geom_bar(aes(fill='gold')) #should be outside aes!
```



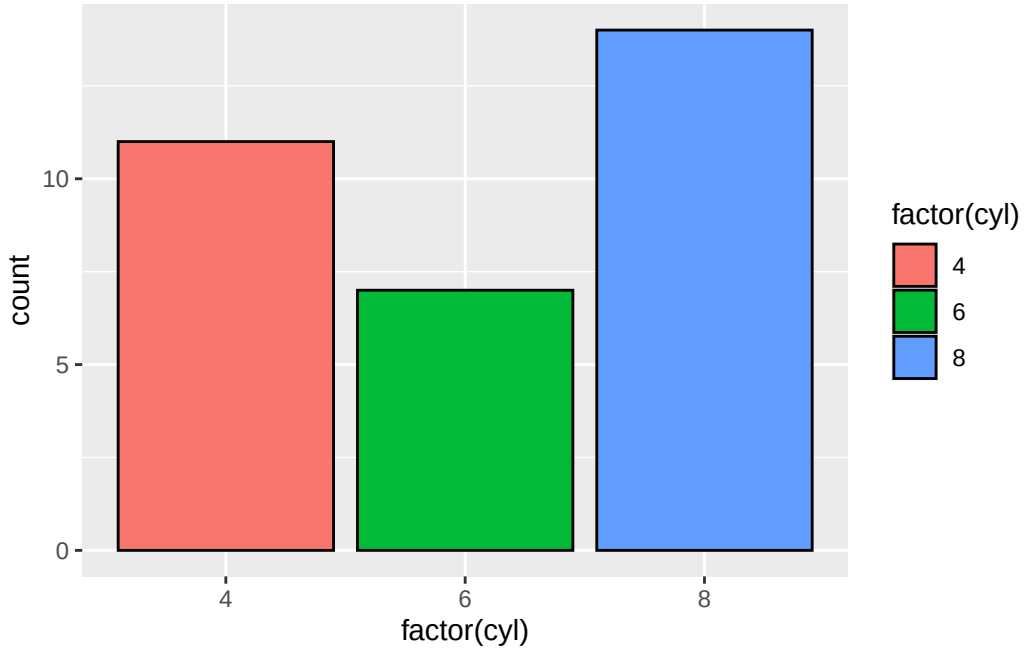
```
ggplot(data=diamonds,aes(x=clarity))+
  geom_bar(aes(fill=cut))
```



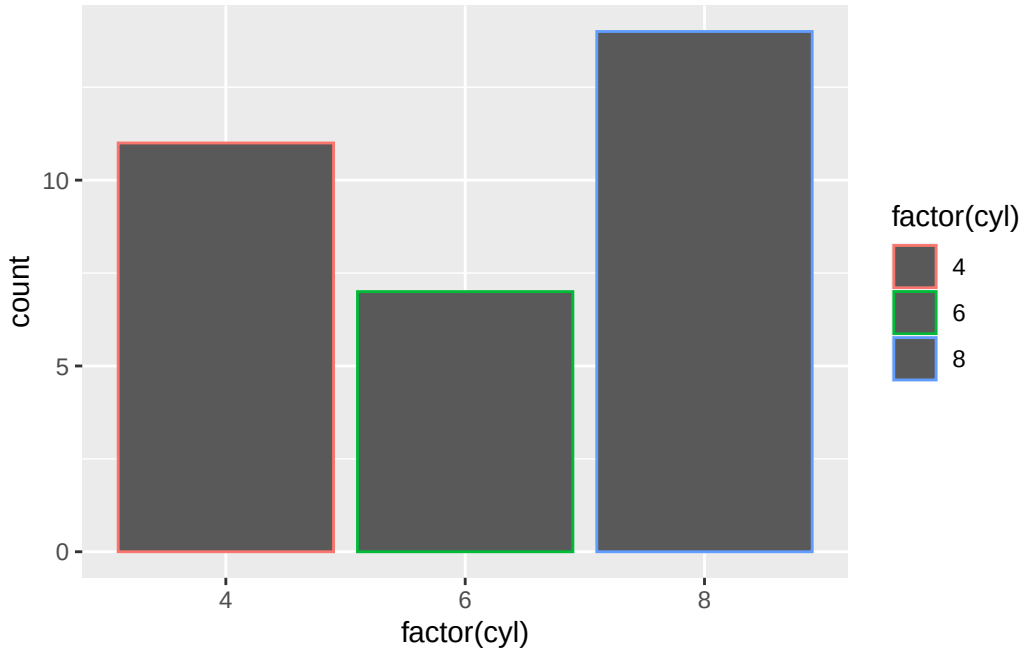

```
#fill/color
ggplot(data=diamonds,aes(x=clarity,color=cut))+
  geom_bar()
```




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



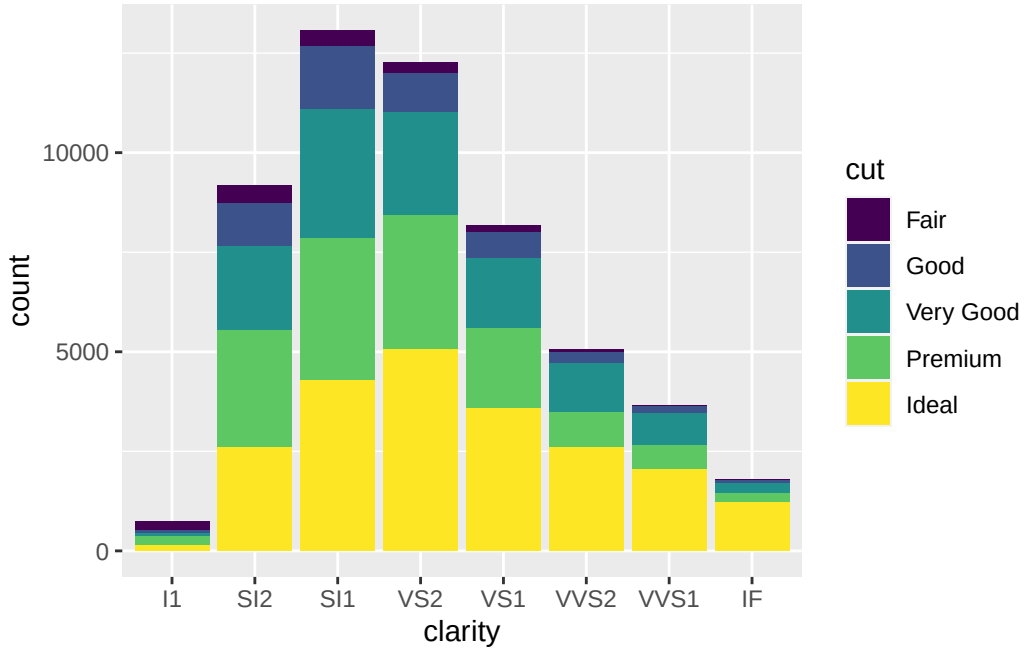
```
ggplot(data=mtcars,aes(factor(cyl),color=factor(cyl)))+
  geom_bar()
```



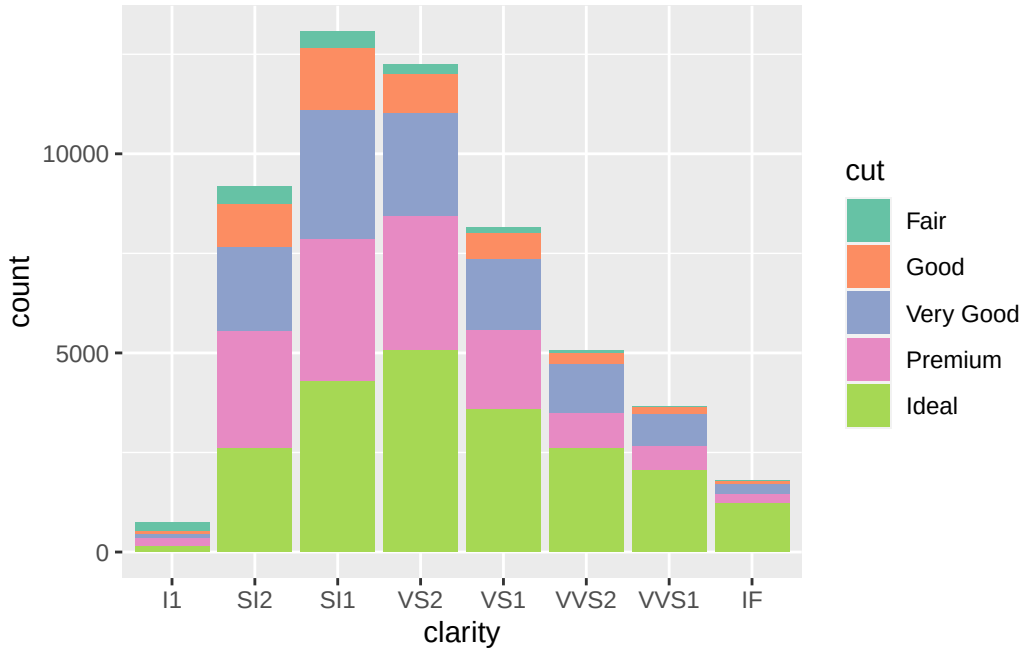

```
help(points)
```

```
starte den http Server für die Hilfe fertig
```

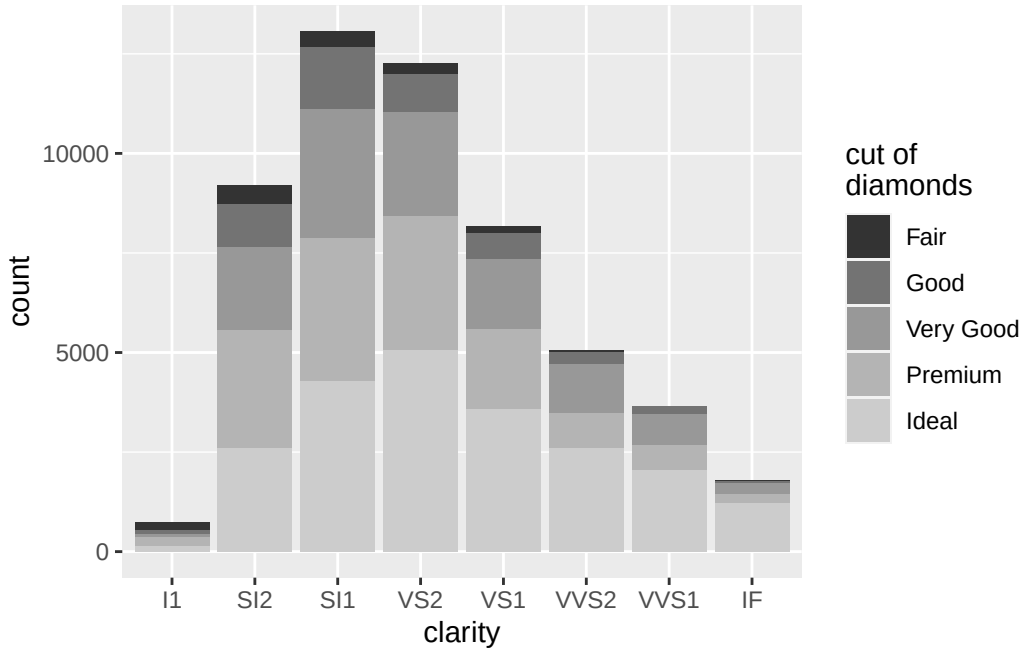
```
#other color systems
(plottemp <- ggplot(data=diamonds,aes(x=clarity,fill=cut))+
    geom_bar())
```



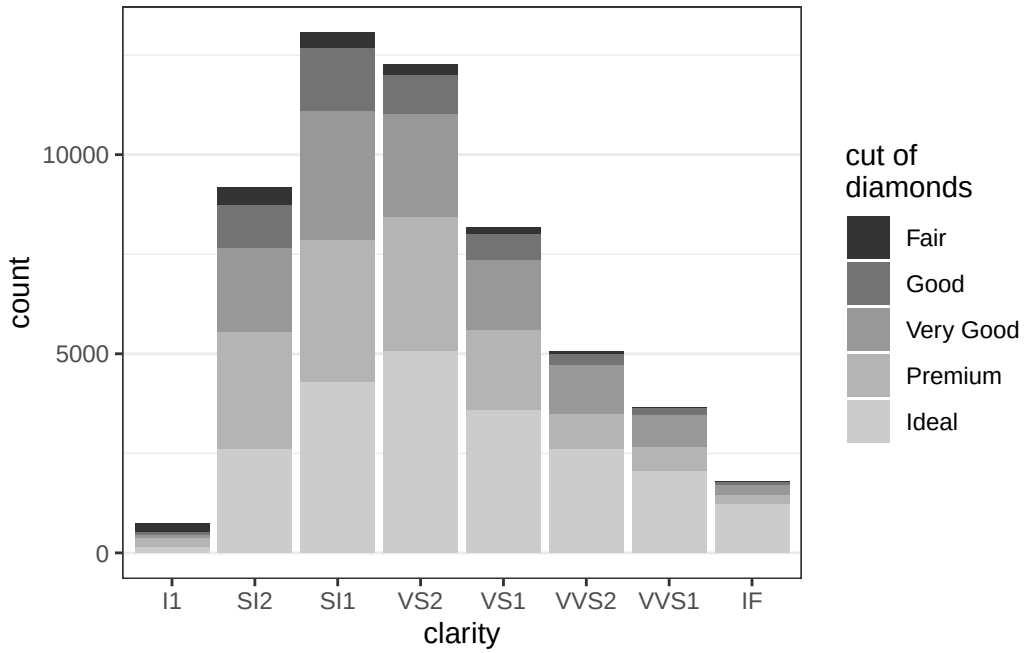

```
plottemp + scale_fill_brewer(palette='Set2') #in-built
```



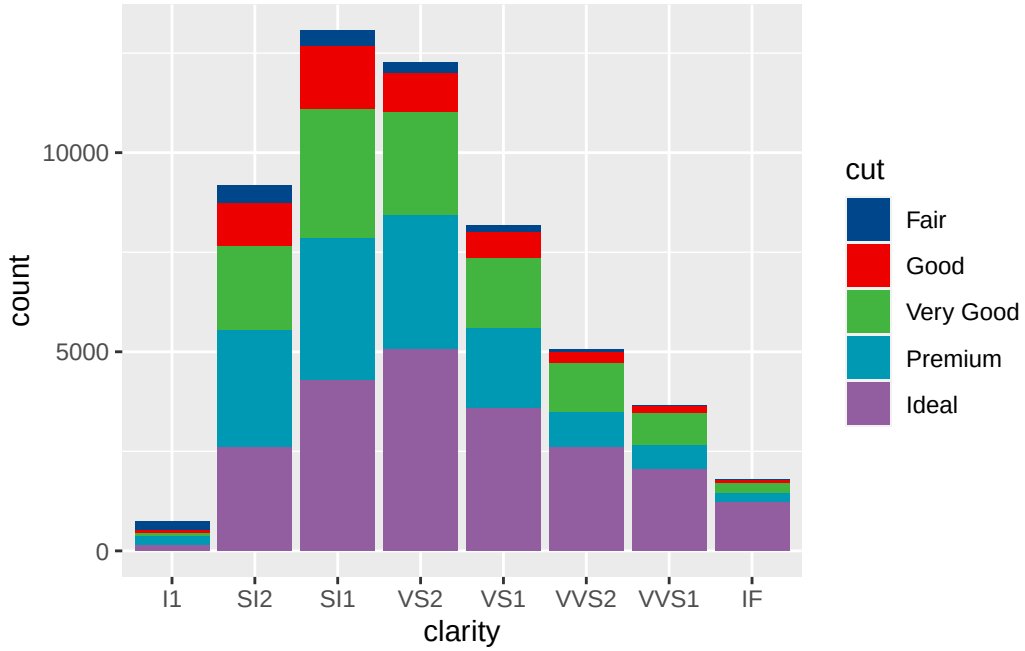
```
plottemp + scale_fill_grey(name = "cut of\ndiamonds")
```



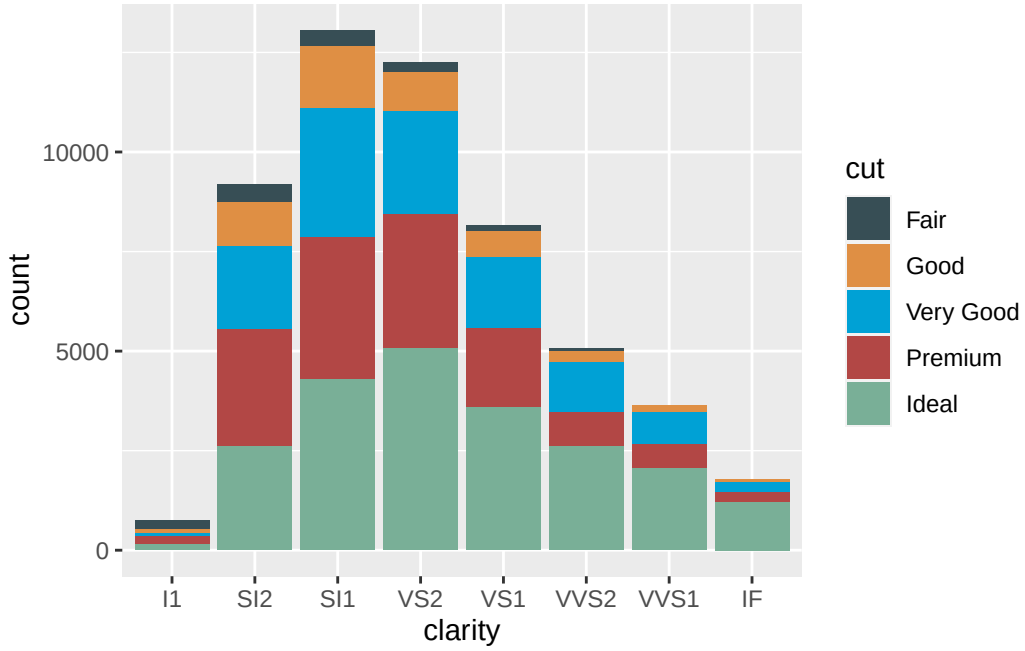

```
plottemp + scale_fill_grey(name = "cut of\ndiamonds") +
  theme_bw()+
  theme(panel.grid.minor.x=element_blank(),
        panel.grid.major.x = element_blank())#+
```



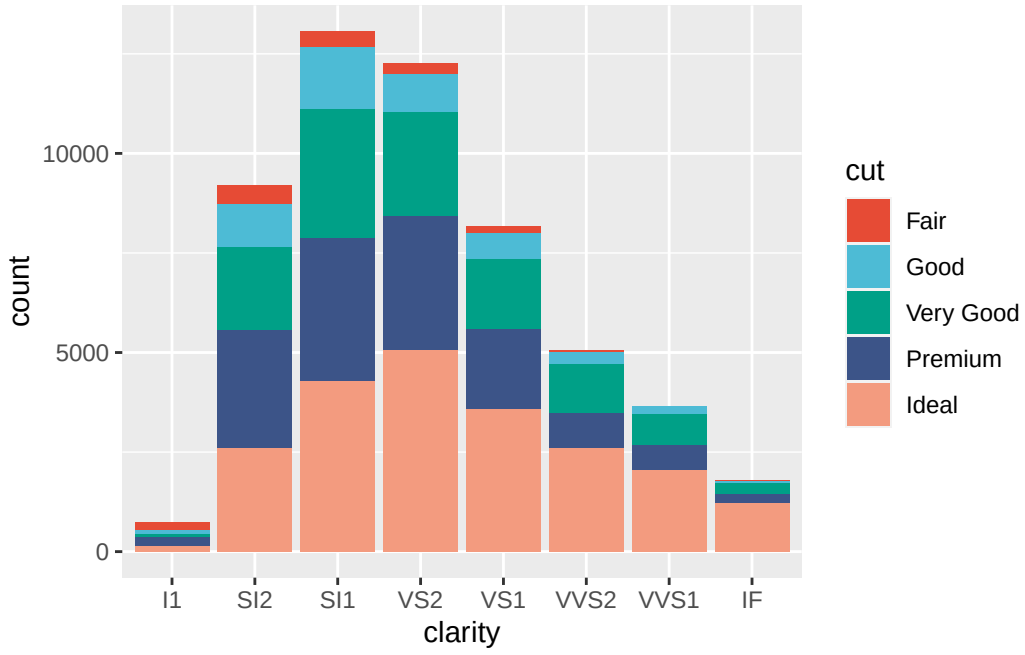

```
# scale_y_continuous(expand = expansion(mult = c(0,.5)))

# ggsci ####
plottemp+scale_fill_lancet()
```



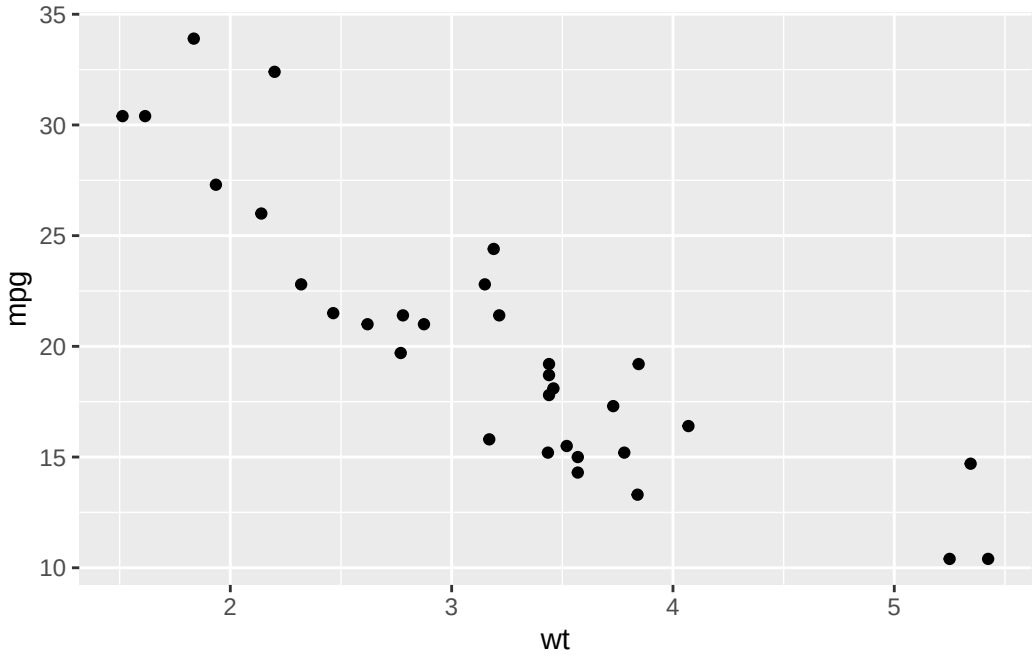

```
plottemp+scale_fill_jama()
```



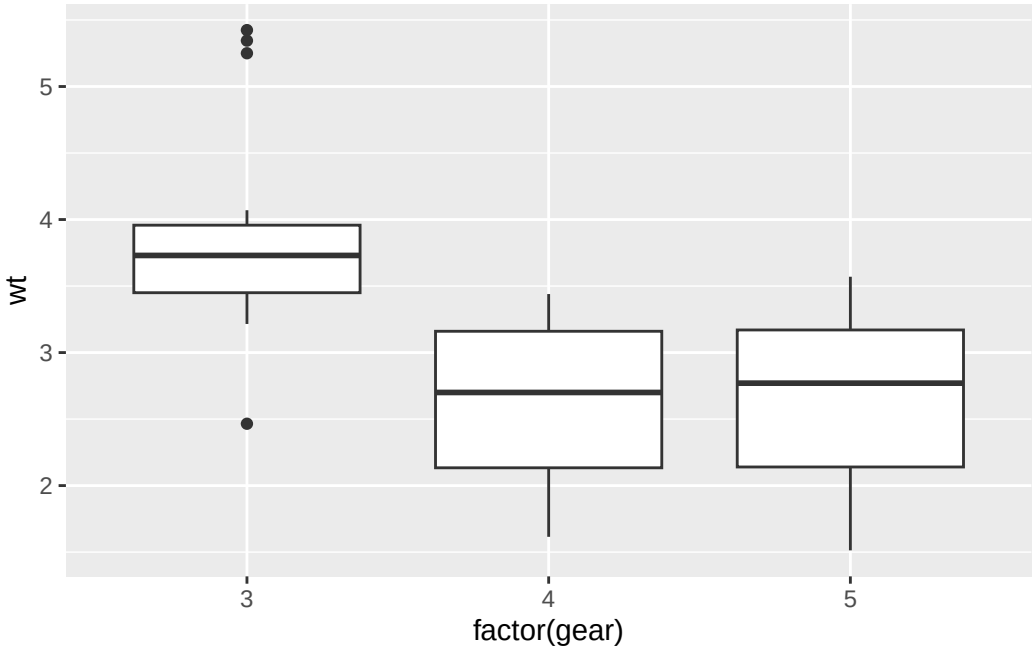
```
plottemp+scale_fill_npg()
```



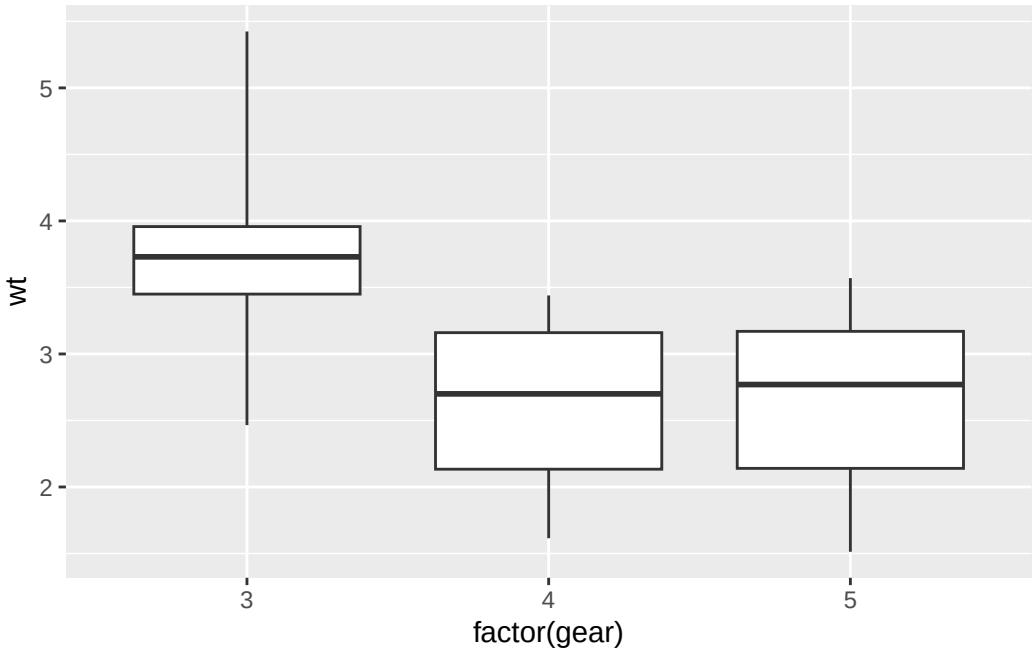

```
printplot <- plottemp+scale_fill_startrek()

#save ggplots
# ggsave(filename = 'Graphs/ggtestplot.png',
#        plot = printplot,
#        width=20,height=20,
#        units='cm',dpi=150)
# alternative:
# png(filename = 'Graphs/ggtestplot2.png',
#     width = 20,height = 20,units = 'cm',res = 150)
# plottemp
# dev.off()
# scatterplot

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



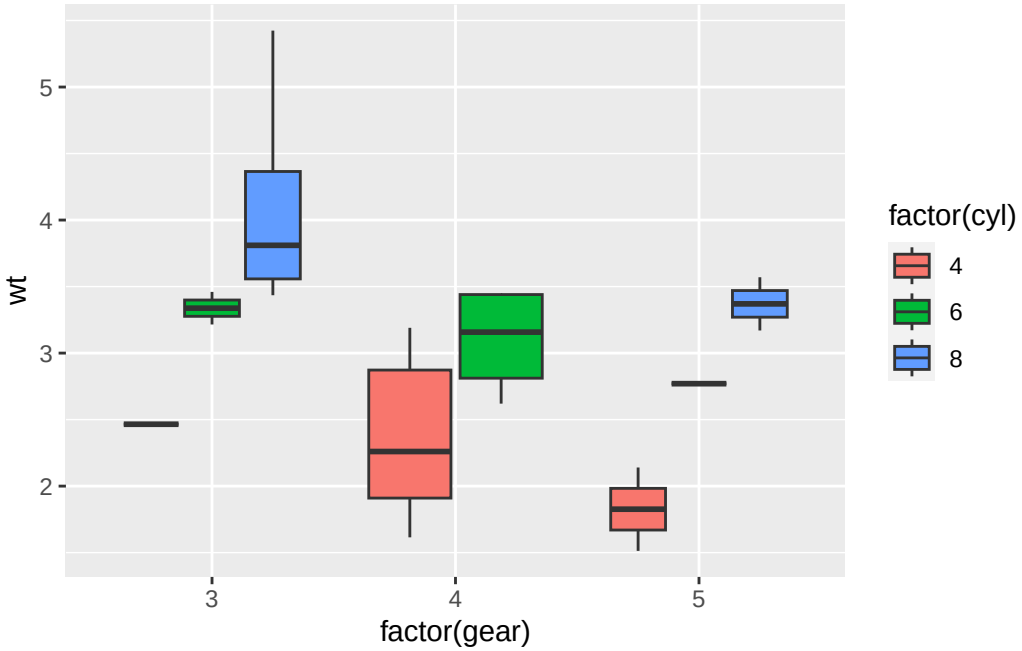

```
ggplot(mtcars,aes(x = factor(gear),y = wt))+
  geom_boxplot() #default 1.5 IQR
```



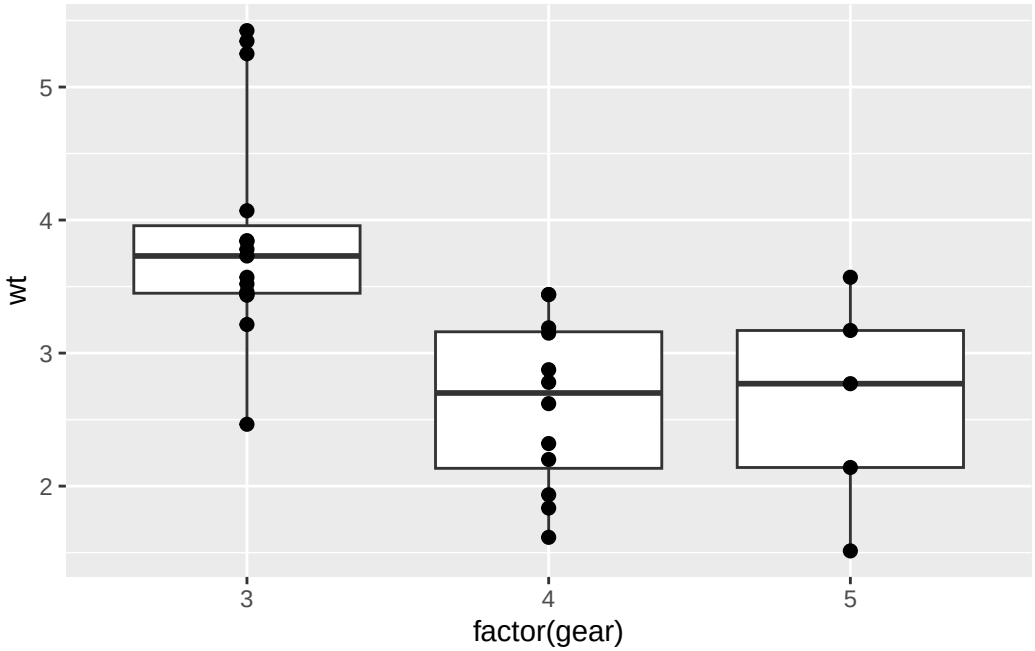
```
ggplot(mtcars,aes(x = factor(gear),y = wt))+
  geom_boxplot(coef=3)
```



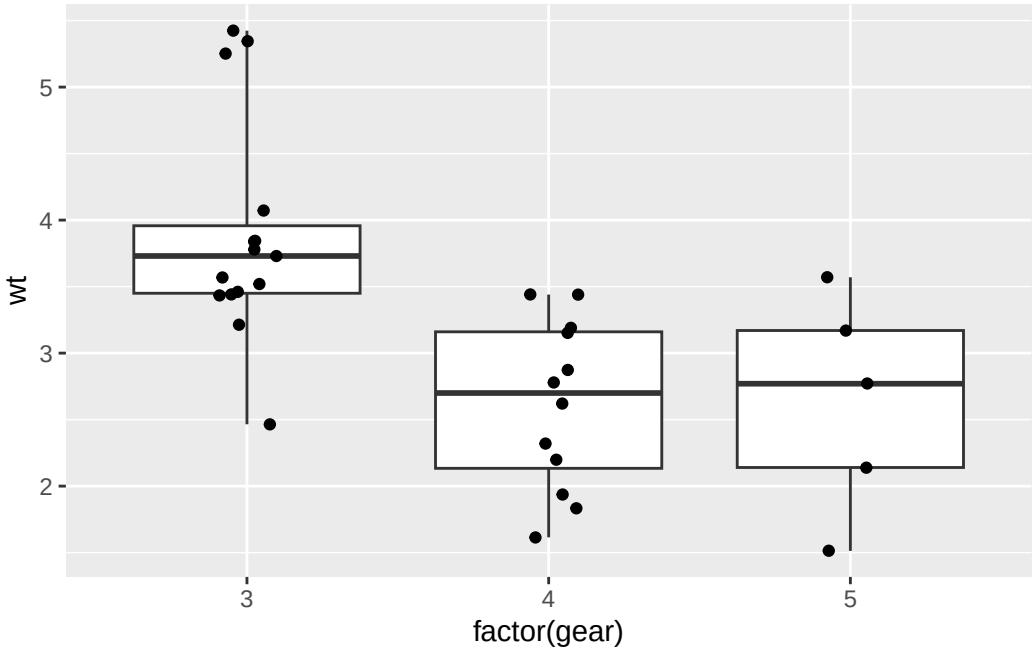

```
ggplot(mtcars,aes(x = factor(gear),y = wt,
                  fill=factor(cyl)))+
  geom_boxplot(coef=3)
```




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

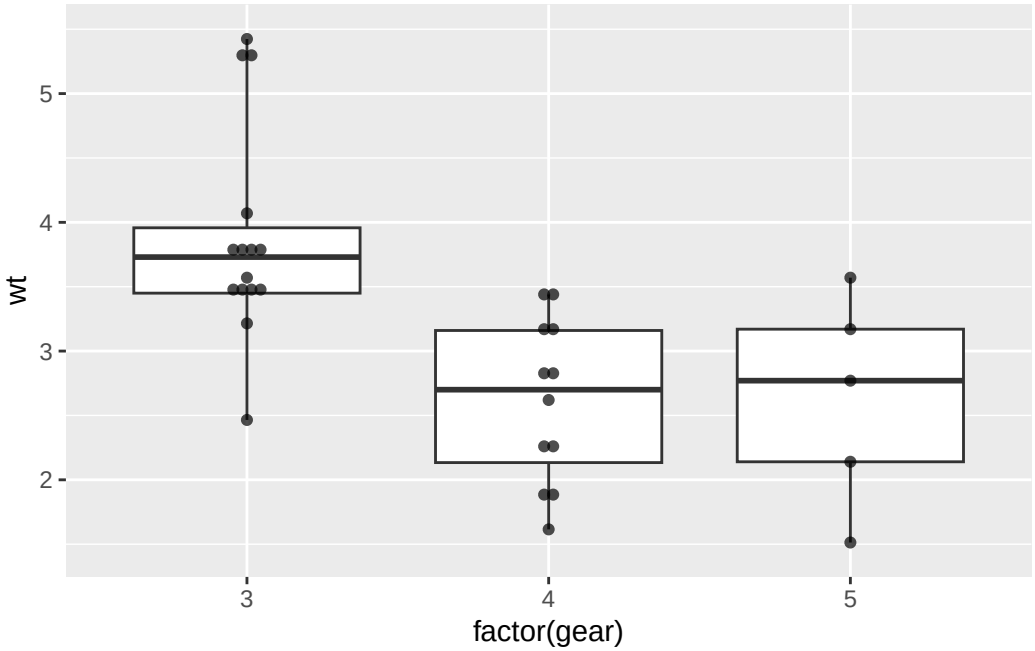



```
ggplot(mtcars,aes(x = factor(gear),y = wt))+
  geom_boxplot(coef=3)+
  geom_point(position = position_jitter(width = .1))
```

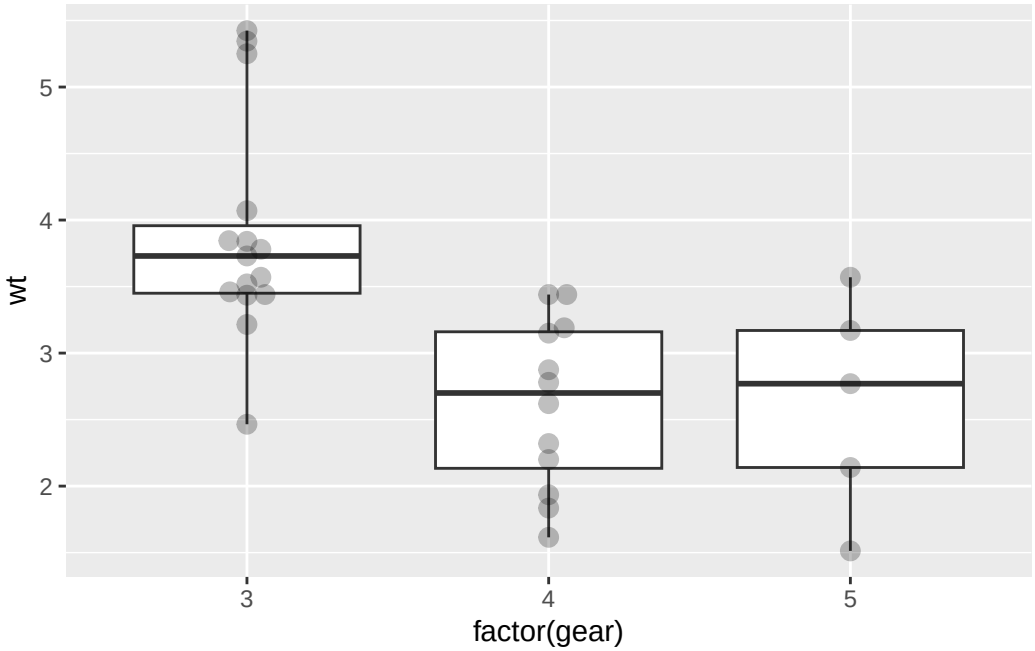



```
ggplot(mtcars,aes(x = factor(gear),y = wt))+
  geom_boxplot(coef=3)+
  geom_dotplot(alpha=.7,
               binaxis = 'y',stackdir = 'center',
               stackratio = .9,dotsize = .6)
```

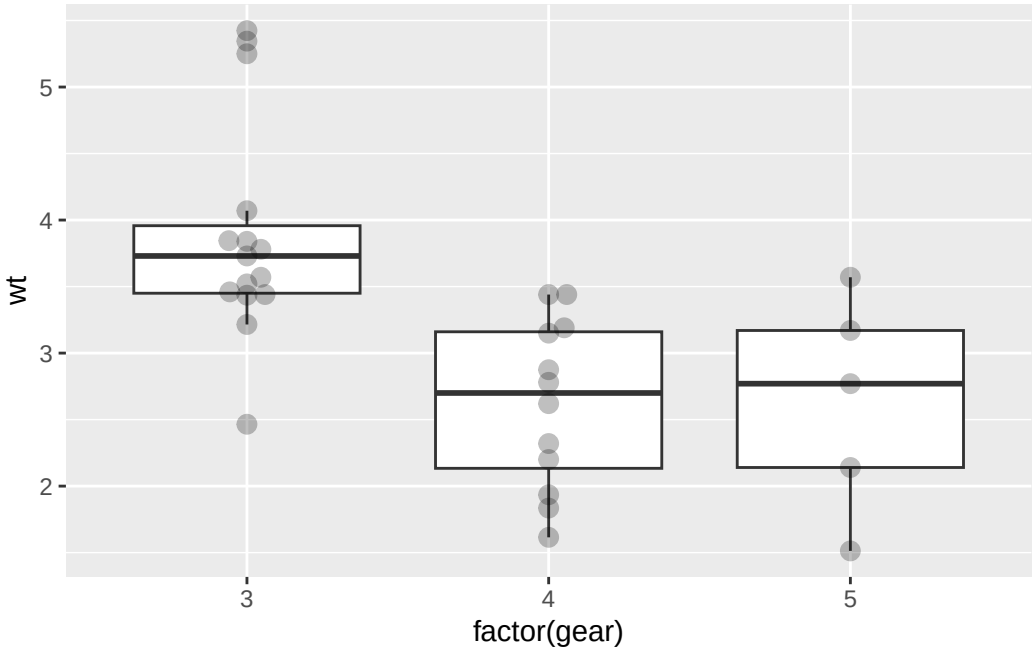
```
Bin width defaults to 1/30 of the range of the data. Pick better value with
`binwidth`.
```



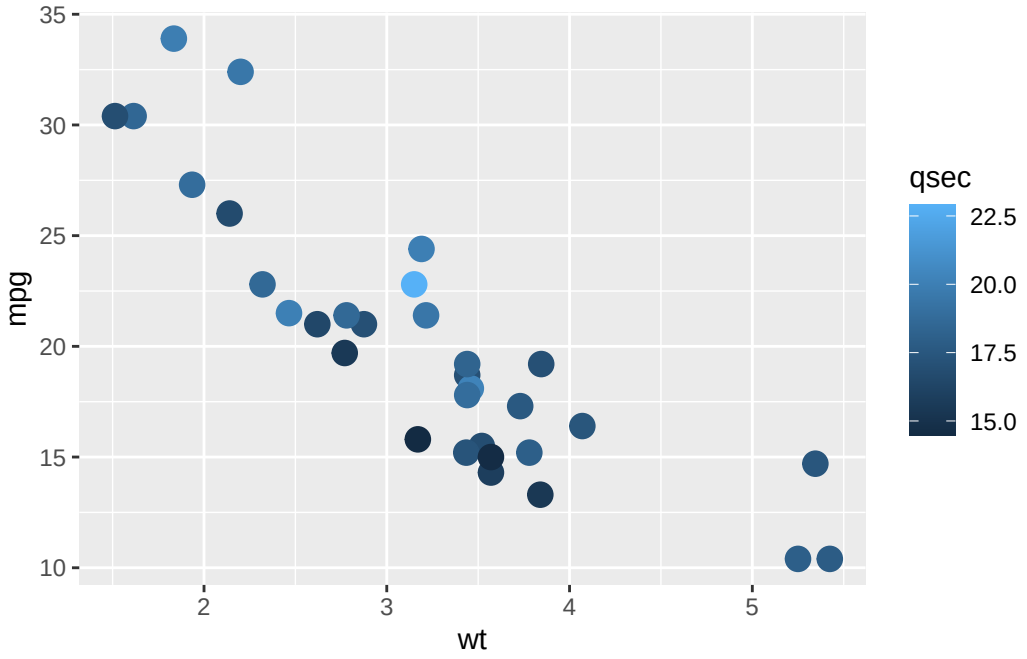

```
ggplot(mtcars,aes(x = factor(gear),y = wt))+
  geom_boxplot(coef=3)+
  ggbeeswarm::geom_beeswarm(cex = 2,size=3,alpha=.25)
```



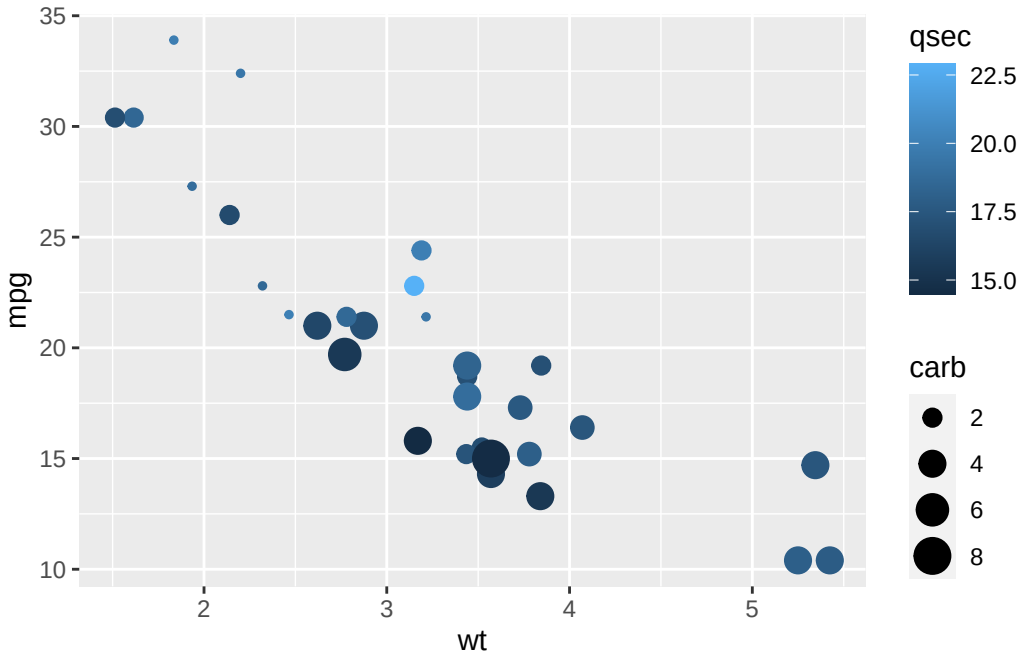

```
ggplot(mtcars,aes(x = factor(gear),y = wt))+
  geom_boxplot(outlier.alpha = 0)+
  geom_beeswarm(cex = 2,size=3,alpha=.25)
```



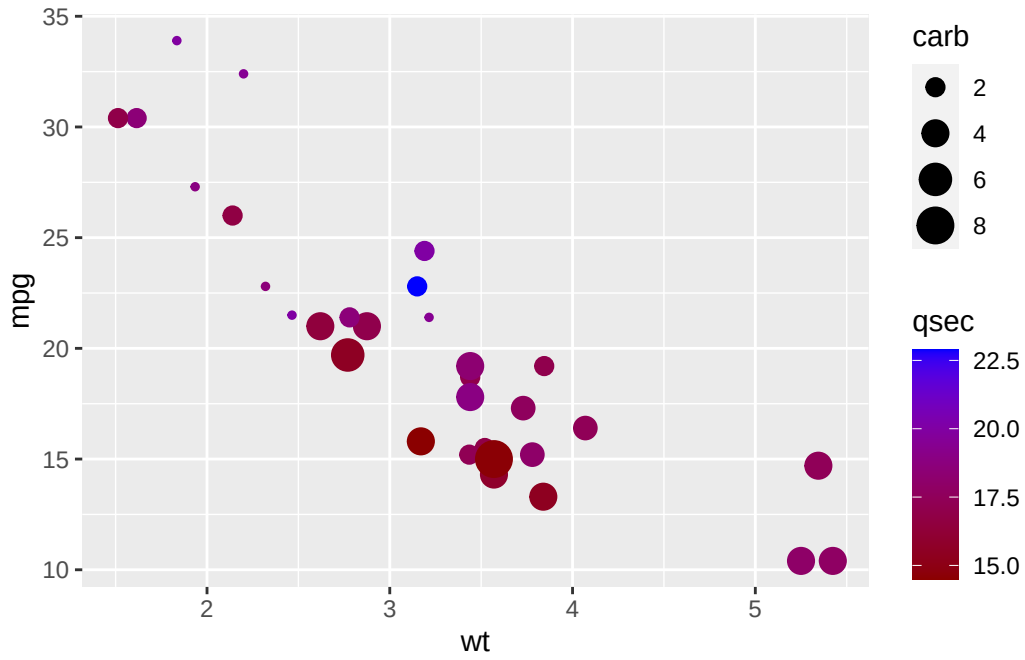

```
#aesthetics again (finetuning)
ggplot(data=mtcars,aes(wt, mpg,color=qsec))+
  geom_point(size=4) #outside aes!
```



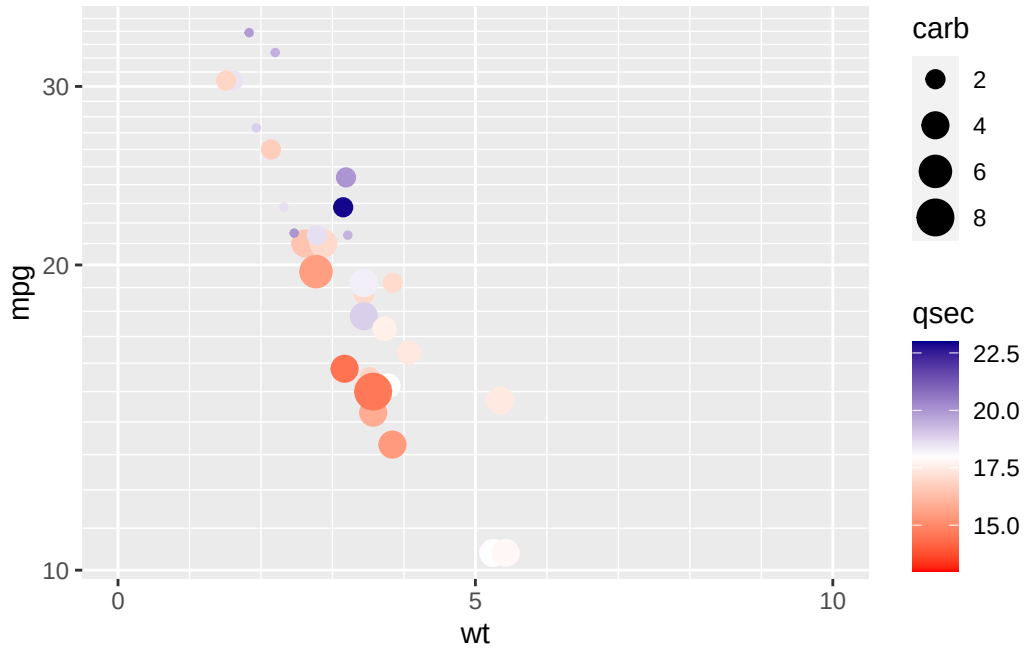

```
ggplot(data=mtcars,aes(wt, mpg,color=qsec, size=carb))+
  geom_point()
```



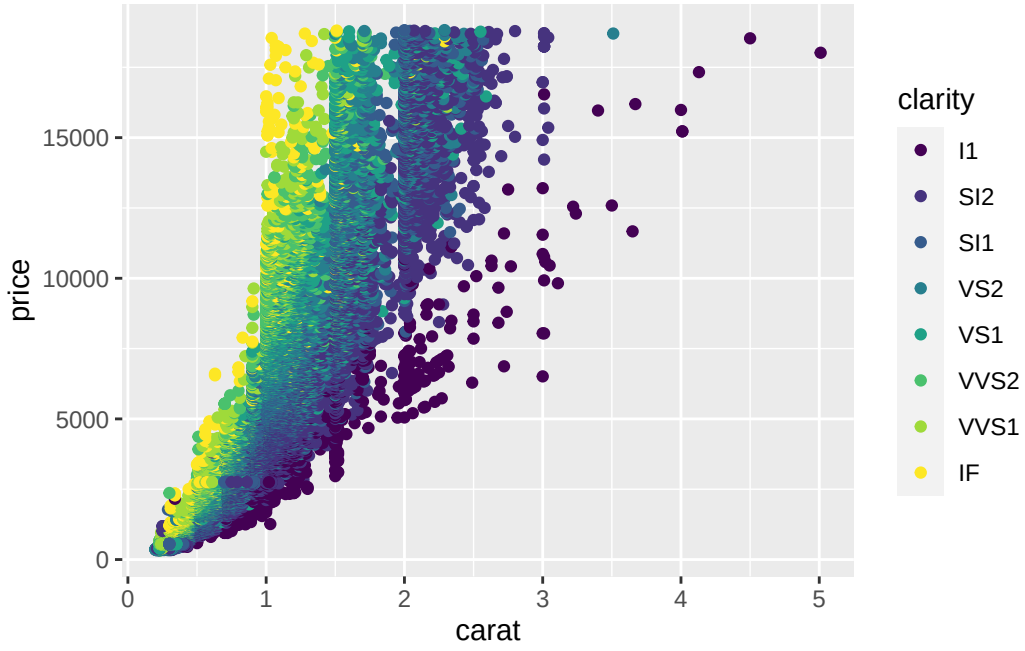
```
ggplot(data=mtcars,aes(wt, mpg,color=qsec, size=carb))+
  scale_color_gradient(low='darkred',high='blue')+
  geom_point()
```



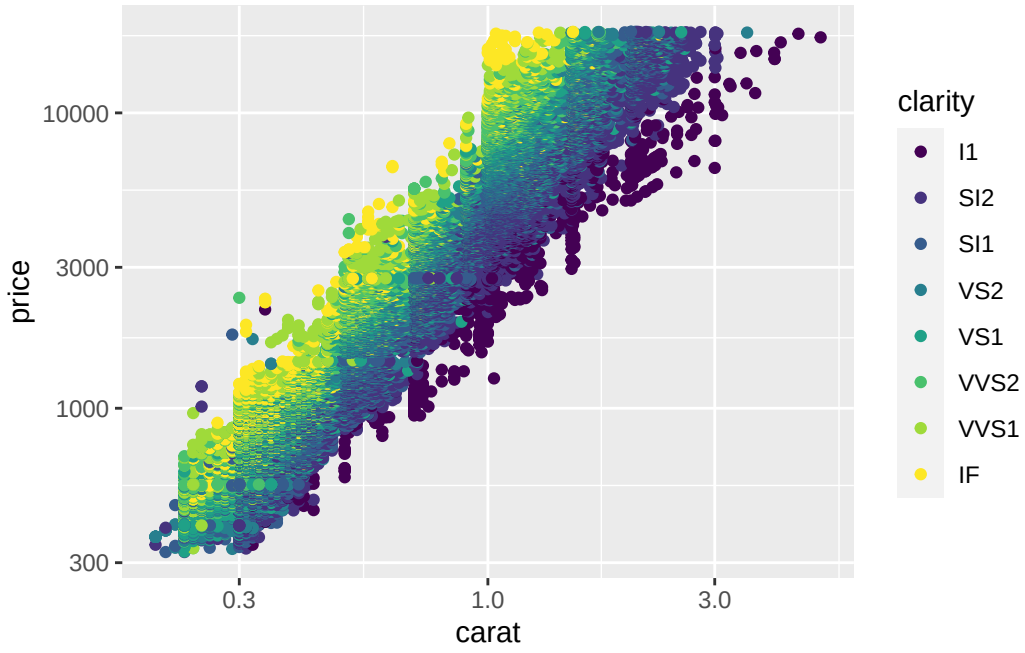

```
ggplot(data=mtcars,aes(wt, mpg,color=qsec, size=carb))+
  scale_color_gradient2(low='red',high='darkblue',
                        mid='white',
                        limits=c(13,23),midpoint=18)+
  geom_point()+
  scale_x_continuous(breaks = seq(0,100,5),
                     minor_breaks=seq(0,100,1),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



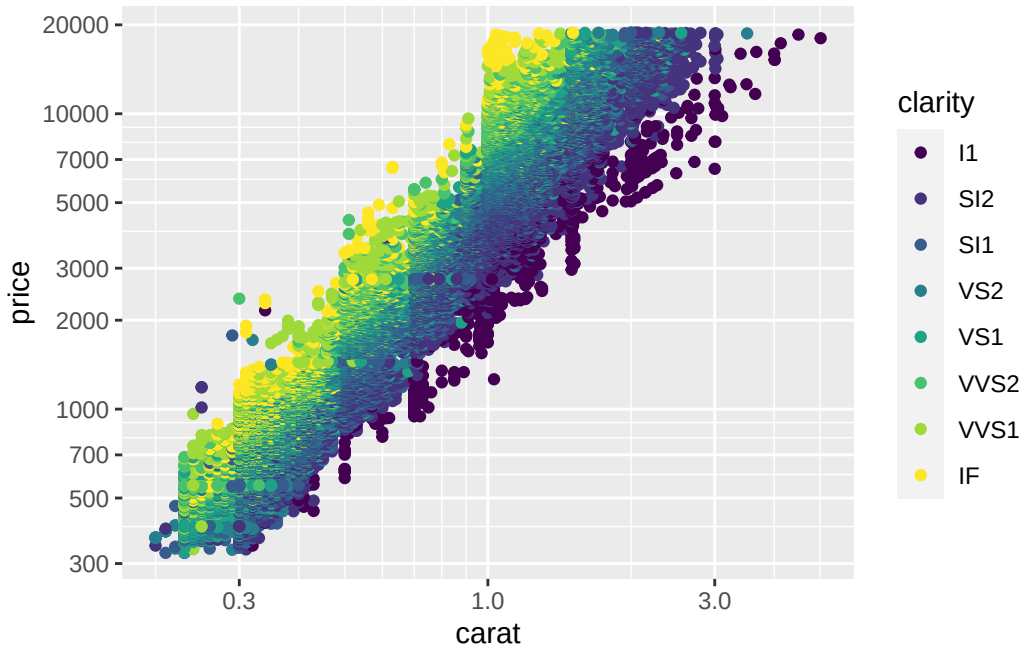

```
ggplot(diamonds,aes(carat,price,color=clarity))+
  geom_point()
```



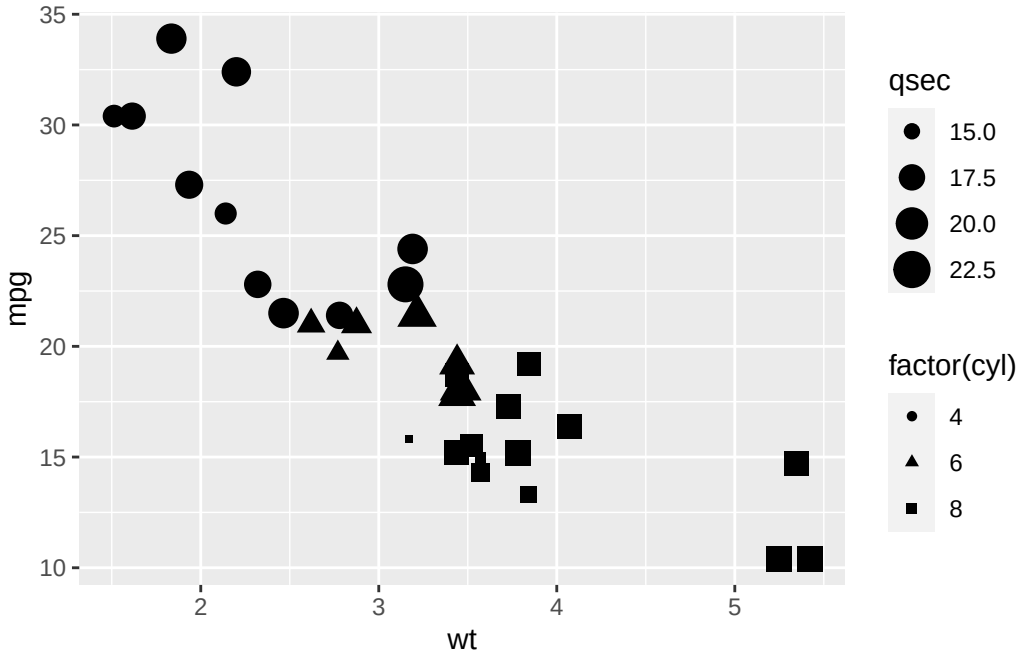
```
ggplot(diamonds,aes(carat,price,color=clarity))+
  geom_point()+
  scale_x_log10()+
  scale_y_log10()
```



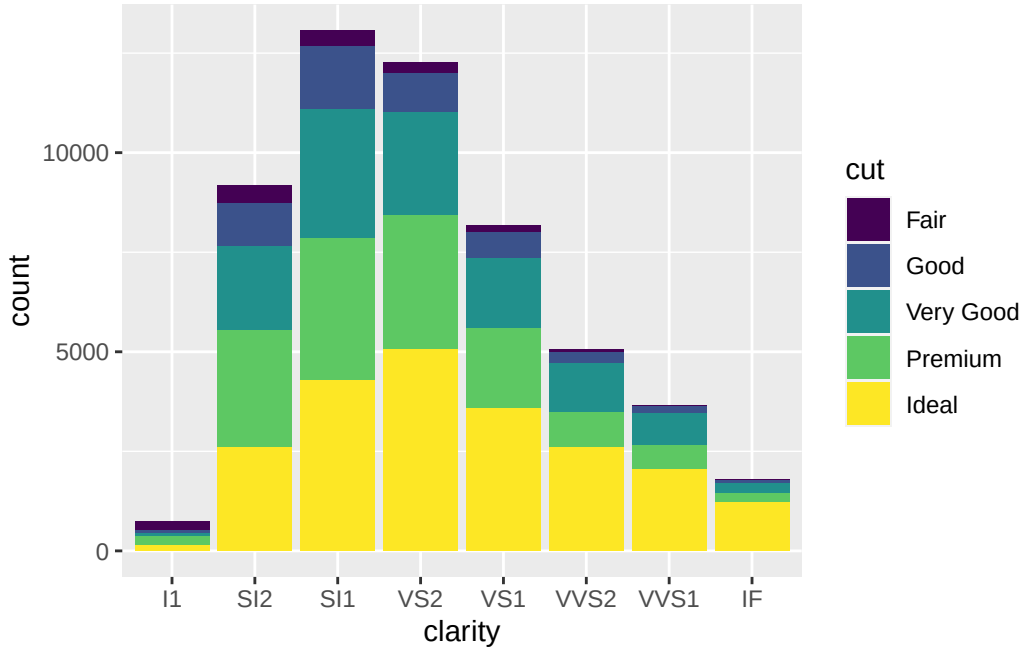

```
ggplot(diamonds,aes(carat,price,color=clarity))+
  geom_point()+
  scale_x_log10(minor_breaks=logrange_123456789)+
  scale_y_log10(
    breaks=logrange_12357,
    minor_breaks=logrange_123456789)
```



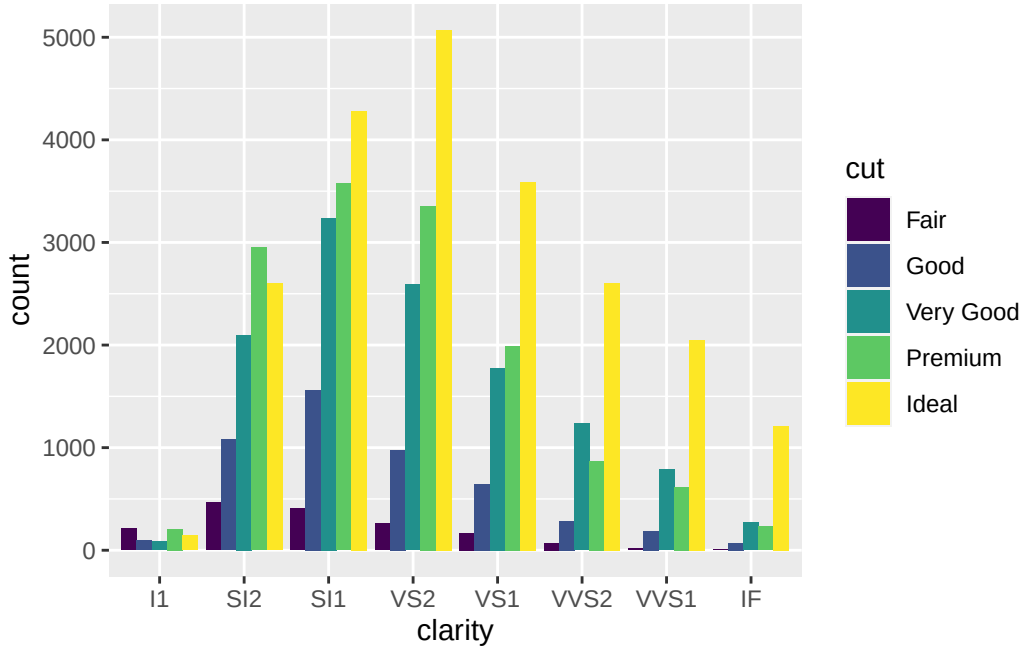

```
# use different aesthetic mappings
ggplot(data=mtcars,
       aes(wt, mpg,size=qsec, shape=factor(cyl)))+
  geom_point()
```



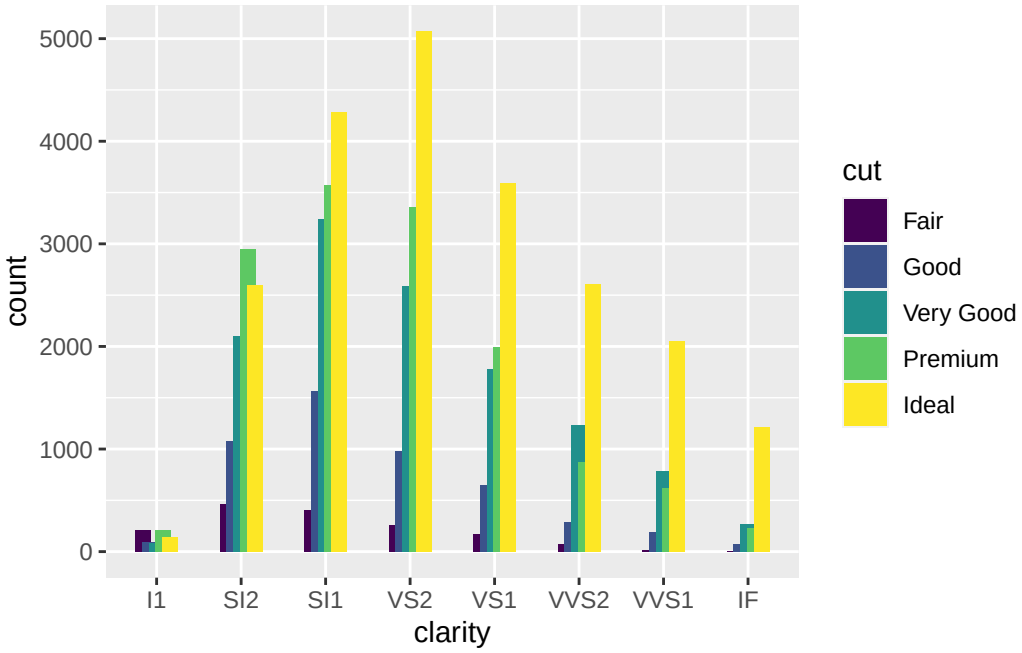

```
# ggplot(data=mtcars,aes(carb, mpg,color=qsec, size=wt))+
#   geom_point(shape='\u2642')

#location, location,position

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



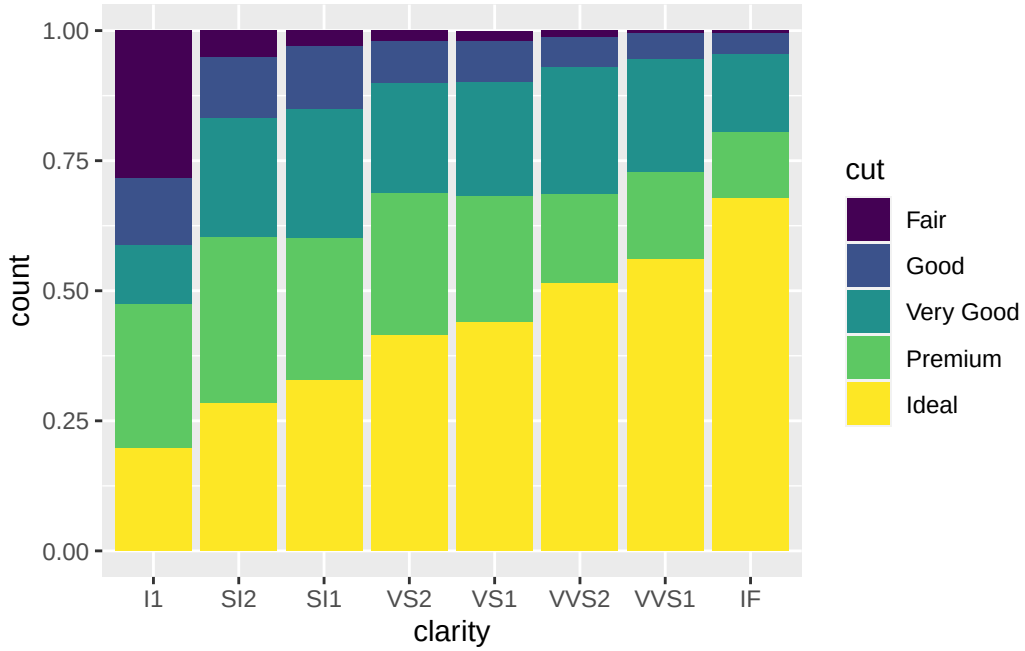

```
p+geom_bar(position="dodge")
```



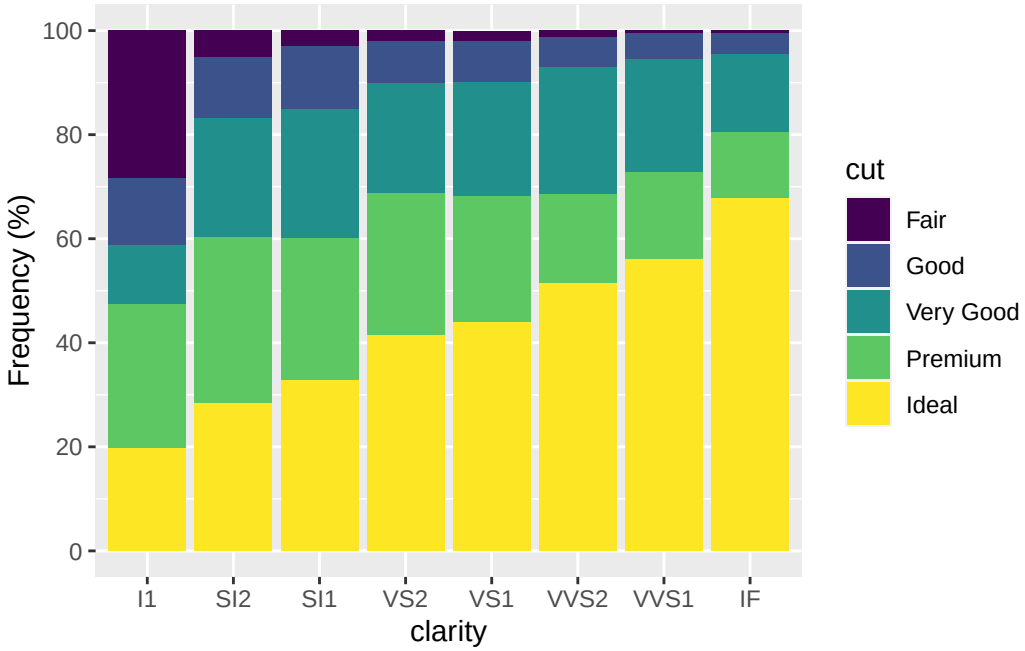
```
p+geom_bar(position=position_dodge(width = .4))
```



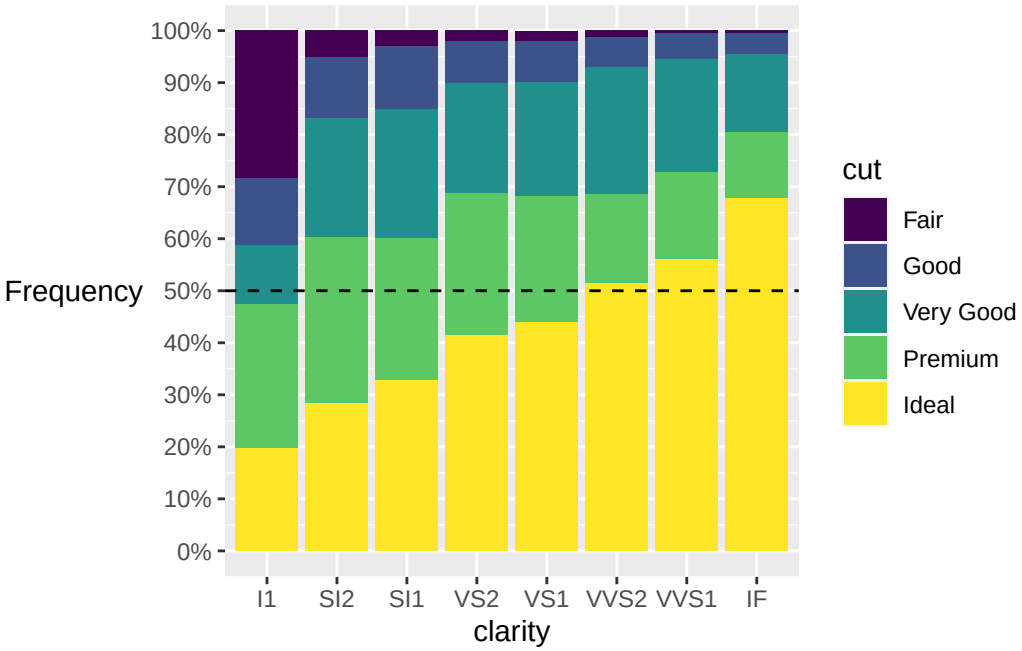

```
p+geom_bar(position="fill")
```



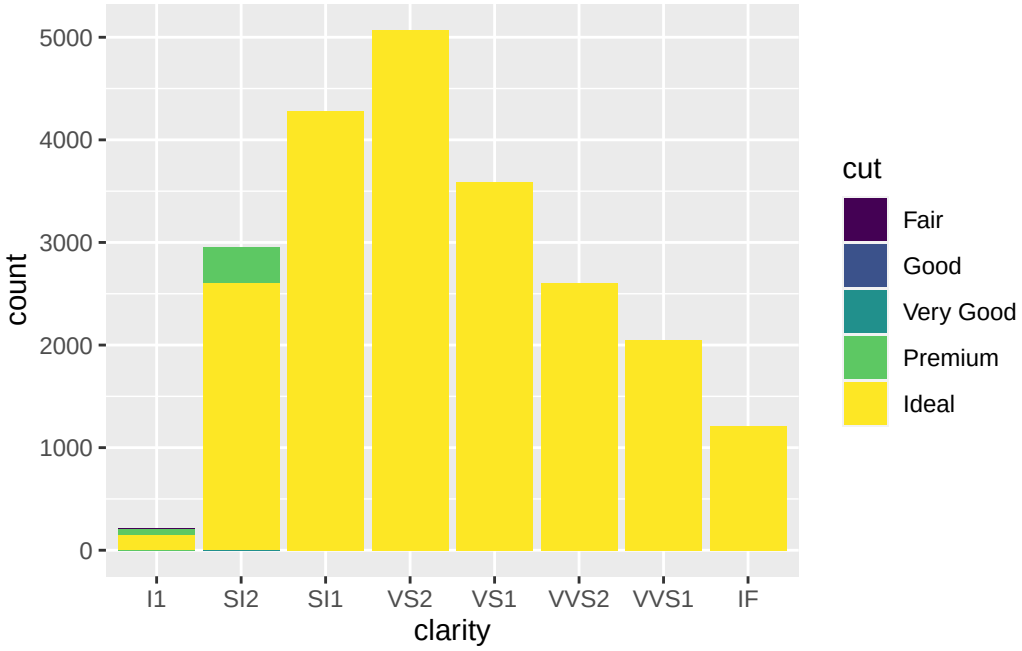

```
p+geom_bar(position="fill")+
  scale_y_continuous('Frequency (%)',
                     breaks=seq(0,1,.2),
                     labels=seq(0,100,20))
```



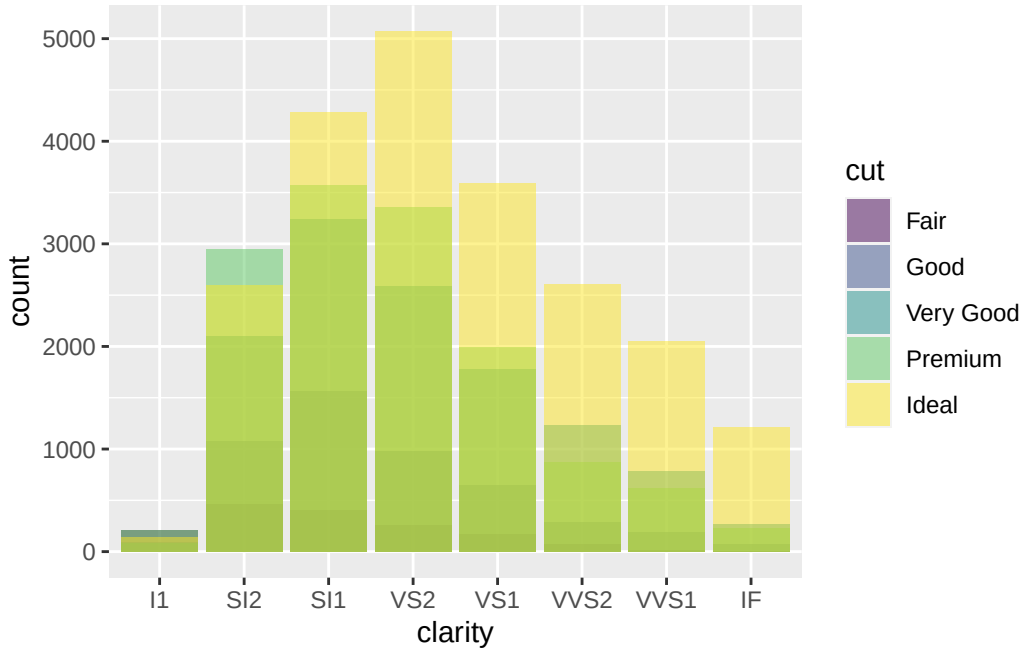

```
p+geom_bar(position="fill")+
  scale_y_continuous('Frequency',
                     breaks=seq(0,1,.1),
                     labels=scales::percent)+
  theme(axis.title.y = element_text(angle = 0,
                                    vjust = .5))+
  geom_hline(yintercept = .5, linetype=2)
```



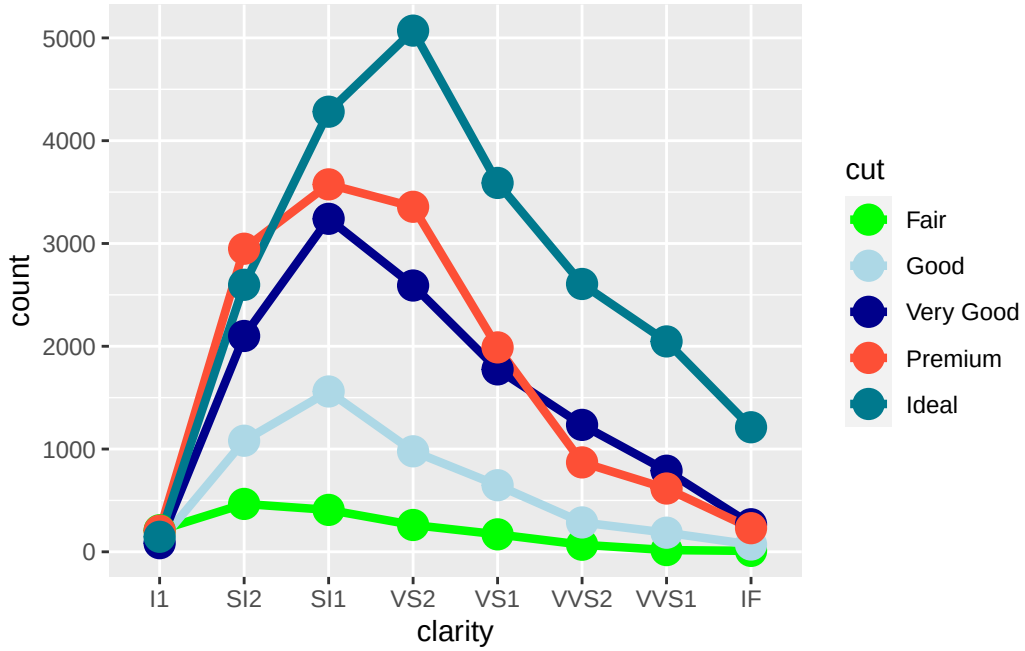

```
p+geom_bar(position="identity")
```



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



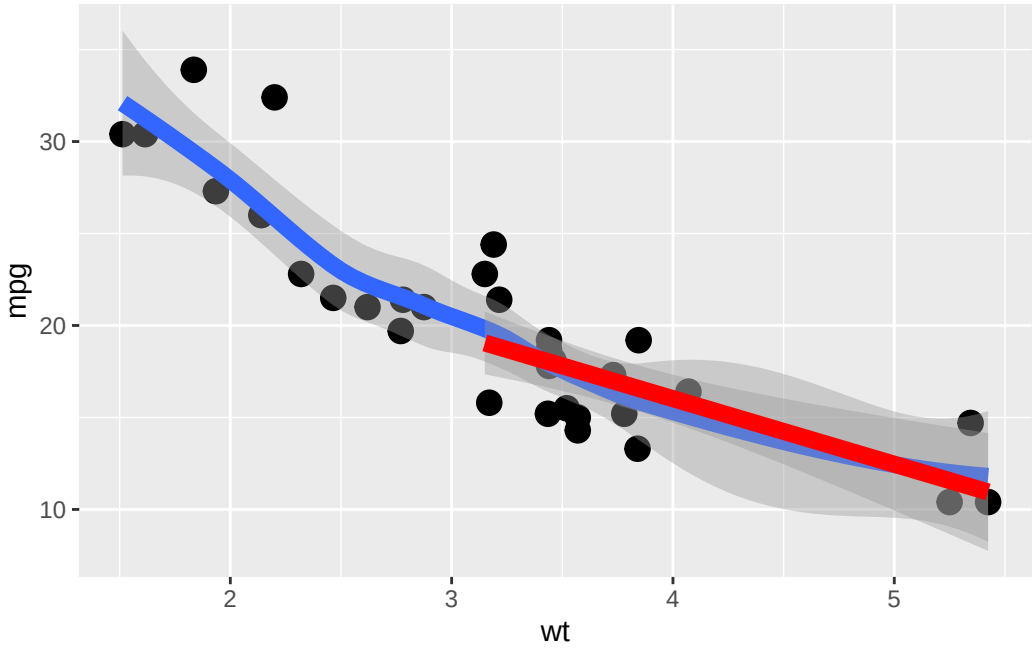

```
ggplot(data=diamonds,aes(clarity,color=cut, group=cut))+
  geom_freqpoly(stat='count',position="identity",lwd=1.5)+
  geom_point(stat='count',size=5)+
  scale_color_manual(values = c('green','lightblue',
                                'darkblue',
                                rgb(253,79,54,maxColorValue = 255),
                                '#00798d'))
```




```
#layer/order / computed geoms
ggplot(data=mtcars,aes(wt, mpg))+
  geom_point(size=4)+
  geom_smooth(size=3)+
  geom_smooth(data=mtcars %>% filter(wt>3),
              method='lm',size=3, color='red')
```

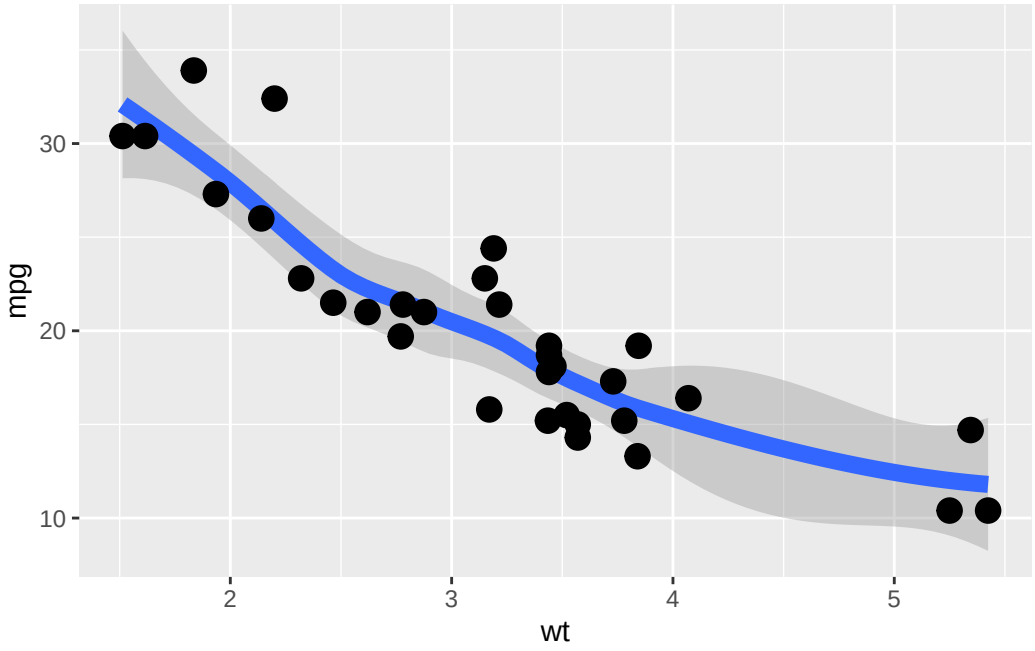
```
Warning: Using `size` aesthetic for lines was deprecated in ggplot2 3.4.0.
i Please use `linewidth` instead.
```

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



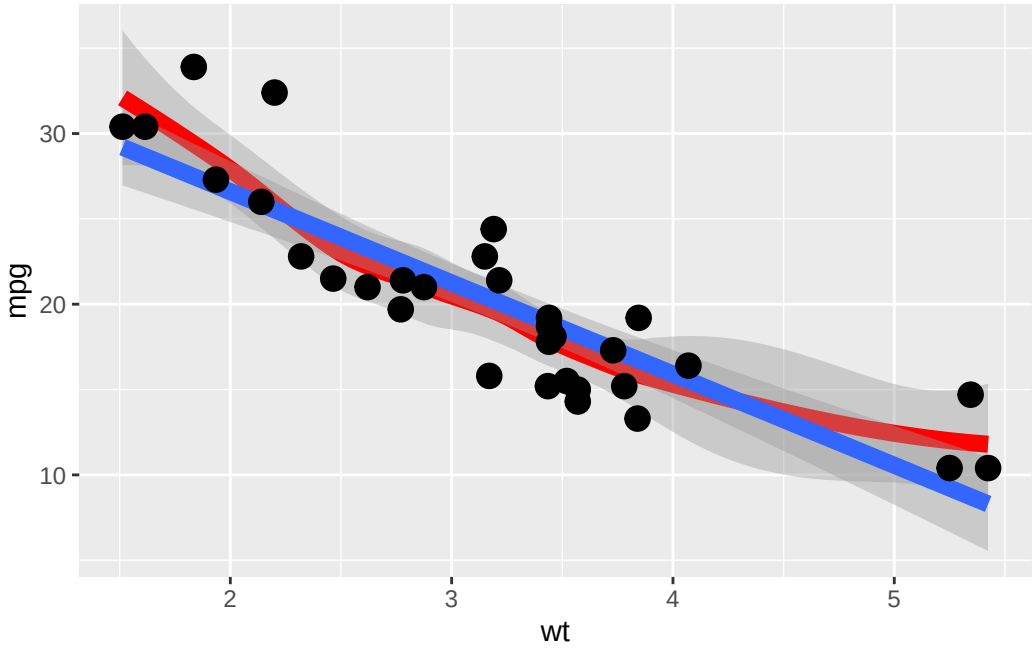

```
ggplot(data=mtcars,aes(wt, mpg))+
  geom_smooth(size=3)+
  geom_point(size=4)
```

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



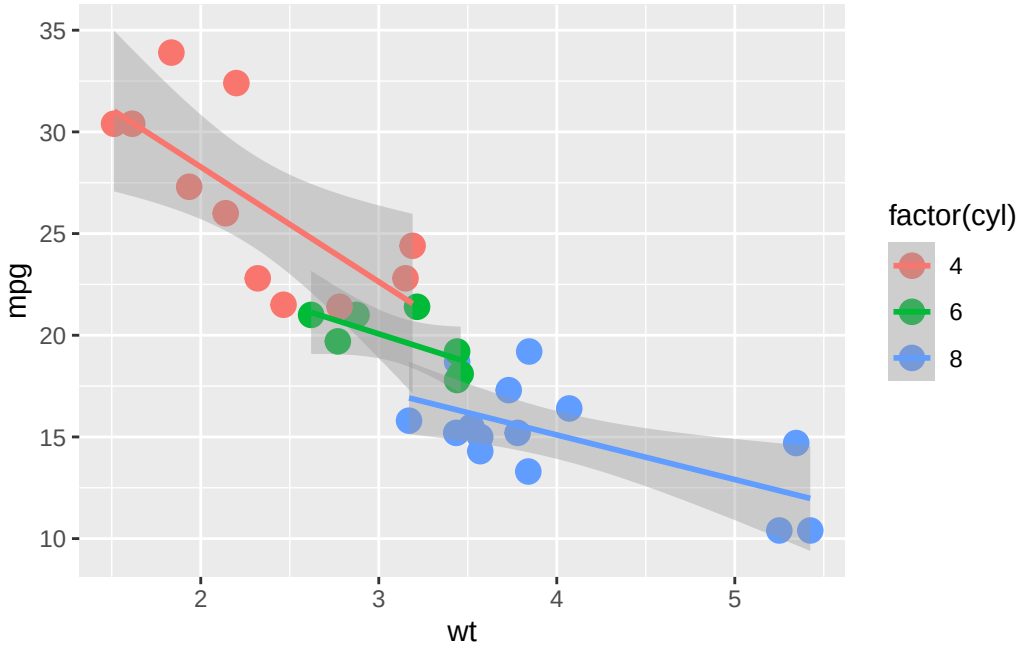

```
ggplot(data=mtcars,aes(wt, mpg))+
  geom_smooth(size=3,color='red')+
  geom_smooth(method='lm',size=3)+
  geom_point(size=4)
```

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



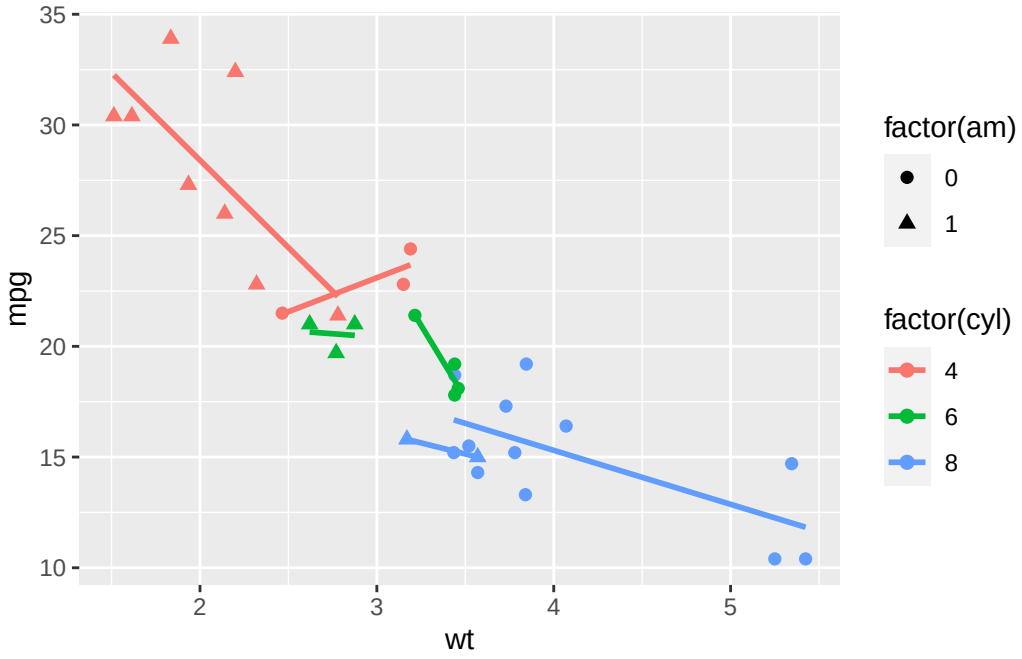

```
  ggplot(data=mtcars,aes(wt, mpg,
                         color=factor(cyl)))+
    geom_point(size=4)+
    geom_smooth(method='lm',size=1)
```

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



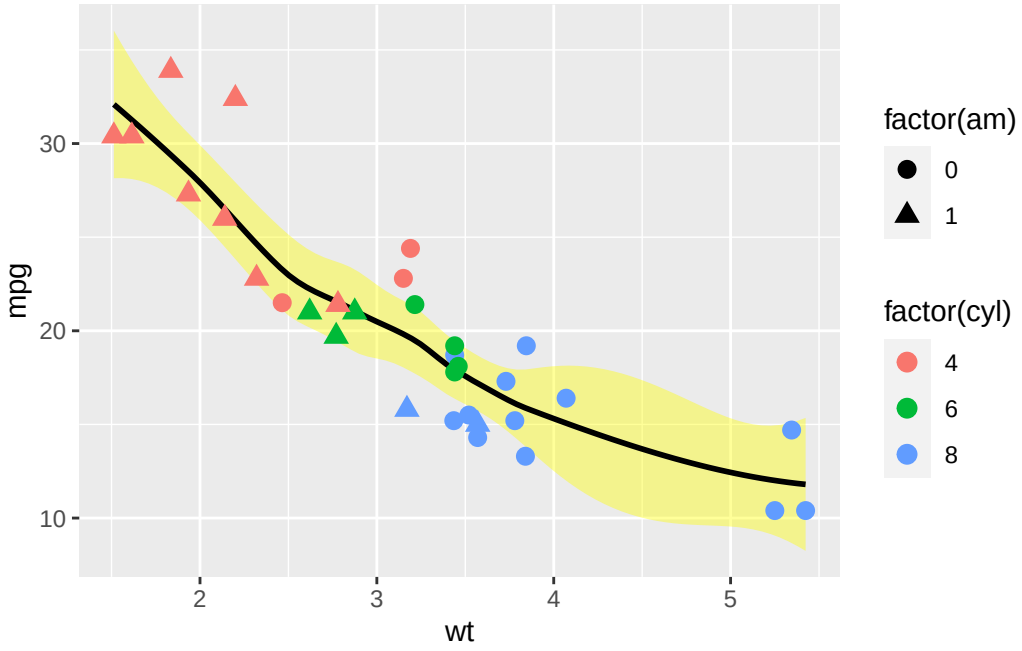

```
ggplot(data=mtcars,aes(wt, mpg,
                       color=factor(cyl),
                       shape=factor(am)))+
  geom_point(size=2)+
  geom_smooth(method='lm',size=1,se=F)
```

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

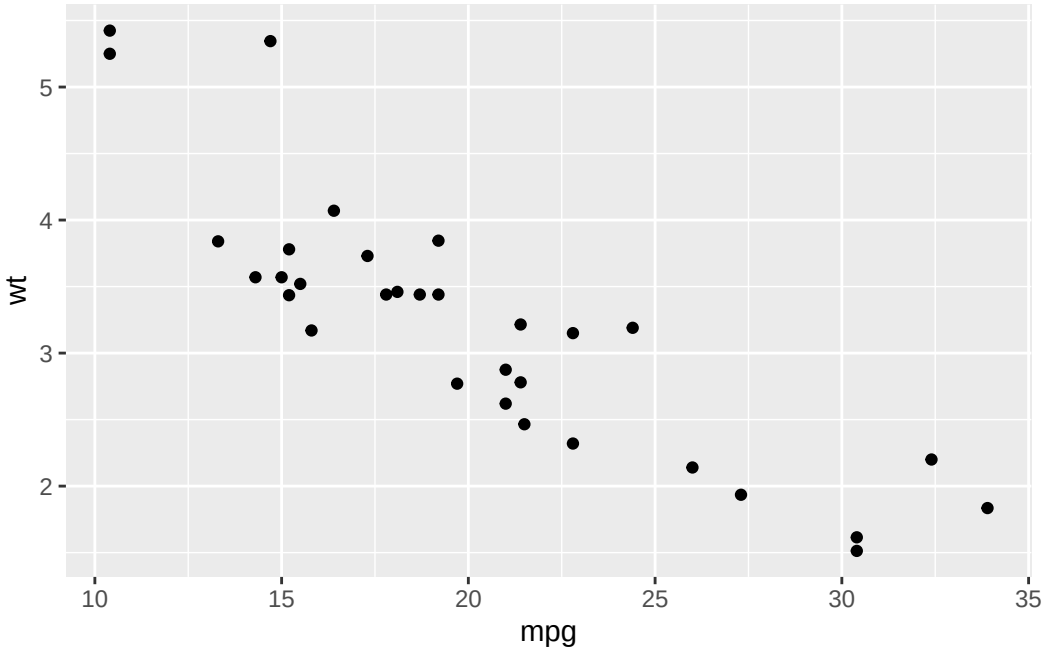



```
#? lm for all?
ggplot(data=mtcars,aes(wt, mpg))+
  geom_smooth(size=1,color='black',fill='yellow')+
  geom_point(size=3,aes(color=factor(cyl),shape=factor(am))) #aes for geom only
```

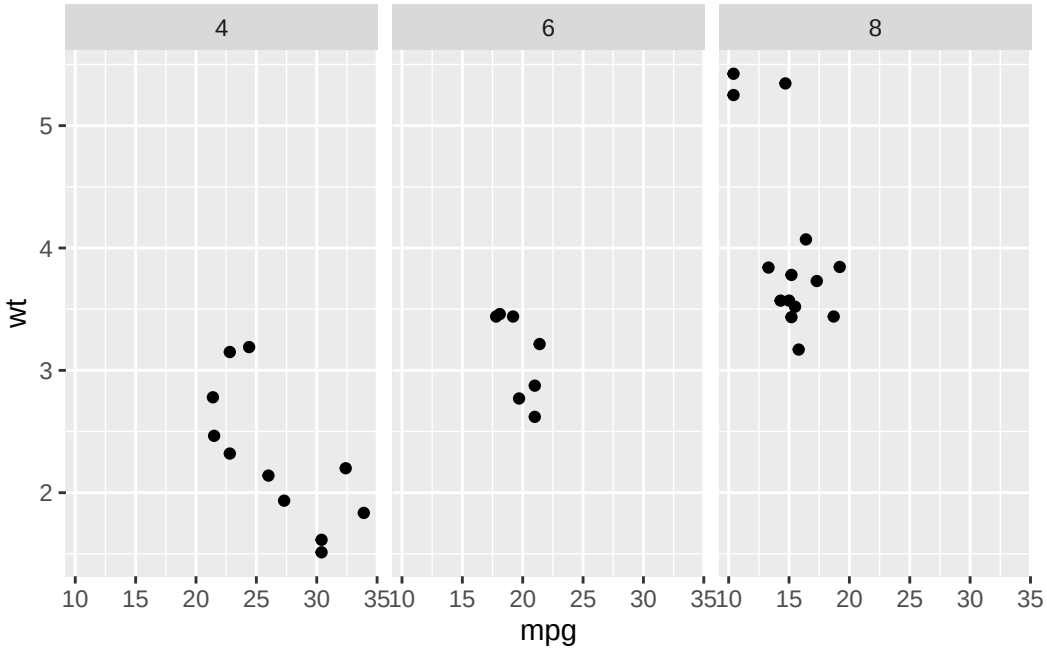
```
`geom_smooth()` using method = 'loess' and formula = 'y ~ x'
```



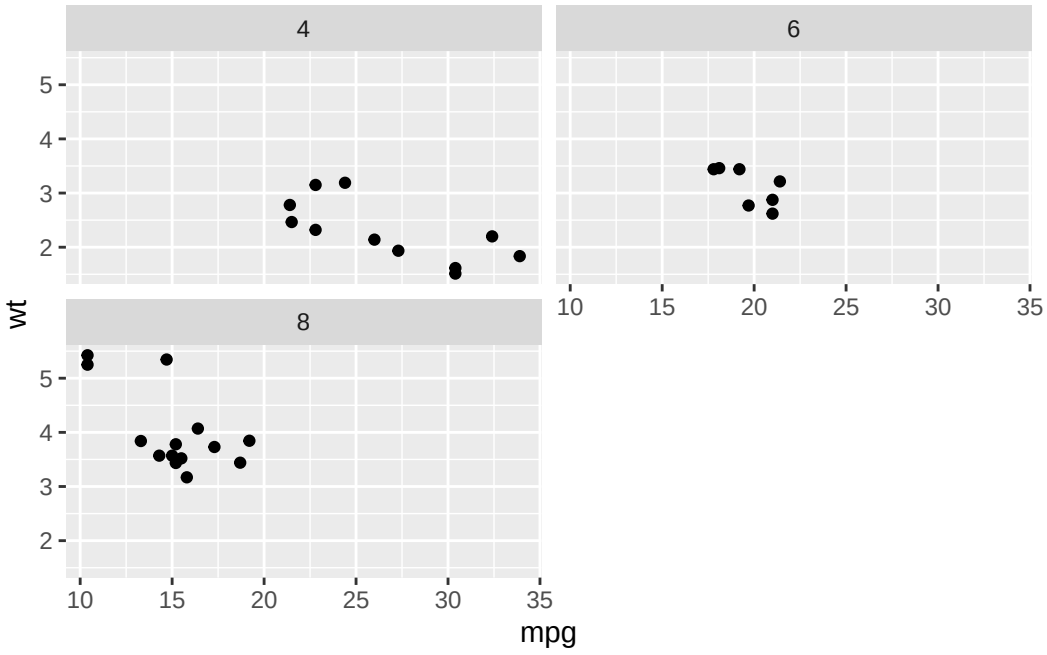

```
# facet_wrap / facet_grid
(p.tmp <- ggplot(mtcars, aes(mpg, wt)) +
    geom_point())
```



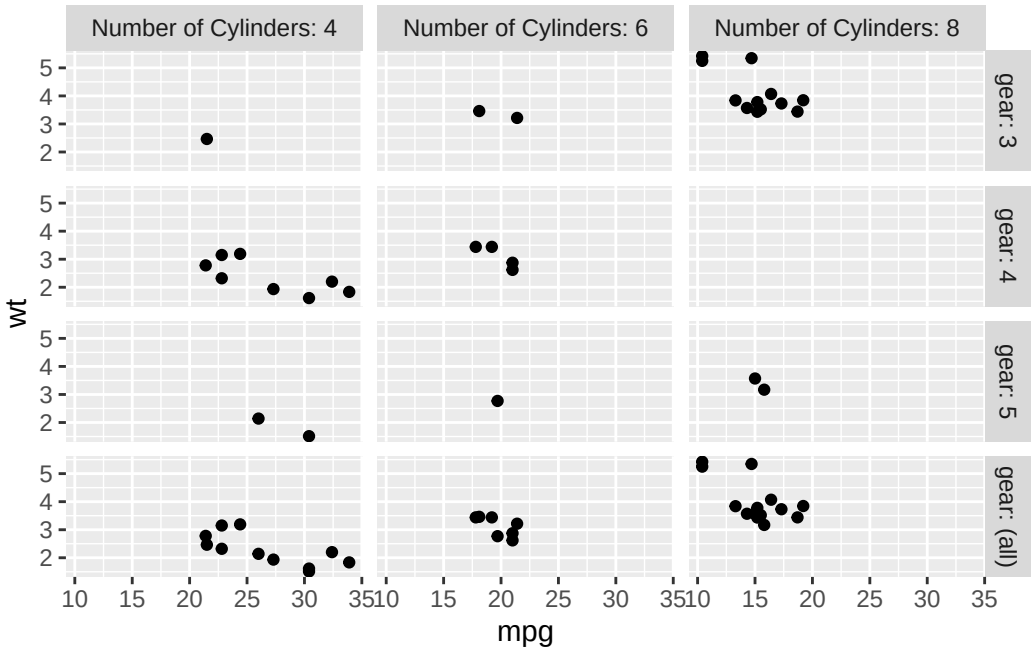

```
p.tmp + facet_wrap(facets = vars(cyl))
```



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

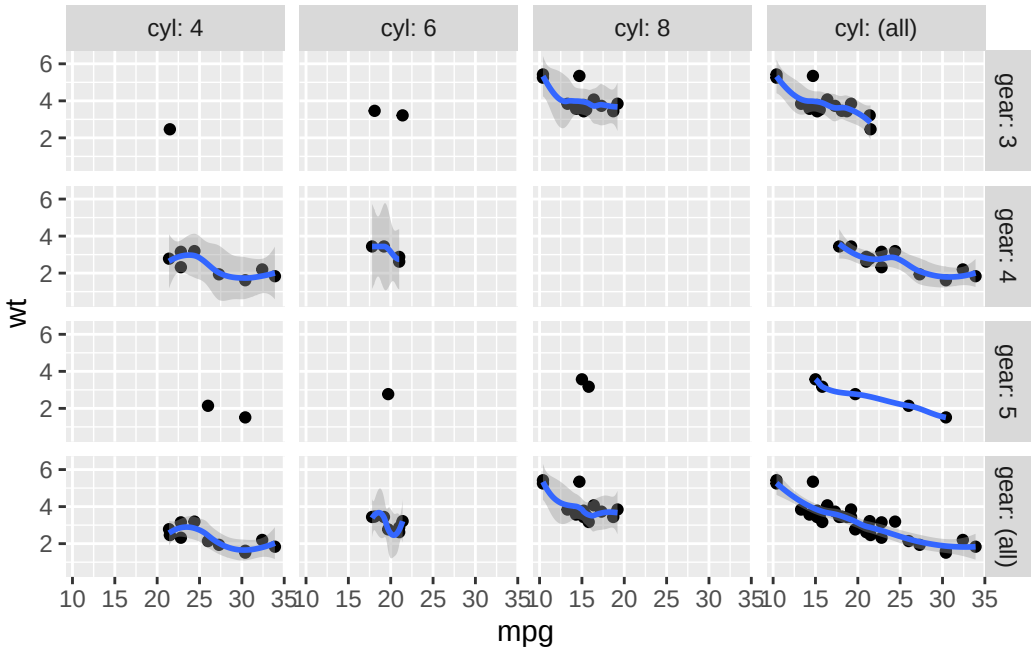



```
#p.tmp + facet_wrap(~cyl, ncol=2)
p.tmp + facet_grid(rows = vars(gear),
                   cols = vars(`Number of Cylinders`=
                               cyl),
                   labeller=label_both,margins='gear')
```

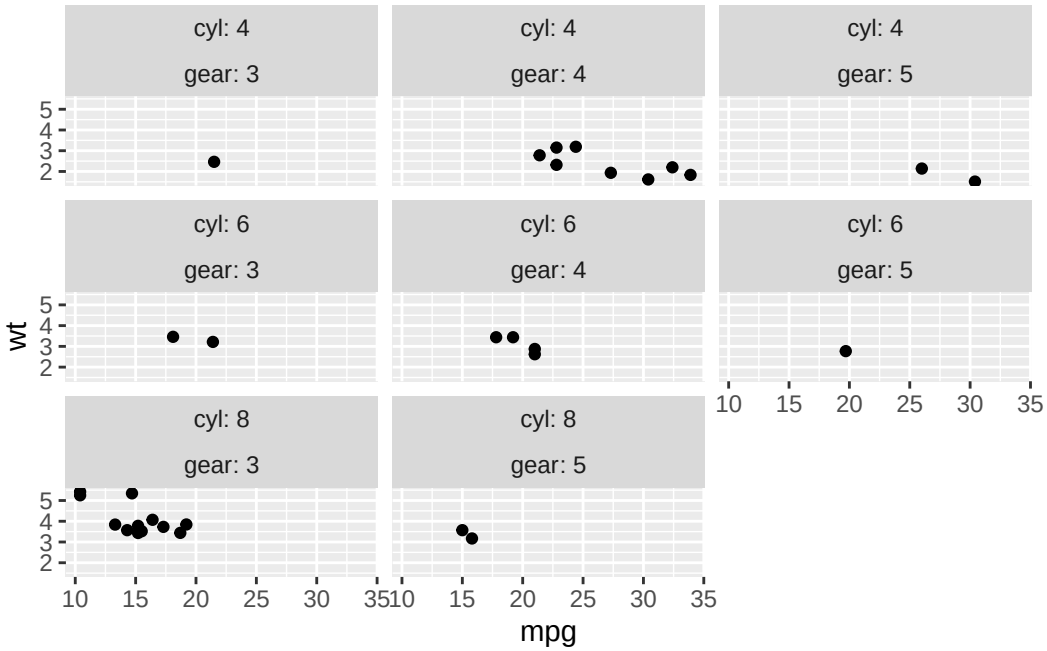



```
options(warn=-1)
p.tmp + geom_smooth()+
  facet_grid(gear~cyl, labeller=label_both,margins=T)
```

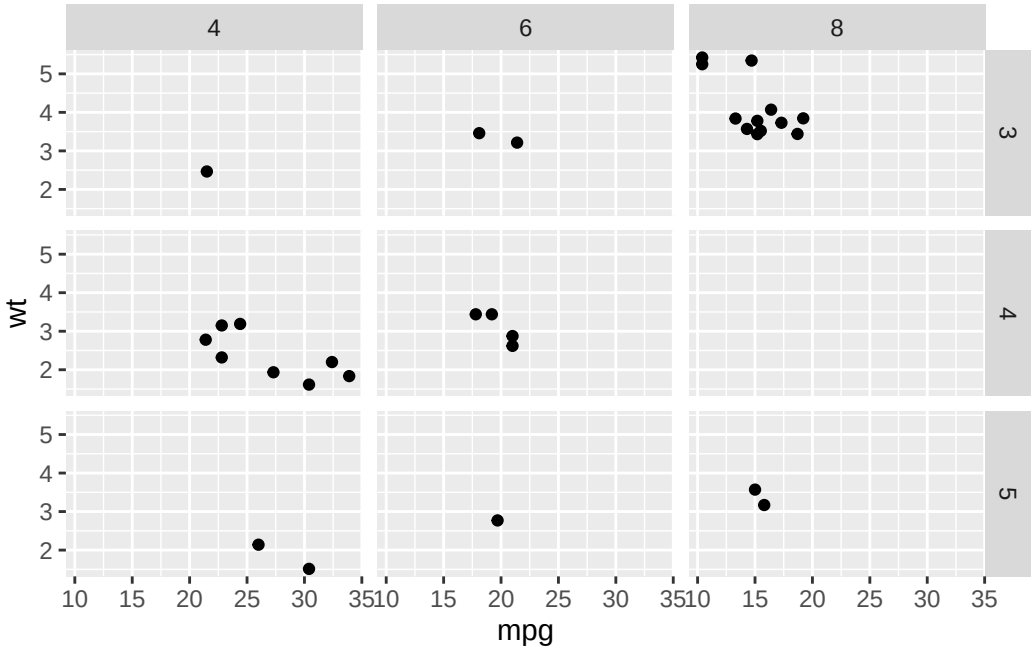
```
`geom_smooth()` using method = 'loess' and formula = 'y ~ x'
```



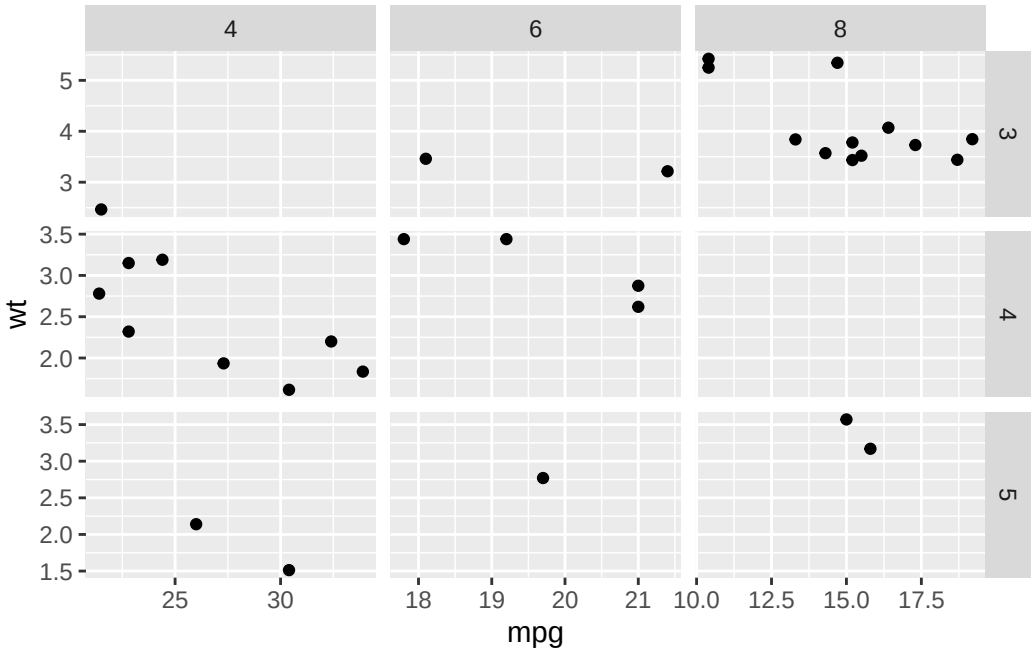

```
options(warn=0)

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



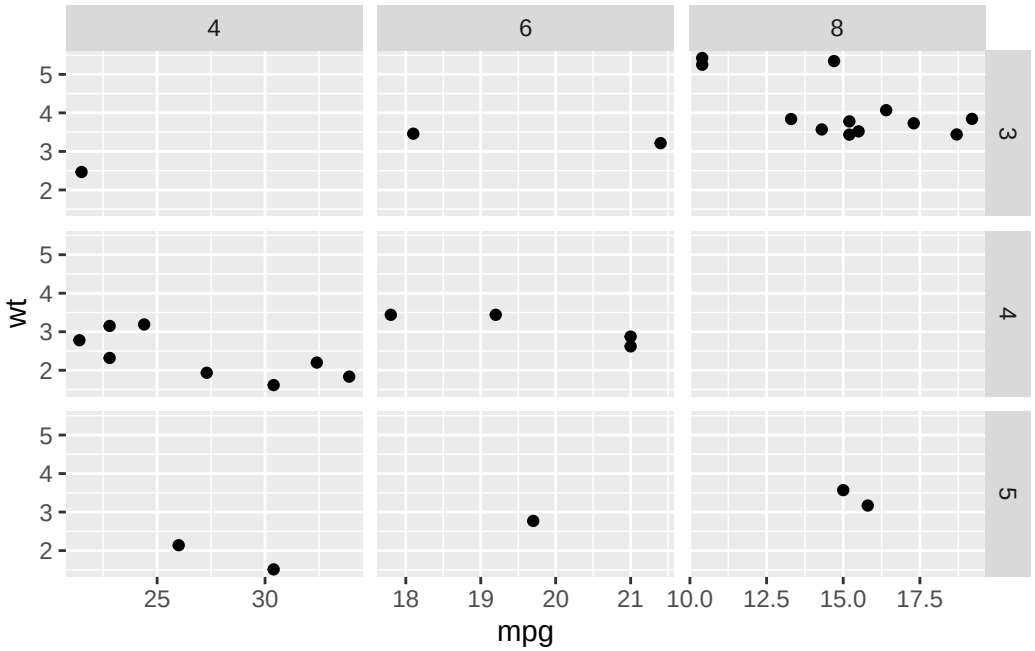

```
# controlling scales in facets (default: scales="fixed")
p.tmp + facet_grid(gear~cyl, scales="fixed")
```



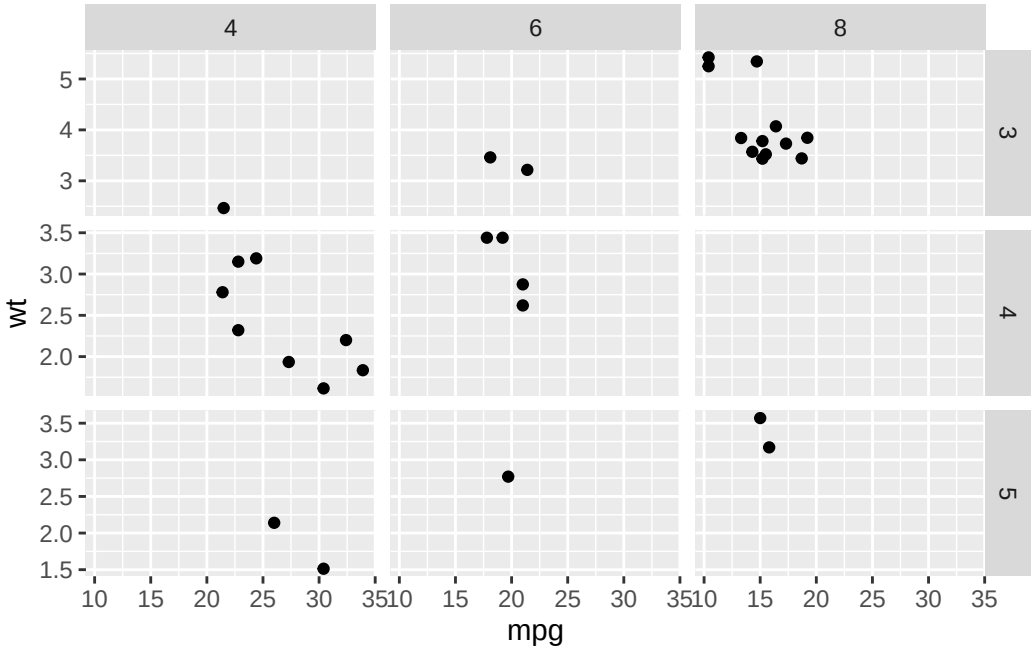
```
p.tmp + facet_grid(gear~cyl, scales="free")
```



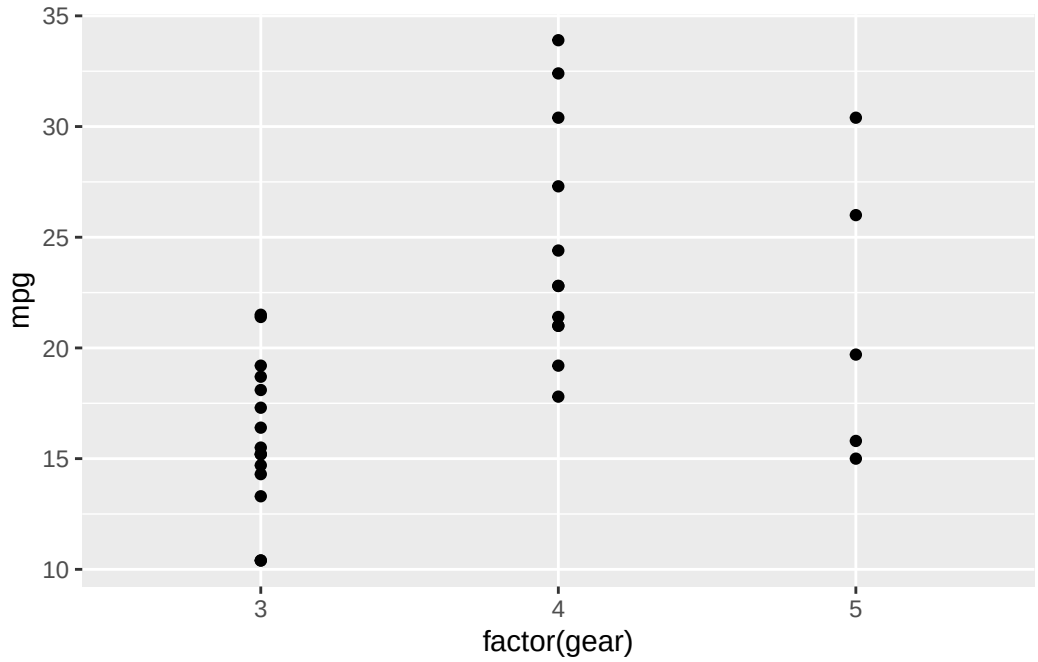

```
p.tmp + facet_grid(gear~cyl, scales="free_x")
```




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

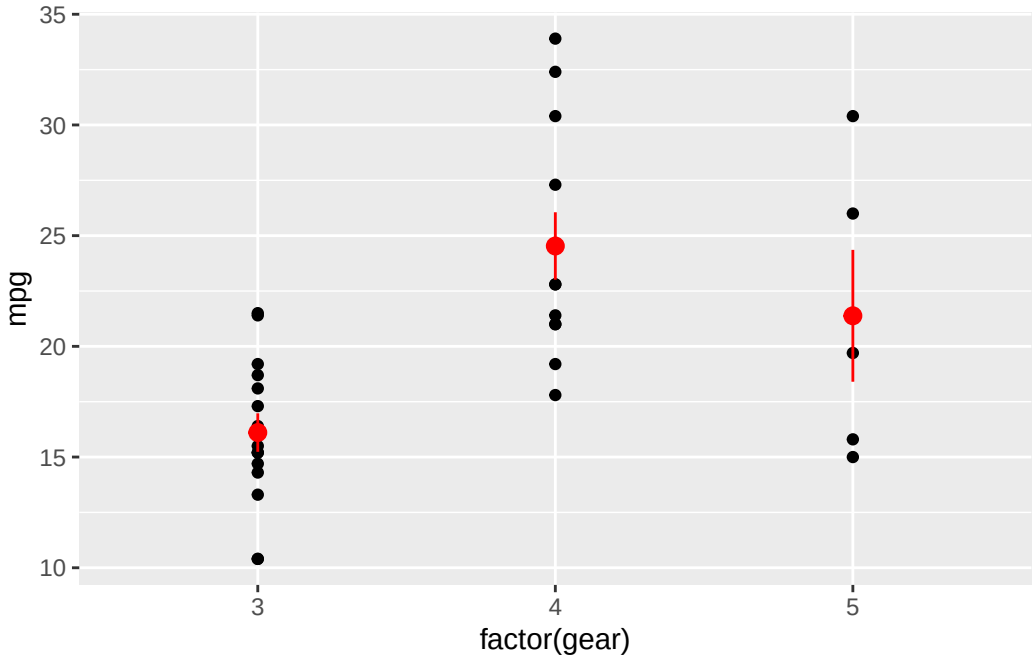


```
# summaries ####
(plottemp <- ggplot(mtcars,aes(factor(gear),mpg))+
   geom_point())
```

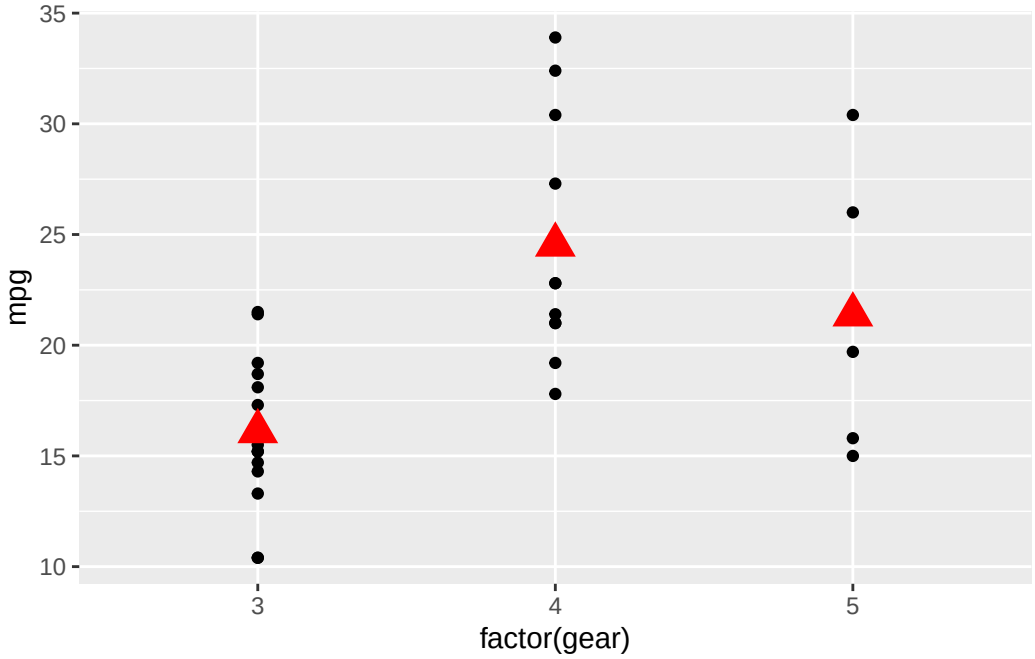



```
plottemp+stat_summary(color='red')
```

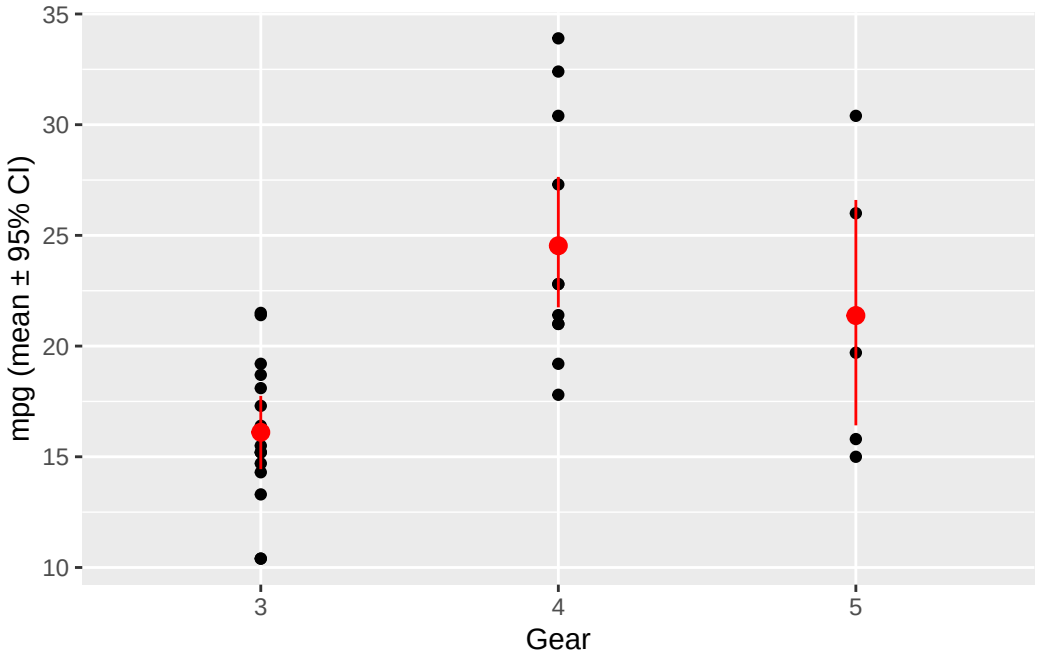
```
No summary function supplied, defaulting to `mean_se()`
```



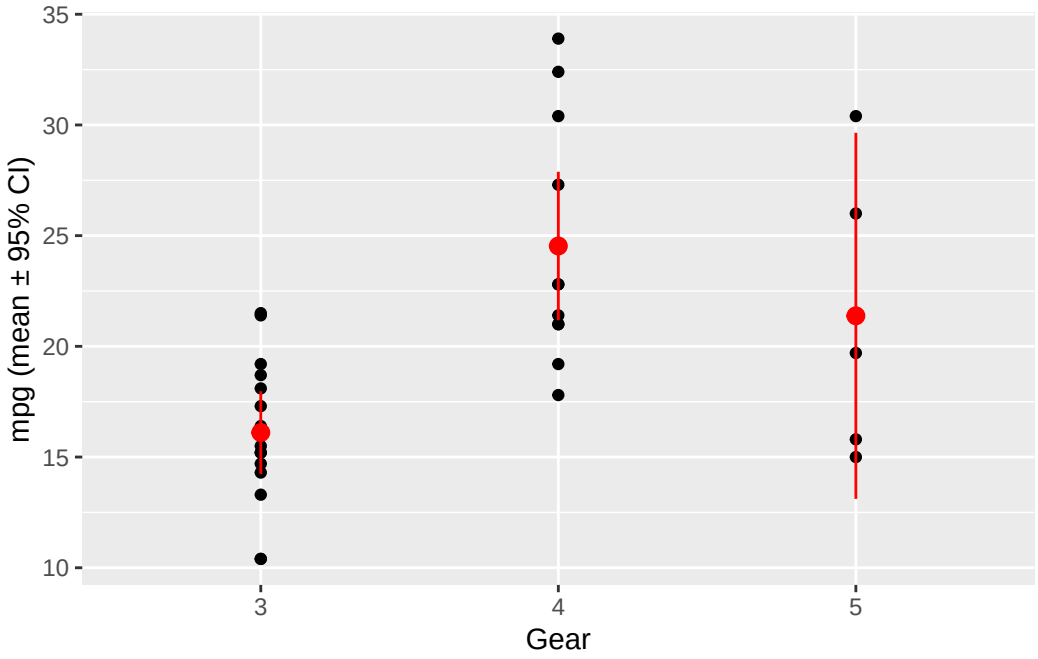

```
plottemp+stat_summary(geom = 'point', shape=17,size=5,
                      fun = 'mean',color='red')
```



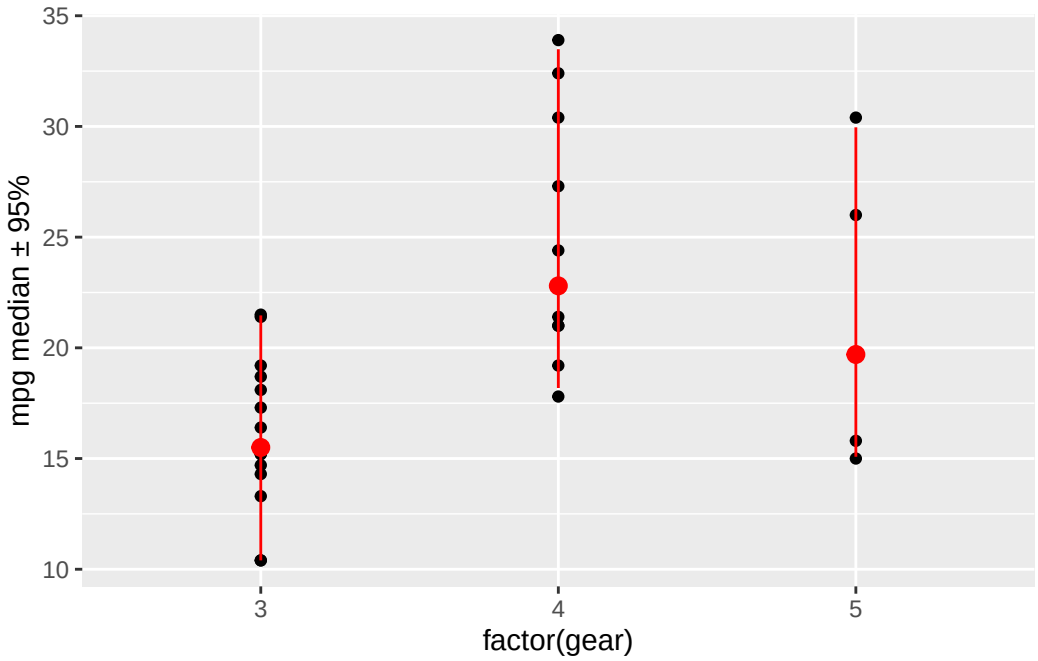
```
plottemp+stat_summary(fun.data='mean_cl_boot',color='red')+
  ylab('mpg (mean \u00b1 95% CI)')+
  xlab('Gear')
```




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



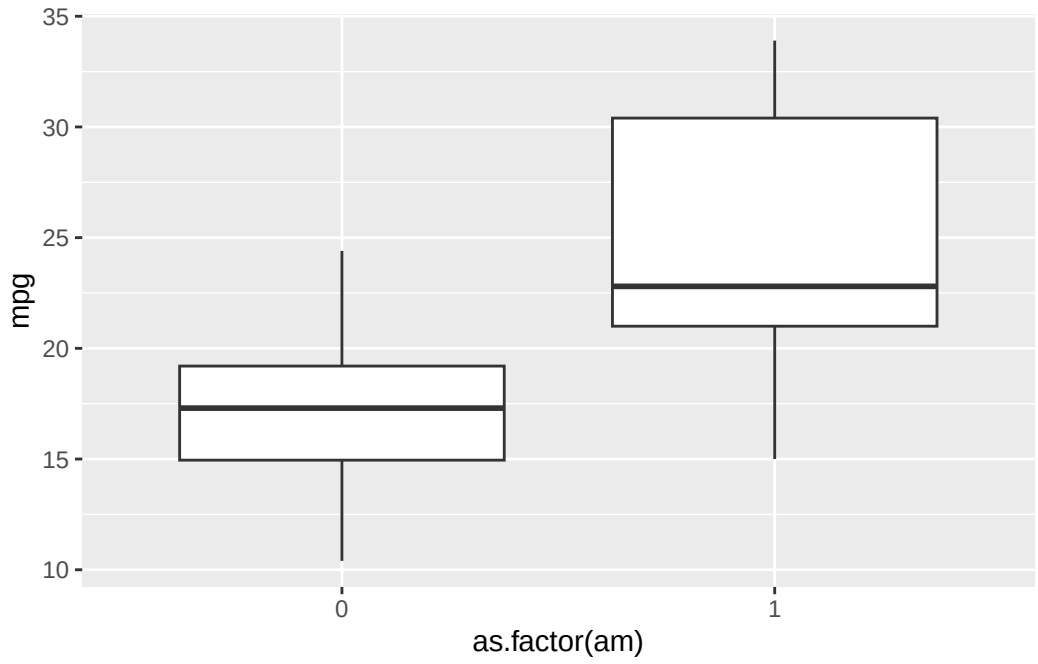

```
plottemp+stat_summary(fun.data='median_hilow',color='red')+
  ylab('mpg median \u00b1 95%')
```



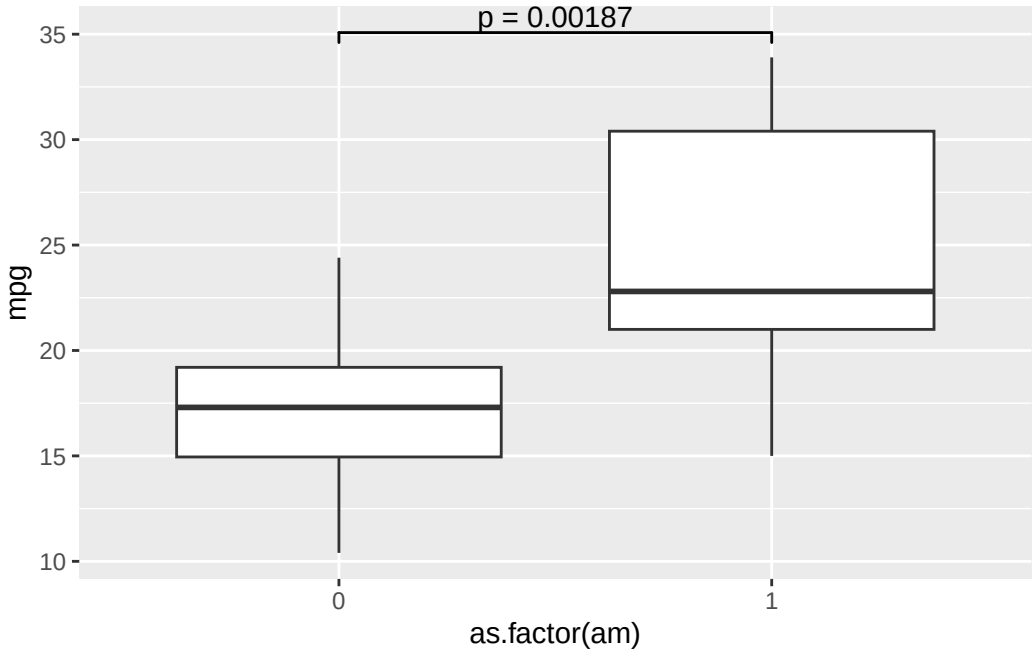
```
# geom_pointrange()

# 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())
```

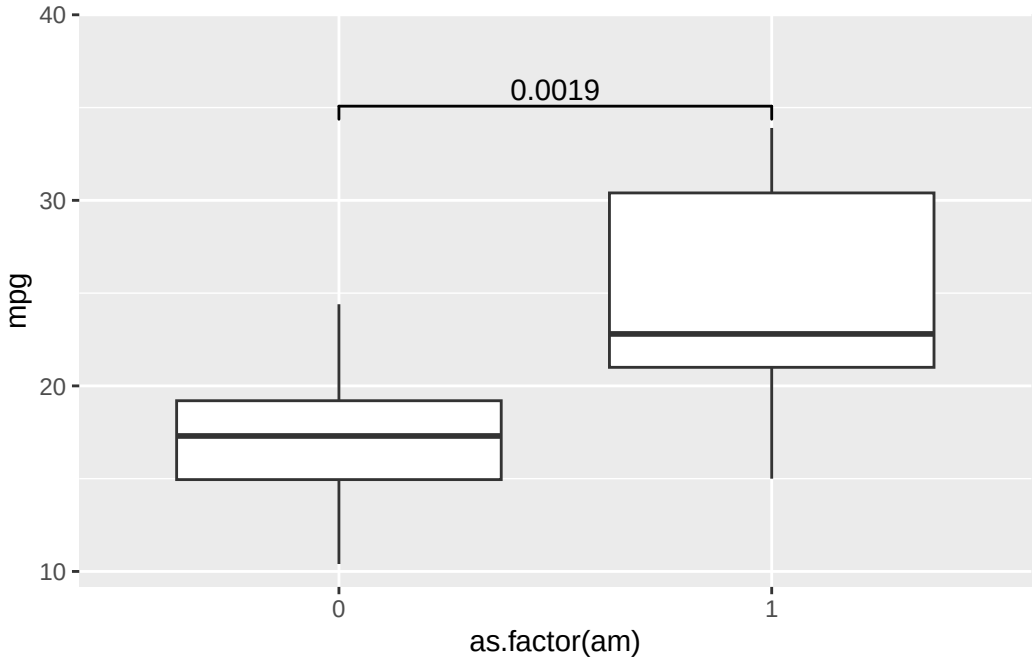



```
plottemp+geom_signif(
  comparisons=list(c(1,2)),
  # aes(y=0),
  # textsize = rel(3), vjust = .0,
  #y_position=max(mtcars$mpg+3),
  annotations=paste0('p = ', p),
  # annotations=p,
  tip_length=.02)
```

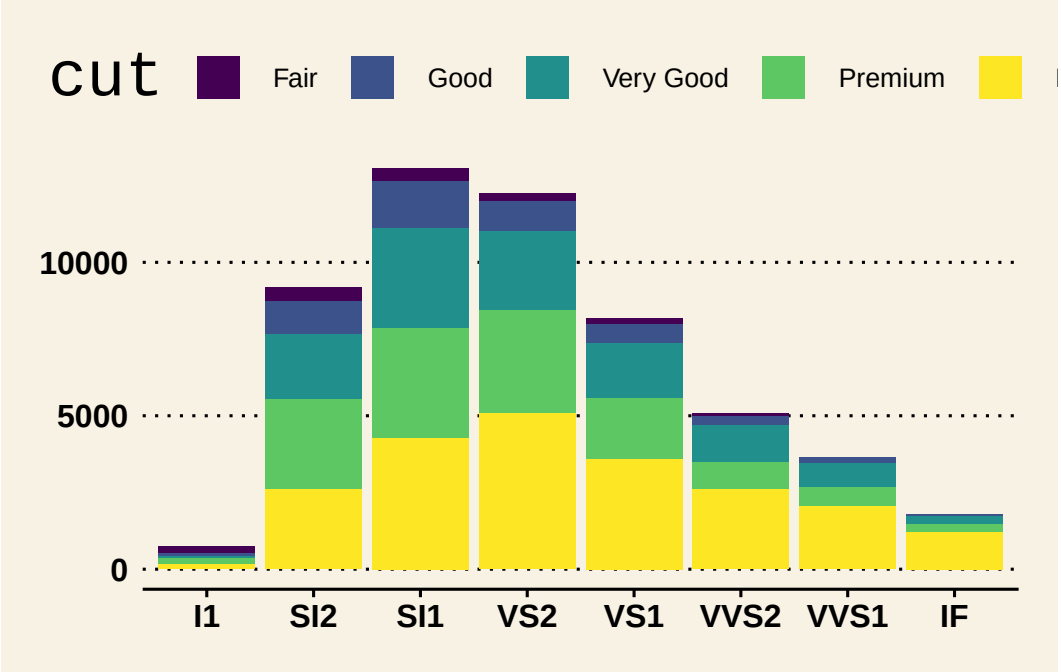



```
plottemp + geom_signif(
  comparisons=list(1:2))+
  scale_y_continuous(expand = expansion(mult=c(0.05,.2)))
```

```
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
```



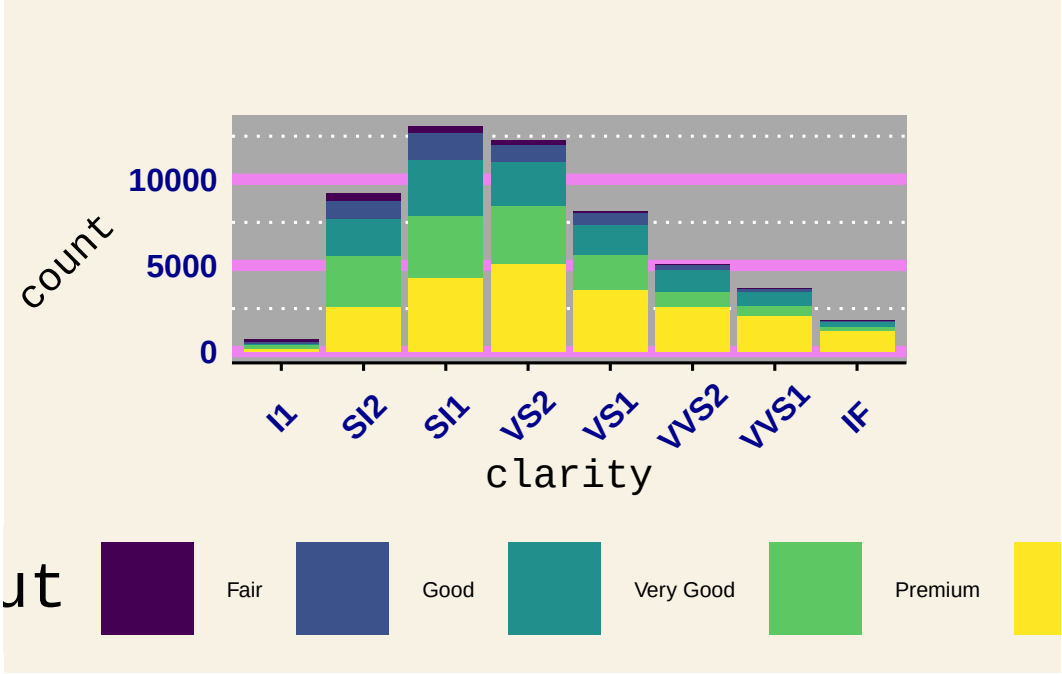

```
old <- theme_set(theme_wsj())
# theme_set(theme_wsj())
ggplot(data=diamonds,aes(x=clarity,fill=cut))+
  geom_bar()
```



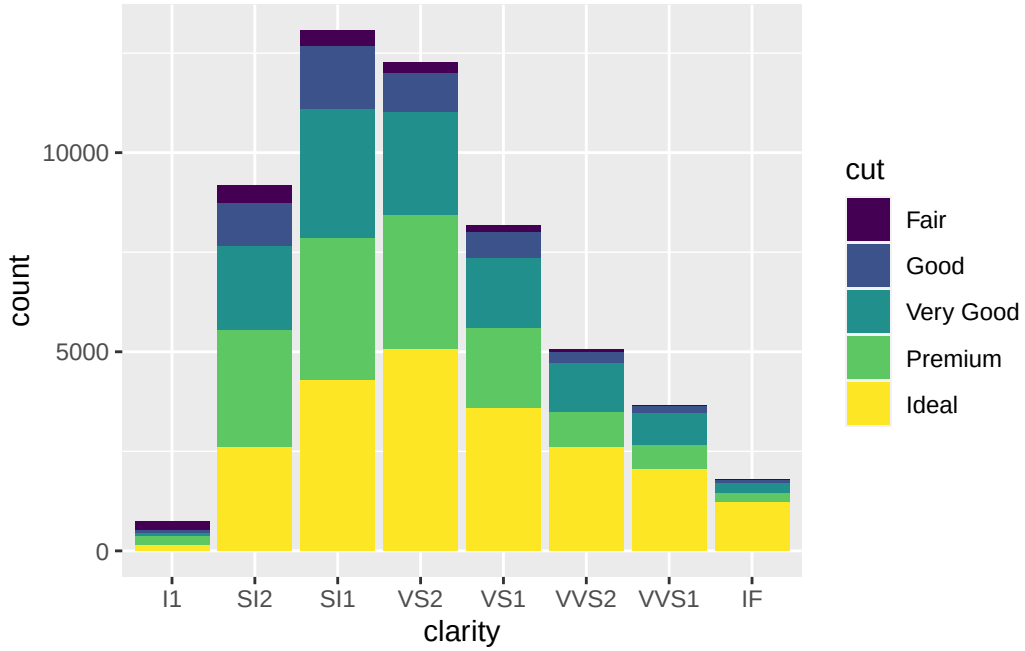

```
theme_update(legend.position="bottom",
             axis.text=element_text(colour = "darkblue",
                                    size=12),
             axis.text.x=element_text(vjust=0.5,angle=45),
             axis.title=element_text(size=15),
             plot.margin=unit(c(3,4,.5,.3),'lines'),    #N,E,S,W
             axis.title.y=element_text(vjust=0.4,angle=45),
             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',size = 2),
             legend.text = element_text(size = 8))
```

```
Warning: The `size` argument of `element_line()` is deprecated as of ggplot2 3.4.0.
i Please use the `linewidth` argument instead.
```

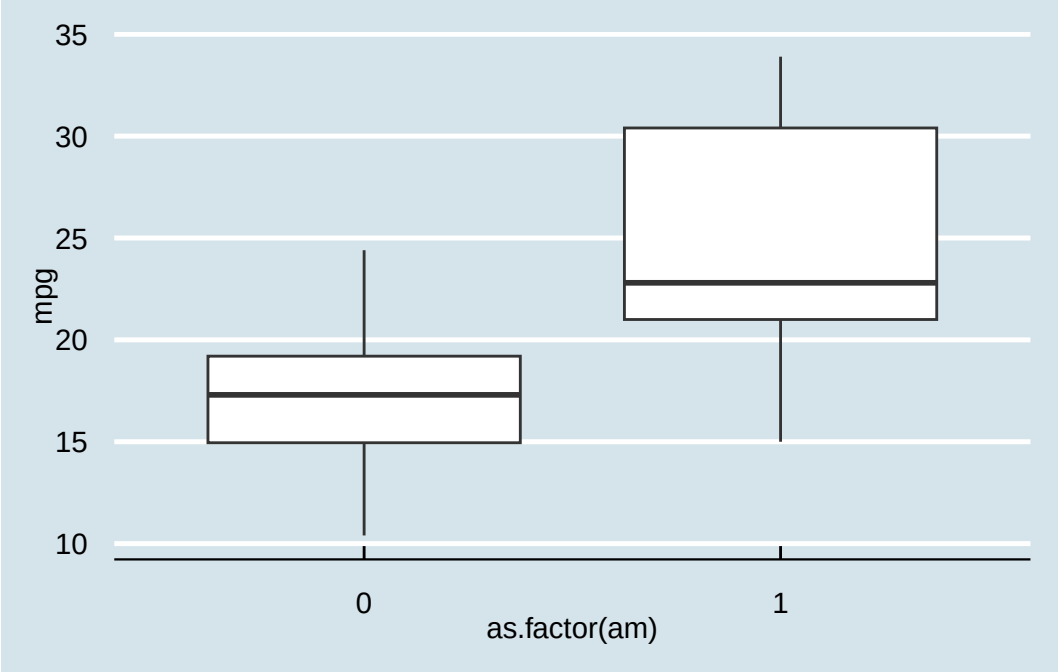
```
ggplot(data=diamonds,aes(x=clarity,fill=cut))+
  geom_bar()
```



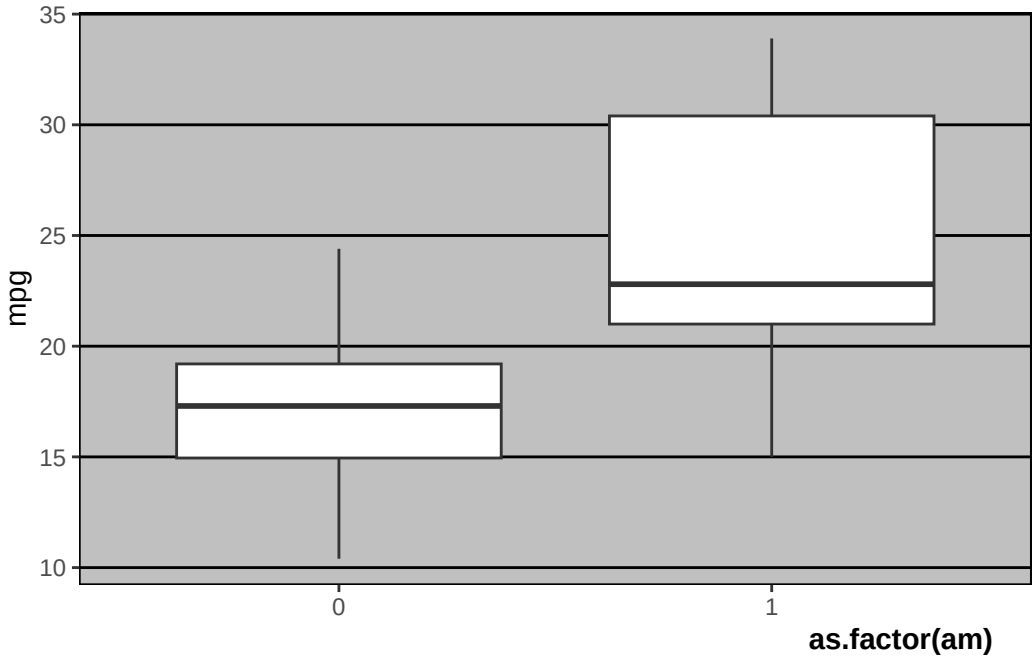

```
theme_set(theme_grey())
#theme_set(old)
ggplot(data=diamonds,aes(x=clarity,fill=cut))+
  geom_bar()
```



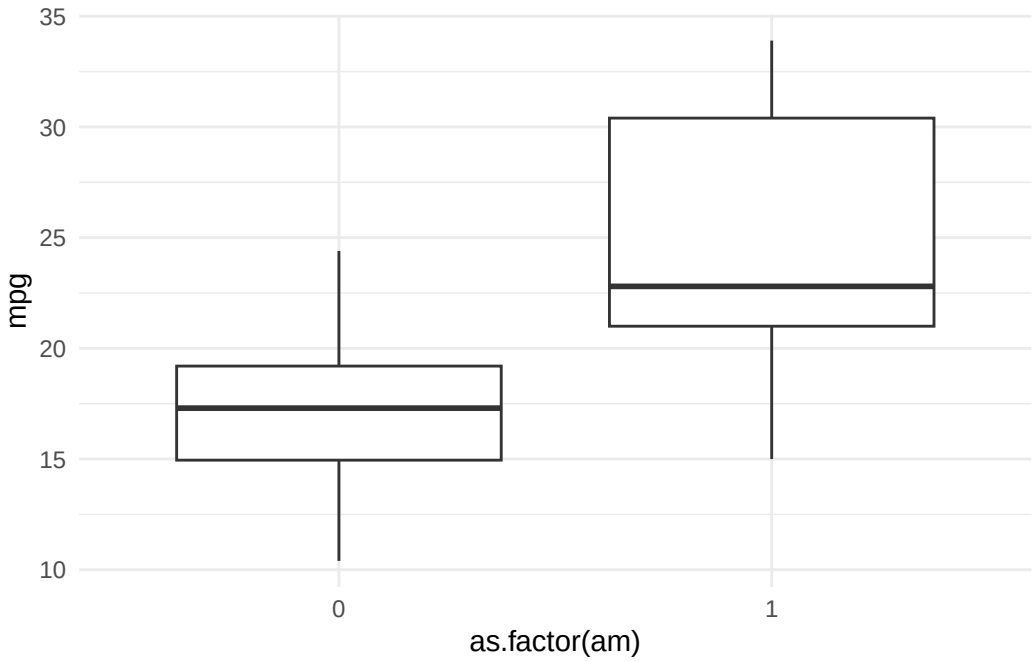

```
# ggthemes ####
plottemp+theme_economist()
```



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




```
plottemp+theme_minimal()
```




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


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

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

6 Descriptive statistics

```
pacman::p_load(tidyverse,wrappedtools,readxl)
#dir('Data/')
rawdata <- read_excel(path = 'data/Medtest_e.xlsx')
rawdata <- rename(rawdata,
                  `Size (cm)`=size,
                  `Weight (kg)`=weight)
rawdata <- select(rawdata,
                  -Sex_m)
save(rawdata,file = "data/testdata.RData")

ggplot(rawdata,aes(sysBP_V0, diaBP_V0))+
  geom_point()+
  geom_smooth(se=F)+
  geom_smooth(method='lm',color='red',
              fill='gold', alpha=.15)
```

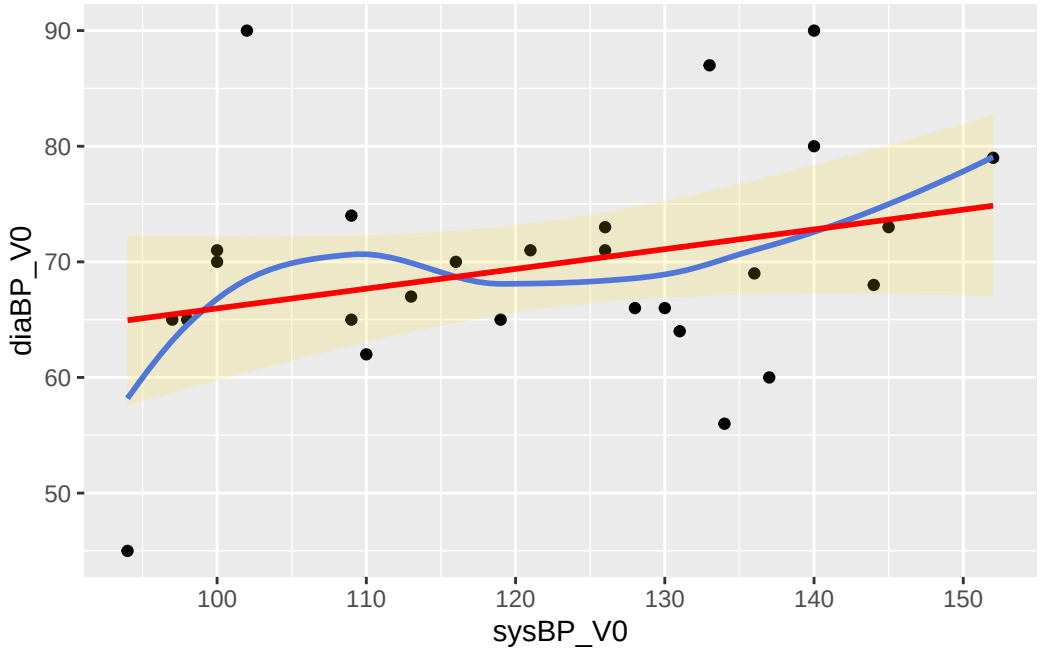
```
`geom_smooth()` using method = 'loess' and formula = 'y ~ x'
```

```
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 = T,add_n = T)
```

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

```
  meansd(rawdata$sysBP_V0, roundDig = 4,range = T,
         add_n = T,.german = T)
```

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

```
  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)"
```

```
  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
```

```
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 = T)
```

```
$level
[1] "f m"

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

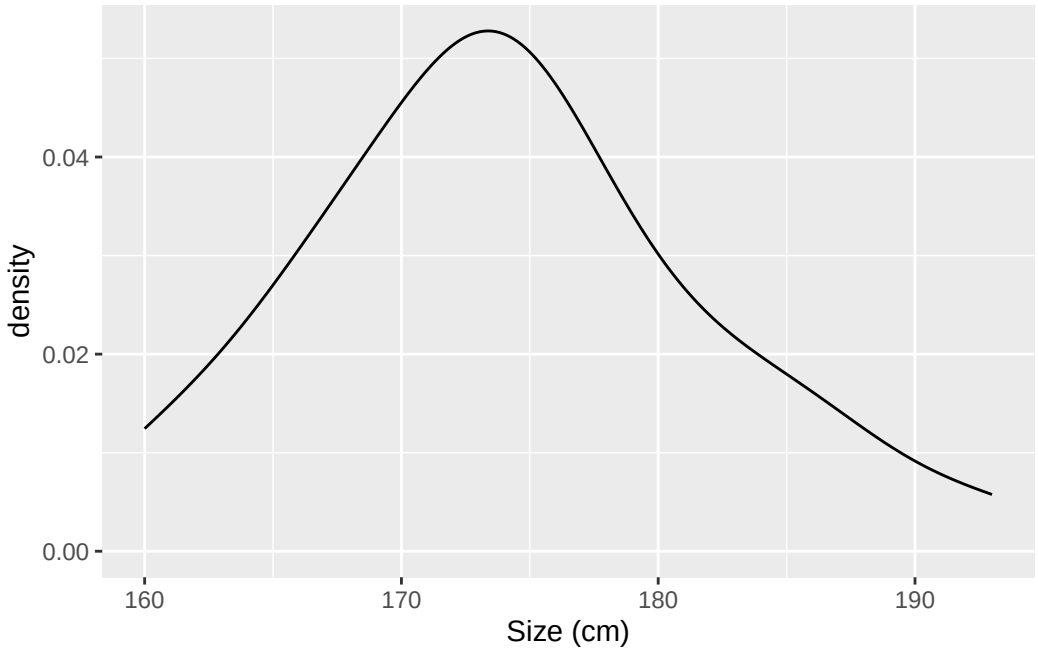
```
rawdata |>
  group_by(sex,testmedication) |>
  summarise(WeightSummary=meansd(`Weight (kg)`))
```

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

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

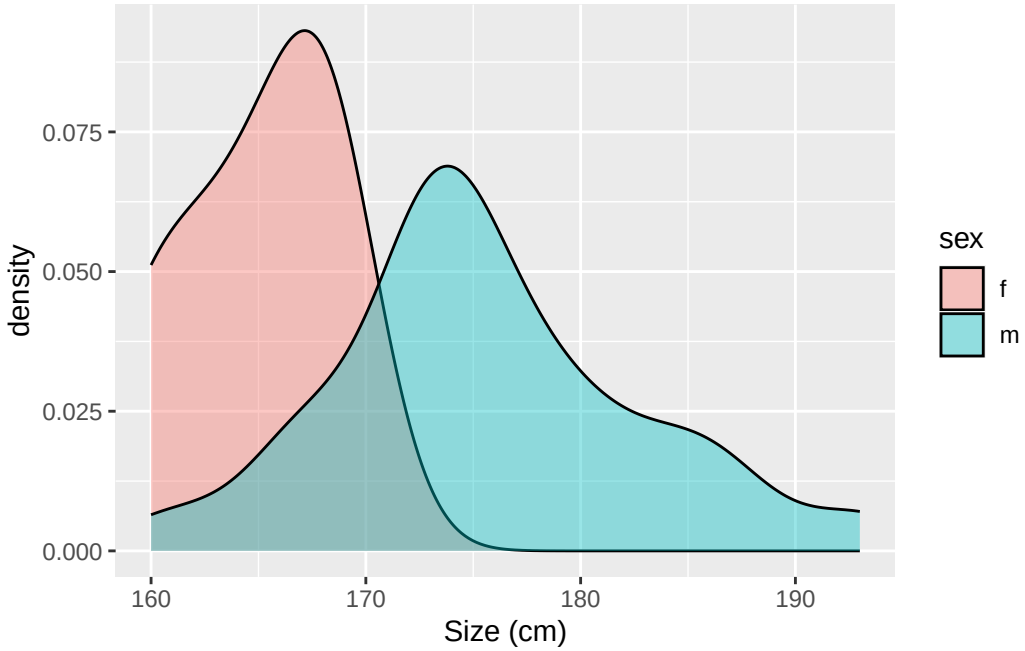
```
compare2numvars(rawdata,
                dep_vars = c( "Size (cm)","Weight (kg)",
                              "sysBP_V0","diaBP_V0"),
                indep_var = 'sex',
                gaussian = F)
```

```
# 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
```

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




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




```
ks.test(rawdata$`Size (cm)`,
        pnorm) #WRONG!!!!!
```

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

```
    Asymptotic one-sample Kolmogorov-Smirnov test

data:  rawdata$`Size (cm)`
D = 1, p-value < 2.2e-16
alternative hypothesis: two-sided
```

```
ks.test(rawdata$`Size (cm)`,
        pnorm,
        mean=mean(rawdata$`Size (cm)`),
        sd=sd(rawdata$`Size (cm)`))
```

```
Warning in ks.test.default(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
```

7 Simple test statistics

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

```
##### Test for normal distribution -----
ks.test(x = rawdata$`Size (cm)`,
        'pnorm',
        mean(rawdata$`Size (cm)`,na.rm=T),
        sd(rawdata$`Size (cm)`,na.rm=T),
        exact=F)
```

```
Warning in ks.test.default(x = rawdata$`Size (cm)`, "pnorm", mean(rawdata$`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
```

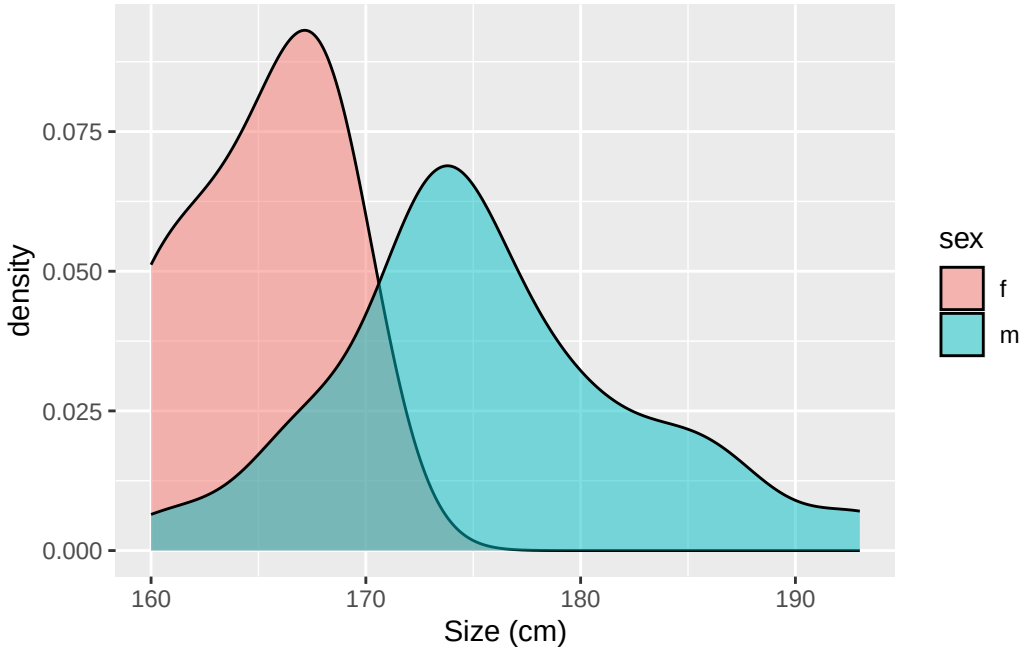
```
ksnormal(rawdata$`Weight (kg)`)
```

```
[1] 0.7598605
```

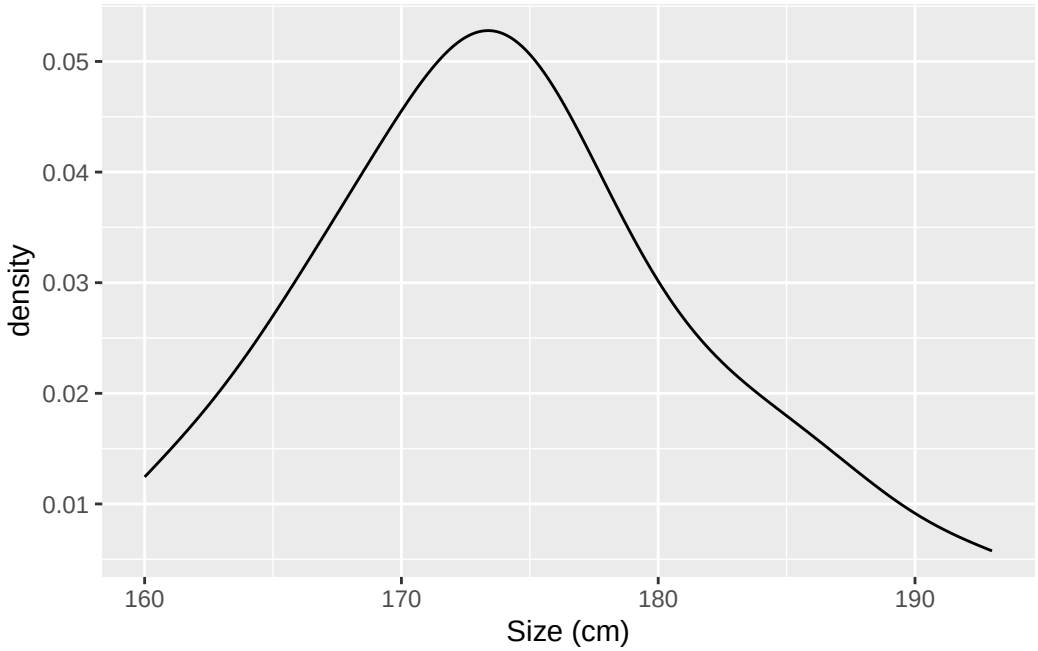
```
shapiro.test(rawdata$`Size (cm)`)
```

```
    Shapiro-Wilk normality test

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

```
ggplot(rawdata,aes(x = `Size (cm)`,fill=sex))+
  geom_density(alpha=.5)
```




```
ggplot(rawdata,aes(x = `Size (cm)`))+
  geom_line(stat='density')
```




```
(ksout<-ksnormal(x = rawdata$`Size (cm)`))
```

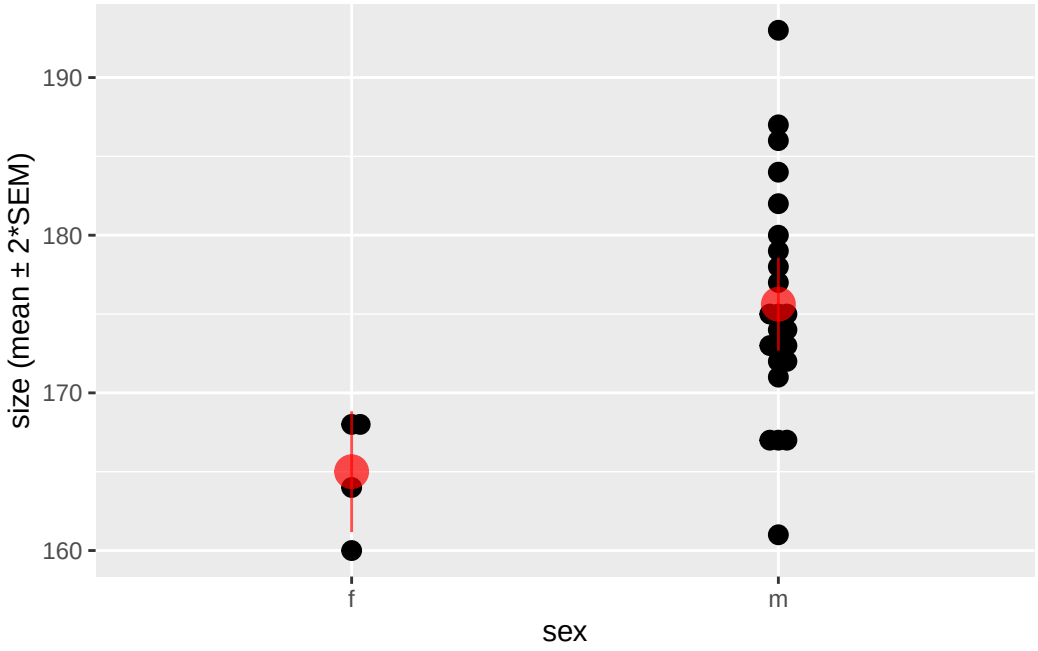
```
[1] 0.7063825
```

```
# test, if log-normal (->then transform)
if (ksnormal(rawdata$`Size (cm)`)<=.05 &
    ksnormal(log(rawdata$`Size (cm)`))>.05) {
  print('lognormal')
  # create new log-transformed variable or just transform...
} else {
  print('not lognormal')
}
```

```
[1] "not lognormal"
```

```
##### 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"
```

```
apply(X=rawdata[quantvars$index],MARGIN=2,
      FUN=meansd,roundDig=2)
```

```
      included       finalized   testmedication        Size (cm)
"0.96 ± 0.19"   "0.86 ± 0.36"    "0.50 ± 0.51"       "174 ± 8"
  Weight (kg)        sysBP_V0         diaBP_V0      lv_edv_mri
    "88 ± 15"      "122 ± 17"       "70 ± 10"      "206 ± 70"
```

```
      lv_esv_mri        lv_ef_mri lv_ef_biplan_mri          ptt_lab
       "110 ± 70"        "50 ± 15"        "49 ± 14"         "32 ± 6"
    ferritin_lab         iron_lab  transferrin_lab         sysBP_V2
     "281 ± 237"        "85 ± 37"       "258 ± 36"       "119 ± 13"
       diaBP_V2              BMI              age          NYHA_V1
        "66 ± 9"         "29 ± 4"         "60 ± 8"      "1.4 ± 0.9"
        NYHA_V2          NYHA_V3
     "1.5 ± 0.9"      "1.8 ± 0.9"
```

```
rawdata %>% group_by(sex) %>%
  summarize(Mean=mean(`Size (cm)`,na.rm=T)) %>%
  ungroup()
```

```
# A tibble: 2 x 2
  sex    Mean
  <chr> <dbl>
1 f      165
2 m      176.
```

```
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$`Size (cm)`[which(rawdata$s
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
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
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 equal to
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')
```

```
    Two Sample t-test

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

```r
print(c(mean(rawdata$sysBP_V0,na.rm=T),
        mean(rawdata$sysBP_V2,na.rm=T)))
```

```
[1] 121.8519 119.4583
```

```r
t.test(rawdata$sysBP_V0,
       rawdata$sysBP_V2,
       alternative='greater', # x>y
       paired=T)  #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
```

```r
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
```

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

```
    One Sample t-test

data:  rawdata$`Size (cm)`
t = 0.75384, df = 27, p-value = 0.4575
```

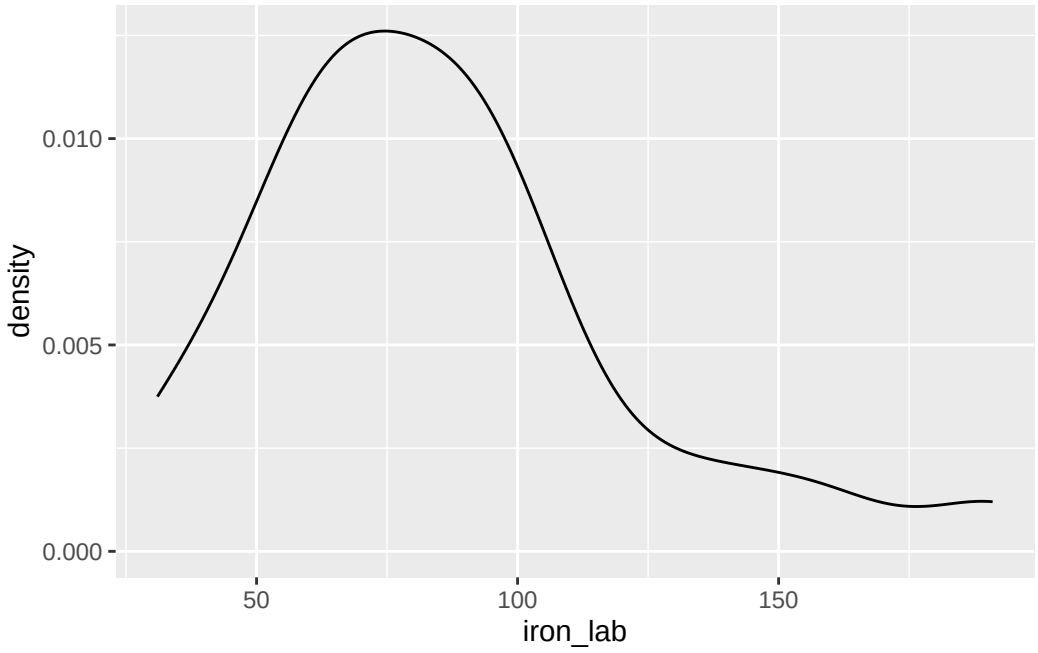
```
alternative hypothesis: true mean is not equal to 173
95 percent confidence interval:
 171.0937 177.1206
sample estimates:
mean of x
 174.1071
```

```
##### 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()`).
```

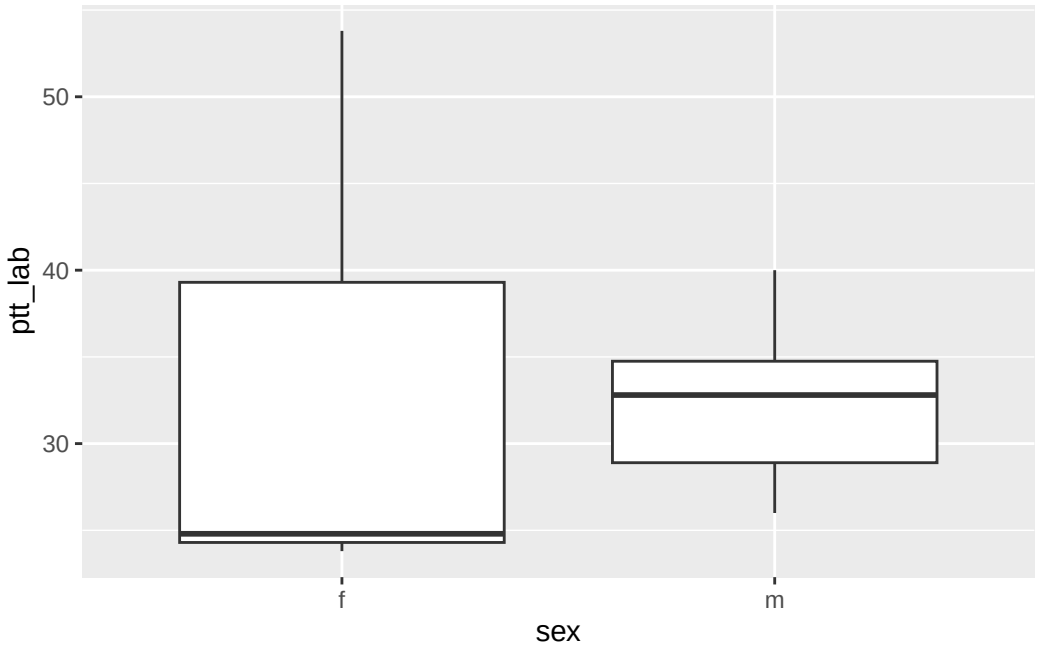


```
by(data = rawdata[[ordvars$index[1]]],
   INDICES = rawdata$sex,FUN = median_quart)
```

```
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=F,
              correct=T,paired=T)
```

```
    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
```

```
  ##### 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 = 0.175
```

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

```
  FALSE TRUE
f     1    3
m    13   11
```

```
prop.table(crosstab1)
```

```
       FALSE       TRUE
f 0.03571429 0.10714286
m 0.46428571 0.39285714
```

```
round(prop.table(crosstab1)*100)
```

```
  FALSE TRUE
f     4   11
m    46   39
```

```
round(prop.table(crosstab1,margin=2)*100) #% per column
```

```
  FALSE TRUE
f     7   21
m    93   79
```

```
round(prop.table(crosstab1,margin=1)*100) #% per row
```

```
  FALSE TRUE
f    25   75
m    54   46
```

```
(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 = 0.5929
```

```
tabletestOut$p.value
```

```
[1] 0.5928541
```

```
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
```

```
groupvars <- ColSeeker(namepattern = c('sex','test'))


##### report -----
# report_qv %<>%
#   mutate(
#     Variable=factor(Variable, levels=quantvars$names),
#     female='', male='',`p sexdiff`="") %>%
#   arrange(Variable)
# for (var_i in 1:quantvars$count) {
#   report_qv[var_i, c('female','male')] <-
#     meansd(rawdata[[quantvars$index[var_i]]],
```

```
#            groupvar = rawdata %>% pull(groupvars$names[2]),#$sex,
#            add_n = T,rangesep = '  ',
#            range = T) %>%
#     as.list()
#   evOut<-var.test((rawdata %>% pull(quantvars$index[var_i]))~
#                     rawdata$sex)
#   tOut<-t.test((rawdata %>% pull(quantvars$index[var_i]))~
#                  rawdata$sex,
#                var.equal=evOut$p.value>.05)
#   report_qv$`p sexdiff`[var_i] <- formatP(tOut$p.value)
#   rm(evOut,tOut)
# }

compare2numvars(data = rawdata,dep_vars = quantvars$names,
                indep_var = "sex",gaussian = T)
```

```
# A tibble: 22 x 5
   Variable       desc_all    `sex f`     `sex m`     p
   <fct>          <chr>       <chr>       <chr>       <chr>
 1 included       0.96 ± 0.19 1.0 ± 0.0   1.0 ± 0.2   0.328
 2 finalized      0.86 ± 0.36 0.75 ± 0.50 0.88 ± 0.34 0.526
 3 testmedication 0.50 ± 0.51 0.50 ± 0.58 0.50 ± 0.51 1.000
 4 Size (cm)      174 ± 8     165 ± 4     176 ± 7     0.009
 5 Weight (kg)    88 ± 15     76 ± 13     90 ± 14     0.072
 6 sysBP_V0       122 ± 17    118 ± 14    123 ± 18    0.587
 7 diaBP_V0       70 ± 10     71 ± 13     69 ± 9      0.780
 8 lv_edv_mri     206 ± 70    235 ± 72    203 ± 71    0.559
 9 lv_esv_mri     110 ± 70    158 ± 56    105 ± 71    0.322
10 lv_ef_mri      50 ± 15     33 ± 3      52 ± 15     0.095
# i 12 more rows
```

```
compare2numvars(data = rawdata,dep_vars = quantvars$names,
                indep_var = "testmedication",gaussian = T)
```

```
# A tibble: 21 x 5
   Variable         desc_all    `testmedication 0` `testmedication 1` p
   <fct>            <chr>       <chr>              <chr>              <chr>
 1 included         0.96 ± 0.19 1.0 ± 0.0          0.9 ± 0.3          0.336
 2 finalized        0.86 ± 0.36 0.79 ± 0.43        0.93 ± 0.27        0.297
```

```
 3 Size (cm)        174 ± 8     173 ± 6           175 ± 9           0.653
 4 Weight (kg)      88 ± 15     90 ± 14           86 ± 16           0.448
 5 sysBP_V0         122 ± 17    122 ± 15          122 ± 19          0.966
 6 diaBP_V0         70 ± 10     70 ± 7            70 ± 12           0.943
 7 lv_edv_mri       206 ± 70    243 ± 77          173 ± 45          0.019
 8 lv_esv_mri       110 ± 70    138 ± 87          86 ± 41           0.108
 9 lv_ef_mri        50 ± 15     48 ± 18           52 ± 12           0.532
10 lv_ef_biplan_mri 49 ± 14     47 ± 17           50 ± 13           0.747
# i 11 more rows
```

```r
for(group_i in seq_len(groupvars$count)){
  resulttmp <- compare2numvars(data = rawdata,dep_vars = quantvars$names,
                  indep_var = groupvars$names[group_i],gaussian = T)
  print(resulttmp)
}
```

```
# A tibble: 21 x 5
   Variable         desc_all    `testmedication 0` `testmedication 1` p
   <fct>            <chr>       <chr>              <chr>               <chr>
 1 included         0.96 ± 0.19 1.0 ± 0.0          0.9 ± 0.3           0.336
 2 finalized        0.86 ± 0.36 0.79 ± 0.43        0.93 ± 0.27         0.297
 3 Size (cm)        174 ± 8     173 ± 6            175 ± 9             0.653
 4 Weight (kg)      88 ± 15     90 ± 14            86 ± 16             0.448
 5 sysBP_V0         122 ± 17    122 ± 15           122 ± 19            0.966
 6 diaBP_V0         70 ± 10     70 ± 7             70 ± 12             0.943
 7 lv_edv_mri       206 ± 70    243 ± 77           173 ± 45            0.019
 8 lv_esv_mri       110 ± 70    138 ± 87           86 ± 41             0.108
 9 lv_ef_mri        50 ± 15     48 ± 18            52 ± 12             0.532
10 lv_ef_biplan_mri 49 ± 14     47 ± 17            50 ± 13             0.747
# i 11 more rows
# A tibble: 22 x 5
   Variable       desc_all    `sex f`     `sex m`     p
   <fct>          <chr>       <chr>       <chr>       <chr>
 1 included       0.96 ± 0.19 1.0 ± 0.0   1.0 ± 0.2   0.328
 2 finalized      0.86 ± 0.36 0.75 ± 0.50 0.88 ± 0.34 0.526
 3 testmedication 0.50 ± 0.51 0.50 ± 0.58 0.50 ± 0.51 1.000
 4 Size (cm)      174 ± 8     165 ± 4     176 ± 7     0.009
 5 Weight (kg)    88 ± 15     76 ± 13     90 ± 14     0.072
 6 sysBP_V0       122 ± 17    118 ± 14    123 ± 18    0.587
 7 diaBP_V0       70 ± 10     71 ± 13     69 ± 9      0.780
 8 lv_edv_mri     206 ± 70    235 ± 72    203 ± 71    0.559
```

```
 9 lv_esv_mri     110 ± 70    158 ± 56    105 ± 71    0.322
10 lv_ef_mri      50 ± 15     33 ± 3      52 ± 15     0.095
# i 12 more rows
```

```
# report_ov

# report_ov %<>%
#   mutate(
#     Variable=factor(Variable, levels=ordvars$names),
#     female='', male='',`p sexdiff`="") %>%
#   arrange(Variable)
# for (var_i in seq_len(ordvars$count)) {
#   report_ov[var_i,c('female','male')] <-
#     # by(rawdata[[ordvars$names[var_i]]],
#     #    rawdata$sex,quantile,probs=c(.25,.75),na.rm=T)
#     median_quart(rawdata[[ordvars$index[var_i]]],
#                  groupvar = rawdata$sex,
#                  add_n = T,rangesep = '  ',
#                  range = T) %>%
#     as.list()
#   wOut<-wilcox.test((rawdata %>% pull(ordvars$index[var_i]))~
#                       rawdata$sex,exact=F)
#   report_ov$`p sexdiff`[var_i] <- formatP(wOut$p.value)
#   plottmp <-
#     rawdata %>% ggplot(aes_string('sex',ordvars$bticked[var_i]))+
#     geom_boxplot()+
#     geom_signif(comparisons = list(c(1,2)),
#                 annotations = paste0('p ',
#                                      formatP(wOut$p.value,
#                                              pretext = T)))+
#     scale_y_continuous(expand = expansion(mult = c(.1,.15)))
#   print(plottmp)
# }

compare2numvars(data = rawdata,dep_vars = ordvars$names,
                indep_var = "sex",gaussian = F)
```

```
# A tibble: 5 x 5
  Variable        desc_all      `sex f`       `sex m`       p
  <fct>           <chr>         <chr>         <chr>         <chr>
1 ptt_lab         33 (28/35)    25 (24/49)    33 (29/35)    0.375
```

```
2 ferritin_lab    222 (162/339) 138 (90/591)  224 (172/316) 0.616
3 iron_lab        80 (61/102)   95 (92/103)   75 (60/99)    0.165
4 transferrin_lab 261 (233/276) 260 (227/299) 262 (235/276) 1.000
5 age             62 (53/67)    66 (58/69)    60 (53/66)    0.250
```

```
# report_cat
groupvar <- 'sex'
# report_cat %<>%
#   mutate(
#     Variable=factor(Variable, levels=factvars$names),
#     female='', male='',`p sexdiff`="") %>%
#   arrange(Variable)
#
# for(var_i in seq_along(factvars$names)){
#   # if(factvars$names[var_i]!=groupvar){
#     report_cat[var_i,c('female','male')] <-
#       cat_desc_stats(rawdata[[factvars$index[var_i]]],
#                      groupvar = rawdata$sex,
#                      singleline = T,separator = ' / ',
#                      return_level = F) %>%
#       as.list()
#     test_out <- fisher.test(rawdata[[factvars$index[var_i]]],
#                             rawdata[[groupvar]])
#     report_cat$`p sexdiff`[var_i] <- formatP(test_out$p.value)
#
#     p1 <- ggplot(rawdata,aes_string(groupvar,
#                                     fill=factvars$bticked[var_i]))+
#       geom_bar()+
#       geom_signif(
#         aes(y=max(table(sex))+2),
#         comparisons = list(c(1,2)),
#         annotations = paste0('p ',
#                              formatP(test_out$p.value,
#                                      pretext = T)))+
#       scale_y_continuous(expand = expansion(mult = c(.1,.15)))
#     p2 <- ggplot(rawdata,aes_string(groupvar,
#                                     fill=factvars$bticked[var_i]))+
#       geom_bar(position='fill')+
#       geom_signif(
#         aes(y=1.05),
#         comparisons = list(c(1,2)),
```

```
#         annotations = paste0('p ',
#                              formatP(test_out$p.value,
#                                      pretext = T)))+
#       scale_y_continuous(expand = expansion(mult = c(.1,.15)),
#                          labels = scales::percent)
#     p3 <- ggplot(rawdata %>%
#                    filter(!is.na(!!sym(factvars$names[var_i]))),
#                  aes_string(groupvar,
#                             fill=factvars$bticked[var_i]))+
#       geom_bar(position='fill')+
#       geom_signif(
#         aes(y=1.05),
#         comparisons = list(c(1,2)),
#         annotations = paste0('p ',
#                              formatP(test_out$p.value,
#                                      pretext = T)))+
#       scale_y_continuous(expand = expansion(mult = c(.1,.15)),
#                          labels = scales::percent)
#     print(p1/(p2+p3))
#     print(p1/(p2+p3)+plot_layout(guides = "collect") &
#             theme(legend.position = 'bottom'))
#   # }
# }

compare2qualvars(rawdata,dep_vars = factvars$names,
                 indep_var = groupvar,spacer = ' ')
```

```
# A tibble: 20 x 5
   Variable         desc_all      `sex f`       `sex m`       p
   <chr>            <chr>         <chr>         <chr>         <chr>
 1 "testmedication" " "           " "           " "           "1.000"
 2 "     0"         "14 (50%)"    "2 (50%)"     "12 (50%)"    " "
 3 "     1"         "14 (50%)"    "2 (50%)"     "12 (50%)"    " "
 4 "sex"            " "           " "           " "           "0.001"
 5 "     f"         "4 (14.29%)"  "4 (100%)"    "0 (0%)"      " "
 6 "     m"         "24 (85.71%)" "0 (0%)"      "24 (100%)"   " "
 7 "NYHA_V1"        " "           " "           " "           "0.097"
 8 "     0"         "2 (11.76%)"  "1 (33.33%)" "1 (7.14%)"   " "
 9 "     1"         "9 (52.94%)"  "0 (0%)"      "9 (64.29%)"  " "
10 "     2"         "3 (17.65%)"  "1 (33.33%)" "2 (14.29%)" " "
11 "     3"         "3 (17.65%)"  "1 (33.33%)" "2 (14.29%)" " "
```

```
12 "NYHA_V2"       " "           " "           " "           "1.000"
13 "     0"        "1 (9.09%)"   "0 (0%)"      "1 (12.5%)"   " "
14 "     1"        "6 (54.55%)"  "2 (66.67%)"  "4 (50%)"     " "
15 "     2"        "2 (18.18%)"  "1 (33.33%)"  "1 (12.5%)"   " "
16 "     3"        "2 (18.18%)"  "0 (0%)"      "2 (25%)"     " "
17 "NYHA_V3"       " "           " "           " "           "0.091"
18 "     1"        "6 (50%)"     "0 (0%)"      "6 (66.67%)"  " "
19 "     2"        "3 (25%)"     "1 (33.33%)"  "2 (22.22%)"  " "
20 "     3"        "3 (25%)"     "2 (66.67%)"  "1 (11.11%)"  " "
```

8 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.

8.1 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()
```

8.2 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.

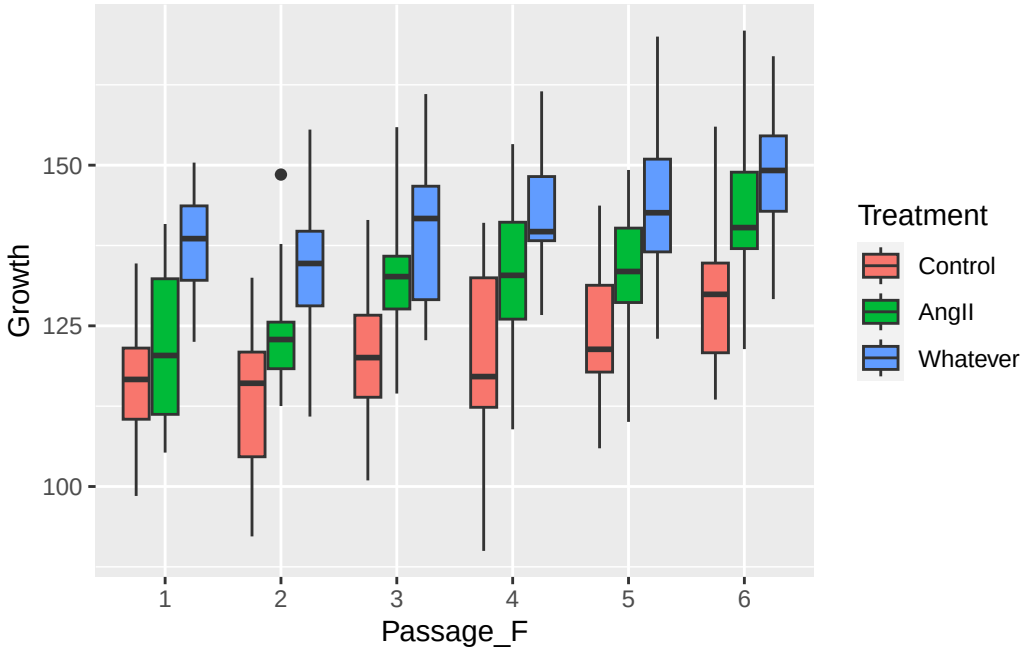
```
rawdata<-foreign::read.spss(file=here('Data/Zellbeads.sav'),
                            use.value.labels=T,to.data.frame=T) %>%
  as_tibble() %>%
  dplyr::select(-ZahlZellen) |>
  rename(Growth=Wachstum,Treatment=Bedingung) |>
  mutate(Passage_F=factor(Passage),
         Treatment=fct_recode(Treatment,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

```
re-encoding from CP1252
```

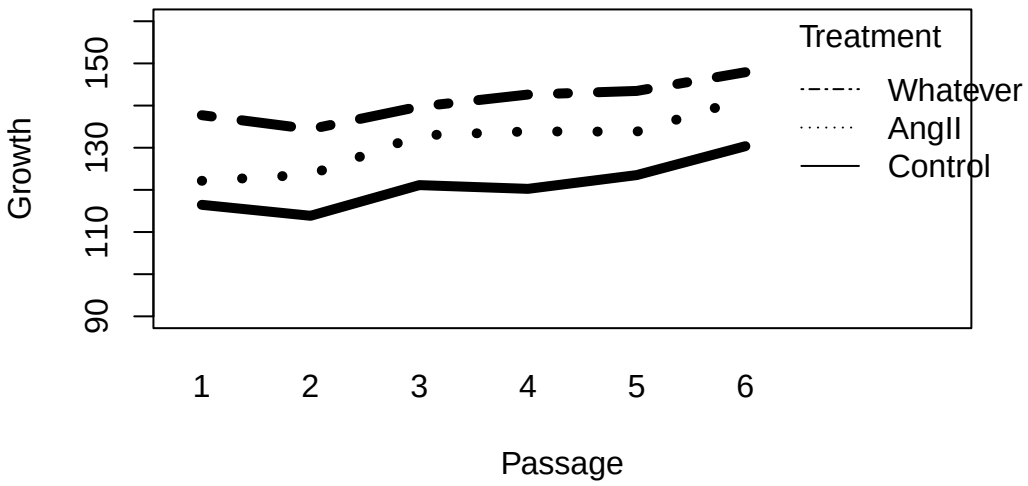
8.3 Graphical exploration

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)
```

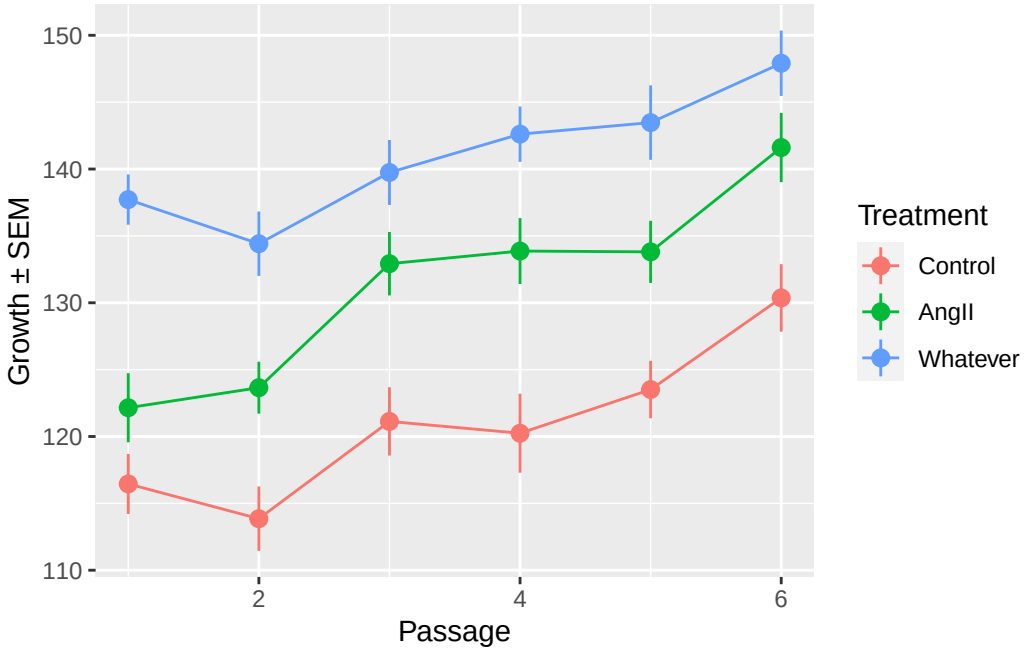



```
with(rawdata, interaction.plot(
  x.factor=Passage, trace.factor=Treatment, response=Growth,
  ylim = c(90, 160), lty = c(1,3,12), lwd = 5,
  ylab = "Growth", xlab = "Passage",
  trace.label = "Treatment"))
```



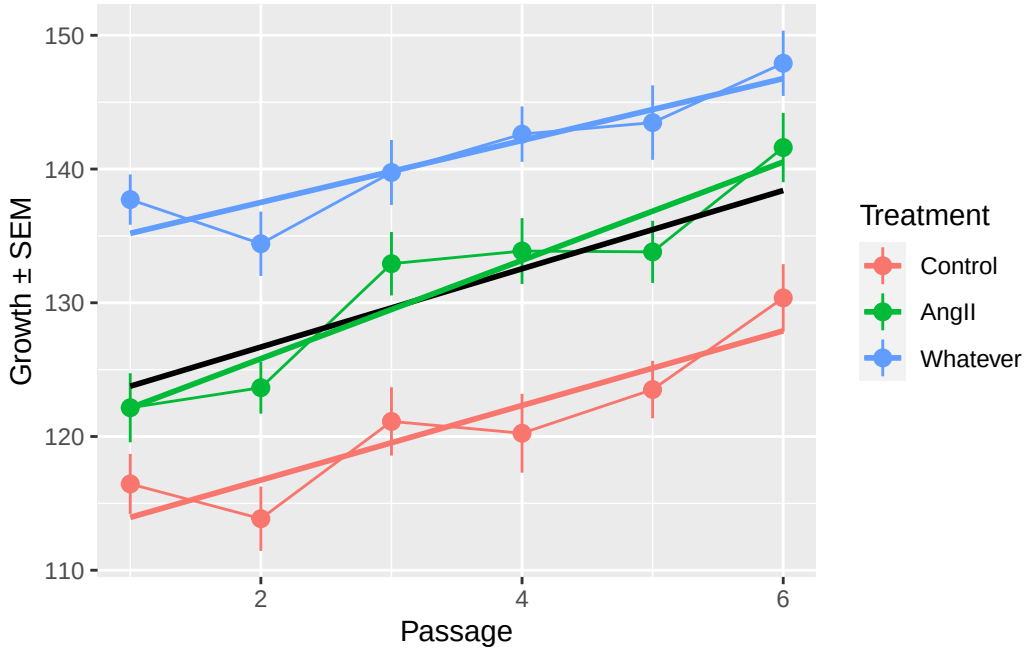

```
# p1<-ggplot(rawdata,aes(x=Passage,y=Growth))+
#    stat_summary(geom='line',fun='mean',aes(color=Treatment))+
#    stat_summary(geom='line',fun='mean')
p1<-ggplot(rawdata,aes(x=Passage,y=Growth))+
  stat_summary(geom='line',fun='mean',aes(color=Treatment))+
  stat_summary(aes(color=Treatment))+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

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



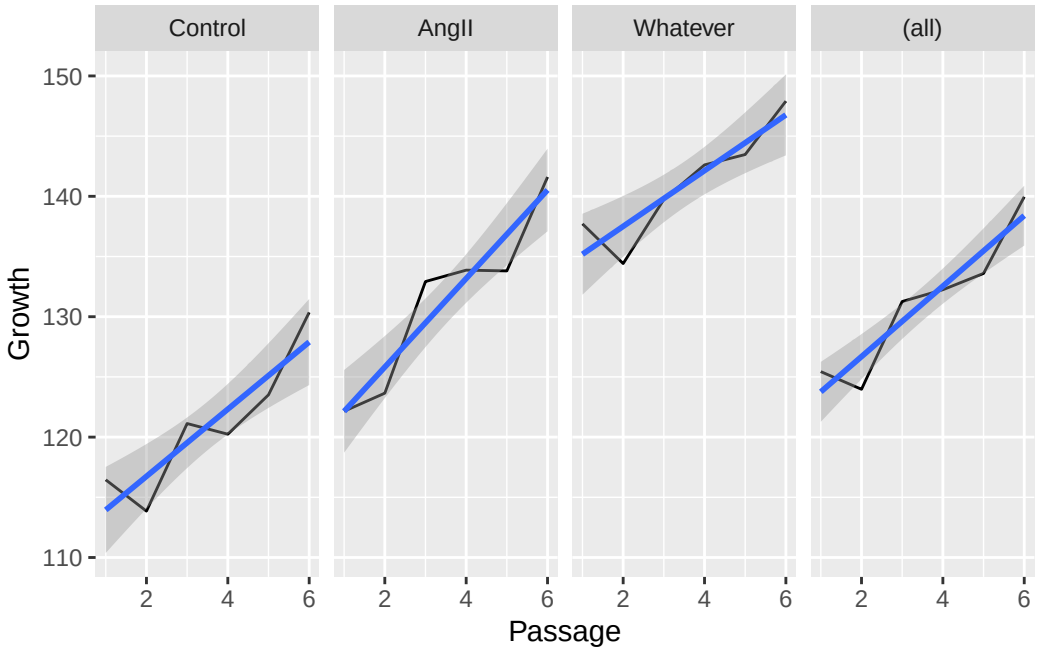

```
p1+geom_smooth(method='lm',color='black',se=F)+
  geom_smooth(method='lm',aes(color=Treatment),se=F)
```

```
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'
```



8.4 Linear Models

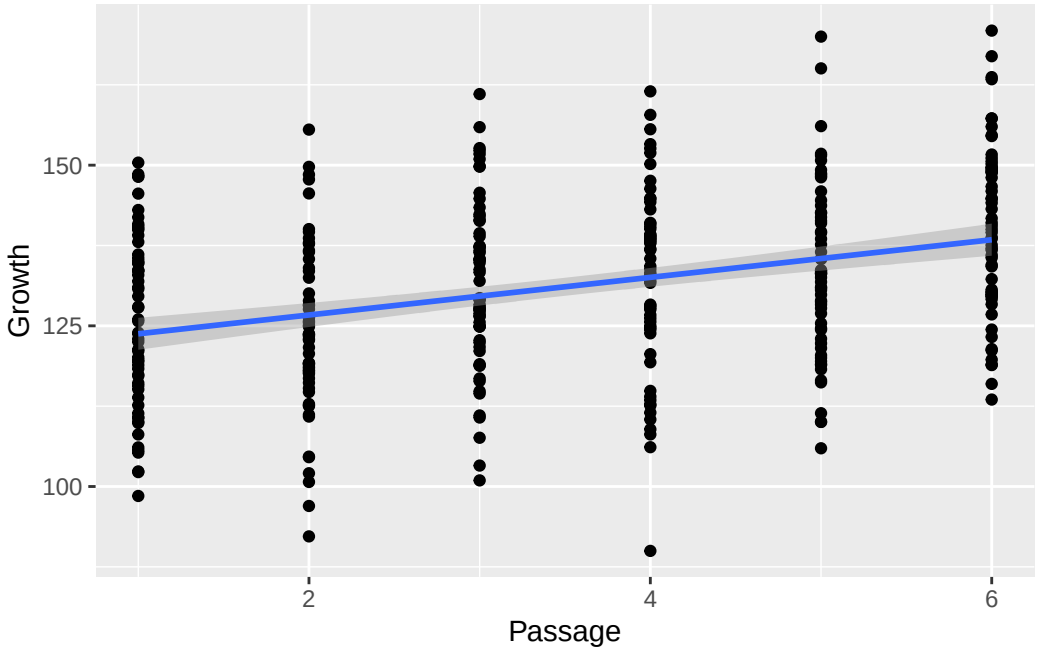
8.4.1 Linear regression

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

8.4.1.1 Graphical exploration

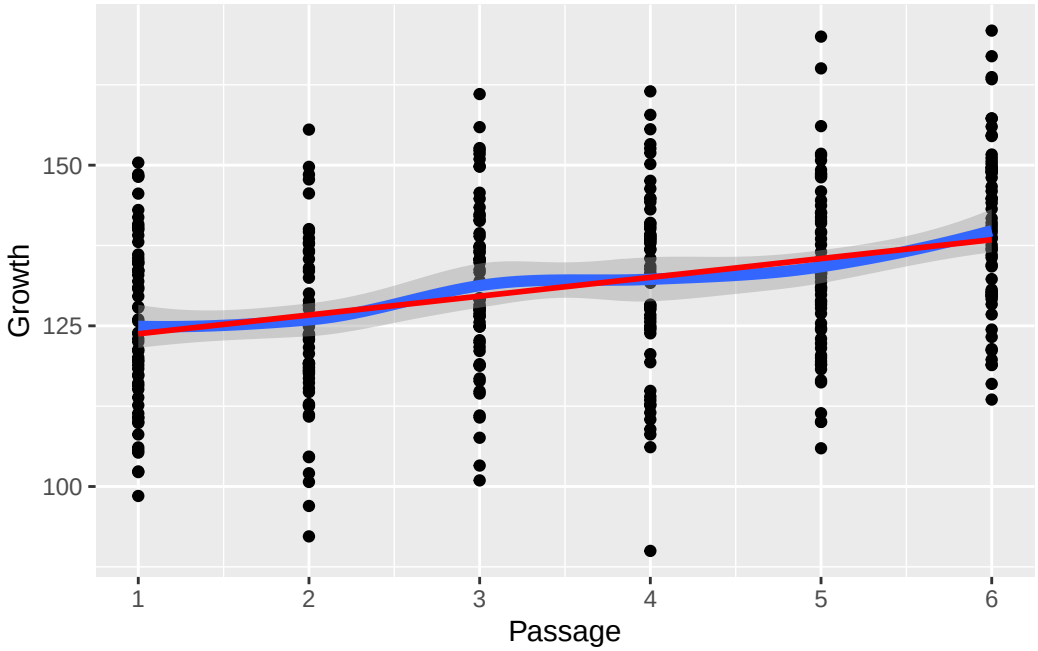
```
ggplot(rawdata,aes(Passage,Growth))+
  geom_point()+
  geom_smooth(method=lm)
```

```
`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'
```



8.4.1.2 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)
```

8.4.1.3 Adjusting

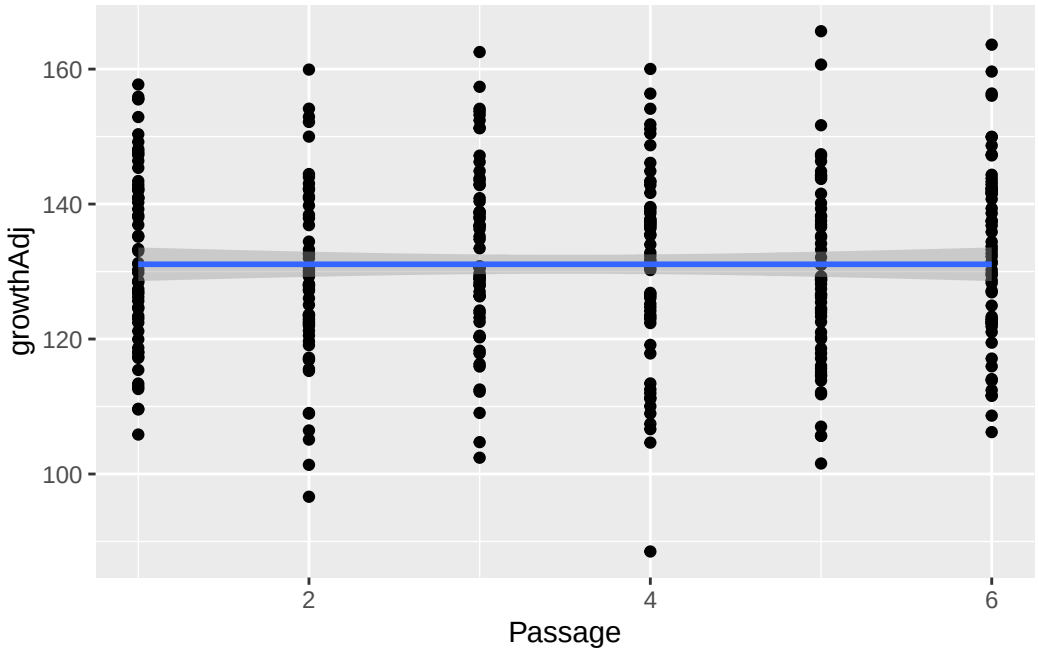
To take out the variance due to Passage effects, we can use the residuals and shift them to the original mean:

```
  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()
```

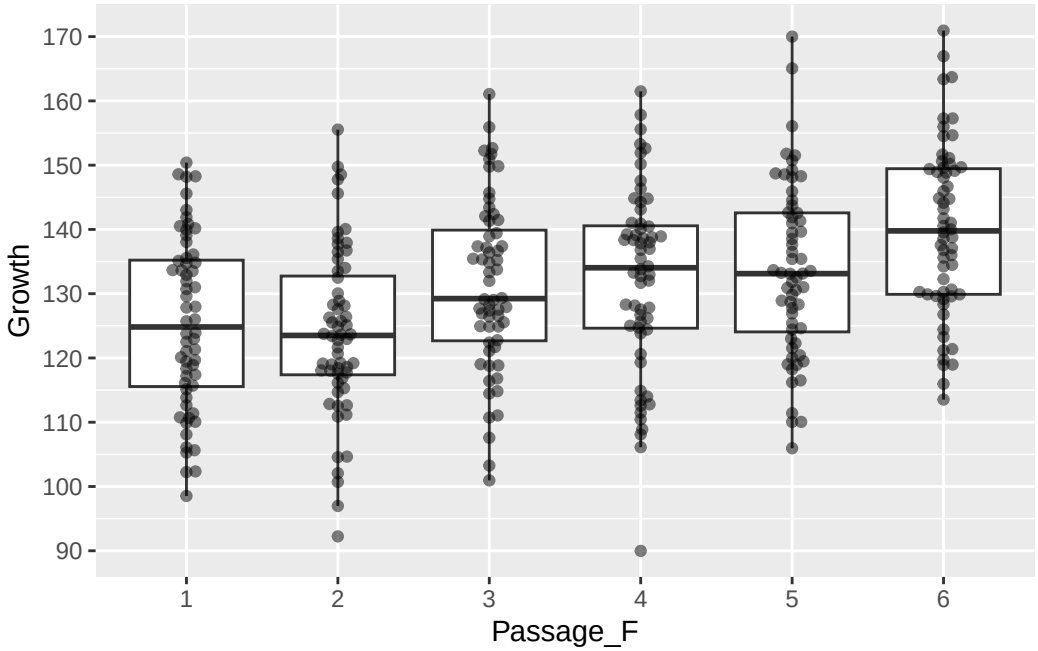
```
# A tibble: 2 x 5
  term        estimate std.error statistic   p.value
  <chr>          <dbl>     <dbl>     <dbl>     <dbl>
1 (Intercept) 1.31e+ 2     1.63   8.05e+ 1 2.04e-231
2 Passage     6.80e-15     0.418  1.63e-14 1.00e+  0
```

8.4.2 ANOVA

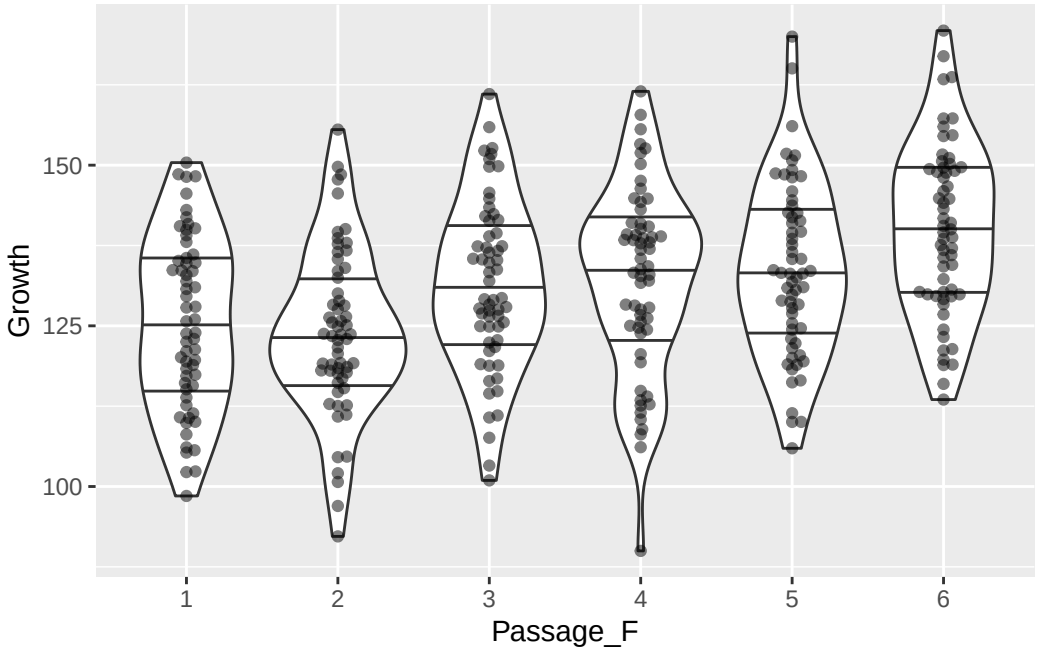
In the linear regression, we had Passage as a continuous IV, estimating a global 'universal' effect supposed to be constant. Now we look at Passege_F and model a discrete IV, allowing for specific effects, and thereby comparing means between groups.

8.4.2.1 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)
```



8.4.2.2 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
```

8.4.2.3 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!

```r
# 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
```

```r
# 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
```

```r
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
```

```r
# 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
```

```r
# 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
```

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

```
[1] 0.55214600 0.00331248 0.69214393 0.58295615 0.01025037
```

```r
# 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
```

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

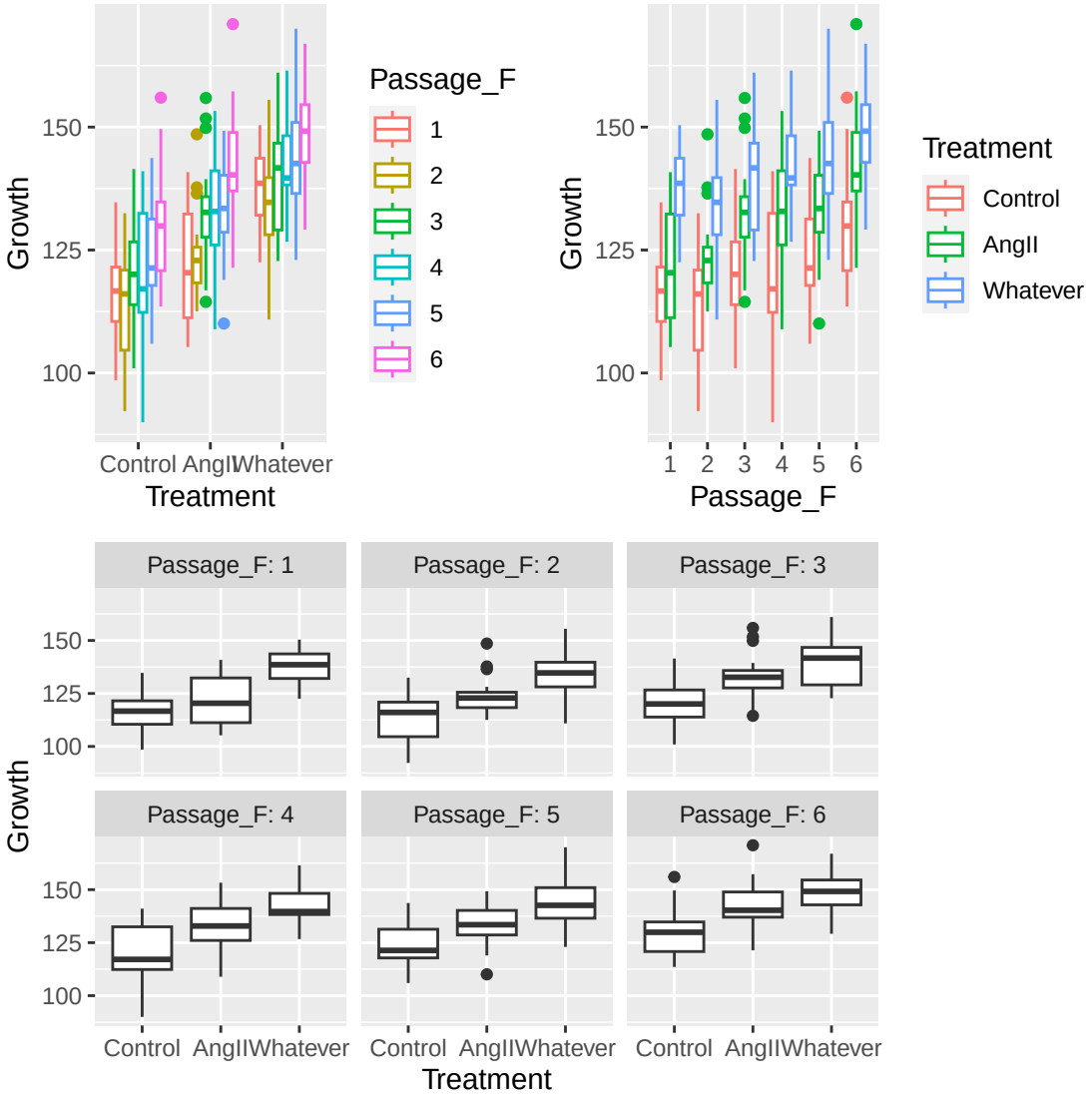
```
[1] "0.552" "0.023" "0.010" "0.003" "0.001"
```

8.4.3 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.

8.4.3.1 Graphical exploration

```r
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
```



8.4.3.2 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(lmOut_additive,type=2)
```

```
Anova Table (Type II tests)

Response: Growth
          Sum Sq  Df F value    Pr(>F)
Passage     8996   1  77.058 < 2.2e-16 ***
Treatment  24137   2 103.372 < 2.2e-16 ***
Residuals  41562 356
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# 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
```

8.4.3.3 Post-hoc analyses

For multivariable models, pairwise.t.test() is not appropriate, Dunnet or Tukey tests (depending on hypothesis) are typical solutions.

```r
summary(glht(model=lmOut_additive,linfct=mcp(Treatment='Dunnett')))
```

```
     Simultaneous Tests for General Linear Hypotheses

Multiple Comparisons of Means: Dunnett 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 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
(Adjusted p values reported -- single-step method)
```

```r
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)
```

```r
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  0.0263 *
5-1  8.156143  1.9335375 14.378748  0.0048 **
6-1 14.520106  8.2975011 20.742712 6.9e-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')])
```

```
[1] 116.4531
```

```
aOut$'Pr(>F)'
```

```
[1] 2.909117e-279  5.549803e-31            NA
```

```
aOut$`Sum Sq`
```

```
[1] 1754742.53   24136.66   50557.95
```

```
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)))
```

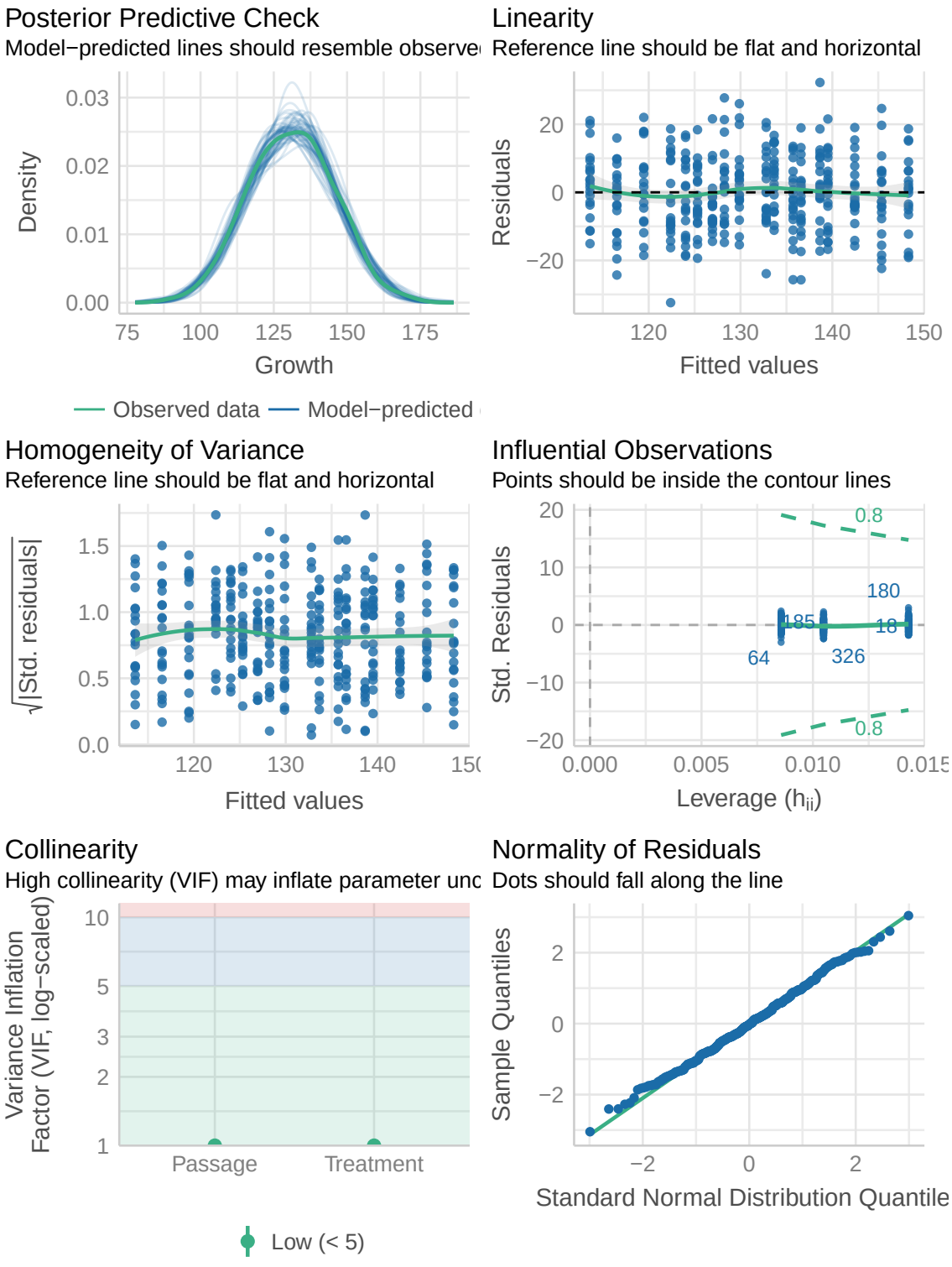
```
# A tibble: 3 x 2
  predictor   p
  <chr>       <chr>
1 (Intercept) "0.00001"
2 Treatment   "0.00001"
3 Residuals   "    NA"
```

```r
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
```

8.4.4 Model exploration with package performance

```
# x11() #interactive only!

# from package performance
check_model(lmOut_additive)
```


Posterior Predictive Check
Model−predicted lines should resemble observe
Density
0.03
0.02
0.01
0.00
75
100
125
150
175
Growth
Observed data
Model−predicted
Linearity
Reference line should be flat and horizontal
Residuals
20
0
−20
120
130
140
150
Fitted values
Homogeneity of Variance
Reference line should be flat and horizontal
√|Std. residuals|
1.5
1.0
0.5
0.0
120
130
140
Fitted values
Influential Observations
Points should be inside the contour lines
Std. Residuals
20
10
0
−10
−20
0.8
180
185
18
64
326
0.8
0.000
0.005
0.010
Leverage (hii)
Collinearity
High collinearity (VIF) may inflate parameter unc
Variance Inflation Factor (VIF, log−scaled)
10
5
3
2
1
Passage
Treatment
Low (< 5)
Normality of Residuals
Dots should fall along the line
Sample Quantiles
2
0
−2
−2
0
2
Standard Normal Distribution Quantile

9 Summary

In summary, this book has no content whatsoever.

```
1 + 1
```

```
[1] 2
```

References