Tutorial

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McGill wins $84 million grant for neuroscience

Great opportunities for undergraduate students with a background in neuro and knowledge of statistics and statistical software!

https://www.mcgill.ca/newsroom/channels/news/mcgill-wins-84-million-grant-neuroscience-262441

To Do Before the Tutorial

Download R

https://cran.r-project.org/

Download R studio

https://www.rstudio.com/products/rstudio/download/

Opening RStudio for the First Time

On the right hand side there is the console. It is where we are going to communicate with R by submitting our instructions.

On the left hand side you have the Environment and the History in the top panel. The Environment lists all the variables that you currently have in your work space (i.e. that you can call in the console). History registers all the operations you have sent to R. You can browse it to see your previous commands in the console.

New Project

I encourage creating a new project for the course as File -> New Project… -> New Directory -> Empty Project -> Directory Name -> R_Tutorial and browse to choose the folder where you want the project to be. It will be easier to manage your project and dataset.

Rmarkdown

You may export your code and graphs easily to MS word or pdf following these instructions.

File -> New File -> R markdown -> select the output format to Word -> Ok -> Knit

Note that what is written in MS Word is not connected to the console, and vice-versa. You will need to write the command in both places if you want to keep their workspaces the same.

To insert code in your file click on "Insert" at the top of the top left panel.

Required Packages

We need to install certain packages for today's tutorial. It can be done this way:

```
# install.packages(c("tidyr", "reshape2"))
```

Tutorial

Use R for Basic Operations

Typping in the console we can use R as a basic calculator.

```
1+2
```

```
## [1] 3
```

```
4/2
```

```
## [1] 2
```

```
5*(1+2)
```

```
## [1] 15
```

```
5^2
```

```
## [1] 25
```

We can also assign value to variable,

```
my_variable <- 7
```

and access it by calling the variable name in the console.

```
my_variable
```

```
## [1] 7
```

Basic Data Structure

Vectors

We can create vectors using the "c" command, where "c" stands for combine.

```
x <- c(6,7,8,9,10)
x
```

```
## [1]  6  7  8  9 10
```

```
x[1]
```

```
## [1] 6
```

```
x[c(2,4)]
```

```
## [1] 7 9
```

```
x*2
```

```
## [1] 12 14 16 18 20
```

```
x <- 1:7
x
```

```
## [1] 1 2 3 4 5 6 7
```

Vectors in R are more general than their mathematical equivalent. They can hold different type of data e.g. string or level.

```
y <- c("hello", "world")
y
```

```
## [1] "hello" "world"
```

However, all elements will be coerce to the same type, they are coerce to string in the following case.

```
y <- c(1, "hello")
y
```

```
## [1] "1"     "hello"
```

Dataframe

Usually, we will have to load our own datasets in R using the "Import Dataset" command in the Environment panel, more on that later. For simplicity, we will now experiment on a build-in dataset in R studio named "mtcars". Using the command "head(mtcars)" let us access the first 6 records of the dataset and their names.

```
dim(mtcars)
```

```
## [1] 32 11
```

```r
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
```

We can use vectors to assess different rows and columns.

```r
mtcars[1:4, c(1,4)]
```

```
##                 mpg  hp
## Mazda RX4      21.0 110
## Mazda RX4 Wag  21.0 110
## Datsun 710     22.8  93
## Hornet 4 Drive 21.4 110
```

Let say that we are interested in the median miles per gallon (mpg) in this dataset. We can use the command "median(mtcars$mpg)", where "mtcars" is the dataset and "mpg" is the column of interest that we accessed with the dollar sign operator "$".

```r
mtcars$mpg
```

```
##  [1] 21.0 21.0 22.8 21.4 18.7 18.1 14.3 24.4 22.8 19.2 17.8 16.4 17.3 15.2
## [15] 10.4 10.4 14.7 32.4 30.4 33.9 21.5 15.5 15.2 13.3 19.2 27.3 26.0 30.4
## [29] 15.8 19.7 15.0 21.4
```

```r
median(mtcars$mpg)
```

```
## [1] 19.2
```

```r
mean(mtcars$mpg)
```

```
## [1] 20.09062
```

```r
var(mtcars$mpg)
```

```
## [1] 36.3241
```

To have more information on a function, we can use the question mark before it e.g. "?mean".

Data Cleaning

Most of the analysis consist of data cleaning. Here is an example of some manipulation that you might be asked to do.

#	Attribute Description
1.	mpg - Miles/(US) gallon
2.	cyl - Number of cylinders
3.	disp - Displacement (cu.in.)
4.	hp - Gross horsepower
5.	drat - Rear axle ratio
6.	wt - Weight (1000 lbs)
7.	qsec - 1/4 mile time
8.	vs - V/S

#	Attribute Description
9.	am - Transmission (0 = automatic, 1 = manual)
10.	gear - Number of forward gears
11.	carb - Number of carburetors

```
str(mtcars)
```

```
## 'data.frame':    32 obs. of  11 variables:
##  $ mpg : num  21 21 22.8 21.4 18.7 18.1 14.3 24.4 22.8 19.2 ...
##  $ cyl : num  6 6 4 6 8 6 8 4 4 6 ...
##  $ disp: num  160 160 108 258 360 ...
##  $ hp  : num  110 110 93 110 175 105 245 62 95 123 ...
##  $ drat: num  3.9 3.9 3.85 3.08 3.15 2.76 3.21 3.69 3.92 3.92 ...
##  $ wt  : num  2.62 2.88 2.32 3.21 3.44 ...
##  $ qsec: num  16.5 17 18.6 19.4 17 ...
##  $ vs  : num  0 0 1 1 0 1 0 1 1 1 ...
##  $ am  : num  1 1 1 0 0 0 0 0 0 0 ...
##  $ gear: num  4 4 4 3 3 3 3 4 4 4 ...
##  $ carb: num  4 4 1 1 2 1 4 2 2 4 ...
```

Should the number of cylinders and the weight be both considered as numeric variable? Weight is a continuous variable while the number of cylinders is categorical e.g. 4,6 or 8 cylinders.

```
mtcars$cyl <- factor(mtcars$cyl)

mtcars$vs <- factor(mtcars$vs)

mtcars$am <- factor(mtcars$am)

mtcars$gear <- factor(mtcars$gear)

mtcars$carb <- factor(mtcars$carb)

str(mtcars)
```

```
## 'data.frame':    32 obs. of  11 variables:
##  $ mpg : num  21 21 22.8 21.4 18.7 18.1 14.3 24.4 22.8 19.2 ...
##  $ cyl : Factor w/ 3 levels "4","6","8": 2 2 1 2 3 2 3 1 1 2 ...
##  $ disp: num  160 160 108 258 360 ...
##  $ hp  : num  110 110 93 110 175 105 245 62 95 123 ...
##  $ drat: num  3.9 3.9 3.85 3.08 3.15 2.76 3.21 3.69 3.92 3.92 ...
##  $ wt  : num  2.62 2.88 2.32 3.21 3.44 ...
##  $ qsec: num  16.5 17 18.6 19.4 17 ...
##  $ vs  : Factor w/ 2 levels "0","1": 1 1 2 2 1 2 1 2 2 2 ...
##  $ am  : Factor w/ 2 levels "0","1": 2 2 2 1 1 1 1 1 1 1 ...
##  $ gear: Factor w/ 3 levels "3","4","5": 2 2 2 1 1 1 1 2 2 2 ...
##  $ carb: Factor w/ 6 levels "1","2","3","4",..: 4 4 1 1 2 1 4 2 2 4 ...
```

It might be annoying to have to remember that 0 stands for automatic and 1 manual transmission. Let us fix it.

```
levels(mtcars$am) <- c("automatic", "manual")
```

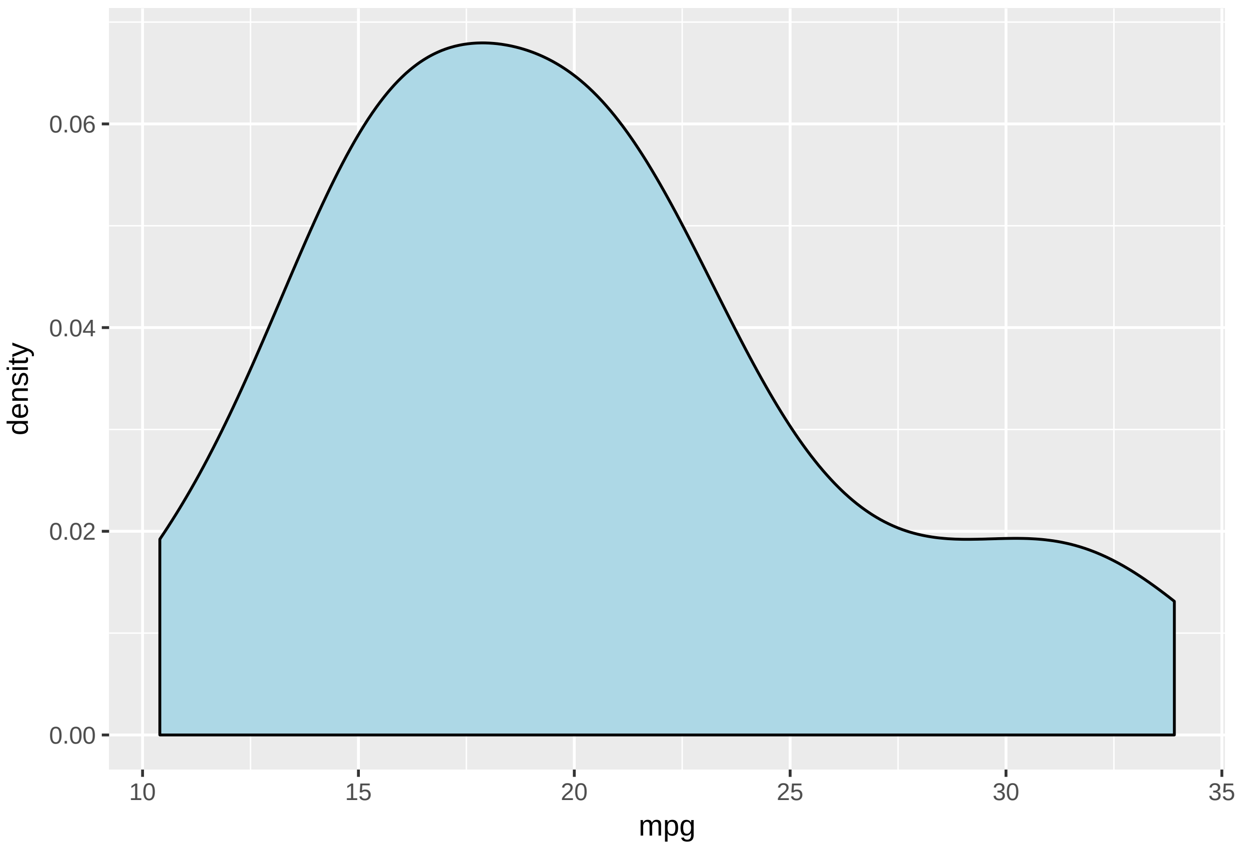
Exploring the Data

Graphing with ggplot2

Exploring the Variability in a Dataset

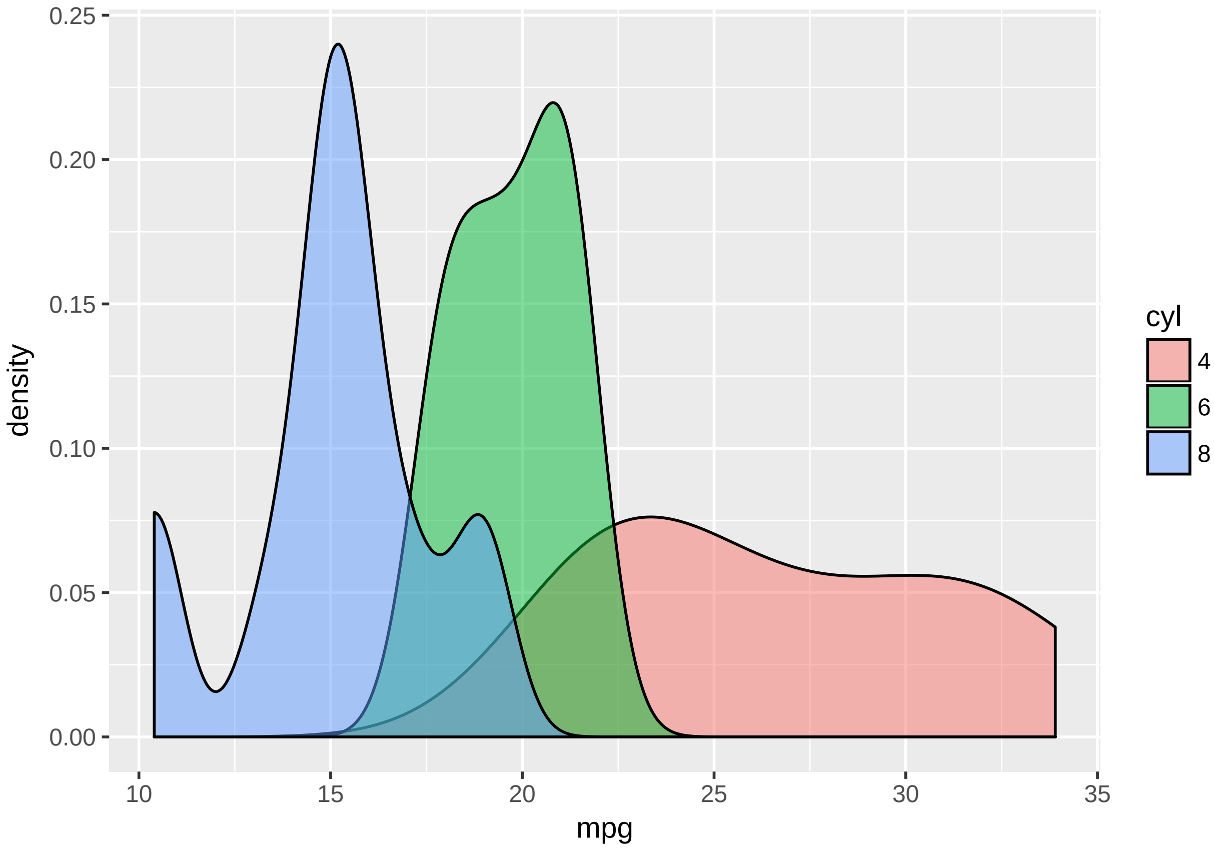
Suppose being interested in the distribution of mpg. The first argument is the dataset name, the second is "aes" (standing for aesthetic) which that the dependent and indepdent variables.

```
# To use the ggplot2 library we have to call it with the library command
# One could think of the command "install.packages" as buying shoes and "library" as putting them on.
library(ggplot2)

ggplot(mtcars, aes(mpg)) + geom_density(fill="lightblue")
```



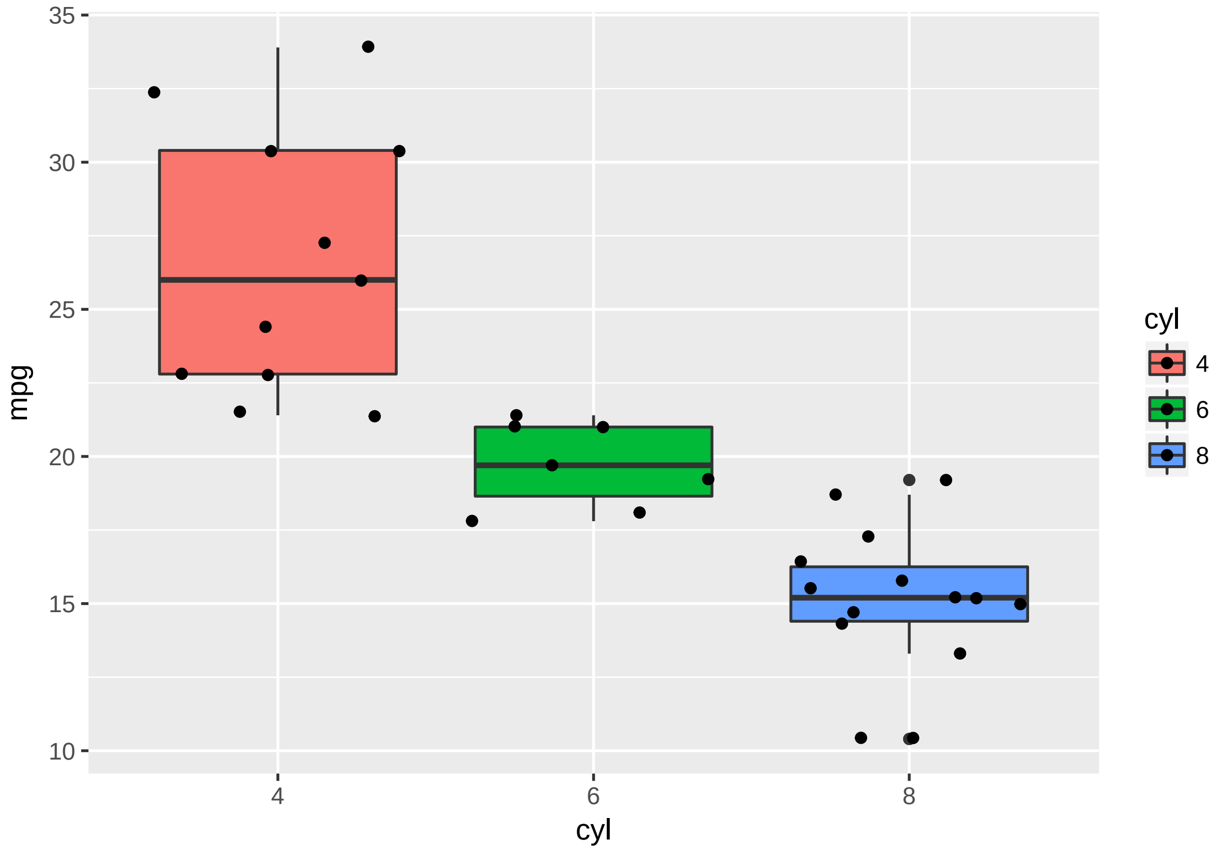
The number of cylinders in a car might impact its consumption.

```
ggplot(mtcars, aes(mpg, fill=cyl)) + geom_density(alpha=.5)
```



It might be useful to be able to see every observation on the graph.

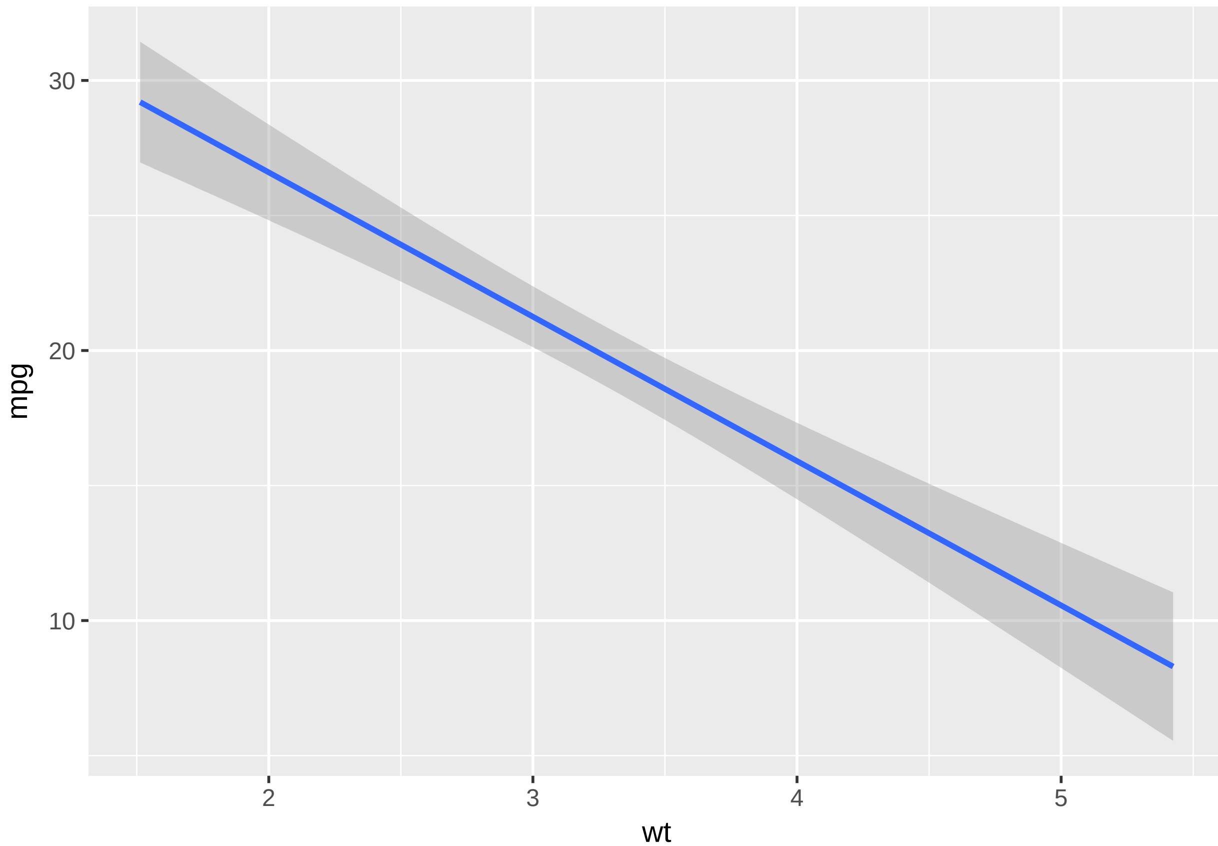
```
ggplot(mtcars, aes(cyl, mpg, fill=cyl)) + geom_boxplot() + geom_jitter()
```



Relationship Across Variables

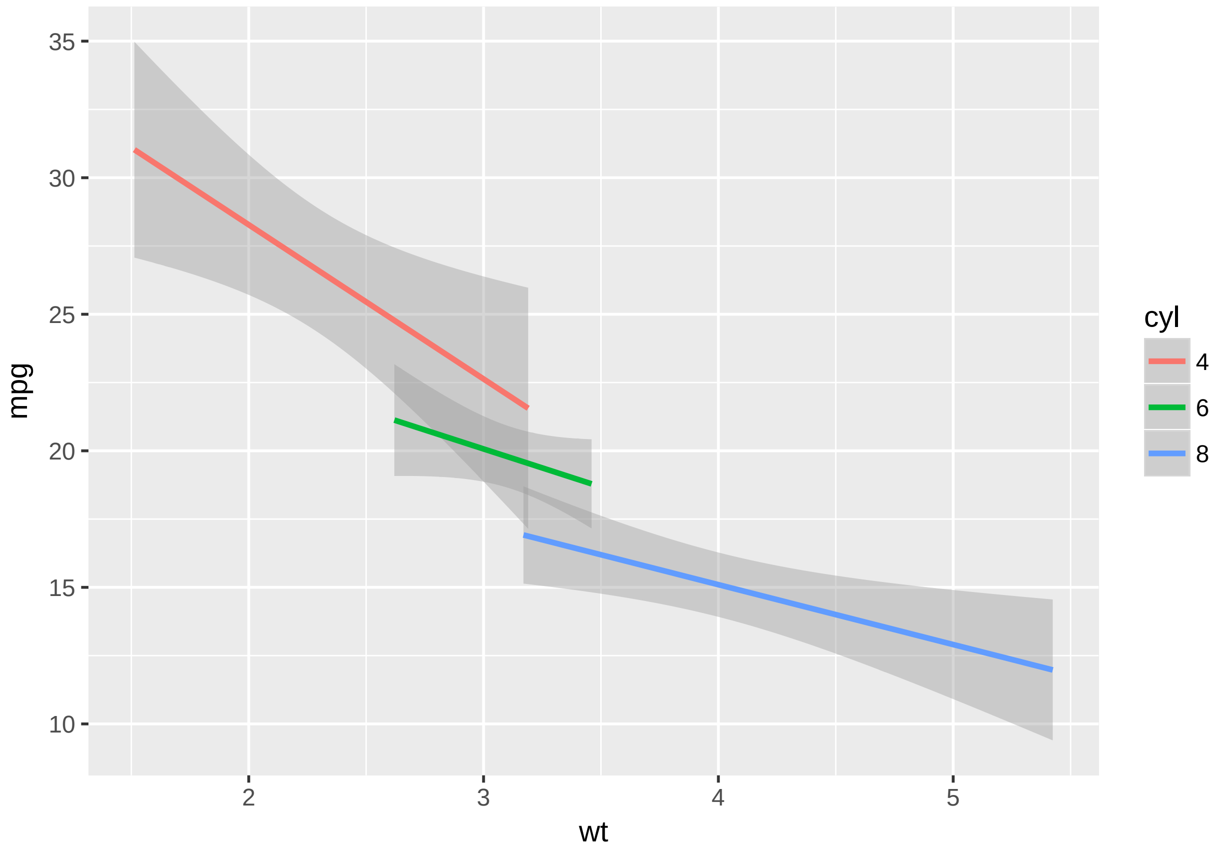
Using the regression, we can clearly see that the heavier a vehicule is the worst Miles per gallon it is going to have.

```
ggplot(mtcars, aes(wt, mpg)) + stat_smooth(method="lm")
```

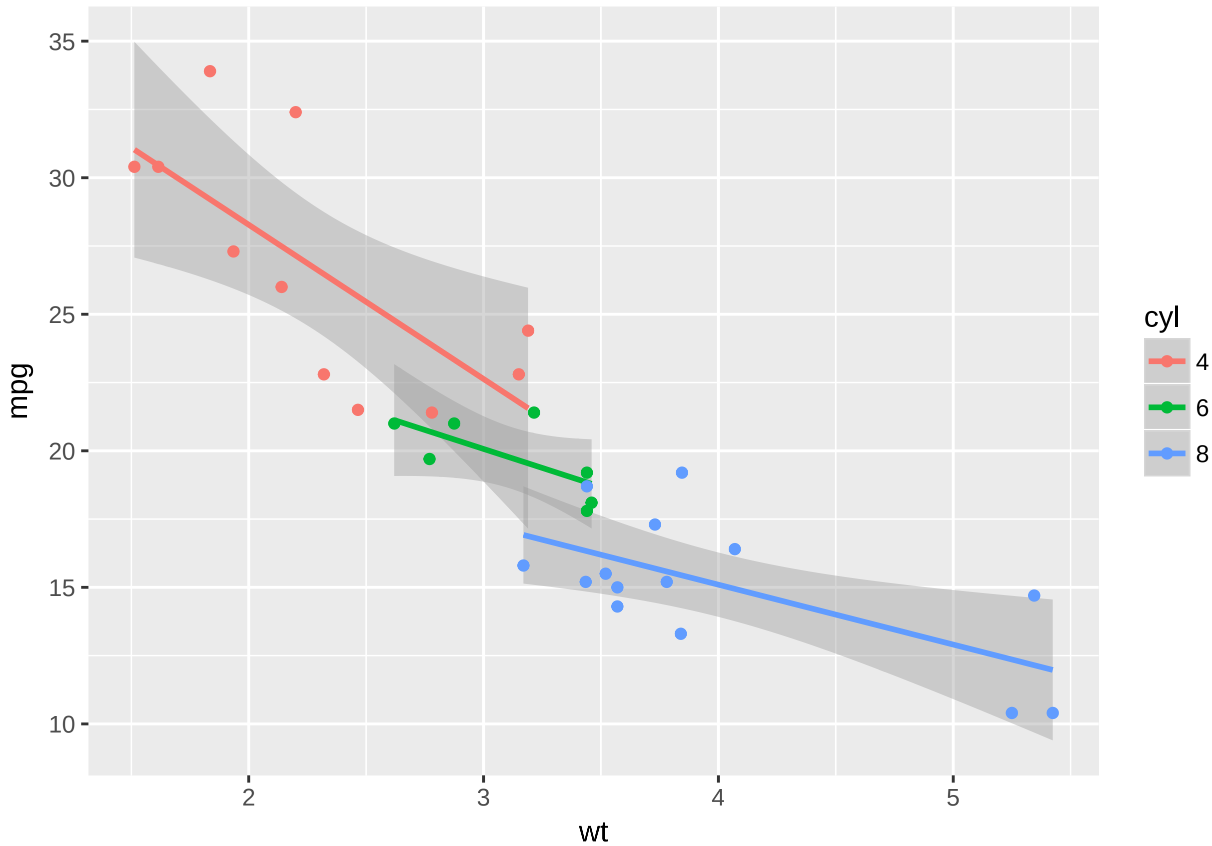


Furthermore, we can divide the regression by the number of cylinders. We can see that the negative correlation is still present, but is not the same for every category.

```
p <- ggplot(mtcars, aes(wt, mpg, color=cyl)) + stat_smooth(method="lm")
p
```



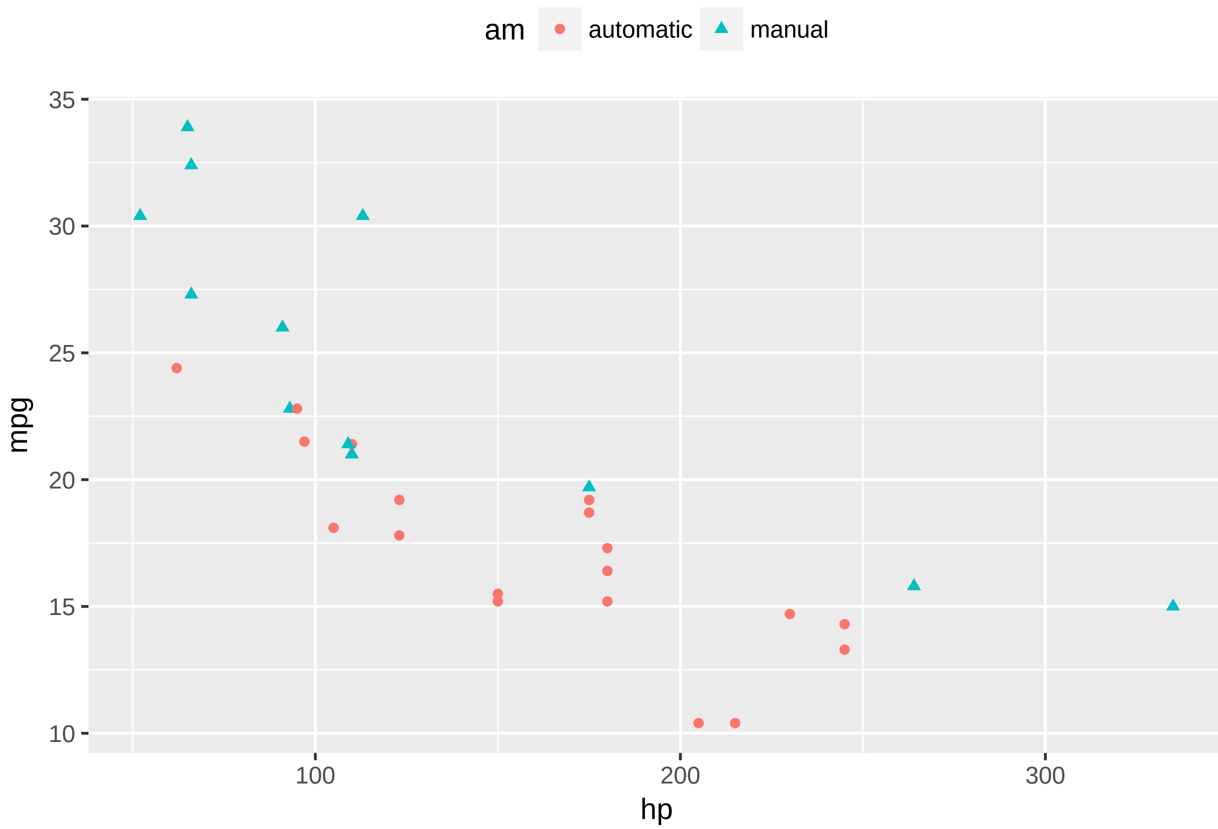

```
p + geom_point()
```



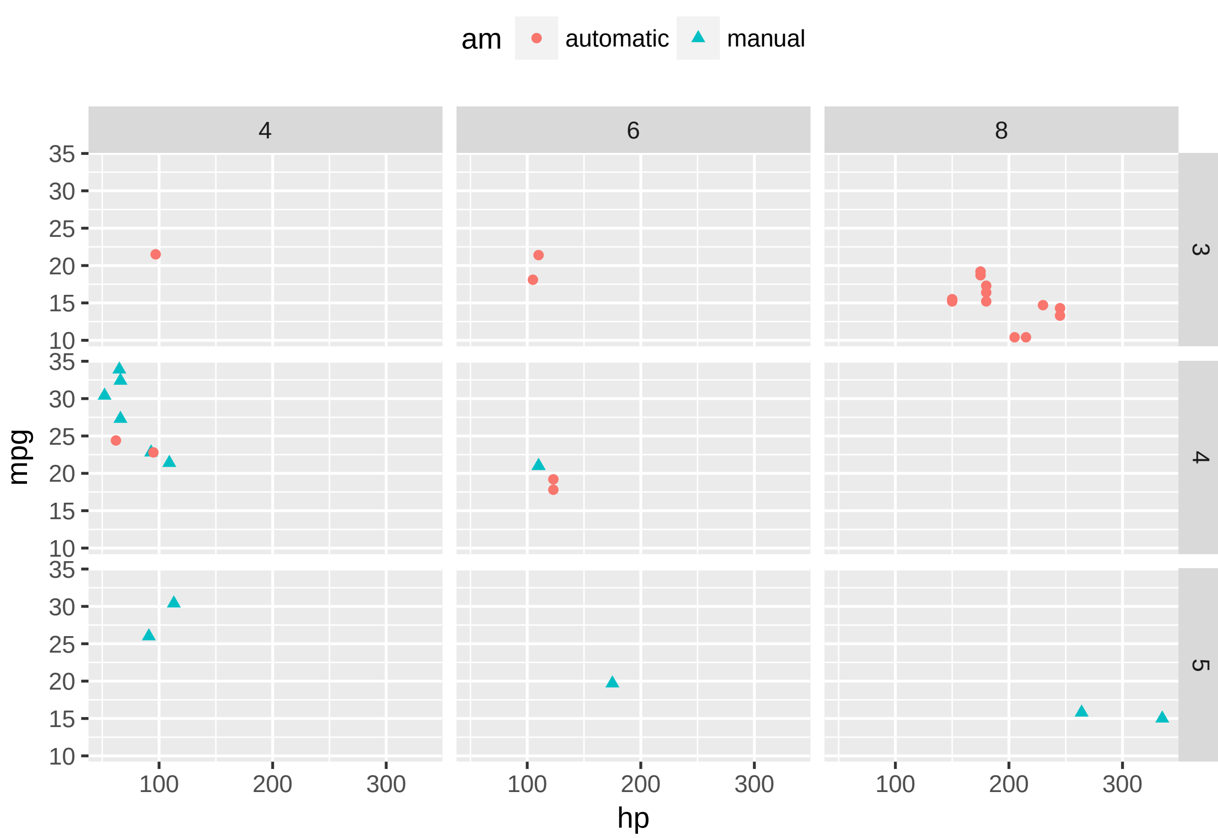
Complex Patterns

We can stratify the data to observe more complex patterns.

```
p <- ggplot(mtcars, aes(hp, mpg, color=am, shape=am)) + geom_point()
p <- p + theme(legend.position="top")
p
```




```
p + facet_grid(gear~cyl)
```



dplyr

```r
library(dplyr)
```

Group by and Summarise

```r
summarise(mtcars, mean_mpg=mean(mpg), mean_wt=mean(wt))
```

```
##   mean_mpg mean_wt
## 1 20.09062 3.21725
```

```r
temp <- group_by(mtcars, cyl)
temp1 <- summarise(temp, mean_mpg=mean(mpg), mean_wt=mean(wt))
temp1
```

```
## # A tibble: 3 × 3
##      cyl mean_mpg  mean_wt
##   <fctr>    <dbl>    <dbl>
## 1      4 26.66364 2.285727
## 2      6 19.74286 3.117143
## 3      8 15.10000 3.999214
```

```r
# one could alternatively chain the operation using the pipe operation %>%
# mtcars %>% group_by(cyl) %>% summarise(mean_mpg=mean(mpg), mean_wt=mean(wt))
```

Select

```r
temp <- mtcars %>% select(mpg, cyl)
temp
```

```
##                      mpg cyl
## Mazda RX4           21.0   6
## Mazda RX4 Wag       21.0   6
## Datsun 710          22.8   4
## Hornet 4 Drive      21.4   6
## Hornet Sportabout   18.7   8
## Valiant             18.1   6
## Duster 360          14.3   8
## Merc 240D           24.4   4
## Merc 230            22.8   4
## Merc 280            19.2   6
## Merc 280C           17.8   6
## Merc 450SE          16.4   8
## Merc 450SL          17.3   8
## Merc 450SLC         15.2   8
## Cadillac Fleetwood  10.4   8
## Lincoln Continental 10.4   8
## Chrysler Imperial   14.7   8
## Fiat 128            32.4   4
## Honda Civic         30.4   4
## Toyota Corolla      33.9   4
## Toyota Corona       21.5   4
## Dodge Challenger    15.5   8
## AMC Javelin         15.2   8
```

```
## Camaro Z28          13.3   8
## Pontiac Firebird    19.2   8
## Fiat X1-9           27.3   4
## Porsche 914-2       26.0   4
## Lotus Europa        30.4   4
## Ford Pantera L      15.8   8
## Ferrari Dino        19.7   6
## Maserati Bora       15.0   8
## Volvo 142E          21.4   4
```

Arrange

```
mtcars %>% select(cyl,am,wt) %>% arrange(cyl,am,wt)
```

```
##    cyl        am    wt
## 1    4 automatic 2.465
## 2    4 automatic 3.150
## 3    4 automatic 3.190
## 4    4    manual 1.513
## 5    4    manual 1.615
## 6    4    manual 1.835
## 7    4    manual 1.935
## 8    4    manual 2.140
## 9    4    manual 2.200
## 10   4    manual 2.320
## 11   4    manual 2.780
## 12   6 automatic 3.215
## 13   6 automatic 3.440
## 14   6 automatic 3.440
## 15   6 automatic 3.460
## 16   6    manual 2.620
## 17   6    manual 2.770
## 18   6    manual 2.875
## 19   8 automatic 3.435
## 20   8 automatic 3.440
## 21   8 automatic 3.520
## 22   8 automatic 3.570
## 23   8 automatic 3.730
## 24   8 automatic 3.780
## 25   8 automatic 3.840
## 26   8 automatic 3.845
## 27   8 automatic 4.070
## 28   8 automatic 5.250
## 29   8 automatic 5.345
## 30   8 automatic 5.424
## 31   8    manual 3.170
## 32   8    manual 3.570
```

Mutate

Let's define heavy as more than 3000 lbs.

```
temp1 <- mtcars %>% mutate(heavy=factor(ifelse(wt < 3, "Light", "Heavy")))
str(temp1)
```

```
## 'data.frame':    32 obs. of  12 variables:
##  $ mpg  : num  21 21 22.8 21.4 18.7 18.1 14.3 24.4 22.8 19.2 ...
##  $ cyl  : Factor w/ 3 levels "4","6","8": 2 2 1 2 3 2 3 1 1 2 ...
##  $ disp : num  160 160 108 258 360 ...
##  $ hp   : num  110 110 93 110 175 105 245 62 95 123 ...
##  $ drat : num  3.9 3.9 3.85 3.08 3.15 2.76 3.21 3.69 3.92 3.92 ...
##  $ wt   : num  2.62 2.88 2.32 3.21 3.44 ...
##  $ qsec : num  16.5 17 18.6 19.4 17 ...
##  $ vs   : Factor w/ 2 levels "0","1": 1 1 2 2 1 2 1 2 2 2 ...
##  $ am   : Factor w/ 2 levels "automatic","manual": 2 2 2 1 1 1 1 1 1 1 ...
##  $ gear : Factor w/ 3 levels "3","4","5": 2 2 2 1 1 1 1 2 2 2 ...
##  $ carb : Factor w/ 6 levels "1","2","3","4",..: 4 4 1 1 2 1 4 2 2 4 ...
##  $ heavy: Factor w/ 2 levels "Heavy","Light": 2 2 2 1 1 1 1 1 1 1 ...
```

Filter

```
temp1 %>% filter(heavy=="Heavy")
```

```
##     mpg cyl  disp  hp drat    wt  qsec vs        am gear carb heavy
## 1  21.4   6 258.0 110 3.08 3.215 19.44  1 automatic    3    1 Heavy
## 2  18.7   8 360.0 175 3.15 3.440 17.02  0 automatic    3    2 Heavy
## 3  18.1   6 225.0 105 2.76 3.460 20.22  1 automatic    3    1 Heavy
## 4  14.3   8 360.0 245 3.21 3.570 15.84  0 automatic    3    4 Heavy
## 5  24.4   4 146.7  62 3.69 3.190 20.00  1 automatic    4    2 Heavy
## 6  22.8   4 140.8  95 3.92 3.150 22.90  1 automatic    4    2 Heavy
## 7  19.2   6 167.6 123 3.92 3.440 18.30  1 automatic    4    4 Heavy
## 8  17.8   6 167.6 123 3.92 3.440 18.90  1 automatic    4    4 Heavy
## 9  16.4   8 275.8 180 3.07 4.070 17.40  0 automatic    3    3 Heavy
## 10 17.3   8 275.8 180 3.07 3.730 17.60  0 automatic    3    3 Heavy
## 11 15.2   8 275.8 180 3.07 3.780 18.00  0 automatic    3    3 Heavy
## 12 10.4   8 472.0 205 2.93 5.250 17.98  0 automatic    3    4 Heavy
## 13 10.4   8 460.0 215 3.00 5.424 17.82  0 automatic    3    4 Heavy
## 14 14.7   8 440.0 230 3.23 5.345 17.42  0 automatic    3    4 Heavy
## 15 15.5   8 318.0 150 2.76 3.520 16.87  0 automatic    3    2 Heavy
## 16 15.2   8 304.0 150 3.15 3.435 17.30  0 automatic    3    2 Heavy
## 17 13.3   8 350.0 245 3.73 3.840 15.41  0 automatic    3    4 Heavy
## 18 19.2   8 400.0 175 3.08 3.845 17.05  0 automatic    3    2 Heavy
## 19 15.8   8 351.0 264 4.22 3.170 14.50  0    manual    5    4 Heavy
## 20 15.0   8 301.0 335 3.54 3.570 14.60  0    manual    5    8 Heavy
```

Real World Problems

Parkinsons

Attribute Information:

#	Attribute Description
1.	subject# - Integer that uniquely identifies each subject
2.	age - Subject age
3.	sex - Subject gender '0' - male, '1' - female
4.	test_time - Time since recruitment into the trial. The integer part is the number of days since recruitment.
5.	motor_UPDRS - Clinician's motor UPDRS score, linearly interpolated

#	Attribute Description
6.	total_UPDRS - Clinician's total UPDRS score, linearly interpolated
7.	Jitter(%),Jitter(Abs),Jitter:RAP,Jitter:PPQ5,Jitter:DDP - Several measures of variation in fundamental frequency
8.	Shimmer,Shimmer(dB),Shimmer:APQ3,Shimmer:APQ5,Shimmer:APQ11,Shimmer:DDA - Several measures of variation in amplitude
9.	NHR,HNR - Two measures of ratio of noise to tonal components in the voice
10.	RPDE - A nonlinear dynamical complexity measure
11.	DFA - Signal fractal scaling exponent
12.	PPE - A nonlinear measure of fundamental frequency variation

```r
# A Tsanas, MA Little, PE McSharry, LO Ramig (2009)
# 'Accurate telemonitoring of Parkinson.s disease progression by non-invasive speech tests',
library(data.table)
```

```
## -------------------------------------------------------------------------

## data.table + dplyr code now lives in dtplyr.
## Please library(dtplyr)!

## -------------------------------------------------------------------------

##
## Attaching package: 'data.table'

## The following objects are masked from 'package:dplyr':
##
##     between, first, last
```

```r
# url <- "https://archive.ics.uci.edu/ml/machine-learning-databases/
# parkinsons/telemonitoring/parkinsons_updrs.data"

#parkinson_dat <- fread(url)
#names(parkinson_dat)[1] <- "subject"

#write.csv(parkinson_dat, file="parkinson_dat.csv")

parkinson_dat <- read.csv("parkinson_dat.csv")

str(parkinson_dat)
```

```
## 'data.frame':    5875 obs. of  23 variables:
##  $ X            : int  1 2 3 4 5 6 7 8 9 10 ...
##  $ subject      : int  1 1 1 1 1 1 1 1 1 1 ...
##  $ age          : int  72 72 72 72 72 72 72 72 72 72 ...
##  $ sex          : int  0 0 0 0 0 0 0 0 0 0 ...
##  $ test_time    : num  5.64 12.67 19.68 25.65 33.64 ...
##  $ motor_UPDRS  : num  28.2 28.4 28.7 28.9 29.2 ...
##  $ total_UPDRS  : num  34.4 34.9 35.4 35.8 36.4 ...
##  $ Jitter...    : num  0.00662 0.003 0.00481 0.00528 0.00335 0.00353 0.00422 0.00476 0.00432 0.00496
##  $ Jitter.Abs.  : num  3.38e-05 1.68e-05 2.46e-05 2.66e-05 2.01e-05 ...
##  $ Jitter.RAP   : num  0.00401 0.00132 0.00205 0.00191 0.00093 0.00119 0.00212 0.00226 0.00156 0.0025
##  $ Jitter.PPQ5  : num  0.00317 0.0015 0.00208 0.00264 0.0013 0.00159 0.00221 0.00259 0.00207 0.00253
##  $ Jitter.DDP   : num  0.01204 0.00395 0.00616 0.00573 0.00278 ...
##  $ Shimmer      : num  0.0256 0.0202 0.0168 0.0231 0.017 ...
```

```
##  $ Shimmer.dB.  : num  0.23 0.179 0.181 0.327 0.176 0.214 0.445 0.212 0.371 0.31 ...
##  $ Shimmer.APQ3 : num  0.01438 0.00994 0.00734 0.01106 0.00679 ...
##  $ Shimmer.APQ5 : num  0.01309 0.01072 0.00844 0.01265 0.00929 ...
##  $ Shimmer.APQ11: num  0.0166 0.0169 0.0146 0.0196 0.0182 ...
##  $ Shimmer.DDA  : num  0.0431 0.0298 0.022 0.0332 0.0204 ...
##  $ NHR          : num  0.0143 0.0111 0.0202 0.0278 0.0116 ...
##  $ HNR          : num  21.6 27.2 23 24.4 26.1 ...
##  $ RPDE         : num  0.419 0.435 0.462 0.487 0.472 ...
##  $ DFA          : num  0.548 0.565 0.544 0.578 0.561 ...
##  $ PPE          : num  0.16 0.108 0.21 0.333 0.194 ...
```

```
parkinson_dat$sex <- factor(parkinson_dat$sex)
levels(parkinson_dat$sex) <- c("male", "female")
```

```
parkinson_dat %>% distinct(subject, .keep_all = TRUE) %>% group_by(sex) %>%
  summarise(count=n(), mean_age=mean(age))
```

```
## # A tibble: 2 × 3
##      sex count mean_age
##   <fctr> <int>    <dbl>
## 1   male    28 64.82143
## 2 female    14 63.57143
```

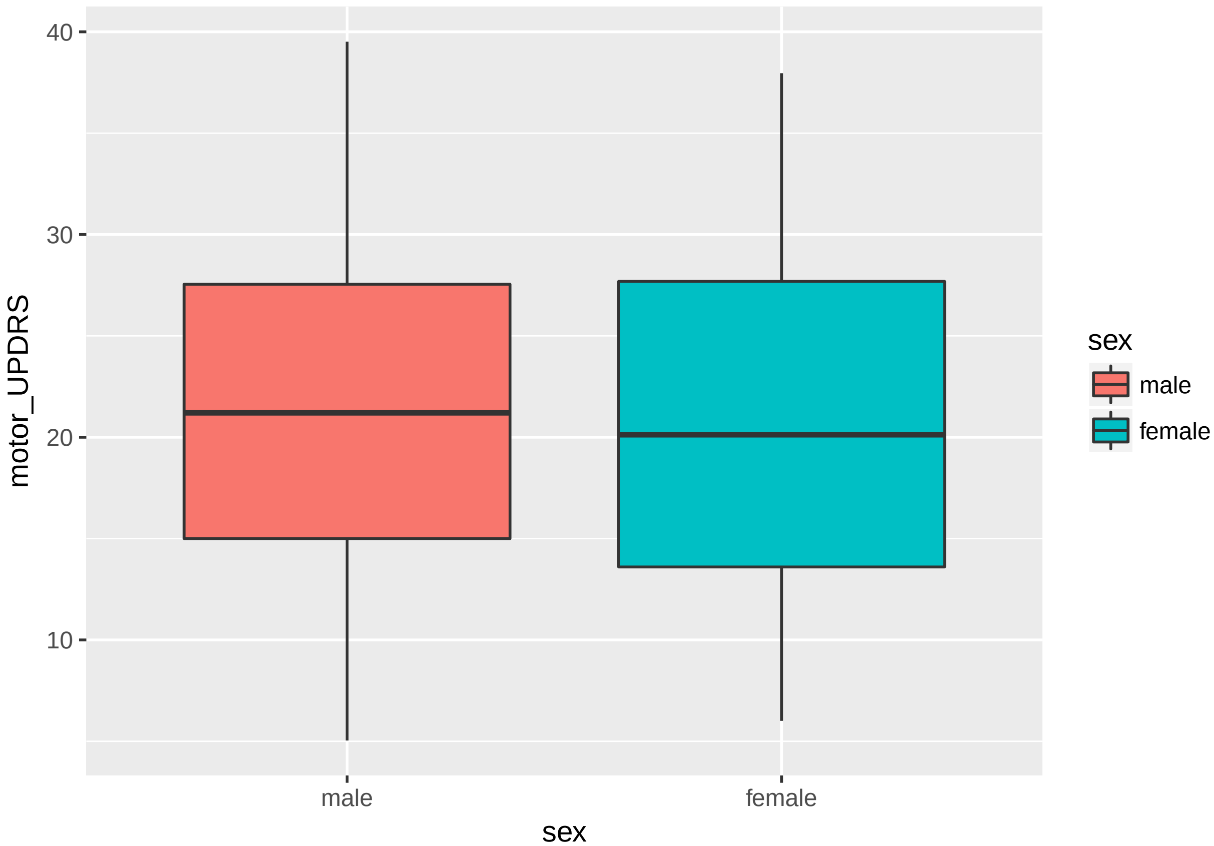
```
parkinson_dat_old <- parkinson_dat %>% filter(age >= 65)
parkinson_dat_old %>% distinct(subject, .keep_all = TRUE) %>% group_by(sex) %>%
  summarise(count=n(), mean_age=mean(age))
```

```
## # A tibble: 2 × 3
##      sex count mean_age
##   <fctr> <int>    <dbl>
## 1   male    16 70.56250
## 2 female     7 72.14286
```

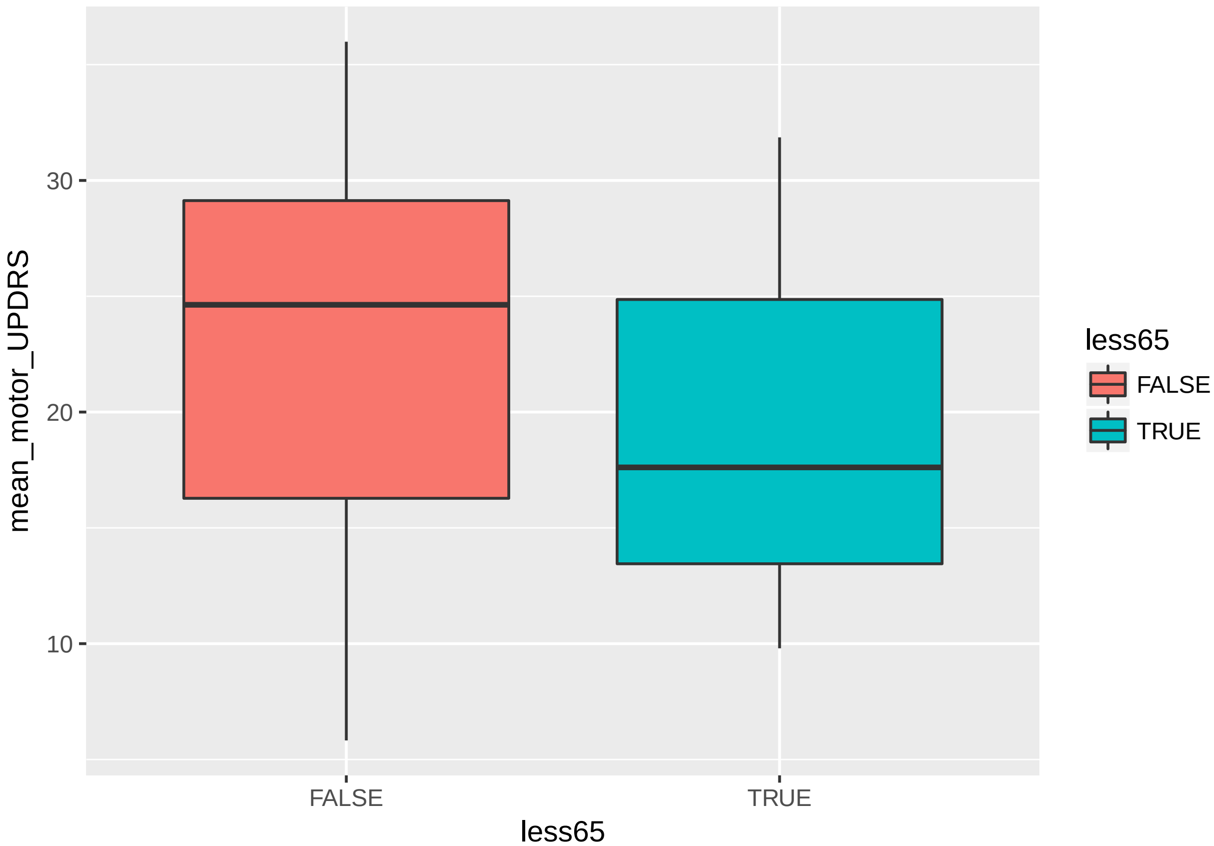
```
new_parkinson_dat <- parkinson_dat %>% group_by(subject) %>%
  summarise(mean_motor_UPDRS = mean(motor_UPDRS), age=mean(age))
new_parkinson_dat
```

```
## # A tibble: 42 × 3
##    subject mean_motor_UPDRS   age
##      <int>            <dbl> <dbl>
## 1        1         31.89893    72
## 2        2         13.81254    58
## 3        3         27.12478    57
## 4        4         15.79082    74
## 5        5         31.63260    75
## 6        6         27.53169    63
## 7        7         16.04706    72
## 8        8         19.88702    73
## 9        9         18.31236    68
## 10      10         13.42442    58
## # ... with 32 more rows
```

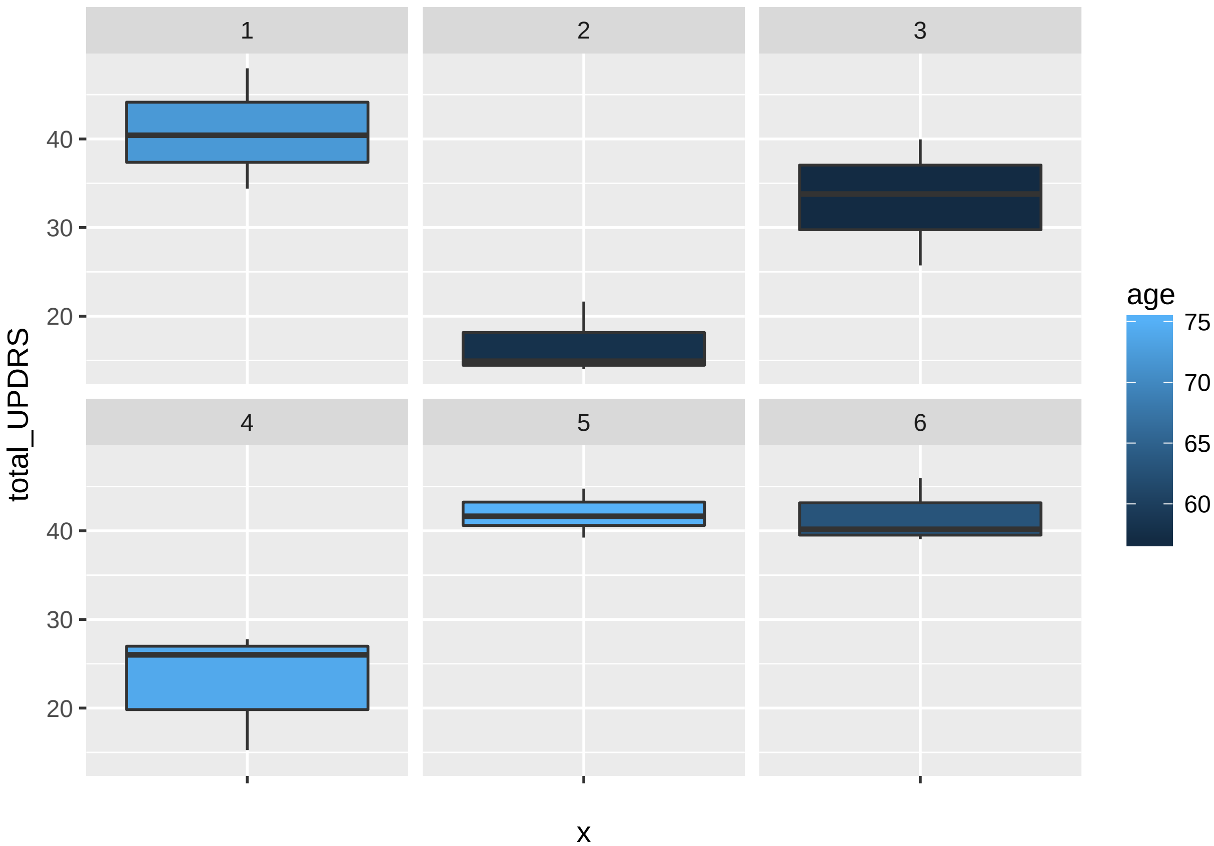
```
library(ggplot2)
ggplot(parkinson_dat, aes(sex, motor_UPDRS, fill=sex)) + geom_boxplot()
```




```
new_parkinson_dat$less65 <- new_parkinson_dat$age < 65
ggplot(new_parkinson_dat, aes(less65, mean_motor_UPDRS, fill=less65)) +
  geom_boxplot() #+ ggtitle("my title") + xlab("x lab") + ylab("y lab")
```




```r
parkinson_dat_sub <- subset(parkinson_dat, subject<=6)
ggplot(parkinson_dat_sub, aes("", total_UPDRS, fill=age)) + geom_boxplot() +
  facet_wrap(~subject, ncol = 3)
```




```
parkinson_dat_select <- parkinson_dat %>% select(total_UPDRS,PPE,DFA)
head(parkinson_dat_select)
```

```
##   total_UPDRS     PPE     DFA
## 1      34.398 0.16006 0.54842
## 2      34.894 0.10810 0.56477
## 3      35.389 0.21014 0.54405
## 4      35.810 0.33277 0.57794
## 5      36.375 0.19361 0.56122
## 6      36.870 0.19500 0.57243
```

```
library(reshape2)
```

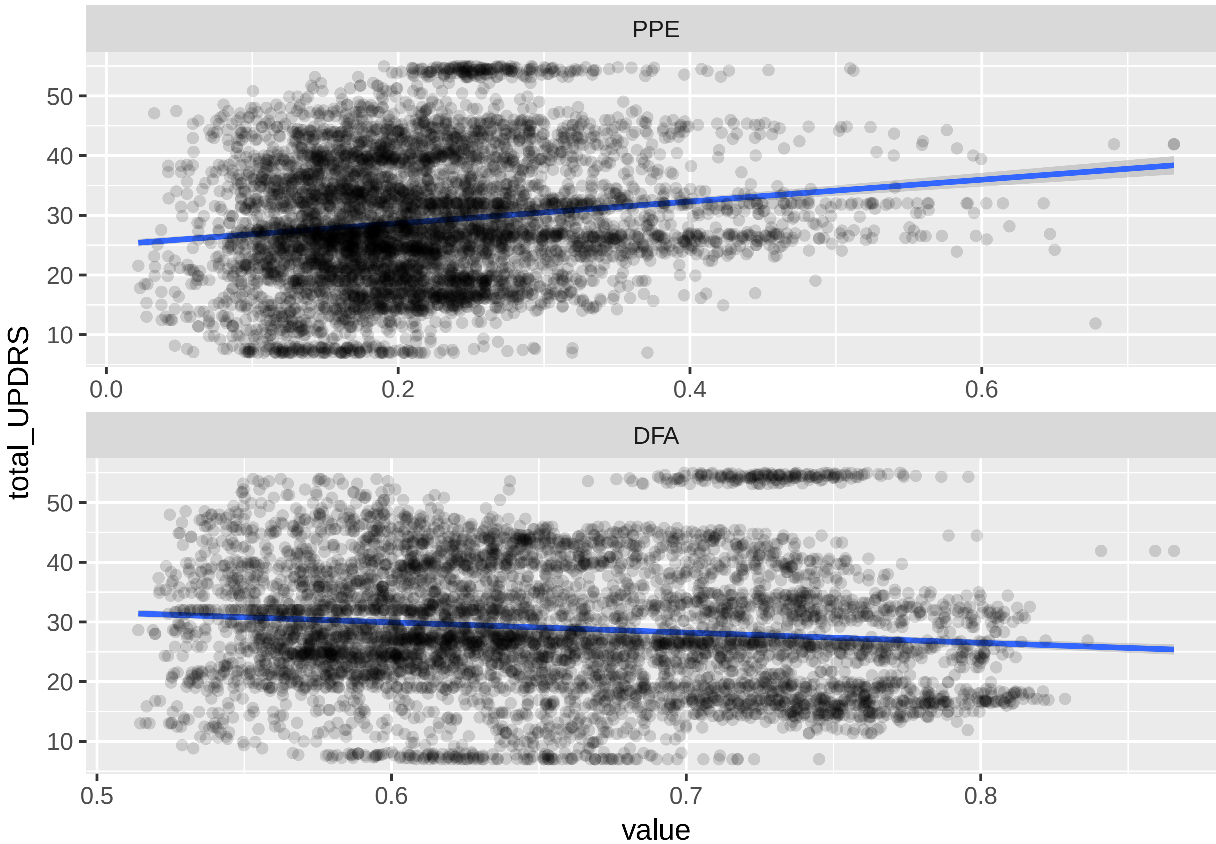
```
##
## Attaching package: 'reshape2'

## The following objects are masked from 'package:data.table':
##
##     dcast, melt
```

```
parkinson_dat_melt <- melt(parkinson_dat_select, id="total_UPDRS")
head(parkinson_dat_melt)
```

```
##   total_UPDRS variable   value
## 1      34.398      PPE 0.16006
## 2      34.894      PPE 0.10810
## 3      35.389      PPE 0.21014
## 4      35.810      PPE 0.33277
## 5      36.375      PPE 0.19361
```

```
## 6      36.870      PPE 0.19500
```

```r
ggplot(parkinson_dat_melt, aes(value, total_UPDRS)) + stat_smooth(method = "lm") +
  geom_point(alpha=0.15) + facet_wrap(~variable, scales="free",ncol=1)
```



Regression

We can do a linear regression to predict the UPDR score from the age, sex, PPE, and DFA variables.

```r
mymodel <- lm(total_UPDRS~age+sex+PPE+DFA+0, parkinson_dat) # + 0 is fot no intercept, coherent with th
summary(mymodel)
```

```
##
## Call:
## lm(formula = total_UPDRS ~ age + sex + PPE + DFA + 0, data = parkinson_dat)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -26.193  -7.441  -1.549   7.402  25.376
##
## Coefficients:
##            Estimate Std. Error t value Pr(>|t|)
## age         0.32456    0.01498   21.67   <2e-16 ***
## sexmale    21.42927    1.68034   12.75   <2e-16 ***
## sexfemale  19.21671    1.64638   11.67   <2e-16 ***
## PPE        21.54042    1.56344   13.78   <2e-16 ***
## DFA       -26.74463    2.03182  -13.16   <2e-16 ***
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 9.919 on 5870 degrees of freedom
## Multiple R-squared:  0.8972, Adjusted R-squared:  0.8971
## F-statistic: 1.025e+04 on 5 and 5870 DF,  p-value: < 2.2e-16
```

Breast Cancer

Attribute Information:

#	Attribute Domain
1.	Sample code number id number
2.	Clump Thickness 1 - 10
3.	Uniformity of Cell Size 1 - 10
4.	Uniformity of Cell Shape 1 - 10
5.	Marginal Adhesion 1 - 10
6.	Single Epithelial Cell Size 1 - 10
7.	Bare Nuclei 1 - 10
8.	Bland Chromatin 1 - 10
9.	Normal Nucleoli 1 - 10
10.	Mitoses 1 - 10
11.	Class: (2 for benign, 4 for malignant)

```r
#breast_cancer <- fread("https://archive.ics.uci.edu/ml/machine-learning-databases/breast-cancer-wiscon
#names(breast_cancer) <- c("id_number", "clump_thickness", "cell_size", "cell_shape", "marginal_adhesio
#write.csv(breast_cancer, file="breast_cancer.csv")

breast_cancer <- read.csv("breast_cancer.csv")
str(breast_cancer)
```

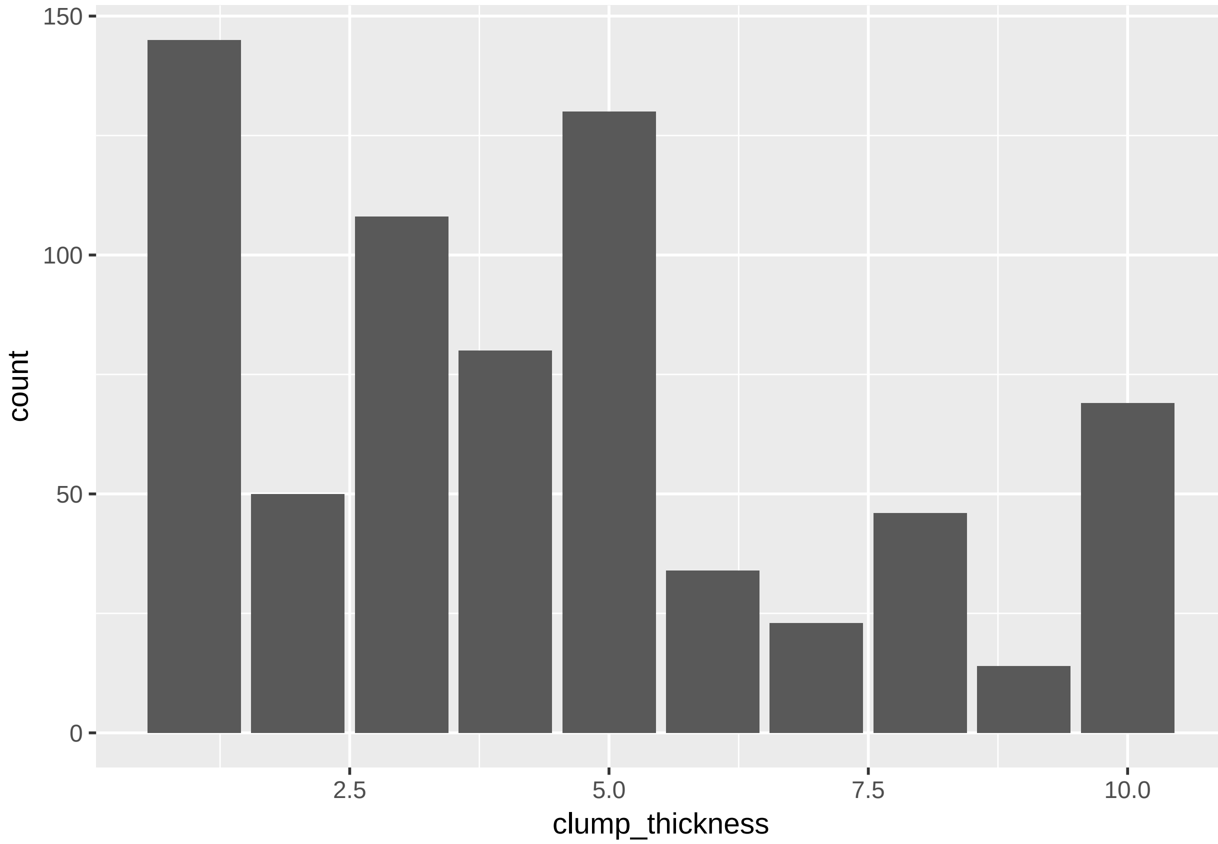
```
## 'data.frame':    699 obs. of  12 variables:
##  $ X                : int  1 2 3 4 5 6 7 8 9 10 ...
##  $ id_number        : int  1000025 1002945 1015425 1016277 1017023 1017122 1018099 1018561 1033078 1
##  $ clump_thickness  : int  5 5 3 6 4 8 1 2 2 4 ...
##  $ cell_size        : int  1 4 1 8 1 10 1 1 1 2 ...
##  $ cell_shape       : int  1 4 1 8 1 10 1 2 1 1 ...
##  $ marginal_adhesion: int  1 5 1 1 3 8 1 1 1 1 ...
##  $ single_epithelial: int  2 7 2 3 2 7 2 2 2 2 ...
##  $ bare_nuclei      : Factor w/ 11 levels "?","1","10","2",..: 2 3 4 6 2 3 3 2 2 2 ...
##  $ bland_chromatin  : int  3 3 3 3 3 9 3 3 1 2 ...
##  $ normal_nucleoli  : int  1 2 1 7 1 7 1 1 1 1 ...
##  $ mitoses          : int  1 1 1 1 1 1 1 1 5 1 ...
##  $ class            : int  2 2 2 2 2 4 2 2 2 2 ...
```

```r
breast_cancer$class <- factor(breast_cancer$class)
levels(breast_cancer$class) <- c("benign", "malignant")
str(breast_cancer)
```

```
## 'data.frame':    699 obs. of  12 variables:
##  $ X                : int  1 2 3 4 5 6 7 8 9 10 ...
##  $ id_number        : int  1000025 1002945 1015425 1016277 1017023 1017122 1018099 1018561 1033078 1
##  $ clump_thickness  : int  5 5 3 6 4 8 1 2 2 4 ...
##  $ cell_size        : int  1 4 1 8 1 10 1 1 1 2 ...
```

```
##  $ cell_shape       : int  1 4 1 8 1 10 1 2 1 1 ...
##  $ marginal_adhesion: int  1 5 1 1 3 8 1 1 1 1 ...
##  $ single_epithelial: int  2 7 2 3 2 7 2 2 2 2 ...
##  $ bare_nuclei      : Factor w/ 11 levels "?","1","10","2",..: 2 3 4 6 2 3 3 2 2 2 ...
##  $ bland_chromatin  : int  3 3 3 3 3 9 3 3 1 2 ...
##  $ normal_nucleoli  : int  1 2 1 7 1 7 1 1 1 1 ...
##  $ mitoses          : int  1 1 1 1 1 1 1 1 5 1 ...
##  $ class            : Factor w/ 2 levels "benign","malignant": 1 1 1 1 1 2 1 1 1 1 ...
```

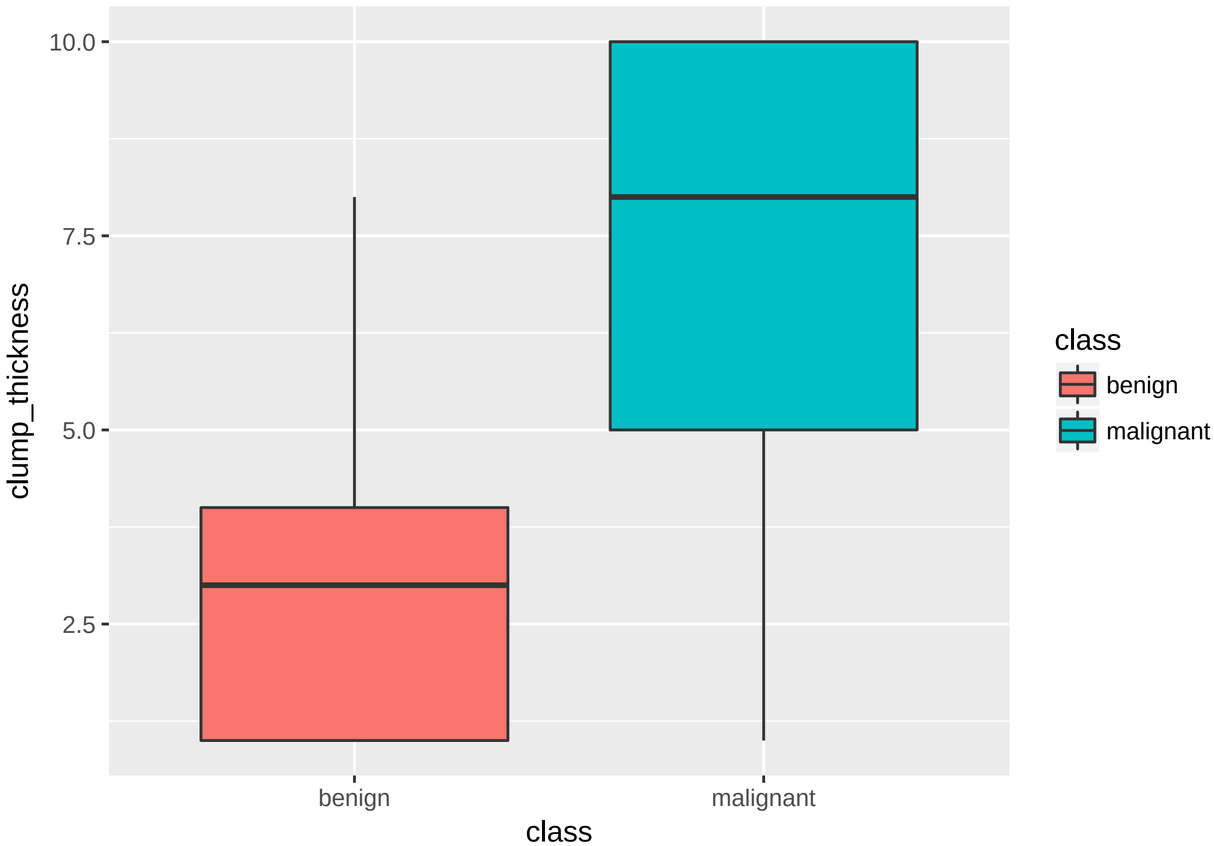
```
ggplot(breast_cancer, aes(clump_thickness)) + geom_bar()
```




```
breast_cancer %>% group_by(class) %>% summarise(count=n())
```

```
## # A tibble: 2 × 2
##       class count
##      <fctr> <int>
## 1    benign   458
## 2 malignant   241
```

```
ggplot(breast_cancer, aes(class, clump_thickness, fill=class)) + geom_boxplot()
```



Classification

Let us use a generalize linear model to classify the tumor into malignant and benign.

```
model <- glm(class~clump_thickness, family = "binomial", data=breast_cancer)
summary(model)
```

```
##
## Call:
## glm(formula = class ~ clump_thickness, family = "binomial", data = breast_cancer)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -2.1986  -0.4261  -0.1704   0.1730   2.9118
##
## Coefficients:
##                 Estimate Std. Error z value Pr(>|z|)
## (Intercept)     -5.16017    0.37795  -13.65   <2e-16 ***
## clump_thickness  0.93546    0.07377   12.68   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 900.53  on 698  degrees of freedom
## Residual deviance: 464.05  on 697  degrees of freedom
## AIC: 468.05
```

```
##
## Number of Fisher Scoring iterations: 6
```

Ressources

Datacamp

https://www.datacamp.com/

R for Data Science

http://r4ds.had.co.nz/

Advanced R

http://adv-r.had.co.nz/