An introduction to the `tidyverse`

Ziv Shkedy et al. (2020)

Part 1: Introduction

Focus: a quick introduction to tidyverse

The `tidyverse`

- The `tidyverse` is a collection of R packages that work in data frames in a tidy format.
- All packages are uploaded in CRAN, and can be installed using `install.packages` .
- In this chapter of the interactive book, we cover materials at an introduction level and follow closely the topics
  presented in Chapter 4 in the book Data Analysis and Prediction Algorithms with R by Rafael A. Irizarry.

What do we cover in this chapter ?

- The chapter is developed at a beginner level.
- We cover few functions from the `tidyverse` packages and illustrate the basic concepts using different examples of the following functions:
  - `mutate()`
  - `filter()`
  - `select()`
  - The pipe: $\%>\%$
  - `summarize()`
  - `group_by()`
  - `arrange()`
  - `top_n()`

`ggplot2`?

- Our aim in this tutorial is not to teach `ggplot2` (this will be done in a different chapter).
- Some functions of the package are used to visualized the main patterns in the datasets we used to illustrate the examples presented in this chapter.

- The following graphical functions are used for visualization:

  - `qplot()`
  - `ggplot() + geom_jitter()`
  - `ggplot() + geom_point()`
  - `gplot() + geom_density()`
  - `stripplot()`

Online references (I)

- Materials about `tidyverse` are widely available online.
  - For a YouTube tutorial about tidyverse in R by Mark Gingrass see **YTtidyverse1**.
  - For a YouTube tutorial about tidyverse in R by Garreet Grolemund see **YTtidyverse2a**.
  - For a YouTube tutorial about tidyverse in R by Garreet Grolemund see **YTtidyverse2b**.
  - For a YouTube tutorial about tidyverse in R by Ben Stenhaug see **YTtidyverse3**.

Online references (II)

- Interactive book for the course: **Booktidyverse1**
- Chapter 4 in the book: Data Analysis and Prediction Algorithms with R by Rafael A. Irizarry see **Chapter4**.

Part 2: the tidyverse package and tidy data

Focus: the center of the distribution

Graphical and numerical summaries

Tidy data

- Tidy data is a data format in which each row represents one measurement for one observation and columns are, as usual, the variables in the data.

The murders data

- The `murders` is an example of a tidy data.
- The information for each state is given in one line.
- Note that in this case, each observation (=state) has information in one data line.

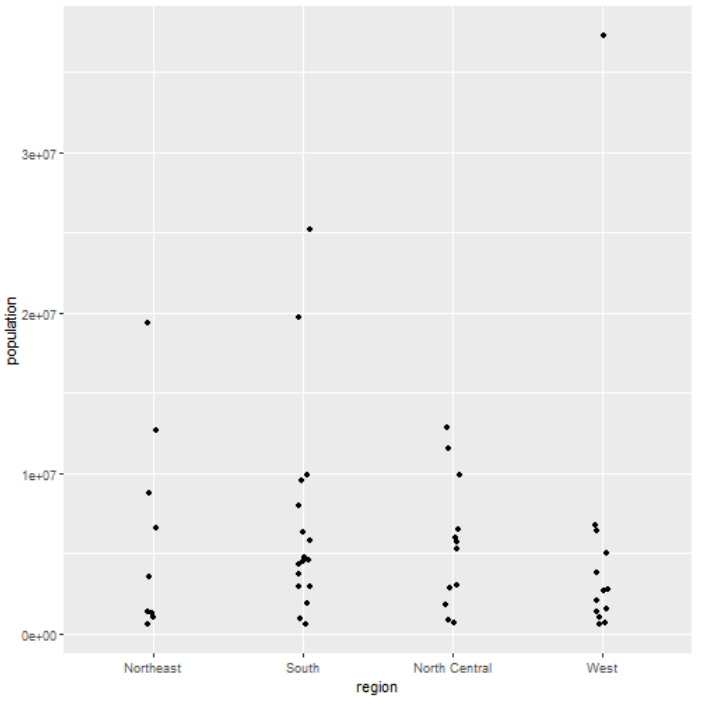
```
data("murders")
head(murders)
```

```
##        state abb region population total
## 1    Alabama  AL  South    4779736   135
## 2     Alaska  AK   West     710231    19
## 3    Arizona  AZ   West    6392017   232
## 4   Arkansas  AR  South    2915918    93
## 5 California  CA   West   37253956  1257
## 6   Colorado  CO   West    5029196    65
```

The murders data

- The murder rate by region is shown in the stripplot.
- It shows clearly that in the west, the murder rate is the lowest.

```
ggplot(murders, aes(region,population)
```



The ChickWeight data

- The Chicken Weight data gives information about weights of chicken in differnt diet groups.
- Each observation is a chick and it was measured in 12 times points.

```
names(ChickWeight)
```

```
## [1] "weight" "Time"   "Chick"  "Diet"
```

```
unique(ChickWeight$Time)
```

```
##  [1]  0  2  4  6  8 10 12 14 16 18 20 21
```

- In the data frame, each measurement is presented in one data line.
- Hence, the `ChickWeight` is a tidy data.

The ChickWeight data

- This implies that that the data for each observation is presented in 12 lines.
- note that NOT ALL subjects were measured in 12 times.
- Data for the first 6 time points of the first chick are listed below.

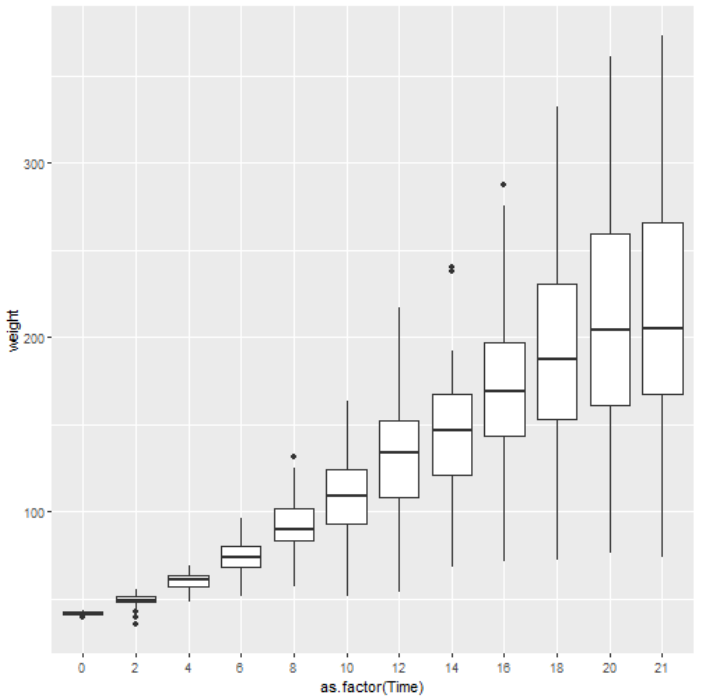
```
head(ChickWeight)
```

```
## Grouped Data: weight ~ Time | Chick
##   weight Time Chick Diet
## 1     42    0     1    1
## 2     51    2     1    1
## 3     59    4     1    1
## 4     64    6     1    1
## 5     76    8     1    1
## 6     93   10     1    1
```

The ChickWeight data

- The boxplot of the chicken weights by time point.
- Itshows the increasing trend of the weight over time.

```
ggplot(ChickWeight, aes(as.factor(Time
```



Part 3: the `mutate()`

Focus: adding a column(s)

Adding a variable (column)

- Suppose that we would like to calculate the murder rate per 100000 people that is

$$\text{rate} = \frac{\text{total}}{\text{population}} \times 100000.$$

- This can be done using the `mutate()` funtion.
- The function has the grneral call of: `mutate(data frame , new variable)` .

The murders data

- For the `murders` data we have

```
data("murders")
murders <- mutate(murders, rate = total / population * 100000)
```

- Note that after calculating the murder rate, the `murders` has an extra column (=variable) for the `rate`.

```
head(murders)
```

```
##        state abb region population total     rate
## 1    Alabama  AL  South    4779736   135 2.824424
## 2     Alaska  AK   West     710231    19 2.675186
## 3    Arizona  AZ   West    6392017   232 3.629527
## 4   Arkansas  AR  South    2915918    93 3.189390
## 5 California  CA   West   37253956  1257 3.374138
## 6   Colorado  CO   West    5029196    65 1.292453
```

The NHANES data

- The BMI of a person is given by

$$\text{BMI} = \frac{\text{weight}}{\text{height}^2}$$

.

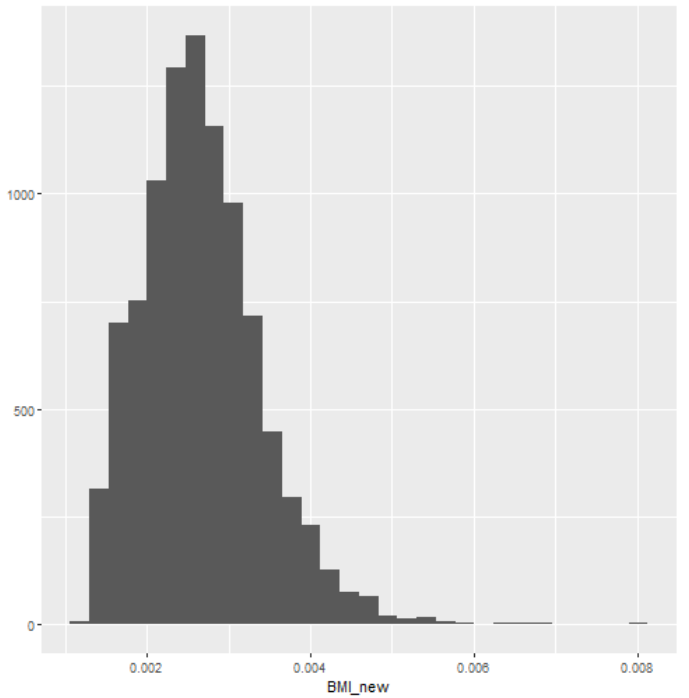
- To calculate the BMI in the `NHANES` we use

```
data("NHANES")
Data_new <- mutate(NHANES, BMI_new = Weight / (Height*Height))
```

The NHANES data

- The histogram of the BMI.

```
qplot(BMI_new , data=Data_new, geom="h
```



Practical session

- For the cars data (`mtcars`):
  - Define a new variable: mile per gallon / weight.
  - Produce a boxplot for the variable mile per gallon / weight by number of number of cylinders.
- For the murders data :
  - Produce a boxplot for the murder rate by region.

Part 4: the `filter()` function

Focus: selection of cases

Filtering

- Selection of observations (=cases) from the data.
- A subset of the data.
- can be done using the function `filter()` .
- The new data: has the same variables.

The murders data

- For murder dataset, we can select all the states with murder rate ≤ 0.71 by

```
filter(murders, rate <= 0.71)
```

```
##           state abb        region population total      rate
## 1        Hawaii  HI          West    1360301     7 0.5145920
## 2          Iowa  IA North Central    3046355    21 0.6893484
## 3 New Hampshire  NH     Northeast    1316470     5 0.3798036
## 4  North Dakota  ND North Central     672591     4 0.5947151
## 5       Vermont  VT     Northeast     625741     2 0.3196211
```

The cars data

- For cars data, suppose that we would like to plot the cars' weight versus the cars mpg for cars with weight ≤ 3.
- We first select all cars with weight smaller or equal to 3:

```
dim(mtcars)
```

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

```
mtcars1<-filter(mtcars, wt <= 3)
dim(mtcars1)
```

```
## [1] 12 11
```

The cars data

- The new data frame `mtcars1` contains the information for all cars with weight lower than 3,

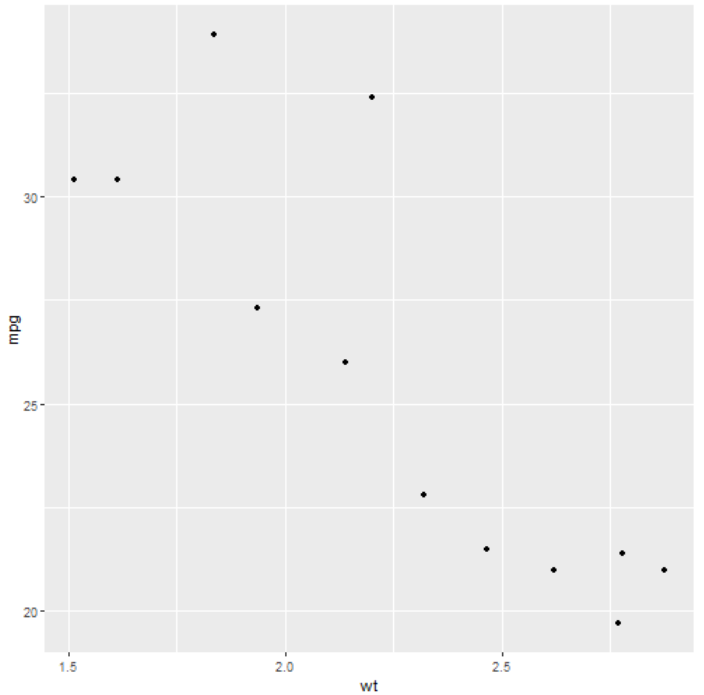
```
mtcars1
```

```
##                  mpg cyl  disp  hp drat    wt  qsec vs am gear carb
## Mazda RX4       21.0   6 160.0 110 3.90 2.620 16.46  0  1    4    4
## Mazda RX4 Wag   21.0   6 160.0 110 3.90 2.875 17.02  0  1    4    4
## Datsun 710      22.8   4 108.0  93 3.85 2.320 18.61  1  1    4    1
## Fiat 128        32.4   4  78.7  66 4.08 2.200 19.47  1  1    4    1
## Honda Civic     30.4   4  75.7  52 4.93 1.615 18.52  1  1    4    2
## Toyota Corolla 33.9   4  71.1  65 4.22 1.835 19.90  1  1    4    1
## Toyota Corona  21.5   4 120.1  97 3.70 2.465 20.01  1  0    3    1
## Fiat X1-9       27.3   4  79.0  66 4.08 1.935 18.90  1  1    4    1
## Porsche 914-2  26.0   4 120.3  91 4.43 2.140 16.70  0  1    5    2
## Lotus Europa    30.4   4  95.1 113 3.77 1.513 16.90  1  1    5    2
## Ferrari Dino    19.7   6 145.0 175 3.62 2.770 15.50  0  1    5    6
## Volvo 142E      21.4   4 121.0 109 4.11 2.780 18.60  1  1    4    2
```

The cars data

- The scaterplot below of the weight versus the mpg can be produce using the following code.

```
ggplot(mtcars1, aes(x=wt, y=mpg)) +
  geom_point()
```



Practical session

- For the NHANES data:
  - Select all the observations for which the BMI is greater or equal to 30.
  - Produce the histogram for the variable BMI for all male.
- For the chick weight data (`chickwts`):
  - Select all chicks with weight smaller than 158.
  - Select all chicks from the `horsebean` feed group.

Part 5: the `select()` function

Focus: selection of variables

Part 6: the pipe %>%

Focus: multiple startments in one run

Part 7: the `summarize()` function

Focus: summary statistics

The summarize function

- The function `summarize()` allows us to produce summery statistics for variables in the data frame.

The heights data

- The height data frame gives the height by gender for 1050 individuals

```
library(dplyr)
library(dslabs)
data(heights)
dim(heights)
```

```
## [1] 1050    2
```

- The first 6 observations in the data are listed below.

```
head(heights)
```

```
##      sex height
## 1   Male     75
## 2   Male     70
## 3   Male     68
## 4   Male     74
## 5   Male     61
## 6 Female     65
```

Mean and standard deviation

- We can calculate the mean and standard deviation for female using the function `summarize ()` .
- Note that we first filter the data and define and subgroup contains the data for female

```
s <- heights %>%  filter(sex == "Female") %>%
  summarize(average = mean(height), standard_deviation = sd(height))
```

- The object `s` stores the results

```
s
```

```
##    average standard_deviation
## 1 64.93942           3.760656
```

Mean and standard deviation

- We can define a vector that contains the results

```
c(s$average,s$standard_deviation)
```

```
## [1] 64.939424  3.760656
```

Summary statistics by group

Alternatively, we can define a vector with the female heights (`height.female`) and calculate the mean and standard deviation for this vector.

```
height.female<-heights$height[heights$sex == "Female"]
mean(height.female)
```

```
## [1] 64.93942
```

```
sd(height.female)
```

```
## [1] 3.760656
```

Quantiles

- The median, minimum and maximum height for female

```
heights %>%
  filter(sex == "Female") %>% summarize(median = median(height), minimum = min(hei
                                        maximum = max(height))
```

```
##     median minimum maximum
## 1 64.98031      51      79
```

Quantiles

- These summary statistics can be also calculate can the function `quantile` .

```
heights %>%  filter(sex == "Female") %>%
  summarize(range = quantile(height, c(0, 0.5, 1)))
```

```
##       range
## 1 51.00000
## 2 64.98031
## 3 79.00000
```

The chicks data

- To calculate the mean and standard deviation for the chick weights we use

```
s <- chickwts %>%  summarize(average = mean(weight), standard_deviation = sd(weigh
s
```

```
##    average standard_deviation
## 1 261.3099            78.0737
```

- Note that for this example we ignore the diet group.

Practical session

- For the NHANES data:
  - Canculate the mean, meadian and standard deviation of the variable BMI.
  - Canculate the mean, meadian and standard deviation of the variable BMI only for male.
- For the cars data:
  - Canculate the mean, meadian and standard deviation of the variable weight.
  - Canculate the mean, meadian and standard deviation of the variable weight only for cars with
    automatic transmission.

Part 8: the `group_by()` function

Focus: summary statistics by group

Analysis by group

- In this section we focus on an analysis in which the analysis is done across a level of a factor in the data frame.
- For example, the diet group in the chick data frame etc.

The heights data

- The mean and standard deviation for the height by gender can be calculate by adding the function `group_by(sex)`

```
heights %>%
  group_by(sex) %>%
  summarize(average = mean(height), standard_deviation = sd(height))
```

```
## # A tibble: 2 x 3
##   sex    average standard_deviation
##   <fct>    <dbl>              <dbl>
## 1 Female    64.9               3.76
## 2 Male      69.3               3.61
```

The heights data

- The same results can be obtained using the function `tapply` .

```
tapply(heights$height,heights$sex,mean)
```

```
##   Female     Male
## 64.93942 69.31475
```

```
tapply(heights$height,heights$sex,sd)
```

```
##   Female     Male
## 3.760656 3.611024
```

The murders data

- The median murder rate by region using the `group_by(region)` and the `summarize()` functions

```
murders %>% group_by(region) %>%
  summarize(median_rate = median(rate))
```

```
## # A tibble: 4 x 2
##   region        median_rate
##   <fct>               <dbl>
## 1 Northeast            1.80
## 2 South                3.40
## 3 North Central        1.97
## 4 West                 1.29
```

The murders data

The median murder rate by region using the `tapply()` function.

```
tapply(murders$rate,murders$region,median)
```

```
##     Northeast         South North Central          West
##      1.802179      3.398069      1.971105      1.292453
```

The chicks data

- Summary statistics by diet group

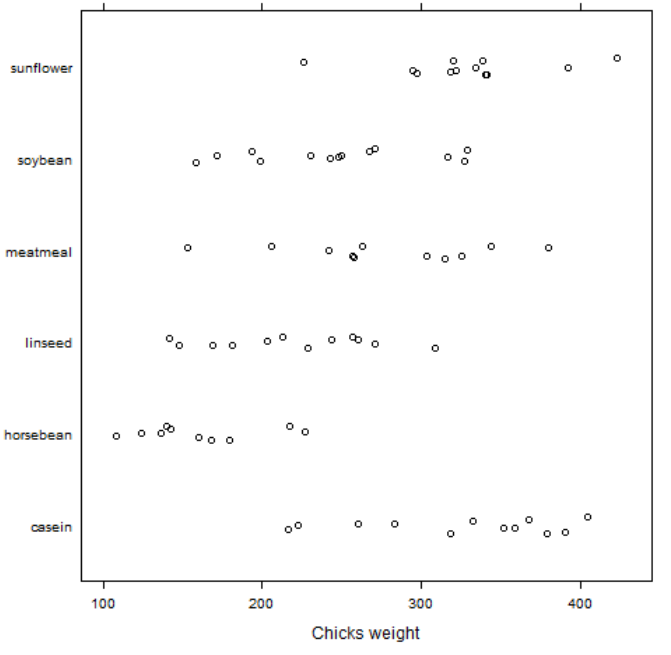
```
chickwts %>%
  group_by(feed) %>%
  summarize(average = mean(weight), standard_deviation = sd(weight))
```

```
## # A tibble: 6 x 3
##   feed      average standard_deviation
##   <fct>       <dbl>              <dbl>
## 1 casein       324.               64.4
## 2 horsebean    160.               38.6
## 3 linseed      219.               52.2
## 4 meatmeal     277.               64.9
## 5 soybean      246.               54.1
## 6 sunflower    329.               48.8
```

The chicks data

- The striptplot reveals that the weights in the horsebean group are, in general, the smallest in the sample.

```
stripplot(feed ~ jitter(weight),
          data = chickwts,
          aspect = 1, jitter = T,
          xlab="Chicks weight", col
```



Practical session

- For the NHANES data:
  - Calculate the mean BMI by gender.
  - Calculate the mean age by diabetes status (the variable `Diabetes`).
- For the cars data:
  - Canculate the mean, meadian and standard deviation of the variable weight by transmission type (automatic vs. manual).
  - Canculate the mean, meadian and standard deviation of the variable miles per gallon by number ofcylinders.

Part 9: the `arrange()` function

Focus: sorting the data

The murders data

- We can sort a data frame by a variable `x` using the function `arrange(x)`.
- For the murder data frame, we sort the data by the population size

```
murders %>%
  arrange(population) %>% head()
```

```
##                  state abb        region population total       rate
## 1              Wyoming  WY          West     563626     5  0.8871131
## 2 District of Columbia  DC         South     601723    99 16.4527532
## 3              Vermont  VT     Northeast     625741     2  0.3196211
## 4         North Dakota  ND North Central     672591     4  0.5947151
## 5               Alaska  AK          West     710231    19  2.6751860
## 6         South Dakota  SD North Central     814180     8  0.9825837
```

The murders data

- The same sorting can be implemented using the function `order()`.
- In this case the rows will be presented in the order of the population.

```
data1<-murders[order(murders$population),]
head(data1)
```

```
##                   state abb        region population total       rate
## 51              Wyoming  WY          West     563626     5  0.8871131
## 9  District of Columbia  DC         South     601723    99 16.4527532
## 46              Vermont  VT     Northeast     625741     2  0.3196211
## 35         North Dakota  ND North Central     672591     4  0.5947151
## 2                Alaska  AK          West     710231    19  2.6751860
## 42         South Dakota  SD North Central     814180     8  0.9825837
```

Sorting and changing the order

- We sort the data frame by rate from the lowest to the highest rate

```
murders %>%
  arrange(rate) %>%
  head()
```

```
##           state abb        region population total      rate
## 1       Vermont  VT     Northeast     625741     2 0.3196211
## 2 New Hampshire  NH     Northeast    1316470     5 0.3798036
## 3        Hawaii  HI          West    1360301     7 0.5145920
## 4  North Dakota  ND North Central     672591     4 0.5947151
## 5          Iowa  IA North Central    3046355    21 0.6893484
## 6         Idaho  ID          West    1567582    12 0.7655102
```

Sorting and changing the order

- We can change the order using the function `desc()` so the data are presented from the highest to the lowest rate in a decreasing order.

```
murders %>%
  arrange(desc(rate)) %>%
  head
```

```
##                  state abb        region population total      rate
## 1 District of Columbia  DC         South     601723    99 16.452753
## 2            Louisiana  LA         South    4533372   351  7.742581
## 3             Missouri  MO North Central    5988927   321  5.359892
## 4             Maryland  MD         South    5773552   293  5.074866
## 5       South Carolina  SC         South    4625364   207  4.475323
## 6             Delaware  DE         South     897934    38  4.231937
```

The Chicken Weight data

- The first 6 observations in the chicken weight data belongs to the first chick at time point 0 to 10.

```
head(ChickWeight)
```

```
## Grouped Data: weight ~ Time | Chick
##   weight Time Chick Diet
## 1     42    0     1    1
## 2     51    2     1    1
## 3     59    4     1    1
## 4     64    6     1    1
## 5     76    8     1    1
## 6     93   10     1    1
```

The Chicken Weight data

- We sort the data frame according to the `Time` variable. After sorting, the first 6 lines in the data frame are the measurements for chock 1-6 at day 21.

```
ChickWeight %>%
  arrange(desc(Time)) %>%
  head
```

```
## Grouped Data: weight ~ Time | Chick
##   weight Time Chick Diet
## 1    205   21     1    1
## 2    215   21     2    1
## 3    202   21     3    1
## 4    157   21     4    1
## 5    223   21     5    1
## 6    157   21     6    1
```

The Chicken Weight data

- We can reverse the order, in this case the first 6 lines are the measurements for check 1-6 at baseline (`Time =0`).

```
ChickWeight %>%
  arrange(Time) %>%
  head
```

```
## Grouped Data: weight ~ Time | Chick
##   weight Time Chick Diet
## 1     42    0     1    1
## 2     40    0     2    1
## 3     43    0     3    1
## 4     42    0     4    1
## 5     41    0     5    1
## 6     41    0     6    1
```

Practical session

- Sort the NHANES data according to the subjects' BMI.
- For the NHANES data, select all subjects with diabetes (the variable `Diabetes`) and sort according to the subjects' age.
- Sort the cars data according to the cars' mpg.

Part 10: Nested sorting

Focus: sorting with two variables

Nested sorting

- Suppose that we want to present the data in an increasing order of `x` across a level of a factor `y` .
- We can sort the data frame by a variable `x` within the factor levels using the function `arrange(y,x)` .

the murder data

- For the murder data frame, we sort the data by murder rate within the region

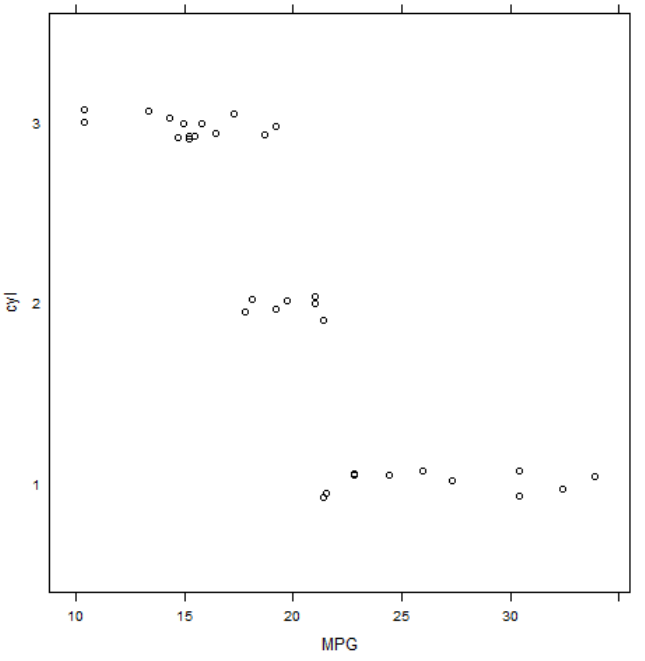
```
murders %>%
  arrange(region, rate) %>%
  head()
```

```
##           state abb    region population total      rate
## 1       Vermont  VT Northeast     625741     2 0.3196211
## 2 New Hampshire  NH Northeast    1316470     5 0.3798036
## 3         Maine  ME Northeast    1328361    11 0.8280881
## 4  Rhode Island  RI Northeast    1052567    16 1.5200933
## 5 Massachusetts  MA Northeast    6547629   118 1.8021791
## 6      New York  NY Northeast   19378102   517 2.6679599
```

The cars data

- The figure shows that `mpg` as the number of cylinders decreases.

```
stripplot(cyl ~ jitter(mpg),
            data = mtcars,
            aspect = 1, jitter = T,
            xlab="MPG", col = 1)
```



The cars data

- We can sort the cars according to their mpg (in an increasing order) by the number of cylinders

```
mtcars %>%
  arrange(cyl, mpg)
```

```
##                      mpg cyl  disp  hp drat    wt  qsec vs am gear carb
## Volvo 142E          21.4   4 121.0 109 4.11 2.780 18.60  1  1    4    2
## Toyota Corona       21.5   4 120.1  97 3.70 2.465 20.01  1  0    3    1
## Datsun 710          22.8   4 108.0  93 3.85 2.320 18.61  1  1    4    1
## Merc 230            22.8   4 140.8  95 3.92 3.150 22.90  1  0    4    2
## Merc 240D           24.4   4 146.7  62 3.69 3.190 20.00  1  0    4    2
## Porsche 914-2       26.0   4 120.3  91 4.43 2.140 16.70  0  1    5    2
## Fiat X1-9           27.3   4  79.0  66 4.08 1.935 18.90  1  1    4    1
## Honda Civic         30.4   4  75.7  52 4.93 1.615 18.52  1  1    4    2
## Lotus Europa        30.4   4  95.1 113 3.77 1.513 16.90  1  1    5    2
## Fiat 128            32.4   4  78.7  66 4.08 2.200 19.47  1  1    4    1
## Toyota Corolla      33.9   4  71.1  65 4.22 1.835 19.90  1  1    4    1
## Merc 280C           17.8   6 167.6 123 3.92 3.440 18.90  1  0    4    4
## Valiant             18.1   6 225.0 105 2.76 3.460 20.22  1  0    3    1
## Merc 280            19.2   6 167.6 123 3.92 3.440 18.30  1  0    4    4
## Ferrari Dino        19.7   6 145.0 175 3.62 2.770 15.50  0  1    5    6
## Mazda RX4           21.0   6 160.0 110 3.90 2.620 16.46  0  1    4    4
## Mazda RX4 Wag       21.0   6 160.0 110 3.90 2.875 17.02  0  1    4    4
## Hornet 4 Drive      21.4   6 258.0 110 3.08 3.215 19.44  1  0    3    1
## Cadillac Fleetwood  10.4   8 472.0 205 2.93 5.250 17.98  0  0    3    4
## Lincoln Continental 10.4   8 460.0 215 3.00 5.424 17.82  0  0    3    4
```

Practical session

- Sort the NHANES data according to the subjects' BMI by Gender.
- Sort the NHANES data according to the subjects' age by smoking status (the variable
  `Smoke100`).
- Sort the Chicks Weights data (`chickwts`) according to the chicks' weight by diet group.

Part 11: The `top_n()` function

Focus: selection of the top K observations

Top n

- To print the top `n` observations according to the variable `x` we can use the function `top_n(n, x)` .

The murders data

- For the murders data, we print the top 5 states with the highest murder rate

```
murders %>% top_n(5, rate)
```

```
##                  state abb        region population total      rate
## 1 District of Columbia  DC         South     601723    99 16.452753
## 2            Louisiana  LA         South    4533372   351  7.742581
## 3             Maryland  MD         South    5773552   293  5.074866
## 4             Missouri  MO North Central    5988927   321  5.359892
## 5       South Carolina  SC         South    4625364   207  4.475323
```

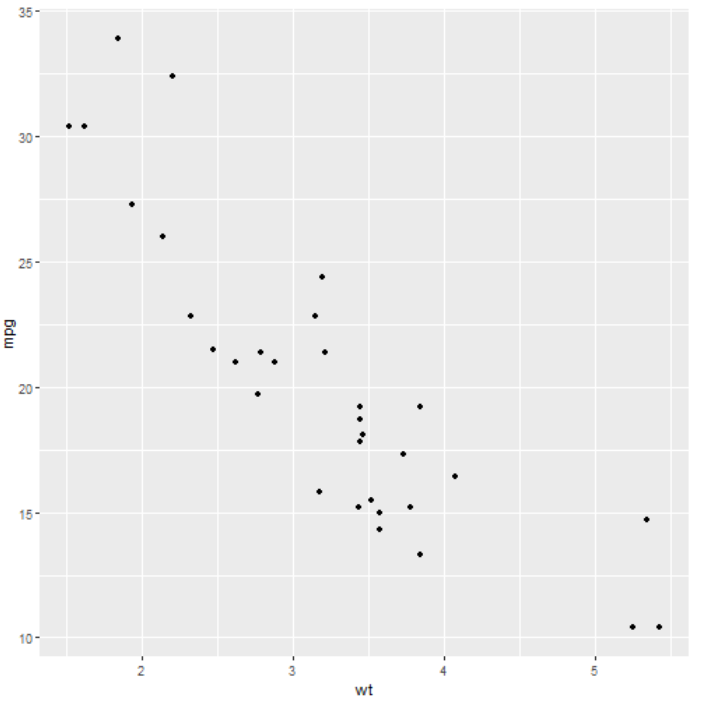
The cars data

- The scaterplot of the cars' weight versus the cars' `mpg`.
- The top 4 cars, with the highest mpg are given below

```
mtcars %>% top_n(4,mpg)
```

```
##                 mpg cyl disp  hp drat
## Fiat 128       32.4   4 78.7  66 4.08 2.2
## Honda Civic    30.4   4 75.7  52 4.93 1.6
## Toyota Corolla 33.9   4 71.1  65 4.22 1.8
## Lotus Europa   30.4   4 95.1 113 3.77 1.5
```

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



Practical session

- Print the 10 observations in the NHANES data with the highest BMI.
- Create a new data frame that contains the top 5 observations with the older age in in the NHANES
  data.