

Ling 411 - Fall 2023

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```
# Seed for random number generation  
set.seed(42)  
knitr::opts_chunk$set(cache.extra = knitr::rand_seed, class.output="r-output")  
source("../source/r_functions.R")
```

Chapter 1

Getting Started

Welcome to the R tutorial for Ling 411. The purpose of these lecture notes is to help remind you some of the R related material we covered in the class. The material here is not intended to be complete and self-contained. These are just lecture notes. You need to attend the classes and Problem Sessions to get a full grasp of the concepts.

1.1 Disclaimer

Some of the material in this book are from Pavel Logachev's class notes for LING 411. I'm indebted to Pavel for his friendship, guidance and support. Without him LING 411 could not exist in its current form.

1.2 Some great resources

- Throughout the semester, I will draw on from the following resources. These are just useful resources and feel free to take a look at them as you wish.
 - Bodo Winter's excellent book: Statistics for Linguists: An Introduction Using R
 - The great introduction materials developed at the University of Glasgow: <https://psyteachr.github.io/>, in particular 'Data Skills for Reproducible Science'.
 - The also pretty great introduction to R and statistics by Danielle Navarro available [here](#).
 - Matt Crump's 'Answering Questions with Data'.
 - Primers on a variety of topics: <https://rstudio.cloud/learn/primers>

- Cheat sheets on a variety of topics: <https://rstudio.cloud/learn/cheat-sheets>
- The following tutorials are great too.
 - ‘The Tidyverse Cookbook’
 - ‘A Ggplot2 Tutorial for Beautiful Plotting in R’
 - ‘R Graphics Cookbook, 2nd edition’

1.3 Blocks

Code, output, and special functions will be shown in designated boxes. The first box below illustrates a **code block**. The code block contains code that you can type in your R interpreter as the source code. You can simply copy and paste it in your R code. The second box indicates the **output** of R given the code in the first box.

```
2+2
```

```
## [1] 4
```

Functions will be introduced in grey boxes. The following grey box describes the `summary()` function.

```
summary(x)
```

Returns the summary statistics of a dataframe.

- `x` A dataframe.

The following code block uses the `summary()` function on the `mtcars` dataframe that comes pre-installed with R.

```
summary(mtcars)
```

```
##           mpg           cyl           disp           hp
##  Min.      :10.40   Min.      :4.000   Min.      : 71.1   Min.      : 52.0
##  1st Qu.:15.43   1st Qu.:4.000   1st Qu.:120.8   1st Qu.: 96.5
##  Median :19.20   Median :6.000   Median :196.3   Median :123.0
##  Mean   :20.09   Mean   :6.188   Mean   :230.7   Mean   :146.7
##  3rd Qu.:22.80   3rd Qu.:8.000   3rd Qu.:326.0   3rd Qu.:180.0
##  Max.   :33.90   Max.   :8.000   Max.   :472.0   Max.   :335.0
```



```
##      drat      wt      qsec      vs
##  Min.   :2.760  Min.   :1.513  Min.   :14.50  Min.   :0.0000
## 1st Qu.:3.080  1st Qu.:2.581  1st Qu.:16.89  1st Qu.:0.0000
## Median :3.695  Median :3.325  Median :17.71  Median :0.0000
## Mean   :3.597  Mean   :3.217  Mean   :17.85  Mean   :0.4375
## 3rd Qu.:3.920  3rd Qu.:3.610  3rd Qu.:18.90  3rd Qu.:1.0000
## Max.   :4.930  Max.   :5.424  Max.   :22.90  Max.   :1.0000
##      am      gear      carb
##  Min.   :0.0000  Min.   :3.000  Min.   :1.000
## 1st Qu.:0.0000  1st Qu.:3.000  1st Qu.:2.000
## Median :0.0000  Median :4.000  Median :2.000
## Mean   :0.4062  Mean   :3.688  Mean   :2.812
## 3rd Qu.:1.0000  3rd Qu.:4.000  3rd Qu.:4.000
## Max.   :1.0000  Max.   :5.000  Max.   :8.000
```

If you want to learn more about the `mtcars` dataset, you can simply put a question mark in front of its name, which will show the documentation for the dataset. The documentation will pop up in the **Help** tab on the bottom right window in RStudio.

```
?mtcars
```


Chapter 2

Basics

You can think of R as a fancy calculator. We could do almost all of the operations we do in R on a calculator. However, that would take a lot of time and effort when we are dealing with a large amount of data. That's (partly) why we're using R. I hope this helps those who might have a bit of anxiety about coding.

You should also note that everything we do in R can also be done in other programming languages. However, R is used a lot by data analysts and statisticians. It is relatively easier to use for data analysis and there are lots of libraries (code someone else has written that makes our life easier) that come quite handy.

Without further ado, let's dive in.

2.1 Basic Math Operations

You can use R to make carry out basic mathematical operations.

Addition

```
2+2
```

```
## [1] 4
```

Subtraction

```
4-2
```

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

Multiplication

```
47*3
```

```
## [1] 141
```

Division

```
9/4
```

```
## [1] 2.25
```

Floor Division

```
9%/%4
```

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

Exponentiation

```
2^3
```

```
## [1] 8
```

2.2 Operators

You can use basic mathematical operators in R.

Equals

`==` is the equals operator. Notice that this is distinct from the `=` operator we are used to. The latter is used for variable assignment in R. We won't use it. When you run `2==2`, R will evaluate this statement and return `TRUE` or `FALSE`.

```
2 == 2
```

```
## [1] TRUE
```

```
2 == 7
```

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

Not Equal

!= is the not equal operator.

```
2 != 2
```

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

```
2 != 7
```

```
## [1] TRUE
```

Other logical operators

<,>,<=,>=

```
2 < 3
```

```
## [1] TRUE
```

```
2 > 5
```

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

```
2 <= 5
```

```
## [1] TRUE
```

```
2 >= 5
```

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

2.3 Variables and Assignment

In R (like in many programming languages), values can be assigned to a variable to be used later. For example, you might want to store someone's age in a variable and then use it later for some purpose. In R, variables created via assignment `<-`. The following code creates a variable called *alex* and assigns it the value 35. Let's assume that this is Alex's age.

```
alex <- 35
```

Next time you want to do anything with the age, you can simply call the variable *alex* and do whatever you want with it (e.g. print, multiply, reassign, etc.). For example, the following code simply prints the value of the *alex* variable.

```
alex
```

```
## [1] 35
```

The following code multiplies it by 2.

```
alex * 2
```

```
## [1] 70
```

Now assume that Alex's friend Emma's is 2 years younger than Alex. Let's assign Emma's age by subtracting 2 from Alex' age. In the following code block, the first line creates the variable *emma* and assigns it the value `alex - 2`. The second line simply prints the value of the variable *emma*.

```
emma <- alex - 2  
emma
```

```
## [1] 33
```

A variable can hold different **types** of data. In the previous examples, we assigned **integers** to variables. We can also assign characters, vectors, etc.

character

```
name <- "emma"  
name
```

```
## [1] "emma"
```

vector

```
age_list <- c(35, 27, 48, 10)  
age_list
```

```
## [1] 35 27 48 10
```

2.4 Data Types

In R, values have **types**:

Data Type	Examples
Integer (Numeric):	..., -3, -2, -1, 0, +1, +2, +3, ...
Double (Numeric):	most rational numbers; e.g., 1.0, 1.5, 20.0, pi
Character:	"a", "b", "word", "hello dear friend, ..."
Logical:	TRUE or FALSE (or: T or F)
Factor:	Restricted, user-defined set of values, internally represented numerically (e.g., Gender {'male', 'female', 'other'})
Ordered factor:	Factor with an ordering (e.g., Starbucks coffee sizes {'venti' > 'grande' > 'tall'})

You need to understand the data types well as some operations are defined only on some data types. For example, you can add two integers or doubles but you cannot add an integer with a character.

```
my_integer_1 <- as.integer(2)
my_integer_2 <- as.integer(5)
my_character <- "two"
my_double <- 2.2
```

Adding, multiplying, deducting, etc. two integers is fine. So is combining two doubles or a double with an integer.

```
my_integer_1 + my_integer_2
```

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

```
my_integer_1 * my_double
```

```
## [1] 4.4
```

However, combining an integer with a character will lead to an error. You should read the errors carefully as they will help you understand where things went wrong.

```
my_integer_1 + my_character
```

```
## Error in my_integer_1 + my_character: non-numeric argument to binary operator
```

2.5 Determining the data type

If you don't know the type of some data, you can use the `typeof()` function to get the type of a particular data item.

```
typeof(my_double)
```

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

```
typeof(my_integer_1)
```

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

```
typeof(my_character)
```

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

2.6 Changing the types

You can change the type of a data item as long as the data is compatible with the type. For example, you can change an integer to a double.

```
as.double(my_integer_2)
```

```
## [1] 5
```

```
as.integer(my_double)
```

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

You can also change a character into an integer if it is a compatible value.


```
as.integer("2")
```

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

However, you cannot change any character into an integer.

```
as.integer("two")
```

```
## Warning: NAs introduced by coercion
```

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

2.7 Installing packages

Packages of code written by other developers for particular needs. They save you a lot of time and effort in carrying out your jobs. All you have to do is to find the right package for your task and learn what the package is capable of and how it works. In this class, we will use several packages that will simplify our lives.

To install a package, simply run `install.packages("your_package_name")`. For example, we will make use of the `tidyverse` package. The official CRAN page for `tidyverse` is [here](#). This is a more user friendly link about `tidyverse`. Finally, this is a bookdown version that looks helpful.

```
install.packages('tidyverse')
```

You need to install a package once. For this reason, you can use the console (bottom left window RStudio) rather than a script (top left window in RStudio). However, either way should work.

Once you install a package, you need to load it before you can use its functions. Just use `library(package_name)` to load the package. The convention is to load all the packages you will use at the beginning of your script. For example, we can import the `tidyverse` package as follows.

```
library(tidyverse)
```

```
## -- Attaching core tidyverse packages ----- tidyverse 2.0.0 --
## v dplyr      1.1.3      v readr      2.1.4
## v forcats    1.0.0      v stringr   1.5.0
## v ggplot2    3.4.3      v tibble    3.2.1
```

```
## v lubridate 1.9.2      v tidyr      1.3.0
## v purrr      1.0.2
## -- Conflicts ----- tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()      masks stats::lag()
## i Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts
```

Tidyverse is a package that contains many useful packages including `ggplot2` (used for plotting), `tibble` (used for efficient dataframes) etc. We will dedicate a chapter to tidyverse but feel free to learn about as you like.

2.8 Plotting

When you are analyzing data, plots are very useful to package information visually. There are various packages that help build nice plots. In this class, we will use the `ggplot2` package for plotting. You might have notices in the output box above that loading `tidyverse` automatically loads `ggplot2` as well. We can go ahead and use the `ggplot2` functions without having to import it again. If we hadn't imported `tidyverse`, then we would have to load `ggplot2` to use its functionality.

Let us start with a simple plot for a linear function.

```
# Let us create a simple data set that satisfies the linear function y = 2x + 1
x <- 1:10
y <- 2*x+1

# print x and y to see what it looks like
x
```

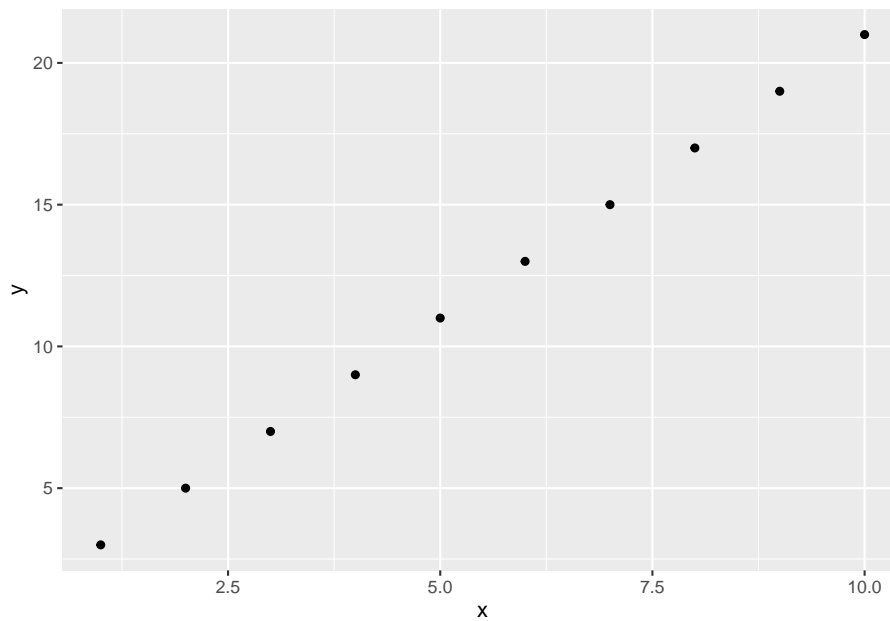
```
## [1] 1 2 3 4 5 6 7 8 9 10
```

```
y
```

```
## [1] 3 5 7 9 11 13 15 17 19 21
```

Let us now plot the data as points.

```
ggplot(data=NULL, aes(x,y)) +
  geom_point()
```



Let us now plot a line to make our plot more informative and better looking.

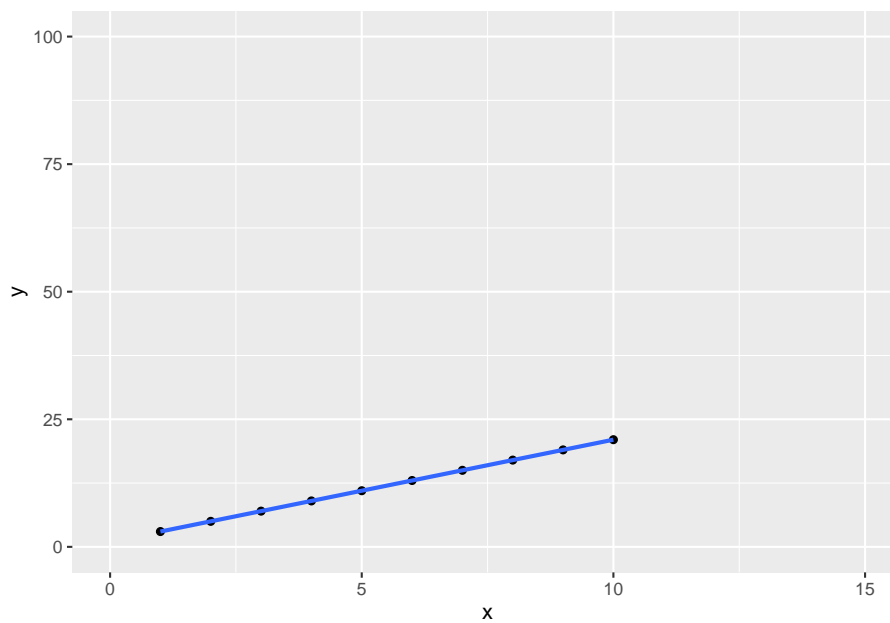
```
# Let us now plot x and y using ggplot2  
ggplot(data=NULL, aes(x,y)) +  
  geom_point() +  
  geom_smooth(method="lm")
```



Notice that playing with the scale sizes will yield dramatic changes in the effects we observe. For this, we can simply use the `xlim()` and `ylim()` functions to identify the lower and upper limits of x and y axes.

```
ggplot(data=NULL, aes(x,y)) +  
  geom_point() +  
  geom_smooth(method="lm")+  
  xlim(0, 15) +  
  ylim(0,100)
```

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



Let us now plot a quadratic function. A quadratic function is one where the base is a variable and the exponent is constant. The following graph plots n^2 .

```
# Let us now plot a and b using ggplot2

a<- 1:10
b <- a^2
ggplot(data=NULL, aes(a,b)) +
  geom_point() +
  geom_smooth(method="lm", formula = y~x +I(x^2), color='orange')
```



Finally, we can plot an exponential function where the variable is the exponent and the base is constant.

```
# Let us now plot a and b using ggplot2

a <- 1:10
b <- exp(a)
ggplot(data=NULL, aes(a,b)) +
  geom_point() +
  geom_smooth(method="lm", color = "orange", formula = (y ~ exp(x)))
```



You can mix and match.

```
# Let us now plot x and y using ggplot2
a<- 1:10
b<- a^2
ggplot(data=NULL, aes(x,y)) +
  geom_smooth(method="lm") +
  geom_smooth(data=NULL, aes(a,b), method="lm", formula = y~x +I(x^2),color= 'orange')
```



2.9 Operators and functions in this section

2.9.1 Operators

$x + y$

Addition

$x - y$

Subtraction

$x * y$

Multiplication

x / y

Division

x^y

Exponentiation

$x \leftarrow y$

Assignment

==

Test for equality. **Don't confuse with a single =, which is an assignment operator (and also always returns TRUE).**

`!=`

Test for inequality

`<`

Test, smaller than

`>`

Test, greater than

`<=`

Test, smaller than or equal to

`>=`

Test, greater than or equal to

2.9.2 Functions

`install.packages(package_name)`

Installs one or several package(s). The argument `package_name` can either be a character (`install.packages('dplyr')`) like or a character vector (`install.packages(c('dplyr', 'ggplot2'))`).

`library(package_name)`

Loads a package called `package_name`.

`typeof(x)`

Determines the type of a variable/vector.

`as.double(x)`

Converts a variable/vector to type **double**.

Chapter 3

Data Structures


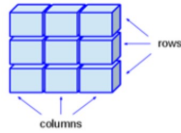
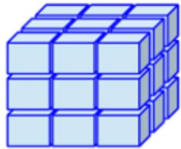
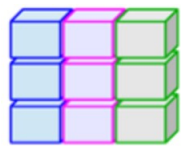
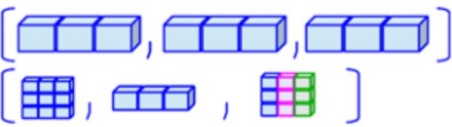
3.1 Data Types in R

In R, value has a *type*:

Data Type	Examples
Integer (Numeric):	..., -3, -2, -1, 0, +1, +2, +3, ...
Double (Numeric):	most rational numbers; e.g., 1.0, 1.5, 20.0, pi
Character:	"a", "b", "word", "hello dear friend, ..."
Logical:	TRUE or FALSE (or: T or F)
Factor:	Restricted, user-defined set of values, internally represented numerically (e.g., Gender {‘male’, ‘female’, ‘other’})
Ordered factor:	Factor with an ordering (e.g., Starbucks coffee sizes {‘venti’ > ‘grande’ > ‘tall’})

3.2 Data Structures in R

- All values in R are organized in data structures. Structures differ in their number of dimensions and in whether they allow mixed data types.
- In this course, we will mainly use vectors and data frames.

	dimensions	types	
Vector	1-dimensional	one type	
Matrix	2-dimensional	one type	
Array	n-dimensional	one type	
Data frame (or tibble)	2-dimensional	mixed types	
List	1-dimensional	mixed types	

(Illustrations from Gaurav Tiwari's article on medium [here](#).)

- Let's look at some examples

```
# create and print vectors, don't save
c(1,2, 1000)
```

```
## [1] 1 2 1000
```

```
c(1,2, 1000, pi)
```

```
## [1] 1.000000 2.000000 1000.000000 3.141593
```

```
1:3
```

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

```
# create and print a data.frame  
data.frame(1:3)
```

```
##      X1.3  
## 1      1  
## 2      2  
## 3      3
```

3.3 Vectors

- Vectors are simply ordered lists of elements, where every element has the same type.
- They are useful for storing sets or sequences of numbers.
- Let's create a simple vector with all integers from 1 to 8 and look at its contents.

```
vector_var <- c(1,2,3,4,5,6,7,8)  
vector_var
```

```
## [1] 1 2 3 4 5 6 7 8
```

- There is even a more elegant ways to do that:

```
vector_var <- 1:8  
vector_var
```

```
## [1] 1 2 3 4 5 6 7 8
```

- Now, let's create a simple vector with integers between 1 and 8, going in steps of 2.

```
vector_var <- seq(1,8, by=2)  
vector_var
```

```
## [1] 1 3 5 7
```

- Some useful vectors already exist in R.

```
letters
```

```
## [1] "a" "b" "c" "d" "e" "f" "g" "h" "i" "j" "k" "l" "m" "n" "o" "p" "q" "r" "s"
## [20] "t" "u" "v" "w" "x" "y" "z"
```

```
LETTERS
```

```
## [1] "A" "B" "C" "D" "E" "F" "G" "H" "I" "J" "K" "L" "M" "N" "O" "P" "Q" "R" "S"
## [20] "T" "U" "V" "W" "X" "Y" "Z"
```

- We can select specific elements of a vector by indexing it with `[]`.

```
# the first letter
letters[1]
```

```
## [1] "a"
```

```
# the 13-th letter
letters[13]
```

```
## [1] "m"
```

- Indices can be vectors too.

```
# both of them
letters[c(1,7)]
```

```
## [1] "a" "g"
```

- We can even take a whole ‘slice’ of a vector.

```
# both of them
letters[6:12]
```

```
## [1] "f" "g" "h" "i" "j" "k" "l"
```

- Indices can even be negative. A negative index $-n$ means ‘everything’ except n .

```
# both of them
letters[-1]
```

```
## [1] "b" "c" "d" "e" "f" "g" "h" "i" "j" "k" "l" "m" "n" "o" "p" "q" "r" "s" "t"
## [20] "u" "v" "w" "x" "y" "z"
```

- Vectors can be named.

```
digits <- c('one'=1, 'two'=2, 'three'=3, 'four'=4, 'five'=5, 'six'=6)
```

- In this case, we can index by the name

```
digits[c('one', 'six')]
```

```
## one six
## 1 6
```

- Believe it or not, everything in R is actually a vector. For example 9 is a vector with only one element, which is 9.

```
9
```

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

- This is why every output begins with [1]. R tries to help you find numbers in printed vectors. Every time a vector is printed, it reminds you at which position in the vector we are.
- The [1] in the output below tells you that "a" is the first element, and the [20] tells you that "t" is the 20-th element.

```
letters # print a vector with all lower-case letters
```

```
## [1] "a" "b" "c" "d" "e" "f" "g" "h" "i" "j" "k" "l" "m" "n" "o" "p" "q" "r" "s"
## [20] "t" "u" "v" "w" "x" "y" "z"
```

3.3.1 What are vectors good for?

- Let's put this knowledge to use.
- Here are two vectors representing the winnings from my recent gambling:

```
poker_payout_t1 <- c(24, 5, -38.1, 12, 103, 15, 5, 187, 13, -23, -45, 36)
```

- ```
sum(horse_bets_payout_t1)
```

```
sum(poker_payout_t1)
```

- Now, we need to determine the length of these vectors:

```
[1] 16
```

```
[1] 12
```

- ```
sum(horse_bets_payout_t1)/length(horse_bets_payout_t1)
```

```
sum(poker_payout_t1)/length(poker_payout_t1)
```

... so which game is more profitable?

- It seems that betting is more profitable.
- Next time, we can accomplish this calculation by calling the function `mean()`.

```
mean(horse_bets_payout_tl)
```

```
## [1] 24.9375
```

```
mean(poker_payout_tl)
```

```
## [1] 24.49167
```

...Now, I forgot to mention that my bookie charges me 1.5 TL per bet on a horse, on average. The poker payouts correspond to the profits, though. ...

- Luckily, we can just add numbers and vectors. Let's just create two new vectors which contain the profits.
- Let's subtract 1.5 from elements of `horse_bets_payout_tl` and save the result as `horse_bets_profits_tl`.
- As you see, this subtraction is applied to every element of the vector.

```
horse_bets_profits_tl <- horse_bets_payout_tl - 1.5
head(horse_bets_profits_tl)
```

```
## [1] 98.5 -51.5 -0.5 98.5 -11.5 -21.5
```

```
head(horse_bets_payout_tl)
```

```
## [1] 100 -50 1 100 -10 -20
```

- For poker, we don't need to change anything. So, we assign the already existing `poker_payout_tl` vector to another vector called `poker_profits_tl`.

```
poker_profits_tl <- poker_payout_tl
```

- Let's compare:

```
horse_bets_payout_t1
```

```
## [1] 100 -50 1 100 -10 -20 250 -40 -30 23 -23 55 14 8 24 -3
```

```
horse_bets_profits_t1
```

```
## [1] 98.5 -51.5 -0.5 98.5 -11.5 -21.5 248.5 -41.5 -31.5 21.5 -24.5 53.5
## [13] 12.5 6.5 22.5 -4.5
```

```
poker_payout_t1
```

```
## [1] 24.0 5.0 -38.1 12.0 103.0 15.0 5.0 187.0 13.0 -23.0 -45.0 36.0
```

```
poker_profits_t1
```

```
## [1] 24.0 5.0 -38.1 12.0 103.0 15.0 5.0 187.0 13.0 -23.0 -45.0 36.0
```

- Which game is more profitable now?

```
mean(horse_bets_profits_t1)
```

```
## [1] 23.4375
```

```
mean(poker_profits_t1)
```

```
## [1] 24.49167
```

3.4 Data Frames

- What I forgot to mention is that I generally gamble on Wednesdays and Fridays. Maybe that matters?
- How can we associate this information with the profits vectors?
- One way is to represent it in two vectors containing days of the week. In that case, every i -th element in `poker_week_days` corresponds to the i -th element in `poker_week_days`.

```
# create two vectors with week days
horse_bets_week_days <- rep(c("Wed", "Fr"), 8)
poker_week_days <- rep(c("Wed", "Fr"), 6)
```

- But this is getting messy. We have to keep track of two pairs of vectors, and the relations between them. Let's represent all poker-related information in one data structure, and all horse race-related information in another structure.
- The best way to represent a pair of vectors where the i -th element in vector 1 corresponds to the i -th element in vector 2 is with data frames. We can create a new data frame with the function `data.frame()`.

```
df_horse_bets <-
  data.frame(wday = horse_bets_week_days,
             profit = horse_bets_profits_t1)
```

```
df_poker <-
  data.frame(wday = poker_week_days,
             profit = poker_payout_t1)
```

- Let's take a look at what we've created.

```
df_horse_bets
```

```
##      wday profit
## 1   Wed   98.5
## 2    Fr  -51.5
## 3   Wed   -0.5
## 4    Fr   98.5
## 5   Wed  -11.5
## 6    Fr  -21.5
## 7   Wed 248.5
## 8    Fr  -41.5
## 9   Wed  -31.5
## 10  Fr   21.5
## 11  Wed  -24.5
## 12  Fr   53.5
## 13  Wed   12.5
## 14  Fr    6.5
## 15  Wed   22.5
## 16  Fr   -4.5
```

- Wow. That's a rather long output ...

- Generally, it's sufficient to see the first couple of rows of a `data.frame` to get a sense of what it contains.
- We'll use the function `head()`, which takes a `data.frame` and a number n , and outputs the first n lines.

```
# let's see the first two rows of the data frame called df_horse_bets
head(df_horse_bets, 2)
```

```
##   wday profit
## 1  Wed   98.5
## 2   Fr  -51.5
```

- An alternative is `View()`, which shows you the entire `data.frame` within a new tab in the RStudio GUI.

```
View(df_poker)
```

- Turning back to our gambling example, we still have two objects, which really belong together.
- Let's merge them into one long data frame.
- The function `rbind()` takes two data frames as its arguments, and returns a single concatenated data frame, where all the rows of the first data frame are on top, and all the rows of the second data frame are at the bottom.

```
df_gambling <- rbind(df_horse_bets, df_poker)
```

- Unfortunately, now, we don't have any information on which profits are from which game.

```
head(df_gambling)
```

```
##   wday profit
## 1  Wed   98.5
## 2   Fr  -51.5
## 3  Wed   -0.5
## 4   Fr   98.5
## 5  Wed  -11.5
## 6   Fr  -21.5
```

- Let's fix this problem by enriching both data frames with this information.

- We can assign to new (or old) columns with our assignment operator `<-`.
- When we assign a value to a specific column, R puts the specified value into every row of the column of the given data frame.
- What the following code says is “Create a new column named `game` in the data frame named `df_horse_bets` and fill the column with the string `horse_bets`.”

```
df_horse_bets$game <- "horse_bets"
df_poker$game <- "poker"
```

- Now, let’s bind them together again. (This overwrites the old data frame called `df_gambling`, which we created previously.)

```
df_gambling <- rbind(df_horse_bets, df_poker)
head(df_gambling)
```

```
##   wday profit      game
## 1  Wed   98.5 horse_bets
## 2   Fr  -51.5 horse_bets
## 3  Wed   -0.5 horse_bets
## 4   Fr   98.5 horse_bets
## 5  Wed  -11.5 horse_bets
## 6   Fr  -21.5 horse_bets
```

3.5 Working with data frames

- Now, we can do very cool things very easily.
- But we’ll need two packages for that: `dplyr`, and `magrittr`.

```
# load the two packages
library(magrittr) # for '%>%'
```

```
##
## Attaching package: 'magrittr'
```

```
## The following object is masked from 'package:purrr':
##
##   set_names
```

```
## The following object is masked from 'package:tidyr':
##
##   extract
```

```
library(dplyr) # for group_by() and summarize()
```

- Now, we can ‘aggregate’ data (= “combine data from several measurements by replacing it by summary statistics”).
- Let’s compute the average profit by game.
- Within the `summarize()` function, we specify new columns.
- In this case, `avg_profit` is the name of our column and its content is mean of the profit column.
- Keep in mind that `summarize()` function is applied at the group level.

```
df_gambling %>%
  group_by(game) %>%
  summarize(avg_profit = mean(profit))
```

```
## # A tibble: 2 x 2
##   game      avg_profit
##   <chr>      <dbl>
## 1 horse_bets    23.4
## 2 poker        24.5
```

- We can also aggregate over several grouping variables at the same time, like game and wday.

```
df_gambling %>%
  group_by(game, wday) %>%
  summarize(avg_profit = mean(profit))
```

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

```
## # A tibble: 4 x 3
## # Groups:   game [2]
##   game      wday avg_profit
##   <chr>      <chr>      <dbl>
## 1 horse_bets Fr         7.62
## 2 horse_bets Wed        39.2
## 3 poker      Fr         38.7
## 4 poker      Wed        10.3
```

- ... and we can do so in various ways. Here we compute the proportion of wins.

```
df_gambling %>%
  group_by(game, wday) %>%
  summarize(avg_proportion_wins = mean(profit>0) )
```

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

```
## # A tibble: 4 x 3
## # Groups:   game [2]
##   game      wday avg_proportion_wins
##   <chr>    <chr>                <dbl>
## 1 horse_bets Fr                0.5
## 2 horse_bets Wed                0.5
## 3 poker     Fr                0.833
## 4 poker     Wed                0.667
```

- Now, we can also plot the results.
- But we'll need to save the summary statistics first.

```
profits_by_game <-
  df_gambling %>%
    group_by(game) %>%
    summarize(avg_profit = mean(profit))
```

```
profits_by_game_and_wday <-
  df_gambling %>%
    group_by(game, wday) %>%
    summarize(avg_profit = mean(profit))
```

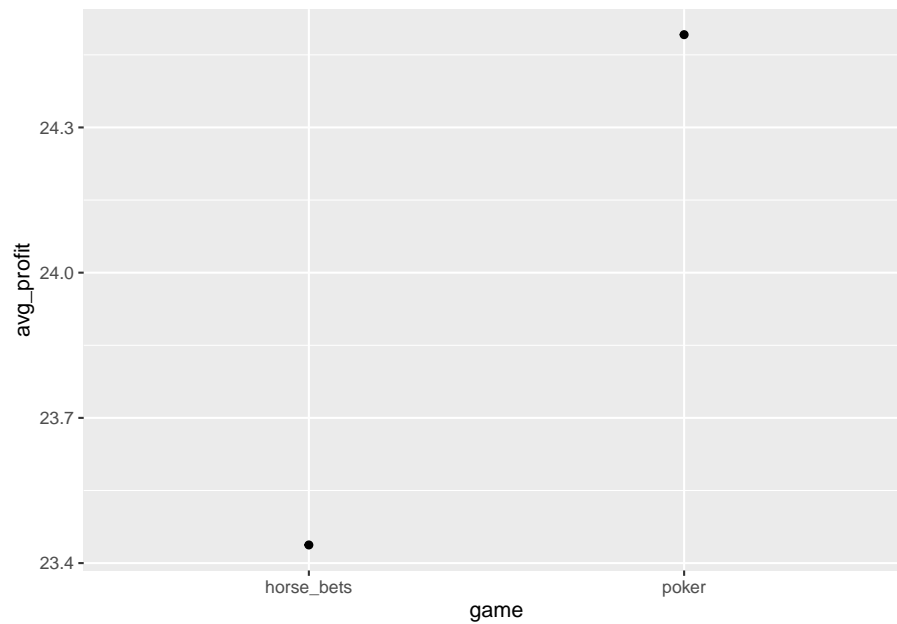
```
## `summarise()` has grouped output by 'game'. You can override using the
## `.groups` argument.
```

- We will also need yet another package (for plotting): `ggplot2`.

```
library(ggplot2)
```

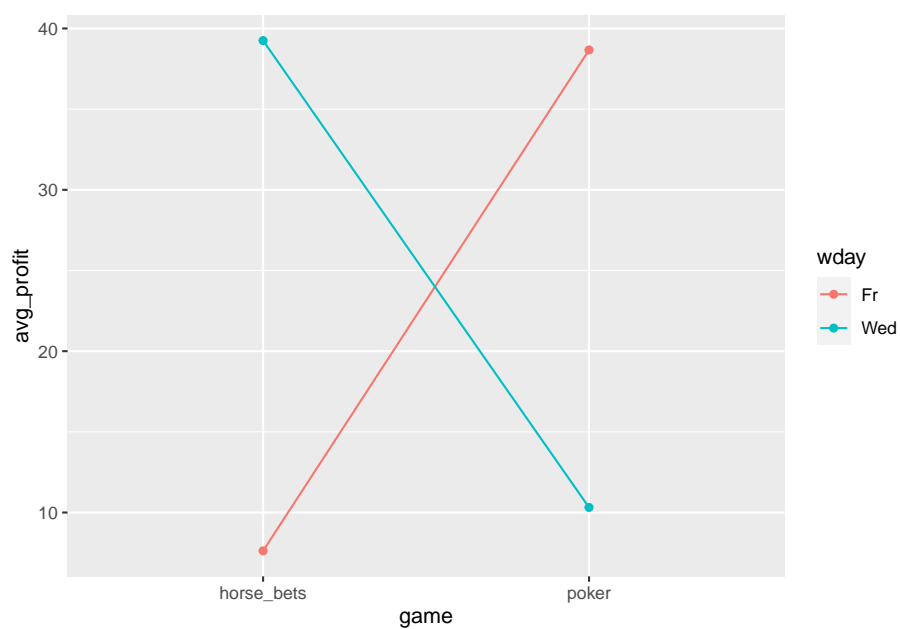
- After loading the package `ggplot2`, we can create plots with the function `ggplot()`. We will be going over the details in the upcoming chapters.

```
ggplot(profits_by_game, aes(game, avg_profit)) + geom_point()
```



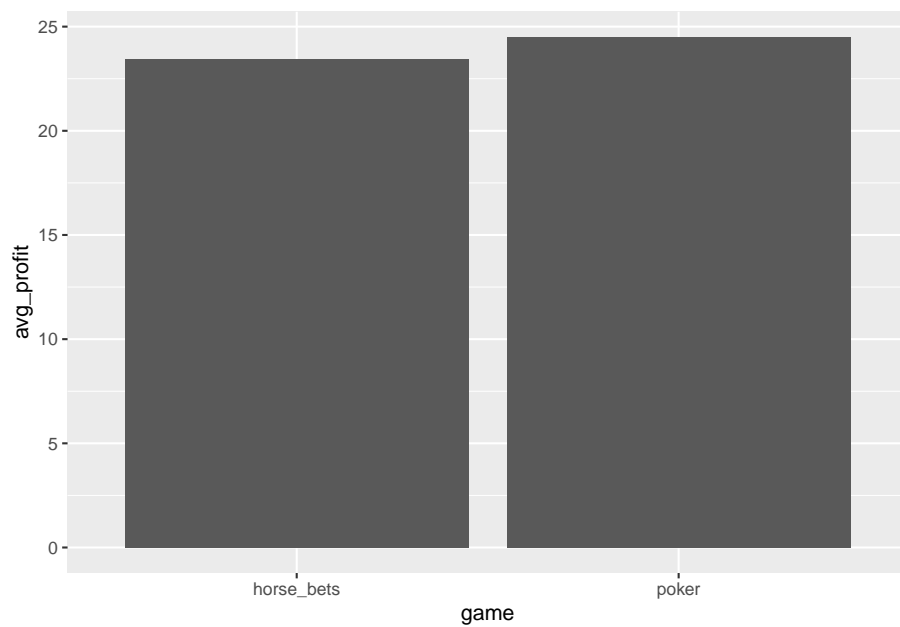
- We may also want lines that connect the points.

```
library(ggplot2)  
ggplot(profits_by_game_and_wday, aes(game, avg_profit, color = wday, group = wday)) + g
```

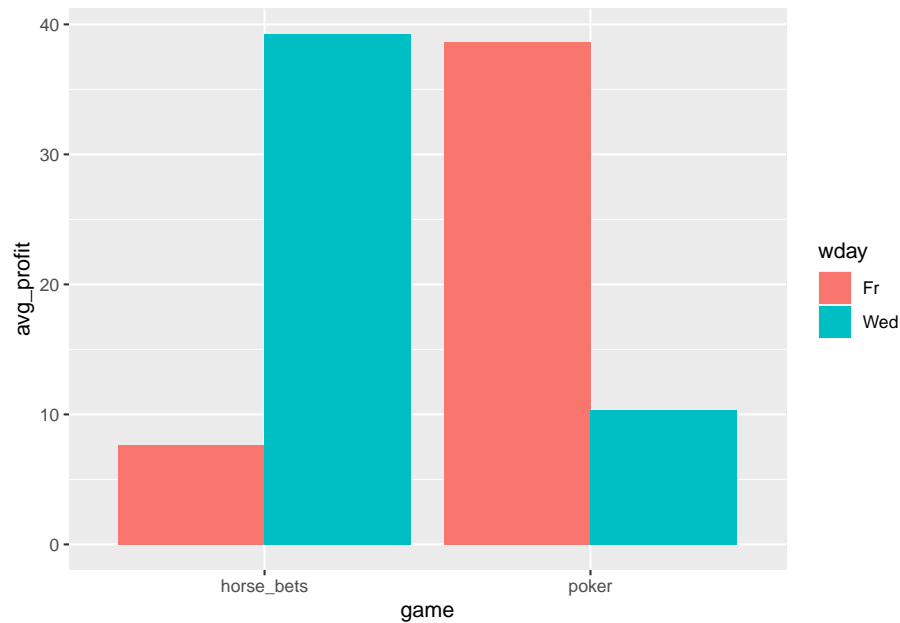



- Or, we may want to have a bar graph.

```
library(ggplot2)
ggplot(profits_by_game, aes(game, avg_profit)) + geom_bar(stat = "identity")
```



```
library(ggplot2)
ggplot(profits_by_game_and_wday, aes(game, avg_profit, fill = wday)) + geom_bar(stat =
```



3.6 Functions in this section

```
data.frame(a = x, b = y, ...)
```

Create a data frame from several vectors. The vectors can be different types.

- **x** A vector with n elements.
- **y** Another vector with n elements.
- **...** More vectors can be provided.

```
View(x)
```

Display a data frame, or another structure.

```
head(df, n=6)
```

Show the first n rows in the data frame `df`.

- **df** Data frame from which to display the first n rows.
- **n** The number of rows to display. The default value for n is 6.

`sum(x)`

Compute the sum of a vector.

`length(x)`

Return the length of a vector.

`mean(x)`

Compute the mean of a vector.

`rep(x, n)`

Repeat the contents of a vector n times

- `x` The vector to be repeated.
- `n` How many times to repeat the vector `x`.

`seq(from, to, by)`

Create a sequence of integers from `from` to `to` in steps of `by`.

- `from` The integer to start from.
- `to` The integer to stop after.
- `by` Size of steps to take. (If `from > to`, `by` needs to be negative.)

`rbind(df1, df2)`

Append `df1` to `df2` and return the resulting data frame. Both data frames need to have the same number of columns with the same names.

- `df1` First data frame.
- `df2` Second data frame.

Chapter 4

Working with Data

In this section, we learn how to work with data in a **dataframe**. A dataframe is a two-dimensional array consisting of *rows* and *columns*. You can simply think of it as a spreadsheet (e.g. MS Excel, Google Sheets, etc.).

4.1 Basic dataframes

R has some prebuilt functions to build dataframes. Let us see a simple example. Consider the following three vectors.

```
name <- c("Sam", "Paulina", "Cenk")
age <- c(23, 34, 19)
height <- c(179, 167, 173)
```

Let us turn the data stored in different vectors into a single dataframe so that we can visualize the data better.

```
#Let us first create the dataframe and assign it to the variable my_df
my_df <- data.frame(name,age,height)

#Let's print the dataframe now
my_df
```

```
##      name age height
## 1    Sam  23    179
## 2 Paulina 34    167
## 3   Cenk  19    173
```

We can select a particular row, column, or cell on a dataframe by using indices. For this we can use the slicing method `my_dataframe[row,column]`.

```
#Let us select the entire first row
my_df[1,]
```

```
##   name age height
## 1  Sam  23    179
```

```
#Now, let us select the first column
my_df[,1]
```

```
## [1] "Sam"      "Paulina" "Cenk"
```

```
#Now, let us find Paulina's height. For this, we need to get the 2nd row and 3rd column
my_df[2,3]
```

```
## [1] 167
```

```
#Now, let us find Paulina's age and height. For this, we need to get the 2nd row and 2nd and 3rd column
my_df[2,2:3]
```

```
##   age height
## 2  34    167
```

```
#Finally, let us get Sam and Paulina's ages.
my_df[1:2,2]
```

```
## [1] 23 34
```

You can also use the column name to select an entire column. Just add the dollar sign `$` after the `df` and then the column name.

```
my_df$age
```

```
## [1] 23 34 19
```

4.2 Tibbles

The standard dataframes in R are good but not great. Often, we will deal with a lot of data we may not know which index to use to find the value we want. So,

we need to be able to have some better ways to access data on our dataframes. We also want to be able to add new data or change some of the existing data easily. For this, we will use various packages in **tidyverse** for better dataframe management.

Let us first load the tidyverse library, which will load the necessary packages for the functionality described in the following sections.

```
library(tidyverse)
```

Next, let us introduce tibbles. A **tibble** is a dataframe with some improved properties. We can turn a regular dataframe into a tibble by calling the `as_tibble()` function on our dataframe.

```
#Let's turn my_df into a tibble
my_tibble <- as_tibble(my_df)

#Let's print my_tibble
my_tibble
```

```
## # A tibble: 3 x 3
##   name      age height
##   <chr>   <dbl> <dbl>
## 1 Sam        23    179
## 2 Paulina    34    167
## 3 Cen        19    173
```

As you can see above, the console output tells you that this is a 3x3 tibble meaning that it has 3 rows and 3 columns. It also tells you the type of the data in each column. You can see the data types right under each column name.

4.3 Beyond Toy Data

So far we have been working with toy data. In real life projects, you will have a lot more data. The data will usually be stored in some file from which you will have to read into a dataframe. Alternatively, it might be some dataset that from a corpus easily accessible to R. Let us see a few ways in which we can load some realistic datasets into a tibble.

4.3.1 Reading data from a csv file

In this course, we will use some of the data sets from Bodo Winter's book. Go to this website to download the `materials` folder. Once your data has

been downloaded, navigate to the `materials/data` folder and locate the `nettle_1999_climate.csv` file.

To read in data from a csv to a tibble, we will use the `read_csv()` function. All we need to do is to provide the path to the csv file we want to read in. If your csv file is in the same folder as your script, you can simply give its name. Otherwise, you need to provide the relevant directory information as well in your path.

```
#Let's read in the data
nettle <- read_csv('data/nettle_1999_climate.csv')
```

```
## Rows: 74 Columns: 5
## -- Column specification -----
## Delimiter: ","
## chr (1): Country
## dbl (4): Population, Area, MGS, Langs
##
## i Use `spec()` to retrieve the full column specification for this data.
## i Specify the column types or set `show_col_types = FALSE` to quiet this message.
```

```
#Let's print the head of the data to see what it looks like
nettle
```

```
## # A tibble: 74 x 5
##   Country      Population Area   MGS Langs
##   <chr>          <dbl> <dbl> <dbl> <dbl>
## 1 Algeria         4.41  6.38  6.6    18
## 2 Angola          4.01  6.1   6.22   42
## 3 Australia       4.24  6.89  6      234
## 4 Bangladesh      5.07  5.16  7.4    37
## 5 Benin           3.69  5.05  7.14   52
## 6 Bolivia         3.88  6.04  6.92   38
## 7 Botswana        3.13  5.76  4.6    27
## 8 Brazil          5.19  6.93  9.71  209
## 9 Burkina Faso    3.97  5.44  5.17   75
## 10 CAR            3.5   5.79  8.08   94
## # i 64 more rows
```

If you want to see the last 5 items, use the `tail()` function.

```
tail(nettle)
```



```
## # A tibble: 6 x 5
##   Country      Population Area   MGS Langs
##   <chr>         <dbl> <dbl> <dbl> <dbl>
## 1 Venezuela      4.31  5.96  7.98   40
## 2 Vietnam        4.83  5.52  8.8    88
## 3 Yemen          4.09  5.72  0       6
## 4 Zaire          4.56  6.37  9.44  219
## 5 Zambia         3.94  5.88  5.43   38
## 6 Zimbabwe       4      5.59  5.29   18
```

If you want to view the entire dataset, you can use `View(nettles)`. This will open a new tab in RStudio and show your data as a table.

4.3.2 Reading data from R data packages

R has various data packages you can install and use. Let us install the `languageR` which has some nice language datasets. Once you install the package and load the library, you can easily use the datasets as tibbles. For all the details and available datasets in `languageR`, you can check the `languageR` documentation on CRAN.

```
#Let's load the library
library(languageR)
```

```
#We'll use the dativeSimplified dataset, which is documented. Let's see the documentation
?dativeSimplified
```

```
#let's use the dativeSimplified data from the languageR
data <- as_tibble(dativeSimplified)
```

```
#Let's print the first few lines of the data
data
```

```
## # A tibble: 903 x 5
##   RealizationOfRec Verb AnimacyOfRec AnimacyOfTheme LengthOfTheme
##   <fct>           <fct> <fct>      <fct>              <dbl>
## 1 NP             feed  animate   inanimate          2.64
## 2 NP             give  animate   inanimate          1.10
## 3 NP             give  animate   inanimate          2.56
## 4 NP             give  animate   inanimate          1.61
## 5 NP             offer animate   inanimate          1.10
## 6 NP             give  animate   inanimate          1.39
## 7 NP             pay   animate   inanimate          1.39
## 8 NP             bring animate   inanimate          0
```

```
## 9 NP      teach animate      inanimate      2.40
## 10 NP     give  animate      inanimate      0.693
## # i 893 more rows
```

Dative Alternation is the phenomenon in English where a recipient of a di-transitive verb can occur as an NP or a PP.

1. Alex gave Sam a book.
2. Alex gave a book to Sam.

Both of these constructions are grammatical and they mean essentially the same thing. The question is what factors are involved in picking one of the forms over the other. Bresnan et al. (2007) used this data to determine the relevant factors. Let us randomly select 10 examples and see what they look like. For that, we can use the following code.

```
# store all possible row indices in a vector
indices_all <- 1:nrow(data)

# set the random seed to make the results reproducible
set.seed(123)

# choose 10 such numbers at random without replacement
indices_random <- sample(indices_all, size = 10)

# use them to index the data frame to get the corresponding rows
data[indices_random,]
```

```
## # A tibble: 10 x 5
##   RealizationOfRec Verb AnimacyOfRec AnimacyOfTheme LengthOfTheme
##   <fct>          <fct> <fct>      <fct>          <dbl>
## 1 NP          give  inanimate  inanimate      1.79
## 2 NP          grant animate  inanimate      1.10
## 3 NP          grant animate  inanimate      2.40
## 4 NP          give  animate  inanimate      2.56
## 5 NP          tell  animate  inanimate      3.26
## 6 PP          give  animate  inanimate      0
## 7 NP          pay   animate  inanimate      0.693
## 8 NP          hand  animate  inanimate      0.693
## 9 NP          give  inanimate inanimate      1.61
## 10 NP         wish  animate  inanimate      1.10
```

4.4 Summarizing Data

Looking at the summary statistics of your data is always a good first step. Let's take a look at the percentage of NP realizations of the recipient by animacy of the theme.

First, let's take a look at the key dependent variable (NP or PP)

```
unique(data$RealizationOfRec)
```

```
## [1] NP PP
## Levels: NP PP
```

now, let's compute the percentages (perc_NP) and the number of observations in each subset
data%>%

```
  group_by(AnimacyOfRec) %>%
  summarize(perc_NP = mean(RealizationOfRec == "NP"),
            N = n()
            )
```

```
## # A tibble: 2 x 3
##   AnimacyOfRec perc_NP      N
##   <fct>         <dbl> <int>
## 1 animate      0.634   822
## 2 inanimate    0.420    81
```

What do the results say?

- There are a total of 822 instances of animate recipients.
- 63% of the animate recipients are NPs.

4.5 Working with dplyr

One of the packages in the `tidyverse` is `dplyr`. We use it to do various manipulations on the data frames. Check out the `dplyr` cheatsheet for further details.

The `arrange` function will arrange your data in an ascending order.

```
arrange(data)
```

```
## # A tibble: 903 x 5
##   RealizationOfRec Verb   AnimacyOfRec AnimacyOfTheme LengthOfTheme
##   <fct>             <fct> <fct>         <fct>          <dbl>
## 1 NP               feed  animate      inanimate      2.64
## 2 NP               give  animate      inanimate      1.10
## 3 NP               give  animate      inanimate      2.56
## 4 NP               give  animate      inanimate      1.61
## 5 NP               offer animate      inanimate      1.10
## 6 NP               give  animate      inanimate      1.39
## 7 NP               pay   animate      inanimate      1.39
## 8 NP               bring animate      inanimate      0
## 9 NP               teach animate      inanimate      2.40
## 10 NP              give  animate      inanimate      0.693
## # i 893 more rows
```

You can arrange the data based on a particular column. In that case, you need to provide the column name.

```
arrange(data, LengthOfTheme)
```

```
## # A tibble: 903 x 5
##   RealizationOfRec Verb   AnimacyOfRec AnimacyOfTheme LengthOfTheme
##   <fct>             <fct> <fct>         <fct>          <dbl>
## 1 NP               bring  animate      inanimate      0
## 2 NP               send  animate      inanimate      0
## 3 NP               bet   animate      inanimate      0
## 4 NP               tell  animate      inanimate      0
## 5 NP               tell  animate      inanimate      0
## 6 NP               give  inanimate    inanimate      0
## 7 NP               give  animate      inanimate      0
## 8 NP               charge animate      inanimate      0
## 9 NP               give  animate      inanimate      0
## 10 NP              pay   animate      inanimate      0
## # i 893 more rows
```

```
arrange(data[1:10,], LengthOfTheme)
```

```
## # A tibble: 10 x 5
##   RealizationOfRec Verb   AnimacyOfRec AnimacyOfTheme LengthOfTheme
##   <fct>             <fct> <fct>         <fct>          <dbl>
## 1 NP               bring  animate      inanimate      0
## 2 NP               give  animate      inanimate      0.693
## 3 NP               give  animate      inanimate      1.10
## 4 NP               offer animate      inanimate      1.10
```

```
## 5 NP      give animate inanimate 1.39
## 6 NP      pay  animate inanimate 1.39
## 7 NP      give animate inanimate 1.61
## 8 NP      teach animate inanimate 2.40
## 9 NP      give animate inanimate 2.56
## 10 NP     feed animate inanimate 2.64
```

If you want to arrange things in a descending order, then you need to put the `desc()` function around the relevant column.

```
arrange(data, desc(LengthOfTheme))
```

```
## # A tibble: 903 x 5
##   RealizationOfRec Verb AnimacyOfRec AnimacyOfTheme LengthOfTheme
##   <fct>           <fct> <fct>      <fct>          <dbl>
## 1 NP            give inanimate inanimate      3.64
## 2 NP            send animate inanimate      3.56
## 3 NP            give animate inanimate      3.53
## 4 NP            pay  animate inanimate      3.50
## 5 NP            give animate inanimate      3.50
## 6 NP            give animate inanimate      3.47
## 7 NP            give animate inanimate      3.47
## 8 NP            give animate inanimate      3.40
## 9 NP            send animate inanimate      3.40
## 10 NP           give animate inanimate      3.37
## # i 893 more rows
```

Another useful function is the `select()` function which allows you to create new dataframes using only columns you want.

```
#Create the new dataframe using select
df <- select(data, Verb, LengthOfTheme)
```

```
#print the head
df
```

```
## # A tibble: 903 x 2
##   Verb LengthOfTheme
##   <fct>          <dbl>
## 1 feed          2.64
## 2 give           1.10
## 3 give           2.56
## 4 give           1.61
## 5 offer          1.10
```

```
## 6 give      1.39
## 7 pay       1.39
## 8 bring      0
## 9 teach     2.40
## 10 give     0.693
## # i 893 more rows
```

Another useful function is `sample_n()` which randomly samples some number of datapoints.

```
sample_n(data, 5)
```

```
## # A tibble: 5 x 5
##   RealizationOfRec Verb  AnimacyOfRec AnimacyOfTheme LengthOfTheme
##   <fct>           <fct> <fct>         <fct>           <dbl>
## 1 NP             give  animate      inanimate        0.693
## 2 NP             sell  animate      inanimate         0
## 3 PP             give  animate      inanimate        1.61
## 4 PP             pay   animate      inanimate        1.39
## 5 PP             offer inanimate    inanimate        1.95
```

Two other useful functions are `group_by()` and `ungroup()`.

#Let's group a small portion of the data by the realization of recipient

```
group_by(data[1:5], RealizationOfRec)
```

```
## # A tibble: 903 x 5
## # Groups:   RealizationOfRec [2]
##   RealizationOfRec Verb  AnimacyOfRec AnimacyOfTheme LengthOfTheme
##   <fct>           <fct> <fct>         <fct>           <dbl>
## 1 NP             feed  animate      inanimate        2.64
## 2 NP             give  animate      inanimate        1.10
## 3 NP             give  animate      inanimate        2.56
## 4 NP             give  animate      inanimate        1.61
## 5 NP             offer  animate      inanimate        1.10
## 6 NP             give  animate      inanimate        1.39
## 7 NP             pay   animate      inanimate        1.39
## 8 NP             bring  animate      inanimate         0
## 9 NP             teach  animate      inanimate        2.40
## 10 NP            give  animate      inanimate        0.693
## # i 893 more rows
```

Now let us group the data by verbs.

```
data_grouped_by_verb <- group_by(data, Verb)
```

An important but complex function is the `summarize()` function.

1. It divides a grouped data frame into subsets, with each subset corresponding to one value of the grouping variable (or a combination of values for several grouping variables).
2. It computes one or several values we specify on each such subset.
3. It creates a new data frame and puts everything together. The first column of this new data frame consists of levels of our grouping variable. In the following columns, the `summarize()` function prints the results of the computations we have specified.

Try to guess the result of the following code. What will you see as an output? What will be the name of the columns?

```
# summarize several variables
summarize(data_grouped_by_verb,
  prop_animate_rec = mean( AnimacyOfRec == "animate" ),
  prop_animate_theme = mean( AnimacyOfTheme == "animate" ),
  N = n()
)
```

```
## # A tibble: 65 x 4
##   Verb      prop_animate_rec prop_animate_theme     N
##   <fct>          <dbl>          <dbl> <int>
## 1 accord            1            0      1
## 2 allocate          0            0      3
## 3 allow            0.833          0      6
## 4 assess            1            0      1
## 5 assure            1            0      2
## 6 award            0.944          0     18
## 7 bequeath          1            0      1
## 8 bet              1            0      1
## 9 bring            0.818          0     11
## 10 carry            1            0      1
## # i 55 more rows
```

Try to interpret the output of the following code.

```
# compute the averages
summarize(data_grouped_by_verb,
  prop_anim = mean(AnimacyOfRec == "animate"),
  prop_inanim = 1-prop_anim,
```

```
prop_v_recip_anim = ifelse(prop_anim > 0.5, "high", "low")
)
```

```
## # A tibble: 65 x 4
##   Verb      prop_anim prop_inanim prop_v_recip_anim
##   <fct>      <dbl>      <dbl> <chr>
## 1 accord      1          0      high
## 2 allocate    0          1      low
## 3 allow       0.833      0.167  high
## 4 assess      1          0      high
## 5 assure      1          0      high
## 6 award       0.944      0.0556 high
## 7 bequeath    1          0      high
## 8 bet         1          0      high
## 9 bring       0.818      0.182  high
## 10 carry      1          0      high
## # i 55 more rows
```

The last line uses the function `ifelse(condition, value1, value2)`, which, for each element of the condition vector returns the corresponding element of the `value1` vector if the condition is true at that element, or an element of `value2` otherwise.

`mutate()` proceeds similarly to `summarize()` in dividing a grouped dataset into subsets, but instead of computing one or several values for each subset, it creates or modifies a column.

The main difference between `mutate()` and `summarize()` is the output. While `mutate()` modifies the original and returns a modified version of it, `summarize()` creates a brand new data frame with one row for every combination of the the grouping variable values.

A very simple application of `mutate()` is to simply create a new column. In this case, we don't even need to group.

```
# these two lines performs exactly the same action,
# except the latter stores the result in df
data$is_realization_NP <- (data$RealizationOfRec == "NP" )
df <- mutate(data, is_realization_NP = (RealizationOfRec == "NP") )

head(df, 2)
```

```
## # A tibble: 2 x 6
##   RealizationOfRec Verb  AnimacyOfRec AnimacyOfTheme LengthOfTheme
##   <fct>          <fct> <fct>      <fct>              <dbl>
## 1 NP            feed  animate    inanimate          2.64
## 2 NP            give  animate    inanimate          1.10
## # i 1 more variable: is_realization_NP <lgl>
```


One final useful function is the `filter()` function. It allows you to find rows by particular values of a column.

```
filter(data, is_realization_NP == FALSE)
```

```
## # A tibble: 348 x 6
##   RealizationOfRec Verb   AnimacyOfRec AnimacyOfTheme LengthOfTheme
##   <fct>            <fct> <fct>         <fct>          <dbl>
## 1 PP              give  animate      inanimate      0
## 2 PP              give  inanimate    inanimate    1.79
## 3 PP              give  animate      inanimate    1.39
## 4 PP              give  animate      inanimate    1.39
## 5 PP              sell  animate      inanimate    1.79
## 6 PP              give  inanimate    inanimate    0.693
## 7 PP              give  inanimate    inanimate    0.693
## 8 PP              give  animate      inanimate    1.39
## 9 PP              send  animate      inanimate    2.56
## 10 PP             offer  animate      inanimate    1.95
## # i 338 more rows
## # i 1 more variable: is_realization_NP <lgl>
```

```
filter(data, LengthOfTheme > 3.5)
```

```
## # A tibble: 3 x 6
##   RealizationOfRec Verb   AnimacyOfRec AnimacyOfTheme LengthOfTheme
##   <fct>            <fct> <fct>         <fct>          <dbl>
## 1 NP              send  animate      inanimate    3.56
## 2 NP              give  animate      inanimate    3.53
## 3 NP              give  inanimate    inanimate    3.64
## # i 1 more variable: is_realization_NP <lgl>
```

4.6 Pipes

4.6.1 The problem

- The code below is really hard to read, even harder to maintain, and `dativeSimplified_grouped_by_AnimacyOfRec_and_AnimacyOfTheme` is a terribly long variable name.

```
dativeSimplified_grouped_by_AnimacyOfRec_and_AnimacyOfTheme <-
  group_by(dativeSimplified, AnimacyOfRec, AnimacyOfTheme)
df <- summarize(dativeSimplified_grouped_by_AnimacyOfRec_and_AnimacyOfTheme,
  perc_NP = mean(RealizationOfRec == "NP") )
```

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

```
df
```

```
## # A tibble: 4 x 3
## # Groups:   AnimacyOfRec [2]
##   AnimacyOfRec AnimacyOfTheme perc_NP
##   <fct>        <fct>         <dbl>
## 1 animate      animate           0.8
## 2 animate      inanimate        0.633
## 3 inanimate     animate           1
## 4 inanimate     inanimate        0.412
```

- This alternative is also quite bad. To read this code, you need to know which bracket matches which other bracket.

```
df <- summarize(group_by(dativeSimplified, AnimacyOfRec, AnimacyOfTheme),
  perc_NP = mean(RealizationOfRec == "NP") )
```

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

```
df
```

```
## # A tibble: 4 x 3
## # Groups:   AnimacyOfRec [2]
##   AnimacyOfRec AnimacyOfTheme perc_NP
##   <fct>        <fct>         <dbl>
## 1 animate      animate           0.8
## 2 animate      inanimate        0.633
## 3 inanimate     animate           1
## 4 inanimate     inanimate        0.412
```

- One nested function call may be OK. But try to read this.

```
df <- dplyr::summarize(group_by(mutate(dativeSimplified, long_theme = ifelse(LengthOfT
  perc_NP = mean(RealizationOfRec == "NP")
  )
```

- Or consider this expression (sqrt is the square root.)

```
sqrt(divide_by(sum(divide_by(2,3), multiply_by(2,3)), sum(3,4)))

## [1] 0.9759001
```

- Luckily, there a better way to write this expression.

4.6.2 Pipes

- The problem is that we have too many levels of embedding.
- In natural language we avoid multiple embeddings of that sort by making shorter sentences, and using anaphors to refer to previous discourse.
- The packages **dplyr** and **magrittr** provide a limited version of such functionality, and we'll need to use **pipe** operators (`%>%` and `%<>%`) to link expressions with an 'anaphoric dependency'.
- Whenever you see `%>%`, you can think about it as the following: "Take whatever is on the left side, and use it in the function that is on the right side."

```
library(dplyr)
library(magrittr)
# Typical notation. Read as "Divide 10 by 2."
divide_by(10, 2)
```

```
## [1] 5
```

```
# Equivalent pipe notation. Read as "Take 10, and divide it by 2."
10 %>% divide_by(., 2)
```

```
## [1] 5
```

```
# Equivalent pipe notation. Read as "Take 2, and divide 10 by it."
2 %>% divide_by(10, .)
```

```
## [1] 5
```

- If the dot operator occurs in the first argument slot, it can be omitted. (R has pro-drop.)

```
# pipe notation with omission of '.'
10 %>% divide_by(2)
```

```
## [1] 5
```

- Let's see how it can resolve the mess below. (Repetition of previous example.)

```
df <- mutate(group_by(dativeSimplified, AnimacyOfRec, AnimacyOfTheme),
              perc_NP = mean(RealizationOfRec == "NP") )
df
```

```
## # A tibble: 903 x 6
## # Groups:   AnimacyOfRec, AnimacyOfTheme [4]
##   RealizationOfRec Verb AnimacyOfRec AnimacyOfTheme LengthOfTheme perc_NP
##   <fct>           <fct> <fct>         <fct>           <dbl>   <dbl>
## 1 NP             feed animate      inanimate        2.64    0.633
## 2 NP             give animate      inanimate        1.10    0.633
## 3 NP             give animate      inanimate        2.56    0.633
## 4 NP             give animate      inanimate        1.61    0.633
## 5 NP             offer animate      inanimate        1.10    0.633
## 6 NP             give animate      inanimate        1.39    0.633
## 7 NP             pay  animate      inanimate        1.39    0.633
## 8 NP             bring animate      inanimate         0      0.633
## 9 NP             teach animate      inanimate        2.40    0.633
## 10 NP            give animate      inanimate        0.693   0.633
## # i 893 more rows
```

- And here is the much more readable version of this code:

```
df <- dativeSimplified %>%
  mutate(long_theme = ifelse(LengthOfTheme > 1.6, "long", "short") ) %>%
  group_by(long_theme) %>%
  dplyr::summarize(perc_NP = mean(RealizationOfRec == "NP") )
```

- We don't actually need the dot:

```
df <- dativeSimplified %>%
  mutate(long_theme = ifelse(LengthOfTheme > 1.6, "long", "short") ) %>%
  group_by(long_theme) %>%
  dplyr::summarize(perc_NP = mean(RealizationOfRec == "NP") )
```

- The %<>% operator is a convenient combination of %>% and <- which you can use to directly modify an object.

```

# load the package magrittr in order to access the assignment pipe operator
library(magrittr)

# create a vector with numbers from 1 to 10
x <- 1:10
# keep only numbers < 5:
#   (i) without %<>%
x <- x[x<5]
#   (i) with %<>%
x %<>% .[.<5]

# lets add several columns to 'dativeSimplified'
dativeSimplified %<>% mutate(A=1, B=2, C=3, D=4)
head(dativeSimplified)

```

##	RealizationOfRec	Verb	AnimacyOfRec	AnimacyOfTheme	LengthOfTheme	A	B	C	D
## 1	NP	feed	animate	inanimate	2.639057	1	2	3	4
## 2	NP	give	animate	inanimate	1.098612	1	2	3	4
## 3	NP	give	animate	inanimate	2.564949	1	2	3	4
## 4	NP	give	animate	inanimate	1.609438	1	2	3	4
## 5	NP	offer	animate	inanimate	1.098612	1	2	3	4
## 6	NP	give	animate	inanimate	1.386294	1	2	3	4

Chapter 5

Plotting

(26 December, 2023, 08:54)

5.1 The basics of ggplot2

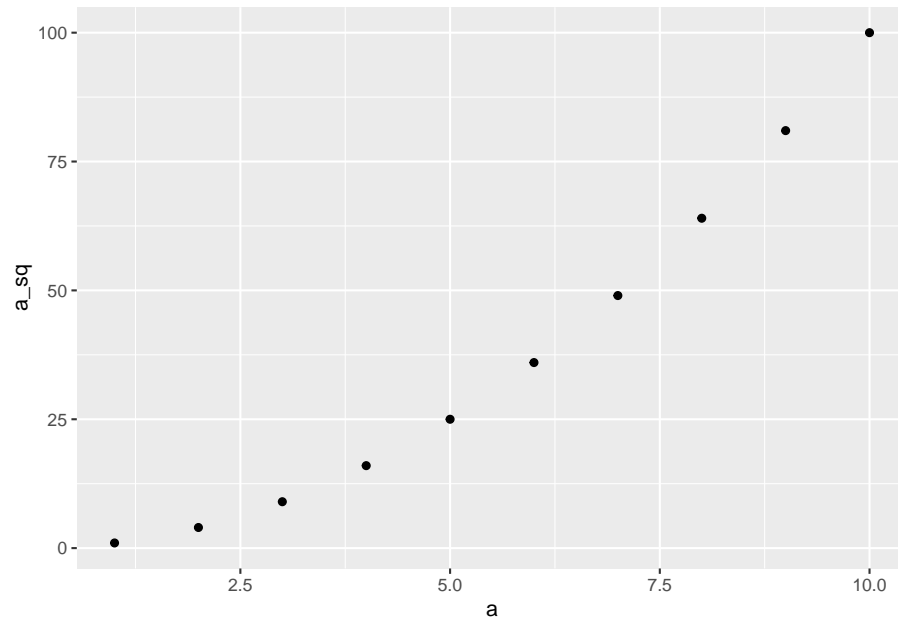
- Let's first take a look at some example plots.
- Create a synthetic data set and load the `ggplot2` package to access the plotting functionality.

```
library(ggplot2)
df <- data.frame(a=1:10, a_sq=(1:10)^2, my_group = c("weekday","weekend"))
df
```

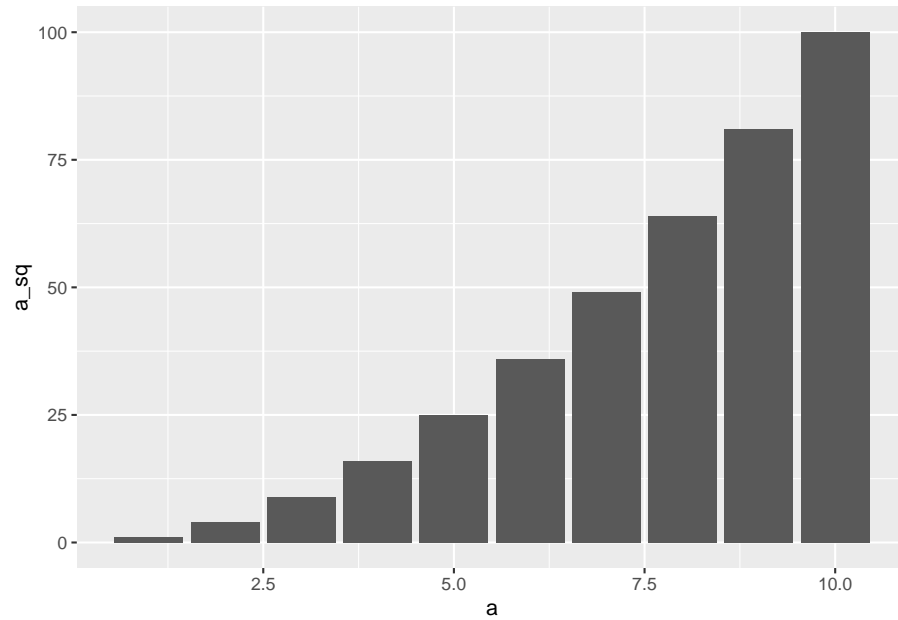
```
##      a a_sq my_group
## 1    1     1 weekday
## 2    2     4 weekend
## 3    3     9 weekday
## 4    4    16 weekend
## 5    5    25 weekday
## 6    6    36 weekend
## 7    7    49 weekday
## 8    8    64 weekend
## 9    9    81 weekday
## 10  10   100 weekend
```

- Take a look at the following code and the resulting plots. Can you tell what parts that start with `geom_...` does?

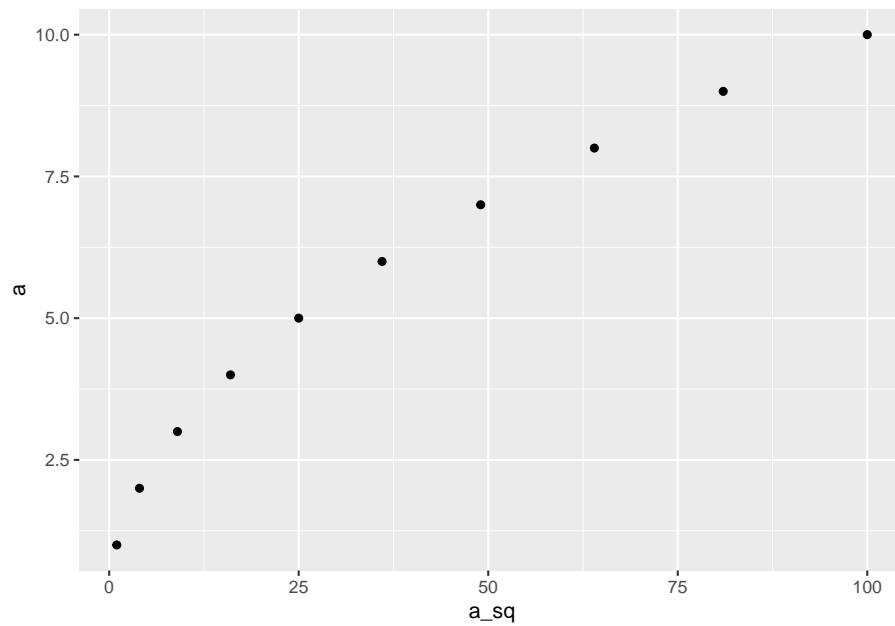
```
ggplot(data = df, mapping = aes(x = a, y = a_sq)) + geom_point()
```



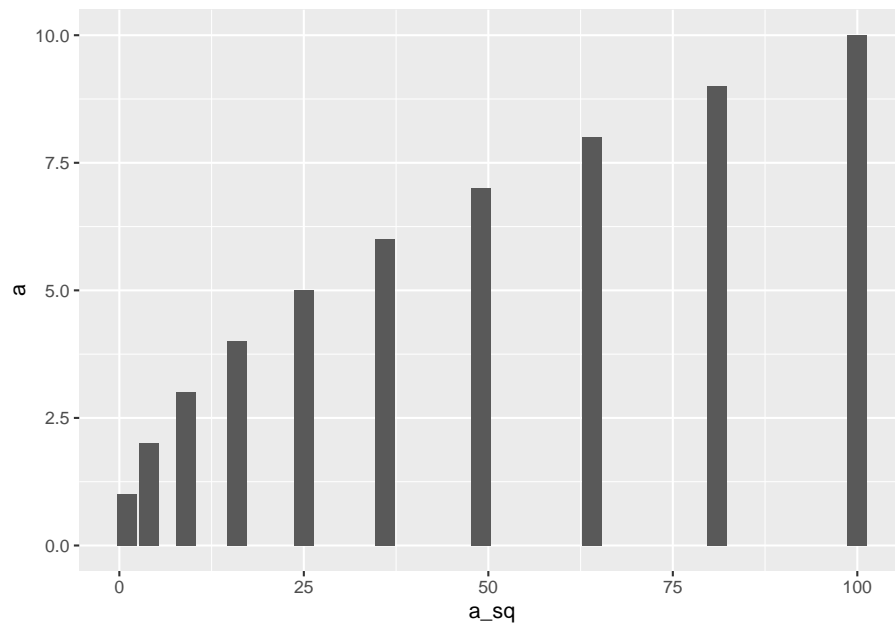
```
ggplot(data = df, mapping = aes(x = a, y = a_sq)) + geom_bar(stat="identity")
```




```
ggplot(data = df, mapping = aes(x = a_sq, y = a)) + geom_point()
```



```
ggplot(data = df, mapping = aes(x = a_sq, y = a)) + geom_bar(stat="identity")
```



5.2 The basics of ggplot2

- So what do those function calls mean?
- Let's take a look at it again: This is pretty much the minimal useful plotting command in R.

```
ggplot(data = df, mapping = aes(x = a, y = a_sq)) + geom_point()
```

- Each ggplot2 plot specification consists, at a minimum, of three parts:
 1. the data to plot
 2. *an abstract specification of the plot* (a rough mapping between variables and axes and other plot elements, such as *groups*, *facets*, etc.)
 3. *concrete instructions on what to draw* (a specification of the actual visual elements to use)
- They correspond to three parts of the `ggplot()` function call
 1. **data:** `data = df`
 2. **'aesthetic':** `mapping = aes(x, y)`
 3. **'geoms':** `+ geom_point()`
- You can read the instruction below as “*Create a plot using the data in data frame df, placing a on the x-axis and a_sq on the y-axis, and visualize the data using points*”.
- Keep in mind that information regarding x and y axes is specified within a function called `aes()`.

```
ggplot(data = df, mapping = aes(x = a, y = a_sq)) + geom_point()
```

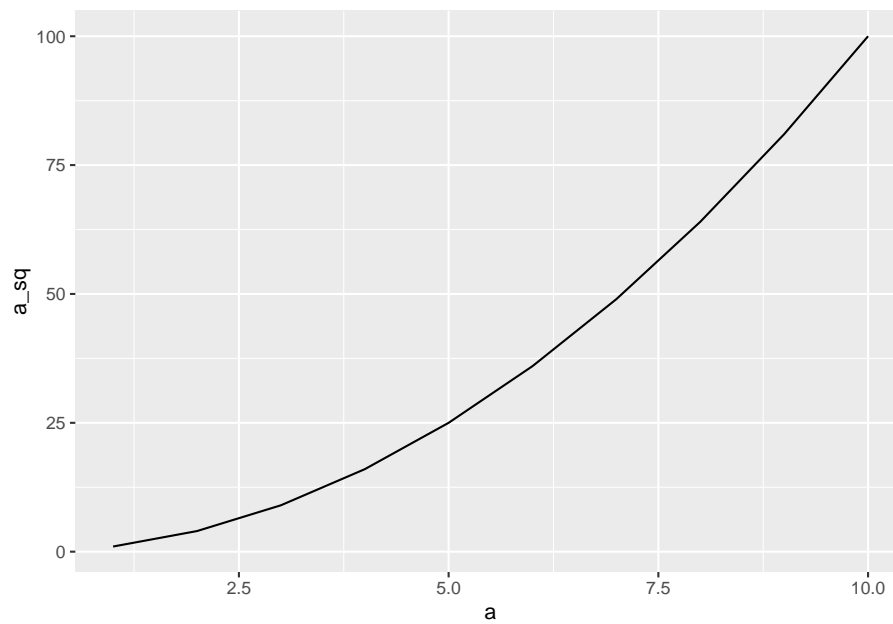
- As an aside: A shorter way to write the same code is below, and I'll mostly use some mixed form.

```
ggplot(df, aes(a, a_sq)) + geom_point()
```

5.3 Using lines in plots

- We already know `geom_point` and `geom_bar`. Let's take a look at some other *geoms*.
- `geom_line` connects the (invisible, in this case) points in the plot.

```
ggplot(df, aes(a, a_sq)) + geom_line()
```



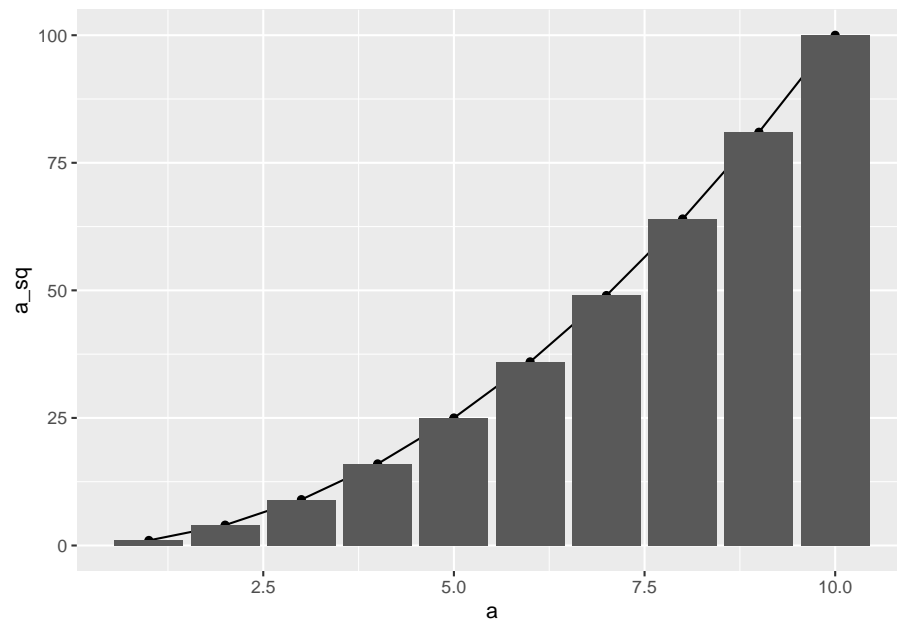
- We can even combine geoms:

```
ggplot(df, aes(a, a_sq)) + geom_point() + geom_line()
```



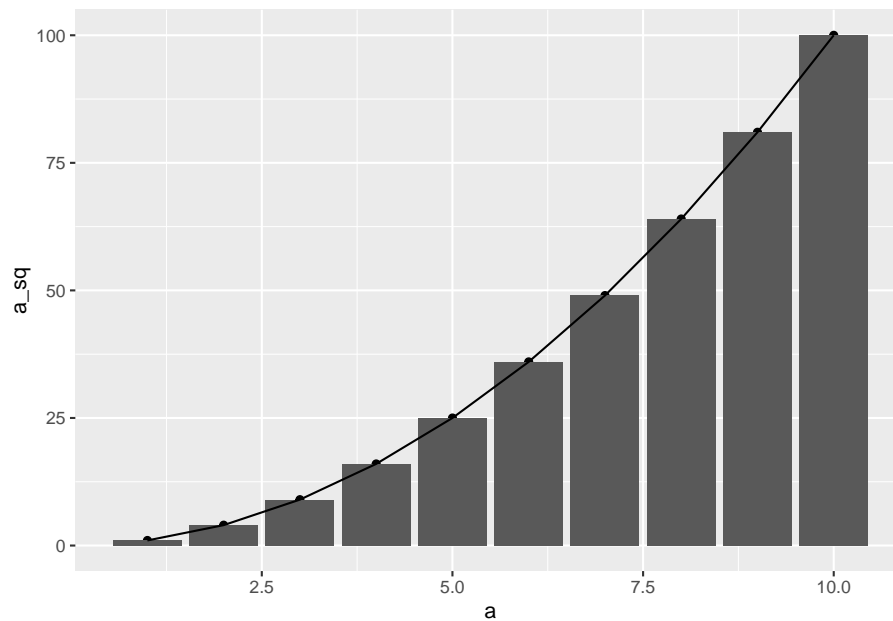
- ... in fact, as many as we want. But there is no guarantee that the result will look good, or even make sense.

```
ggplot(df, aes(a, a_sq)) + geom_point() + geom_line() + geom_bar(stat = "identity")
```



- The order of their specification matter a little bit. Here, the line is plotted over the bars, in contrast to the previous plot.

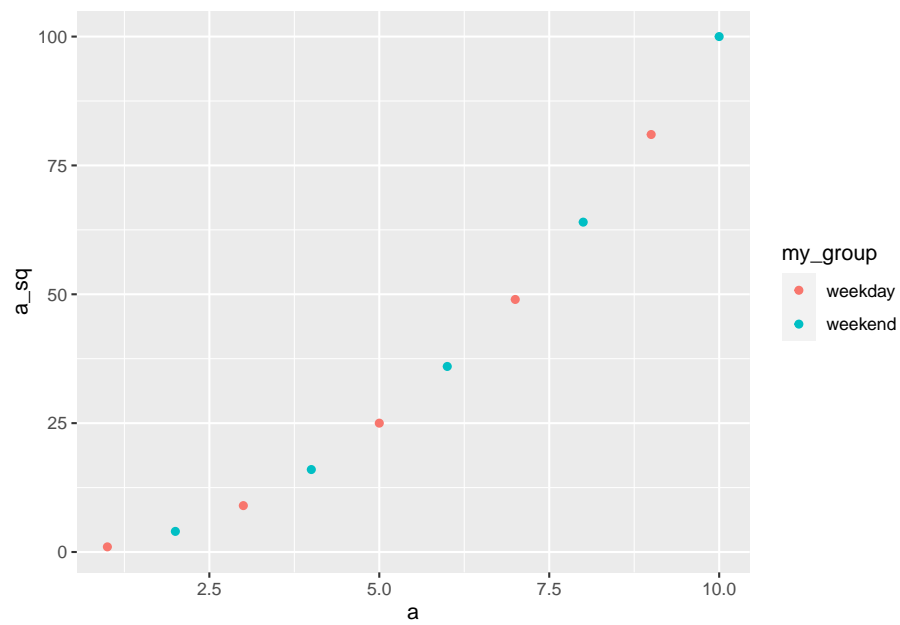
```
ggplot(df, aes(a, a_sq)) + geom_point() + geom_bar(stat = "identity") + geom_line()
```



5.4 Color and fill

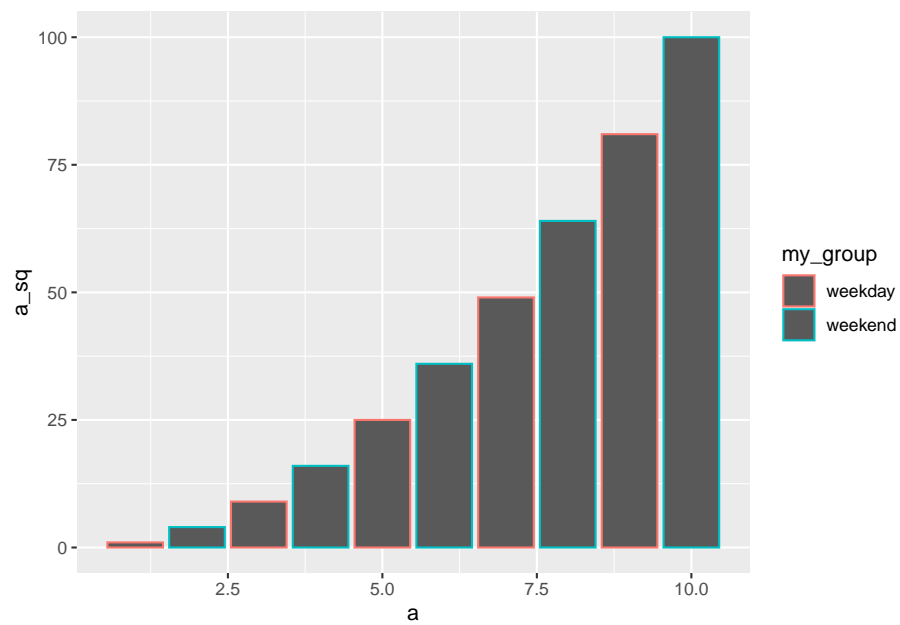
- Relationships between two variables are usually easy to visualize, but often there is a third variable.
- There are various ways for dealing with it.
- Let's first try using color coding for the third variable.

```
ggplot(df, aes(a, a_sq, color = my_group)) + geom_point(stat = "identity")
```



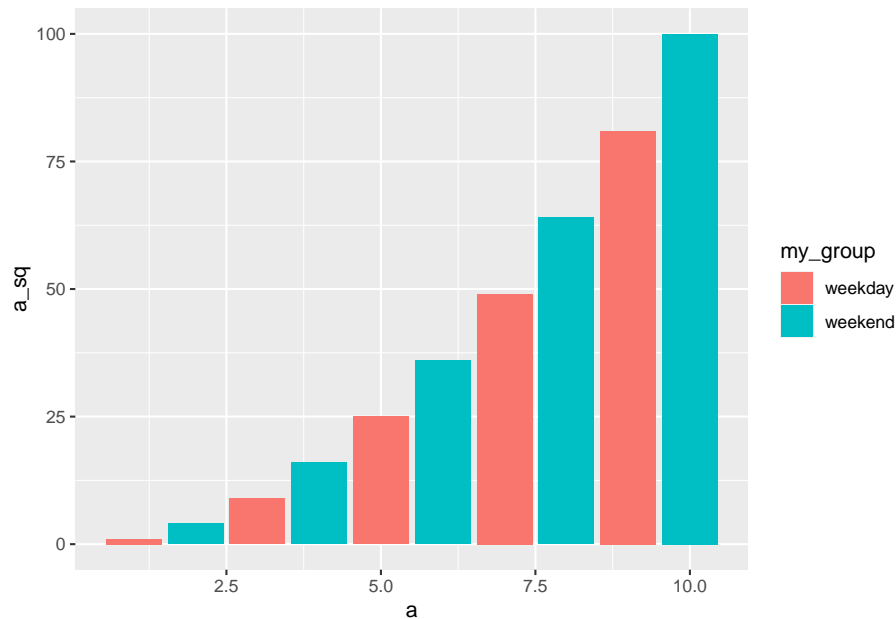
- Let's try this with bar plots. Not at all what you expected, is it?

```
ggplot(df, aes(a, a_sq, color = my_group)) + geom_bar(stat = "identity")
```



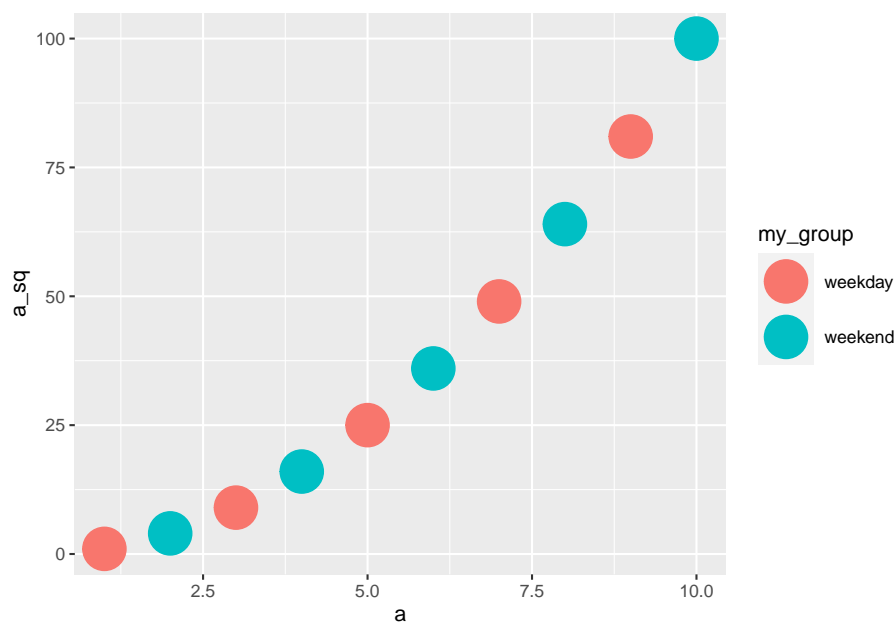
- This is what we wanted. The right argument for bar plots is `fill`.

```
ggplot(df, aes(a, a_sq, fill = my_group)) + geom_bar(stat = "identity")
```



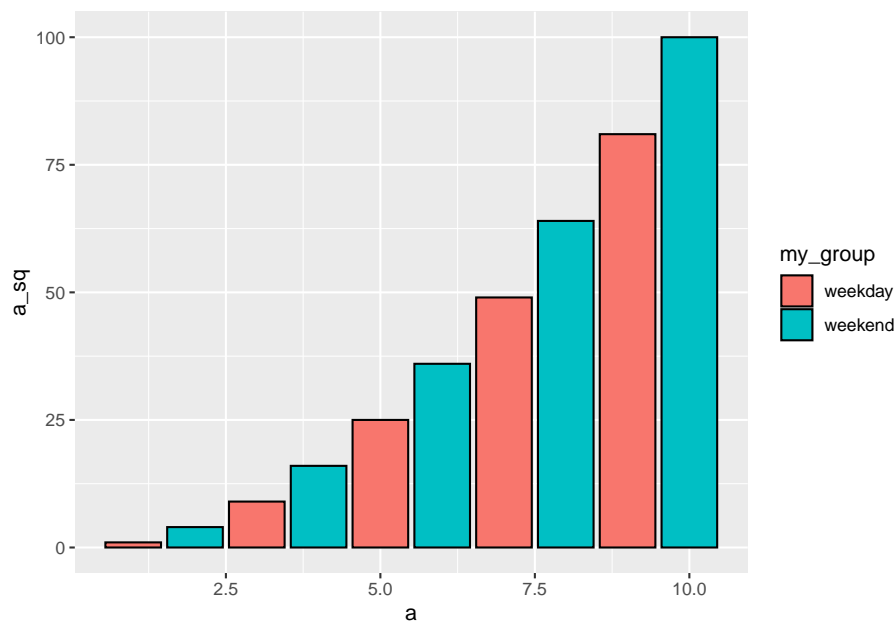
- So why isn't the aesthetic argument for bar plots not also `color`?
- Because geoms in ggplot2 have `fill` (the color of the inner part of the object), and a `color` (the color of the line with which they are drawn).
- Points don't have a fill. (Don't ask me why.)
- We can try, if you do not believe me. See that even though we specify a `fill` argument for `geom_point`, `color` argument overwrites it.

```
ggplot(df, aes(a, a_sq, color = my_group)) + geom_point(size=10, fill = "black")
```



- If points had a fill, we would expect the argument that comes last to overwrite the previous one. - Bars have both fill and color arguments.

```
ggplot(df, aes(a, a_sq, fill = my_group)) + geom_bar(stat="identity", color = "black")
```



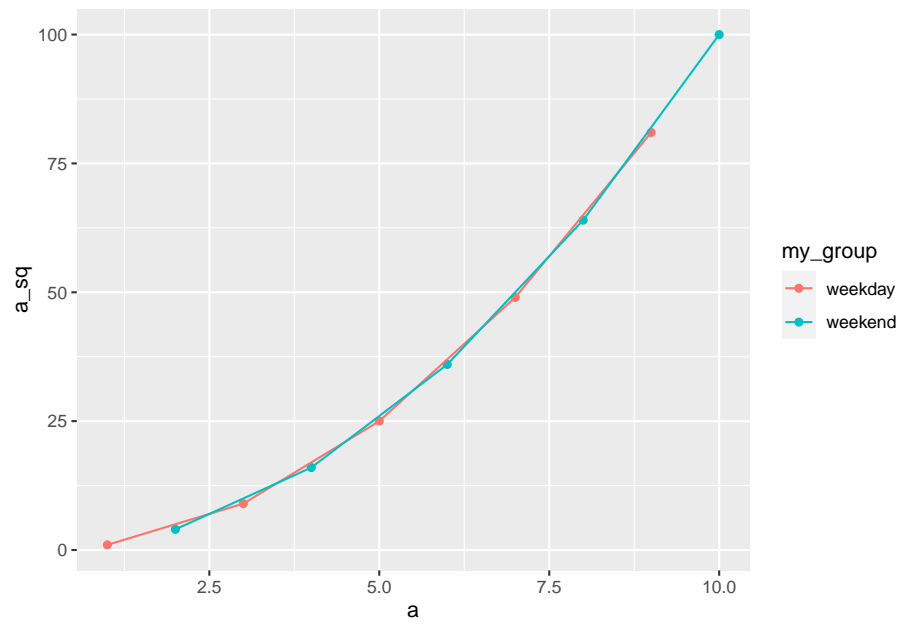

```
ggplot(df, aes(a, a_sq, color = my_group)) + geom_bar(stat="identity", fill = "black")
```



5.5 Grouping and facets

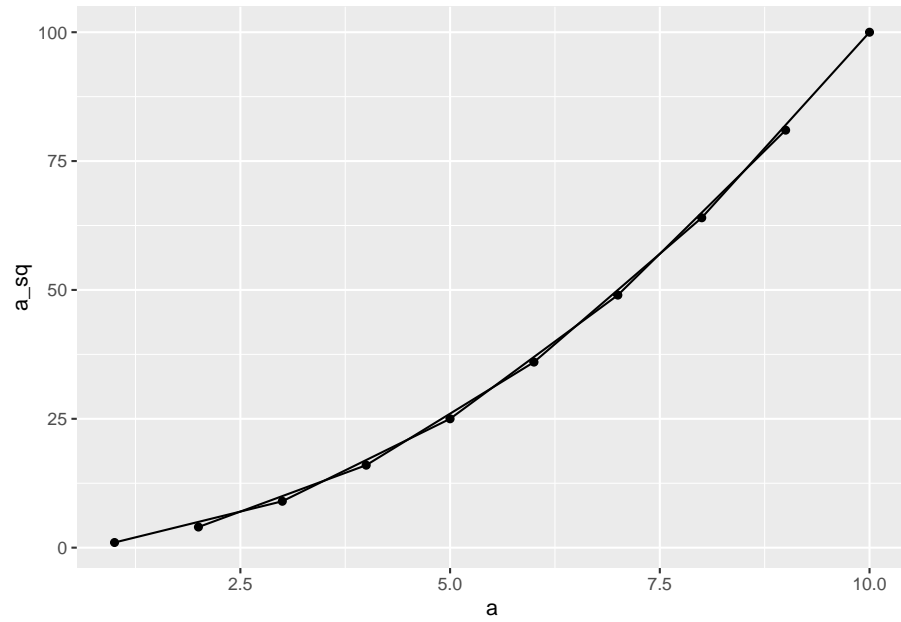
- Color, fill, etc. implicitly group the data set into different subgroups.
- You can see that better if you connect the points by lines.

```
ggplot(df, aes(a, a_sq, color = my_group)) + geom_point() + geom_line()
```



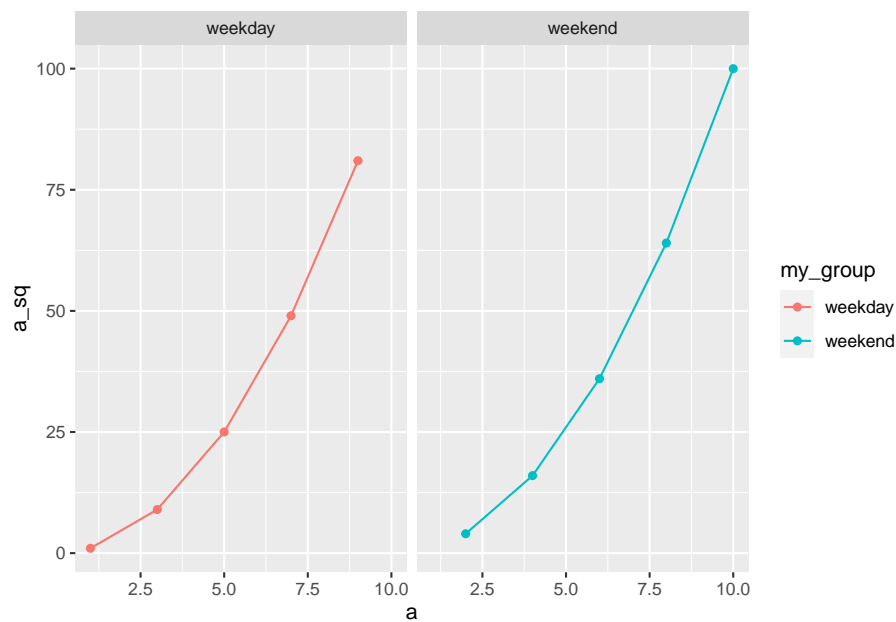
- This can be done explicitly as well.

```
ggplot(df, aes(a, a_sq, group = my_group)) + geom_point() + geom_line()
```



- Now it's very hard to see which line is which, so let's at least separate it into different **facets** (aka '*panels*').
- We can introduce our new facets with the function `facet_wrap()`. Keep in mind that the grouping variable is introduced with `~`.
- The name of the groups can be seen at the top of the plots.

```
ggplot(df, aes(a, a_sq, color = my_group)) + geom_point() + geom_line() + facet_wrap(~my_group)
```



Chapter 6

Descriptive Statistics

Anytime you have some data, one of the first tasks you need to do is to find ways to summarize your data neatly. Raw data by itself will not make much sense. So, you want to calculate some summary statistics that describes your data. This is **descriptive statistics** (as opposed to **inferential statistics**).

Let us start with a simple dataset about the mammalian sleep hours.

```
library(tidyverse)
library(magrittr)
library(lsr)
mammalian_sleep <-
  read_csv("./data/msleep_ggplot2.csv") %>%
  select(name, sleep_total, bodywt) %>%
  rename(sleep_total_h = sleep_total, bodywt_kg = bodywt) %>%
  mutate(sleep_total_h = round(sleep_total_h) )
```

```
## Rows: 83 Columns: 11
## -- Column specification -----
## Delimiter: ","
## chr (5): name, genus, vore, order, conservation
## dbl (6): sleep_total, sleep_rem, sleep_cycle, awake, brainwt, bodywt
##
## i Use `spec()` to retrieve the full column specification for this data.
## i Specify the column types or set `show_col_types = FALSE` to quiet this message.
```

```
head(mammalian_sleep)
```

```
## # A tibble: 6 x 3
##   name                sleep_total_h bodywt_kg
##   <chr>                <dbl>      <dbl>
## 1 Cheetah                12        50
## 2 Owl monkey             17        0.48
## 3 Mountain beaver       14        1.35
## 4 Greater short-tailed shrew 15        0.019
## 5 Cow                    4        600
## 6 Three-toed sloth       14        3.85
```

- There are three variables here, `name`, `sleep_total_h` and `bodywt_kg`. For each animal named in `name`, the `sleep_total_h` variable contains the average number of hours animals of this kind sleep per day. The variable `bodywt_kg` contains the average weight of that animal in kg.
- Let's have a look at the `sleep_total_h` variable:

```
print(mammalian_sleep$sleep_total_h)
```

```
## [1] 12 17 14 15 4 14 9 7 10 3 5 9 10 12 10 8 9 17 5 18 4 20 3 3 10
## [26] 11 15 12 10 2 3 6 6 8 10 3 19 10 14 14 13 12 20 15 11 8 14 8 4 10
## [51] 16 10 14 9 10 11 12 14 4 6 11 18 5 13 9 10 8 11 11 17 14 16 13 9 9
## [76] 16 4 16 9 5 6 12 10
```

- This output doesn't make it easy to get a sense of what the data are actually saying. Just "looking at the data" isn't a terribly effective way of understanding data. In order to get some idea about what's going on, we need to calculate some descriptive statistics and draw some nice pictures.

```
ggplot(mammalian_sleep, aes(sleep_total_h)) +
  geom_histogram(binwidth=1,
                 color = 'black',
                 fill = 'lightblue')
```

6.1 Distributions

Let us see a couple more data examples to get a sense of what data might look like in the wild. First, let us generate some random data with a **uniform distribution** using the `runif()` function.

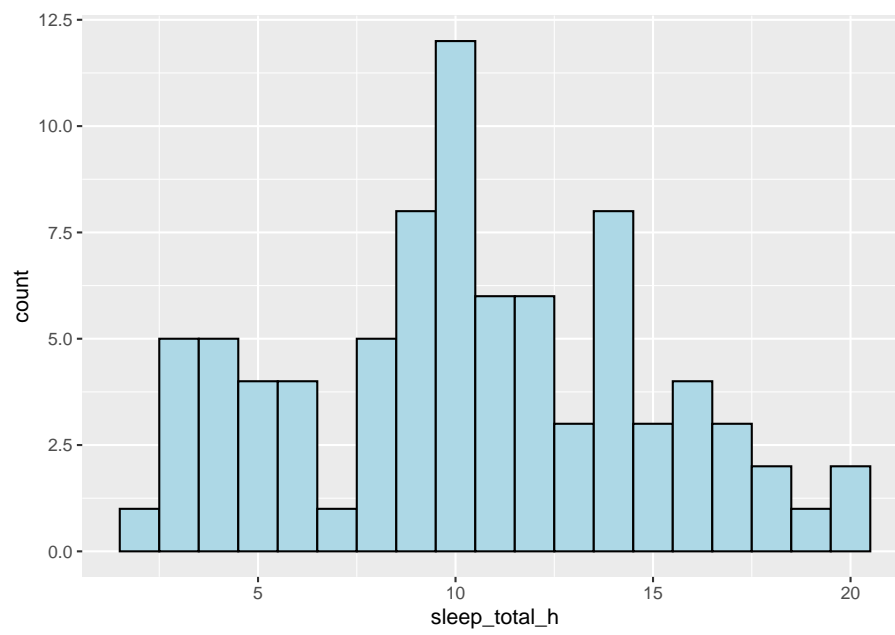


Figure 6.1: A histogram of the average amount of sleep by animal (the `sleep_total_h` variable). As you might expect, the larger the margin the less frequently you tend to see it.

```
uniform <- as_tibble_col(runif(120, min = 1, max = 6), column_name = "some_value")
```

```
uniform
```

```
## # A tibble: 120 x 1
##   some_value
##   <dbl>
## 1      2.23
## 2      1.21
## 3      2.64
## 4      5.77
## 5      5.45
## 6      4.46
## 7      4.20
## 8      5.97
## 9      4.28
## 10     4.54
## # i 110 more rows
```

Let us plot the uniformly distributed data using a histogram.

```
ggplot(uniform, aes(some_value)) +
  geom_histogram(binwidth=0.5, boundary=0,
    color = 'black',
    fill = 'lightblue')
```

This looks good but it doesn't make as much intuitive sense as we'd like. Let us tweak this slightly. Assume that you have a fair dice with 6 sides. So, whenever we roll the dice, each side has an equal probability (i.e. $1/6$). Let us simulate this. The data is going to be very similar, except that this time we will need **discrete** values rather than **continuous** values. For that, we need to use the `rdunif()` function which generates random values with a discrete uniform distribution.

```
uniform <- as_tibble_col(rdunif(120, 6, 1), column_name="dice_value")
```

```
## Warning: `rdunif()` was deprecated in purrr 1.0.0.
## This warning is displayed once every 8 hours.
## Call `lifecycle::last_lifecycle_warnings()` to see where this warning was
## generated.
```

```
uniform
```

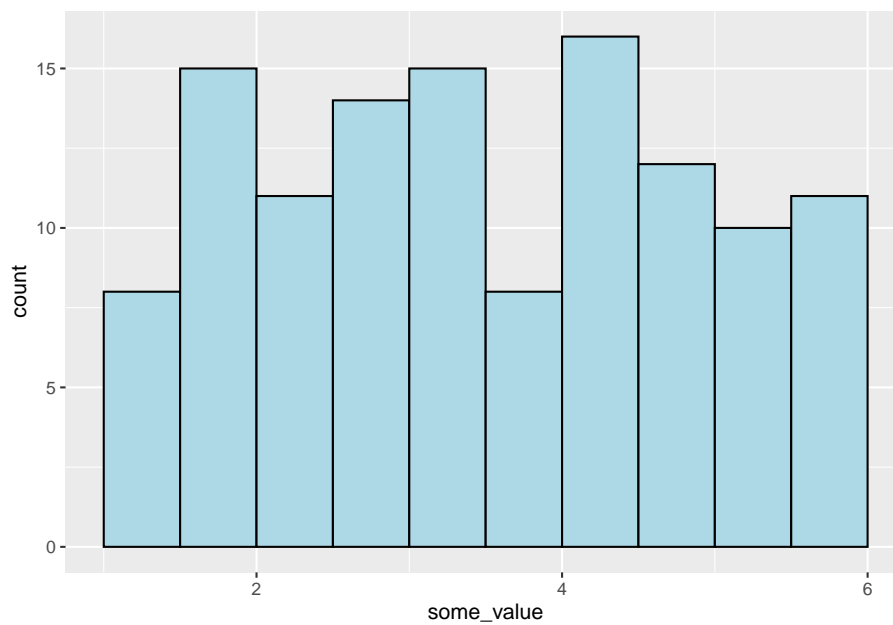
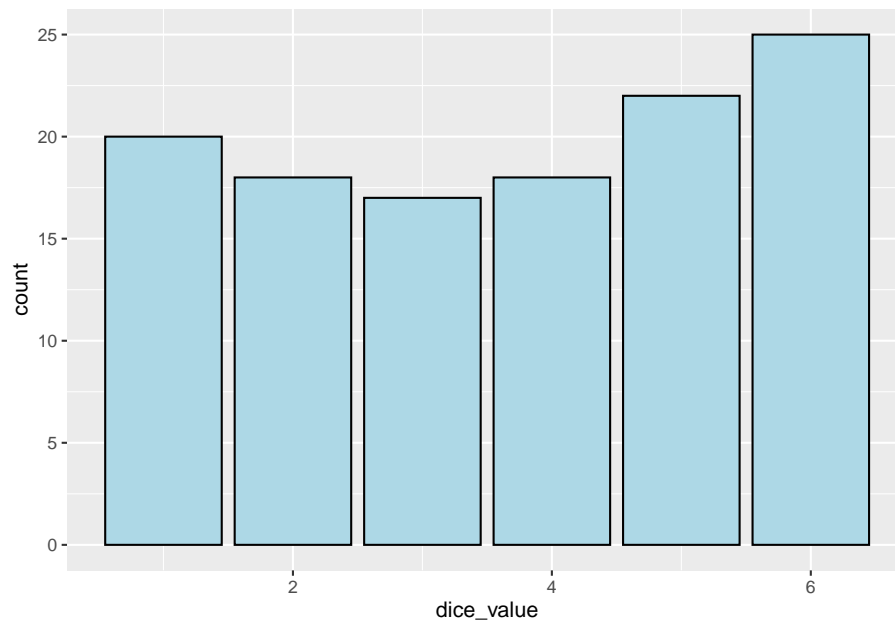



Figure 6.2: Histogram of a uniform distribution.

```
## # A tibble: 120 x 1
##   dice_value
##   <dbl>
## 1         2
## 2         2
## 3         6
## 4         4
## 5         4
## 6         6
## 7         1
## 8         6
## 9         6
## 10        6
## # i 110 more rows
```

```
ggplot(uniform, aes(dice_value)) +
  geom_bar(color = 'black',
           fill = 'lightblue')
```



Just a quick point to think about. Why did we use a histogram for the continuous uniform distribution and a bar graph for a discrete one?

Now, let us generate some random data with a **normal distribution** using the `rnorm()` function.

```
normal <- as_tibble(rnorm(160))
```

Let us plot the normally distributed data using a histogram.

```
ggplot(normal, aes(value)) +  
  geom_histogram(binwidth=0.2,  
                 color = 'black',  
                 fill = 'lightblue')
```

Here's another one where we provide the **mean** and **standard deviation** parameters.

```
normal2 <- as_tibble(rnorm(160, mean = 8, sd = 0.5))
```

Let us plot the second normally distributed data using a histogram.

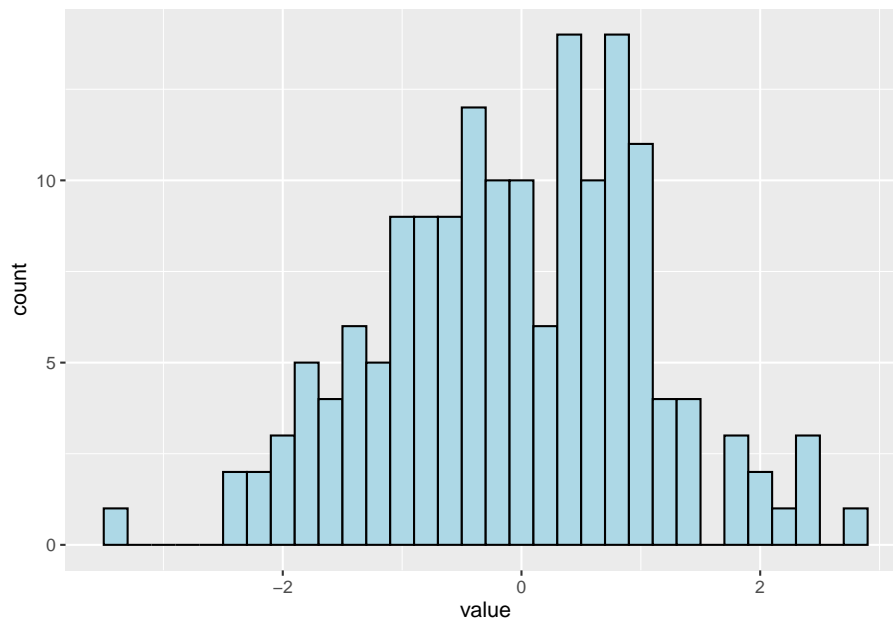


Figure 6.3: Histogram of a normal distribution.

```
ggplot(normal2, aes(value)) +
  geom_histogram(binwidth=0.2,
                 color = 'black',
                 fill = 'steelblue')
```

Finally, let us plot both of the normally distributed data on the same plot to see them side by side.

```
ggplot(normal, aes(value)) +
  geom_histogram(binwidth=0.2,
                 color = 'black',
                 fill = 'lightblue') +
  geom_histogram(data=normal2, binwidth=0.2, boundary=0,
                 color = 'black',
                 fill = 'steelblue')
```

6.2 Measures of central tendency

Drawing pictures of the data, as I did in Figure 6.1 is an excellent way to convey the “gist” of what the data is trying to tell you, it’s often extremely useful to try

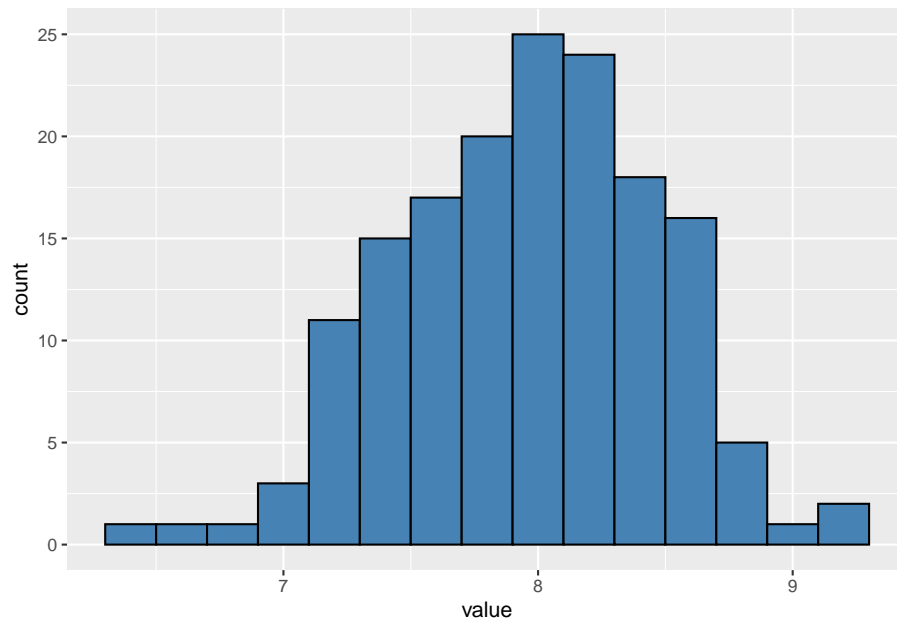


Figure 6.4: Histogram of a normal distribution.

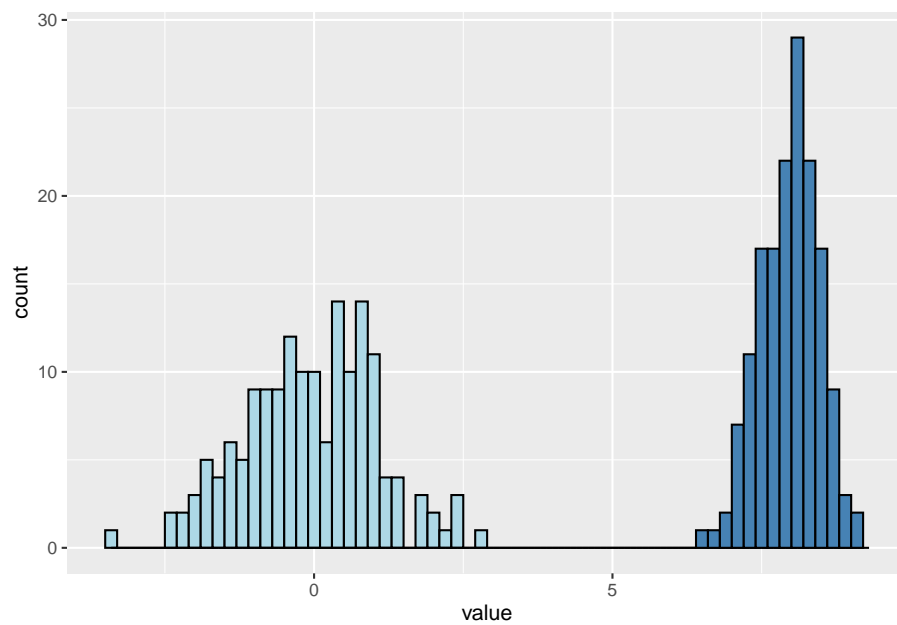


Figure 6.5: Histogram of two normal distributions side by side.

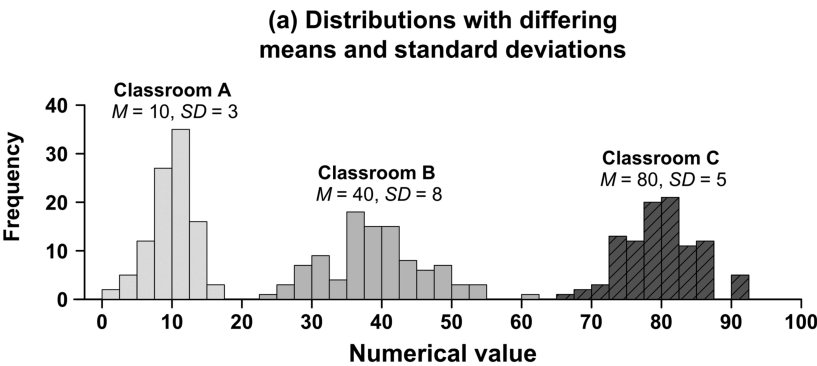


Figure 6.6: Distributions with different means and standard deviations.

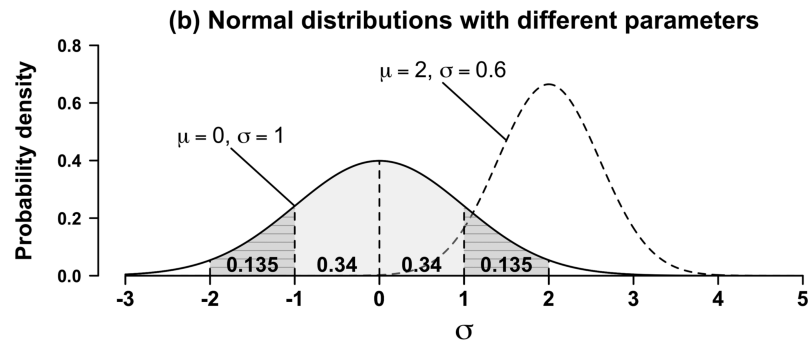


Figure 6.7: Distributions with different means and standard deviations. The light gray area covers the 68% of the data and the total of the gray areas cover the 95% of the data.

to condense the data into a few simple “summary” statistics. In most situations, the first thing that you’ll want to calculate is a measure of **central tendency**. That is, you’d like to know something about the “average” or “middle” of your data lies. The three most commonly used measures are the **mean**, **median** and **mode**; occasionally people will also report a trimmed mean. I’ll explain each of these in turn, and then discuss when each of them is useful.

6.2.1 The mean

- The **mean** of a set of observations is just a normal, old-fashioned average: add all of the values up, and then divide by the total number of values. The first five animals’ typical amount of sleep is $12 + 17 + 14 + 15 + 4$, so the mean of these observations is just:

$$\frac{12 + 17 + 14 + 15 + 4}{5} = \frac{62.4}{5} = 12.48$$

- Of course, this definition of the mean isn’t news to anyone: averages (i.e., means) are used so often in everyday life that this is pretty familiar stuff. However, since the concept of a mean is something that everyone already understands, I’ll use this as an excuse to start introducing some of the mathematical notation that statisticians use to describe this calculation, and talk about how the calculations would be done in R.
- The first piece of notation to introduce is N , which we’ll use to refer to the number of observations that we’re averaging (in this case $N = 5$).
- Next, we need to attach a label to the observations themselves. It’s traditional to use X for this, and to use subscripts to indicate which observation we’re actually talking about.
- That is, we’ll use X_1 to refer to the first observation, X_2 to refer to the second observation, and so on, all the way up to X_N for the last one. Or, to say the same thing in a slightly more abstract way, we use X_i to refer to the i -th observation. Just to make sure we’re clear on the notation, the following table lists the 5 observations in the `sleep_total_h` variable, along with the mathematical symbol used to refer to it, and the actual value that the observation corresponds to:

the observation	its symbol	the observed value
Cheetah (animal 1)	X_1	12 hours
Owl monkey (animal 2)	X_2	17 hours
Mountain beaver (animal 3)	X_3	14 hours
Greater short-tailed shrew (animal 4)	X_4	15 hours
Cow (animal 5)	X_5	4 hours

- Okay, now let's try to write a formula for the mean. By tradition, we use \bar{X} as the notation for the mean. So the calculation for the mean could be expressed using the following formula:

$$\bar{X} = \frac{X_1 + X_2 + \dots + X_{N-1} + X_N}{N}$$

- This formula is entirely correct, but it's terribly long, so we make use of the **summation symbol** Σ to shorten it.¹ If I want to add up the first five observations, I could write out the sum the long way, $X_1 + X_2 + X_3 + X_4 + X_5$ or I could use the summation symbol to shorten it to this:

$$\sum_{i=1}^5 X_i$$

- Taken literally, this could be read as “the sum, taken over all i values from 1 to 5, of the value X_i ”. But basically, what it means is “add up the first five observations”. In any case, we can use this notation to write out the formula for the mean, which looks like this:

$$\bar{X} = \frac{1}{N} \sum_{i=1}^N X_i$$

- In all honesty, I can't imagine that all this mathematical notation helps clarify the concept of the mean at all. In fact, it's really just a fancy way of writing out the same thing I said in words: add all the values up, and then divide by the total number of items. However, that's not really the reason I went into all that detail.
- My goal was to try to make sure that everyone reading this book is clear on the notation that we'll be using throughout the book: \bar{X} for the mean, Σ for the idea of summation, X_i for the i th observation, and N for the total number of observations.
- We're going to be re-using these symbols a fair bit, so it's important that you understand them well enough to be able to “read” the equations, and to be able to see that it's just saying “add up lots of things and then divide by another thing”.

¹The choice to use Σ to denote summation isn't arbitrary: it's the Greek upper case letter sigma, which is the analogue of the letter S in that alphabet. Similarly, there's an equivalent symbol used to denote the multiplication of lots of numbers: because multiplications are also called “products”, we use the Π symbol for this; the Greek upper case pi, which is the analogue of the letter P.

6.2.2 Calculating the mean in R

Okay that's the maths, how do we get the magic computing box to do the work for us? If you really wanted to, you could do this calculation directly in R. For the first numbers, do this just by typing it in as if R were a calculator...

```
(12 + 17 + 14 + 15 + 4) / 5
```

```
## [1] 12.4
```

... in which case R outputs the answer 12.4, just as if it were a calculator.

- However, we learned quicker ways of doing that

```
sum( mammalian_sleep$sleep_total_h[1:5] ) / 5
```

```
## [1] 12.4
```

```
# or:
```

```
mean( mammalian_sleep$sleep_total_h[1:5] )
```

```
## [1] 12.4
```

6.2.3 The median

- The second measure of central tendency that people use a lot is the *median*, and it's even easier to describe than the mean. The median of a set of observations is just the middle value.
- As before let's imagine we were interested only in the first 5 animals: They sleep 12, 17, 14, 15, and 4 hours respectively. To figure out the median, we sort these numbers into ascending order:

4, 12, 14, 15, 17

- From inspection, it's obvious that the median value of these 5 observations is 14, since that's the middle one in the sorted list (I've put it in red to make it even more obvious). Easy stuff.
- But what should we do if we were interested in the first 6 animals rather than the first 5? Since the sixth animal sleeps for 14 hours, our sorted list is now:

4, 12, 14, 14, 15, 17

- That's also easy. It's still 14.
- But what we do if we were interested in the first 8 animals? Here is our new sorted list.

4, 7, 9, 12, 14, 14, 15, 17

- There are now *two* middle numbers, 12 and 14. The median is defined as the average of those two numbers, which is of course 13.
- To understand why, think of the median as the value that divides the sorted list of numbers into two halves – those on its left, and those on its right.
- As before, it's very tedious to do this by hand when you've got lots of numbers. To illustrate this, here's what happens when you use R to sort all the sleep durations. First, I'll use the `sort()` function to display the 83 numbers in increasing numerical order:

```
sort( mammalian_sleep$sleep_total_h )
```

```
## [1]  2  3  3  3  3  3  4  4  4  4  4  5  5  5  5  6  6  6  6  7  8  8  8  8  8
## [26]  9  9  9  9  9  9  9  9 10 10 10 10 10 10 10 10 10 10 10 11 11 11 11 11
## [51] 11 12 12 12 12 12 12 12 13 13 13 14 14 14 14 14 14 14 14 15 15 15 16 16 16 16
## [76] 17 17 17 18 18 19 20 20
```

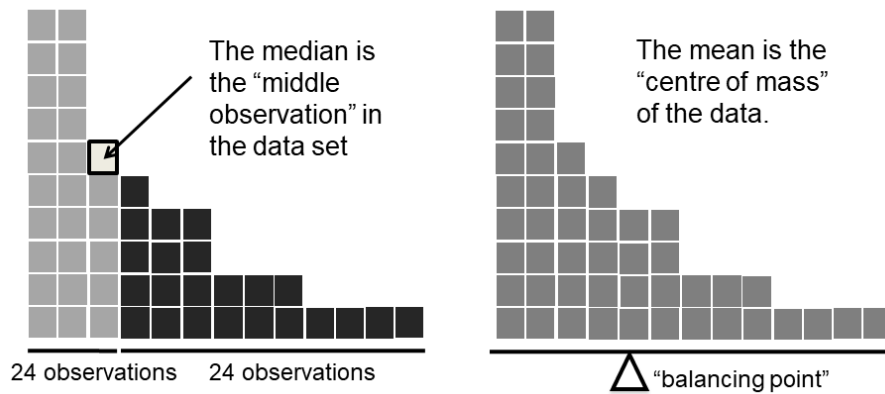
- Because the vector is 83 elements long, the middle value is at position 42. This means that the median of this vector is 10. In real life, of course, no-one actually calculates the median by sorting the data and then looking for the middle value. In real life, we use the median command:

```
median( mammalian_sleep$sleep_total_h )
```

```
## [1] 10
```

which outputs the median value of 10.

6.2.4 Mean or median? What's the difference?



- Knowing how to calculate means and medians is only a part of the story. You also need to understand what each one is saying about the data, and what that implies for when you should use each one. This is illustrated in Figure ?? the mean is kind of like the “centre of gravity” of the data set, whereas the median is the “middle value” in the data. What this implies, as far as which one you should use, depends a little on what type of data you’ve got and what you’re trying to achieve. As a rough guide:
- One consequence is that there’s systematic differences between the mean and the median when the histogram is asymmetric (skewed). This is illustrated in Figure ?? notice that the median (right hand side) is located closer to the “body” of the histogram, whereas the mean (left hand side) gets dragged towards the “tail” (where the extreme values are).
- To give a concrete example, suppose Bob (income \$50,000), Kate (income \$60,000) and Jane (income \$65,000) are sitting at a table: the average income at the table is \$58,333 and the median income is \$60,000. Then Bill sits down with them (income \$100,000,000). The average income has now jumped to \$25,043,750 but the median rises only to \$62,500. If you’re interested in looking at the overall income at the table, the mean might be the right answer; but if you’re interested in what counts as a typical income at the table, the median would be a better choice here.

6.2.5 Trimmed mean

- One of the fundamental rules of applied statistics is that the data are messy. Real life is never simple, and so the data sets that you obtain are

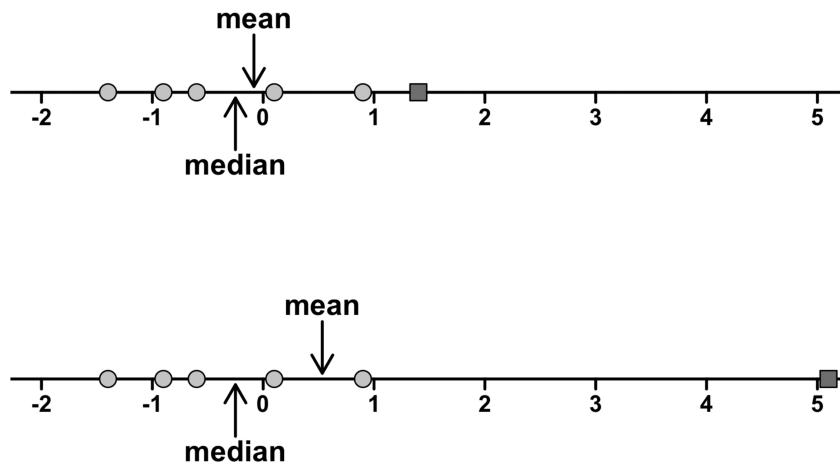


Figure 6.8: Another example of mean and median where mean is moved by the outliers but median is constant.

never as straightforward as the statistical theory says.² This can have awkward consequences. To illustrate, consider this rather strange looking data set (nevermind what it represents):

$$-100, 2, 3, 4, 5, 6, 7, 8, 9, 10$$

- If you were to observe this in a real life data set, you'd probably suspect that something funny was going on with the -100 value. It's probably an **outlier**, a value that doesn't really belong with the others. You might consider removing it from the data set entirely, and in this particular case I'd probably agree with that course of action.
- In real life, however, you don't always get such cut-and-dried examples. For instance, you might get this instead:

$$-15, 2, 3, 4, 5, 6, 7, 8, 9, 12$$

- The -15 looks a bit suspicious, but not anywhere near as much as that -100 did. In this case, it's a little trickier. It *might* be a legitimate observation, it might not.
- When faced with a situation where some of the most extreme-valued observations might not be quite trustworthy, the mean is not necessarily a

²Or at least, the basic statistical theory – these days there is a whole subfield of statistics called *robust statistics* that tries to grapple with the messiness of real data and develop theory that can cope with it.

good measure of central tendency. It is highly sensitive to one or two extreme values, and is thus not considered to be a **robust** measure.

- One remedy that we’ve seen is to use the median. A more general solution is to use a “trimmed mean”. To calculate a trimmed mean, what you do is “discard” the most extreme examples on both ends (i.e., the largest and the smallest), and then take the mean of everything else. The goal is to preserve the best characteristics of the mean and the median:
 - just like a median, you aren’t highly influenced by extreme outliers, but ...
 - like the mean, you “use” more than one of the observations.
- Generally, we describe a trimmed mean in terms of the percentage of observation on either side that are discarded. So, for instance, a 10% trimmed mean discards the largest 10% of the observations *and* the smallest 10% of the observations, and then takes the mean of the remaining 80% of the observations.
- Not surprisingly, the 0% trimmed mean is just the regular mean, and the 50% trimmed mean is the median. In that sense, trimmed means provide a whole family of central tendency measures that span the range from the mean to the median.
- For our toy example above, we have 10 observations, and so a 10% trimmed mean is calculated by ignoring the largest value (i.e., 12) and the smallest value (i.e., -15) and taking the mean of the remaining values. First, let’s enter the data

```
dataset <- c( -15,2,3,4,5,6,7,8,9,12 )
```

Next, let’s calculate means and medians:

```
mean( dataset )
```

```
## [1] 4.1
```

```
median( dataset )
```

```
## [1] 5.5
```

- That’s a fairly substantial difference, but I’m tempted to think that the mean is being influenced a bit too much by the extreme values at either end of the data set, especially the -15 one. So let’s just try trimming the mean a bit. If I take a 10% trimmed mean, we’ll drop the extreme values on either side, and take the mean of the rest:

```
mean( dataset, trim = .1)
```

```
## [1] 5.5
```

- In this case it gives exactly the same answer as the median. Note that, to get a 10% trimmed mean you write `trim = .1`, not `trim = 10`.

6.2.6 Mode

- The *mode* is the last measure of central tendency we'll look at. It is very simple: it is the value that occurs most frequently.
- Let's look at the some soccer data: specifically, the European Cup and Champions League results in the time from 1955-2016.
- Lets find out which team has won the most matches. The command below tells R we just want the first 25 rows of the data.frame.

6.2.7 Summary

- There are multiple measures of central tendency that can be used to summarize an aspect of a distribution: **__ (arithmetic) mean, median, and mode__**.
- They answer different questions about distribution. For example, in the distribution of number of goals per game in the previous section
 - mean: “If the same number of goals were scored in each game, how many goals would be scored?”
 - median: “What is a ‘mediocre’ game like?”
 - mode: “What is the most typical game like?”

6.3 Measures of variability

- The statistics that we've discussed so far all relate to *central tendency*. That is, they all talk about which values are “in the middle” or “popular” in the data.
- The second thing that we really want is a measure of the *variability* of the data.
 - That is, how “spread out” are the data?
 - In other words, how ‘representative’ is our measure of central tendency of most data points.
- Let's consider interval and ratio scale data.

6.3.1 Range

- The *range* of a variable is very simple: it's the biggest value minus the smallest value. For the sleep data, the maximum value is 20, and the minimum value is 2. We can calculate these values in R using the `max()` and `min()` functions:

```
max( mammalian_sleep$sleep_total_h )
```

```
## [1] 20
```

```
min( mammalian_sleep$sleep_total_h )
```

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

where I've omitted the output because it's not interesting.

- The other possibility is to use the `range()` function; which outputs both the minimum value and the maximum value in a vector, like this:

```
range( mammalian_sleep$sleep_total_h )
```

```
## [1] 2 20
```

- Although the range is the simplest way to quantify the notion of “variability”, it's one of the worst. Recall from our discussion of the mean that we want our summary measure to be robust. If the data set has one or two extremely bad values in it, we'd like our statistics not to be unduly influenced by these cases. If we look once again at our toy example of a data set containing very extreme outliers...

$$-100, 2, 3, 4, 5, 6, 7, 8, 9, 10$$

... it is clear that the range is not robust, since this has a range of 110, but if the outlier were removed we would have a range of only 8.

6.3.2 Quantiles and percentile

- A key concept we will need to build on to conceptualize several other measures of variability are *quantiles* or *percentiles*.
- A *percentile* is the smallest value in a dataset such that a set percentage is smaller than it. (A *quantile* does pretty much the same but is more generic.)

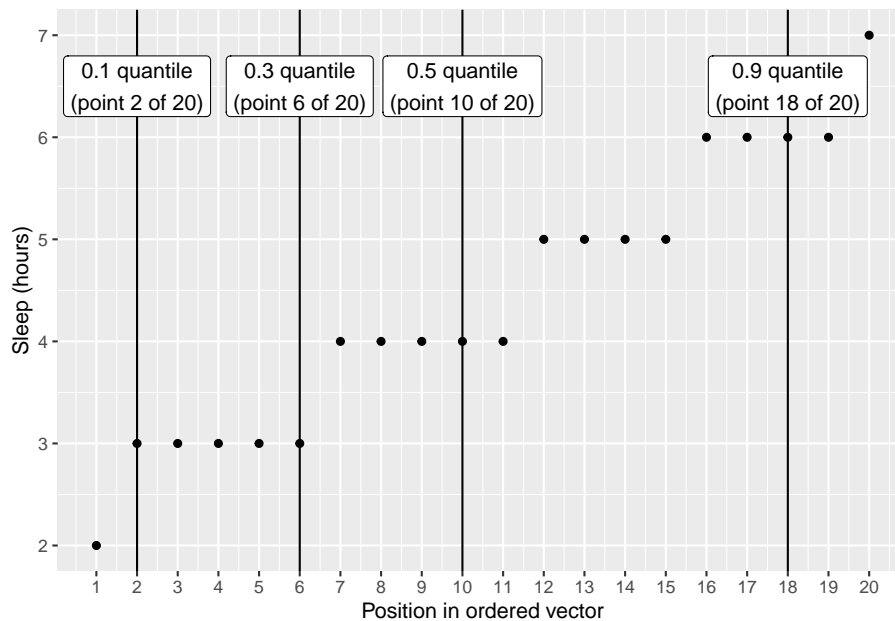
- For example, if the 10-th percentile (i.e., the 0.1 quantile) of a list of values is 73, this means that 10 percent of the values are smaller than or equal to 73.
- Let's take a look at the 20 shortest sorted sleep durations and determine the 10-th percentile (0.1 quantile), 30-th percentile (0.3 quantile), 50-th percentile (0.5 quantile), and the 90-th percentile (0.9 quantile).
- Here are the values:

```
sort(mammalian_sleep$sleep_total_h)[1:20]
```

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

- And here is a sorted plot of the 20 smallest values:

```
quantile <- c(0.1,0.3,0.5,0.9)
quantile_points <- c(0.1,0.3,0.5,0.9)*20
quantile_labels <- sprintf("%0.1f quantile\n(point %d of 20)", quantile, quantile_points)
ggplot(data=NULL, aes(x=1:20, y=sort(mammalian_sleep$sleep_total_h)[1:20])) +
  geom_point() +
  geom_vline(xintercept = quantile_points) +
  geom_label(aes(x=quantile_points, y=6.5, label=quantile_labels)) +
  scale_x_continuous(breaks = 1:20) + xlab("Position in ordered vector") + ylab("Sleep (hours)")
```



- As you can see:
 - 10-th percentile (0.1 quantile): 3 [to be found at position 2, since 2 data points constitute 10 percent of the data]
 - 30-th percentile (0.3 quantile): 3 [to be found at position 6, since 6 data points constitute 30 percent of the data]
 - 50-th percentile (0.5 quantile): 4 [to be found at position 10, since 10 data points constitute 50 percent of the data]
 - 90-th percentile (0.9 quantile): 6 [to be found at position 18, since 18 data points constitute 90 percent of the data]
- The 50-th percentile is the median.

6.3.3 Interquartile range

- The *interquartile range* (IQR) is like the range, but instead of calculating the difference between the biggest and smallest value, it calculates the difference between the 25th quantile and the 75th quantile.
- R provides you with a way of calculating quantiles, using the (surprise, surprise) `quantile()` function. Let's use it to calculate the median sleep durations:

```
quantile( x = mammalian_sleep$sleep_total_h, probs = .5)
```

```
## 50%
## 10
```

- And not surprisingly, this agrees with the answer that we saw earlier with the `median()` function. Now, we can actually input lots of quantiles at once, by specifying a vector for the `probs` argument. So let's do that, and get the 25th and 75th percentile:

```
quantile( x = mammalian_sleep$sleep_total_h, probs = c(.25,.75) )
```

```
## 25% 75%
## 8 14
```

- And, by noting that $14 - 8 = 6$, we can see that the interquartile range for the sleep durations is 6. Of course, that seems like too much work to do all that typing, so R has a built in function called `IQR()` that we can use:


```
IQR( x = mammalian_sleep$sleep_total_h )
```

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

- While it's obvious how to interpret the range, it's a little less obvious how to interpret the IQR. The simplest way to think about it is like this: the interquartile range is the range spanned by the “middle half” of the data. That is, one quarter of the data falls below the 25th percentile, one quarter of the data is above the 75th percentile, leaving the “middle half” of the data lying in between the two. And the IQR is the range covered by that middle half.
- IQR is used to identify the outliers (i.e. extreme values). Any value above $Q3 + IQR * 1.5$ or below $Q1 - IQR * 1.5$ is considered to be an outlier.

6.3.4 Mean absolute deviation

- The range and the interquartile range, both rely on the idea that we can measure the spread of the data by looking at the quantiles of the data.
- However, this isn't the only way to think about the problem. A different approach is to select a meaningful reference point (usually the mean or the median) and then report the “*typical*” *deviations* from that reference point.
- Let's go through the *mean absolute deviation* (AAD for average absolute deviation, since MAD is reserved for the median absolute deviation) from the mean a little more slowly. One useful thing about this measure is that the name actually tells you exactly how to calculate it:

$$AAD(X) = \frac{1}{N} \sum_{i=1}^N |X_i - \bar{X}|$$

- Let's compute the AAD for the first data points in the sleep data:

12, 17, 14, 15, 4

- The mean of the dataset is 12.4. That is, $\bar{X} = 12.4$
- The deviations $X_i - \bar{X}$ are:

-0.4, 4.6, 1.6, 2.6, -8.4

- The absolute deviations $|X_i - \bar{X}|$ are:

0.4, 4.6, 1.6, 2.6, 8.4

- The sum of the absolute deviations $\sum_{i=1}^N |X_i - \bar{X}|$ is 17.6.
- And $N = 5$, which means, that, in our case: $AAD(X) = \frac{1}{N} \sum_{i=1}^N |X_i - \bar{X}| = 3.52$
- In R, we can compute it for the entire vector.

```
mean_sleep <- mean(mammalian_sleep$sleep_total_h)
deviation_sleep <- mean_sleep - mammalian_sleep$sleep_total_h
mean( abs(deviation_sleep) )
```

```
## [1] 3.576717
```

- An alternative, more compact way to write it is using (lots) pipes:

```
mammalian_sleep$sleep_total_h %>% subtract(., mean(.)) %>% abs() %>% mean()
```

```
## [1] 3.576717
```

- The interpretation of the AAD is quite straightforward: It is the average distance from the average. When it's big, the values are quite spread out. When it's small, they are close. The units are the same (hours in our case).

6.3.5 Variance

- Although the mean absolute deviation measure has its uses, it's not the best measure of variability to use.
- For a number of practical reasons, there are some solid reasons to prefer squared deviations rather than absolute deviations. A measure of variability based on *squared deviations* has a number of useful properties in *inferential statistics* and *statistical modeling*.³
- If we do that, we obtain a measure is called the **variance**, which for a specific set of observations X is written s_X^2 . It is the most wide-spread measure of variability because it is a key concept in *inferential statistics*.

³I will very briefly mention the one that I think is coolest, for a very particular definition of “cool”, that is. Variances are *additive*. Here's what that means: suppose I have two variables X and Y , whose variances are $\text{Var}(X)$ and $\text{Var}(Y)$ respectively. Now imagine I want to define a new variable Z that is the sum of the two, $Z = X + Y$. As it turns out, the variance of Z is equal to $\text{Var}(X) + \text{Var}(Y)$. This is a *very* useful property, but it's not true of the other measures that I talk about in this section.

Table 6.1: Regular, absolute, and squared deviations

Notation [English]	x_i [animal]	X_i [value]	$X_i - \bar{X}$ [deviation from mean]	$(X_i - \bar{X})^2$
	1	12	-0.4	0.16
	2	17	4.6	21.16
	3	14	1.6	2.56
	4	15	2.6	6.76
	5	4	-8.4	70.56

- The formula that we use to calculate the variance of a set of observations is as follows:

$$s_X^2 = \frac{1}{N-1} \sum_{i=1}^N (X_i - \bar{X})^2$$

- As you can see, it's basically the same formula that we used to calculate the mean absolute deviation, except that:
 1. Instead of using “absolute deviations” we use “squared deviations”.
 2. Instead of dividing by N (which gives us the average deviation), we divide by $N - 1$ (which gives us ‘*sort-of-the-average*'). [We will talk about this in a little while.]
- Now that we've got the basic idea, let's have a look at a concrete example. Once again, let's use the first five sleep durations. If we follow the same approach that we took last time, we end up with the following table:
- That last column contains all of our squared deviations, so all we have to do is average them. If we do that by typing all the numbers into R by hand...

```
( 0.16+21.16+2.56+6.76+70.56 ) / (5-1)
```

```
## [1] 25.3
```

- We end up with a variance of 25.3. Exciting, isn't it? For the moment, let's ignore the burning question that you're all probably thinking (i.e., what the heck does a variance of 25.3 actually mean?) and instead talk a bit more about how to do the calculations in R.
- As always, we want to avoid having to type in a whole lot of numbers ourselves. And as it happens, we have the vector `X` lying around, which we created in the previous section. With this in mind, we can calculate the variance of `X` by using the following command,

```
X <- mammalian_sleep$sleep_total_h[1:5]
(X - mean(X) )^2 / (length(X) - 1)
```

```
## [1] 0.04 5.29 0.64 1.69 17.64
```

and as usual we get the same answer as the one that we got when we did everything by hand. However, I *still* think that this is too much typing. Fortunately, R has a built in function called `var()` which does calculate variances. So we could also do this...

```
var(X)
```

```
## [1] 25.3
```

and you get the same answer. Great.

6.3.6 Standard deviation

- One problem with the variance is that it is expressed in odd units. In the case above it's h^2 (*hours squared*). I know what m^2 is, but what are h^2 ? No idea.
- Suppose that you'd like to have a measure that is expressed in the same units as the data itself (i.e., points, not points-squared). What should you do?
- The solution to the problem is obvious: take the square root of the variance, known as the ***standard deviation***, also called the “root mean squared deviation”, or RMSD. This solves out problem fairly neatly.
- While nobody has a clue what “*a variance of 19.95 hours-squared*” really means, it's much easier to understand “*a standard deviation of 4.5 hours*”, since it's expressed in the original units.
- It is traditional to refer to the standard deviation of a sample of data as s_x , though “sd” and “std dev.” are also used at times. Because the standard deviation is equal to the square root of the variance, you probably won't be surprised to see that the formula is:

$$s_x = \sqrt{\frac{1}{N-1} \sum_{i=1}^N (X_i - \bar{X})^2}$$

- Interpreting standard deviations is slightly more complex. Because the standard deviation is derived from the variance, and the variance is a quantity that has little to no meaning that makes sense to us humans, the standard deviation doesn't have a simple interpretation.

- As a consequence, most of us just rely on a **simple rule of thumb**: “in general, you should expect 68% of the data to fall within 1 standard deviation of the mean, 95% of the data to fall within 2 standard deviation of the mean, and 99.7% of the data to fall within 3 standard deviations of the mean”. This rule tends to work pretty well most of the time, but it’s not exact: it’s actually calculated based on an *assumption* that the histogram is symmetric and “bell shaped”. (Strictly, the assumption is that the data are *normally* distributed, which is an important concept that we’ll discuss more later).

```
p <- mammalian_sleep %>%
  ggplot(aes(sleep_total_h)) +
  geom_histogram(binwidth = 1,
                 color = "black",
                 fill = "lightgrey")

sleep_sd <- sd(mammalian_sleep$sleep_total_h)
sleep_mean <- mean(mammalian_sleep$sleep_total_h)
bars <- c(sleep_mean-sleep_sd, sleep_mean, sleep_mean+sleep_sd)
bar_labels <- c("mean-1*sd", "mean", "mean+1*sd")
p <- p + geom_vline(xintercept = bars, color = "red") +
  geom_label(data=NULL, aes(x=bars[1], y= 10, label = bar_labels[1])) +
  geom_label(data=NULL, aes(x=bars[2], y= 10, label = bar_labels[2])) +
  geom_label(data=NULL, aes(x=bars[3], y= 10, label = bar_labels[3]))
p
```

```
with(mammalian_sleep, mean(sleep_total_h>(sleep_mean-sleep_sd) & sleep_total_h<(sleep_mean+sleep_sd)))
```

```
## [1] 0.6385542
```

6.3.6.1 Bessel’s correction: What’s up with all those $N - 1$ s in the denominator?

- Now, what’s going on with that $N - 1$, and why do I still call the sample variance a ‘*sort-of-the-average*’ of the squared deviations? Let’s address these questions in turn.
- The important thing to note about variance and standard deviation is they serve *two* purposes: They are used to (i) describe a **sample**, but also to (ii) tentatively characterize the larger population from which the sample is.
- You are *usually* not really interested in the variance of a particular set of numbers, but rather in what they represent. So function number (ii) is the far more dominant use.

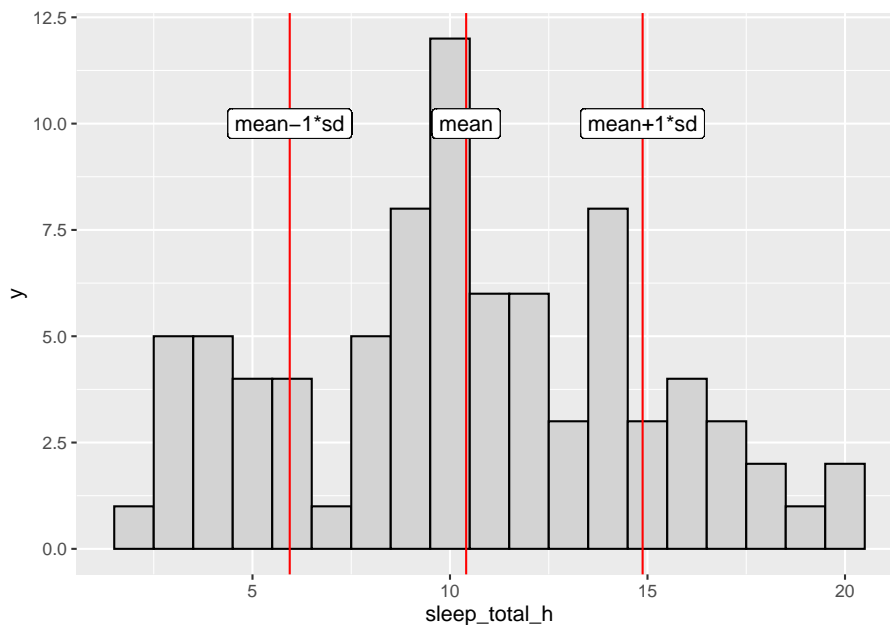


Figure 6.9: An illustration of the standard deviation.

- In our case, when I want to quantify the variability of the sleep durations dataset, it is not these 83 specific mammals I am interested in – I want to get a sense of the variability among mammals in general. That is, I want to know – how much do mammals vary *in general*. These just happen to be a **sample** (83 mammals) from the **population** (all mammals).
- What I actually want to compute are not the (squared) deviations from the **sample mean** (\bar{X} ; the average sleep duration of **these** mammals), but from the actual **population mean** (μ ; the average sleep duration of **all** mammals). That is, I don't want $(X_i - \bar{X})^2$, I want $(X_i - \mu)^2$.
- But I don't know μ , and the *best guess* I have about it is \bar{X} . And this has consequences: $(X_i - \bar{X})^2$ underestimates the distance between X_i and μ because we use the same data points (X_i) to compute the mean (\bar{X}) and then determine the distance to them.
- The problem becomes smaller as N increases, because it becomes less and less likely that all N points are squarely on one side of the mean.
- Dividing by $N - 1$ 'corrects' this underestimation problem:
 - Dividing by a smaller number makes the estimate of the variance bigger.

- As N increases the difference between dividing by N and $N - 1$ becomes less and less important, and ultimately negligible.

6.3.6.1.1 Summary

- To recap, these are the two estimators of the variance, but the second one requires knowledge of the true population mean μ , which we don't know.
- Therefore, we use the first one (s_X^2), and divide by $N - 1$ to avoid underestimating the 'true variance'.

$$s_X^2 = \frac{1}{N-1} \sum_{i=1}^N (X_i - \bar{X})^2$$

$$\text{Var}_X = \frac{1}{N} \sum_{i=1}^N (X_i - \mu)^2$$

6.3.7 Which measure to use?

We've discussed quite a few measures of spread (range, IQR, variance and standard deviation). Below is a quick summary. In short, the IQR and the standard deviation are easily the two most common measures used to report the variability of the data.

- *Range.* Gives you the full spread of the data. It's very vulnerable to outliers, and as a consequence it isn't often used unless you have good reasons to care about the extremes in the data.
- *Interquartile range.* Tells you where the "middle half" of the data sits. It's pretty robust, and complements the median nicely. This is used a lot.
- *Variance.* Tells you the average squared deviation from the mean. It's mathematically elegant, and is probably the "right" way to describe variation around the mean, but it's completely uninterpretable because it doesn't use the same units as the data. Almost never used except as a mathematical tool; but it's buried "under the hood" of a very large number of statistical tools.
- *Standard deviation.* This is the square root of the variance. It's fairly elegant mathematically, and it's expressed in the same units as the data so it can be interpreted pretty well. In situations where the mean is the measure of central tendency, this is the default. This is by far the most popular measure of variation.

6.4 Getting an overall summary of a variable

- It's kind of annoying to have to separately calculate means, medians, standard deviations, etc. Wouldn't it be nice if R had some helpful functions that would do all these tedious calculations at once? Something like `summary()`, perhaps?
- The basic idea behind the `summary()` function is that it prints out some useful information about whatever object it receives (e.g., a vector or data frame).
- Let's take a look at some examples:

6.4.1 Summarising a vector

6.4.1.1 Numerical vectors

- For numeric variables, we get a whole bunch of useful descriptive statistics. It gives us the minimum and maximum values (and thus the range), the first and third quartiles (25th and 75th percentiles; and thus the IQR), the mean and the median.
- In sum, it gives us a pretty good collection of descriptive statistics related to the central tendency and the spread of the data.

```
summary( mammalian_sleep$sleep_total_h )
```

```
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##      2.00    8.00   10.00   10.41   14.00   20.00
```

6.4.1.2 Logical vectors

- Returns the number of TRUE and FALSE values.

```
summary( mammalian_sleep$sleep_total_h > 10 )
```

```
##      Mode  FALSE  TRUE
## logical     45    38
```

6.4.1.3 Factors vectors

- Returns the number of observations for each factor level.


```
summary( as.factor(mammalian_sleep$name[1:10]) )
```

```
##           Cheetah           Cow
##           1           1
##           Dog Greater short-tailed shrew
##           1           1
##           Mountain beaver           Northern fur seal
##           1           1
##           Owl monkey           Roe deer
##           1           1
##           Three-toed sloth           Vesper mouse
##           1           1
```

6.4.1.4 Character vectors

- Returns almost no useful information except for length.

```
summary( mammalian_sleep$name )
```

```
##      Length      Class      Mode
##      83 character character
```

6.4.2 Summarising a data frame

- `summary()` can also be called on a data frame, in which case it returns summaries of all variables.

```
summary( mammalian_sleep )
```

```
##      name      sleep_total_h      bodywt_kg
## Length:83      Min.   : 2.00      Min.   : 0.005
## Class :character 1st Qu.: 8.00      1st Qu.: 0.174
## Mode  :character Median :10.00      Median : 1.670
##              Mean  :10.41      Mean  : 166.136
##              3rd Qu.:14.00      3rd Qu.: 41.750
##              Max.  :20.00      Max.  :6654.000
```

6.5 Correlations

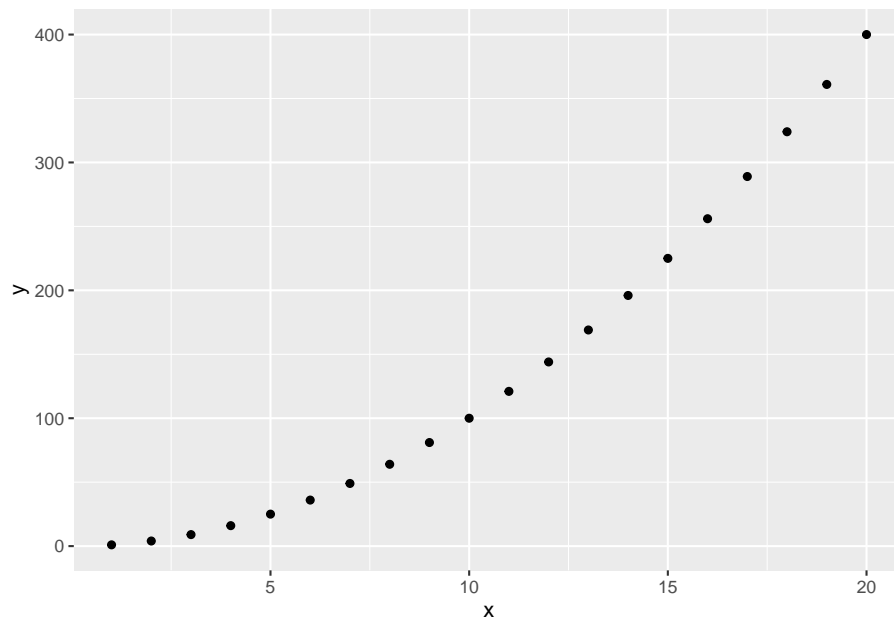
The descriptive statistics we discussed so far were all about a single variable. Sometimes, we want to describe the relation between two variables. For this we

need to calculate **correlations**. Correlations range between -1 and 1. 0 means no correlation, 1 means strong positive correlation and -1 means strong negative correlation. Correlation is indicated by the letter **r**.

In R, we can calculate the correlations of two variables using the `cor()` function. Consider the following example.

```
x <- 1:20
y <- (x^2)

ggplot(data=NULL, aes(x = x, y=y)) +
  geom_point()
```



```
cor(x,y)
```

```
## [1] 0.9713482
```

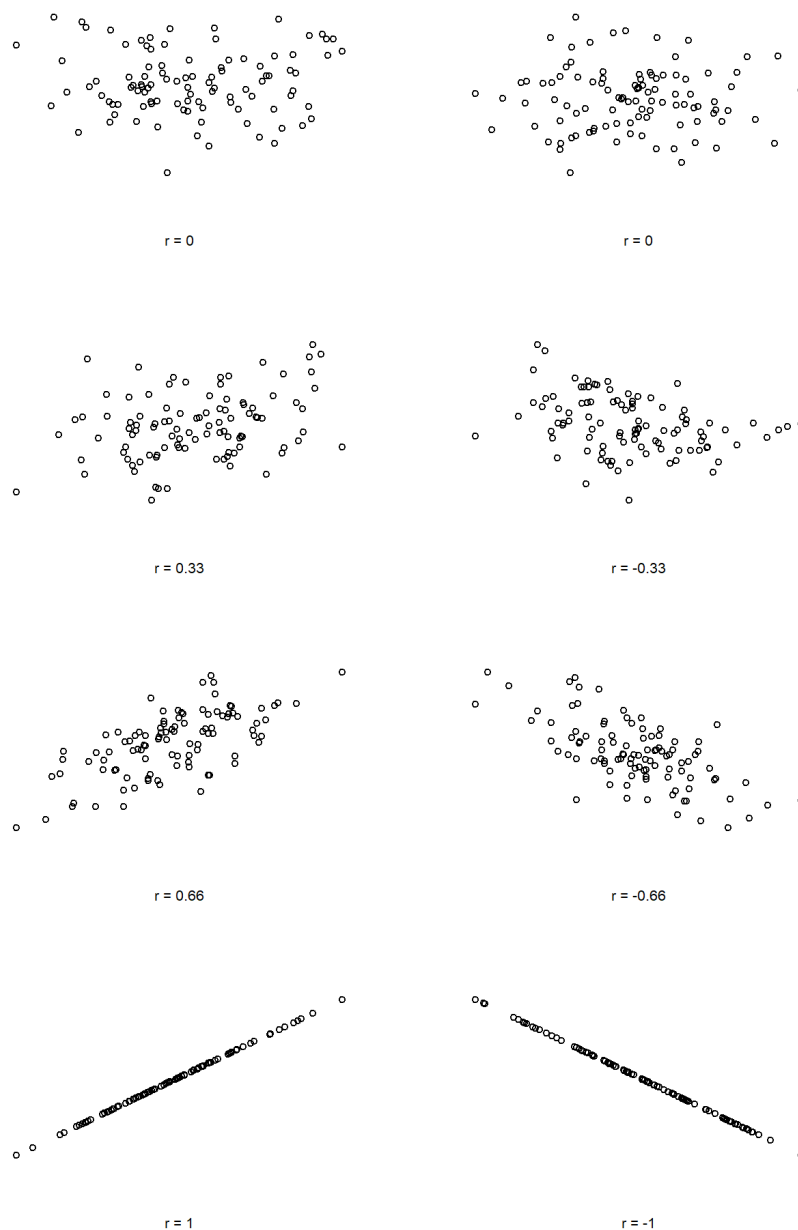


Figure 6.10: Different correlations.

Chapter 7

Linear Regression with one Predictor

In the previous section, we looked at some descriptive statistics about data. In all of these cases, we looked at the descriptive statistics of a **single variable**. For example, we looked at the mean and standard deviation of total sleep hours for various animals. The variable we considered was `total_sleep_hours`. This is also called **univariate statistics** because we were interested in the statistics of a **single variable**.

Now, we are moving onto **bivariate statistics**. In other words, we will analyze the relationship between two variables. Instead of calculating the **mean** of a single variable, we will calculate the **conditional mean** of a variable based on some other variable. For example, we could try calculating the relationship between `total_sleep_hours` and `bodyweight`.

7.1 Word Frequency Effects

Instead of looking at animal sleep hours, this time let's look at something more relevant for linguistics. Earlier, we discussed the role of frequency in processing.

- Our hypothesis was that more frequent words will be processed more easily.
- We operationalized this hypothesis by picking
 - **word frequency** as our **independent variable** (also called a **predictor**)
 - **reaction time** as our **dependent variable** (also called **response** or **outcome variable**)

The typical dataset we will be working with has a structure similar to the one below:

dependent var.(Y)	predictor		
	1(X_1)	predictor 2(X_2)	(other predictors)
705	1.2	2.2	(...)
209	8.3	-4.0	(...)
334	7.2	-1.4	(...)
...	(...)

- What the variables represent will depend on the problem you're studying and the question you're asking
 - dependent variable (e.g., reaction time)
 - predictor 1 (e.g., frequency)
 - predictor 2 (e.g., familiarity)

Let us take a look at a linear regression model where x = frequency and y =response time.

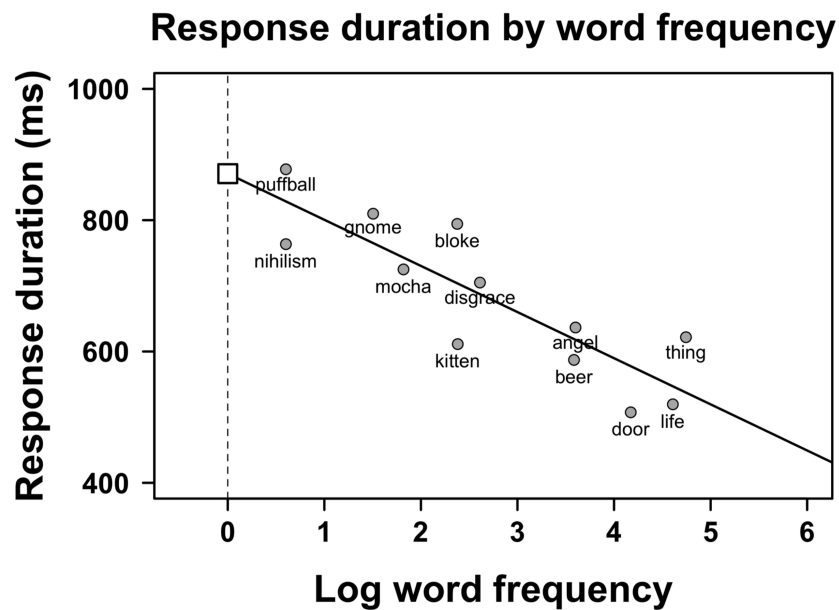


Figure 7.1: Response duration as a function of word frequency. The frequencies are not raw frequencies. Instead, log frequencies are used. We'll talk more about this.

- Each point on the plot above indicates the average response time of multiple participants.
- The somewhat diagonal line is called the **regression line**.

7.2 Simple Linear Regression

In simple regression, our goal is to find the **regression line** as IT IS our model. The line extends to infinity and makes predictions about every point on its path. For example, our **model** can make a prediction about the reaction time if I were to find a word that has the log frequency 7. It would tell me that the reaction time would be a little below 400 milliseconds.

An important point regarding simple linear regression is that it can be used for data where the dependent variable is **continuous** (e.g. 436 milliseconds) but not **categorical** (e.g. grammatical/ungrammatical).

7.3 Finding the Regression Line

In simple linear regression, the value for a **dependent variable** is a **linear function of the predictor variable**. A linear function looks like the following.

$$y = a + b * x$$

Let us try to understand these values a bit.

$$\underbrace{Y}_{\text{dependent variable}} = \underbrace{\overbrace{a}^{\text{additive term}}}_{\text{intercept}} + \underbrace{\overbrace{b * X}^{\text{additive term}}}_{\substack{\text{slope} \quad \text{predictor}}}$$

Mathematically, a line is defined in terms of an **intercept** and **slope**.

- **Slope** can be defined as the amount of change in y as x changes one unit.

$$slope = \frac{\Delta y}{\Delta x}$$

- A rising slope will have a positive value whereas a descending slope will have a negative value.
- For example, the slope in the Response Duration Model above is -70. This means that for each unit of increase in frequency, we observe a 70ms decrease in reaction time.

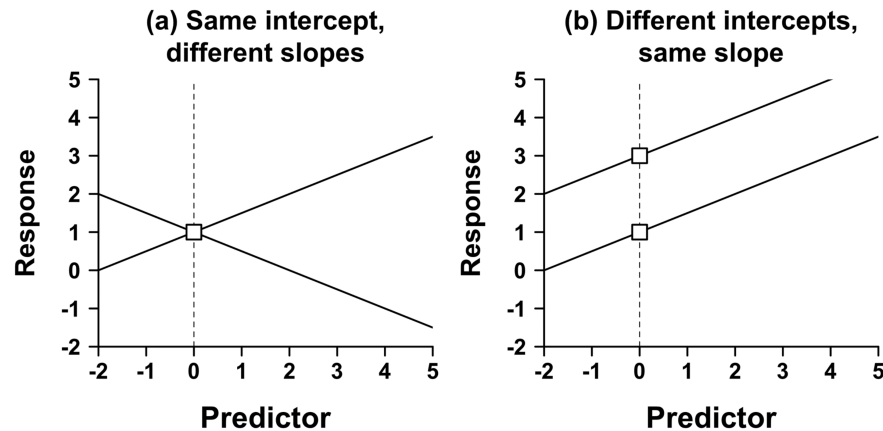


Figure 7.2: Lines with different intercept and slope values.

A slope is not enough to define a line on a plot. There can be an infinite number of lines that have the same slope. We also need the **intercept**. Intercept determines the value predicted for y when x is 0. Consider the following graphs.

The intercept for the data Response Duration Model above is 880ms. So, our Response Duration Model is:

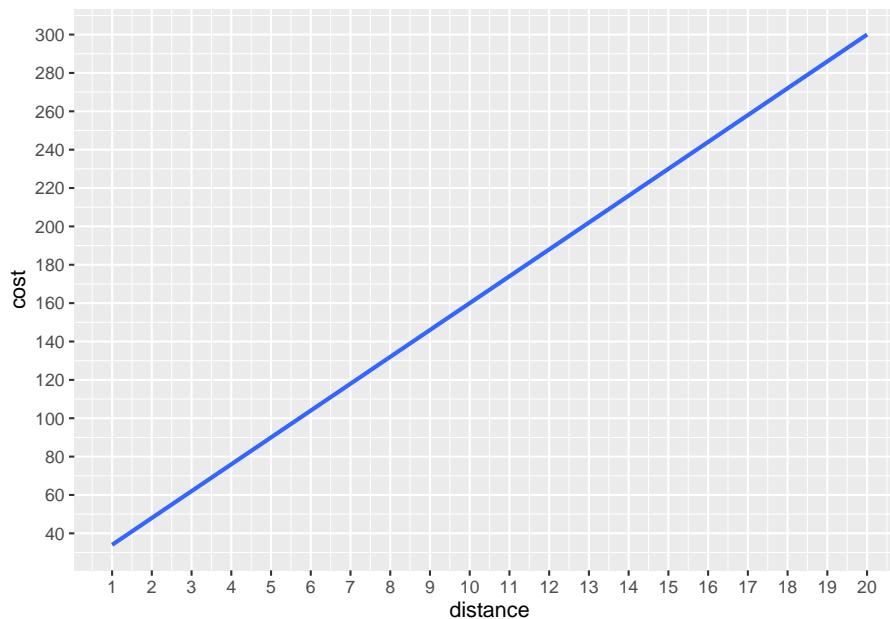
$$\text{response duration} = 880\text{ms} + \left(-70 \frac{\text{ms}}{\text{freq}}\right) * \text{word frequency}$$

A good way to remember the intercept and the slope and a linear model is to remember the **taxi fares**. The taxi fares will usually start with a constant fee (a minimum fee). This is your intercept. It's the 0th kilometers and it already costs you 7 TLs. Then the cost for each kilometer is your slope. At the time of writing these notes, it is 6TLs.

```
library(ggplot2)

distance = 1:20
cost = 20+(14*distance)

ggplot(data=NULL, aes(distance,cost)) +
  scale_x_continuous(breaks = seq(0, 20, by =1)) +
  scale_y_continuous(breaks = seq(0, 500, by = 20)) +
  geom_smooth(method="lm", formula =y~x + I(20+14*x))
```

Slope and **intercept** are the **coefficients** of our linear regression model. Our task is to find the **coefficients** from the data.

7.4 Estimating the Coefficients

A Linear Regression analysis of a particular data is essentially all about **estimating coefficients** and **interpreting the results**. In the **taxi model**, we already knew the coefficients. So, we had a model about the world and we can use the model to make predictions about taxi costs. In the Response Duration Model, the coefficients were learnt from the data but I gave them to you directly. So, how are we going to estimate the coefficients when what we have is just data but nothing else?

Let's not get into the weeds of how to find the right linear regression model. Instead, let's just use R to estimate the coefficients. This is called **fitting a model**. So, let's fit a linear model on the taxi model and interpret its results. We'll start with the taxi model simply because we already know the coefficients. We'll let R estimate some coefficients for us and then compare them with the coefficients we used to generate the **cost** data above from the **distance** variables and our coefficients.

The simplest way to fit a linear model on some data is the **lm()** function. **lm()** takes two variables **x** (predictor) and **y** (dependent variable) and fits a model by modeling **y** as a linear function of **x**. The tilde **~** means: element on the left as a function of element on the right.

For our taxi model, we will model cost as a function of duration. The following lines of code does that.

```
# fit a linear regression model of cost as a function of distance
taxi_model <- lm(cost ~ distance)

# print the model coefficients
taxi_model
```

```
##
## Call:
## lm(formula = cost ~ distance)
##
## Coefficients:
## (Intercept)      distance
##           20           14
```

Unbelievable! The model estimated the intercept (start cost) as 20 and the slope (cost per km) as 14. Simple as that. Notice that the model estimated these coefficients simply from the data but nothing else.

The model object that we stored in the variable `taxi_model` has a lot more information. Let us take a look at the results of our model. To do this, we'll take use the `glance()` function from the `broom` package.

```
library(broom)
library(tidyverse)
glance(taxi_model)
```

```
## Warning in summary.lm(x): essentially perfect fit: summary may be unreliable
## Warning in summary.lm(x): essentially perfect fit: summary may be unreliable

## # A tibble: 1 x 12
##   r.squared adj.r.squared  sigma statistic  p.value    df logLik    AIC
##   <dbl>      <dbl>      <dbl>    <dbl>    <dbl> <dbl> <dbl> <dbl>
## 1         1          1          1 2.58e-14  1.96e32 8.70e-281    1  598. -1191.
## # i 4 more variables: BIC <dbl>, deviance <dbl>, df.residual <int>, nobs <int>
```

There are a lot of details. For now, we'll focus on only two values **R²** and the **p value**.

```
results <- glance(taxi_model) %>%
  select(r.squared, p.value)
```

```
## Warning in summary.lm(x): essentially perfect fit: summary may be unreliable
```

```
## Warning in summary.lm(x): essentially perfect fit: summary may be unreliable
```

```
results
```

```
## # A tibble: 1 x 2
##   r.squared  p.value
##     <dbl>    <dbl>
## 1         1 8.70e-281
```

Without going into any detail yet, I can tell you that we got an excellent model. Our **R²** is 1, which is perfect and our p value is very small **1.51e-287** (This means that there are 286 zeroes after 0. and before 151. So, a very small number). When the p value is so small, we can conclude that the relation between distance and cost is **statistically significant** (i.e. not random).

7.5 Data is messy

In the taxi model above, we worked with a very simplistic and ideal dataset. We know that in theory that is what a tax fare should look like. However, İstanbul is a crowded city and there are lots of traffic jams and traffic is quite unpredictable as there are so many random variables. Since the taxi charges you not only for the distance but also the duration you wait at the lights, there is always going to be some random addition to the fare. Let us incorporate that randomness to our taxi cost data and rerun our model to see what it looks like.

All we are going to do is to add some random values to our taxi prices. Let's generate some random numbers and bind it to a new cost variable.

```
set.seed(42)
hidden_cost <- rnorm(20, mean=7.5, sd=4.5)
total_cost <- cost + hidden_cost
```

Let us plot the theoretical costs and the total costs side by side. We'll use the `gridExtra` package to plot two plots side by side.

```
library(gridExtra)
```

```
##
## Attaching package: 'gridExtra'
```

```
## The following object is masked from 'package:dplyr':
```

```
##
```

```
##      combine
```

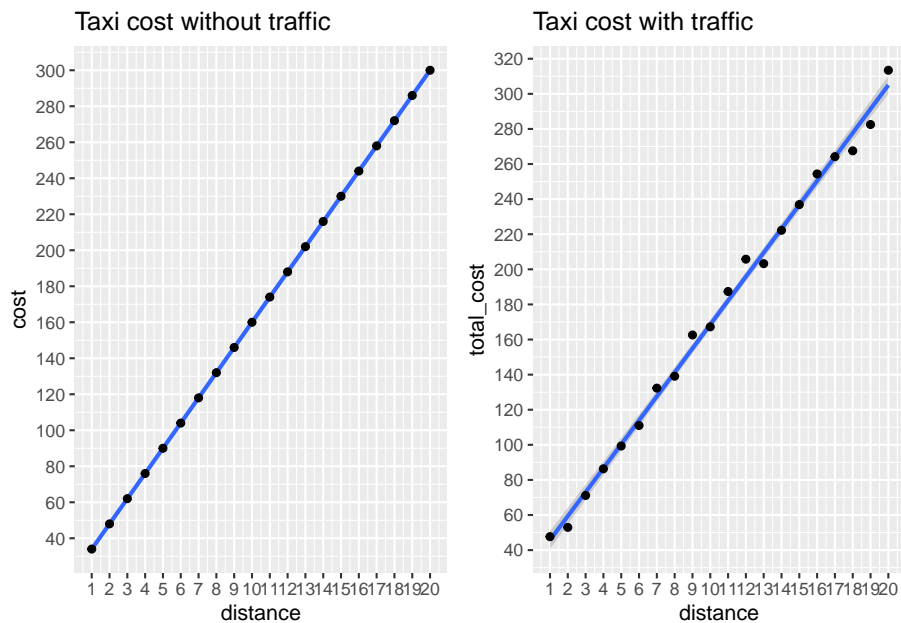
```
plot1 <- ggplot(data=NULL, aes(distance, cost)) +
  scale_x_continuous(breaks = seq(0, 20, by = 1)) +
  scale_y_continuous(breaks = seq(0, 500, by = 20)) +
  geom_smooth(method="lm") +
  geom_point() +
  ggtitle("Taxi cost without traffic")

plot2 <- ggplot(data=NULL, aes(distance, total_cost)) +
  scale_x_continuous(breaks = seq(0, 20, by = 1)) +
  scale_y_continuous(breaks = seq(0, 500, by = 20)) +
  geom_smooth(method="lm") +
  geom_point() +
  ggtitle("Taxi cost with traffic")

grid.arrange(plot1, plot2, ncol=2)
```

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

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



OK, now it looks like we have some more realistic data. Let us rerun our linear model to see what the coefficients look like.

```
better_taxi_model <- lm(total_cost~distance)

better_taxi_model
```

```
##
## Call:
## lm(formula = total_cost ~ distance)
##
## Coefficients:
## (Intercept)      distance
##      32.08         13.65
```

Notice that we got a new intercept and slope. It's kinda weird. We know that the taxi start fare is 20TL. However, our intercept is a lot higher (this will differ as each time you run your code as the traffic cost we calculated is random unless you set some seed number to generate the random values). This is quite off given our original intercept.

Notice that the slope is a little off too. It's not exactly 14 but it's not way off like the intercept. So, did our linear model do well? Before answering this question more formally, I'll draw your attention to one point. Our model predicts that your initial taxi fare will be a little higher at the beginning and it will sort of even out as your distance increases. Even though our model doesn't guess the intercept correctly, it still does a very decent job in modeling the real life taxi costs (or a simulation of it). Just add up the intercept and slope and that should give you around the minimum cost you'll pay for a taxi ride.

```
coef(better_taxi_model)[1] + coef(better_taxi_model)[2]

## (Intercept)
##      45.72571
```

At this point, I want to remind you that taxi rides in İstanbul have a minimum of 70 TLs for short distance trips (2km or less). So, our model does pretty good for a real life scenario.

7.6 Simplified Frequency Data

Let us use a simple frequency data. Go ahead and download the `log10ELP_frequency.csv` file from Moodle. This is the same data in

Bodo Winter's ELP_frequency.csv file with an added column for log10 normalization. We will plot the data using a scatterplot with `geom_point` and also draw a regression line.

We will use log normal values as the x axis and the reaction time as the y axis.

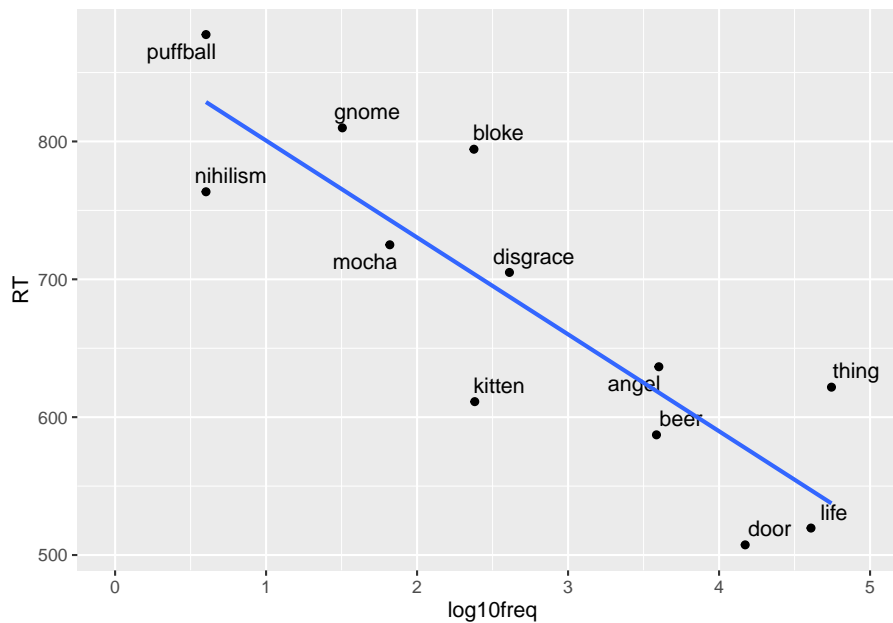
```
library(ggrepel)

freq_data <- read_csv("/Users/umit/ling_411/data/log10ELP_frequency.csv")

## Rows: 12 Columns: 4
## -- Column specification -----
## Delimiter: ","
## chr (1): Word
## dbl (3): RT, Freq, log10freq
##
## i Use `spec()` to retrieve the full column specification for this data.
## i Specify the column types or set `show_col_types = FALSE` to quiet this message.

ggplot(freq_data, aes(x=log10freq, y=RT)) +
  scale_x_continuous(limits = c(0,5)) +
  geom_text_repel(aes(label = Word)) +
  geom_point() +
  geom_smooth(method="lm", se=F)

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



```
freq_model <- lm(freq_data$RT ~ freq_data$log10freq)
```

OK, let us also get a glance at our model. We'll first take a look at the slope and the intercept and then **R2** and the **p value**.

```
coef(freq_model)
```

```
##      (Intercept) freq_data$log10freq
##      870.90539      -70.27646
```

```
glance(freq_model)
```

```
## # A tibble: 1 x 12
##   r.squared adj.r.squared sigma statistic p.value    df logLik   AIC   BIC
##   <dbl>      <dbl> <dbl>      <dbl>   <dbl> <dbl> <dbl> <dbl> <dbl>
## 1    0.737        0.711  63.3      28.1 0.000348     1  -65.7  137.  139.
## # i 3 more variables: deviance <dbl>, df.residual <int>, nobs <int>
```

7.7 Residuals

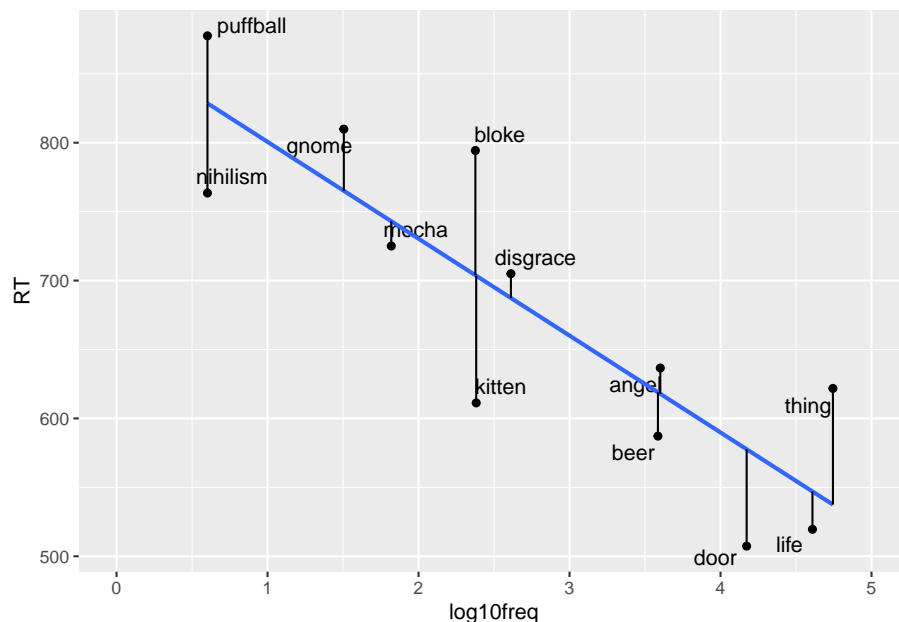
So far, we built and plotted linear models by estimating the intercept and slope of a line that seems to best describe our data. In the simple taxi model, we were

in a perfect position. Our model had a **perfect fit** on our data. However, once we introduced some **random noise** (e.g. random traffic jams) into our data, our linear model still did a decent job but it was not a perfect fit.

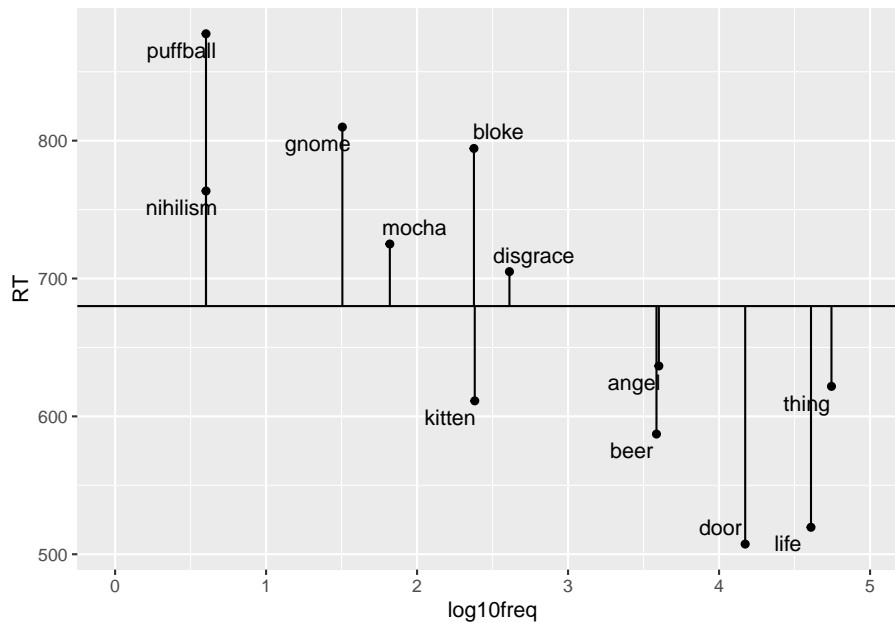
Next, we tried modeling the simple frequency data and we got a decent model that describes the trend in our data but the fit is not perfect. Can we find a way to quantify how good our model fits our data (“goodness of fit”). That’s what we will do here. Let us reconsider the frequency data plot. This time, we’ll draw lines from the data points to the regression line. The distance for each data point is called a **residual**. It describes the amount by which our model missed the actual value.

```
freq_model <- lm(freq_data$RT ~ freq_data$log10freq)
ggplot(freq_data, aes(x=log10freq, y=RT)) +
  scale_x_continuous(limits = c(0,5)) +
  geom_text_repel(aes(label = Word)) +
  geom_point() +
  geom_smooth(method="lm", se=F) +
  geom_segment(aes(x = log10freq, y = RT,
                  xend = log10freq, yend = fitted(freq_model)))
```

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




```
ggplot(freq_data, aes(x=log10freq, y=RT)) +
  scale_x_continuous(limits = c(0,5)) +
  geom_text_repel(aes(label = Word)) +
  geom_point() +
  geom_hline(yintercept = 680) +
  geom_segment(aes(x = log10freq, y = RT,
                  xend = log10freq, yend = 680))
```



Now, we have two models:

- A model where there is a relation between frequency and reaction time
- A null model where there is no relation between frequency and reaction time (reaction time is independent of frequency)

7.7.1 Sum of Squared Errors

One way to describe the errors of the model is to sum the squares of each error value. This is called the Sum of Squared Errors.

To do this, we need to get the residuals of the model, square them and then sum them. Let us do this for the linear model.

```
SSE_freq_model <- sum((residuals(freq_model))^2)
SSE_freq_model
```

```
## [1] 40114.97
```

Let us also calculate it for the null model. The intercept for the null model was 680 I found this value by taking the average reaction time. This will be my null model. The mean was 679.9167. So, we'll deduce the the mean from the actual values to find the residuals. The rest is just the same.

```
null_model_residuals <- freq_data$RT - 680
SSE_null_model <- sum(null_model_residuals^2)
SSE_null_model
```

```
## [1] 152743.3
```

These numbers are very similar to what Bodo Winter reports in his chapter. He might not have done the rounding I did. We use the null model to calculate a **standardized measure of fit**. One measure is **R2** and it is calculated as follows.

$$R^2 = 1 - \frac{SSE_{model}}{SSE_{null}}$$

Let's calculate **R2**.

```
r_squared <- 1 - (SSE_freq_model/SSE_null_model)
r_squared
```

```
## [1] 0.73737
```

Excellent! We've calculated **R2** and it is the same as what we found earlier when we took a look at the model report using the **glance()** function.

So, what is this **R2**? When we interpret **R2**, we say “n” amount of the variance in the dependent variable (RT) can be accounted for by incorporating the independent variable (word frequency). In this case, 73% of the variance is due to word frequency. The remaining 27% is due to chance or some other factors we didn't consider.

Chapter 8

Linear Regression with Many Predictors

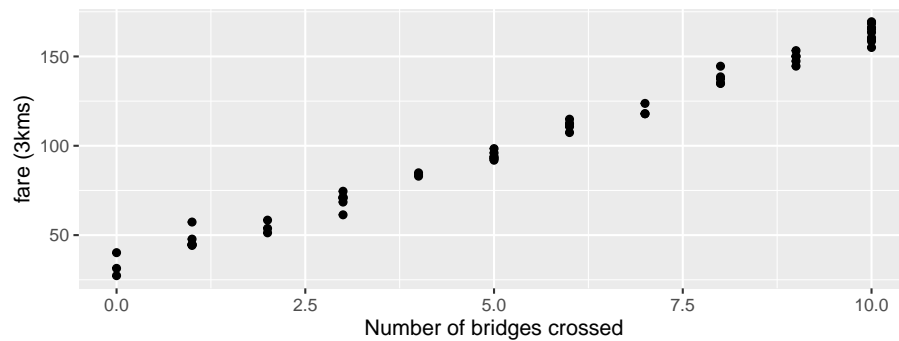
In the previous section, we built linear models with **one predictor**. In other words, we had only one dependent variable and one independent variable.

Model	Dependent Variable	Predictor
Taxi	Cost	Travel Distance
Processing	Reaction Time	Word Frequency

In many real life scenarios, multiple factors will be involved in the outcome of a particular experiments. In other words, a particular dependent variable will be the outcome of more than one independent variable (predictors).

Let us consider our taxi example again. While our taxi model is primarily based on the distance we travel, sometimes we need to cross bridges or toll roads. These factors will obviously increase the cost as they get added to our total cost. The following is a simple example. You can download the data from Moodle or by just clicking this [data link](#).

Let us see if there is any relationship between the number of bridges and the cost when we travel only 3 kilometers.



It looks like there is a decent positive correlation between the fare and the number of bridges crossed. So, we need to find a way to incorporate this into our linear model. The nice thing about linear models is that they allow us to incorporate multiple predictors each with its own slope.

$$\begin{array}{ccccccc}
 \underbrace{Y}_{\text{dependent variable}} & = & \underbrace{a}_{\text{intercept}} & + & \underbrace{b_1 * X_1}_{\substack{\text{slope} \quad \text{predictor}}} & + & \underbrace{b_2 * X_2}_{\substack{\text{slope} \quad \text{predictor}}} + \dots
 \end{array}$$

In R, fitting a linear model with multiple predictors is quite simple. All we have to do is to add the predictors with a + in the `lm()` function as in `lm(dependent variable ~ Predictor 1 + Predictor 2 + ...)`.

```
taxi_model_two_preds <- lm(cab_fares$taxi_fare ~ cab_fares$distance_km + cab_fares$n_bridges)

taxi_model_two_preds
```

```
##
## Call:
## lm(formula = cab_fares$taxi_fare ~ cab_fares$distance_km + cab_fares$n_bridges)
##
## Coefficients:
##          (Intercept)  cab_fares$distance_km  cab_fares$n_bridges
##              14.366              5.991              13.024
```

The model is doing pretty well. The data coefficients I used to generate the data are as follows:

- intercept = 7
- distance slope = 6
- bridge slope = 13

I also added some random noise with the mean=7.5, sd=4.5. Let us also glance at the **R²** and the **p.values** using the summary function. Alternatively, we

could use the `glance()` function from the `broom` package. Give it a shot to see if you observe any differences.

```
summary(taxi_model_two_preds)
```

```
##
## Call:
## lm(formula = cab_fares$taxi_fare ~ cab_fares$distance_km + cab_fares$n_bridges)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -15.0456  -2.9538   0.0829   3.0946  15.9076
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    14.36644    0.42465   33.83  <2e-16 ***
## cab_fares$distance_km  5.99074    0.02746  218.16  <2e-16 ***
## cab_fares$n_bridges   13.02431    0.04447  292.89  <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 4.515 on 997 degrees of freedom
## Multiple R-squared:  0.9923, Adjusted R-squared:  0.9923
## F-statistic: 6.414e+04 on 2 and 997 DF,  p-value: < 2.2e-16
```

```
library(broom)
tidy(taxi_model_two_preds)
```

```
## # A tibble: 3 x 5
##   term                estimate std.error statistic  p.value
##   <chr>              <dbl>     <dbl>     <dbl>    <dbl>
## 1 (Intercept)        14.4       0.425      33.8 1.04e-167
## 2 cab_fares$distance_km  5.99     0.0275     218. 0
## 3 cab_fares$n_bridges   13.0     0.0445     293. 0
```

8.1 Fitting two Linear Models

In the previous section, we fit a linear model with two variables. The **R²** we got was quite high. Let us run two models with one variable and see how the **R²** values change.

```
distance_model <- lm(cab_fares$taxi_fare ~ cab_fares$distance_km)
bridge_model <- lm(cab_fares$taxi_fare ~ cab_fares$n_bridges)
```

```
distance_model
```

```
##
## Call:
## lm(formula = cab_fares$taxi_fare ~ cab_fares$distance_km)
##
## Coefficients:
##           (Intercept)  cab_fares$distance_km
##                85.194                5.656
```

```
bridge_model
```

```
##
## Call:
## lm(formula = cab_fares$taxi_fare ~ cab_fares$n_bridges)
##
## Coefficients:
##           (Intercept)  cab_fares$n_bridges
##                85.99                12.62
```

It looks like the models are still doing pretty well in identifying the slopes. Let us now take a look at their **R²** values.

```
glance(distance_model)$r.squared
```

```
## [1] 0.328751
```

```
glance(bridge_model)$r.squared
```

```
## [1] 0.6241472
```

The results are very interesting. It looks like the number of bridges explains the cost more than the distance. Let us add the two **R²** values to see if they add up to the same value as our multiple regression model did.

```
glance(taxi_model_two_preds)$r.squared
```

```
## [1] 0.9922884
```

```
glance(distance_model)$r.squared + glance(bridge_model)$r.squared
```

```
## [1] 0.9528982
```

Very close. Not too bad. It looks like when both of the predictors are taken into account, we might be able to explain even more variance but the difference is not huge.

What is **kinda weird** is that the bridge costs seem to be more important factor than the distance in this model. Consider the same kind of data except now the distances are longer and the number of bridges are still the same. It looks like the coefficients are still the same but the **R²** values change. This is an important point to stop and think a bit about how your data impacts your results and what kind of conclusions you'll draw from the data. It also shows the importance of the **representativeness** of your data. The key point is to get data that represents a **typical** taxi ride for a particular area (population)**. In most cases, we don't cross that many paid bridges. Nor do we ride such long distances either.

```
distance_model_2 <- lm(cab_fares_2$taxi_fare_2 ~ cab_fares_2$distance_km)
bridge_model_2 <- lm(cab_fares_2$taxi_fare_2 ~ cab_fares_2$n_bridges)
```

```
#Print coefficients
distance_model_2
```

```
##
## Call:
## lm(formula = cab_fares_2$taxi_fare_2 ~ cab_fares_2$distance_km)
##
## Coefficients:
##          (Intercept)  cab_fares_2$distance_km
##              127.33              13.82
```

```
bridge_model_2
```

```
##
## Call:
## lm(formula = cab_fares_2$taxi_fare_2 ~ cab_fares_2$n_bridges)
##
## Coefficients:
##          (Intercept)  cab_fares_2$n_bridges
##              472.26              14.14
```

```
#Print R squared.  
glance(distance_model_2)$r.squared
```

```
## [1] 0.90287
```

```
glance(bridge_model_2)$r.squared
```

```
## [1] 0.06932796
```


Chapter 9

Linear & Non-Linear Transformations

9.1 Linear Transformations

A **linear transformation** of a value is addition, subtraction, multiplication, or division with a constant value. Consider the following data:

- [2, 4, 6, 8]

Each of the number on the right is 2 more than the number on the left. Adding 1 to each of the values is a linear transformation of this data.

- [3, 5, 7, 9]

While the numbers themselves change, the relationship among them does not.

Linear transformations are especially useful in describing data at a level of measurement that is useful to you. For example, the following descriptions are equal and they are linear transformations of each other.

Measured Value	Metric 1	Metric 2
Distance	700m	0.7km
Time	2100ms	2.1s

The crucial point in linear transformations is that they won't change the relationship among your data point and thus won't impact your models significantly. There are many different types of linear transformations. For our purposes we will focus on two linear transformations **centering** and **standardizing**.

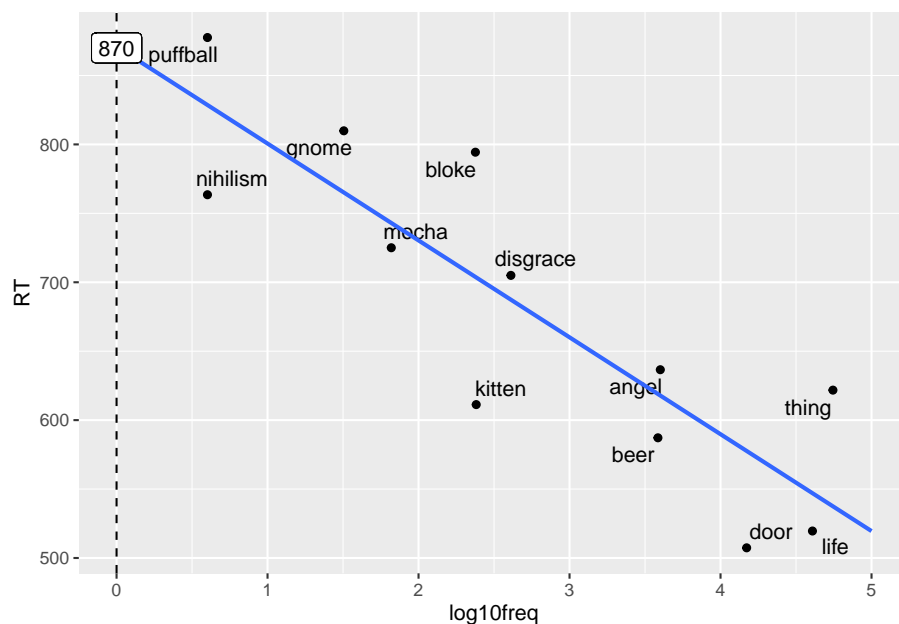
9.1.1 Centering

Let us consider one of our previous examples.

```
library(tidyverse)
library(ggrepel)

freq_data <- read_csv("/Users/umit/ling_411/data/log10ELP_frequency.csv")

ggplot(freq_data, aes(x=log10freq, y=RT)) +
  scale_x_continuous(limits = c(0,5)) +
  geom_text_repel(aes(label = Word)) +
  geom_point()+
  geom_smooth(method="lm",se=F, fullrange=TRUE)+
  geom_vline(xintercept = 0, linetype = "dashed")+
  geom_label(data=NULL, aes(x=0, y= 870, label="870"))
```



Overall, our model does a decent job in showing us that there is a trend in our data. As the frequency of a word increases, reaction time decreases. However, the model also makes some hard to interpret prediction. Our model predicts that when the frequency of a word is 0, RT is expected to be 870. But that's kinda odd. What does it mean for a word to have 0 frequency. If a word has 0 frequency, does it even exist?

At this point, we can step back and ask ourselves a question regarding the **intercept**. When we defined the intercept, we defined it as the value y takes

when x is 0. We mentioned that this was the way to define a line mathematically. But why $x=0$?

Maybe setting the intercept as the value y takes when $x=0$ is mathematically meaningful. We can assume that $x=0$ is the **center** of the positive and negative integers both of which go to infinity. However, our data are usually finite and their center is usually not 0. We have talked about various measures of **central tendency** to identify the center of our data (e.g. mean, median, mode). How about we take the **mean** as the center of our data. In other words, how about we take the mean to be our $x=0$ point? This is called **centering**.

When you **center** your data, your intercept becomes the value y assumes when $x = \text{mean}(x)$. Thus, everything is interpreted relative to the mean. In other words, instead of measuring the distance from the absolute 0, we measure the distance from the mean.

To center a predictor variable, we subtract the mean from each of the predictor variables. Let us center the log frequency data and plot it again.

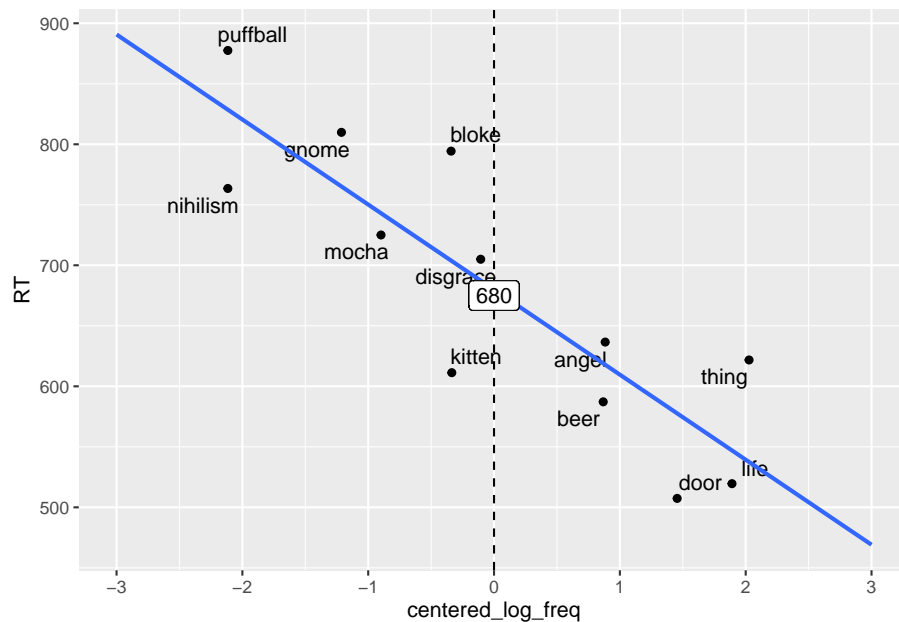
```
centered_freq_data <- mutate(freq_data, centered_log_freq = log10freq - mean(log10freq))
```

```
centered_freq_data
```

```
## # A tibble: 12 x 5
##   Word      RT  Freq log10freq centered_log_freq
##   <chr>   <dbl> <dbl>    <dbl>         <dbl>
## 1 thing    622.  55522    4.74          2.03
## 2 life     520.  40629    4.61          1.89
## 3 door     507.  14895    4.17          1.46
## 4 angel    637.   3992    3.60          0.884
## 5 beer     587.   3850    3.59          0.868
## 6 disgrace  705.    409    2.61         -0.106
## 7 kitten   611.    241    2.38         -0.336
## 8 bloke    794.    238    2.38         -0.341
## 9 mocha    725.     66    1.82         -0.898
## 10 gnome   810.     32    1.51         -1.21
## 11 nihilism 764.      4    0.602        -2.12
## 12 puffball 878.      4    0.602        -2.12
```

We can see that the centered data has smaller values compared to the log frequencies. We also observe that there are negative values. What does a negative value mean? How can the frequency of a word be negative? In this case, the negative value is relative to the mean. Thus, it means that it is less than the mean (but still above 0).

```
ggplot(centered_freq_data, aes(x=centered_log_freq, y=RT)) +
  scale_x_continuous(limits = c(-3,3), n.breaks=6) +
  geom_text_repel(aes(label = Word)) +
  geom_point() +
  geom_smooth(method="lm", se=F, fullrange=TRUE) +
  geom_vline(xintercept = 0, linetype = "dashed") +
  geom_label(data=NULL, aes(x=mean(centered_log_freq), y= 675, label="680"))
```



Let us take a look at the intercept and slope values of the two models as well as their **R²** values to see if centering has any effect on the model and its interpretation.

```
## # A tibble: 2 x 2
##   names          x
##   <chr>         <dbl>
## 1 (Intercept)    871.
## 2 freq_data$log10freq -70.3
```

```
## # A tibble: 2 x 2
##   names          x
##   <chr>         <dbl>
## 1 (Intercept)    680.
## 2 centered_freq_data$centered_log_freq -70.3
```

```
## [1] 0.7373698
```

```
## [1] 0.7373698
```

You can see that both the slope and the **R²** values remain unchanged. This shows that the model is remaining the same in all the crucial aspects except that it's now treating its 0 point as the mean. This is more meaningful for most measurements. In addition, centering helps interpreting the coefficients especially when multiple predictors interact (to be discussed later).

9.1.2 Standardizing

The second type of linear transformation that is very common is **standardizing** a.k.a. **z-scoring**. Standardizing also helps identifying a **standard scale** that helps us define a metric in terms of the sample mean and standard deviation. This is a little counter-intuitive but helps a lot especially when we are interpreting models with multiple predictor variables.

Imagine that you have your taxi data set with the fare and distance variables. One very basic question you have to answer is what metric to use to report the distance. Should you use kilometers, miles, yards, meters, etc. Now, further imagine that you're comparing two data sets with different reported distance measures (e.g. mile vs km). This is actually a relatively simple problem as you can transform miles to kms and vice versa. However, what if you are trying to measure the relative impact of distance and the number of bridges you pass. These are two different variables with two different measurement units. We cannot directly compare kilometers with the number of bridges. They're not on the same scale. Standardizing helps us make such comparisons (sometimes).

To standardize a variable, we divide the centered values by the standard deviation of the (sample) values.

```
centered_freq_data <- mutate(centered_freq_data, z_log_freq = centered_log_freq/sd(log10freq))
```

```
centered_freq_data
```

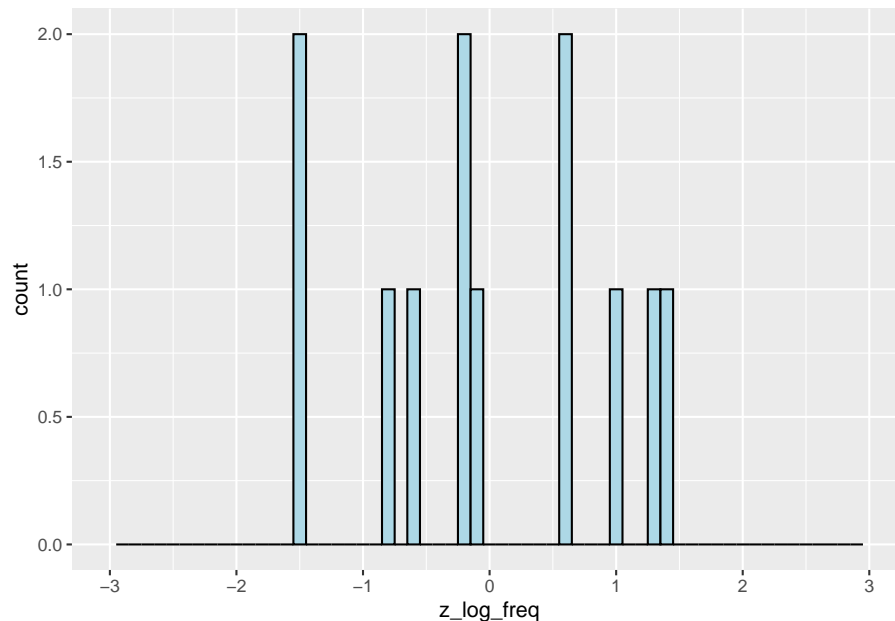
```
## # A tibble: 12 x 6
##   Word      RT  Freq log10freq centered_log_freq z_log_freq
##   <chr>    <dbl> <dbl>    <dbl>          <dbl>        <dbl>
## 1 thing    622.  55522    4.74          2.03         1.41
## 2 life     520.  40629    4.61          1.89         1.31
## 3 door     507.  14895    4.17          1.46         1.01
## 4 angel    637.   3992    3.60          0.884        0.614
## 5 beer     587.   3850    3.59          0.868        0.603
```

##	6	disgrace	705	409	2.61	-0.106	-0.0736
##	7	kitten	611.	241	2.38	-0.336	-0.233
##	8	bloke	794.	238	2.38	-0.341	-0.237
##	9	mocha	725.	66	1.82	-0.898	-0.624
##	10	gnome	810.	32	1.51	-1.21	-0.842
##	11	nihilism	764.	4	0.602	-2.12	-1.47
##	12	puffball	878.	4	0.602	-2.12	-1.47

Let us plot a histogram of z scores to see what they look like.

```
ggplot(centered_freq_data, aes(z_log_freq)) +
  scale_x_continuous(limits = c(-3,3), n.breaks=6) +
  geom_histogram(binwidth=0.1,
                 color = 'black',
                 fill = 'lightblue')
```

Warning: Removed 2 rows containing missing values (`geom_bar()`).



9.2 Scaling and Standardizing in R

In the previous sections, we calculated the centered values and the standardized values by hand. R has a dedicated function `scale()` which does both.

```
library(tidyverse)
cab_fares <- read_csv('data/cab_fares.csv')
cab_fares
```

```
## # A tibble: 1,000 x 3
##   distance_km n_bridges taxi_fare
##   <dbl>      <dbl>    <dbl>
## 1         20         3      180.
## 2         10        10      202.
## 3         15         4      158.
## 4         19         5      196.
## 5         18         1      137.
## 6         16         7      201.
## 7         14         8      209.
## 8         18         8      226.
## 9          5         2       79.6
## 10         9         2       94.2
## # i 990 more rows
```

```
# only centering
cab_fares <- mutate(cab_fares, distance_c = scale(distance_km, scale = FALSE))

# centering and standardizing
cab_fares <- mutate(cab_fares, distance_c_z = scale(distance_km))

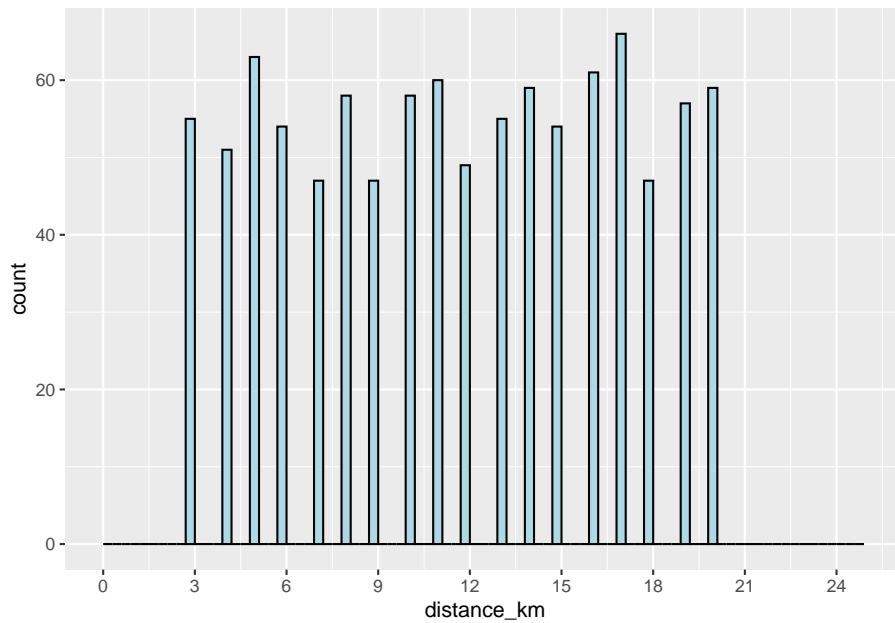
#printing the dataframe
cab_fares
```

```
## # A tibble: 1,000 x 5
##   distance_km n_bridges taxi_fare distance_c[,1] distance_c_z[,1]
##   <dbl>      <dbl>    <dbl>      <dbl>      <dbl>
## 1         20         3      180.         8.39         1.61
## 2         10        10      202.        -1.61        -0.309
## 3         15         4      158.         3.39         0.651
## 4         19         5      196.         7.39         1.42
## 5         18         1      137.         6.39         1.23
## 6         16         7      201.         4.39         0.843
## 7         14         8      209.         2.39         0.459
## 8         18         8      226.         6.39         1.23
## 9          5         2       79.6        -6.61        -1.27
## 10         9         2       94.2        -2.61        -0.501
## # i 990 more rows
```

Let us plot a histogram of the raw, centered and the z_scored data.

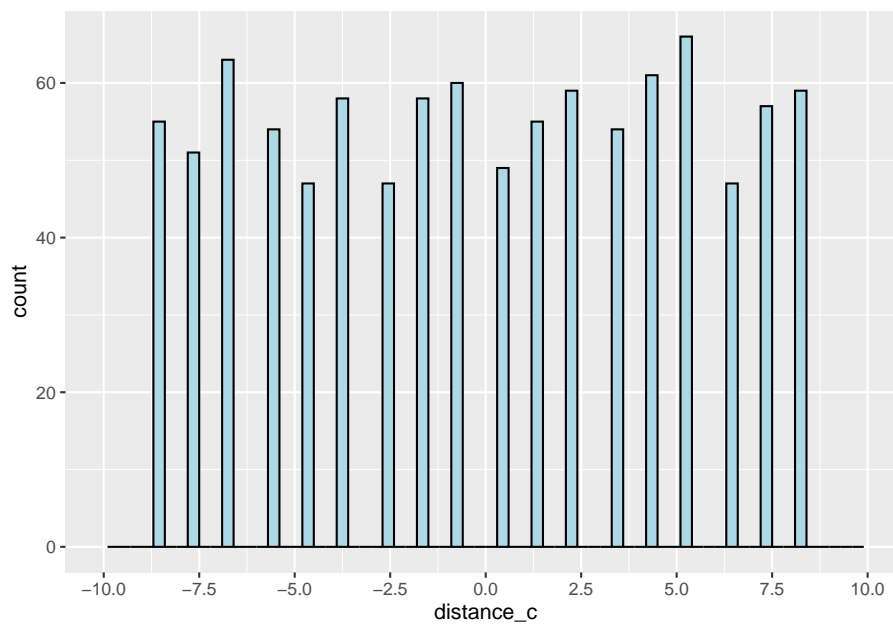
```
library(gridExtra)
ggplot(cab_fares, aes(distance_km)) +
  scale_x_continuous(limits = c(0, 25), n.breaks=10)+
  geom_histogram(binwidth=0.3,boundary=0,
    color = 'black',
    fill = 'lightblue')
```

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

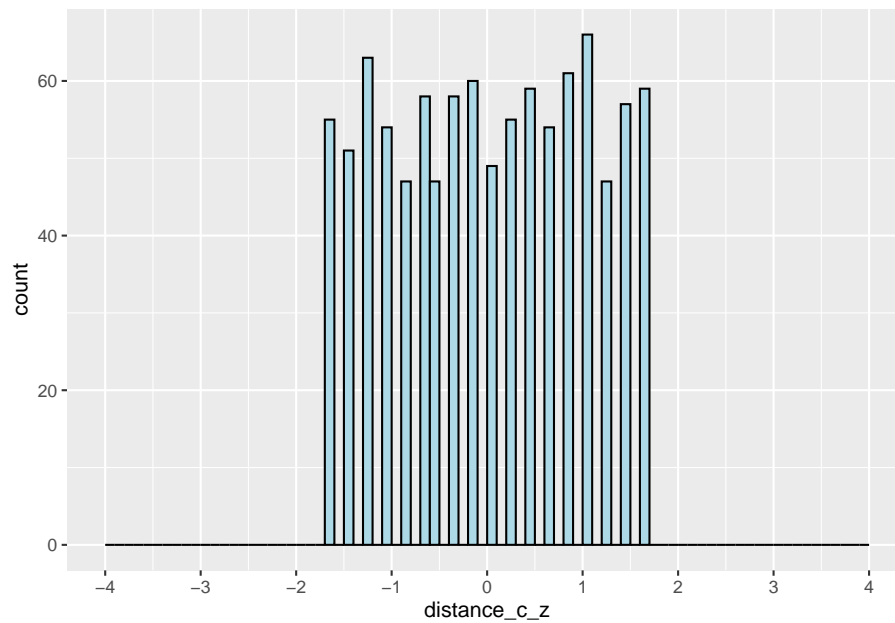


```
ggplot(cab_fares, aes(distance_c)) +
  scale_x_continuous(limits = c(-10, 10), n.breaks=10)+
  geom_histogram(binwidth=0.3,boundary=0,
    color = 'black',
    fill = 'lightblue')
```

```
## Warning: Removed 2 rows containing missing values (`geom_bar()`).
```

```
ggplot(cab_fares, aes(distance_c_z)) +  
  scale_x_continuous(limits = c(-4, 4), n.breaks=10) +  
  geom_histogram(binwidth=0.1, boundary=0,  
                 color = 'black',  
                 fill = 'lightblue')
```



Important A z-score above 3 or below -3 is usually interpreted as an extreme value.

9.3 Non-linear Transformations

9.3.1 Logarithms & Log Transformation

One of the problems we often face in raw data is **skewness**. Technically, skewness is a measure of asymmetry in the data. In practice, it looks like the bulk of the data is rested on one side of a histogram plot with a long tail on the other side. When the tail of the data extends towards a positive value, data is **positively skewed**. When the tail extends towards a negative value, we call it **negatively skewed**.

Many types of data in linguistics have a positive skew. For example, frequency data is highly skewed. Let us take a look at a frequency data for 50K words from Turkish. (I got this data from some corpus but I don't remember where. Apologies for not being able to provide credit.)

```
turkish_freq <- read_csv("data/tr_50k_freq.csv", col_names = c("word", "frequency"))  
  
turkish_freq
```

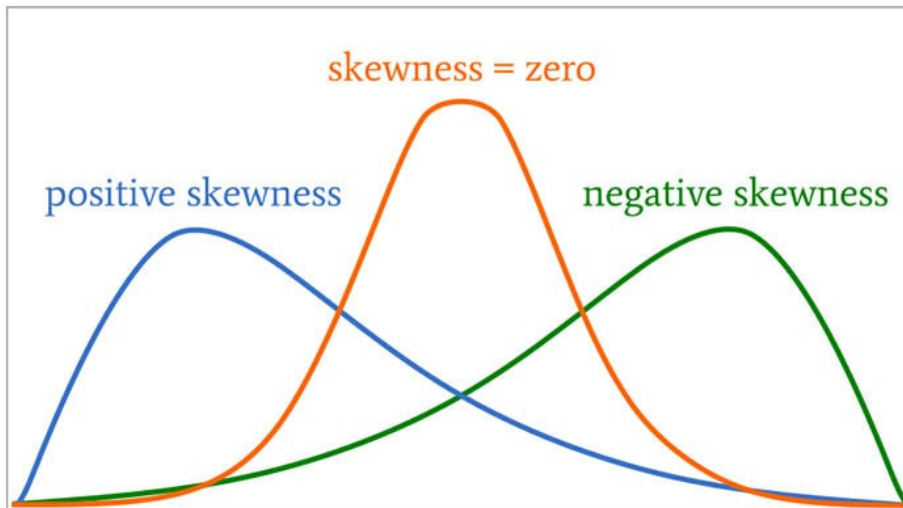


Figure 9.1: Skewness. Image by Robert Keim

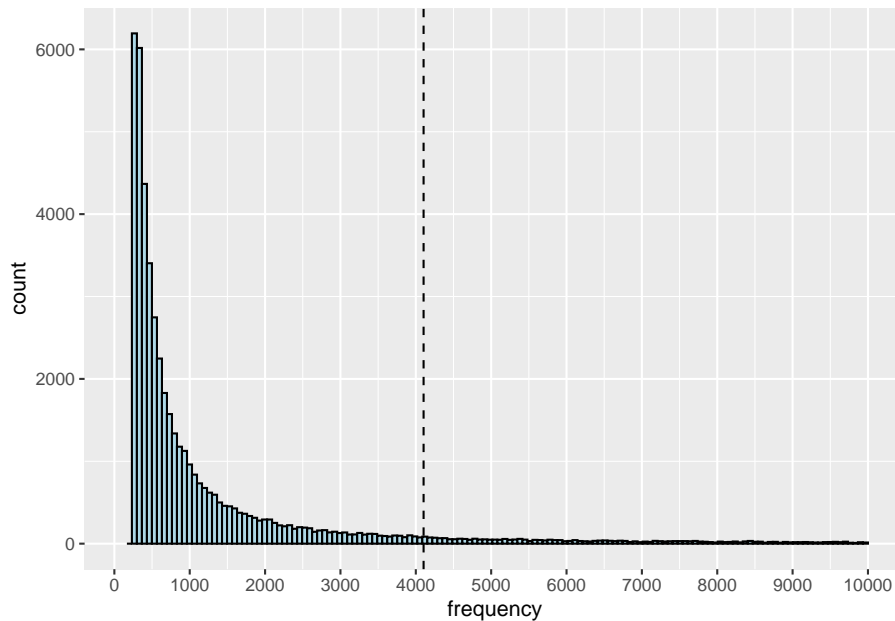
```
## # A tibble: 50,000 x 2
##   word frequency
##   <chr>      <dbl>
## 1 bir      6034903
## 2 bu       3529532
## 3 ne       2550646
## 4 ve       2544175
## 5 için     1795506
## 6 mi       1713472
## 7 de       1647867
## 8 o        1639226
## 9 ben      1597395
## 10 çok     1572658
## # i 49,990 more rows
```

Let us now get a histogram to see what the data distribution looks like.

```
ggplot(turkish_freq, aes(frequency)) +
  scale_x_continuous(limits = c(0, 10000), n.breaks=10) +
  geom_histogram(bins=150,
                 color = 'black',
                 fill = 'lightblue') +
  geom_vline(xintercept = mean(turkish_freq$frequency), linetype="dashed" )
```

```
## Warning: Removed 2288 rows containing non-finite values (`stat_bin()`).
```

```
## Warning: Removed 2 rows containing missing values (`geom_bar()`).
```



It looks like most of the words are quite infrequent and a handful of words are very frequent. In fact, word frequencies are skewed in a very interesting way and they have a special distribution name called **Zipfian** distribution named after George Kingsley Zipf. But we're not interested in that for now.

The important point to notice is where the mean is in this distribution. The mean is shown with the dashed line and it does not in any way reflect the majority of the data. What is more important is that when the data is skewed, its linear modeling will usually result in **residuals that are not normal**. If the residuals are not normal, then the model will lose its validity. It is important that you notice what matters is the **normality of the residuals** not the normality of the data. Non-normal data is still fine for liner models as long as the residuals are normal.

So, what are logarithms and how do they help?

Logarithms are inverses of exponentiation.

Logatihm	Exponentiation
$\log_{10}(1) = 0$	$10^0 = 1$
$\log_{10}(10) = 1$	$10^1 = 10$
$\log_{10}(100) = 2$	$10^2 = 100$
$\log_{10}(1000) = 3$	$10^3 = 1000$

Logatihm	Exponentiation
$\log_{10}(10000) = 4$	$10^4 = 10000$

Transforming the data into a log space has a very interesting normalizing impact on your data. It shrinks your data in a non-linear fashion by reducing smaller numbers less than the big numbers. Consider the following example.

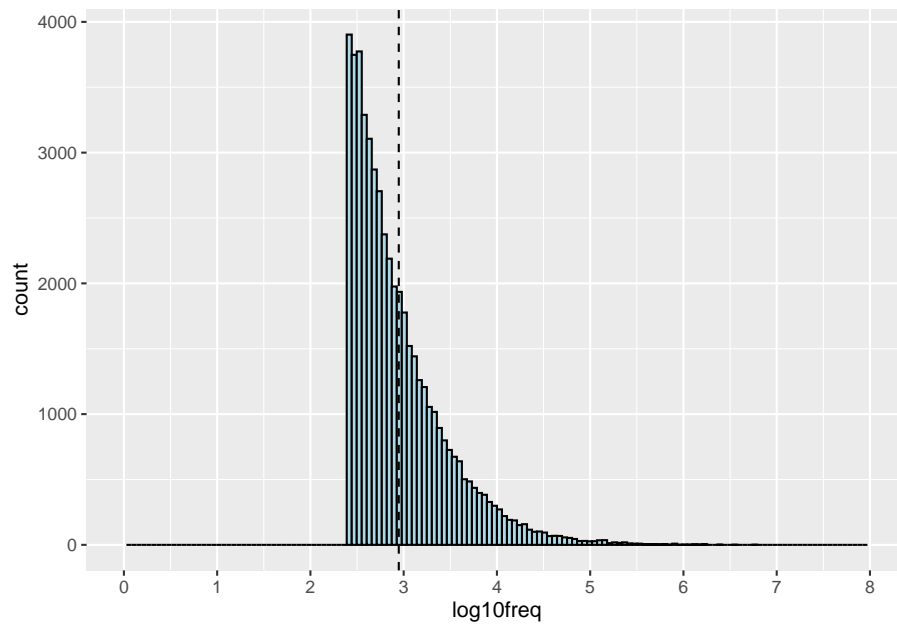
Raw Value	log10 Value	Difference	% Shrunk
10	1	9	90%
100	2	98	98%
1000	3	997	99.7%

Log transformation keeps some of the relation among data points but removes a decent bit of information as well. When we log transform our data, it becomes **more normal** and **less skewed**. It doesn't always become completely normal but it is more normal.

Let us log10 transform the frequency data for Turkish and plot a histogram to see what the data looks like now.

```
# create a new column with the log10 frequency values
turkish_freq <- mutate(turkish_freq, log10freq = log10(frequency))

#plot a histogram of the log10 frequency values
ggplot(turkish_freq, aes(log10freq)) +
  scale_x_continuous(limits = c(0, 8), n.breaks=8)+
  geom_histogram(bins=150,
                 color = 'black',
                 fill = 'lightblue')+
  geom_vline(xintercept = mean(turkish_freq$log10freq), linetype="dashed" )
```



Notice that the data is still skewed but it's not as bad as before and the mean is closer to the bulk of the data.

9.3.2 Linear Regression with Log Transformation

You should run a linear model with and without log transformation to see how the model performs. You can do that by looking at various values.

- SSE
- R²
- p value

You can also fit a linear regression plot against a point plot to see how they differ. Let us do this for the `log10ELP_frequency` data. It's the smaller dataset. You should also consider log10 transforming your dependent variable as well.

Chapter 10

Categorical Predictors

Remember that we talked about four basic types of models in terms of their dependent and independent variable types. Variables can assume **continuous** values (e.g. reaction time, voicing duration, word count, etc.) or **categorical** values (e.g. positive-negative, gender, agreement type, word order (SVO - SOV) etc.).

Predictor Type (independent var.)	Outcome Type (dependent var.)
Continuous	Continuous
Categorical	Continuous
Continuous	Categorical
Categorical	Categorical

So far we built models where both the predictor and the outcome are **continuous**. Now, we are moving to modeling data where the predictors are **categorical** and the outcomes are **continuous**.

10.1 Categorical Predictor - Continuous Outcome

Models with categorical predictors are quite common in linguistics as well as in many fields that rely on data analytics. Here are some examples:

- What are the reaction times of children vs. adults for a picture naming task?

- How does pro-drop impact the acceptability ratings of clauses. (Assuming ratings are continuous).
- How does NP ellipsis impact time to comprehend a linguistic expression?

Outside linguistics, especially in UX Research, people carry out a lot of A/B testing. For example, they check to see if a particular change to the UI has a significant impact on the user behavior. Here are some examples:

- What is the impact of the background color on the length of stay on a webpage?
- How much money do people from different cities spend on our platform?
- How does the language of a campaign affect the amount of donations made by people?

Categorical predictors are used whenever you compare two or more groups based on some classification (e.g. age, education level, native speaker status, and so on.).

10.2 Taste vs. Smell Words

The data and analysis for this section comes from Bodo Winter’s Chapter 7.

Smell words have been claimed to be more negative than taste words. I don’t know if this is true for every language or not but Turkish presents some very nice data points in this direction. Consider the following two expressions.

- Burası (çok) kokuyor.
- Bu (çok) tatlı.

Just the verb *kok* “smell” seems to have a negative connotation. On the other hand, the adjective *tatlı* “tasty” whose root *tat* “taste” and the suffix *-lı* simply means “with” has a positive connotation. While this is simply a hunch, we don’t have enough evidence for Turkish to claim that this is in fact true. Let’s hope that someone will run an experiment for Turkish and report the results. For now, we’ll use the **senses_valence** dataset from Bodo Winter’s book.

Let us read in the dataset and see what it looks like.

```
#Import tidyverse
library(tidyverse)
#Read in the data
data <- read_csv('data/winter_2016_senses_valence.csv')
#print the head to see what it looks like
data
```



```
## # A tibble: 405 x 3
##   Word      Modality   Val
##   <chr>    <chr>    <dbl>
## 1 abrasive Touch      5.40
## 2 absorbent Sight      5.88
## 3 aching   Touch      5.23
## 4 acidic   Taste      5.54
## 5 acrid     Smell      5.17
## 6 adhesive Touch      5.24
## 7 alcoholic Taste      5.56
## 8 alive     Sight      6.04
## 9 amber     Sight      5.72
## 10 angular  Sight      5.48
## # i 395 more rows
```

The dataset consists of three variables:

- **Word:** A word associated with some sense.
- **Modality:** Modality of the sense (touch, smell, etc.)
- **Valence:** A numeric value representing the attractiveness-aversiveness of a word.
 - Higher Valence is better. See Wikipedia for more on valence.

For now, we're only interested in **smell** and **taste**. Yet, it looks like the data has more than that. Let's print the unique values in the Modality column to see all the categories.

```
unique(data$Modality)
```

```
## [1] "Touch" "Sight" "Taste" "Smell" "Sound"
```

Let's now select the rows that have only **smell** and **taste** values. For this, we will use the filter function.

```
# Filter the data
senses_data <- filter(data, Modality %in% c('Smell', 'Taste'))

# Check the unique values to make sure
unique(senses_data$Modality)
```

```
## [1] "Taste" "Smell"
```

Let us quickly get some summary statistics using the 'summarize()' function.

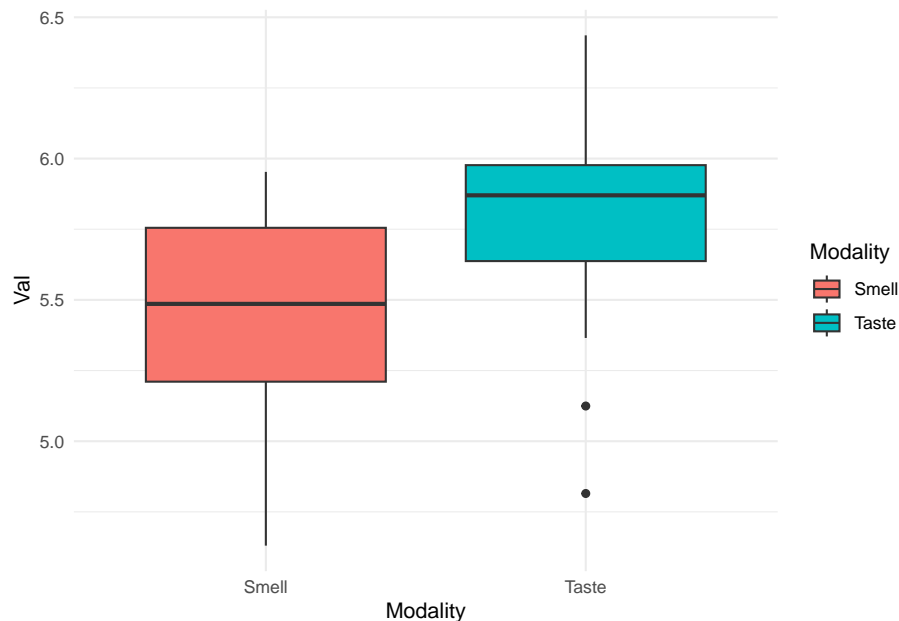
```
#pipe the data to a group_by function
#then pipe the groupings to the summarize function
# create the summary variables for mean and sd
senses_data %>% group_by(Modality) %>%
  summarize(M = mean(Val), SD = sd(Val))
```

```
## # A tibble: 2 x 3
##   Modality      M      SD
##   <chr>    <dbl> <dbl>
## 1 Smell      5.47 0.336
## 2 Taste      5.81 0.303
```

It looks like the mean valence for the two groups (smell and taste) are slightly different. Without fitting a model, we won't yet know if this difference is significant (i.e. meaningful but not by chance).

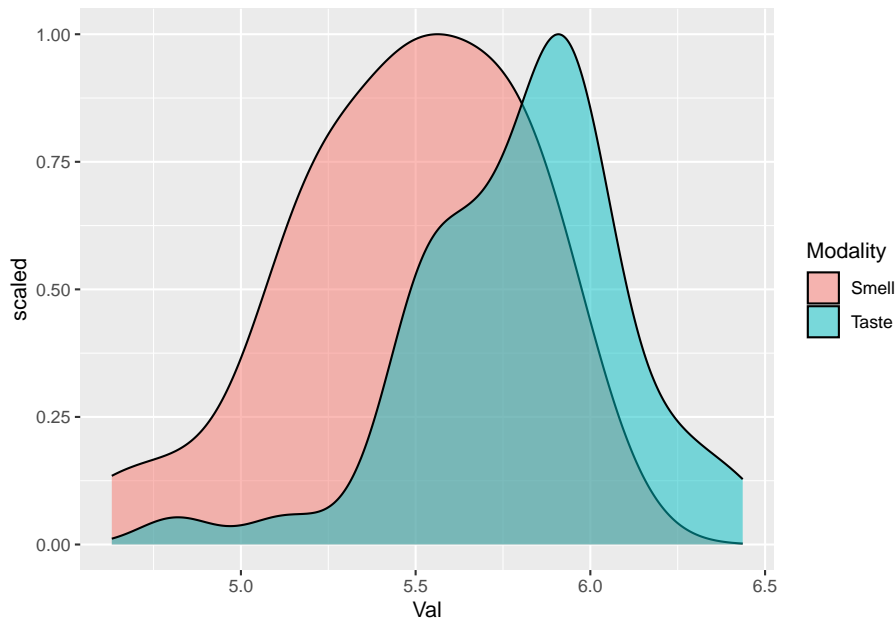
Before fitting a model though, let us visualize the data to see what it looks like. For categorical variables, it is often useful to plot a box-and-whiskers plot.

```
senses_data %>% ggplot(aes(x = Modality, y = Val, fill = Modality)) +
  geom_boxplot() +
  theme_minimal()
```



An alternative way to plot the data is to use density graphs, which are essentially smoothed histograms.

```
senses_data %>% ggplot(aes(x = Val, fill = Modality, after_stat(scaled))) +  
  geom_density(alpha=0.5)
```



10.3 Contrasts & Coding

Linear models are essentially linear equations. This means that they are defined on numeric values (e.g. 5, 0.2, etc.) but not categorical values (e.g. child-adult, SOV-VSO, etc.). To be able to use linear models with categorical values, we need to convert our categories into some numeric values that can be used in a linear equation. This conversion of categorical values into numeric values is called **contrast coding**. There are various ways in which this coding can be done and they have slightly different interpretations. While numbers are somewhat arbitrary, the interpretation of the coefficients depends on the choice of the coding technique.

10.3.1 Treatment Coding.

One way of coding the difference between two categories is to convert them into ones and zeroes. This is called **treatment coding**. Sometimes it is also called **dummy coding**.

Word	Category	Treatment Coding
odor	smell	0
sweet	taste	1
acid	smell	0

Let us do this by hand before training a model.

```
# Create a new column with 0 for smell and 1 for taste
senses_data <- mutate(senses_data, treatment = ifelse(Modality == 'Taste', 1, 0))

senses_data
```

```
## # A tibble: 72 x 4
##   Word      Modality   Val treatment
##   <chr>    <chr>   <dbl>   <dbl>
## 1 acidic   Taste    5.54     1
## 2 acrid    Smell    5.17     0
## 3 alcoholic Taste    5.56     1
## 4 antiseptic Smell    5.51     0
## 5 aromatic Smell    5.95     0
## 6 astringent Taste    5.96     1
## 7 barbecued Taste    6.05     1
## 8 beery     Taste    6.07     1
## 9 bitter    Taste    5.12     1
## 10 bland    Taste    5.75     1
## # i 62 more rows
```

Now that our categories are turned into numeric values, we can run a model. Let us fit a model where **valence** is a function of **modality** using our **treatment** codes.

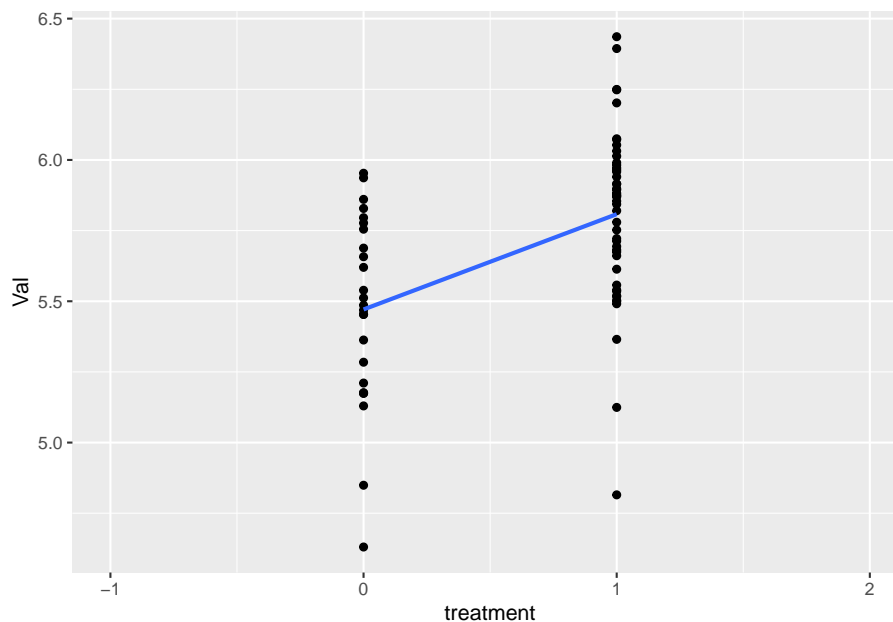
```
model_1 <- lm(Val ~ treatment, data = senses_data)

model_1

##
## Call:
## lm(formula = Val ~ treatment, data = senses_data)
##
## Coefficients:
## (Intercept)      treatment
##      5.4710         0.3371
```

In treatment coding, the intercept becomes the mean of one of your variables whereas the slope is the difference between the two means. You can see this clearly once you plot a linear function between the two variables.

```
ggplot(senses_data, aes(x= treatment, y= Val))+
  scale_x_continuous(limits = c(-1,2)) +
  geom_point()+
  geom_smooth(method='lm', se=F)
```



Let us now take a look at the usual numbers R2 and p-value to interpret how our model is doing.

```
summary(model_1)
```

```
##
## Call:
## lm(formula = Val ~ treatment, data = senses_data)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.99315 -0.20870  0.04343  0.19115  0.62788
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
```

```
## (Intercept)  5.47101    0.06297  86.889  < 2e-16 ***
## treatment    0.33711    0.07793   4.326 4.95e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.3148 on 70 degrees of freedom
## Multiple R-squared:  0.2109, Adjusted R-squared:  0.1997
## F-statistic: 18.71 on 1 and 70 DF,  p-value: 4.951e-05
```

Normally, you don't have to do the treatment coding by hand. R will do it automatically for you. We did it manually to make sure we understand what's under the hood.

```
model_2 <- lm(Val ~ Modality, data = senses_data)
```

```
model_2
```

```
##
## Call:
## lm(formula = Val ~ Modality, data = senses_data)
##
## Coefficients:
## (Intercept) ModalityTaste
##          5.4710          0.3371
```

Interpreting the coefficients: Our model is simply the following mathematical model.

$$valence = 5.8 + (-0.3) * modality$$

So, our model predicts only two values.

```
#Create a dataset consisting of categories in the data
preds <- tibble(Modality = unique(senses_data$Modality))
# Print to see what they look like
preds
```

```
## # A tibble: 2 x 1
##   Modality
##   <chr>
## 1 Taste
## 2 Smell
```

```
# See the predictions
predict(model_2, preds)
```

```
##          1          2
## 5.808124 5.471012
```

10.3.2 Sum Coding

Sum coding is a slightly different coding mechanism. Instead of using 0 and 1 as the coding scheme, we use -1 and 1 as the coding scheme. This has the benefit of having the mean of the means as the intercept. To be able to use R's coding functionality, we should convert our categorical values as **factors**.

```
senses_data <- mutate(senses_data, Modality = factor(Modality))
senses_data
```

```
## # A tibble: 72 x 4
##   Word      Modality  Val treatment
##   <chr>    <fct>    <dbl>    <dbl>
## 1 acidic   Taste     5.54      1
## 2 acrid    Smell     5.17      0
## 3 alcoholic Taste     5.56      1
## 4 antiseptic Smell    5.51      0
## 5 aromatic Smell     5.95      0
## 6 astringent Taste     5.96      1
## 7 barbecued Taste     6.05      1
## 8 beery     Taste     6.07      1
## 9 bitter    Taste     5.12      1
## 10 bland    Taste     5.75      1
## # i 62 more rows
```

Next, we can use the contrasts function to see what the current coding scheme looks like.

```
contrasts(senses_data$Modality)
```

```
##      Taste
## Smell    0
## Taste    1
```

We can also use R's built in cont function to get various coding types.

For treatment coding:

```
#Treatment coding with two variables
contr.treatment(2)
```

```
##      2
## 1 0
## 2 1
```

For Sum coding:

```
#Sum coding with two variables
contr.sum(2)
```

```
##      [,1]
## 1      1
## 2     -1
```

More than 2 variables:

```
#Treatment coding with 3 variables
contr.treatment(3)
```

```
##      2 3
## 1 0 0
## 2 1 0
## 3 0 1
```

```
#Sum coding with 3 variables
contr.sum(3)
```

```
##      [,1] [,2]
## 1      1    0
## 2      0    1
## 3     -1   -1
```

More than 2 variables:

```
#Treatment coding with 5 variables
contr.treatment(5)
```

```
##      2 3 4 5
## 1 0 0 0 0
## 2 1 0 0 0
## 3 0 1 0 0
## 4 0 0 1 0
## 5 0 0 0 1
```



```
#Sum coding with 5 variables
contr.sum(5)
```

```
##      [,1] [,2] [,3] [,4]
## 1      1      0      0      0
## 2      0      1      0      0
## 3      0      0      1      0
## 4      0      0      0      1
## 5     -1     -1     -1     -1
```

Let us use sum coding on our data.

```
#Create a new column by copying the modality factors (Taste and Smell)
senses_data <- mutate(senses_data, sum_coding=Modality)
#Use sum coding using contrasts() and contr.sum()
contrasts(senses_data$sum_coding) <- contr.sum(2)
#run contrasts to see if it worked
contrasts(senses_data$sum_coding)
```

```
##      [,1]
## Smell      1
## Taste     -1
```

Now we can fit a linear model and see what the coefficients look like.

```
model_3 <- lm(Val ~ sum_coding, data=senses_data)

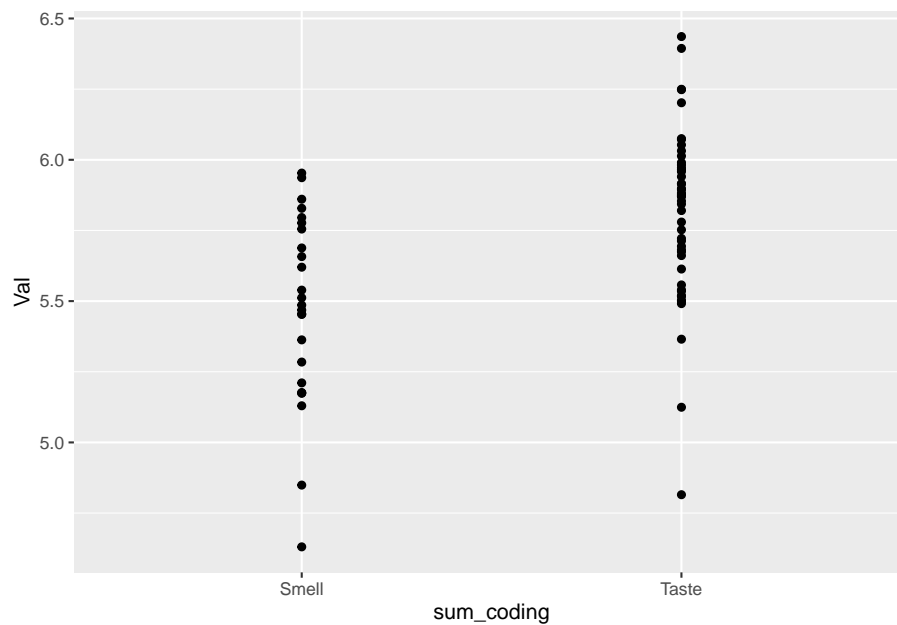
model_3
```

```
##
## Call:
## lm(formula = Val ~ sum_coding, data = senses_data)
##
## Coefficients:
## (Intercept)  sum_coding1
##      5.6396      -0.1686
```

The intercept is now the mean of the means. The slope is halved.

Let us also plot the model to see where the intercept is.

```
ggplot(senses_data, aes(x= sum_coding, y= Val))+
  geom_point()
```



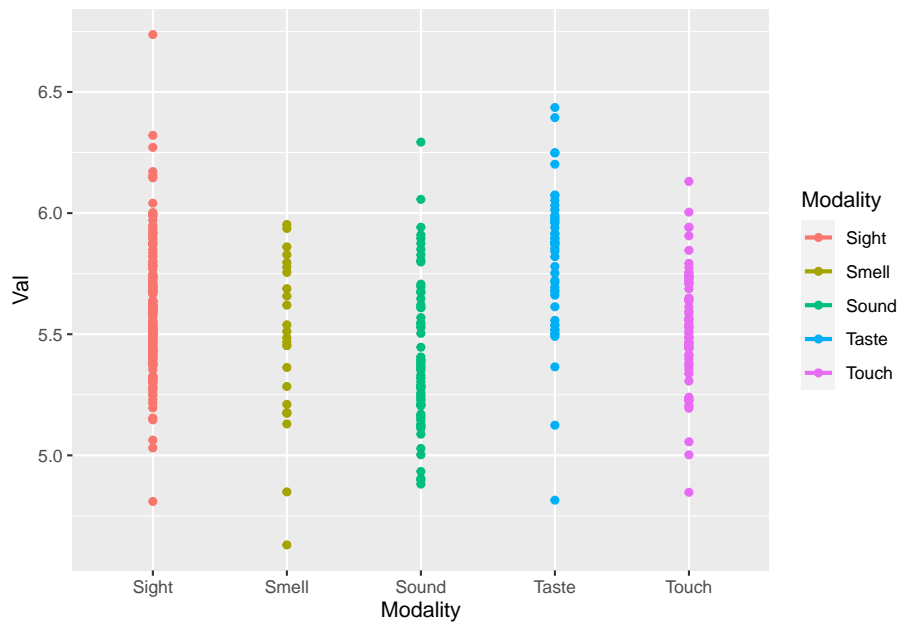
10.4 Categorical Predictors with more than 2 levels

Remember that originally our data had 5 levels (“Touch” “Sight” “Taste” “Smell” “Sound”). Let us build a linear model that includes all of them.

```
model_4 <- lm(Val ~ Modality, data=data)
model_4
```

```
##
## Call:
## lm(formula = Val ~ Modality, data = data)
##
## Coefficients:
## (Intercept)  ModalitySmell  ModalitySound  ModalityTaste  ModalityTouch
##      5.57966      -0.10865      -0.17447       0.22846      -0.04523
```

```
ggplot(data, aes(x= Modality, y= Val, color=Modality))+
  geom_point()+
  geom_smooth(method='lm', se=F)
```



Chapter 11

Effect Size & Significance

Often times, we will observe a difference between the means of two groups. These groups could be variables of any factor. For example, age could be a factor as we are investigating the difference in voice pitch between children and adults. Or, we could be looking at the difference between the frequency of using the word **darlamak** between members of Gen X and Gen Z. Yet another example would be looking at the difference between the average valence of smell and taste words.

In all these cases, we are comparing two means. So, let's say we collect data from 100 adults and 100 children and observe that on average children's fundamental frequencies in their voice pitch is 100Hz higher than those of adults.

What have we found? Is this a big difference? (As humans we are usually able to distinguish between an adult and a child when they speak. So, assuming that fundamental frequency is a predictor of adult vs child, then we know that some level of difference in Hertz is the source of this difference. But what is that level?)

Let's say we run another experiment with 5 children and 5 adults. Now, we find the average difference to be 200. So, once again, we face the same question. Is 100 big? Is 200 big? Obviously 200 is bigger than 100 but we don't know if these are big numbers or not.

Once again, we need to think of magnitude not in terms of absolute values but relative to a population (e.g. humans, children, adults, men, women, etc.). So, it would be great if we could figure out a way to calculate the **effect size** of a predictor (e.g. being adult or being a child) in a **standardized way**. If we have a standard definition of effect size, then we can compute this for any kind of metric.

As we are trying to figure out a standardized effect size (and other values), we'll keep three main points in mind:

- **Magnitude of difference**
 - The bigger the difference between (means of) two sample groups, the more you should expect to see a difference in the population.
- **Variability in the data**
 - The less variability in the data, the more certain you'll be about the estimate.
- **Sample Size**
 - The bigger the sample size, the more accurate is your measurement of the difference.

11.1 Cohen's d

Cohen's d is the measure used to quantify the **strength** of a difference between two means (m_1 and m_2). The formula for Cohen's d is given below:

$$d = \frac{m_1 - m_2}{s}$$

where:

m_1 = mean of group 1

m_2 = mean of group 2

s = pooled standard deviation

We'll calculate s using the formula below for **pooled** standard deviation:

$$s = \sqrt{\frac{(n_1 - 1) * sd_1^2 + (n_2 - 1) * sd_2^2}{n_1 + n_2 - 2}}$$

where:

n_1 = number of items in group 1

n_2 = number of items in group 2

sd_1 = standard deviation of group 1

sd_2 = standard deviation of group 2

The reason why we are calculating the **pooled** standard deviation is to make sure that our standard deviations that come from different means (i.e. groups of data) are weighted. Below, we'll see that the pooled standard deviation has a slightly different value than the standard deviation of the whole data.

Let us try Cohen's d for the Smell and Taste data.

First, load the data and select the relevant data using the filter function.

```
#Import tidyverse
library(tidyverse)
#Read in the data
data <- read_csv('data/winter_2016_senses_valence.csv')
#filter in the data for the relevant conditions (Taste and Smell)
senses_data <- filter(data, Modality %in% c('Taste', 'Smell'))
#print the head to see what it looks like
data
```

```
## # A tibble: 405 x 3
##   Word      Modality  Val
##   <chr>    <chr>    <dbl>
## 1 abrasive Touch     5.40
## 2 absorbent Sight    5.88
## 3 aching   Touch     5.23
## 4 acidic   Taste     5.54
## 5 acrid    Smell     5.17
## 6 adhesive Touch     5.24
## 7 alcoholic Taste     5.56
## 8 alive    Sight     6.04
## 9 amber    Sight     5.72
## 10 angular Sight     5.48
## # i 395 more rows
```

Let us get the means for each category.

```
#calculate means for each condition (Taste, Smell)
means <- senses_data %>%
  group_by(Modality) %>%
  summarize(avg = mean(Val))

#print means to see what it looks like
means
```

```
## # A tibble: 2 x 2
##   Modality  avg
##   <chr>    <dbl>
```

```
## 1 Smell      5.47
## 2 Taste      5.81
```

Let us get the length of each group (i.e. number of items in each group).

```
#get the number of items for each condition (Taste, Smell)
lengths <- senses_data %>%
  group_by(Modality) %>%
  summarize(N = n())
```

Let us now calculate s (pooled standard deviation).

```
#calculate standard deviation for each condition (Taste, Smell)
s_devs <- senses_data %>%
  group_by(Modality) %>%
  summarize(s = sd(Val))

#calculate pooled standard deviation using the formula above
s <- sqrt(((lengths$N[1]-1)*(s_devs$s[1]^2) + (lengths$N[2]-1)*(s_devs$s[2]^2))/(lengths$N[1]+lengths$N[2]-2))

#print the pooled standard deviation
s
```

```
## [1] 0.3148274
```

```
#calculate and print the standard deviation of the whole data for comparison
sd(senses_data$Val)
```

```
## [1] 0.3519115
```

Now we can calculate Cohen's d .

```
d = (means$avg[1] - means$avg[2]) / s
d
```

```
## [1] -1.070784
```

We can also use the package `effsize` to calculate Cohen's d . You'll see observe a difference between our calculation and the calculation given by the `effsize` package. This is mainly because they use a slightly different way of calculating variation in the data (the denominator). That's not a huge difference.


```
library(effsize)
cohen.d(Val ~ Modality, data = senses_data)

##
## Cohen's d
##
## d estimate: -1.070784 (large)
## 95 percent confidence interval:
##      lower      upper
## -1.5955866 -0.5459824
```

How to interpret Cohen's d ?

Cohen's d	Magnitude
0.2	small
0.5	medium
0.8	large

11.2 Standard Error

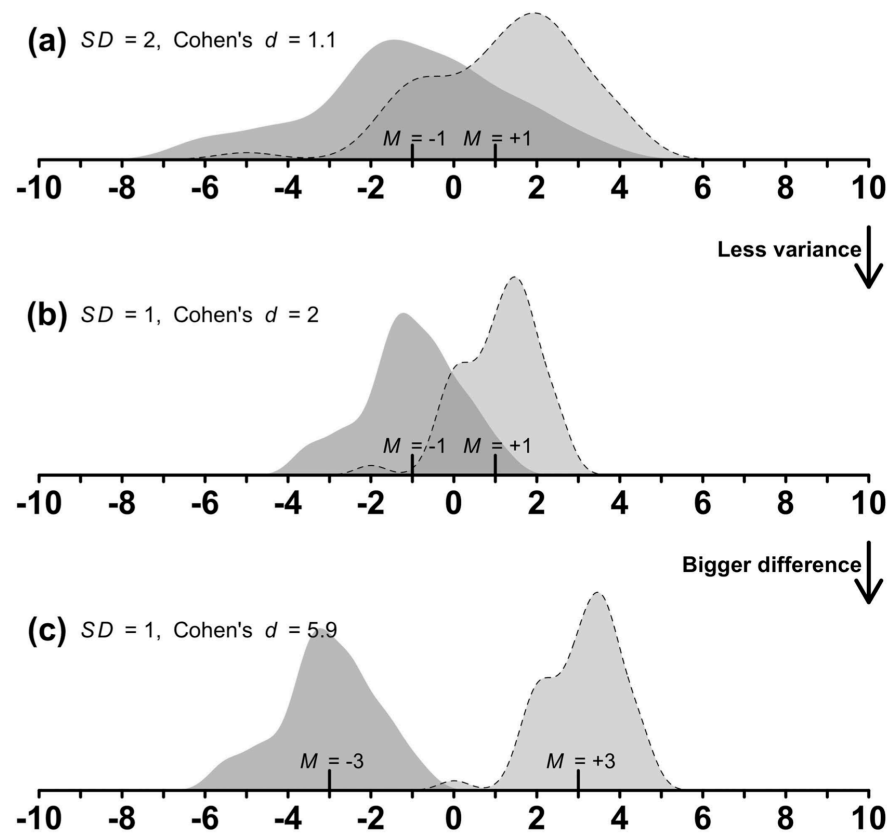
Cohen's d is a standard measure of difference in magnitude between two samples. It does not care about the sample size though. Your sample size for each group could be 2, 200, 2K, 2M, and so on.

Although, Cohen's d can tell us whether the difference between the two samples is large, it won't tell us much about our population.

Here's a small example. I want to test if there is a difference between the voice pitch of people who wear **blue shirts** and people who wear **red shirts**. Assume that the following is my data.

Participant (by shirt color)	Fundamental Frequency
Blue 1	175
Blue 2	125
Red 1	220
Red 2	190

Let us run Cohen's d on this data to see what the magnitude of the difference is.

Figure 11.1: Cohen's d .

```
blue = c(175,125)
red = c(220,190)
mean(blue) - mean(red)
```

```
## [1] -55
```

```
cohen.d(blue,red)
```

```
##
## Cohen's d
##
## d estimate: -1.886484 (large)
## 95 percent confidence interval:
##      lower      upper
## -7.058361  3.285392
```

We get a large effect. However, there's no way we can conclude that shirt color has anything to do with someone's voice pitch. We cannot generalize to the population. We observe a difference but we probably have a decent error margin in our prediction. To quantify this error, we need to introduce a new metric **standard error**.

Standard Error (SE) is a combination of the **variability** in the data and the **sample size**

$$SE = \frac{s}{\sqrt{N}}$$

- s = standard deviation
- N = sample size

The bigger the standard error, the less accurate is your estimation of the population parameters. This means your estimation (of the parameters, i.e. mean and standard deviation) is less reliable. The smaller the SE, the more accurate is your calculation of the population parameter estimates.

As you can see from the formula:

- SE will increase as your standard deviation grows (i.e. there is more variance in the data)
- SE will decrease as your sample size grows

Let us calculate the standard error for each of our means.

```
#Calculate Standard Errors
SE_blue <- sd(blue)/sqrt(2)
SE_red <- sd(red)/sqrt(2)

#print Standard Error for blue shirts
SE_blue
```

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

```
#print Standard Error for red shirts
SE_red
```

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

Standard Error tells us how close or far away from the true population mean. In this example, we were trying to get the average voice pitch for people wearing a blue shirt and people wearing a red shirt. In each sample, we have only 2 samples. Obviously, this is very little data and the Standard Errors are going to be big.

11.3 Confidence Interval

Confidence interval is a metric that helps you determine the level of confidence in your population parameter estimates. The formula for 95% Confidence Interval is as follows:

$$CI = [mean \pm 1.96 * SE]$$

Let us decompose this formula a bit.

- **mean** is the sample mean of some sample
- **SE** is the standard error of the sample
- \pm indicates that the value is going to be somewhere between *mean plus* or *minus some value*.
- **1.96** is a special number that indicates the 95% CI.¹

As the name suggests, CI is an interval and the numbers returned define the range of possible values for 95% of the time.

Let us calculate the 95% confidence intervals for our means for the blue and red data.

¹In fact, it corresponds to the z-score value of 95%. For calculating the 90% interval, we would use the corresponding z-score value 1.64.

```

#calculate means
mean_blue <- mean(blue)
mean_red <- mean(red)

#calculate CIs
CI_blue <- c(mean_blue - 1.96 * SE_blue, mean_blue + 1.96 * SE_blue)
CI_red <- c(mean_red - 1.96 * SE_red, mean_red + 1.96 * SE_red)

name <-c('mean', 'SE', 'CI_min', 'CI_max')
val_blue<-c(mean_blue, SE_blue, CI_blue)
val_red<-c(mean_red, SE_red, CI_red)

#print mean, SE, and CI for blue
blue_st <- data.frame(name, val_blue)
blue_st

```

```

##      name val_blue
## 1   mean      150
## 2    SE       25
## 3 CI_min     101
## 4 CI_max     199

```

```

#print mean, SE, and CI for red
red_st <- data.frame(name, val_red)
red_st

```

```

##      name val_red
## 1   mean    205.0
## 2    SE     15.0
## 3 CI_min    175.6
## 4 CI_max    234.4

```

11.4 Standard Error of the difference of two means

In the previous sections, we calculated the SE and CI for each sample (blue and red). However, what we are ultimately interested in is the difference in the means between two groups. The difference in the mean is what will tell us if there is a significant difference between the voice pitches of people wearing different colors. To calculate the Standard Error for the difference in mean of two samples, we use the formula below.

$$SE_{diff} = \sqrt{\frac{SD_1^2}{n_1} + \frac{SD_2^2}{n_2}}$$

Let us calculate the SE of the difference in mean.

```
#calculate standard deviations

sd_blue <- sd(blue)
sd_red <- sd(red)

# calculate SE_diff
SE_diff <- sqrt(sd_blue^2/2 + sd_red^2/2)

#print SE_diff
SE_diff
```

```
## [1] 29.15476
```

Let us now calculate the 95% CI for the difference in means.

```
#calculate the difference in means
diff_mean <- mean_blue - mean_red

#calculate the 95% CI
CI_diff <- c(diff_mean-1.96*SE_diff, diff_mean+1.96*SE_diff)

#print the CI_diff by rounding the numbers to 2 decimal point
round(CI_diff, 2)
```

```
## [1] -112.14 2.14
```

11.5 Hypothesis Testing

Remember that throughout the semester we talked about forming and testing hypotheses. Let us form our hypotheses and then test them.

Let us build our **alternative hypothesis**.

- H1: There is a difference in voice pitch between people who wear blue and people who wear red.

Now, let us build our null hypothesis.

- H_0 : There is **no** difference in voice pitch between people who wear blue and people who wear red.

In hypothesis testing framework, we do not try proving our alternative hypothesis (H_1). Instead, we try **rejecting the null hypothesis**.

To reject the null hypothesis we do the following:

1. Make an observation.
 - In this case, our observation is the difference in means between two colors.
2. Calculate the probability of making this observation.
 - This means we need to find the **p-value** of the observation.
3. Check the **p-value** against a **critical value** called alpha (α).
 - If the **p-value** is smaller than the **critical value**, then we **reject** the null hypothesis.
 - else, we maintain the null hypothesis.

What is the **critical value**. Critical value is a value that we define depending on the nature of our question. It's up to us and how we want to interpret the results. The scientific community has converged on using several critical values.

- $\alpha = 0.05$ (commonly adopted for social sciences)
- $\alpha = 0.01$
- $\alpha = 0.001$

So, how do we calculate the p-value for our null hypothesis?

In other words, how do we calculate the p-value for the difference we observe between people who wear blue and red? To do this, we need a particular method that allows us to calculate some statistics for the **difference between two means**. For this, we will use a **t-test** which allows us to calculate a standardized **t-score** which comes from a particular distribution called **t-distribution**. Once we have a **t-score**, we can check it against the **t-distribution** to calculate its **p-value**.

11.6 Calculating the t-score

t-score is calculated using the following formula.

$$t = \frac{mean1 - mean2}{SE_{diff}}$$

What the t-score encodes is 1) magnitude of the difference, 2) Variability in the data 3) Sample size. So, all of the information we need.

Let us calculate the t-score for our data.

```
#calculate the t-score
t <- diff_mean / SE_diff
#print the t-score
t
```

```
## [1] -1.886484
```

How do we interpret the t-score t-score is going to be a value from a t-distribution. A t-distribution is very similar to a normal distribution except that it has **heavier tails**. What this means is that there is a higher probability of having more extreme values especially with small data sets. Let's take a look at the t-and normal distributions.

A t-distribution is like a normal distribution but has an additional parameter called **degrees of freedom**. This is relatively vague concept we won't go into. You can google it and find what it means intuitively. For our purposes, we will just assume that degrees of freedom is calculated by deducing 1 from our sample size.

- `df_blue = sample_size_blue - 1`
- `df_red = sample_size_red - 1`

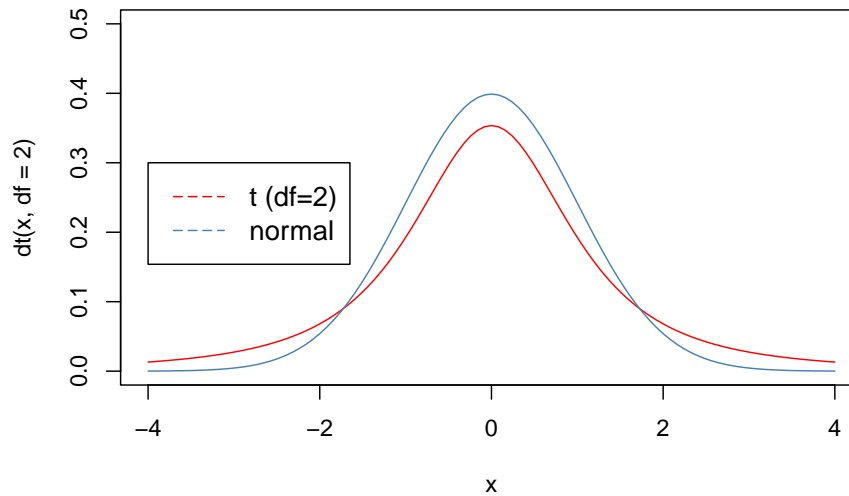
When we are calculating the degrees of freedom for both samples, then we calculate it using the formula below:

- `df = sample_size_blue + sample_size_red - 2`

Given that we have a total of 4 data points, then our df will be 2.

```
curve(dt(x, df=2), from=-4, to=4, col = 'red',ylim=c(0,0.5)) # 2 degrees of freedom
curve(dnorm(x), from=-4, to=4, col = 'steelblue',add=TRUE)

legend(-4, .3, legend=c("t (df=2)", "normal"),
      col=c("red", "steelblue" ), lty=5, cex=1.2)
```

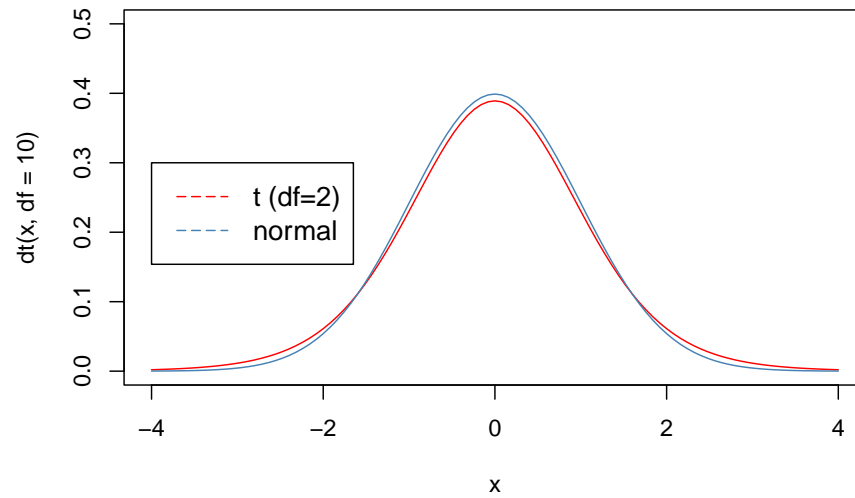



t-distribution approaches normal distribution (for z-scores) as the degrees of freedom increases. At 30 degrees of freedom or above, it becomes very similar to normal distribution.²

```
curve(dt(x, df=10), from=-4, to=4, col = 'red',ylim=c(0,0.5)) #10 degrees of freedom
curve(dnorm(x), from=-4, to=4, col = 'steelblue',add=TRUE)

legend(-4, .3, legend=c("t (df=2)", "normal"),
      col=c("red", "steelblue" ), lty=5, cex=1.2)
```

²This is part of the reason why people aim for at least 30 participants in each group.

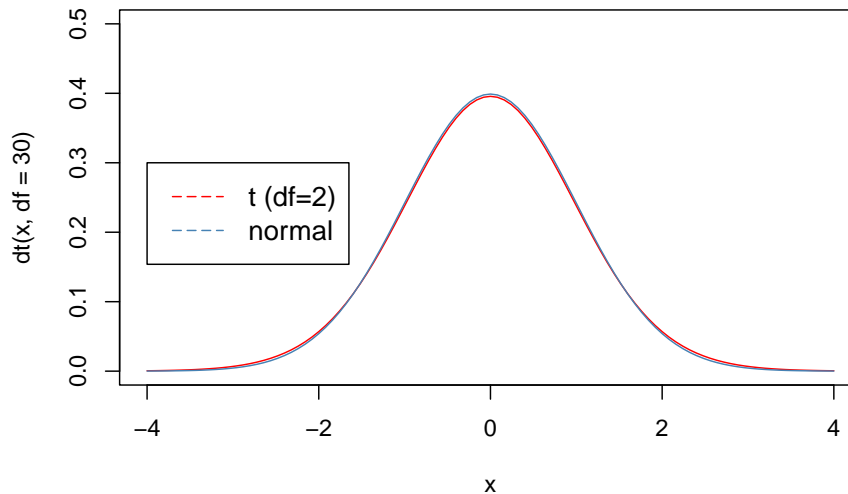


```

curve(dt(x, df=30), from=-4, to=4, col = 'red',ylim=c(0,0.5)) #30 degrees of freedom
curve(dnorm(x), from=-4, to=4, col = 'steelblue',add=TRUE)

legend(-4, .3, legend=c("t (df=2)", "normal"),
      col=c("red", "steelblue" ), lty=5, cex=1.2)

```



11.7 p-value

p-value is the probability of observing a particular t-score given a t-distribution. So, all we need to do now is to calculate the p-value for the t-score we observed above. There are various ways of doing this. Many people use a t-table to do the calculation. See [this link](#).

Alternatively, we can calculate it using the `pt()` function, which takes the following arguments.

- t-score
- degrees of freedom
- A Boolean for `lower.tail` (optional)

```
pt(abs(t), 1.6374, lower.tail = FALSE)
```

```
## [1] 0.1135606
```

The value we get is going to be the probability of t-score on one tail of the distribution (called **one-tailed**). This is used for a directional hypothesis (e.g. red shirts have a higher voice pitch than blue ones). In our case, we are interested in the difference regardless of the direction. For this, we can simply multiply our p-value by 2 to get a **two-tailed** distribution.

```
2*pt(abs(t),1.6374, lower.tail = FALSE)
```

```
## [1] 0.2271212
```

It looks like our p -value is larger than the critical value $\alpha = 0.05$. So, we must **cannot reject** our null hypothesis. This means that, there is a big chance of observing such a difference in mean when we have only a total of 4 data points.

Even though our effect size is large as can be seen below, our results are **not significant**. In other words, the big difference is due to chance and we cannot conclude that there is a difference in the voice pitches of people who wear blue and people who wear red.

```
cohen.d(blue,red)
```

```
##
## Cohen's d
##
## d estimate: -1.886484 (large)
## 95 percent confidence interval:
##      lower      upper
## -7.058361   3.285392
```

11.8 Type I and Type II Errors

Sometimes, we might find $p < 0.05$ which suggests that we have found a significant result. However, this is not always true. Such errors are called Type I error (also known as False Positive). Other times, there might be a significant difference between our two groups but we might fail to identify this significance because we got $p \geq 0.05$. Such errors are called Type II errors (a.k.a. False Negative). Such errors usually occur when we don't have sufficient data (i.e. sample size is too small).

Error Type	Explanation	a.k.a.
Type I	$p < 0.05$ but in fact there is no significant difference	False Positive
Type II	$p \geq 0.05$ but in fact there is a significant difference	False Negative

11.8.1 Type I Error

Remember that the difference between two groups of data is **statistically significant** means that there is an actual meaningful difference in the way these data are generated. This difference can be small or big in terms of its effect size. This difference might be caused by one factor or by many factors. What matters is that there is an underlying difference in the mechanism that is generating the data. This underlying difference is causing the actual variance in the data from two distinct groups.

Also remember that the variance within or across two groups can also be caused by completely random factors. For example, when you are measuring the reaction time, a little insect in the room might lead to a bit of a distraction and increase the reaction time.

Given all this background, let us see a little bit of a random data that was generated from a single distribution.

```
data_1 <- rnorm(10,mean =1, sd = 1)
data_2 <- rnorm(10,mean =1, sd = 1)
```

```
data_1
```

```
## [1] -0.2918083  1.3658382  0.8477967  0.2659059  0.2180279  1.5515670
## [7] -0.6108410  1.7481764  1.4492960  0.1299375
```

```
data_2
```

```
## [1]  0.902252069  1.893100214  2.350915095  2.488970394  1.371067213
## [6]  0.785526756  1.455494590  0.741888890 -0.002923752  1.844143483
```

You see that the data points are different but the parameters are the same. So underlyingly, they come from the same distribution, same data generation process, there is no actual difference between the two datasets in terms of the underlying mechanism.

Let us now pass the data through a t test for a few times to see if we can ever find a statistically significant difference.

```
set.seed(42)
t.test(rnorm(10,mean =1, sd = 1),rnorm(10,mean =1, sd = 1))
```

```
##
## Welch Two Sample t-test
##
```

```
## data:  rnorm(10, mean = 1, sd = 1) and rnorm(10, mean = 1, sd = 1)
## t = 1.2268, df = 13.421, p-value = 0.241
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -0.5369389  1.9584459
## sample estimates:
## mean of x mean of y
## 1.5472968 0.8365433
```

```
t.test(rnorm(10,mean =1, sd = 1),rnorm(10,mean =1, sd = 1))
```

```
##
##  Welch Two Sample t-test
##
## data:  rnorm(10, mean = 1, sd = 1) and rnorm(10, mean = 1, sd = 1)
## t = 0.36582, df = 17.977, p-value = 0.7188
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -0.8814711  1.2531201
## sample estimates:
## mean of x mean of y
## 0.8219205 0.6360959
```

```
t.test(rnorm(10,mean =1, sd = 1),rnorm(10,mean =1, sd = 1))
```

```
##
##  Welch Two Sample t-test
##
## data:  rnorm(10, mean = 1, sd = 1) and rnorm(10, mean = 1, sd = 1)
## t = -0.082117, df = 16.257, p-value = 0.9356
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -1.0340503  0.9568318
## sample estimates:
## mean of x mean of y
## 0.9797846 1.0183939
```

```
t.test(rnorm(10,mean =1, sd = 1),rnorm(10,mean =1, sd = 1))
```

```
##
##  Welch Two Sample t-test
##
## data:  rnorm(10, mean = 1, sd = 1) and rnorm(10, mean = 1, sd = 1)
## t = 2.3062, df = 17.808, p-value = 0.03335
```

```
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  0.06683172 1.44707262
## sample estimates:
## mean of x mean of y
## 1.5390768 0.7821246
```

As you can see, the fourth model came out to be statistically significant. This is a Type I Error.

11.8.2 Type II Error

Now, let us create data with different parameters. This time, the means are going to be different.

```
data_1 <- rnorm(10,mean =0, sd = 1)
data_2 <- rnorm(10,mean =1, sd = 1)

data_1

## [1] 1.51270701 0.25792144 0.08844023 -0.12089654 -1.19432890 0.61199690
## [7] -0.21713985 -0.18275671 0.93334633 0.82177311

data_2

## [1] 2.3921164 0.5238261 1.6503486 2.3911105 -0.1107889 0.1392074
## [7] -0.1317387 -0.4592140 1.0799826 1.6532043
```

Now, let's run the model a few times again.

```
set.seed(42)
t.test(rnorm(10,mean =0, sd = 1),rnorm(10,mean =1, sd = 1))

##
## Welch Two Sample t-test
##
## data:  rnorm(10, mean = 0, sd = 1) and rnorm(10, mean = 1, sd = 1)
## t = -0.49924, df = 13.421, p-value = 0.6257
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -1.5369389 0.9584459
## sample estimates:
## mean of x mean of y
## 0.5472968 0.8365433
```

```
t.test(rnorm(10,mean =0, sd = 1),rnorm(10,mean =1, sd = 1))

##
## Welch Two Sample t-test
##
## data:  rnorm(10, mean = 0, sd = 1) and rnorm(10, mean = 1, sd = 1)
## t = -1.6028, df = 17.977, p-value = 0.1264
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -1.8814711  0.2531201
## sample estimates:
## mean of x mean of y
## -0.1780795  0.6360959
```

```
t.test(rnorm(10,mean =0, sd = 1),rnorm(10,mean =1, sd = 1))

##
## Welch Two Sample t-test
##
## data:  rnorm(10, mean = 0, sd = 1) and rnorm(10, mean = 1, sd = 1)
## t = -2.209, df = 16.257, p-value = 0.04186
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -2.03405031 -0.04316822
## sample estimates:
## mean of x mean of y
## -0.02021535  1.01839391
```

```
t.test(rnorm(10,mean =0, sd = 1),rnorm(10,mean =1, sd = 1))

##
## Welch Two Sample t-test
##
## data:  rnorm(10, mean = 0, sd = 1) and rnorm(10, mean = 1, sd = 1)
## t = -0.74048, df = 17.808, p-value = 0.4687
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.9331683  0.4470726
## sample estimates:
## mean of x mean of y
## 0.5390768 0.7821246
```

As you can see, the results end up being not significant despite an actual difference in the parameters that generate data.

11.8.3 Statistical Power

The rate at which a model would makes a Type II error is called Type II Error rate represented as β . We want to minimize β as much as possible. The lower the error rate, the more powerful our model is. A standard way of measuring how powerful our model is the concept of **statistical power**.

- Statistical power = $1-\beta$

The higher the statistical power of a model, the more reliable it is. Often people aim for a value above 80%. To calculate the statistical power of a t test in r, we can use the following code.

```
effect_size <- cohen.d(rnorm(10,mean =0, sd = 1), rnorm(10,mean =1, sd = 1))$estimate
n <- 10
alpha <- 0.05

power <- power.t.test(n = n, delta = effect_size, sd = 1, sig.level = alpha, type = "two.sample")

power
```

```
## [1] 0.3273469
```

Now, let us try the same data with an increased number of observations.

```
effect_size <- cohen.d(rnorm(10,mean =0, sd = 1), rnorm(10,mean =1, sd = 1))$estimate
n <- 300
alpha <- 0.05

power <- power.t.test(n = n, delta = effect_size, sd = 1, sig.level = alpha, type = "two.sample")

power
```

```
## [1] 0.9999999
```


Chapter 12

Logistic Regression

So far, we built linear models where the outcome (i.e. dependent variable) was a continuous value (e.g. reaction time, frequency, etc.). Now, we turn to modeling data where the outcome is a **categorical** value. In particular, we will use **logistic regression** to model **categorical** outcomes where the number of categories is **two**. Some examples are:

- acceptable – unacceptable expression
- NP NP construction – NP PP construction
- SOV – SVO word order
- accusative present – accusative absent
- adult – child

For example, we can use **average utterance length** as an indicator of **child speech** vs. **adult speech**. Consider the following artificial toy dataset.

Utterance length	Utterer
2	child
8	adult
12	adult
3	adult
3	child
6	adult
5	???

Given the data set above, can we predict whether it was uttered by a child or an adult?

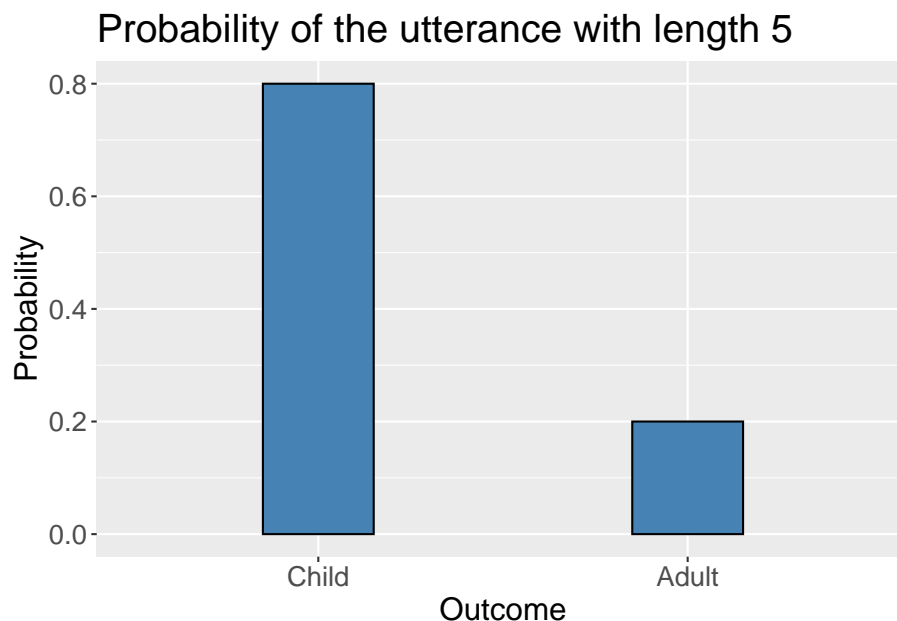
Notice that the answer is not that straightforward as it is possible that the utterance belongs to a child because it is shortish but on the other hand, we do see that the adults also produce short sentences (e.g. utterance length of 3).

12.1 The Intuition

The core intuition behind logistic regression is very simple. The task is to **model the probability of an outcome given a predictor**. Going back to our toy example above, we would like a model that can produce probabilities like the following.

- $p(\text{child}|\text{length} = 5)$
 - read as *probability of the utterer being a child given that the utterance length is 5*
- $p(\text{adult}|\text{length} = 5)$
 - read as *probability of the utterer being an adult given that the utterance length is 5*

For example, we want to build a model that returns something like the following.



Once we estimate the probabilities, we have a model that can:

- **predict** the categorical outcome (e.g. adult vs. child)
- help us **interpret** the relationship between a predictor and the outcome

Let us now turn to the math behind how the logistic regression works.

12.2 The Math

Remember that our **linear regression** models assumed that our data is **normally distributed**. Normal distribution is a distribution of continuous values. Similarly, for **logistic regression**, we assume that the **outcome variables** come from a certain probability distribution.

12.2.1 Binomial & Bernoulli Distributions

12.2.1.1 Binomial Distribution

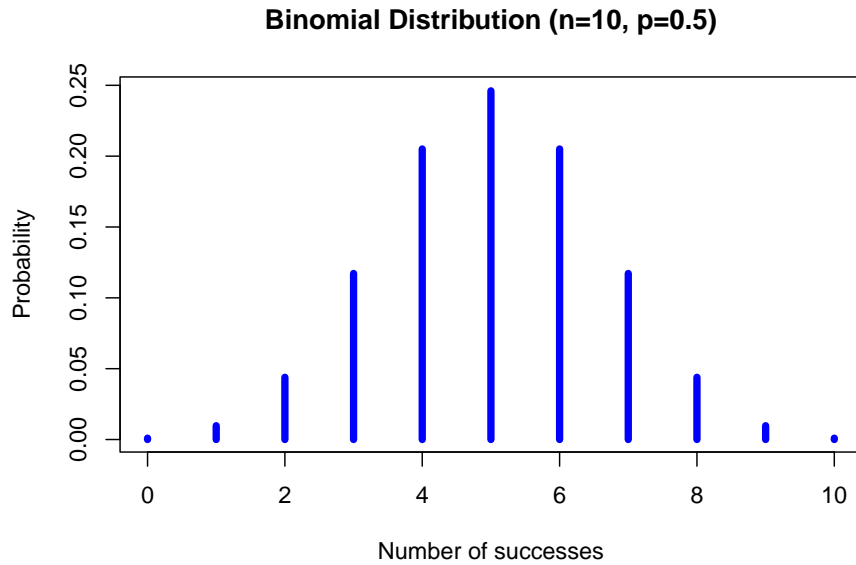
The **Binomial Distribution** is a discrete probability distribution with a fixed number of **Bernoulli trials** with the parameters:

- n trials
- p probability

where each trial has only two possible outcomes: **success** or **failure**. Success can be associated with any outcome that is relevant to you as long as there are only two outcomes. For example:

- success = child – failure = adult
- success = acceptable – failure = unacceptable
- success = SVO – failure = SOV
- ...

A good way of understanding the binomial distribution is to think of a coin-flip experiment. Imagine that you have a fair coin and you flip the coin 10 times. What is the probability that you will have 5 heads (i.e. successes)?



To get the actual probability values in R, we can use the `dbinom()` function.

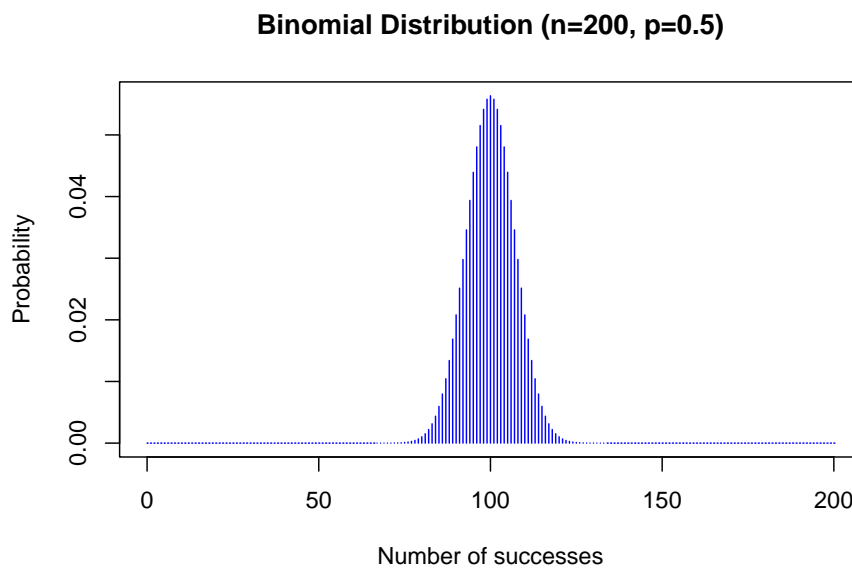
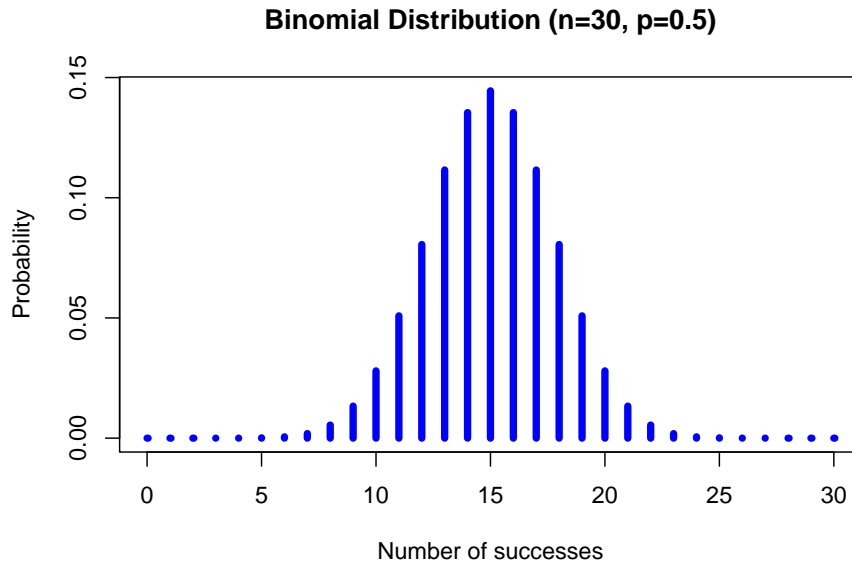
```
n = 10 #number of trials
p = 0.5 #probability of success (e.g. heads)
s = 5 #number of successes in n trials (e.g. number of heads in 10 trials)

dbinom(s,n,p)
```

```
## [1] 0.2460938
```

Try it with different parameters to see how the probabilities change.

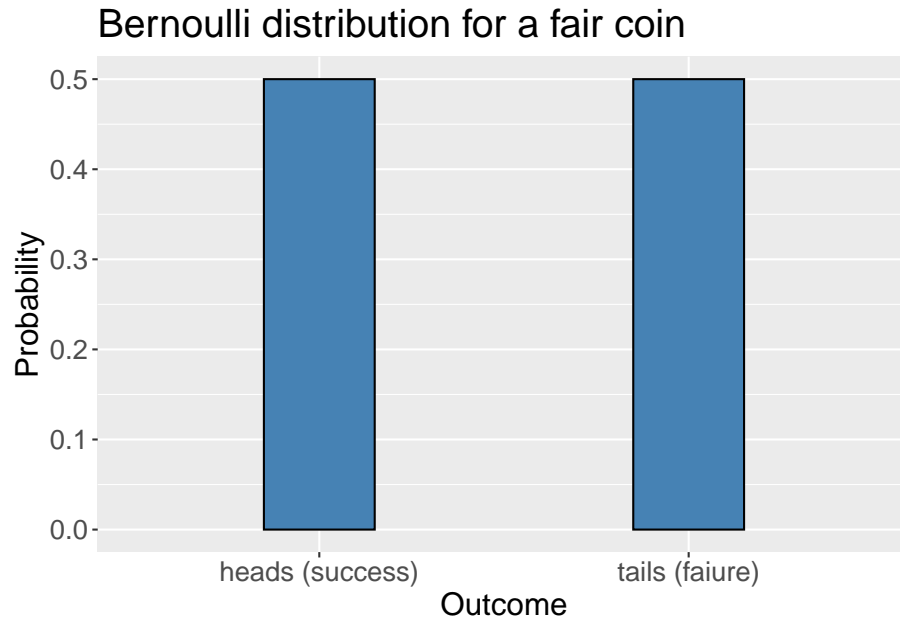
Notice that the binomial distribution is a discrete distribution (not continuous) but the plot looks very similar to a normal distribution especially when the number of trials is at or above 30.



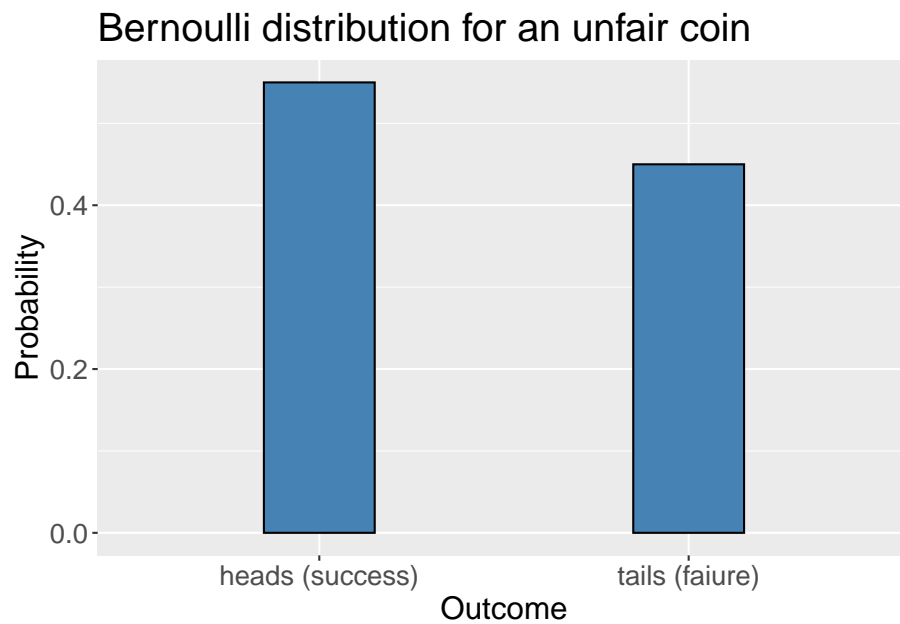
12.2.1.2 Bernoulli distribution

A Bernoulli distribution is a special case of a binomial distribution with where the number of trials is 1. The only relevant parameter is the p . Thus, Bernoulli

distribution for a fair coin would look like the following.

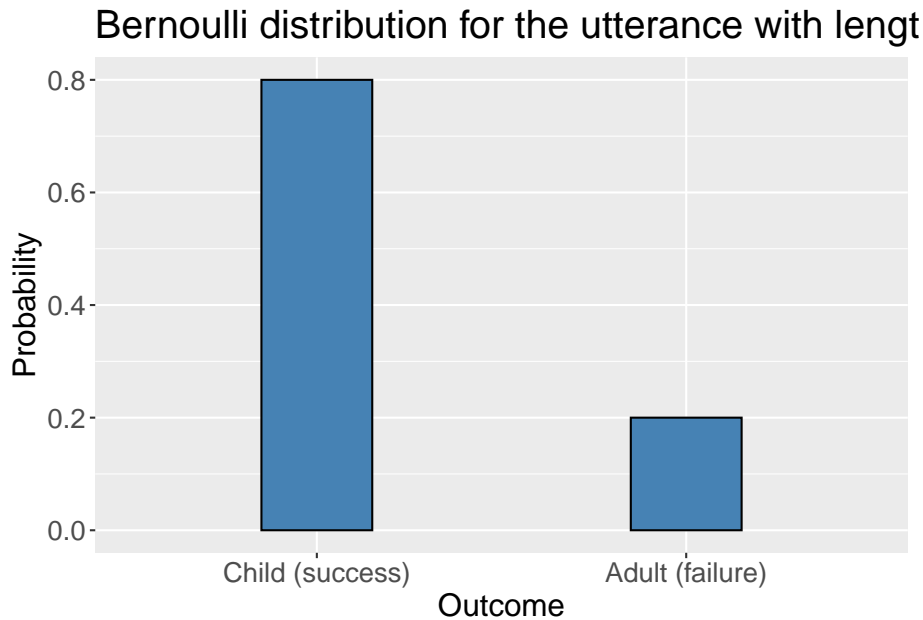


What if the coin were a bit unfair. Assume that you want to cheat but not too much to avoid getting caught.



Finally, going back to our toy example from above about the length of utter-

ances. Notice that this is also a Bernoulli distribution.



Bernoulli distribution will vary based on a single parameter p , which is the probability of success for a given condition.

12.3 Logistic Regression

Remember that in **linear regression**, the goal was to estimate the model parameters that can describe a line.

$$\underbrace{Y}_{\text{dependent variable}} = \underbrace{\underbrace{a}_{\text{intercept}}}_{\text{additive term}} + \underbrace{\underbrace{\underbrace{b}_{\text{slope}} * \underbrace{X}_{\text{predictor}}}_{\text{additive term}}}$$

In other words, our model took input some data, assumed that the variance in the data can be described by a line, then tried to estimate the parameters (i.e. intercept and slope). For example, we tried to estimate the taxi fare cost and our linear model could predict it as follows:

- cost = Intercept + Slope * Distance (in km)
- cost = 20 + 14 * 5

The values for the intercept and the slope were estimated by the model after analyzing the input data. The output of the model (i.e. the cost) is an **arbitrary number** (e.g. 90 TL).

In **logistic regression**, we don't want an arbitrary number. Instead, we want a **category** (e.g. adult or child) along with a **probability**. In fact, what we need is a probability for success and the Bernoulli distribution will handle the rest.

- $y \sim \text{Bernoulli}(p)$
 - read as *y as a function of Bernoulli(p)*
 - y is the predicted category

So, we need a way to convert **arbitrary numbers** (output of the linear equation) to **probabilities**. Remember that probabilities range between $[0,1]$.

In mathematics, there is a really nice function that will squeeze arbitrary numbers between $[0,1]$. The name of this function is the **logistic function**.

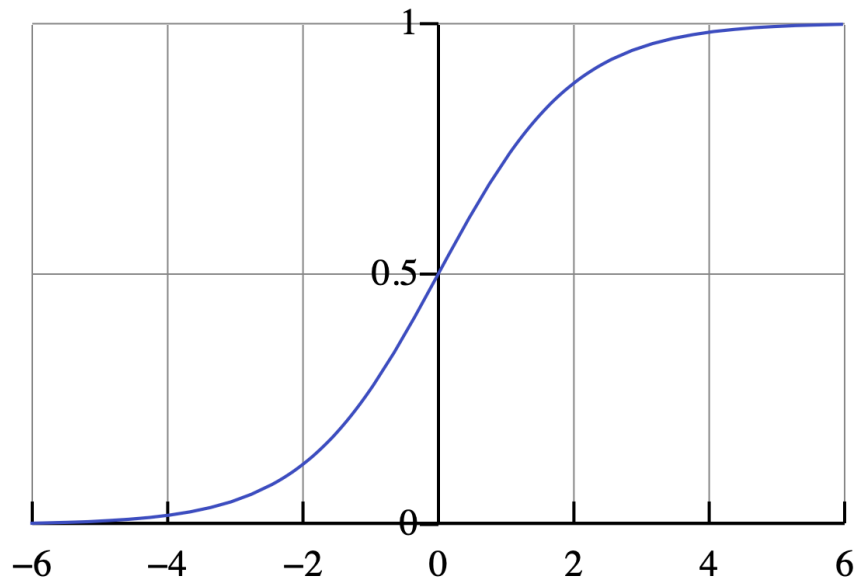


Figure 12.1: Logistic Function

In R, we can use the `plogis()` function to apply the logistic function to an arbitrary number. Try the following code with various values to see what you get.

```
plogis(90)
```

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

```
plogis(2.1)
```

```
## [1] 0.8909032
```

```
plogis(0)
```

```
## [1] 0.5
```

```
plogis(-3)
```

```
## [1] 0.04742587
```

This is nice because we can use the logistic function to convert the output of our linear function to probabilities. Once we have the probabilities, we can get a Bernoulli distribution to predict the category we are interested in.

By now, it should be clear where the name **logistic regression** comes from.

12.3.1 Log Odds & Logits

In a nutshell, the logistic regression model works as follows:

- $p = \text{logistic}(\text{output})$
- $y \sim \text{Bernoulli}(p)$

You calculate some output:

- $(\text{output} = \text{Intercept} + \text{Slope} * \text{input})$

You convert it to a probability:

- $p = \text{logistic}(\text{output})$

The rest is just a Bernoulli distribution with the parameter p :

- $y \sim \text{Bernoulli}(p)$

There is an important difference though. In **linear regression** the output is just an arbitrary number :

- $(\text{output} = \text{Intercept} + \text{Slope} * \text{input}).$

In **logistic regression**, the model output is a **logit**. So, we calculate the probability of logits rather than arbitrary numbers.

- $\text{logit}(p) = \text{intercept} + \text{slope} * x$

12.3.1.1 Odds, Log Odds, and Logits

You understand **logits**, we need to understand the concept of **odds**. You must have heard questions like:

- What are the **odds** that our team will win this week?
- The **odds** are in my favor.
- The **odds** are 1 to 1.

The **odds** express the probability of an event occurring (p) over the probability of an event not occurring ($1 - p$).

$$\bullet \text{ odds}(X = \text{win}) = \frac{P(X=\text{win})}{1-P(X=\text{win})}$$

Logits are log odds ($\log(\text{odd})$). Converting the odds to log odds (i.e. logits) turns them into a **continuous scale** from negative infinity to positive infinity. Thus, it allows us to model **categorical outcomes** similar to **continuous outcomes**.

Probability	Odds	log odds (logits)
0.1	0.11 to 1	-2.20
0.4	0.67 to 1	-0.41
0.5	1 to 1	0.00
0.8	4 to 1	+1.39
0.9	9 to 1	+2.20

Logistic Regression models estimate coefficients (intercept and slope) as **logits**. We can turn logits into probabilities, simply by feeding them into the **logistic function**.

12.4 Logistic Regression in R

12.4.1 Data

Let us see **logistic regression** in action by using it on a dataset from Bodo Winter's book. For this task, we will use the **speech_errors** dataset.

```
library(tidyverse)
data <- read_csv '~/ling_411/data/speech_errors.csv')
```

```
## Rows: 40 Columns: 2
## -- Column specification -----
## Delimiter: ","
## dbf (2): BAC, speech_error
##
## i Use `spec()` to retrieve the full column specification for this data.
## i Specify the column types or set `show_col_types = FALSE` to quiet this message.
```

```
data
```

```
## # A tibble: 40 x 2
##       BAC speech_error
##   <dbl>         <dbl>
## 1 0.0737           0
## 2 0.0973           0
## 3 0.234            0
## 4 0.138            1
## 5 0.0933           0
## 6 0.262            1
## 7 0.357            0
## 8 0.237            1
## 9 0.352            1
## 10 0.379           1
## # i 30 more rows
```

The data consists of two columns:

- **BAC**: A continuous value representing the level of Blood Alcohol Concentration
- **speech_error**: A binary value representing the presence and absence of a speech error.
 - 1 = speech error
 - 0 = no speech error

12.4.2 Model

In R, we will use the `glm()` function, which stands for **generalized linear model**. `glm()` takes input

- an output variable,
- predictors
- a dataset
- a **family** parameter, which will be `'binomial'` for our purposes

```
speech_error_model <- glm(speech_error ~ BAC, data = data,
                          family = 'binomial'
                          )
```

Simple as that, we have modeled the presence and absence of speech errors as a function of blood alcohol concentration using **logistic regression**. Let us inspect the model coefficients to understand what our model learnt from the data.

```
library(broom)
tidy(speech_error_model)

## # A tibble: 2 x 5
##   term          estimate std.error statistic  p.value
##   <chr>          <dbl>    <dbl>    <dbl>    <dbl>
## 1 (Intercept)   -3.64      1.12     -3.24  0.00118
## 2 BAC           16.1      4.86      3.32  0.000903
```

We learn a few things:

- The slope of BAC is positive (16.1). This means that an increase in BAC will lead to an increase in speech errors.
- We also see that the $p < 0.05$. This indicates that our conclusion is statistically significant.
- Remember that the output of logistic regression is a **logit**. Thus our coefficients (intercept and slope) are in logit units.

The results of the model can be reported as:

- There was a reliable effect of BAC (logit coefficient: +16.11, SE = 4.86, $z=3.3$, $p = 0.0009$).

12.4.3 From logits to probabilities

Logits are a bit confusing. Let us turn our logits to probabilities to get a more intuitive understanding of the model results.

First, let us convert the intercept to a probability. Remember that the intercept is the logit for $BAC = 0$.

```
intercept <- tidy(speech_error_model)$estimate[1]
slope <- tidy(speech_error_model)$estimate[2]

plogis(intercept)
```

```
## [1] 0.02549508
```

This shows that a sober person will make a speech error with the probability $P = 0.025$, quite a small probability.

Now let us check the probability of a person with a BAC of 0.4 making speech errors.

```
logit <- intercept + slope * 0.3
probability <- plogis(logit)
probability
```

```
## [1] 0.7670986
```

That is a huge jump. Our model predicts that someone with a $BAC = 0.3$ will make a speech error with a probability $P = 0.76$, a lot more likely.

Let's see what the data looks like.

```
data_bac_0.3 <- filter(data, BAC >= 0.3)
data_bac_0.3
```

```
## # A tibble: 9 x 2
##   BAC speech_error
##   <dbl>         <dbl>
## 1 0.357           0
## 2 0.352           1
## 3 0.379           1
## 4 0.306           0
## 5 0.382           1
## 6 0.308           1
## 7 0.394           1
## 8 0.332           1
## 9 0.395           1
```

Not bad. Using **logistic regression** we can:

- understand the relationship between variables where the outcome is categorical (two categories)
- make predictions

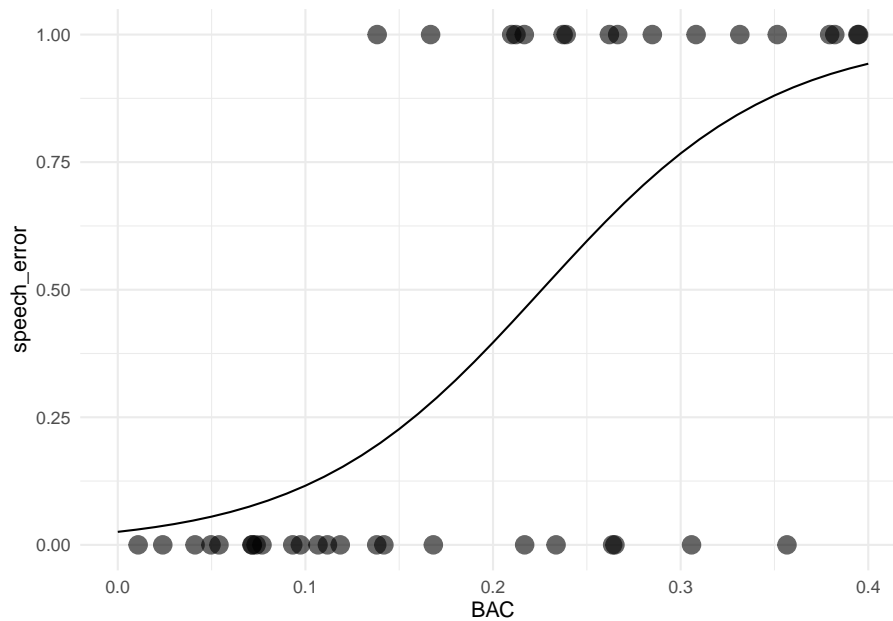
Now that we have the model coefficients, we can predict some values and plot them.

```
BAC_vals <- seq(0, 0.4, 0.01)
y_preds <- plogis(intercept + slope * BAC_vals)

mdl_preds <- tibble(BAC_vals, y_preds)
mdl_preds
```

```
## # A tibble: 41 x 2
##   BAC_vals y_preds
##   <dbl>   <dbl>
## 1      0     0.0255
## 2    0.01     0.0298
## 3    0.02     0.0349
## 4    0.03     0.0407
## 5    0.04     0.0475
## 6    0.05     0.0553
## 7    0.06     0.0644
## 8    0.07     0.0748
## 9    0.08     0.0867
## 10   0.09     0.100
## # i 31 more rows
```

```
ggplot(data, aes(x = BAC, y = speech_error)) +
  geom_point(size = 4, alpha = 0.6) +
  geom_line(data = mdl_preds,
            aes(x = BAC_vals, y = y_preds)) +
  theme_minimal()
```

12.4.4 Dative Dataset

Let us now turn to another dataset we discussed earlier in the semester. This is the dative dataset by Bresnan et al. (2007). The main goal of the experiment was to identify the factors in determining the dative alternation in English:

- Alex gave Sam a book. (NP NP)
- Alex gave a book to Sam. (NP PP)

The dative data set can be found directly using the `languageR` library. Let us take a look at the columns in the dataset and also some values to get a sense of what it looks like.

```
library(languageR)
```

```
colnames(dative)
```

```
## [1] "Speaker"           "Modality"          "Verb"
## [4] "SemanticClass"     "LengthOfRecipient" "AnimacyOfRec"
## [7] "DefinOfRec"        "PronomOfRec"       "LengthOfTheme"
## [10] "AnimacyOfTheme"    "DefinOfTheme"      "PronomOfTheme"
## [13] "RealizationOfRecipient" "AccessOfRec"       "AccessOfTheme"
```

```
head(dative,3)
```

```
##   Speaker Modality Verb SemanticClass LengthOfRecipient AnimacyOfRec DefinOfRec
## 1   <NA>   written feed              t                1      animate   definite
## 2   <NA>   written give              a                2      animate   definite
## 3   <NA>   written give              a                1      animate   definite
##   PronomOfRec LengthOfTheme AnimacyOfTheme DefinOfTheme PronomOfTheme
## 1   pronominal           14      inanimate   indefinite nonpronominal
## 2 nonpronominal           3      inanimate   indefinite nonpronominal
## 3 nonpronominal          13      inanimate    definite nonpronominal
##   RealizationOfRecipient AccessOfRec AccessOfTheme
## 1                    NP      given          new
## 2                    NP      given          new
## 3                    NP      given          new
```

Next, let us take a look at the possible values for the RealizationOfRecipient column to see what they look like.

```
levels(dative$RealizationOfRecipient)
```

```
## [1] "NP" "PP"
```

```
levels(dative$AnimacyOfRec)
```

```
## [1] "animate" "inanimate"
```

OK so, we have only two values. This is a good task for logistic regression. Let us for now model the RealizationOfRecipient as a function of the AnimacyOfRec.

```
model_1 <- model <- glm(RealizationOfRecipient ~ AnimacyOfRec, dative, family='binomial')
tidy(model)
```

```
## # A tibble: 2 x 5
##   term                estimate std.error statistic    p.value
##   <chr>              <dbl>     <dbl>     <dbl>    <dbl>
## 1 (Intercept)        -1.15     0.0426    -27.1  1.15e-161
## 2 AnimacyOfRecinanimate  1.23     0.136      9.02  1.87e- 19
```

```
model_2 <- glm(RealizationOfRecipient ~ AnimacyOfRec+LengthOfTheme+LengthOfRecipient+An.
tidy(model)
```

```
## # A tibble: 2 x 5
##   term                estimate std.error statistic    p.value
##   <chr>                <dbl>    <dbl>    <dbl>    <dbl>
## 1 (Intercept)        -1.15    0.0426   -27.1  1.15e-161
## 2 AnimacyOfRecinanimate    1.23    0.136     9.02  1.87e- 19
```

Now let us compare the two models.

```
library(lmtest)
```

```
## Loading required package: zoo
```

```
##
```

```
## Attaching package: 'zoo'
```

```
## The following objects are masked from 'package:base':
```

```
##
```

```
##      as.Date, as.Date.numeric
```

```
lr_test <- lrtest(model_1, model_2)
print(lr_test)
```

```
## Likelihood ratio test
```

```
##
```

```
## Model 1: RealizationOfRecipient ~ AnimacyOfRec
```

```
## Model 2: RealizationOfRecipient ~ AnimacyOfRec + LengthOfTheme + LengthOfRecipient +
```

```
##      AnimacyOfTheme
```

```
##   #Df  LogLik Df  Chisq Pr(>Chisq)
```

```
## 1    2 -1831.1
```

```
## 2    5 -1379.5  3 903.19 < 2.2e-16 ***
```

```
## ---
```

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

12.5 Testing the model

```
test_data <- select(dative, AnimacyOfRec, LengthOfTheme, LengthOfRecipient, AnimacyOfTheme, RealizationOfTheme)
head(test_data)
```

```
##   AnimacyOfRec LengthOfTheme LengthOfRecipient AnimacyOfTheme
## 1   animate      14           1   inanimate
## 2   animate      3           2   inanimate
## 3   animate     13           1   inanimate
## 4   animate      5           1   inanimate
## 5   animate      3           2   inanimate
## 6   animate      4           2   inanimate
##   RealizationOfRecipient
## 1                NP
## 2                NP
## 3                NP
## 4                NP
## 5                NP
## 6                NP
```

```
# Make predictions on the test set
predictions <- predict(model, newdata = test_data, type = "response")

# For binary classification, calculate accuracy
predicted_classes <- ifelse(predictions > 0.5, 'PP', 'NP')

accuracy <- mean(predicted_classes == test_data$RealizationOfRecipient)

accuracy

## [1] 0.7425682
```

Chapter 13

Modeling Poisson Distribution

Counting is an inherently **discrete process** (not continuous). For example, a sentence can have 4 words or 5 words. However, it cannot have 4.5 words. In addition, counting has no negative values. For example, a sentence can have 2, 3 or 20 words in it but it cannot have -1 words in it. It just doesn't make sense. Thus, technically, we cannot model **count data** with a normal distribution assumption. Instead, count processes are modeled with what is called a **Poisson distribution** named after Siméon Denis Poisson. When the outcome (dependent variable) is a count, it is more appropriate to use modeling techniques that make a Poisson assumption.

13.1 Poisson Distribution

Poisson Distribution models count distributions. It has a single parameter λ which builds in both the central tendency and spread (so to speak). λ is the average rate at which an event would occur at a specified time. It tells you the average number of events you would expect to occur in a given interval.

For example, assume that on average you get **5 email per day**. A day is your interval and λ is the average number of emails. Given $\lambda = 5$, the Poisson distribution of emails per day looks like the following.

```
# Set the lambda parameter for the Poisson distribution
lambda <- 5

# Generate values for x (number of events) and their corresponding probabilities
x <- 0:15
```

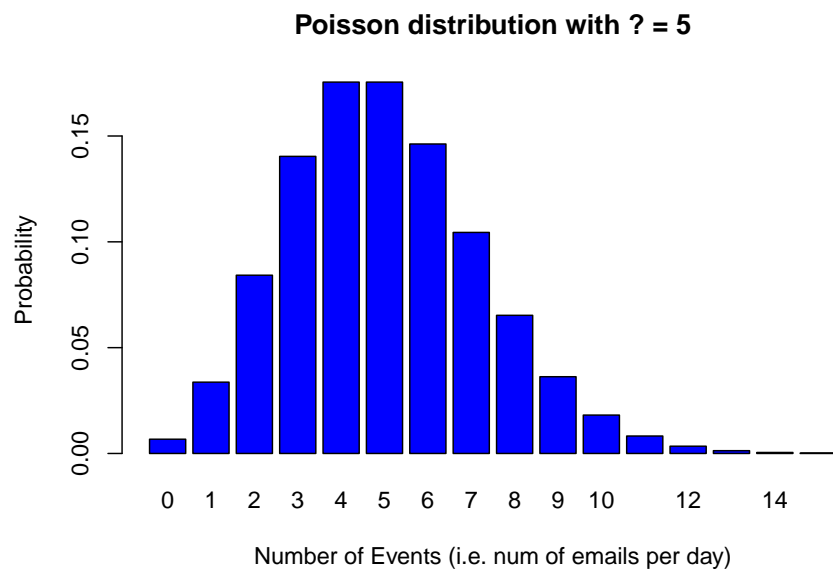
```

probabilities <- dpois(x, lambda)

barplot(probabilities, names.arg = x, col = "blue",
        xlab = "Number of Events (i.e. num of emails per day)",
        ylab = "Probability")

# Add a title and labels to the plot
title(paste("Poisson distribution with ", lambda))

```



The bar plot above plots the **probability density** of each event. In other words, it just gives us a probability for each number of emails per day. As you can see, when $\lambda = 5$, it is more likely to get 4 or 5 emails than 15 emails per day. Let us play with the number of events to see what the probability distribution looks like.

```

# Set the lambda parameter for the Poisson distribution
lambda <- 5

# Generate values for x (number of events) and their corresponding probabilities
x <- 0:50
probabilities <- dpois(x, lambda)

barplot(probabilities, names.arg = x, col = "blue",
        xlab = "Number of Events (i.e. num of emails per day)",

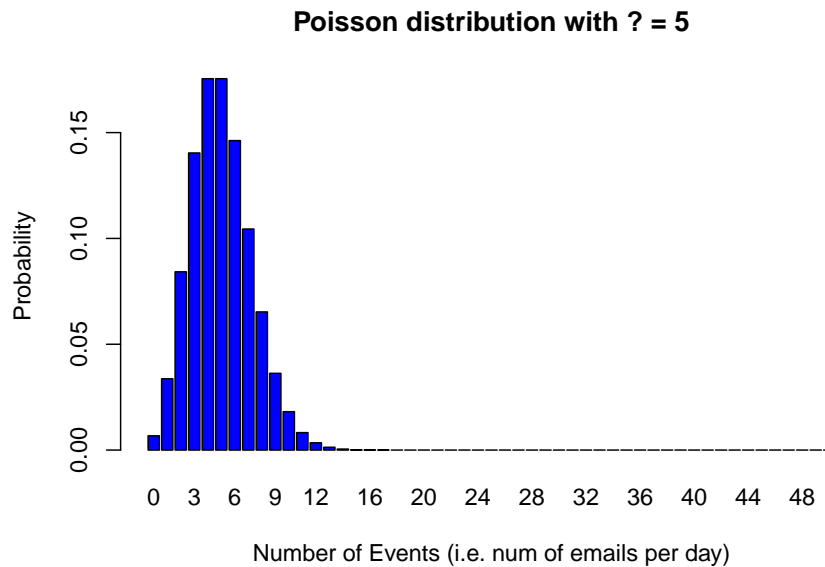
```

```

      ylab = "Probability")

# Add a title and labels to the plot
title(paste("Poisson distribution with  $\lambda =$ ", lambda))

```



Notice how we kept λ constant and merely increased the number of emails per day. We now have a long tail with probabilities close to 0. This just simply means ‘if you are receiving on average 5 emails per day, then the probability of getting 50 emails on a given day is very low (close to 0).’

Let us now change our λ to see what it looks like. Assume that on average you get 20 emails per day.

```

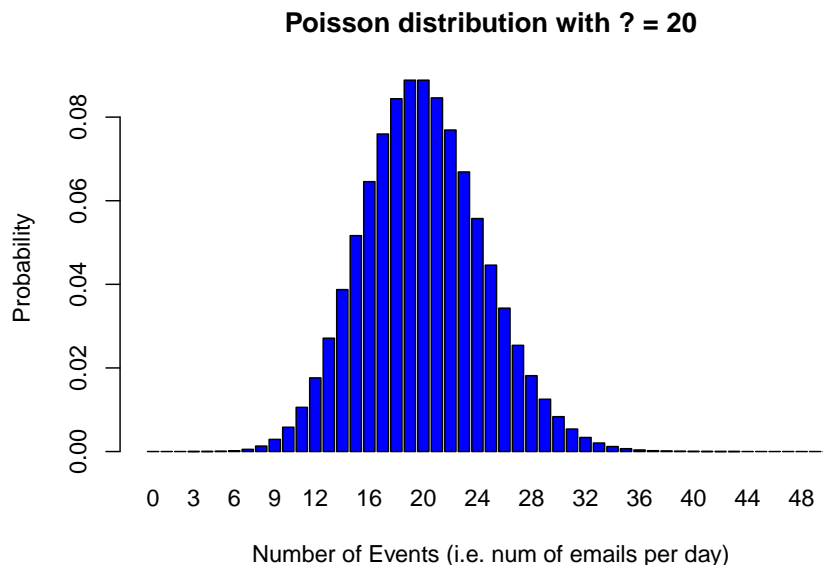
# Set the lambda parameter for the Poisson distribution
lambda <- 20

# Generate values for x (number of events) and their corresponding probabilities
x <- 0:50
probabilities <- dpois(x, lambda)

barplot(probabilities, names.arg = x, col = "blue",
        xlab = "Number of Events (i.e. num of emails per day)",
        ylab = "Probability")

```

```
# Add a title and labels to the plot
title(paste("Poisson distribution with ", lambda))
```



So far, we have used the `dpois()` function to generate the probability distributions of possible events. It takes in an array of possible event values and a λ and returns the probability associated with each event given λ . These are theoretical values. What the barplot above tells us is the following: ‘For any given day, you are likely to get 20 emails. It is also equally likely that you’ll get 18 or 21 emails. It is also possible that you only get 9 emails but it is a lot less likely. It is very unlikely that you’ll get no emails at all.’

Given the probabilities above, how does a real day look like then? For simulating real life scenarios, we need to randomly sample some data using the probabilities above. For that, we’ll use the `rpois()` function. The `r` prefix before distributions suggests that we want to do some random sampling. We’ve seen this several times.

- `dnorm()` – `rnorm()`
- `dbinom()` – `rbinom()`
- `dpois()` – `rpois()`

Let us now simulate a single day with $\lambda = 20$. Think of it like ‘On average I get 20 emails per day. Given that today is just another day in the office, how many emails am I getting today?’ Each time we run the code below, we’ll get a slightly different number as the sampling is random.


```
# Number of samples and lambda
rpois(1,lambda=20)
```

```
## [1] 37
```

Now, let us project what a month will look like in terms of the number of emails I receive. For that, we just need to sample not once but 30 times.

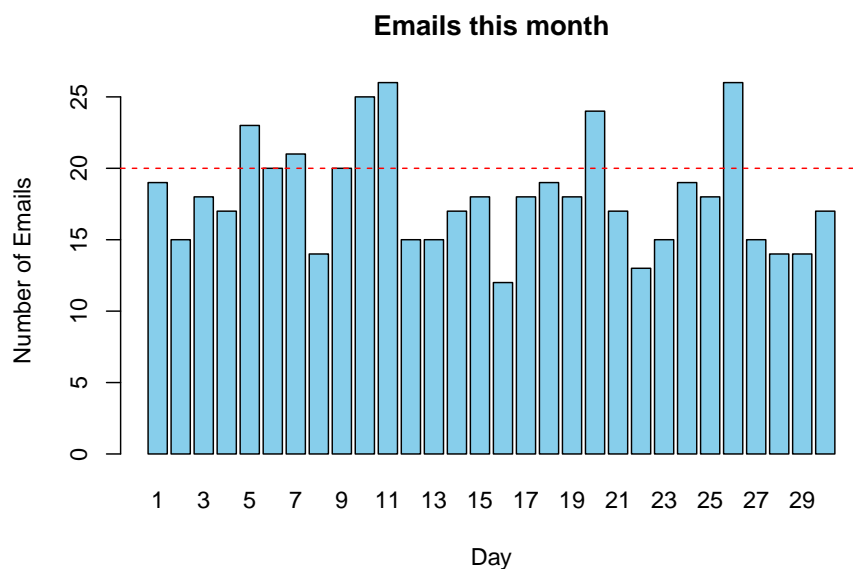
```
# Number of samples and lambda
emails_this_month <- rpois(30,lambda=20)
emails_this_month
```

```
## [1] 19 15 18 17 23 20 21 14 20 25 26 15 15 17 18 12 18 19 18 24 17 13 15 19 18
## [26] 26 15 14 14 17
```

Let us plot the emails to get a better visual.

```
# Plot a bar graph
barplot(emails_this_month, names.arg = 1:30, col = "skyblue",
        main = "Emails this month",
        xlab = "Day", ylab = "Number of Emails")

# Add a horizontal line representing the average rate (lambda)
abline(h = lambda, col = "red", lty = 2)
```



13.2 Modeling with Poisson distribution

When modeling data where the outcome is a count, we should assume a Poisson distribution and model our data accordingly. To do this, we'll use generalized linear models with a Poisson assumption. Our goal is to estimate the λ parameter. For any given set of independent variables, we assume that the outcome will be:

- $y \sim \text{Poisson}(\lambda)$

Let us first get some data though.

13.2.1 Data

We'll use the Nettle (1999) data which we used earlier in the semester.

```
library(tidyverse)
nettle <- read_csv('/Users/umit/ling_411/data/nettle_1999_climate.csv')
```

```
## Rows: 74 Columns: 5
## -- Column specification -----
## Delimiter: ","
## chr (1): Country
## dbl (4): Population, Area, MGS, Langs
##
## i Use `spec()` to retrieve the full column specification for this data.
## i Specify the column types or set `show_col_types = FALSE` to quiet this message.
```

```
nettle
```

```
## # A tibble: 74 x 5
##   Country      Population Area   MGS Langs
##   <chr>          <dbl> <dbl> <dbl> <dbl>
## 1 Algeria         4.41  6.38  6.6    18
## 2 Angola          4.01  6.1   6.22   42
## 3 Australia       4.24  6.89  6      234
## 4 Bangladesh     5.07  5.16  7.4    37
## 5 Benin           3.69  5.05  7.14   52
## 6 Bolivia         3.88  6.04  6.92   38
## 7 Botswana       3.13  5.76  4.6    27
## 8 Brazil         5.19  6.93  9.71  209
## 9 Burkina Faso   3.97  5.44  5.17   75
## 10 CAR           3.5   5.79  8.08   94
## # i 64 more rows
```

The data consists of *population*, *area*, *mean growing season* (MGS), and *number of languages* spoken in a country. For now, we'll just try to predict the number of language spoken in a country as a function of the MGS.

```
library(broom)
mgs_model <- glm(Langs ~ MGS, data = nettle,
                 family = 'poisson')

tidy(mgs_model)
```

```
## # A tibble: 2 x 5
##   term      estimate std.error statistic  p.value
##   <chr>      <dbl>    <dbl>    <dbl>    <dbl>
## 1 (Intercept)  3.42    0.0392    87.1  0
## 2 MGS         0.141   0.00453    31.2 2.42e-213
```

Let us interpret the coefficients. We observe that the intercept is positive and the p-value is very small. This indicates a positive correlation between the number of languages and mean number growing seasons and the relationship is statistically significant. There's one thing to pay attention though. The coefficients in `glm poisson` are expressed in logarithms. In order for them to make a bit more sense, we need to exponentiate them (remember that exponentiation is the inverse of logarithms).

```
intercept <- tidy(mgs_model)$estimate[1]
slope <- tidy(mgs_model)$estimate[2]

exp(intercept)
```

```
## [1] 30.45637
```

```
exp(slope)
```

```
## [1] 1.151545
```

The intercept is 30.45637. This means that on average, a country with 0 months of growing season (e.g. desert or ice/snow) will have 30 languages. Let us predict other values.

```
langs <- exp(intercept + 1:12 * slope)
langs
```

```
## [1] 35.07188 40.38685 46.50727 53.55521 61.67123 71.01719 81.77948
## [8] 94.17275 108.44415 124.87831 143.80298 165.59559
```

```
filter(nettle, MGS == 0 | MGS == 12)
```

```
## # A tibble: 6 x 5
##   Country      Population Area   MGS Langs
##   <chr>          <dbl> <dbl> <dbl> <dbl>
## 1 Guyana          2.9   5.33   12    14
## 2 Oman            3.19  5.33    0     8
## 3 Solomon Islands 3.52  4.46   12    66
## 4 Suriname        2.63  5.21   12    17
## 5 Vanuatu          2.21  4.09   12   111
## 6 Yemen            4.09  5.72    0     6
```

```
mgs_model_1 <- mgs_model <- glm(Langs ~ MGS, data = nettle,
                                family = 'poisson')

mgs_model_2 <- mgs_model <- glm(Langs ~ Population + Area + MGS, data = nettle,
                                family = 'poisson')

library(lmtest)

lr_test <- lrtest(mgs_model_1, mgs_model_2)
print(lr_test)
```

```
## Likelihood ratio test
##
## Model 1: Langs ~ MGS
## Model 2: Langs ~ Population + Area + MGS
##   #Df LogLik Df  Chisq Pr(>Chisq)
## 1    2 -4576.2
## 2    4 -2861.7  2 3428.9 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
library(MASS)
```

```
##
## Attaching package: 'MASS'

## The following object is masked from 'package:dplyr':
##
##   select
```

```
mgs_model_3 <- mgs_model <- glm.nb(Langs ~ Population + Area + MGS, data = nettle)
```

```
tidy(mgs_model_3)
```

```
## # A tibble: 4 x 5
##   term          estimate std.error statistic  p.value
##   <chr>         <dbl>     <dbl>     <dbl>    <dbl>
## 1 (Intercept)  -4.01      1.25     -3.21  1.35e- 3
## 2 Population    0.401     0.188     2.14  3.25e- 2
## 3 Area          0.870     0.245     3.55  3.88e- 4
## 4 MGS           0.238     0.0363    6.55  5.74e-11
```

```
lr_test <- lrtest(mgs_model_2, mgs_model_3)
lr_test
```

```
## Likelihood ratio test
##
## Model 1: Langs ~ Population + Area + MGS
## Model 2: Langs ~ Population + Area + MGS
##   #Df   LogLik Df  Chisq Pr(>Chisq)
## 1    4 -2861.73
## 2    5 -379.84  1 4963.8 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```