R Fundamentals Part 4: For-loops and functions

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Learning objectives

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Load your `sleep_VIM.csv` file from Part 2:

```
sleep <- read.csv("sleep_VIM.csv", header=TRUE, stringsAsFactors = FALSE)
```

0. Functionals

0. Functionals/

A functional is a function that takes functions as arguments.

0. Functionals/ The wrong way to be functional

Imagine you want to apply a function to the columns of a dataframe (which is a list!). You could do something like this:

```
?mean

mean(sleep[,2], na.rm=TRUE)

## [1] 283.1342

mean(sleep[,3], na.rm=TRUE)

## [1] 8.672917

mean(sleep[,4], na.rm=TRUE)

## [1] 1.972
```

0. Functionals/ the right way to be functional

```
?lapply

lapply(sleep, mean)

## $BodyWgt
## [1] 198.79
##
## $BrainWgt
## [1] 283.1342
##
## $NonD
```

```
## [1] NA
##
## $Dream
## [1] NA
##
## $Sleep
## [1] NA
##
## $Span
## [1] NA
##
## $Gest
## [1] NA
##
## $Pred
## [1] 2.870968
##
## $Exp
## [1] 2.419355
##
## $Danger
## [1] 2.612903
```

Or equivalently, sapply()

```
?sapply

sapply(sleep, mean)

##    BodyWgt   BrainWgt       NonD      Dream      Sleep       Span
Gest       Pred        Exp     Danger
## 198.789984 283.134194         NA         NA         NA         NA
NA   2.870968   2.419355   2.612903

sapply(sleep, mean, simplify=FALSE)

## $BodyWgt
## [1] 198.79
##
## $BrainWgt
## [1] 283.1342
##
## $NonD
## [1] NA
##
## $Dream
## [1] NA
##
## $Sleep
## [1] NA
##
```

```
## $Span
## [1] NA
##
## $Gest
## [1] NA
##
## $Pred
## [1] 2.870968
##
## $Exp
## [1] 2.419355
##
## $Danger
## [1] 2.612903
```

However, `lapply()` has limits. We can't do something like the following:

```
lapply(sleep, mean(na.rm = TRUE))
```

1. Introduction

Commands in R are built on many small functions that can be grouped together in smart ways to do powerful things. You assign functions in a way similar to how you assign an object (with <-). Functions are generally meant to be mapped to data structures or are used to write other functions. Using functions might allow you to write your code more efficiently.

However, before we get to functions, let us review for loops because many functions have for loops embedded in them.

Set working directory and load the `animals` data frame - we will return to this a little later:

```
getwd()
```

```
## [1] "/Users/E/Desktop/R-Fundamentals-master"
```

```
setwd("/Users/E/Desktop/R-Fundamentals-master")
animals <- read.csv("animals.csv", header=TRUE, stringsAsFactors=FALSE)
str(animals)
```

```
## 'data.frame':    20 obs. of  5 variables:
##  $ Name    : chr  "Dog" "Pig" "Dog" "Cat" ...
##  $ Healthy : logi  FALSE TRUE TRUE FALSE FALSE TRUE ...
##  $ Weight  : num  4.06 4.49 5.29 6.63 3.81 ...
##  $ Height  : int  10 6 7 6 8 6 7 9 5 10 ...
##  $ Progress: num  1.512 0.39 -0.621 -2.215 1.125 ...
```

2. For-loops

Before we introduce how functions work and learn how to write them, let us discuss how a for-loop works in R. A for-loop repeats a block of code a certain number of times until a certain condition is met, telling the code to stop and potentially print/return some sort of output.

Many functions often have for-loops embedded in them, hence it will be useful to understand looping first. The basic syntax looks like this:

syntax: `for(variable in sequence){statement}`

All for-loops are precluded by `for` so that R knows you want to iterate over a loop.

The `variable` in `(variable in sequence)` is generally denoted with an `i`, which stands for "iterator". However, `i` should be thought of as a placeholder and can be represented by other ways (e.g., `x`, `donut`, `n`, etc.). `sequence` is some sequence of numbers telling R how many times you want to iterate the code.

"{statement}" refers to the code that you want run over the sequence at each iteration `i`. Notice that it is contained within curly braces { } - this defines the boundary of the statement in the for-loop.

2. For-loops/ Example 1

Let's create a matrix of 2 to the power of `i` where `i` is 1 to 10. First we create a null vector called `mat` which will serve as a placeholder for the output of the loop.

```
?rep

mat <- c(rep(NA, 10))
mat

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

Now, let's create a matrix of 2 to the power of i where i is 1 to 10

```
for(i in 1:10){
    mat[i] <- 2^(i)
    }
mat

##  [1]    2    4    8   16   32   64  128  256  512 1024
```

This code tells R that we want to raise 2 to the power of `i`, where `i` is 1:10.

We can also use indexing to modify only some elements. We now have an object called `mat` with defined values. What if we want to replace the first 5 elements of `mat` with 3 to the power of `i` instead?

You can change the `sequence` to to tell R just to overwrite the first five positions!

```
for(i in 1:5){
    mat[i] <- 3^i
    }
mat

##  [1]    3    9   27   81  243   64  128  256  512 1024

#This has changed only the first five entries of `mat`
```

This can also be a character vector. First, create a name vector:

```
animal.names <- c("Cat", "Dog", "Pig", "Elephant", "Giraffe")
animal.names

## [1] "Cat"      "Dog"      "Pig"      "Elephant" "Giraffe"
```

Then, we create a NULL vector of the same length like we did above:

```
animals.length <- rep(NA, length(animal.names))
animals.length

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

Now give the null vector names:

```
names(animals.length) <- animal.names
animals.length  #See how we are building this from scratch?

##      Cat      Dog      Pig Elephant  Giraffe
##       NA       NA       NA       NA       NA
```

Finally, perhaps you want to perform some operation across `animals.length`. For example, count the number of characters in each animal name like this:

```
?nchar

for(i in animal.names){
  animals.length[i] <- nchar(i)
}
animals.length

##      Cat      Dog      Pig Elephant  Giraffe
##        3        3        3        8        7
```

2. For-loops/ `break` and `stopifnot`

For long loops, many intermediate commands can help us "end the looping" once a condition is met, or when a condition is no longer satisfied. Two particular useful ones are `break` and `stopifnot`.

`break` ends the looping once a certain condition is met.

`stopifnot` ends the loop when a certain condition is NOT met.

Let's begin by writing a for-loop that outputs the numbers of the sequence 1:100

```
for(i in 1:100){
    print(i)
    }
```

`if` statements are frequently used to specify code to be evaluated when the condition is held. Here we tell the code that when `i` is equal to 50, stop the code:

```
?break

for(i in 1:100){
    print(i)
    if(i == 50) break
}
#Numbers up to and including 50 are printed!
```

`stopifnot` works similarly. Here we tell the code to stop if `i` is no longer less than or equal to <= 50:

```
?stopifnot

for(i in 1:100){
    stopifnot(i<=50)
    print(i)
}
```

Challenge 1

1. Write a for-loop that outputs something
2. Insert a `break` or `stopifnot` command to tell it when to stop

2. For-loops/ `if`, `else`, and `ifelse`

`if` and `else` statements are control structures that let you control how a code should be iterated within a single for-loop. You saw `if` above and is handy when you want to assign different tasks to different subsets of data using a single for-loop.

`if` something happens, do "this" if something `else` happens, do "that"!

syntax: if(condition){statement} else{other statement}

```
?"if"

x <- 7
if(x > 7){
  print(x)
  }else{   #`else` should not start its own line. Always let it be
preceded by a closing brace on the same line.
```

```
  print("NOT BIG ENOUGH!!")
  }
```

```
## [1] "NOT BIG ENOUGH!!"
```

Reassign x <- 10 here - what happens?

This also works in a loop. Here, we get all outputs for the loop:

```
x <- 1:10
for (i in 1:10){
    if(x[i] > 7){
        print(x[i])
        }else{
            print("NOT BIG ENOUGH!!")}
    }
```

```
## [1] "NOT BIG ENOUGH!!"
## [1] "NOT BIG ENOUGH!!"
## [1] "NOT BIG ENOUGH!!"
## [1] "NOT BIG ENOUGH!!"
## [1] "NOT BIG ENOUGH!!"
## [1] "NOT BIG ENOUGH!!"
## [1] "NOT BIG ENOUGH!!"
## [1] 8
## [1] 9
## [1] 10
```

```
#Super cool! :)
```

The ``ifelse" function can be handy to recode data as long as you have two conditions that are binary/mutually exclusive.

syntax: `ifelse(test, yes, no)`

Let us begin by generating 10 random draws of two common housepets "cat" and "dog":

```
?"ifelse"

set.seed(1)
animal <- sample(c("cat", "dog"), 10, replace=TRUE)
animal
```

```
##  [1] "cat" "cat" "dog" "dog" "cat" "dog" "dog" "dog" "dog" "cat"
```

Now we can recode the character data to numeric using `ifelse()`:

```
animal <- ifelse(animal=="cat", 1, 0)
animal
```

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

... or recode the numeric data to some other character type:

```
animal <- ifelse(animal==1, "meow!?", "WOOF")
animal
```

```
##  [1] "meow!?" "meow!?" "WOOF"   "WOOF"   "meow!?" "WOOF"   "WOOF"
"WOOF"   "WOOF"   "meow!?"
```

... and recode the new character data type to logical type:

```
animal <- ifelse(animal=="meow!?", TRUE, FALSE)
animal
```

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

Challenge 2

1. Write a for-loop that uses `if`
2. Write a for-loop that uses `if` and `else`
3. Create and then recode some binary data using `ifelse`

3. Functions

In R, a function is a set of code that might be more useful if it is self-contained and/or is to be used repeatedly. For example, if you want to run the same satatistical tests on several datasets, you might want to write a function that contains instructions for all the tests once, so that you do not have to rewrite the code each time.

Every function has four parts and its basic syntax looks like this:

function.name <- function(x){ body of function }

1. `function.name` - like objects in R, it is helpful if you give your function a relevant name.
2. `function(x)` - `function` lets R know you are writing a function and `(x)` contains the inputs/arguments.
3. `{body of function}` - the body of the function is contained within curly braces { } and denotes the statements that you want R to evaluate.
4. The `environment` (global environment) that the function operates within.

For example:

```
?"function"

test_function <- function(x){
  x + 1
}
```

```
class(test_function)        # Returns the class of `test_function`

## [1] "function"

formals(test_function)      # Shows the defined arguments

## $x

body(test_function)         # Displays the statements to be evaluated

## {
##     x + 1
## }

environment(test_function)  # Returns the "global" environment

## <environment: R_GlobalEnv>

test_function               # Shows your function as you have written
it

## function(x){
##   x + 1
## }
```

See how our function has `R_GlobalEnv` as it's environment? that's because we defined it in the global environment. This means that if you tell a function to look for an `object`, it will look in the global namespace - not within the function itself.

To evaluate this function, call the name of the function with your argument `x` within parantheses. R then evaluates the body of the function and returns the desired output for the specified input.

If we want to see what `x + 1` is equal to when x = 2, we type:

```
test_function(2)

## [1] 3
```

3. Functions/ default arguments

We can also add a predetermined value for one or more arguments, which serves as a default value that we can change in particular applications. Define a function called `f`. We will tell R to hold the y input/argument constant at "3", and leave `x` and `z` to our choosing:

```
f <- function(x, y=3, z){
  (x + y) / z
}
f(x = 1, z = 1) #here, we only specify `x` and `z` because `y` is held
constant.
```

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

If we want, we can also change the default arguments within the function call itself:

```
f(x = 2, y = 1, z = 10)

## [1] 0.3
```

3. Functions/ functions-within-functions

It is also common for functions to be declared within another function.

```
f <- function(x) {
  y <- 1
  g <- function (x) {
    x + y
  }
  g(x)
}
f(1)

## [1] 2
```

What is going on here? Does g show up in your global environment? Why not? (hint: because it was defined in the functional environment instead of the global environment!)

This is important because it means that functions can be separated from the state of your computer (which is what makes them easy to parallelize). What we really mean here is that anything created inside the function environment doesn't show up in the global environment.

side note - R automatically returns the value of the last expression, so there is no need for an explicit `return` statement unless you want to break the function early

For example:

```
f <- function(x) {
    if (x>5) {return("ERROR")}
    y <- 4
    g <- function (x) {
    x + y
  }
  g(x)
}
f(x=1)

## [1] 5

f(x=10)

## [1] "ERROR"
```

3. Functions/ unit conversion example

Unit conversion is a common obstacle in research. Let us write a function that converts inches to centimeters. For now however, pretend that we think that one inch is equal to 2.5 centimeters - we will show you how to update it below.

Define a function called `in_to_cm` and then enter Evan's height (74 inches):

```
in_to_cm <- function(x){
  x * 2.5
}
in_to_cm(74)

## [1] 185

#Evan is 185 cm tall (incorrectly assuming that 1 inch = 2.5 cm)
```

What if we want to know how tall I am in meters?

You could type:

```
function(x){
  x * 2.5 / 100
  }
```

...but this would be repeating yourself!

Then, when you figure out that the conversion factor is really *2.54*, not 2.5, you might update one function and forget to update the other - these inconsistencies can cause problems.

Instead, let's define a new function called `in_to_m` so that the output of `in_to_cm` is used in the new function!

```
in_to_m <- function(x){
  in_to_cm(x) / 100
}
in_to_m(74)

## [1] 1.85
```

Now, if we go back and update `in_to_cm`, those changes automatically get propogated to `in_to_m` and we do not have to worry about updating it!

```
in_to_cm <- function(x){
  x * 2.54
}
in_to_m(74)

## [1] 1.8796

#Evan is actually 1.8796 meters tall
```

R is a bit quirky in that there is no such thing as an uncontained value, e.g. the number 74 is really a vector with length of one, and a value of 74 in position 1

```
74 == c(74)

## [1] TRUE
```

This means that R automatically broadcasts functions across vectors of any length.

```
height.vec <- c(74,64,73,82)
in_to_m(height.vec)

## [1] 1.8796 1.6256 1.8542 2.0828
```

Note this doesn't work with lists:

```
height.list <- list(74,64,73,82)

in_to_m(height.list)
```

```

NOTE: Here, the error message shows the incorrect inches to centimeter conversion of 2.5 instead of 2.54

Instead, a functional such as `lapply()` might be used to do so. Remember that a functional is a function that takes functions as arguments.

```
lapply(height.list, in_to_m)

[[1]]
[1] 1.8796
##
[[2]]
[1] 1.6256
##
[[3]]
[1] 1.8542
##
[[4]]
[1] 2.0828
```

## 3. Functions/ Day 3 statistical tests function

Remember back to Day 3 when you learned a t-test, ANOVA, cor.test, and lm? We can block these into a function quite conveniently, and we can even include plots!

First, refer back to your `animals` data frame.

```
str(animals)

'data.frame':   20 obs. of 5 variables:
$ Name   : chr "Dog" "Pig" "Dog" "Cat" ...
$ Healthy : logi FALSE TRUE TRUE FALSE FALSE TRUE ...
```
```

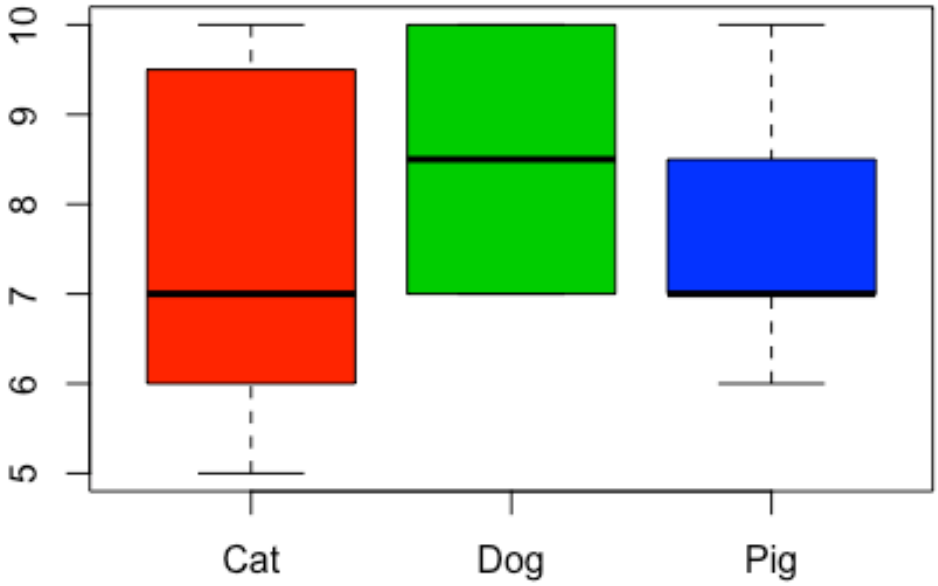
```
##  $ Weight  : num  4.06 4.49 5.29 6.63 3.81 ...
##  $ Height  : int  10 6 7 6 8 6 7 9 5 10 ...
##  $ Progress: num  1.512 0.39 -0.621 -2.215 1.125 ...

head(animals)

##   Name Healthy   Weight Height    Progress
## 1  Dog   FALSE 4.062035     10  1.51178117
## 2  Pig    TRUE 4.488496      6  0.38984324
## 3  Dog    TRUE 5.291413      7 -0.62124058
## 4  Cat   FALSE 6.632831      6 -2.21469989
## 5  Pig   FALSE 3.806728      8  1.12493092
## 6  Cat    TRUE 6.593559      6 -0.04493361
```

Then write your function to include ANOVA, Pearson correlation, and linear model information (as well as a boxplot). Notice that we are defining four objects within the function itself:

```
stats_tests <- function(x){
  sum_aov <- summary(aov(Height ~ Name, data=animals))
  Pearson <- cor.test(animals$Height, animals$Weight)
  sum_lm <- summary(lin.mod <- lm(Height ~ Weight, data=animals))
  box <- boxplot(Height ~ Name, data=animals, col=c(2,3,4))
stats_list <- list(sum_aov, Pearson, sum_lm, box)
names(stats_list)[1:4] <- c("ANOVA summary info", "Pearson correlation
info", "Linear model summary info", "Boxplot info")
list(stats_list)
}
```

All we have to do is call the function on the argument x

```
stats_tests(x)
```

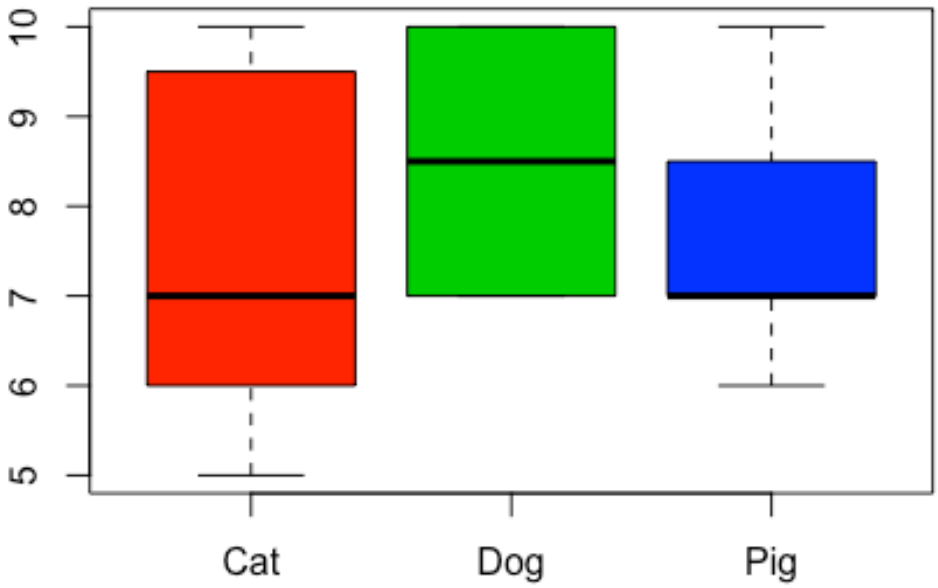



```
## [[1]]
## [[1]]$`ANOVA summary info`
##             Df Sum Sq Mean Sq F value Pr(>F)
## Name         2   3.16   1.579    0.53  0.598
## Residuals   17  50.64   2.979
##
## [[1]]$`Pearson correlation info`
##
##  Pearson's product-moment correlation
##
## data:  animals$Height and animals$Weight
## t = -1.8502, df = 18, p-value = 0.08076
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  -0.71566804  0.05196763
## sample estimates:
##       cor
## -0.399746
##
##
## [[1]]$`Linear model summary info`
##
## Call:
```

```
## lm(formula = Height ~ Weight, data = animals)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -2.7262 -1.0758 -0.1898  1.2445  2.6226
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  10.9685     1.6958   6.468 4.39e-06 ***
## Weight       -0.5878     0.3177  -1.850   0.0808 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.585 on 18 degrees of freedom
## Multiple R-squared:  0.1598, Adjusted R-squared:  0.1131
## F-statistic: 3.423 on 1 and 18 DF,  p-value: 0.08076
##
##
## [[1]]$`Boxplot info`
## [[1]]$`Boxplot info`$stats
##      [,1] [,2] [,3]
## [1,]  5.0  7.0  6.0
## [2,]  6.0  7.0  7.0
## [3,]  7.0  8.5  7.0
## [4,]  9.5 10.0  8.5
## [5,] 10.0 10.0 10.0
## attr(,"class")
##       Cat
## "integer"
##
## [[1]]$`Boxplot info`$n
## [1] 7 6 7
##
## [[1]]$`Boxplot info`$conf
##          [,1]      [,2]     [,3]
## [1,] 4.909856  6.564903 6.104224
## [2,] 9.090144 10.435097 7.895776
##
## [[1]]$`Boxplot info`$out
## numeric(0)
##
## [[1]]$`Boxplot info`$group
## numeric(0)
##
## [[1]]$`Boxplot info`$names
## [1] "Cat" "Dog" "Pig"
```

We can subset the output like you learned in Part 2. For example, to return only the results of the Pearson correlation:

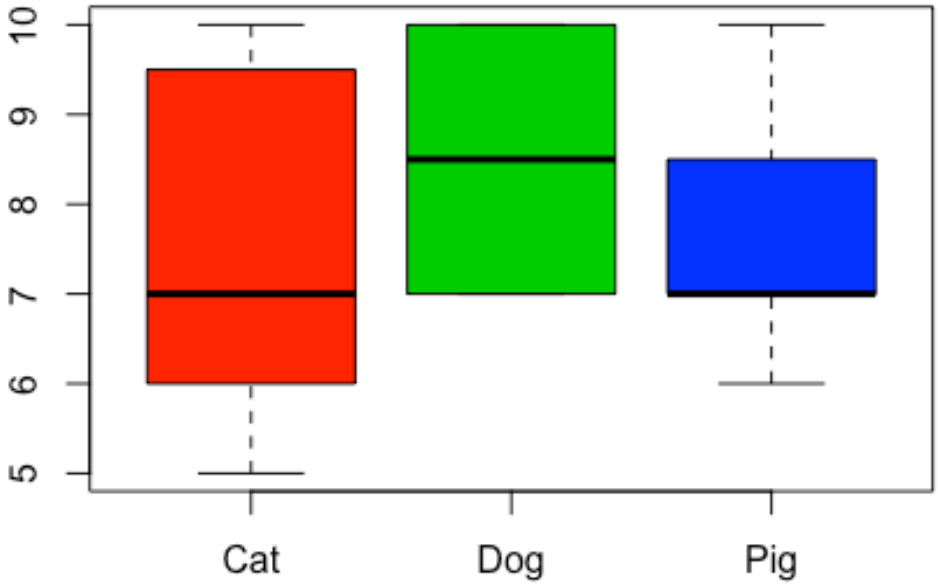
```
stats_tests(x)[[1]][2]
```




```
## $`Pearson correlation info`
##
##  Pearson's product-moment correlation
##
## data:  animals$Height and animals$Weight
## t = -1.8502, df = 18, p-value = 0.08076
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  -0.71566804  0.05196763
## sample estimates:
##       cor
## -0.399746
```

Or return only the results of the linear model:

```
stats_tests(x)[[1]][3]
```




```
## $`Linear model summary info`
##
## Call:
## lm(formula = Height ~ Weight, data = animals)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -2.7262 -1.0758 -0.1898  1.2445  2.6226
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  10.9685     1.6958   6.468 4.39e-06 ***
## Weight       -0.5878     0.3177  -1.850   0.0808 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.585 on 18 degrees of freedom
## Multiple R-squared:  0.1598, Adjusted R-squared:  0.1131
## F-statistic: 3.423 on 1 and 18 DF,  p-value: 0.08076
```

etc...

4. Monte Carlo simulations

A Monte Carlo simulation is an algorithm that relies on repeated random sampling to obtain numerical results. In R, loops and functions are key for Monte Carlo simulations.

For example, we can simulate a die roll by taking a random sample from a 1:6 vector.

```
sample(1:6, 1)

## [1] 2

# We can also use the sample function to simulate 100 die rolls...
sample(1:6, 100, replace=TRUE)

##   [1] 2 5 3 5 3 5 6 3 5 6 2 4 1 2 3 1 3 6 3 3 4 3 2 5 5 5 1 5 3 5 4
5 4 4 5 1 3 5 5 3 6 3 2 1 1 2 4 4 3 6 2 3 2 4 2 3 5
##  [58] 1 6 3 6 3 3 3 6 6 3 5 6 3 5 3 2 5 2 5 1 2 1 2 1 4 6 5 5 3 3 5
4 4 3 2 6 4 2 1 3 6 4 6
```

But what if we wanted to repeat the process 200 times and get the mean of the die rolls for each iteration? One option is to do that with a loop:

```
iter <- 200
nr_rolls <- 100
for (i in 1:iter){
    rolls <- sample(1:6, nr_rolls, replace=TRUE)
    print(rolls)
    print(mean(rolls))
}
```

Another alternative is to write a function that produces one iteration of the process and then use the `replicate` command to repeat the process 100 times.

4. Monte Carlo simulations/ Step 1

Write a function that works through the process once

```
die_roll_mean <- function(nr_rolls){
    rolls <- sample(1:6, nr_rolls, replace=TRUE)
    mean(rolls)
}

die_roll_mean(nr_rolls = 100)

## [1] 3.56
```

4. Monte Carlo simulations/ Step 2

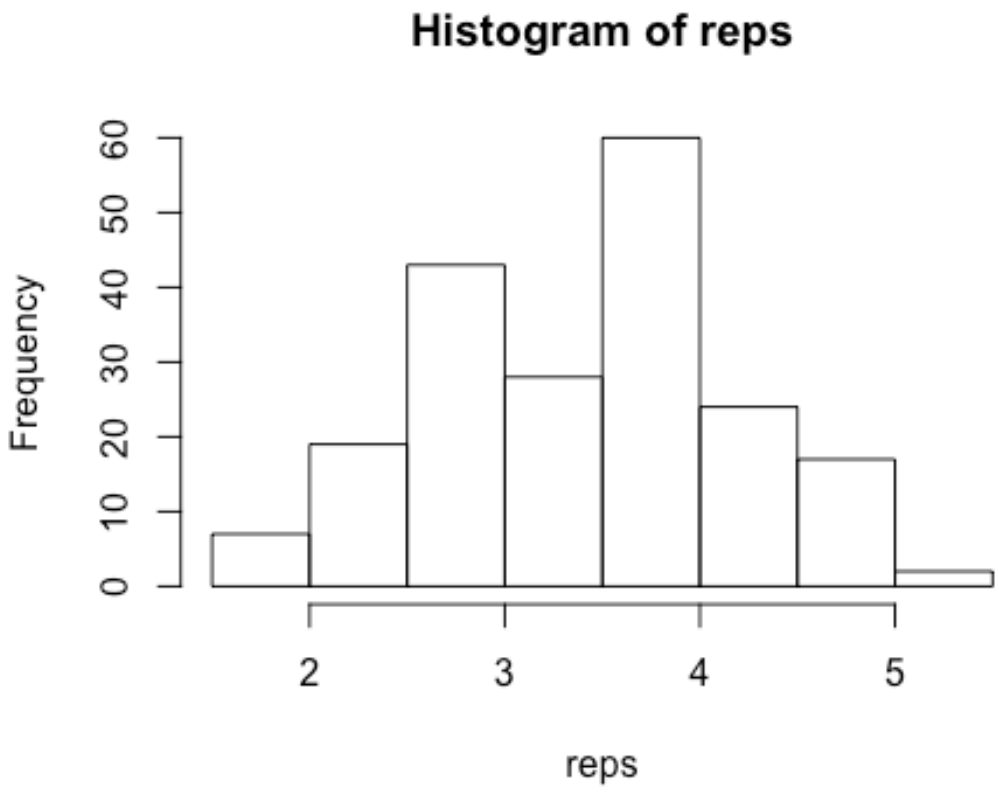
Now we use `replicate` to iterate the function 200 times:

```
?replicate

reps <- replicate(200, die_roll_mean(nr_rolls = 100))

reps

reps <- replicate(200, die_roll_mean(nr_rolls = 5))

reps
```

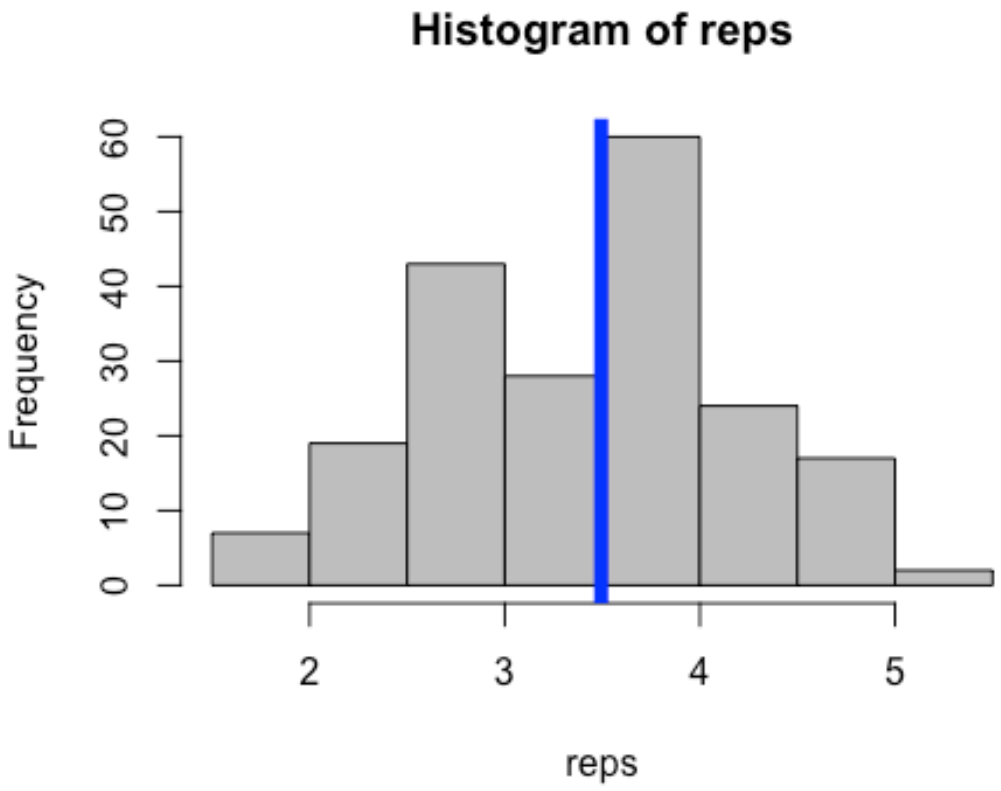
4. Monte Carlo simulations/ include a plotting function

Again, we can use functions with plotting functions as well:

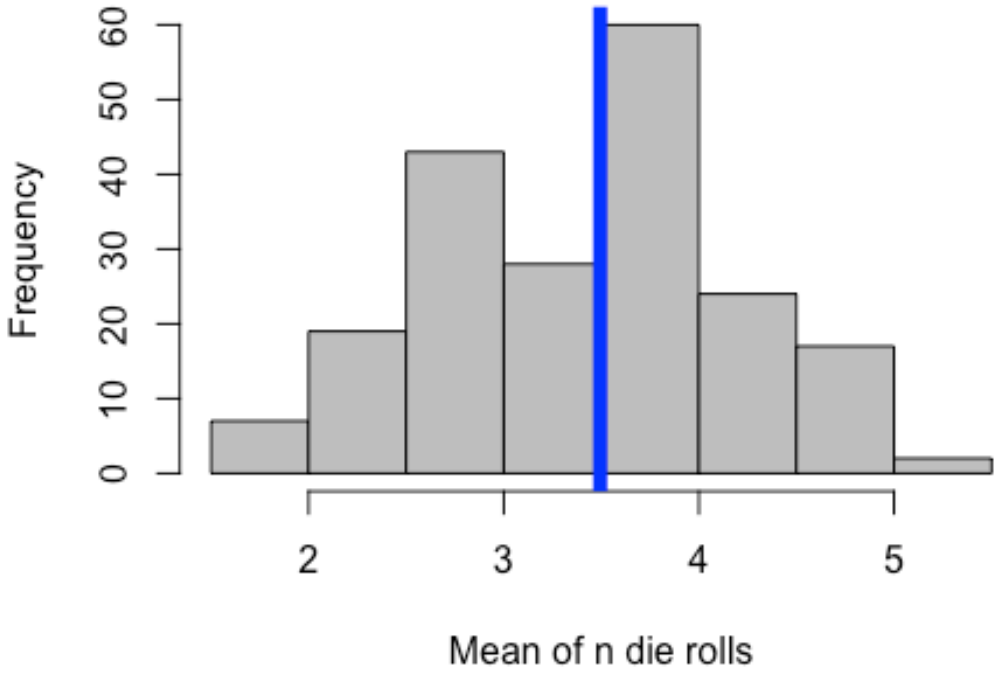
```
hist(reps)
```




```
hist(reps, col="grey")
abline(v=mean(reps), col="blue", lwd=6)
```



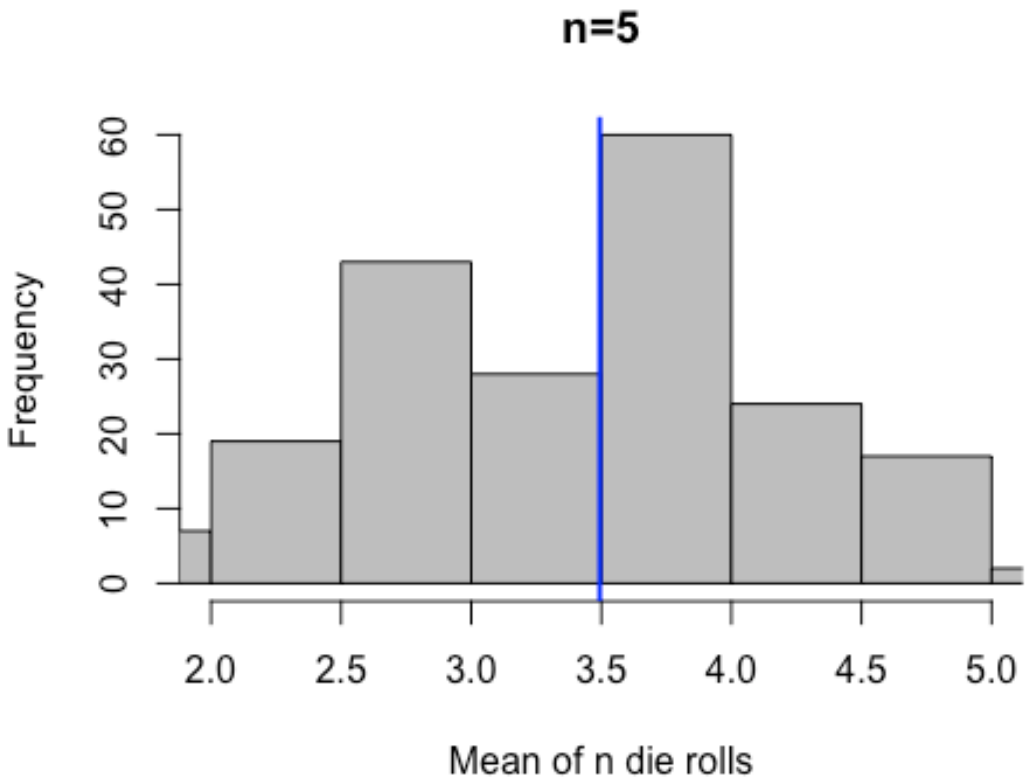

```
my_hist <- function(sims){
    hist(sims, col="grey", xlab="Mean of n die rolls", main="")
    abline(v=mean(sims), col="blue", lwd=6)
}

my_hist(sims=reps)
```



4. Monte Carlo simulations/ Step 3

How would we update the function to add the number of die rolls as the title of the plot?

```
my_hist <- function(sims, n){
    hist(sims, col="grey",  xlab="Mean of n die rolls",
         main=paste0("n=",n), xlim=c(2,5))
    abline(v=mean(sims), col="blue", lwd=2)
    }

my_hist(sims=reps, n=5)
```



How can we use everything we learned today to analyze the changes in the the sampling distribution of the mean of the die rolls as the number of die rolls change?

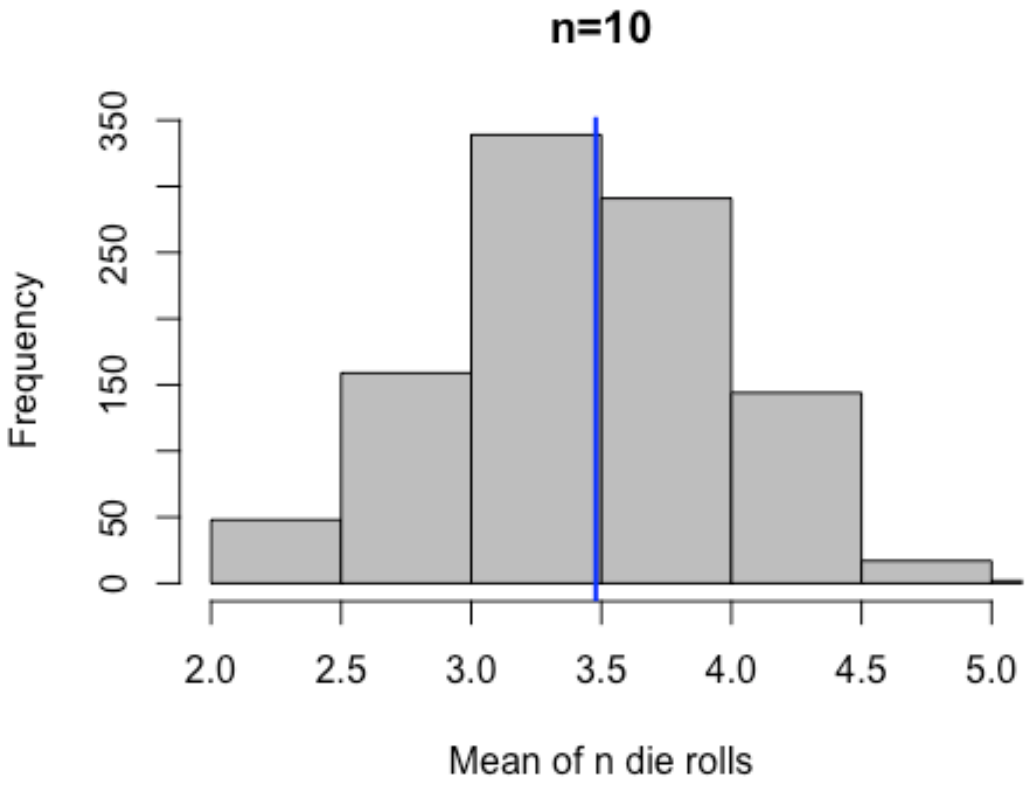
We can integrate what we did above and write a loop that varies the number of die rolls over which we take the mean and plots the sampling distribution each time.

Say we want to see the sampling distribution for $n = 10$, $n = 25$, $n = 50$, $n = 100$, $n = 200$, and $n = 500$.

```
nr_die_rolls <- c(10, 25, 50, 100, 200, 500)
```

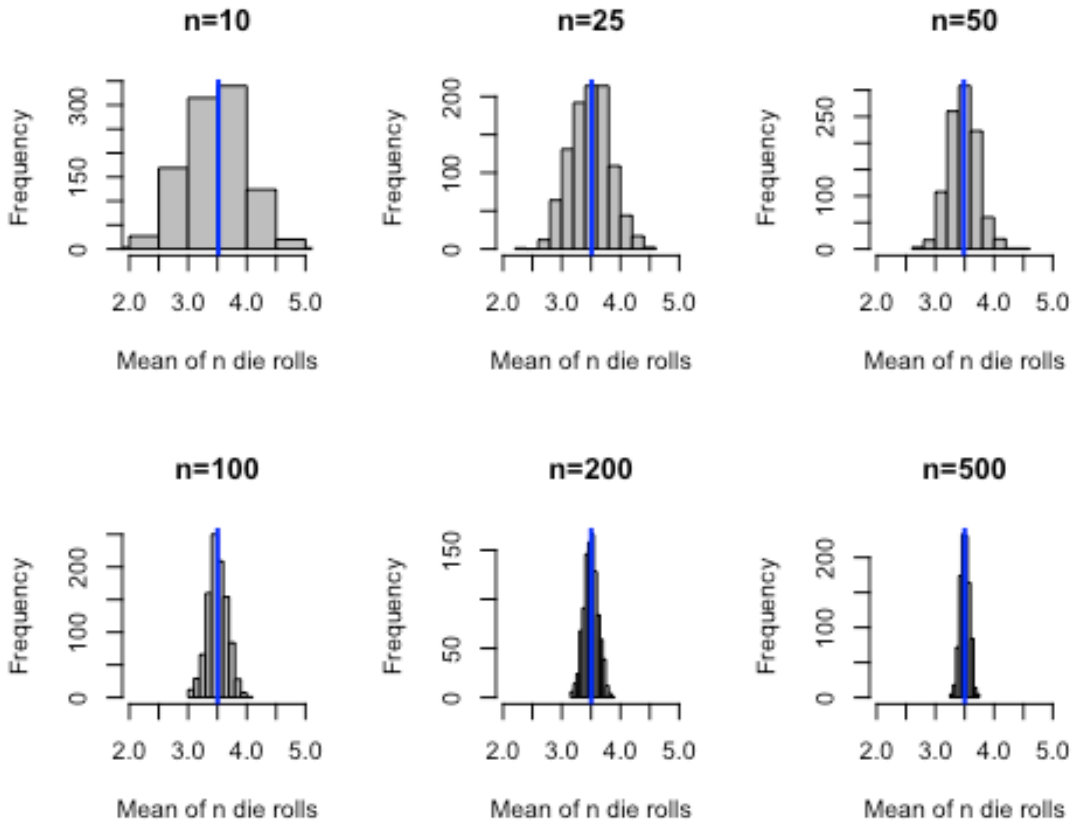
Let's see how we can first write this for $n = 10$. Remember this is the first element of the vector, so we can get it using 1 as the index, `nr_die_rolls[1]`.

```
reps <- replicate(1000, die_roll_mean(nr_rolls = nr_die_rolls[1]))
my_hist(sims=reps, n=nr_die_rolls[1])
```



We can now write a loop that works through the vector with the numnber of die rolls and produced the relevant plot for each iteration:

```
par(mfrow=c(2,3))

for (i in 1:length(nr_die_rolls)){
    reps <- replicate(1000, die_roll_mean(nr_rolls = nr_die_rolls[i]))
    my_hist(sims=reps, n=nr_die_rolls[i])
}
```



5. *Challenge 3:* The Birthday Problem

Say we choose 25 people at random. What is the probability two or more of them have the same birthday?'

Model simplifications: * Ignore leap years * Assume the probability of having a birthday in any of the 365 days of the year is equally likely.

Let's start by thinking of one room. We need to sample 25 birthdays and check how many are repeated.

```
set.seed(94702)  #UC Berkeley zip code seed!
birthdays <- sample(1:365, 25, replace=TRUE)
birthdays
```

```
##  [1] 231 343 265 236 256 130 273 272 175 199 169 198 139 334 269  82
318  87 261 227 124  37 189 110 357
```

We now want to know how many of those birthdays are repeated. For that we can use the `unique()` command.

```
unique(birthdays)
```

```
##  [1] 231 343 265 236 256 130 273 272 175 199 169 198 139 334 269  82
318  87 261 227 124  37 189 110 357
```

```
length(unique(birthdays))
```

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

All 25 dates are unique. We have no repeated birthdays.

Note this is just one realization of the process. To use R to approximate the probability we would need to repeat this process many, many times.

For this we can start by writing a function that goes through the process one time and then use the `replicate` function as we did above.

We start by writing the function:

```
birthday_function <- function(people=25){

    # we populate the room
    birthdays <- sample(1:365, people, replace=TRUE)

    # get the unique number of bdays
    unique_bdays <- length(unique(birthdays))

    # and return a 1 if at least one bday is repeated.
    as.numeric(unique_bdays!=people)
}

birthday_function(people=25)
```

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

Thus, we have one repeat birthday!

Now we can use `replicate` to repeat the process 1,000 times:

```
many_sims <- replicate(1000, birthday_function(people=25))

many_sims
```

To approximate the probability of at least one matching birthday, we can just take the mean of this vector:

```
mean(many_sims)
```

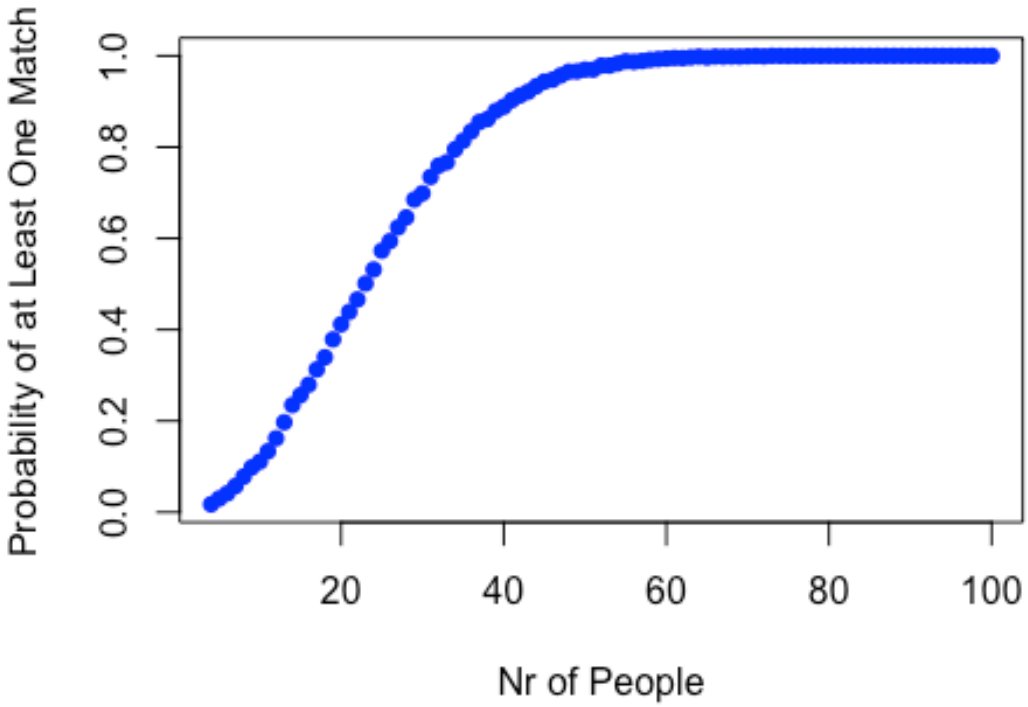
```
## [1] 0.573
```

Say we now want to use R to see how this probability changes as the number of people in the room changes. How can we do this? We can use our function but incorporating it into a loop which varies the number of people in the room:

```r
people <- 4:100
sims <- matrix(NA, length(people), 2)

for(i in 1:length(people)){
    many_sims <- replicate(5000, birthday_function(people=people[i]))
    sims[i,] <- c(people[i], mean(many_sims))
}

head(sims)
```

```
##      [,1]   [,2]
## [1,]    4 0.0174
## [2,]    5 0.0300
## [3,]    6 0.0414
## [4,]    7 0.0574
## [5,]    8 0.0780
## [6,]    9 0.0982
```

```r
par(mfrow=c(1,1))
plot(sims[,1], sims[,2], pch=16, col="blue",
     xlab="Nr of People", ylab="Probability of at Least One Match")
```



Acknowledgements

Software Carpentry Hadley Wickham more Hadley Wickham