Lab 1: Pooled Covid Testing

Stephen R. Proulx, Taom Sakal

Bayesian Statistical Modeling Winter 2024

Lab Exercise, Week 1

When is this lab due? Labs are due on the Thursday after they are assigned. However, in many cases you can complete them during the lab period itself. This assignment is due on Thursday, 1/18/2024. You must answer all the problems, which are written in **bold**.

These problems follow up on the example of estimating the percentage of the earth's surface that is water. But first we will briefly go over how to use R Markdown. Feel free to skip this section if you are already wise in its ways.

How to R Markdown (A very very short tutorial)

R Markdown blends text with code. This is a great way to communicate understandable code to others (and to future you once you inevitably forget what you wrote). This is text right now. Below is a code chunk.

```r
print("Roses are red,")
```

```
## [1] "Roses are red,"
```

```r
print("violets are blue,")
```

```
## [1] "violets are blue,"
```

```r
print("R's pretty rad,")
```

```
## [1] "R's pretty rad,"
```

```r
print("and Bayes' rule rules.")
```

```
## [1] "and Bayes' rule rules."
```

Put your cursor on one line of the code chunk and press *ctrl-enter* (the actual keystroke may be version specific) to run it. Or place your cursor anywhere in the chunk and press *ctrl-shift-enter* to run the entire thing. You can also press the green play button at the top right of the chunk.

Try creating your own code chunk. You can either type out the code or you can press *ctrl-alt-I* (or *cmd-option-I* for Mac). Below is an empty chunk but try creating your own and running it.

You'll notice the chunks in the code below have names. You can navigate by chunk name in the tiny pop-up menu at the bottom of this editor window.

```r
# This chunk has a name!
# These lines with '#' are comments.
# The computer ignores them but humans don't.
# You can use them to clarify code.
#
# It is good coding style to use comments
# to clarify any confusing lines.

2 + 3 + 5  # Addition
```

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

```r
2 * 3 * 5  # Multiplication
```

```
## [1] 30
```

```r
(2 ^ 3) ^ 5  # Exponentiation
```

```
## [1] 32768
```

There's also a nice document outline button on the top right corner of the editor window. This will let you jump around this R markdown file with ease.

We can save data into a variable to use later. This is the '=' notation. You'll often see '<-' used in R too. We'll try to use '<-' as it is clearer and most style guides recommend it. (But some of your instructors come from programming traditions where '=' is the norm, so we'll slip up. And many people use the '=' notation, so you should be able to read both.)

```r
# Three variables
a <- 42
b = 42
a <- TRUE # Overwrite a with a new value
word_variable <- 'words go in quotes!'  # Variable names don't have spaces

# A named list of the three variables (see https://www.geeksforgeeks.org/named-list-in-r-programming/ f
#This allows us to store a collection of variables and retreive them by name
list_of_data <- list(logical= a, number=b, word= word_variable)
print(list_of_data)
```

```
## $logical
## [1] TRUE
##
## $number
## [1] 42
##
## $word
## [1] "words go in quotes!"
```

```r
#see what is in the "number" slot
list_of_data$number
```

```
## [1] 42
```

```r
#You can also still pull out the stored information by position in the list
list_of_data[3]
```

```
## $word
## [1] "words go in quotes!"
```

You can see all active variables in the *Environment* panel on your right. These will stay as they are until you change them. If you have run something else in this same R session, you may have variables hanging around from your prior calculations.

You can clear your workspace and/or restart R by accessing commands in the "Session" menu.

Finally, you can create a pdf of everything by pressing the Knit button at the top of the editor. You'll need to run the code chunk below to get that button to appear. You'll be turning in the original R Markdown file along with a pdf generated from knitr. Try this now. (If the button just looks like "preview" then choose "Knit to pdf" and save it.)

That's all you need to know for this lab. We've skipped a lot but we'll introduce more concepts throughout the class and labs. As you code try your best to use a consistent style. It makes things more readable for others and is a good habit as you go further into science. The R tidyverse style guide is at https://style.tidyverse.org/. As you have time you can check it out to learn how to space and indent things. Otherwise explore R Studio. Don't be afraid to press buttons and mess around.

Lab Problem

In a not-so-far-off dystopian future COVID-20 has appeared. It's everywhere and we only have one test for it: a PCR spit test. This test is so advanced that it can perfectly detect any COVID material in any sample of spit.

Sadly, this technology is expensive and these tests are limited. While we'd like to administer the test to everybody there's simply not enough. Is there any way to do better than one test per person while still identifying everybody who has COVID?

One potential strategy is to pool k people's spit and test the pool. If even one person in the group has covid then the test will come back positive and we re-test all k people individually to find out who it is. Otherwise if the test came back negative we know nobody has COVID. In this way each pool that is positive generates *k+1* tests but a pool that is negative generates *1* test.

This pooling strategy sounds promising, but does it really use fewer tests than than testing each person individually? And if so what k is the best pool size?

We can answer this by simulating the strategy in R. First we will simulate data by creating a bunch of people and giving some of them COVID. We can then take those people and see how the pooling strategy does, and try the pooling with many values for k.

Create Data

Before we create the data we need to setup R by loading any packages we need. Running the code chunk below will give us all we need. If you are not on the VM then you might need to install the tidyverse package. In R studio you can do this by going to Tools > Install Packages.

```r
library(tidyverse)  # Import the tidyverse package
```

```
## -- 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   3.4.4     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 to become error
```

```r
knitr::opts_chunk$set(echo = TRUE)  # ready knitr
```

Now we can simulate some data. We will first create a bunch of pools and fill them with people. We will call the pools "samples," as each are samples of our data.

```r
k <- 10  # Number of people in a pool
samps <- 10000  # The total number of pools we test.
```

Some of these pools will have people that test positive and some will not. Because each person in the pool has the same, independent chance of having COVID we can get the number of sick people in the pool by drawing from a binomial distribution. If you don't remember what the bionomial distribution is or why we use it see this video: https://www.youtube.com/watch?v=8idr1WZ1A7Q&t=50s&ab_channel=3Blue1Brown. (This video also builds up Bayesian ideas, so it and the channel's other probability videos are worth a watch even if you do remember.)

We will assume that 5% of people have covid for now.

```r
pos_rate <- 0.05  # The rate at which people have COVID. This is now a variable and is saved.
rbinom(1, size = k, prob = pos_rate)  # This randomly picks the number of people with covid in one pool
```

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

The *rbinom(1, size=k,prob=pos_rate)* simulates the number of people in one pool where each person has a *pos_rate* of having covid. As a reminder, something like *rbinom()* is a function. It takes in arguments and gives an output. This one stands for *random binomial* and will return a random draw from a binomial distribution. Try rerunning the *rbinom* line above a couple times. It won't always give the same value.

If we replace 1 with another number then this will give a *vector* of numbers. We can use variables for the function arguments or write in the numbers directly.

```r
# Make 42 random draws from the binomial distribution.
rbinom(42, size = k, prob = pos_rate)
```

```
##  [1] 0 0 1 0 0 0 0 0 1 0 0 0 0 2 0 1 0 1 0 0 0 0 0 0 1 0 0 1 1 1 1 0 0 2 0 0 0 0
## [39] 1 1 0 0
```

```r
# If we want to type in the values directly, we can do this.
#Make 10 random draws, from a pool of 10, with positive rate of 50%.
rbinom(10, size = 10, prob = 0.5)
```

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

Problem 1 Make a vector of 200 random draws from a binomial distribution. Let the size of the pools be 100 and the positive rate be 50%.

```
# Write your answer here.

rbinom(200, size = 100, prob = 0.5)
```

```
##   [1] 46 48 58 51 52 46 48 48 53 49 51 53 52 47 47 56 50 55 53 56 40 54 42 58 50
##  [26] 50 59 50 51 51 49 52 39 59 43 53 49 53 39 47 57 51 40 49 48 62 47 41 54 42
##  [51] 45 51 54 53 48 42 45 56 53 45 51 48 52 59 51 46 48 48 40 53 55 49 50 42 56
##  [76] 58 50 55 42 49 51 53 60 47 56 43 49 48 46 50 48 63 45 47 51 44 46 50 49 50
## [101] 49 48 57 48 49 60 41 59 50 50 48 38 49 59 52 42 44 52 56 53 50 54 46 47 55
## [126] 55 50 45 49 45 49 46 52 53 52 54 54 50 50 52 38 51 42 45 53 51 61 45 53 49
## [151] 50 50 47 45 48 51 45 56 45 45 56 47 50 54 53 54 48 52 48 53 43 54 49 57 46
## [176] 49 42 52 46 53 46 51 46 54 58 44 54 43 48 53 54 44 49 46 52 51 49 49 38 52
```

Problem 2 We can look up the documentation for a function by putting your cursor on a function and pressing *F1*. Or you can type *?function_name* and run it. The documentation will appear in the lower right-hand panel.

Using the documentation on *rbinom* will pull up documentation for many binomial functions R has. There are four of them, each of which do different things.What are their names?

```
?rbinom

# Write down the three other types of bionomial function's names.
# dbinom gives the density
# pbinom gives the distribution function
# qbinom gives the quantile function
# rbinom generates random deviates
```

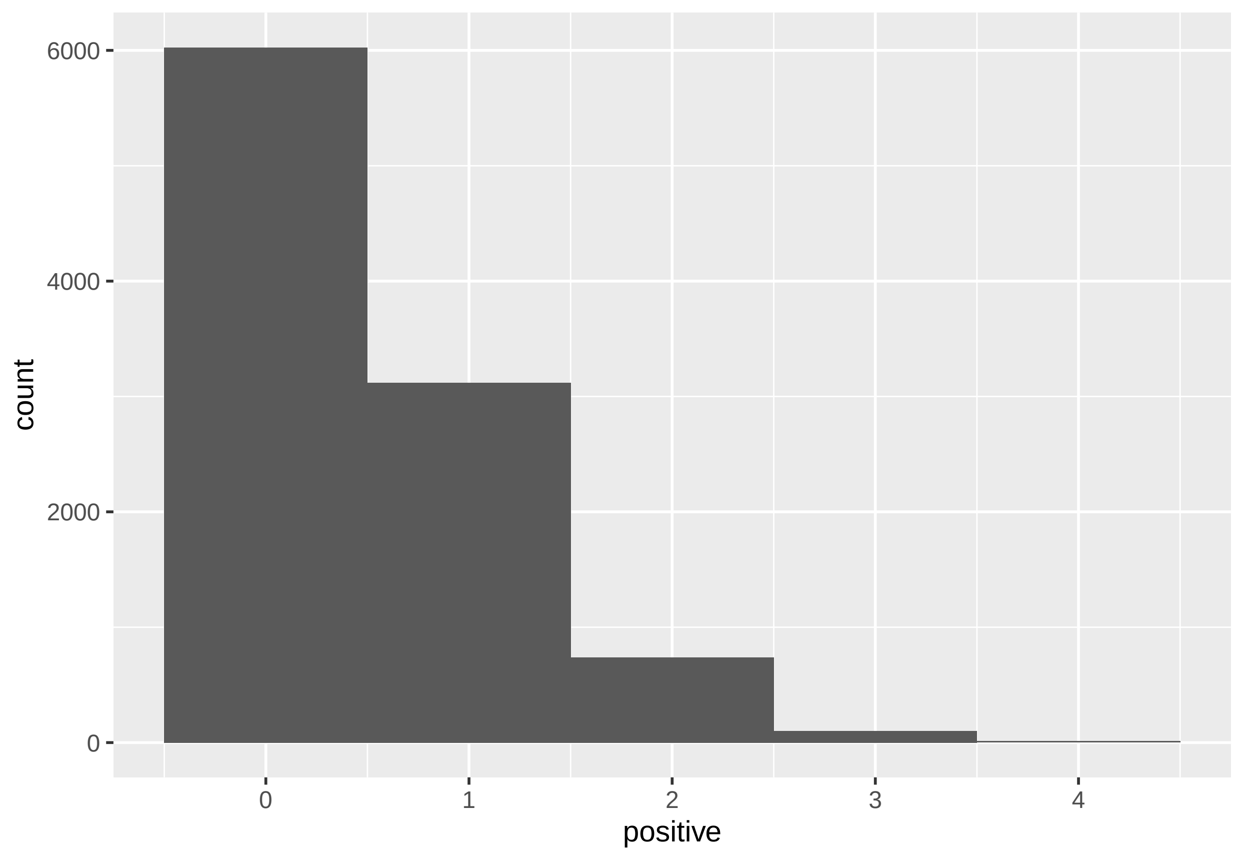
Playing with the data

Now we can make a list of the number of people with COVID in all 10000 pools and arrange the data in a *tibble*. (A tibble is a more modern dataframe-like object which works well with the tidyverse.)

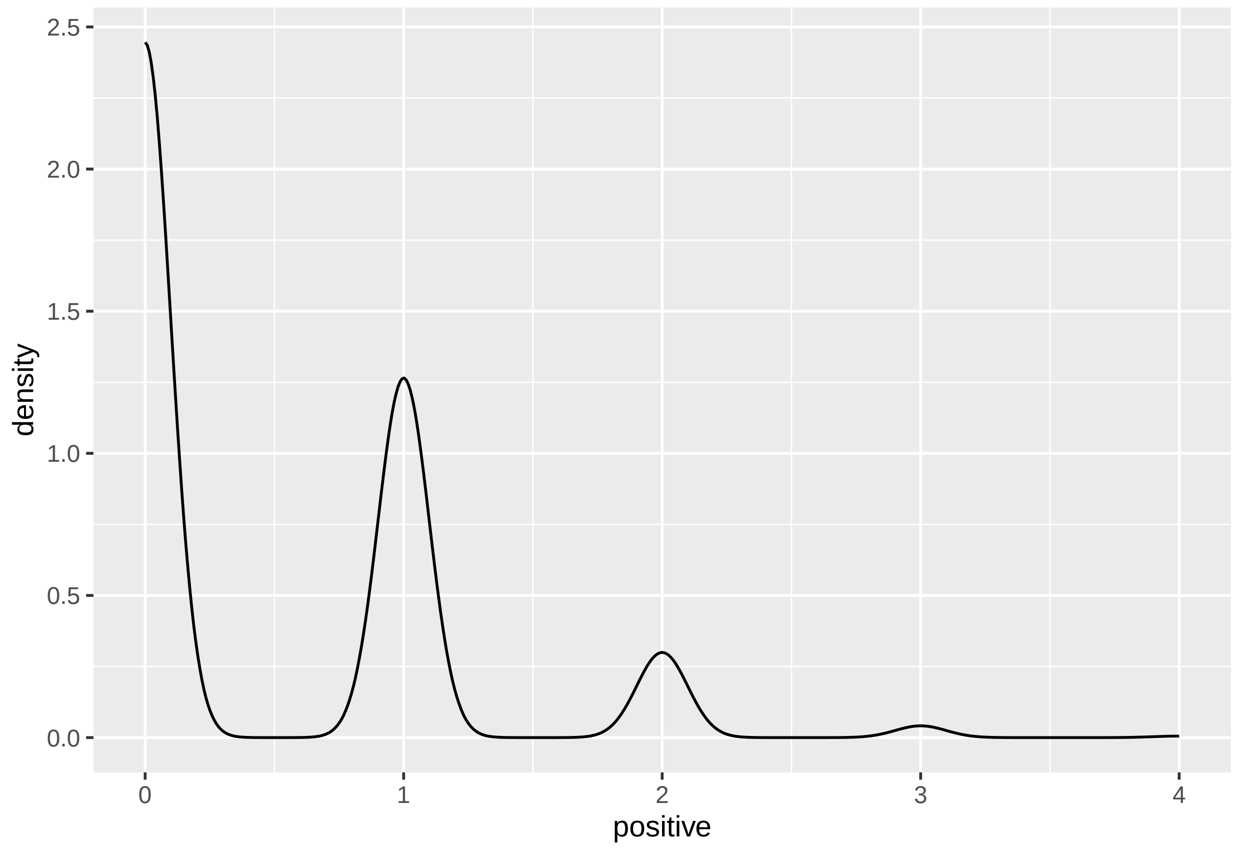
```
# Make a vector of all the pools,
# where the i'th pool has the number of people with COVID in it.
positive <- rbinom(n = samps, size = k, prob = pos_rate)

# Arrange data in a tibble.
# Look in your Environment panel and click pools to see what this data looks like.
pools <- as_tibble(positive)
```

Next lets plot the number of people with covid in each pool. We will use the *ggplot2* package (which comes with the tidyverse) for visualization. If you need a refresher on it head here: https://r4ds.had.co.nz/data-visualisation.html

```
# Make a plot and say what data we will plot
ggplot(data = pools, aes(x = positive)) +
  geom_histogram(binwidth = 1)
```



```r
ggplot(data = pools, aes(x = positive)) +
  geom_density()
```



What we've just made is some simulated pool data that mimics what we expect from real life. We can now use this data to test our pooling strategy. First need to count up how many tests we have to do.

The code below makes a new column with the number of tests we would have to do for each pool. Any pool with at least one person with COVID will test positive, so in that pool we will have to retest everybody and will have a grand total of $1 + 10 = 11$ tests. Otherwise we spent one test for the entire pool, it came back negative, we know nobody has COVID, and we are done.

```
# 'mutate' adds two columns to the data frame, one called 'retest'
# and one called 'tests'. These columns are filled with the values provided.
# You can look at the pools variable before and after running this to see what changed!
pools <- mutate(pools, retest = sign(positive) , tests = 1 + retest * k)

# Take mean number of tests needed
mean(pools$tests) / k
```

```
## [1] 0.4974
```

The output here is the average number of tests run per person in the entire population. If this is less than 1, we are doing better than testing everyone.

Problem 3 What does the *sign* function in mutate do? Use the documentation to find out. Write your answer as text below.

```
?sign
```

< Put your answer here >

Sign returns a vector with the signs of the corresponding elements of x The sign of a real number is 1, 0, -1, which corresponds to positive, zero, or negative

Piping

A quick aside for some common syntax: the pipe. This is one of the great boons of R that many other languages don't have. It makes a lot of code more readable. We could rewrite the mutate code above with pipe syntax

```
pools <- pools %>%
  mutate(retest = sign(positive) , tests = 1 + retest * k)
```

We can chain pipes together. The code below takes an imaginary number, then takes the real part of it, then takes the square root, then finally prints it.

```
z = -10 + 3i  # The imaginary number -10 + 3i

z %>%
  Re() %>%  # Take the real part...
  abs() %>% # then take the absolute value...
  log(base = 10)  # then take log base ten.
```

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

```
# Same thing but now save it as the variable a
a <- z %>%
  Re() %>%  # Take the real part...
  abs() %>% # then take the absolute value...
  log(base = 10)  # the take the log base ten.

print(a)
```

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

Piping is encouraged as it is more readable than the typical nested way of writing this.

```
z = -10 + 3i

a = log(abs(Re(z)), base = 10)

print(a)
```

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

Problem 4 Take the pipe code and modify it to take the square root after the absolute value but before taking the log. Also use the natural log instead of base 10. You might have to use Google to figure our how to do this. (But half of programming is being great at looking things up.) You should get 1.151293 as your final answer.

```
# Modify this code.

z = -10 + 3i  # The imaginary number -10 + 3i

z %>%
  Re() %>%  # Take the real part...
  abs() %>% # then take the absolute value...
  sqrt() %>% # take the square root
  log()  # then take the natural log.
```

```
## [1] 1.151293
```

Functions

Taking the mean number of tests we need per group is a good metric – the lower the mean the more efficient our pooling strategy is. We could rerun the code above to test different values of k and see which is best, but it is easier to make our own function that takes in a value for k and return the average number of tests per person.

```
# This function takes in a pool size k and
# returns the mean number of tests needed
# to identify everybody that has COVID.

calc_tests <- function(k) {

  pos_rate <- 0.05
  samps <- 10000
  positive = rbinom(n = samps, size = k, prob = pos_rate)  # Make new data for each run
  pools <-  as_tibble(positive)

  pools <- pools %>%
    mutate(retest = sign(positive) , tests= 1 + retest * k)

  output <- mean(pools$tests) / k

  output  # Return the mean

}
```

We can run this function like so.

```
calc_tests(7)  # Mean tests needed for when pools have three people each
```

```
## [1] 0.4442571
```

Problem 5 Try changing the pool size in the chunk above to see how the mean number of tests change. Why do the numbers change each time we run it? Why is *calc_tests(1)* not exactly equal to 1?

< *Type your response here* > The numbers change each time we run it because the function is based off of random draws from a binomial distribution. Each time the draws change so the value of the mean changes.

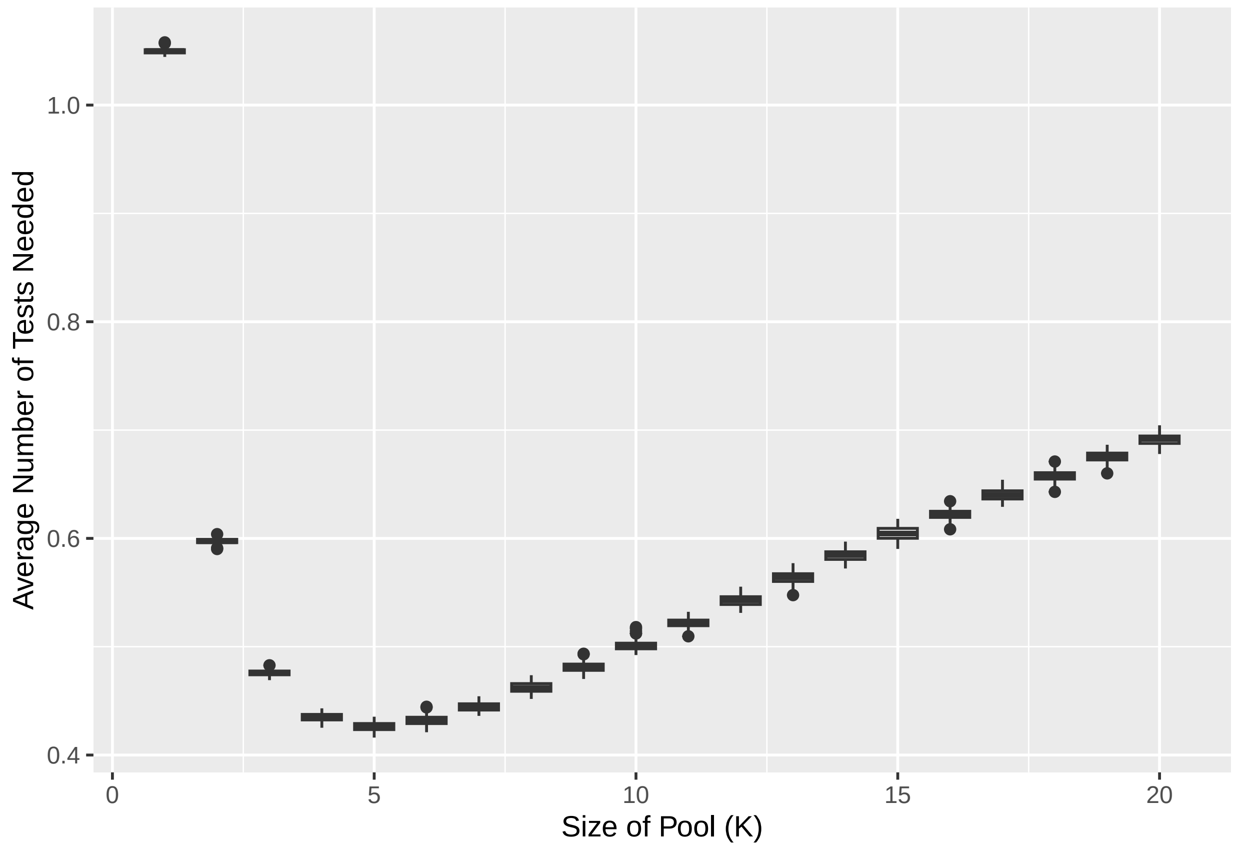
Running the test with one person each doesn't give a value of exactly one because when we obtain a positive result, (per our function) we retest that pool. So it adds a test.

The best pool size

Now armed with the *calc_test* function we can figure out which *k* is best. This is a simple matter of running through a bunch of possible pool sizes and recording the mean tests needed. Because each run is random we will take the average of 100 runs.

For now you don't need to understand the nitty gritty of the code. But if you're feeling daring then use the documentation, view the variables that are made, and try to reverse engineer the code.

```
# make a new tibble that contains the pool size *k*
# for each replicate and does each replicate 100 times.
keffects <- tibble(k = rep(seq(20), 100))

# Calculate the average number of tests needed
keffects <- keffects %>%
  rowwise() %>% # Group input by rows (doing it one row at a time)
  mutate(ave_tests = calc_tests(k), poolsize = as.integer(k))  # convert *k* to an integer to get geom_

ggplot(data = keffects, aes(x = k, y = ave_tests, group = poolsize)) +
  geom_boxplot() +
  labs(y = "Average Number of Tests Needed", x = "Size of Pool (K)")
```



#### Problem 6

Does the pooling strategy use less tests than the naive one-test-per-person strategy? If so, what is the best pool size k to use?

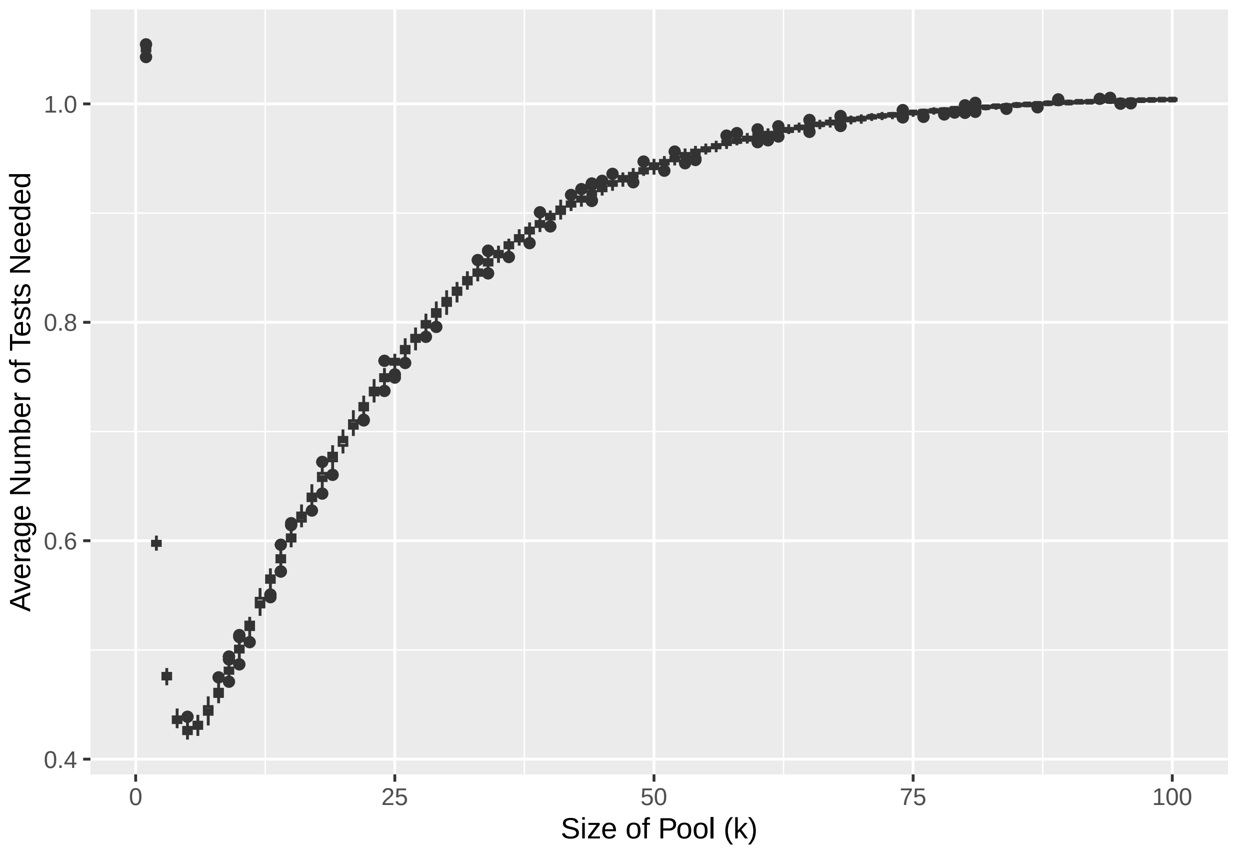
Type answer here

Yes the pooling strategy uses less tests than the one-test strategy. The best poolsize K to use appears to be 5.

Problem 7 (Bonus) Modify the above code to try up to pool size 100. What do you see? (This will take a few minutes to run!)

Type answer here

```
keffects2 <- tibble(k = rep(seq(100), 100))

keffects2 <- keffects2 %>%
  rowwise() %>%
  mutate(ave_tests = calc_tests(k), poolsize = as.integer(k))

ggplot(data = keffects2, aes(x = k, y = ave_tests, group = poolsize)) +
  geom_boxplot() +
  labs( x = "Size of Pool (k)", y = "Average Number of Tests Needed")
```



Average Number of Tests Needed
1.0
0.8
0.6
0.4
0
25
50
75
100
Size of Pool (k)