Solution to Lab 6

Univariate Statistics with R

It is finally time to do some stats!

So in today's lab we are going to start working with some data that looks a little more "real". What do I mean by real, well, messy! Up until now we have largely been working with complete data sets where all the values for every variable are within the range we expect and there are no unusual cases. But for any of you who have previously had your hands on real raw data, you will know it rarely looks so neat. So our aims for today are to show you some more R skills for exploring your data to highlight potentially problematic values, and then to put these, and all your other skills to the test to answer some simple research questions using some real (messy) data.

So let's get started.

Some more R skills

Two types of subscripting

Create a vector called "vec" with 10 numbers in it (you could use one of the following functions, `sample()`, or `seq()`, for example).

```
vec =  seq(2, 20, 2)
```

What does the next command do?

```
vec[8]
```

```
## [1] 16
```

What about the following command?

```
vec[c(2, 8)]
```

```
## [1]  4 16
```

Now try:

```
vec[c(F, T, F, F, F, F, F, T, F, F)]
```

```
## [1]  4 16
```

So what is going on here? In one case the subscripting is being done by *index*; in the other, it's being done by truth value (these are called *logical* subscripts). Having both gives R enormous flexibility when it comes to manipulating data. In general, indexes are what you type in if you want to target specific values, but logical subscripts are the results of tests. Try the following and observe and in each case think about what the output represents:

```
vec2 <- c(1, 2, NA, 4, 5, 6)
is.na(vec2)
```

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

```
vec2 > 4
```

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

```
vec2/2 == 2
```

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

what will the next two commands do? Think about it first and then try them out:

```
vec2[vec2 > 4]
```

```
## [1] NA  5  6
```

```
vec2[vec2 > 4] <- NA
```

For matrices, R indexes by row, then by column in the format `matrix[row, column]`.

Let's create a matrix:

```
mat <- matrix(rnorm(20, 100, 15), ncol = 5, nrow = 4)
# Here we specify some values (20 from a normal(100, 15) distribution)
# and then tell R how to organise the matrix (col and row sizes)
```

What does the next command point to (you have seen this before in previous labs - think about adding values to the empty matrix)?

```
mat[2, 3]
```

```
## [1] 89.74633
```

What about the next one?

```
mat[ , 3]
```

```
## [1] 125.98554  89.74633 112.28819  96.31343
```

What's the difference between the folllowing two commands?

```
mat[2, 3]
```

```
## [1] 89.74633
```

```
mat[c(2, 3), ]
```

```
##          [,1]     [,2]      [,3]     [,4]     [,5]
## [1,] 92.14175 90.50177  89.74633 75.58787 112.4091
## [2,] 81.44043 87.58729 112.28819 75.92976 116.3344
```

Note that logical tests respect the shape of the input, as much as possible. To see what this means, try the following and as usual think about what you expect the output to look like first:

```
mat > 100
```

```
##       [,1]  [,2]  [,3]  [,4]  [,5]
## [1,]  TRUE  TRUE  TRUE  TRUE FALSE
## [2,] FALSE FALSE FALSE FALSE  TRUE
## [3,] FALSE FALSE  TRUE FALSE  TRUE
## [4,]  TRUE  TRUE FALSE  TRUE FALSE
```

You can use the matrix of truth values like so (the rows and columns are implicit because the truth values come as a matrix):

```
mat[mat > 100] <- 100  # cap maximum score at 100 throughout
```

Your Turn

If you've followed all this, you should be able to have a good go at the following:

1. Create a 20-row, 2-column matrix called 'mat2' filled with random numbers drawn from a normal population with mean 100 and sd 15;

2. change the value at the 14th and 18th rows of the first column to 200 (in one command);

3. change the value of the 3rd row of the second column to 200;

4. find the mean and the sd of all the values (using mean() and sd());

5. A typical task we want to carry out when 'cleaning' data prior to carrying out our formal analysis is to look for **outliers** and follow a protocol for dealing with them. For this particular analysis you have been told to exclude any values that are **2 standard deviations above the mean**. Therefore you need to convert any values in the matrix that fit this criteria to NA. This is a natural extension to some of the examples given above and while the code you produce may look scary it is just a case of joining together multiple parts.

6. check that your code has worked by looking at the matrix either in the console or in the editor view in RStudio. Imagine you had a matrix with 10, 000 rows and had just completed the same task and now wanted to check which values had been converted to NA. It would be difficult to do this by simply looking at the matrix. Try:

```
which(is.na(mat2[ , 1]))
```

What does which() do? (hint: try `is.na(mat2[ , 1])` on its own).

If you have time: Repeat the exercise above (create a new matrix called mat3). This time, replace the values greater than 2 sds above the mean in *column 1 only*. (hint: your command will start with something like "mat3[, 1][mat3[, 1] > .]")

```
### ANSWERS to above exercise ###

# Step 1
mat2 <- matrix(rnorm(40, 100, 15), nrow = 20, ncol = 2)

# Step 2
mat2[c(14, 18), 1] <- 200

# Step 3
mat2[3, 2] <- 200

# Step 4
mean.mat2 <- mean(mat2)
sd.mat2 <- sd(mat2)

# Step 5
cutoff <- mean.mat2 + (2 * sd.mat2)
mat2[mat2 > cutoff] <- NA

#Step 6
# which() returns the index values where the evaluation of the given condition is TRUE.
# Hence in this case we definitely get 14 and 18 as we set those values to 200.
# You may also have got other values depending on the random values selected initially.

# The 'If you have time....'
mat3 <- matrix(rnorm(40, 100, 15), nrow = 20, ncol = 2)
mat3[c(14, 18), 1] <- 200
```

```r
mat3[3, 2] <- 200
cutoff <- mean(mat3) + (2 * sd(mat3))
mat3[ , 1][mat3[ , 1] > cutoff] <- NA
mat3
```

```
##             [,1]      [,2]
##  [1,] 104.48359 113.71041
##  [2,]  99.17096 105.30951
##  [3,]  93.19930 200.00000
##  [4,]  94.77964 105.76290
##  [5,] 113.96566  56.28477
##  [6,] 110.44209 101.00112
##  [7,] 113.77535  87.99485
##  [8,]  85.97432  80.91249
##  [9,]  88.88026  90.94978
## [10,]  94.07255  70.05949
## [11,] 119.45447 105.90463
## [12,] 100.31180 103.12901
## [13,]  91.35538 106.92424
## [14,]        NA 103.88036
## [15,] 102.20205 139.05392
## [16,] 103.52356  91.12184
## [17,]  70.35739  94.77257
## [18,]        NA  94.63254
## [19,]  97.82936 124.75142
## [20,] 112.89514  96.40057
```

```r
# Notice the 3rd value in column 2 is still 200 and not NA, so the code worked.
```

Real Data

OK, now let's have a look at analysing some real data to answer some research questions. The questions will require you to use the methods from todays lecture, as well as your previously learnt R skills (cleaning data, describing data, plotting etc.).

Though some elements may be repetitive, it is good practice to think through your analyses from start to finish each time. Think about what the question is asking and what is needed to answer - basic descriptives of the variables, plots, tests of assumptions, etc.

The data

The data set is saved on LEARN as a .csv file (Under the Lab/Lecture 6 tab). You can open this file by downloading it and saving it to a a given location, and using the `read.csv()` to open the file. We have have used `read.csv()` previously so if you cant recall how it works, then look back at lab 3 and use `?read.csv`.

The data for this lab come from a study of exercise and cognitive ability in early and later adulthood. All participants were male and randomly sampled within age groups. Data were collected on 325 individuals, 151 from a young adulthood group (aged 20-28 years) and 174 from a later adulthood group (aged 50-58 years). Each person was asked to categorized the regularity of their exercise, and were given an IQ test.

The data are in the file called `healthIQ.csv`. The variables are as follows:

1. ID
2. AgeGroup: 1 = Young adulthood; 2 = Later adulthood

3. ExGroup: 1 = No exercise; 2 = moderate exercise; 3 = intense exercise
4. IQ score: Standardized IQ score (mean 100)

In addition to this data, the researchers were given some seperate data from a colleague which used the same IQ test on a sample men of approximately the same age as the later adulthood sample. This group had been tested at 2 points in time 3 years apart. The data file `repeatIQ.csv` contatins this data.The variables are:

1. ID
2. IQ score wave 1: Standardized IQ score (mean 100)
3. IQ score wave 2: Standardized IQ score (mean 100)

The questions

Data Inspection/Cleanse: You are going need to use your newly aquired indexing skills, as well as some of your already established skills to check all variables ahead of the analyses. What you should do here is use some tools (perhaps describe() in the psych package as a starting point?) to get a feel for the data. Are there any strange values such as impossible values based on the codebook for the variables given above? Any outliers? Is R treating each variable as the appropriate class (type) of data? e.g. factor or numeric. . . .

This should take you a little bit of time, it is an open ended exercise where you need to use your R skills and judgement to assess the data and fix any problems you encounter before moving on to the following questions:

```
### ANSWER ###

# reading in and checking the data (my data files are in my project folder)
health =  read.csv("healthIQ.csv", header = T)
repIQ =  read.csv("repeatIQ.csv", header = T)

# Basic eyeball
library(psych)
describe(health)
```

```
##           vars   n   mean    sd median trimmed    mad min    max  range
## ID           1 325 163.00 93.96 163.00  163.00 120.09   1 325.00 324.00
## Agegroup     2 325   1.54  0.52   2.00    1.55   0.00   1   4.00   3.00
## ExGroup      3 325   4.72 55.33   2.00    1.63   0.00   1 999.00 998.00
## IQ           4 325 100.00 15.34  99.82  100.18  14.74  20 135.92 115.92
##            skew kurtosis   se
## ID         0.00    -1.21 5.21
## Agegroup   0.16    -0.54 0.03
## ExGroup   17.86   317.95 3.07
## IQ        -0.46     1.70 0.85
```

```
# This tells us a few things. There are no * so we can see that at the moment,
# AgeGroup and ExGroup are not being treated as factors. Second, we can see that
# the max value for AgeGroup is 4, yet we know from the code book that there are
# only 2 groups. So we have a coding error here. Third, there is a max value of 999
# for ExGroup - which is again out of range (we have 3 groups). Lastly, our minimum
# value for IQ is 20. This is VERY low. On a standardized IQ scale, we should not
# be seeing a value this low. This suggests we have a data entry problem. So lets
# sort these out.


# check factor versus numeric
is.factor(health$Agegroup)
```

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

```
is.factor(health$ExGroup)
```

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

```
health$Agegroup <- as.factor(health$Agegroup)
health$ExGroup <- as.factor(health$ExGroup)

# Now they are factors let's deal with the levels
levels(health[ , 2])
```

```
## [1] "1" "2" "4"
```

```
# so we have got a 4 where we dont need it. So lets give that NA
# NA is R generic code for missing data
levels(health[ , 2]) <- c("Young", "Older", NA)
levels(health[ , 2])
```

```
## [1] "Young" "Older"
```

```
# And the same for Exercise Group
levels(health[ , 3])
```

```
## [1] "1"   "2"   "3"   "999"
```

```
levels(health[ , 3]) <- c("None", "Mod", "Intense", NA)
levels(health[ , 3])
```

```
## [1] "None"    "Mod"     "Intense"
```

```
# Let's have a look at the effect of using NA
describe(health)
```

```
##            vars   n   mean    sd median trimmed    mad min    max  range
## ID            1 325 163.00 93.96 163.00  163.00 120.09   1 325.00 324.00
## Agegroup*     2 324   1.54  0.50   2.00    1.55   0.00   1   2.00   1.00
## ExGroup*      3 324   1.65  0.58   2.00    1.63   0.00   1   3.00   2.00
## IQ            4 325 100.00 15.34  99.82  100.18  14.74  20 135.92 115.92
##             skew kurtosis   se
## ID          0.00    -1.21 5.21
## Agegroup* -0.15    -1.98 0.03
## ExGroup*    0.20    -0.71 0.03
## IQ         -0.46     1.70 0.85
```

```
# What we can see here is that we now have * and we have an n of 324 for Age group and
# Exercise group. In other words, R is now recognising that we have some missing data.


# We can now do exactly the same for the lo IQ value and then the second data set

# For the IQ data, we can use what you have learnt above
health$IQ[health$IQ < 25] <- NA
summary(health$IQ)
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
##   55.78   90.19   99.83  100.24  110.51  135.92       1
```

```
# And the second data set
describe(repIQ)
```

```
##          vars  n   mean    sd median trimmed   mad    min    max  range
## ID          1 80 250.26 45.90 256.00  250.69 60.05 174.00 324.00 150.00
## wave1_IQ    2 80  99.33 14.53  98.51   99.36 14.28  64.61 135.83  71.21
## wave2_IQ    3 80  96.55 14.70  96.39   96.56 14.86  63.78 148.10  84.32
##           skew kurtosis   se
## ID       -0.10    -1.35 5.13
## wave1_IQ  0.07     0.08 1.62
## wave2_IQ  0.24     0.74 1.64
```

```
# This one looks OK

# you may have made different decisions, or encountered different potential issues.
# As long as you engaged with the data and highlighted that it wasn't perfectly
# fit for analysis as it was and took steps to fix it, then you passed the Qu!

# Now to the analysis
```

For the following questions you need to be thinking about what you learned in your lecture this week. Perhaps bring up your lecture notes to remind yourself. You need to think about what statistical procedure you can use to answer each question, and then implement it using R.

Q1. Are age category (young versus old) and health activity category independent?

```
### ANSWER ###

# Chi-Square Test of Independence
# Assumptions
# We know each case is only measured once
# Look at cell counts using xtabs:
xtabs(~ Agegroup + ExGroup, data = health)
```

```
##          ExGroup
## Agegroup None Mod Intense
##    Young   38 100      11
##    Older   90  78       6
```

```
# some counts (Intense) are quite low so we will run with correction

library(lsr)
results = chisq.test(health[ , 2], health[ , 3], correct = T)
results
```

```
##
##  Pearson's Chi-squared test
##
## data:  health[, 2] and health[, 3]
## X-squared = 23.521, df = 2, p-value = 7.808e-06
```

```
# And look at some residuals
results$residuals
```

```
##            health[, 3]
## health[, 2]      None       Mod   Intense
##       Young -2.738935  1.974118  1.127668
##       Older  2.534547 -1.826803 -1.043518
```

Q2. A researcher has a hypothesis that extreme exercise is quite rare and no/moderate exercise are equally probable. Construct a single sample test for exercise volume with appropriate probabilities to test this hypothesis.

```
### ANSWER ###

# This is a Chi-Square Goodness of Fit Test
observed =  table(health$ExGroup)
chisq.test(x = observed, p = c(.45, .45, .10))
```

```
##
##  Chi-squared test for given probabilities
##
## data:  observed
## X-squared = 16.367, df = 2, p-value = 0.0002792
```

```
# The test is significant, suggesting that the proposed distribution
# is not reflected in the data
```

Q3. Do younger and older individuals differ in IQ score at wave 1?

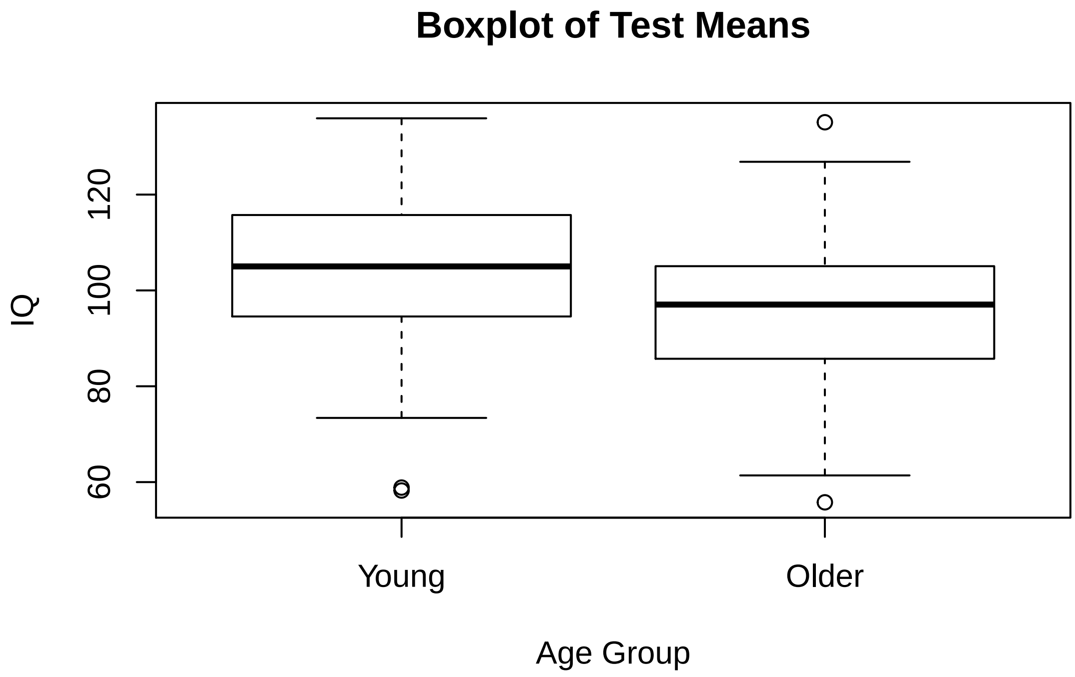
```
### ANSWER ###

# This is an independent sample t-test
bygroup =  describeBy(health, health$Agegroup)
# describes the data for each factor level seperately
bygroup$Young[4, c(2:4, 11:12)] # narrow selection to what we are interested in
```

```
##      n   mean    sd  skew kurtosis
## IQ 149 105.24 14.45 -0.28     0.18
```

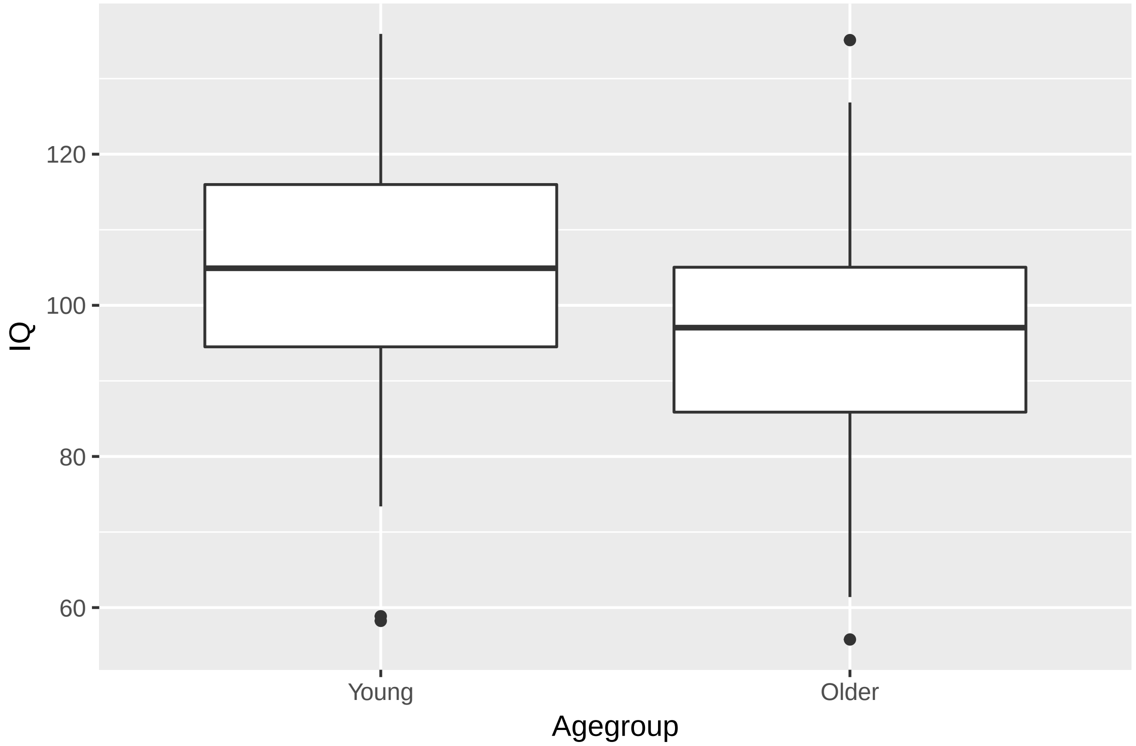
```
bygroup$Older[4, c(2:4, 11:12)] # narrow selection to what we are interested in
```

```
##      n  mean    sd  skew kurtosis
## IQ 174 95.99 13.61 -0.02    -0.14
```

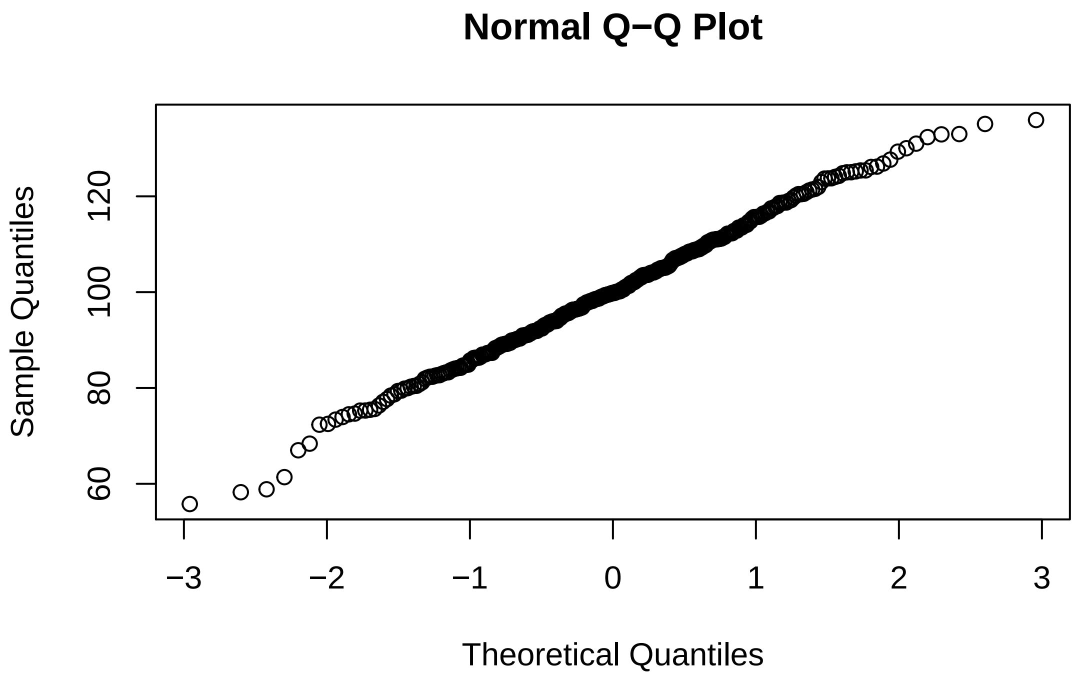
```
# plot it
boxplot(health$IQ ~ health$Agegroup,
        main = "Boxplot of Test Means",
        xlab = "Age Group", ylab = "IQ")
```



```
# Or using ggplot2
library(ggplot2)
iq_plot <- ggplot(data =  na.omit(health), aes(x =  Agegroup, y =  IQ))
# use na.omit() to remove the case with NA value for Age Group.
# Otherwise we get a box plot for the NA group....
iq_plot + geom_boxplot()
```



```
#Assumptions
qqnorm(y = health$IQ)
```



```
shapiro.test(health$IQ)
```

```
##
##  Shapiro-Wilk normality test
##
## data:  health$IQ
## W = 0.99598, p-value = 0.5807
```

```
library(car)
leveneTest(health$IQ ~ health$Agegroup)
```

```
## Levene's Test for Homogeneity of Variance (center = median)
##        Df F value Pr(>F)
## group   1  0.5643 0.4531
##       321
```

```
# Test
q3 =  t.test(formula =  IQ ~ Agegroup, data = health, var.equal = T)
q3$statistic
```

```
##        t
## 5.916355
```

```
q3$parameter
```

```
##  df
## 321
```

```
q3$p.value
```

```
## [1] 8.436336e-09
```

Q4. Did IQ scores significantly increase across time points in the later adulthood sample?

```
### ANSWER ###

# This is a paired sample t-test
describe(repIQ[ , c(2, 3)]) # Descriptive look at the variables
```

```
##          vars  n  mean    sd median trimmed   mad   min    max range skew
## wave1_IQ    1 80 99.33 14.53  98.51   99.36 14.28 64.61 135.83 71.21 0.07
## wave2_IQ    2 80 96.55 14.70  96.39   96.56 14.86 63.78 148.10 84.32 0.24
##          kurtosis   se
## wave1_IQ     0.08 1.62
## wave2_IQ     0.74 1.64
```

```
# Essentially follow the instructions for previous question except make sure
# to set the paired value to TRUE in t.test() and take note of the directional
# hypothesis using the alternative = "greater" argument.
q4 =  t.test(repIQ$wave2_IQ, repIQ$wave1_IQ, alternative = "greater", paired =  TRUE)
q4$statistic
```

```
##         t
## -2.088266
```

```
q4$parameter
```

```
## df
## 79
```

```
q4$p.value
```

```
## [1] 0.9800024
```