Answer Key for EDA

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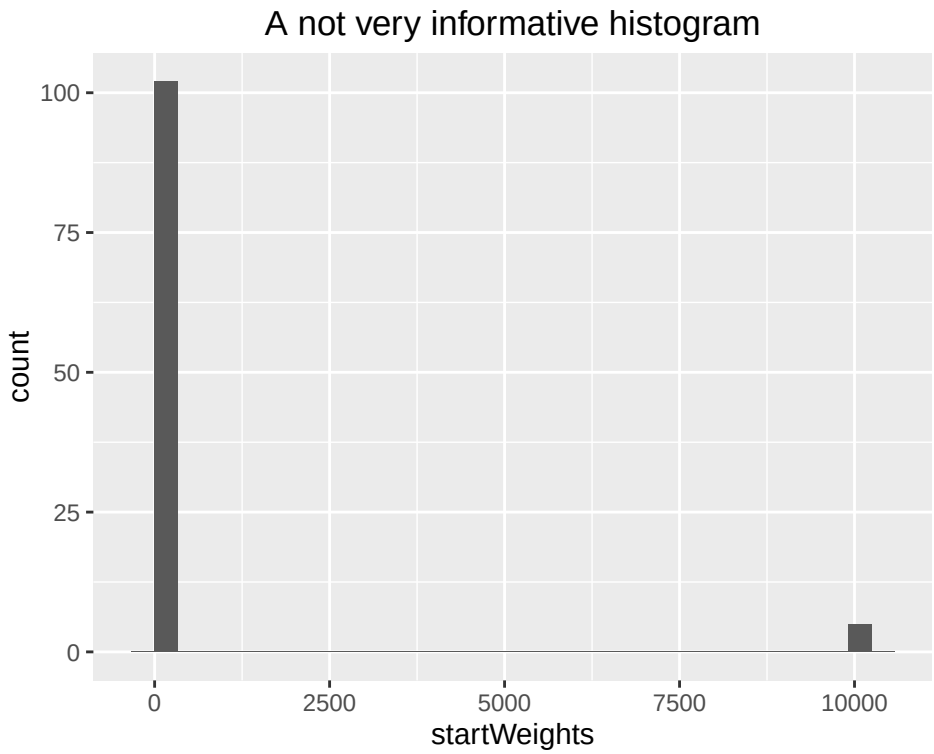
Dataset A

There are two things to notice for dataset A. The first can be noticed by looking at the data dictionary. The value of `9999` indicates an error on the scale. If they did not catch it via the data dictionary, then they will notice it when they look at the summaries, histogram and boxplots.

```
library(ggplot2)
library(dplyr)
datasetA <- read.delim("../data/datasetA.txt",row.names = 1)
#show summary of data
summary(datasetA)
```

```
##   startWeights       endWeights          treatment   timeElapsed
##  Min.   :  91.83   Min.   :  85.65   Control  :54   Min.   :10.00
##  1st Qu.: 129.10   1st Qu.: 124.50   Treatment:53   1st Qu.:25.00
##  Median : 154.30   Median : 150.70                  Median :35.00
##  Mean   : 610.49   Mean   : 607.04                  Mean   :35.61
##  3rd Qu.: 177.65   3rd Qu.: 169.70                  3rd Qu.:48.00
##  Max.   :9999.00   Max.   :9999.00                  Max.   :60.00
##  staffID1 staffID2    gender        age
##  N1:33    N1:33    female:60   Min.   :20.00
##  N2:31    N2:31    male  :37   1st Qu.:23.00
##  N3:43    N3:43    NA's  :10   Median :26.00
##                                Mean   :25.36
##                                3rd Qu.:28.00
##                                Max.   :30.00
```

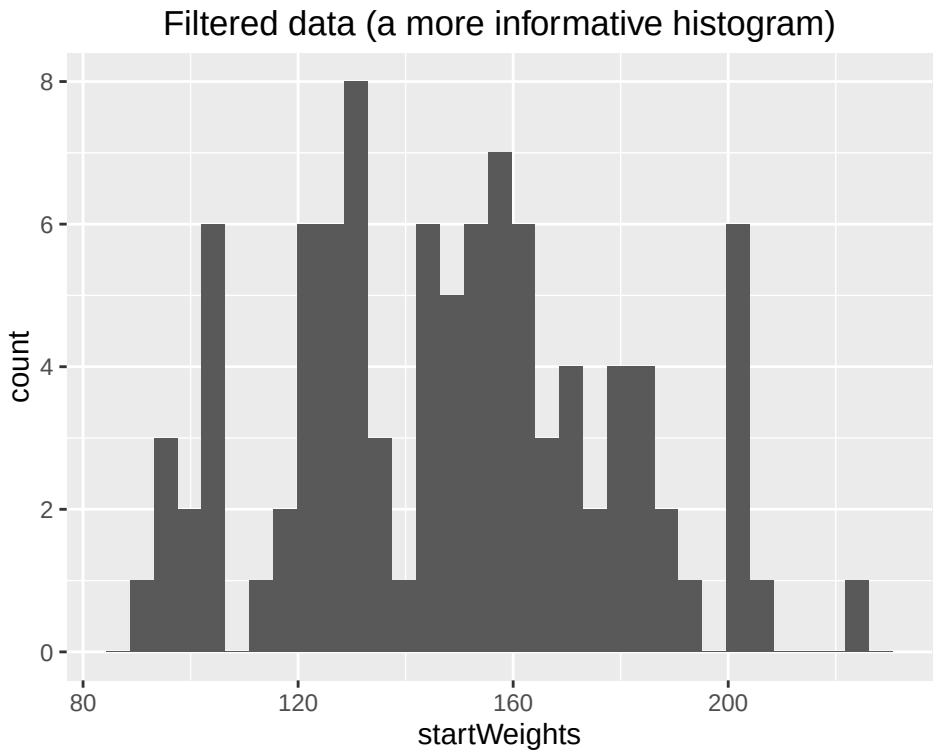
```
#show histogram of startWeights - is not very informative because of error value!
ggplot(datasetA, aes(x=startWeights)) + geom_histogram() +
  ggtitle("A not very informative histogram")
```



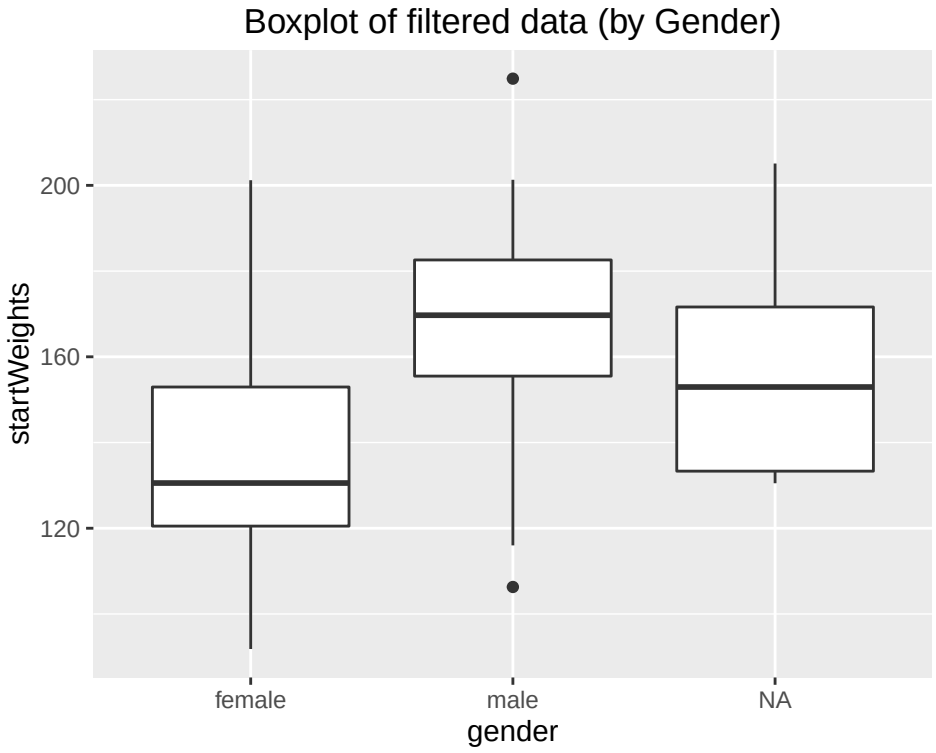
So the first step is remove rows with these values. After removing those rows with error values, the histogram looks much more informative.

```
#do filtering to remove those lines with error values
datasetA <- datasetA %>% filter(startWeights != 9999 & endWeights != 9999)

#do the histogram again
ggplot(datasetA, aes(x=startWeights)) + geom_histogram() +
  ggtitle("Filtered data (a more informative histogram)")
```




```
#Also there is a difference in weight among genders (most easily seen in boxPlots)
ggplot(datasetA, aes(x=gender, y=startWeights)) + geom_boxplot() +
  ggtitle("Boxplot of filtered data (by Gender)")
```

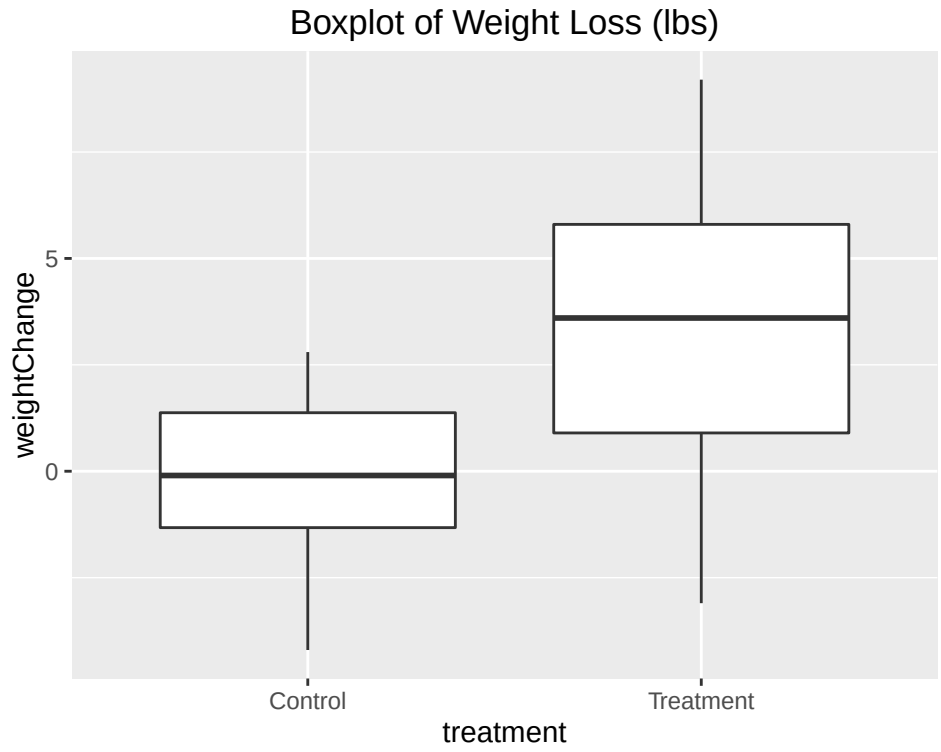


The second thing to notice is that the data needs to be transformed somehow in order to see the weight loss effect. Here I define a new variable called `weightChange`, which is just `startWeights - endWeights`. Because timeElapsed is variable, I also try to scale `weightChange` by the `timeElapsed` in order to look for a possible linear relationship between the two.

An optional step is to omit NAs, which occur in gender.

```
datasetA <- datasetA %>% mutate(weightChange = startWeights - endWeights,
                                weightChangePerDay = weightChange / timeElapsed)
datasetA <- na.omit(datasetA)

#show that there is a weightChange effect in those treated
#versus those who are not
ggplot(datasetA, aes(x = treatment, y= weightChange)) + geom_boxplot() +
  ggtitle("Boxplot of Weight Loss (lbs)")
```



Dataset B

Dataset B is a little trickier. Reading the data dictionary, we notice that the units for `startWeight` and `endWeight` are in kg, so that complicates comparing the two datasets. Also, there are patients who do not have a second measurement. Referring to the data dictionary, these patients are ones who dropped out of the study and are thus uninformative to our research question, so we'll remove them.

```
datasetB <- read.csv("../data/datasetB.csv", row.names= 1)
#show summary before
summary(datasetB)
```

```
##       age            gender       treatment    startWeight
```

```
##  Min.   :64.00   Female:30   Control  :30   Min.   : 51.00
##  1st Qu.:69.00   Male  :42   Treatment:42   1st Qu.: 51.00
##  Median :73.50                             Median : 82.40
##  Mean   :74.75                             Mean   : 76.16
##  3rd Qu.:80.00                             3rd Qu.: 90.50
##  Max.   :88.00                             Max.   :118.00
##
##    endWeight       timeElapsed    staffID1 staffID2
##  Min.   : 57.50   Min.   :30.00   S1: 9    S1:22
##  1st Qu.: 77.58   1st Qu.:40.00   S2:20    S2:23
##  Median : 86.90   Median :55.00   S3:21    S4:27
##  Mean   : 84.79   Mean   :54.75   S4:22
##  3rd Qu.: 93.17   3rd Qu.:67.50
##  Max.   :115.00   Max.   :80.00
##  NA's   :14
```

```
datasetB <- na.omit(datasetB)
#show summary after removing NAs
summary(datasetB)
```

```
##       age           gender       treatment   startWeight
##  Min.   :64.00   Female:24   Control  :24   Min.   : 51.00
##  1st Qu.:69.25   Male  :34   Treatment:34   1st Qu.: 51.00
##  Median :73.50                             Median : 83.25
##  Mean   :75.05                             Mean   : 76.81
##  3rd Qu.:80.00                             3rd Qu.: 92.22
##  Max.   :88.00                             Max.   :118.00
##    endWeight       timeElapsed    staffID1 staffID2
##  Min.   : 57.50   Min.   :30.00   S1: 6    S1:19
##  1st Qu.: 77.58   1st Qu.:38.00   S2:18    S2:18
##  Median : 86.90   Median :54.00   S3:17    S4:21
##  Mean   : 84.79   Mean   :53.81   S4:17
##  3rd Qu.: 93.17   3rd Qu.:67.00
##  Max.   :115.00   Max.   :80.00
```

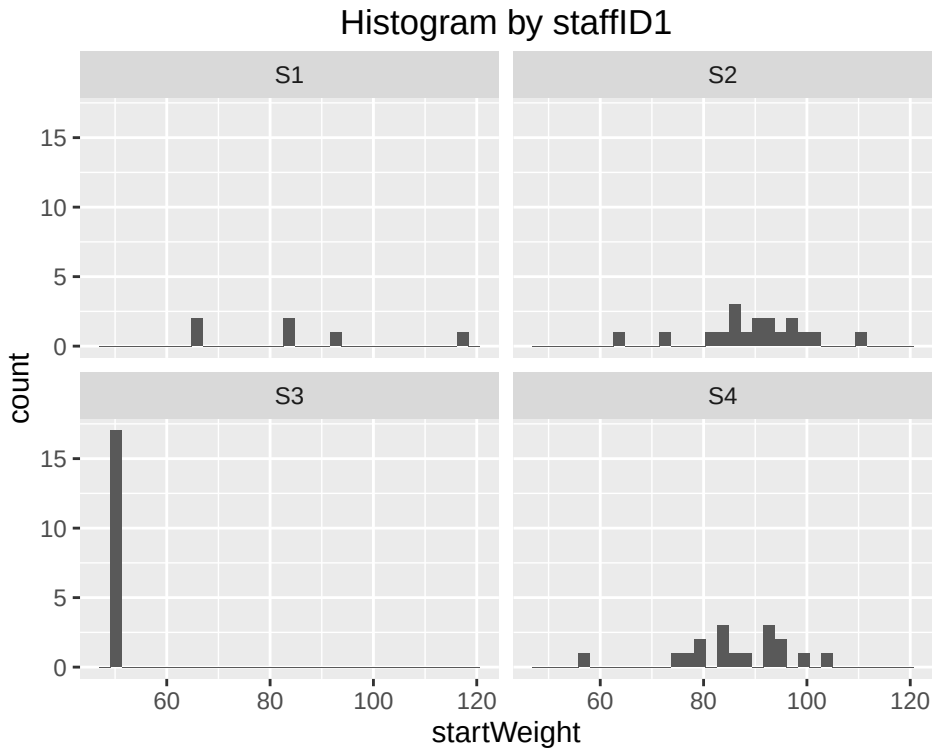
However, all is not well. We should start getting suspicious if we look at the crosstabs between staffID1 and staffID2. Why is there `S3` in `staffID1`, but not `staffID2`?

```
table(datasetB$staffID1, datasetB$staffID2)
```

```
##
##      S1 S2 S4
##   S1  2  1  3
##   S2  4  5  9
##   S3  5  7  5
##   S4  8  5  4
```

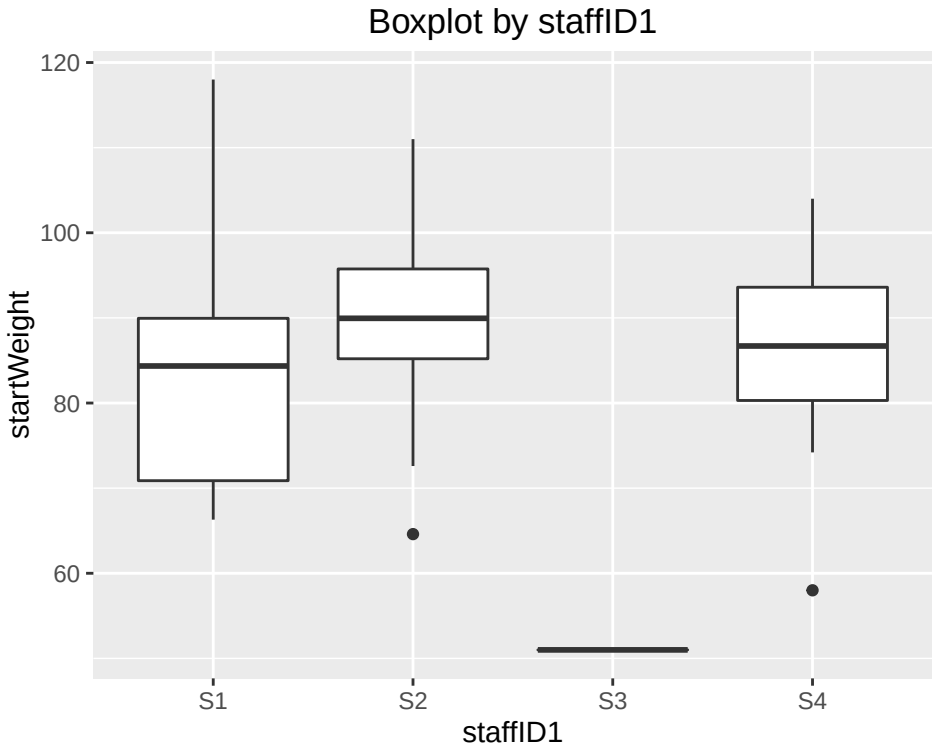
Doing our detective work, we start looking at histograms and boxplots of `startWeight`. Hmm, the weights for S3 look strange. They're all the same value!

```
ggplot(datasetB, aes(x = startWeight)) + geom_histogram() +
  facet_wrap(facet=c("staffID1")) +
  ggtitle("Histogram by staffID1")
```



Looking at the boxplots will also show this.

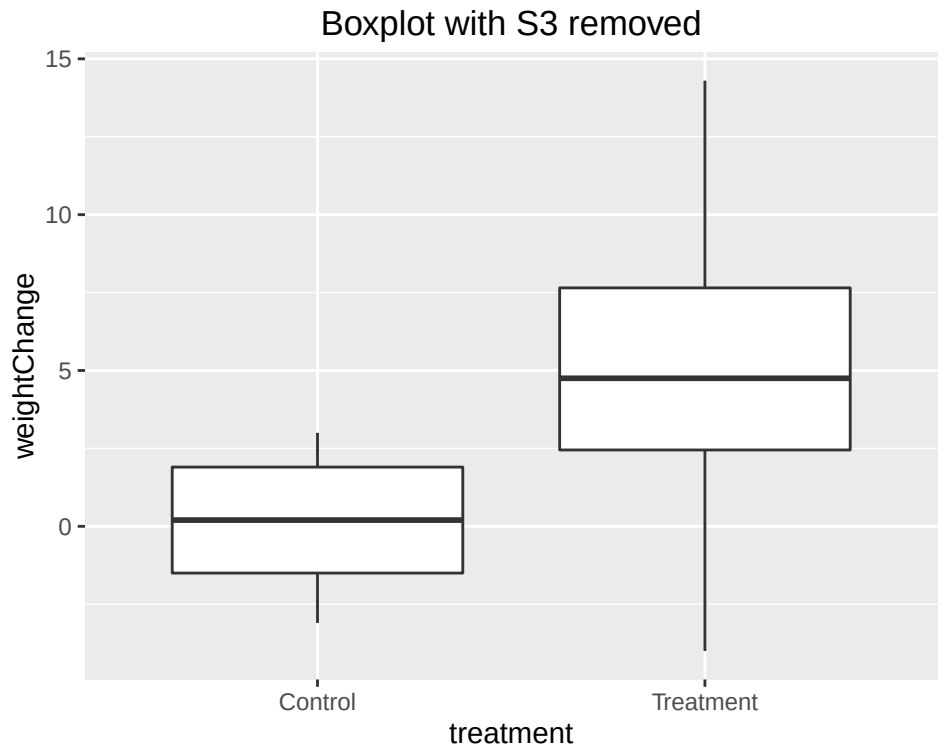
```
ggplot(datasetB, aes(x= staffID1, y = startWeight)) + geom_boxplot() +
  ggtitle("Boxplot by staffID1")
```



Is this data valid? Better not risk it. We'll take it out. We'll calculate the weight change as weightChange

```
datasetB <- datasetB %>% mutate(weightChange = startWeight - endWeight)
ggplot(datasetB, aes(x=treatment, y=weightChange)) + geom_boxplot() +
  ggtitle("Boxplot with all staff")
```

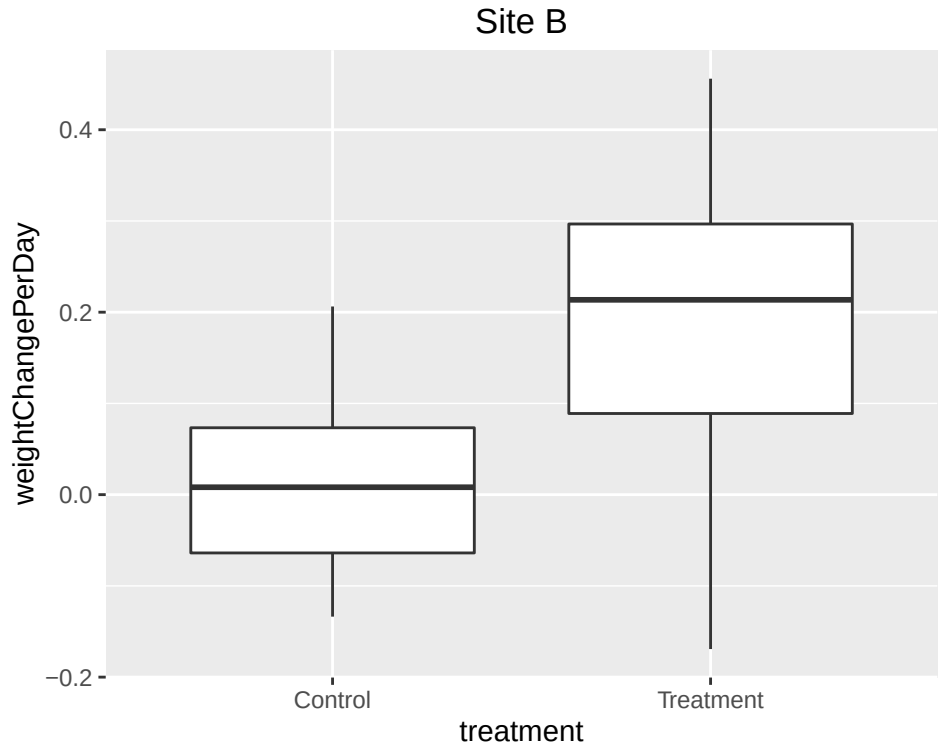

```
datasetB <- datasetB %>% filter(staffID1 != "S3")
ggplot(datasetB, aes(x=treatment, y=weightChange)) + geom_boxplot() +
  ggtitle("Boxplot with S3 removed")
```



Here I convert datasetB's weight loss to pounds, and also scale the weightLoss per day, which seems to be a reasonable way to compare the weight loss across individuals.

```
datasetB <- datasetB %>% mutate(weightChangeLb = weightChange * 2.2, weightChangePerDay =
                                weightChangeLb / timeElapsed)

ggplot(datasetB, aes(x=treatment, y=weightChangePerDay)) + geom_boxplot() +
  ggtitle("Site B")
```



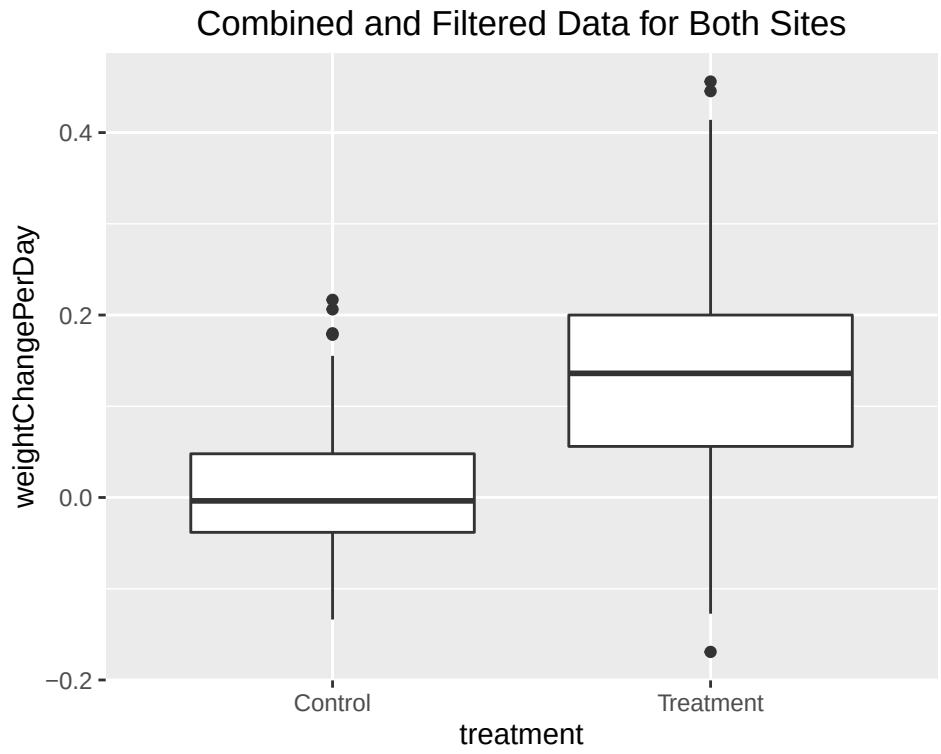
Combining the Data

What is the best way to compare the two datasets? Since the timeElapsed seems to differ among the two datasets, we should compare using `weightChangePerDay`. Students should also note the demographics (especially age) are different between the two datasets.

```
datasetAselect <- datasetA %>% mutate(site="A") %>% select(treatment, weightChangePerDay, site)
datasetBselect <- datasetB %>% mutate(site="B") %>% select(treatment, weightChangePerDay, site)

datasetCombined <- rbind(datasetAselect, datasetBselect)

#plot all combined data together
ggplot(datasetCombined, aes(x=treatment, y=weightChangePerDay)) +
  geom_boxplot() + ggtitle("Combined and Filtered Data for Both Sites")
```




```
#plot all combined data conditioned by site
ggplot(datasetCombined, aes(x=treatment, y=weightChangePerDay)) +
  geom_boxplot() + facet_wrap(facet=c("site")) +
  ggtitle("Combined Data By Site")
```