CSI 2300: Intro to Data Science

In-Class Exercise 03: Introduction to R and RStudio

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The data for today's exercises are the Colorado Covid-19 data used in the lecture.

1. Download the data, and then load it into R. To verify that this has been accomplished, show the column names of the data frame, using the `colnames()` command.

```
covid <- read.csv("~/Documents/dat/lecture3dataset.csv", header=TRUE)
colnames(covid)
# [1] "Date"                                "Utility"
# [3] "SARS_CoV_2_copies_L"                 "Number_of_New_COVID19_Cases_by_"
# [5] "ObjectId"
```

2. Let's do some light data wrangling of this dataset. First, remove the redundant last column, and overwrite the dataset name with this new dataset containing 4 instead of 5 columns. Show the first 6 rows of the updated dataset to demonstrate.

```
covid <- covid[ ,-5]
head(covid)
#         Date                        Utility SARS_CoV_2_copies_L
# 1 08/15/2020 Metro Wastewater RWHTF - PRC                    NA
# 2 08/11/2020                   Broomfield                    NA
# 3 08/15/2020                   Northglenn                    NA
# 4 08/11/2020     CO Springs - JD Phillips                    NA
# 5 08/11/2020       CO Springs - Las Vegas                    NA
# 6 08/15/2020                       Pueblo                    NA
#   Number_of_New_COVID19_Cases_by_
# 1                              36
# 2                               0
# 3                               0
# 4                               6
# 5                              22
# 6                               5
```

3. The names of the last two columns could be better. Replace the existing names with the names `sars_rna_copies` and `new_covid_cases`.

```
colnames(covid)[3:4] <- c("sars_rna_copies","new_covid_cases")
```

4. How many missing values are there in the `sars_rna_copies` variable? What proportion of the dataset is this?

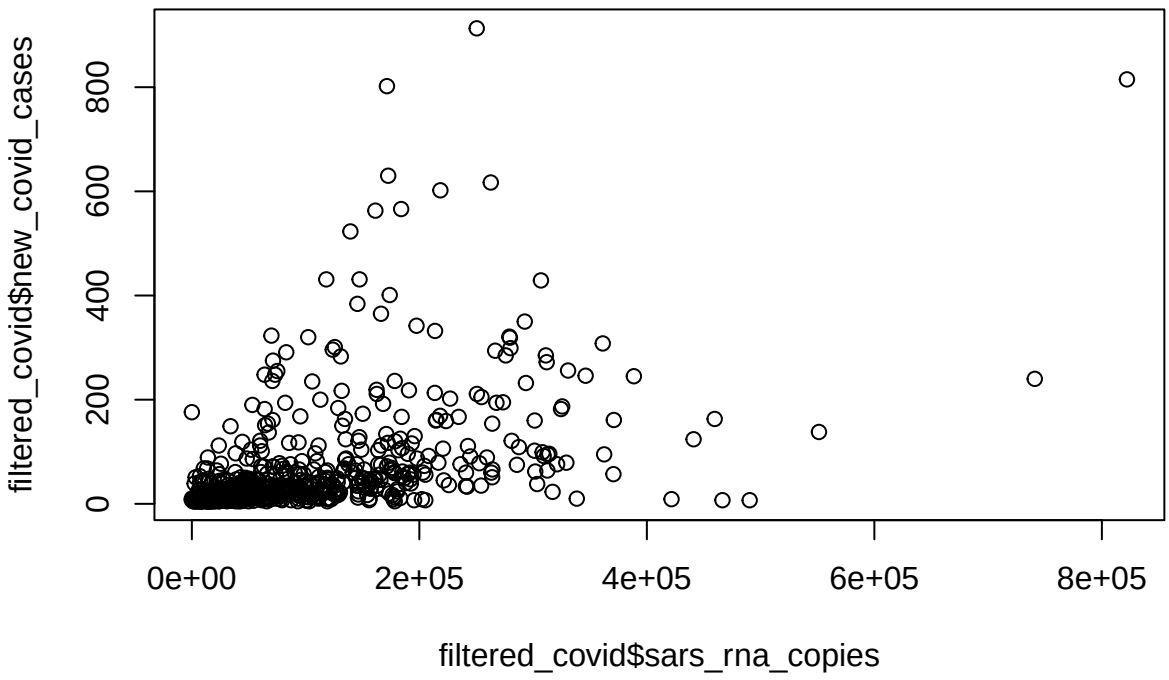
```r
missing_val <- covid[is.na(covid$sars_rna_copies), ]
nrow(missing_val) / nrow(covid) * 100
# [1] 75.67181
```

5. Another issue with the data is that when the count of new cases of Covid-19 is less than 5, the count of new cases is reported as 0 to maintain patient privacy. Filter the data so that only non-NA `sars_rna_copies` are present AND all `new_covid_cases` are 5 or greater. Show the first few rows of this new data frame to demonstrate that you filtered out the undesirable rows.

```r
filtered_covid <- covid[!is.na(covid$sars_rna_copies) & (covid$new_covid_cases >= 5), ]
head(filtered_covid)
#          Date                      Utility sars_rna_copies new_covid_cases
# 16 08/06/2020  Metro Wastewater RWHTF - CC         17308.9              40
# 20 08/06/2020 Metro Wastewater RWHTF - PRC          7078.3              53
# 23 08/02/2020     CO Springs - JD Phillips         24177.4               5
# 29 08/02/2020       CO Springs - Las Vegas         50393.5              15
# 31 08/06/2020                      Pueblo         17677.7               6
# 41 08/06/2020           South Adams County             0.0               7
```

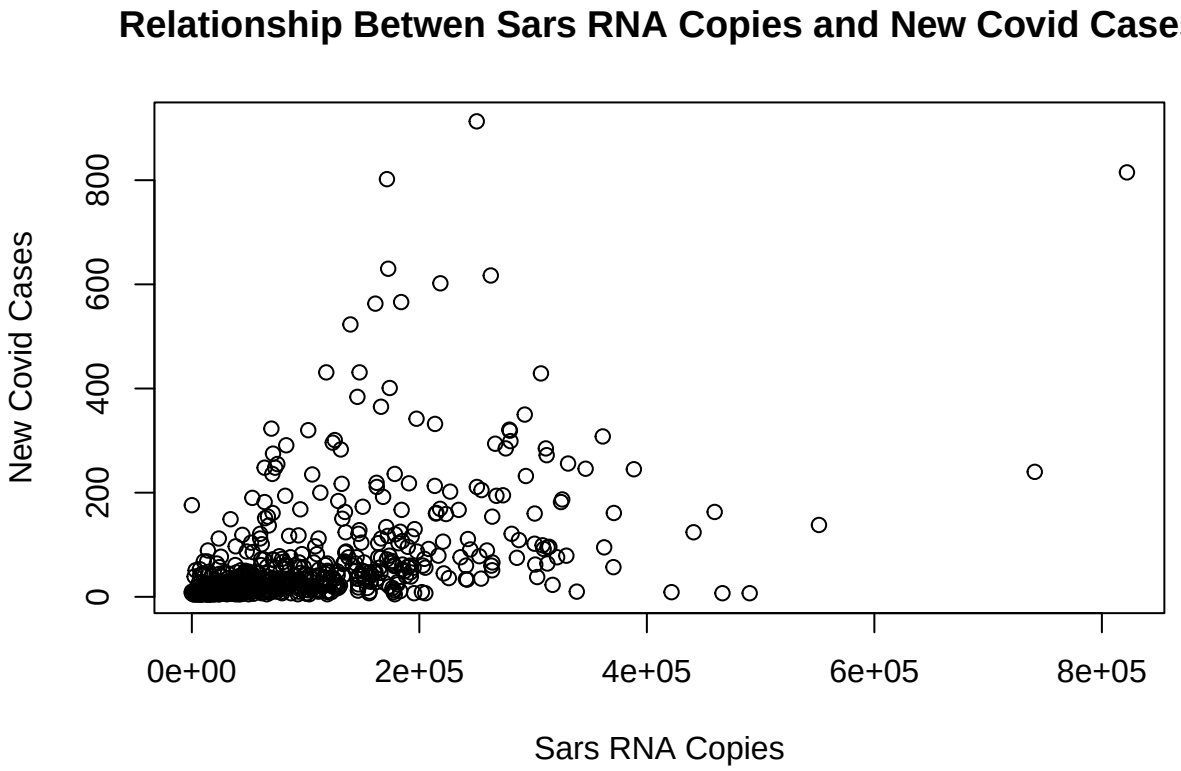
6. Let's do a simple plot of the `new_covid_cases` versus `sars_rna_copies` using the filtered data. Given that we expect the number of new cases to depend on the RNA copies measured, put `new_covid_cases` on the y-axis and `sars_rna_copies` on the x-axis. Comment on what you observe in this plot.

```r
plot(x=filtered_covid$sars_rna_copies,y=filtered_covid$new_covid_cases)
```



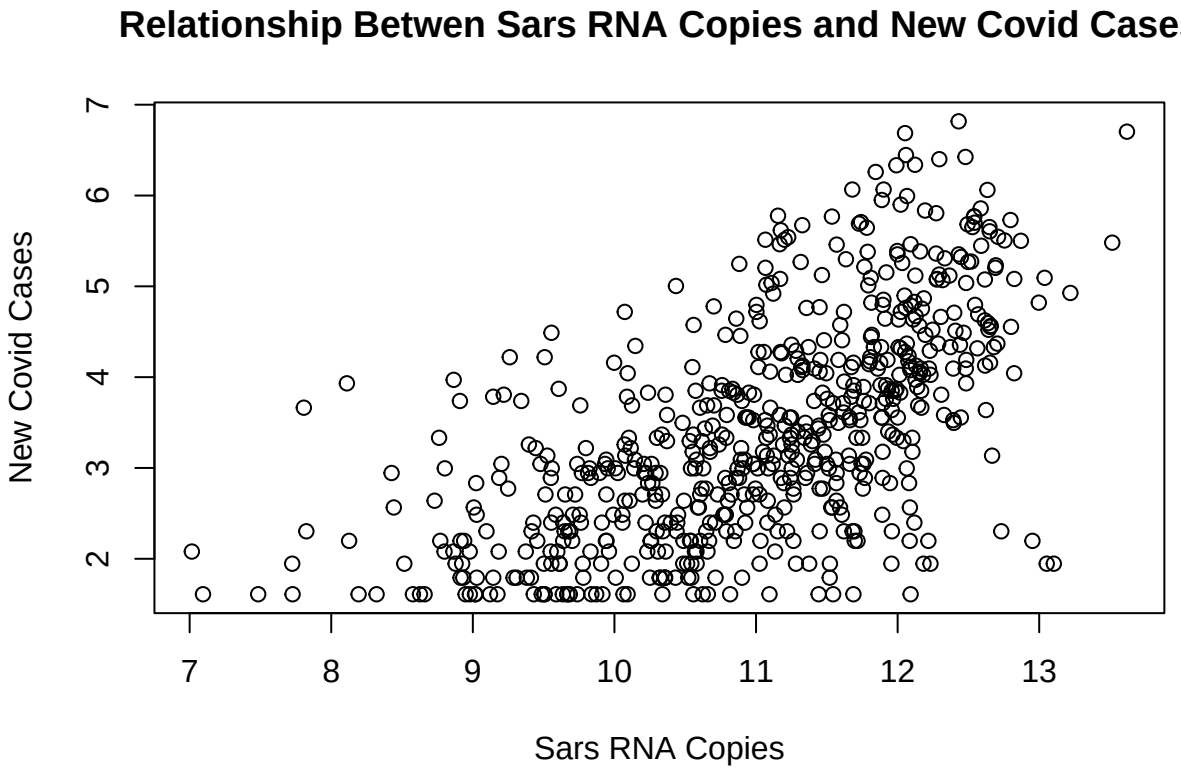
7. Add nicer labels to the plot by including the arguments `xlab="X Label"` and `ylab="Y Label"` and `main="Overall Title"` in the plot command. Change the labels to something appropriate for this figure.

```
plot(x=filtered_covid$sars_rna_copies,y=filtered_covid$new_covid_cases,
     xlab = "Sars RNA Copies",
     ylab = "New Covid Cases",
     main = "Relationship Betwen Sars RNA Copies and New Covid Cases")
```



8. A lot of the points are squished into the bottom left of the figure. They can be spread apart to see the relationship between the two variables more clearly by applying the log to each of the variables. Replot the figure applying the `log()` function to each variable.

```
plot(x=log(filtered_covid$sars_rna_copies),y=log(filtered_covid$new_covid_cases),
     xlab = "Sars RNA Copies",
     ylab = "New Covid Cases",
     main = "Relationship Betwen Sars RNA Copies and New Covid Cases")
```



9. Describe what you see in the figure from the prior question.

It has zoomed into the section where the points were squished together. It is now easier to see the points in this plot. As the number of Sars RNA Copies increase, the number of new covid cases also increases.

10. Now, let's go back to the full dataset and examine the new case counts in one county, Boulder county. First, filter the data to obtain just the Boulder utility's observations. Then, sort the `new_covid_cases` from smallest to largest. What do you observe?

```
covid_boulder <- covid[covid$Utility == "Boulder",]
sort(covid_boulder$new_covid_cases)
#   [1]   0   0   0   0   0   0   0   0   0   0   0   0   0   0   0   0   0   0   0
#  [19]   0   5   5   5   5   5   5   6   6   6   6   7   7   7   7   8   8   8
#  [37]   8   8   9   9   9   9  10  10  10  10  10  10  11  12  12  12  12  13
#  [55]  13  13  14  14  14  15  15  15  15  16  16  16  16  17  17  17  17  18
#  [73]  19  19  19  20  20  20  20  20  21  21  21  21  21  22  22  22  24  24
#  [91]  24  24  25  26  27  27  27  29  30  30  30  30  31  31  31  31  33  33
# [109]  34  34  35  35  35  35  36  37  38  40  41  41  43  44  46  46  47  47
# [127]  47  48  52  53  53  55  55  55  56  57  58  58  58  58  58  60  60  61
```

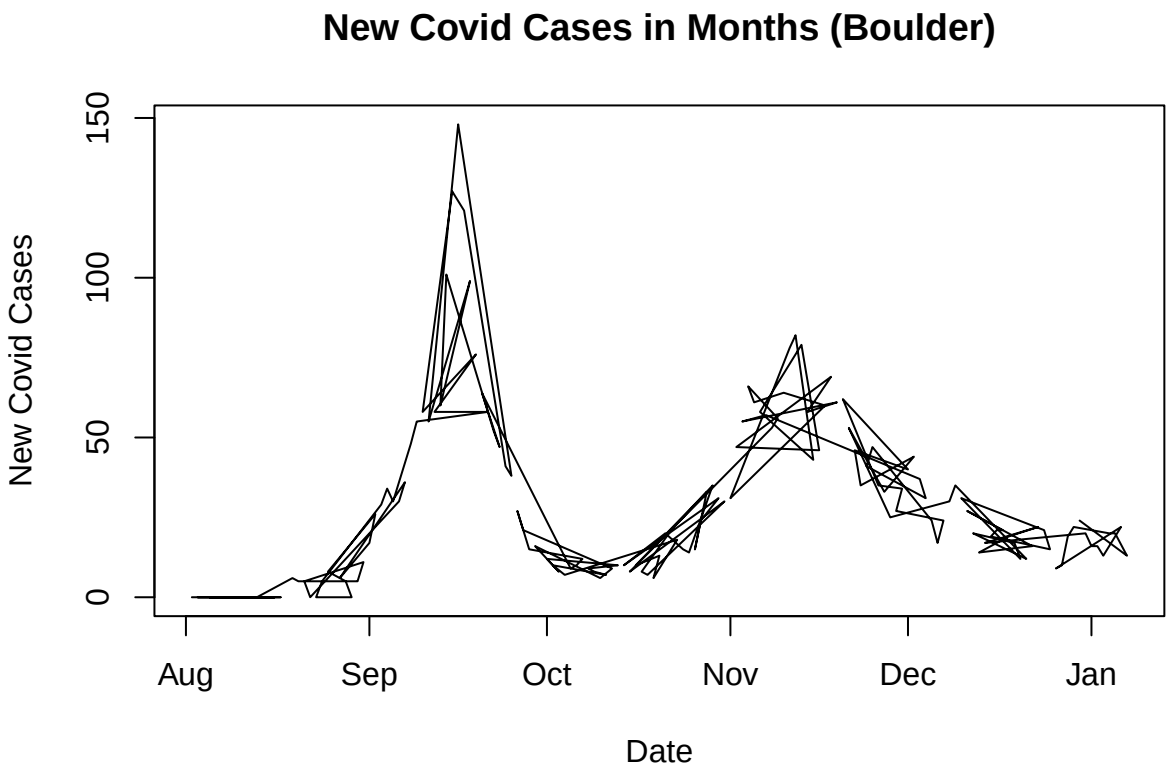
```
# [145]  61  62  64  64  66  69  76  78  79  82  99 101 121 127 148
# There are several zeroes, the majority of the numbers range from 20-40, and only
#a few of the cases are in the higher end (90+).
```

11. Now we want to plot the new covid cases for Boulder over time, similar to the website where the data are reported[1]. To do this, we want to plot the date on the x-axis and the number of new cases on the y-axis with the following additional instructions:

- install and load the `lubridate` library
- wrap `covid_boulder$Date` with the `mdy()` command from the `lubridate` library, which can then be used as the variable to plot on the x-axis.
- inside the `plot()` command, add the argument `type="l"`
- add sensible labels to x and y axes

```
library(lubridate)
#
# Attaching package: 'lubridate'
# The following objects are masked from 'package:base':
#
#     date, intersect, setdiff, union
plot(x=mdy(covid_boulder$Date),y=covid_boulder$new_covid_cases,
     type="l",
     xlab = "Date",
     ylab= "New Covid Cases",
     main = "New Covid Cases in Months (Boulder)")
```

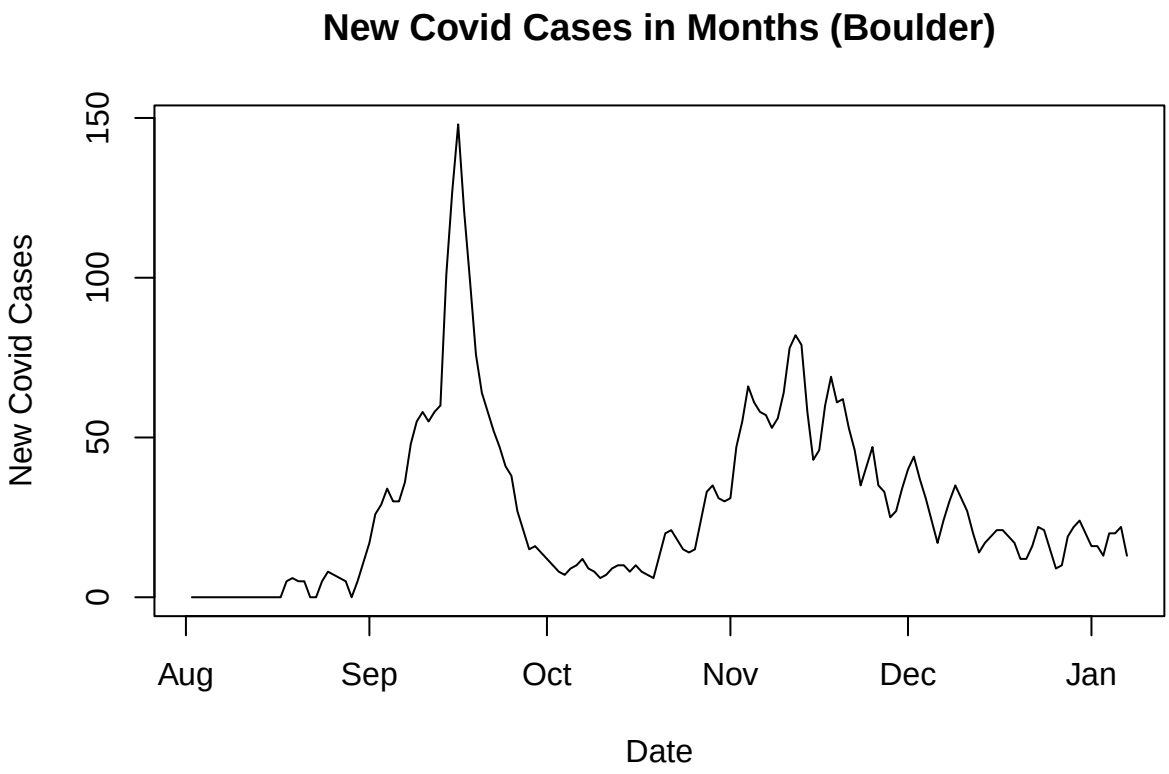
[1] https://cdphe.maps.arcgis.com/apps/opsdashboard/index.html#/d79cf93c3938470ca4bcc4823328946b



12. The lines in the prior plot should not be criss-crossing over themselves. What is the cause of this problem? See if you can fix it. You may find the `order()` command to be useful.

```
# The dates are out of order.
correct_order <- order(mdy(covid_boulder$Date))

plot(mdy(covid_boulder$Date)[correct_order],
     covid_boulder$new_covid_cases[correct_order],
     type = "l",
     xlab = "Date",
     ylab = "New Covid Cases",
     main = "New Covid Cases in Months (Boulder)")
```



13. What patterns do you observe in the plot from the prior question?

The days between September to October, there are a spike in covid cases. After that, it dies down significantly but rises again from November-December.