# Statistical Methods Example Project Rough Draft

John Tipton

## 1 Malaria deaths

For this project, I am examining the malaria deaths by age dataset contained in the `malaria_deaths_age.csv` file on the Tidy Tuesday website. The data consists of 30780 observations of 5 variables. The variable `entity` is a factor with 228 levels that represents the region for the deaths. The variable `code` is a factor with 196 levels which represents a three letter code for the country/region. The variable `year` is a discrete integer variable that records the years between 1990 and 2016. The variable `age_group` is a discrete ordered factor with 5 levels that groups the population into age groups under 5, 5-14, 15-49, 50-69 and 70 or older. The variable `deaths` records the number of deaths from malaria for each region, year, and age group. Initial exploration shows that the largest variability in the number of deaths occurs across age groups with the largest number of deaths occurring in children under 5. Other variability in deaths occurs when examining death rates by region.

The second dataset we use to understand malaria is the incidence rate of malaria given in the `malaria_inc.csv` file on the Tidy Tuesday website. The malaria incidence rate is the average number of people who contract malaria per 1000 people at risk. The malaria incidence dataset has 508 observations of 4 variables: the variable `Entity`, which is a factor with 127 levels, that represents the region for the malaria cases, the variable `Code`, which is a factor with 101 levels, that represents a three letter code for the country/region, the variable `year`, which is a discrete integer variable that records the years between 2000 and 2015 in an interval of 5 years, and the variable `Incidence` which records the number of malaria cases per 1000 people at risk.

To perform our analyses, we need to filter out the data that does not come from a country. These include the following:

### 1.1 Question 1:

First, is there a significant difference in malaria deaths by age group. If so, which groups are different. First, we summarize the annual deaths by age group.

```
## factor in increasing ages
age_levels <- c("Under 5", "5-14", "15-49", "50-69", "70 or older")

dat2 %>%
  mutate(age_group = fct_relevel(age_group, age_levels)) %>%
  filter(!(entity %in% non_countries)) %>%
  group_by(age_group) %>%
  summarize(total_deaths = sum(deaths),
            sd_deaths = sd(deaths),
            count = n()) %>%
  mutate(prop_deaths = total_deaths / sum(total_deaths))
```

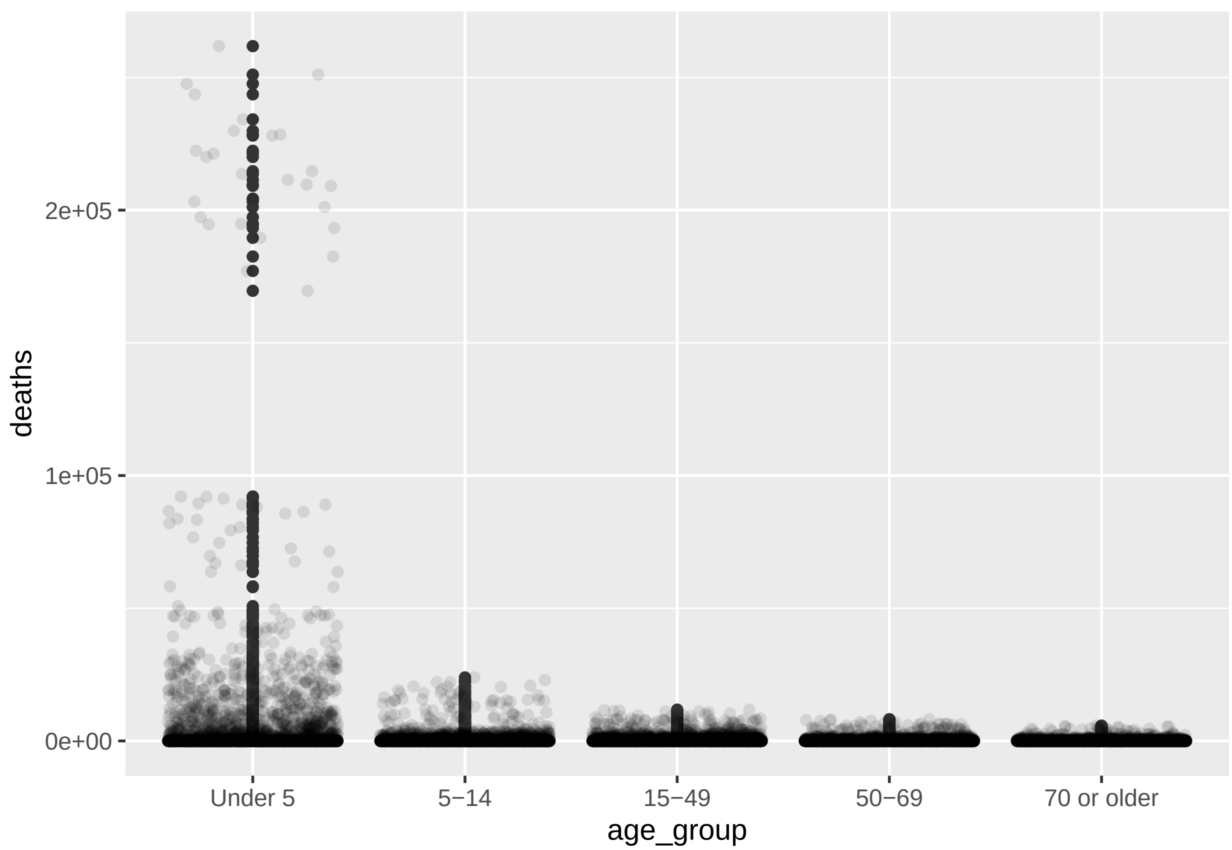
```
## `summarise()` ungrouping output (override with `.groups` argument)
```

```
## # A tibble: 5 x 5
##   age_group   total_deaths sd_deaths count prop_deaths
##   <fct>              <dbl>     <dbl> <int>       <dbl>
```

```
## 1 Under 5        17679161.    17044.  5373       0.759
## 2 5-14             2161707.     1755.  5373       0.0928
## 3 15-49            1810052.     1102.  5373       0.0777
## 4 50-69            1016814.      689.  5373       0.0437
## 5 70 or older       624677.      437.  5373       0.0268
```

From the summary table, we see that the Under 5 age group is the largest proportion of deaths (76.7%) with the next highest death rate fo the 5-14 age group. The dataset shows that there is a very large amount of variability around total deaths. Next, we visualize this result to better highlight the differences. However, the data is really hard to visualize on the original data scale.

```
dat2 %>%
  mutate(age_group = fct_relevel(age_group, age_levels)) %>%
  filter(!(entity %in% non_countries)) %>%
  mutate(age_group = fct_relevel(age_group, age_levels)) %>%
  filter(!(entity %in% non_countries)) %>%
  ggplot(aes(x = age_group, y = deaths)) +
  geom_boxplot() +
  geom_point(position = "jitter", alpha = 0.1)
```




There seems to be a pretty interesting grouping happening. Maybe this is related to country/region?

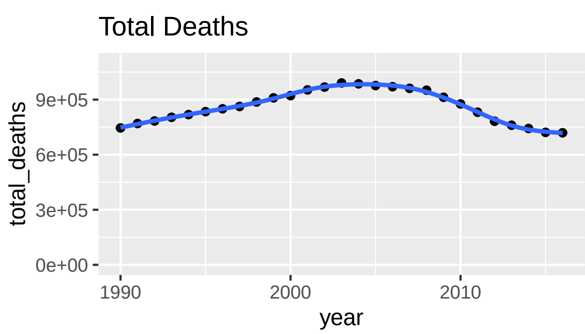
## 1.2 Question 2:

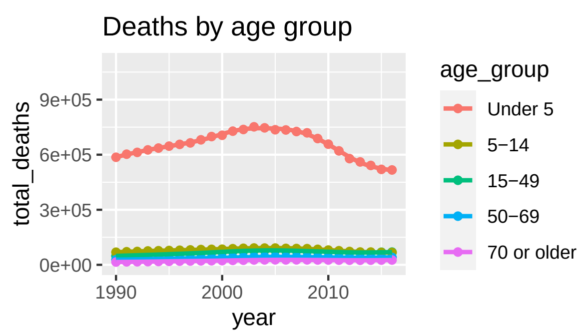
Second, I want to test whether the death rate from malaria changed over time?

```
dat2 %>%
  filter(!(entity %in% non_countries)) %>%
```

```
  group_by(year) %>%
  summarize(total_deaths = sum(deaths)) %>%
  ggplot(aes(x = year, y = total_deaths)) +
  geom_point() +
  stat_smooth(method = "gam") +
  ylim(c(0, 1100000)) +
  ggtitle("Total Deaths")

## plot time varying response
dat2 %>%
  filter(!(entity %in% non_countries)) %>%
  group_by(year, age_group) %>%
  summarize(total_deaths = sum(deaths)) %>%
  mutate(age_group = fct_relevel(age_group, age_levels)) %>%
  ggplot(aes(x = year, y = total_deaths, group = age_group, color = age_group)) +
  geom_point() +
  stat_smooth(method = "gam", se = FALSE) +
  # stat_smooth(method = "lm") +
  ylim(c(0, 1100000)) +
  ggtitle("Deaths by age group")
```

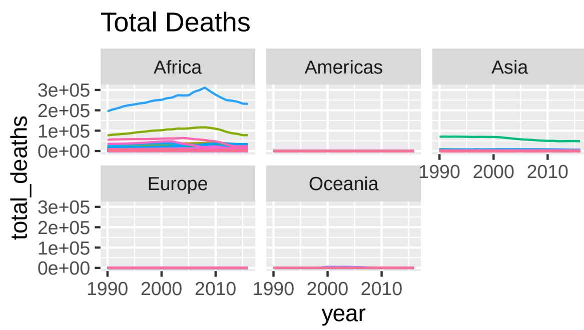



From these graphics, it appears that there is a change in total deaths over time, with an increase in young child mortality until the mid 2000s and then a relatively rapid decrease in child mortality in the late 2000s and 2010s.

To get a better understanding of the mortality patterns, I will plot the total mortality by country. To visualize this, I will group the country-level data by region.

```
dat2 %>%
  filter(!(entity %in% non_countries)) %>%
  left_join(dat_codes, by = c("code" = "alpha-3")) %>%
  group_by(year, entity, region) %>%
  ## remove the NA values corresponding to the British Isles
  filter(!is.na(region)) %>%
  summarize(total_deaths = sum(deaths)) %>%
  ggplot(aes(x = year, y = total_deaths, group = entity, color = entity)) +
  geom_line() +
  facet_wrap(~ region) +
  ggtitle("Total Deaths") +
  theme(legend.position = "none")
```




Form this graphic, we can see that the African continent has been the primary driver of Malaria deaths with some deaths in Asia. We also see a large drop in Malaria deaths in the mid 2000s for many African countries.

This leads to an interesting question: What are the countries that have had the highest Malaria deaths during the study period?

```
dat2 %>%
  mutate(age_group = fct_relevel(age_group, age_levels)) %>%
  filter(!(entity %in% non_countries)) %>%
  group_by(entity) %>%
  summarize(total_deaths = sum(deaths)) %>%
  arrange(desc(total_deaths))
```

```
## `summarise()` ungrouping output (override with `.groups` argument)
```

```
## # A tibble: 199 x 2
##    entity                           total_deaths
##    <chr>                                   <dbl>
##  1 Nigeria                              6781688.
##  2 Democratic Republic of Congo         2626521.
##  3 India                                1635914.
##  4 Uganda                               1385068.
##  5 Burkina Faso                          871502.
##  6 Tanzania                              840409.
##  7 Mozambique                            815691.
##  8 Cote d'Ivoire                         743532.
##  9 Niger                                 703402.
## 10 Cameroon                              673736.
## # ... with 189 more rows
```

The highest Malaria deaths occurred in Nigeria, Democratic Republic of Congo, India, and down the line. This is not surprising as these are the largest countries in the tropical region where the *Anopheles* mosquitoes that spread Malaria live.

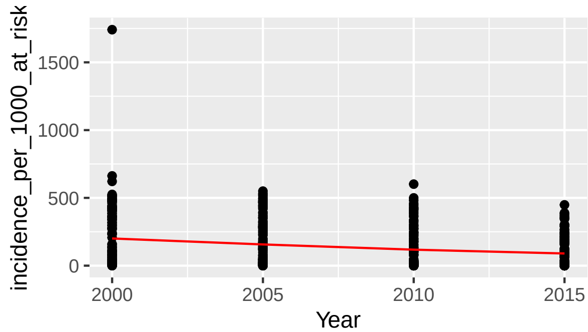
### 1.3 Question 3:

The third question is whether the incidence of malaria per 100K people at risk changed over time? This is a better indicator of risk as it is the same across countries with large and small populations.

```
dat3 %>%
  filter(!(Entity %in% non_countries)) %>%
  group_by(Year) %>%
  # summarize(mean_incidence = mean(incidence_per_1000_at_risk)) %>%
  ggplot(aes(x = Year, y = incidence_per_1000_at_risk)) +
  geom_point() +
```

```
  stat_summary(fun = "mean", geom = "line", color = "red")
  ggtitle("Malaria incidence per 100K")
```

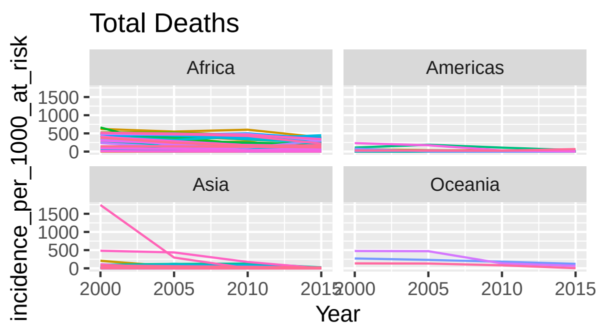
```
## $title
## [1] "Malaria incidence per 100K"
##
## attr(,"class")
## [1] "labels"
```




From this graphics, it appears that there is a decrease in Malaria incidence over time.

To get a better understanding of the Malaria incidence patterns, I will plot the incidence over time by country To visualize this, I will group the country-level data by region.

```
dat3 %>%
  filter(!(Entity %in% non_countries)) %>%
  left_join(dat_codes, by = c("Code" = "alpha-3")) %>%
  group_by(Year, Entity, region) %>%
  ## remove the NA values corresponding to the British Isles
  filter(!is.na(region)) %>%
  ggplot(aes(x = Year, y = incidence_per_1000_at_risk, group = Entity, color = Entity)) +
  geom_line() +
  facet_wrap(~ region) +
  ggtitle("Total Deaths") +
  theme(legend.position = "none")
```




Form this graphic, we can see that the African continent has the highest incidence of Malaria although in Asia, one country has had a very large decrease in Malaria incidence. The incidence rates in Africa have been slowly declining.

This leads to an interesting question: What are the countries that have had the highest Malaria incidence during 2000?

```r
dat3 %>%
  filter(!(Entity %in% non_countries)) %>%
  filter(Year == "2000") %>%
  arrange(desc(incidence_per_1000_at_risk))
```

```
## # A tibble: 124 x 4
##    Entity                       Code   Year incidence_per_1000_at_risk
##    <chr>                        <chr> <dbl>                      <dbl>
##  1 Turkey                       TUR    2000                      1741 
##  2 Ethiopia                     ETH    2000                       662.
##  3 Burkina Faso                 BFA    2000                       622.
##  4 Cote d'Ivoire                CIV    2000                       525.
##  5 Togo                         TGO    2000                       518.
##  6 Uganda                       UGA    2000                       517.
##  7 Mozambique                   MOZ    2000                       516.
##  8 Democratic Republic of Congo COD    2000                       508.
##  9 Nigeria                      NGA    2000                       498.
## 10 Liberia                      LBR    2000                       497.
## # ... with 114 more rows
```

The highest Malaria incidence in 2000 was in Turkey, with many African countries also having high incidence.

We can compare this to 2015 to see what has changed:

```r
dat3 %>%
  filter(!(Entity %in% non_countries)) %>%
  filter(Year == "2015") %>%
  arrange(desc(incidence_per_1000_at_risk))
```

```
## # A tibble: 124 x 4
##    Entity        Code   Year incidence_per_1000_at_risk
##    <chr>         <chr> <dbl>                      <dbl>
##  1 Mali          MLI    2015                       449.
##  2 Burkina Faso  BFA    2015                       389.
##  3 Nigeria       NGA    2015                       381.
##  4 Guinea        GIN    2015                       368.
##  5 Niger         NER    2015                       356.
##  6 Cote d'Ivoire CIV    2015                       349.
##  7 Togo          TGO    2015                       345.
##  8 Sierra Leone  SLE    2015                       303.
##  9 Rwanda        RWA    2015                       301.
## 10 Mozambique    MOZ    2015                       298.
## # ... with 114 more rows
```

In 2015, the countries with the highest Malaria incidence have changed but are all in Africa. The overall Malaria incience in the top-10 most affected countries has also decreased.

### 1.4 Conclusion:

TBD

## 2 Covid-19 data analysis

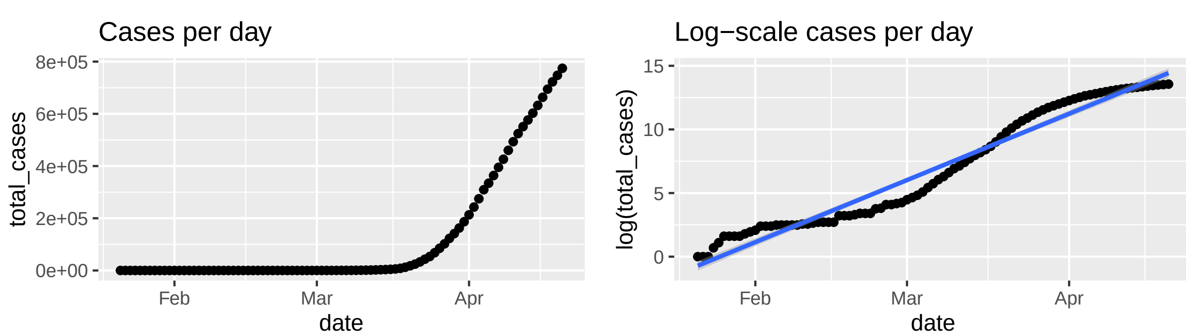
### 2.1 Data

Using data available on GitHub from the NY Times, I am going to investigate the ongoing Covid-19 pandemic in the United States. The variables in the Covid-19 data include the date, the state, the federal id code (fips), the number of cases recorded in the state for the given date, and the number of deaths recorded in the state for the given date. The US population data is from the US Census Bureau website. There are 151 variables in the US Census data – we will use the `NAME` variable (state variable) and the estimated population in 2019 `POPESTIMATE2019`.

### 2.2 Question 1:

Does the number of people being infected with covid-19 each day from late January to late April follow an exponential growth curve? To explore this question, we visualize the total number of cases on both a linear scale and a logarithmic scale. Exponential growth is characterized by a linear response to log-transformed data.

```
dat %>%
    group_by(date) %>%
    summarise(total_cases = sum(cases)) %>%
  ggplot(aes(x = date, y = total_cases)) +
  geom_point() +
  ggtitle("Cases per day")
dat %>%
    group_by(date) %>%
    summarise(total_cases = sum(cases)) %>%
  ggplot(aes(x = date, y = log(total_cases))) +
  geom_point() +
  ggtitle("Log-scale cases per day") +
  stat_smooth(method = "lm")
```




Based on the visualizations, there is evidence that the growth in number of covid-19 cases from late January to late April in the United States was exhibiting exponential growth. This can be seen by the steep increase (hockey-stick shape) in the data over time for the non-transformed data and a nearly linear response in the log-transformed data.

### 2.3 Question 2:

The next question is whether the average rate of cases in the US grown slower in April (post social distancing), than March, the month prior (less social distancing). The rate of cases is defined as the ratio of new cases from day to day.

```
dat_April <-
  dat %>% subset(date >= "2020-04-01")
```

```r
dat_March <-
  dat %>% subset(date >= "2020-03-01" & date < "2020-04-01")

rates_April <- dat_April %>%
  group_by(date) %>%
  summarise(total_cases = sum(cases)) %>%
  mutate(rate_increase = total_cases / lag(total_cases),
         month = "April")
```

```
## `summarise()` ungrouping output (override with `.groups` argument)
```

```r
rates_March <- dat_March %>%
  group_by(date) %>%
  summarise(total_cases = sum(cases)) %>%
  mutate(rate_increase = total_cases / lag(total_cases),
                  month = "March")
```

```
## `summarise()` ungrouping output (override with `.groups` argument)
```

```r
dat_rates <- rbind(rates_March, rates_April)
dat_rates$month <- factor(dat_rates$month, levels = c("March", "April"))
```

Next, we compare the average ratio of cases from day to day for the two time periods

```r
dat_rates %>%
  group_by(month) %>%
  filter(!is.na(rate_increase)) %>%
  summarise(mean_ratio = mean(rate_increase))
```

```
## `summarise()` ungrouping output (override with `.groups` argument)

## # A tibble: 2 x 2
##   month mean_ratio
##   <fct>      <dbl>
## 1 March       1.29
## 2 April       1.07
```

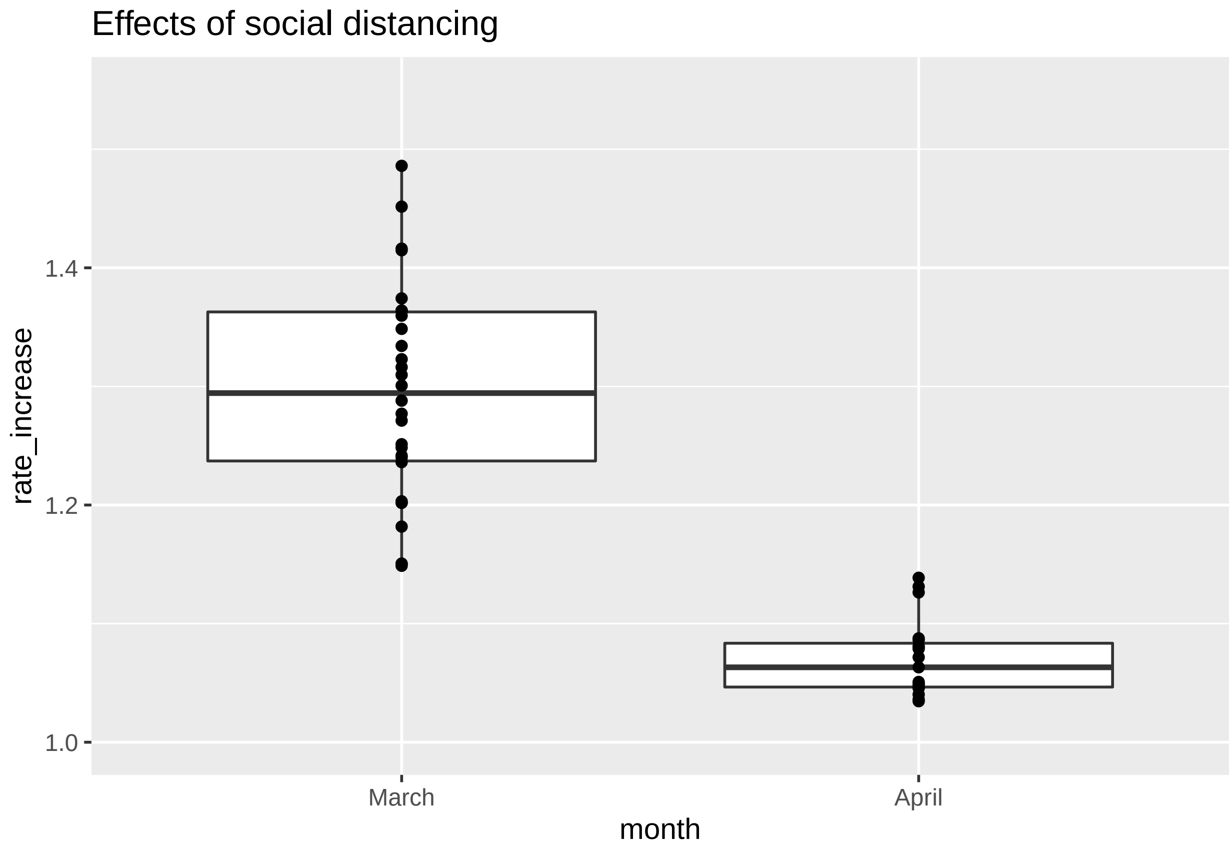
which supports that the daily ratio of the number of cases in March was higher than in April (cases grew faster on a relative scale in March than April). Next we visuallize the data

```r
dat_rates %>%
  ggplot(aes(x = month, y = rate_increase)) +
  geom_boxplot() +
  # scale_color_viridis() +
  geom_point(position = position_dodge()) +
  ggtitle("Effects of social distancing") +
  ylim(c(1.0, 1.55))
```

```
## Warning: Removed 2 rows containing non-finite values (stat_boxplot).

## Warning: Width not defined. Set with `position_dodge(width = ?)`

## Warning: Removed 2 rows containing missing values (geom_point).
```




From the graphic above, the relative increase in the number of cases was high in March (pre social distancing measures) than in April (post social distancing measures). There has been a lot in the news about the $R_0$ of the virus (the reproduction rate). Based on this very simple visualization of the data, there is some evidence that social distancing measures in the United States in the spring may have reduced the $R_0$ for covid-19. We cannot conclude definitively that this result is a direct consequence of social distancing from the data alone, however, there is strong epidemiological evidence that social distancing is the primary cause of this decline in case growth rate. Also note, the growth rate is still greater than 1 suggesting the number of cases is still increasing nationwide.

## 2.4 Question 3:

Using the the week April 10-17, has the number of new cases per 100K people (using population data available here) over the this week, is there a difference in infection rate based on spatial region in the US (northwest, south, northeast, etc.).

```r
## state region data from https://stackoverflow.com/questions/46066974/add-column-to-label-u-s-states-b
dat_NE <- data.frame(
  name = c("Connecticut","Maine","Massachusetts","New Hampshire",
              "Rhode Island","Vermont","New Jersey","New York",
              "Pennsylvania"),
  abbr = c("CT","ME","MA","NH","RI","VT","NJ","NY","PA"),
  region = "NE"
)

dat_MW <- data.frame(
  name = c("Indiana","Illinois","Michigan","Ohio","Wisconsin",
            "Iowa","Kansas","Minnesota","Missouri","Nebraska",
```

```r
           "North Dakota","South Dakota"),
  abbr = c("IN","IL","MI","OH","WI","IA","KS","MN","MO","NE",
           "ND","SD"),
  region = "MW"
)
dat_S <- data.frame(
  name = c("Delaware","District of Columbia","Florida","Georgia",
           "Maryland","North Carolina","South Carolina","Virginia",
           "West Virginia","Alabama","Kentucky","Mississippi",
           "Tennessee","Arkansas","Louisiana","Oklahoma","Texas"),
  abbr = c("DE","DC","FL","GA","MD","NC","SC","VA","WV","AL",
           "KY","MS","TN","AR","LA","OK","TX"),
  region = "S"
)
dat_W <- data.frame(
  name = c("Arizona","Colorado","Idaho","New Mexico","Montana",
            "Utah","Nevada","Wyoming","Alaska","California",
            "Hawaii","Oregon","Washington"),
  abbr = c("AZ","CO","ID","NM","MT","UT","NV","WY","AK","CA",
            "HI","OR","WA"),
  region = "W"
)

dat_region = rbind(dat_NE, dat_MW, dat_S, dat_W)

## plot of number cases per 100K  grouped by state
dat_cases_per_100K_by_region <- dat_merged %>%
  left_join(dat_region, by = c("state" = "name")) %>%
  subset(date >= "2020-04-10" & date <= "2020-04-17") %>%
  group_by(state, date, region) %>%
  summarise(total_cases_per_100K = sum(cases_per_100K)) %>%
  mutate(new_cases_per_100K = total_cases_per_100K - lag(total_cases_per_100K))
```

```
## `summarise()` regrouping output by 'state', 'date' (override with `.groups` argument)
```

```r
dat_cases_per_100K_by_region %>%
  group_by(region) %>%
  summarize(
    region_mean = mean(total_cases_per_100K),
    region_sd   = sd(total_cases_per_100K),
    count = n()
  )
```

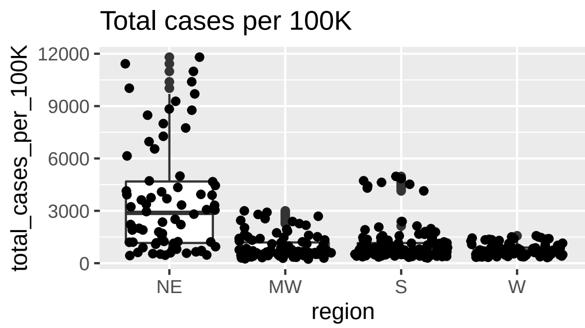
```
## `summarise()` ungrouping output (override with `.groups` argument)
```

```
## # A tibble: 4 x 4
##   region region_mean region_sd count
##   <fct>        <dbl>     <dbl> <int>
## 1 NE           3666.     3176.    72
## 2 MW            918.      677.    96
## 3 S            1070.     1006.   128
## 4 W             761.      350.    88
```

Based on this summary, we see that there was a much higher incidence of covid-19 in the northeast and the south of the United States. This makes intuitive sense as the northeast and south are more densely populated than the midwest and west.

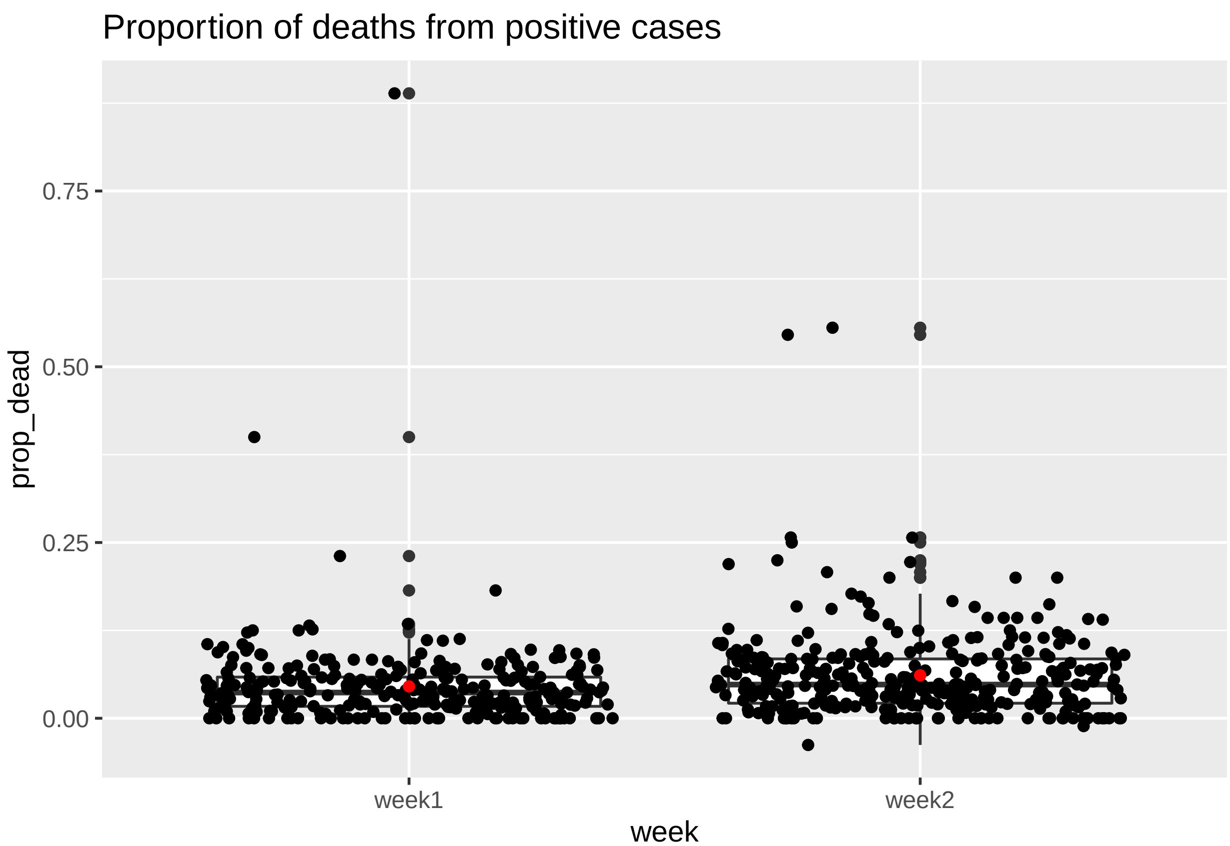
We can also visualize the incidence rates as below:

```
dat_cases_per_100K_by_region %>%
  ggplot(aes (x = region, y = total_cases_per_100K)) +
  geom_boxplot() +
  geom_point(position = "jitter") +
  ggtitle("Total cases per 100K")
```




## 2.5 Question 4:

Is there a difference in the proportion of deaths per cases for the week April 3-10 vs. April 10-17.




Based on this graphic, it does appear that the average proportion of positive cases resulting in death is higher in the week of April 10-17 compared to April 3-10.

# 3 Conclusion:

TBD