Homework #4

Sang Doan 10/15/2020

Problem 1

See data_munge.R.

Problem 2

See data.R.

Problem 3

```
pop <- getPop()
facts <- getFacts()
deaths <- getDeaths()
head(get_counties(pop))

## county state
## 1 Autauga County AL
## 2 Baldwin County AL
## 3 Barbour County AL
## 4 Bibb County AL
## 5 Blount County AL</pre>
```

Problem 4

6 Bullock County

```
dem1 <- 'AGE775214'
head(map_counties(deaths, pop, facts, dem1))</pre>
```

```
##
            county state
                            deathRate statistic
## 1 Autauga County
                      AL 0.0004295763
                                           13.8
## 2 Baldwin County
                   AL 0.0002060618
                                           18.7
## 3 Barbour County
                    AL 0.0002835615
                                           16.5
                   AL 0.0004018934
## 4
       Bibb County
                                           14.8
## 5 Blount County AL 0.0002075191
                                           17.0
## 6 Bullock County
                    AL 0.0013860014
                                           14.9
```

AL

Problem 5

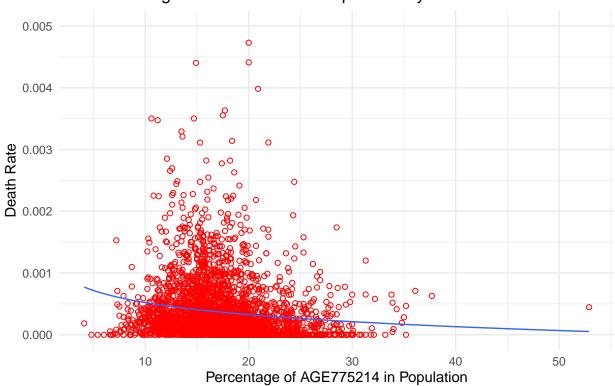
Five demographics I chose are:

- (1) AGE775214 Persons 65 years and over, percent, 2014
- (2) EDU685213 Bachelor's degree or higher, percent of persons age 25+, 2009-2013
- (3) RHI225214 Black or African American alone, percent, 2014
- (4) RHI325214 American Indian and Alaska Native alone, percent, 2014

People 65 years and over

plotDem(deaths, pop, facts, 'AGE775214') %>% format(scientific = F)

Relationship between Covid-19 Death Rate and Percentage of AGE775214 in Population by Counties

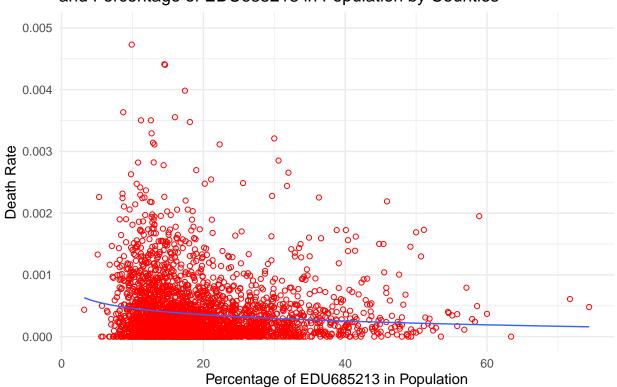


[1] "-0.00001802184"

People with a Bachelor's degree or higher

plotDem(deaths, pop, facts, 'EDU685213') %>% format(scientific = F)

Relationship between Covid–19 Death Rate and Percentage of EDU685213 in Population by Counties

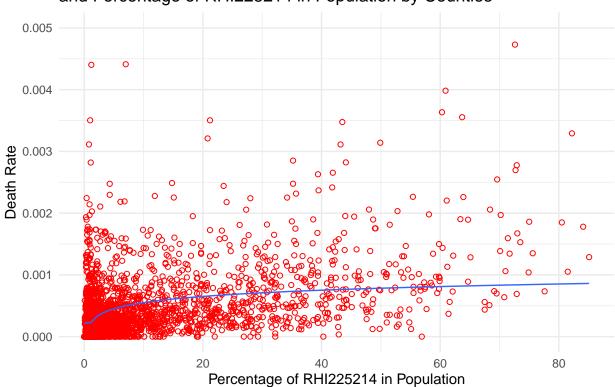


[1] "-0.0000465274"

Black or African Americans

plotDem(deaths, pop, facts, 'RHI225214') %>% format(scientific = F)

Relationship between Covid–19 Death Rate and Percentage of RHI225214 in Population by Counties

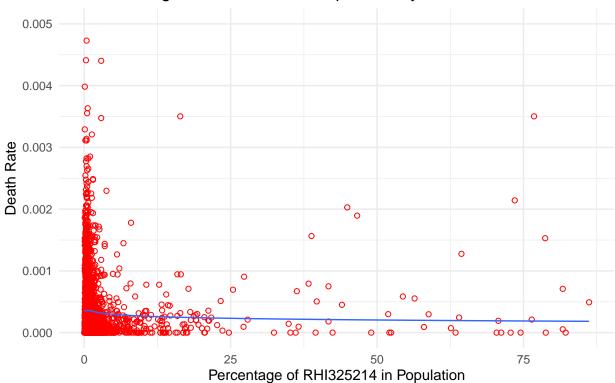


[1] "0.00001762311"

American Indians and Alaska Natives

plotDem(deaths, pop, facts, 'RHI325214') %>% format(scientific = F)

Relationship between Covid–19 Death Rate and Percentage of RHI325214 in Population by Counties

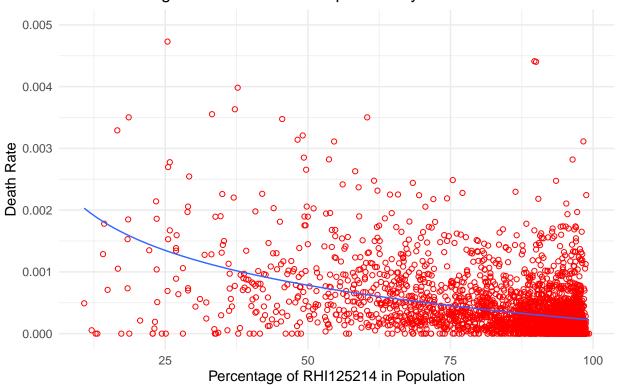


[1] "0.0000004150738"

Whites

plotDem(deaths, pop, facts, 'RHI125214') %>% format(scientific = F)

Relationship between Covid–19 Death Rate and Percentage of RHI125214 in Population by Counties



[1] "-0.00001406819"

Old age is the best predictor of Covid-19 deaths among the five demographics, but all correlations assessed above are insignificant.

Code

```
data_munge.R
deaths <- read.csv('../raw_data/covid_deaths.csv', header=T, stringsAsFactors = F)</pre>
facts <- read.csv('../raw_data/county_facts.csv', header=T, stringsAsFactors = F)</pre>
pop <- read.csv('../raw_data/county_population.csv', header=T, stringsAsFactors = F)</pre>
names(deaths)[1:3] <- c('FIPS', 'county', 'state')</pre>
names(facts)[1:3] <- c('FIPS', 'county', 'state')</pre>
names(pop)[1:3] <- c('FIPS', 'county', 'state')</pre>
write.csv(deaths, '../processed_data/processed_covid_deaths.csv', row.names = F)
write.csv(facts, '../processed_data/processed_county_facts.csv', row.names = F)
write.csv(pop, '../processed_data/processed_county_population.csv', row.names = F)
data.R
getFacts <- function() {</pre>
  return(read.csv('.../processed data/processed county facts.csv', header = T,
                   stringsAsFactors = F))
}
getDeaths <- function() {</pre>
  return(read.csv('../processed_data/processed_covid_deaths.csv', header = T,
                   stringsAsFactors = F))
}
getPop <- function() {</pre>
  return(read.csv('../processed_data/processed_county_population.csv',
                   header = T, stringsAsFactors = F))
analysis.R
get_counties <- function(d) {</pre>
  return(dplyr::select(d, county, state))
map_counties <- function(cd, cp, cf, demographic) {</pre>
  #It appears that all data frames are already arranged in an ascending order by FIPS.
  #In such case, the following three lines are unnecessary.
  cd <- cd %>% arrange(FIPS)
  cf <- cf %>% arrange(FIPS)
  cp <- cp %>% arrange(FIPS)
  counties <- get_counties(cd)</pre>
  counties$deathRate <- rowSums(select(cd, -FIPS, -county, -state, -stateFIPS)) / cp$population</pre>
  counties$statistic <- cf[[demographic]]</pre>
  return(counties)
plotDem <- function(cd, cp, cf, dem) {</pre>
thisDem <- select(map_counties(cd, cp, cf, dem), deathRate, statistic)
```

```
thisPlot <- ggplot(data = thisDem, aes(x = statistic, y = deathRate)) +</pre>
    ggtitle(paste('Relationship between Covid-19 Death Rate \nand Percentage of', dem,
                  'in Population by Counties')) +
    geom_point(color = 'red', size = 1.5, fill = 'blue', shape = 1, stroke = 0.5) +
    xlab(paste('Percentage of', dem, 'in Population')) +
    geom\_smooth(method = 'lm', formula = y ~ ifelse(is.finite(log(x)), log(x), 0),
                se = F, size = 0.5) +
    scale_y_continuous(name = 'Death Rate', limits = c(0, 0.005)) +
    theme_minimal()
  print(thisPlot)
  return(coef(lm(deathRate ~ statistic, thisDem))[[2]])
config.R
source('data.R')
source('analysis.R')
library(tidyverse)
library(magrittr)
```