DATA 608 Module 3

Jun Pan 3/11/2019

Overview Data

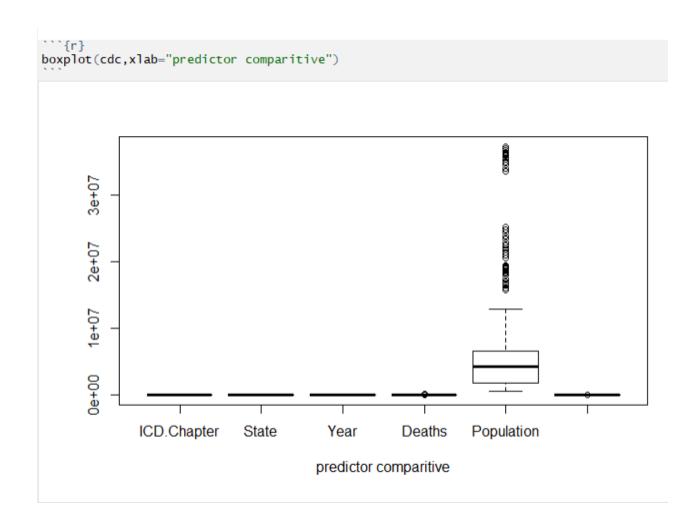
cdc <-read.csv("https://raw.githubusercontent.com/johnpannyc/Jun-Pan-DATA-608-Project-3/master/cleaned-cdc-mortality-1999-2010-2

```{r}

```
.csv")
```{r}
glimpse(cdc)
                                                                                                               Observations: 9.961
Variables: 6
$ ICD.Chapter <fct> Certain infectious and parasitic diseases, Certain infectious and parasitic diseases, Certain infe...
$ State
             $ Year
             <int> 1999, 2000, 2001, 2002, 2003, 2004, 2005, 2006, 2007, 2008, 2009, 2010, 1999, 2000, 2001, 2002, 20...
$ Deaths
             <int> 1092, 1188, 1211, 1215, 1350, 1251, 1303, 1312, 1241, 1385, 1381, 1358, 61, 51, 58, 67, 61, 53, 68...
$ Population <int> 4430141, 4447100, 4467634, 4480089, 4503491, 4530729, 4569805, 4628981, 4672840, 4718206, 4757938....
$ Crude.Rate <dbl> 24.6, 26.7, 27.1, 27.1, 30.0, 27.6, 28.5, 28.3, 26.6, 29.4, 29.0, 28.4, 9.8, 8.1, 9.2, 10.4, 9.4, ...
 ```{r}
 ## X
 summary(cdc)
 ICD.Chapter
 Deaths
 State
 Year
 Certain conditions originating in the perinatal period
 : 612
 CA
 : 209
 Min.
 :1999
 Min. : 10
 Certain infectious and parasitic diseases
 : 612
 : 207
 1st Qu.:2002
 1st Qu.: 177
 Congenital malformations, deformations and chromosomal abnormalities: 612
 : 205
 Median :2005
 Median: 667
 Diseases of the circulatory system
 : 612
 TL
 : 205
 Mean
 :2005
 Mean : 2929
 Diseases of the digestive system
 : 612
 NY
 : 205
 3rd ou.:2008
 3rd Ou.: 2474
 Diseases of the genitourinary system
 : 612
 : 204
 :2010
 :96511
 GΑ
 Max.
 Max.
 (Other)
 :6289
 (Other):8726
 Population
 Crude.Rate
 : 491780
 : 0.00
 Min.
 1st Ou.: 1728292
 1st Qu.: 4.60
 Median: 24.00
 Median : 4219239
 Mean : 5937896
 Mean : 52.15
 3rd Qu.: 6562231
 3rd Qu.: 50.50
 Max.
 :37253956
 Max.
 :478.40
```

## No missing data





```{r} head(cdc, 100)

| | _ | • | |
|--|---|---|--|
| | | | |
| | | | |

| | ICD.Chapter <fctr></fctr> | State
<fctr></fctr> | Year
<int></int> | Deaths
<int></int> | Population <int></int> | |
|--------|---|------------------------|---------------------|-----------------------|------------------------|-----------|
| 1 | Certain infectious and parasitic diseases | AL | 1999 | 1092 | 4430141 | 24.6 |
| 2 | Certain infectious and parasitic diseases | AL | 2000 | 1188 | 4447100 | 26.7 |
| 3 | Certain infectious and parasitic diseases | AL | 2001 | 1211 | 4467634 | 27.1 |
| 4 | Certain infectious and parasitic diseases | AL | 2002 | 1215 | 4480089 | 27.1 |
| 5 | Certain infectious and parasitic diseases | AL | 2003 | 1350 | 4503491 | 30.0 |
| 6 | Certain infectious and parasitic diseases | AL | 2004 | 1251 | 4530729 | 27.6 |
| 7 | Certain infectious and parasitic diseases | AL | 2005 | 1303 | 4569805 | 28.5 |
| 8 | Certain infectious and parasitic diseases | AL | 2006 | 1312 | 4628981 | 28.3 |
| 9 | Certain infectious and parasitic diseases | AL | 2007 | 1241 | 4672840 | 26.6 |
| 10 | Certain infectious and parasitic diseases | AL | 2008 | 1385 | 4718206 | 29.4 |
| 1-10 c | of 100 rows | | | Previous 1 | 2 3 4 5 | 6 10 Next |

After briefly review the data, I feel that the data is clean and ready to be used for further analysis.

Question 1:

 As a researcher, you frequently compare mortality rates from particular causes across different States. You need a visualization that will let you see (for 2010 only) the crude mortality rate, across all States, from one cause (for example, Neoplasms, which are effectively cancers). Create a visualization that allows you to rank States by crude mortality for each cause of death.

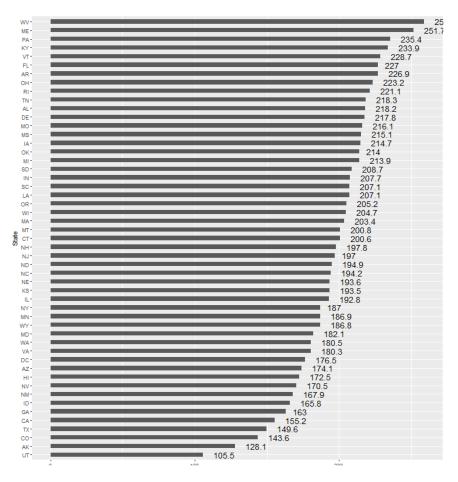
```
library(shiny)
library(forcats)
library(ggplot2)
library(dplyr)
cdc <- read.csv("https://raw.githubusercontent.com/johnpannyc/Jun-Pan-DATA-608-Project-3/master/cleaned-cdc-mortality-1999-2010-2.</pre>
#Define UI for application
ui <- fluidPage(
  # Create a title for the panel
 titlePanel("Mortality Rates Across State in USA"),
  # Sidebar layout with input and output definitions
  sidebarLayout(
    # Define input
   sidebarPanel(
     helpText("year 2010")
    # Create Output
    mainPanel(
     plotOutput("Plot")
```

```
#Define server function required to create the barplot.
server <- function(input, output){</pre>
 output$Plot <- renderPlot({
    cdc_data <- cdc %>%
     filter(Year == 2010) %>%
     filter(ICD.Chapter == input$cause) %>%
      select(c(ICD.Chapter,State,Crude.Rate))
    cdc_data %>%
      mutate(State = fct_reorder(State, Crude.Rate)) %>%
      ggplot( aes(x=State, y=Crude.Rate,width=.5)) +
      geom_bar(stat="identity",position="identity") +
      geom_text(size = 5, aes(label = Crude.Rate), position = position_dodge(width = 1),
                inherit.aes = TRUE.
                hjust = -0.5) +
      coord_flip()}, height = 800, width = 750)
#Create the shiny app object
shinyApp(ui = ui, server = server)
```

Mortality Rates of Neoplasm in 2010

Mortality Rates Across State in USA





Question 2:

 Often you are asked whether particular States are improving their mortality rates (per cause) faster than, or slower than, the national average. Create a visualization that lets your clients see this for themselves for one cause of death at the time. Keep in mind that the national average should be weighted by the national population.

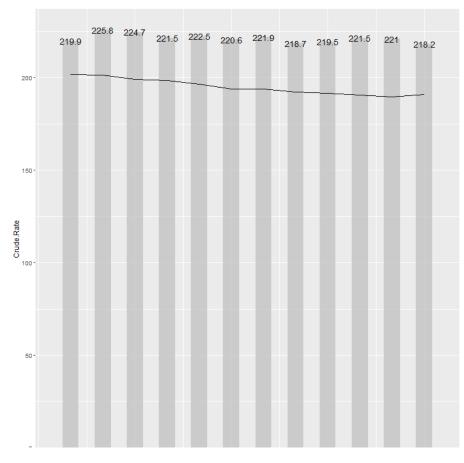
```
library(shiny)
library(ggplot2)
library(dplyr)
library(forcats)
cdc <-read.csv("https://raw.githubusercontent.com/johnpannyc/Jun-Pan-DATA-608-Project-3/master/cleaned-cdc-mortality-1999-2010-2.
#Define UI
ui <- fluidPage(
  # Title of Panel
  titlePanel("Mortality Rate by Year: black line = national average"),
  # Sidebar Layout
  sidebarLayout(
    # Define input
    sidebarPanel(
      selectInput("cause", "Select a Cause:",
      choices=as.character(unique(cdc$ICD.Chapter))),
selectInput("state", "Select a State:",
                   choices=as.character(unique(cdc$State)))
    ),
    # Define output
    mainPanel(
      plotOutput("Plot")
```

```
#Define Server function to create bar plot
server <- function(input, output){</pre>
 output$Plot <- renderPlot({
    clean_data <- cdc %>%
     filter(ICD.Chapter == input$cause) %>%
      group_by(Year) %>%
      mutate(weight=(Population/sum(Population))*Crude.Rate) %>%
      mutate(avg=sum(weight)) %>%
     filter(State == input$state)
    clean data %>%
      ggplot( aes(x=Year, y=Crude.Rate,width=.5)) +
      geom_bar(stat="identity",position="identity",fill="grey", alpha = 0.7) +
      geom_text(size = 5, aes(label = Crude.Rate), position = position_dodge(width = 1),
                inherit.aes = TRUE,
                hjust = 0.5) +
      geom_line(aes(x=Year, y=avg)) +
      theme(axis.text=element_text(size=10),
            axis.title=element_text(size=12))}, height = 800, width = 750)
#Create a shiny app object
shinyApp(ui = ui, server = server)
```

Mortality Rate of Neoplasm is higher in Alabama than National Average

Mortality Rate by Year: black line = national average

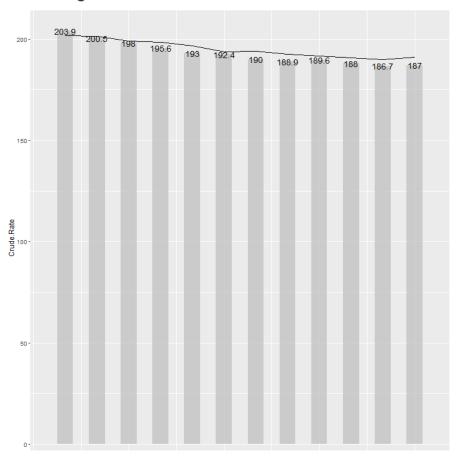




Mortality Rate of Neoplasm is Close to National Average in New York

Mortality Rate by Year: black line = national average





Mortality Rate of Neoplasm is lower in Utah Compared to National Average

Mortality Rate by Year: black line = national average



