

# Temitope Oshinowo

## SML 310 Final Project

Choropleths to better understand the data. I observed the number of cases, deaths, and beds per 1,000, as well as the median household income, all per county.

```
# County Cases choropleth
#source: https://arilamstein.com/us-county-choropleths/

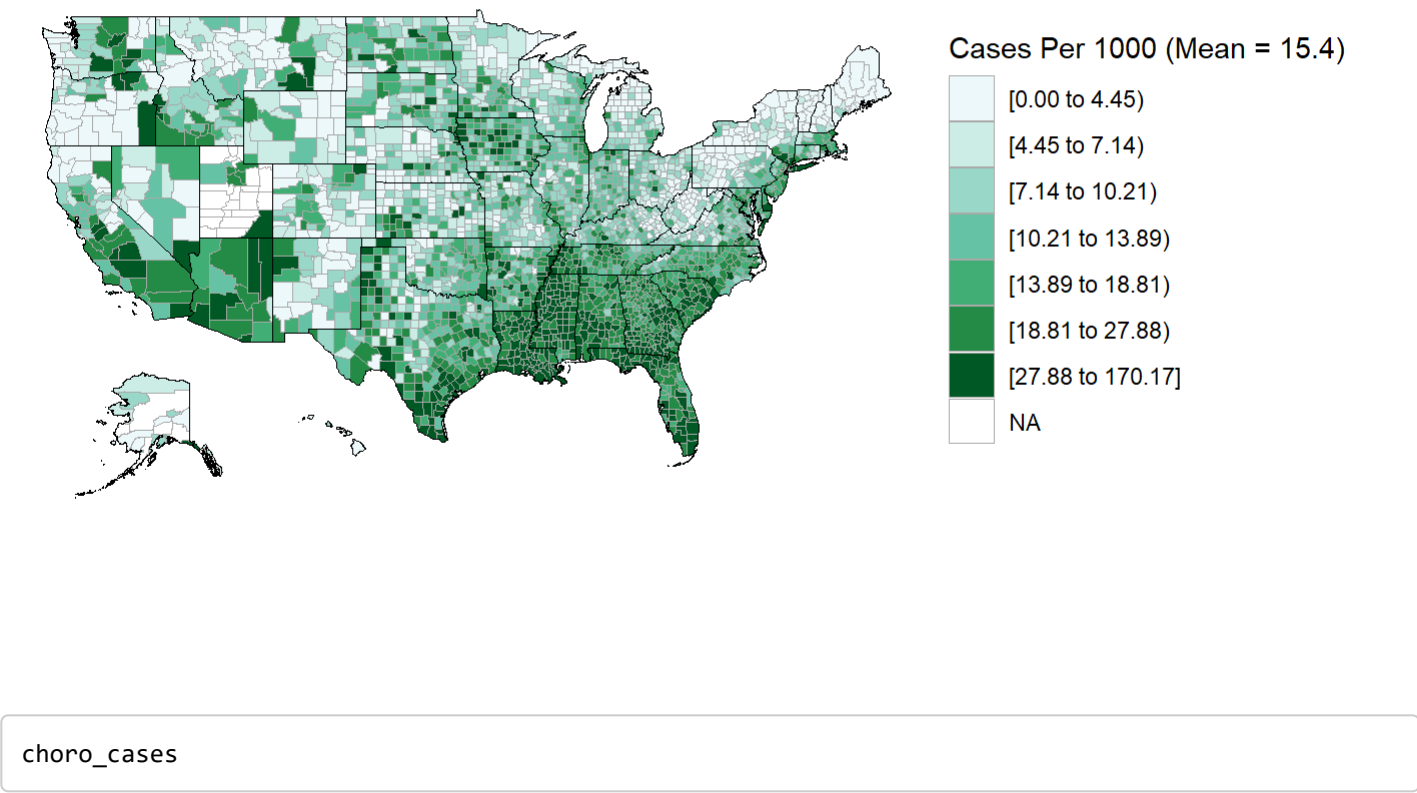
# Load in the county confirmed cases data from the csv
cases_Data_full <- read.csv("C:/Users/Temi/Downloads/select_counties_confirmed.csv")
cases_df <- data.frame(cases_Data_full)
mean(cases_df[["value"]])
```

```
## [1] 15.42118
```

```
choro_cases = CountyChoropleth$new(cases_df)
choro_cases$title = "US Covid Cases Per 1000 by County"
choro_cases$ggplot_scale = scale_fill_brewer(name="Cases Per 1000 (Mean = 15.4)", palette=2, drop=FALSE)
choro_cases$render()
```

```
## Warning in self$bind(): The following regions were missing and are being set to
## NA: 25007, 49001, 49007, 2105, 49009, 49013, 49019, 49023, 46113, 2164, 49039,
## 49057, 49027, 49033, 49041, 49055, 2198, 15005, 49005, 49017, 2170, 51515,
## 51720, 2290, 49015, 49021, 49025, 49003, 25019, 49047, 49053, 49029, 49031,
## 2195, 2230, 2261, 2270, 2275
```

US Covid Cases Per 1000 by County



```
## <CountyChoropleth>
## Inherits from: <USACHoropleth>
## Public:
##   add_state_outline: TRUE
##   bind: function ()
##   choropleth.df: data.frame
##   clip: function ()
##   clone: function (deep = FALSE)
##   discretize: function ()
##   format_levels: function (x, nsep = " to ")
##   get_bounding_box: function (long_margin_percent, lat_margin_percent)
##   get_choropleth_as_polygon: function (alpha)
##   get_max_lat: function ()
##   get_max_long: function ()
##   get_min_lat: function ()
##   get_min_long: function ()
##   get_reference_map: function ()
##   get_scale: function ()
##   get_x_scale: function ()
##   get_y_scale: function ()
##   get_zoom: function ()
##   ggplot_polygon: LayerInstance, Layer, ggproto, gg
##   ggplot_scale: ScaleDiscrete, Scale, ggproto, gg
##   ggplot_sf: list
##   initialize: function (user.df)
##   legend:
##   map.df: data.frame
##   prepare_map: function ()
##   projection: CoordQuickmap, CoordCartesian, Coord, ggproto, gg
##   projection_sf: CoordSf, CoordCartesian, Coord, ggproto, gg
##   render: function ()
##   render_helper: function (choropleth.df, scale_name, theme)
##   render_state_outline: function (states)
##   render_with_reference_map: function (alpha = 0.5)
##   set_num_colors: function (num_colors)
##   set_zoom: function (zoom)
##   theme_clean: function ()
##   theme_inset: function ()
##   title: US Covid Cases Per 1000 by County
##   user.df: data.frame
##   warn: TRUE
## Private:
##   has_invalid_regions: FALSE
##   num_colors: 7
##   zoom: arizona arkansas louisiana minnesota mississippi montana ...
```

```
# County Deaths choropleth
```

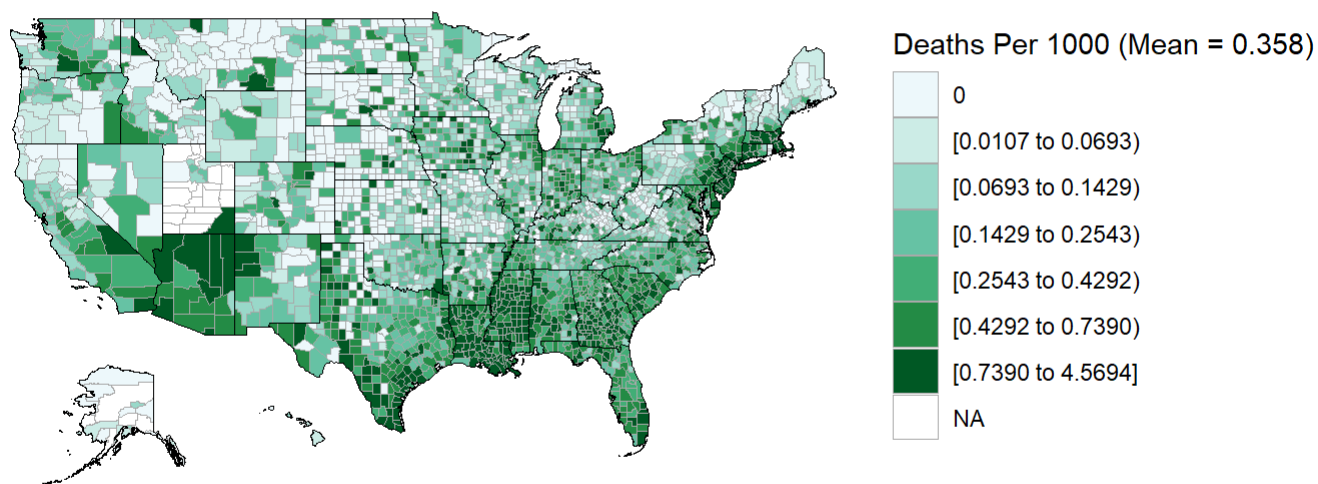
```
# Load in the county confirmed deaths data from the csv
deaths_Data_full <- read.csv("C:/Users/Temi/Downloads/select_counties_deaths.csv")
deaths_df <- data.frame(deaths_Data_full)
mean(deaths_df[["value"]])
```

```
## [1] 0.3584977
```

```
choro_deaths = CountyChoropleth$new(deaths_df)
choro_deaths$title = "US Covid Deaths Per 1000 by County"
choro_deaths$ggplot_scale = scale_fill_brewer(name="Deaths Per 1000 (Mean = 0.358)", palette=2,
drop=FALSE)
choro_deaths$render()
```

```
## Warning in self$bind(): The following regions were missing and are being set to
## NA: 25007, 49001, 49007, 2105, 49009, 49013, 49019, 49023, 46113, 2164, 49039,
## 49057, 49027, 49033, 49041, 49055, 2198, 15005, 49005, 49017, 2170, 51515,
## 51720, 2290, 49015, 49021, 49025, 49003, 25019, 49047, 49053, 49029, 49031,
## 2195, 2230, 2261, 2270, 2275
```

## US Covid Deaths Per 1000 by County



```
choro_deaths
```

```
## <CountyChoropleth>
## Inherits from: <USACHoropleth>
## Public:
##   add_state_outline: TRUE
##   bind: function ()
##   choropleth.df: data.frame
##   clip: function ()
##   clone: function (deep = FALSE)
##   discretize: function ()
##   format_levels: function (x, nsep = " to ")
##   get_bounding_box: function (long_margin_percent, lat_margin_percent)
##   get_choropleth_as_polygon: function (alpha)
##   get_max_lat: function ()
##   get_max_long: function ()
##   get_min_lat: function ()
##   get_min_long: function ()
##   get_reference_map: function ()
##   get_scale: function ()
##   get_x_scale: function ()
##   get_y_scale: function ()
##   get_zoom: function ()
##   ggplot_polygon: LayerInstance, Layer, ggproto, gg
##   ggplot_scale: ScaleDiscrete, Scale, ggproto, gg
##   ggplot_sf: list
##   initialize: function (user.df)
##   legend:
##   map.df: data.frame
##   prepare_map: function ()
##   projection: CoordQuickmap, CoordCartesian, Coord, ggproto, gg
##   projection_sf: CoordSf, CoordCartesian, Coord, ggproto, gg
##   render: function ()
##   render_helper: function (choropleth.df, scale_name, theme)
##   render_state_outline: function (states)
##   render_with_reference_map: function (alpha = 0.5)
##   set_num_colors: function (num_colors)
##   set_zoom: function (zoom)
##   theme_clean: function ()
##   theme_inset: function ()
##   title: US Covid Deaths Per 1000 by County
##   user.df: data.frame
##   warn: TRUE
## Private:
##   has_invalid_regions: FALSE
##   num_colors: 7
##   zoom: arizona arkansas louisiana minnesota mississippi montana ...
```

*#a number of beds choropleth*

```
# Load in the csv
beds_Data_full <- read.csv("C:/Users/Temi/Downloads/bed_count.csv")
beds_df <- data.frame(beds_Data_full)
mean(beds_df[["value"]])
```

```
## [1] 1.474561
```

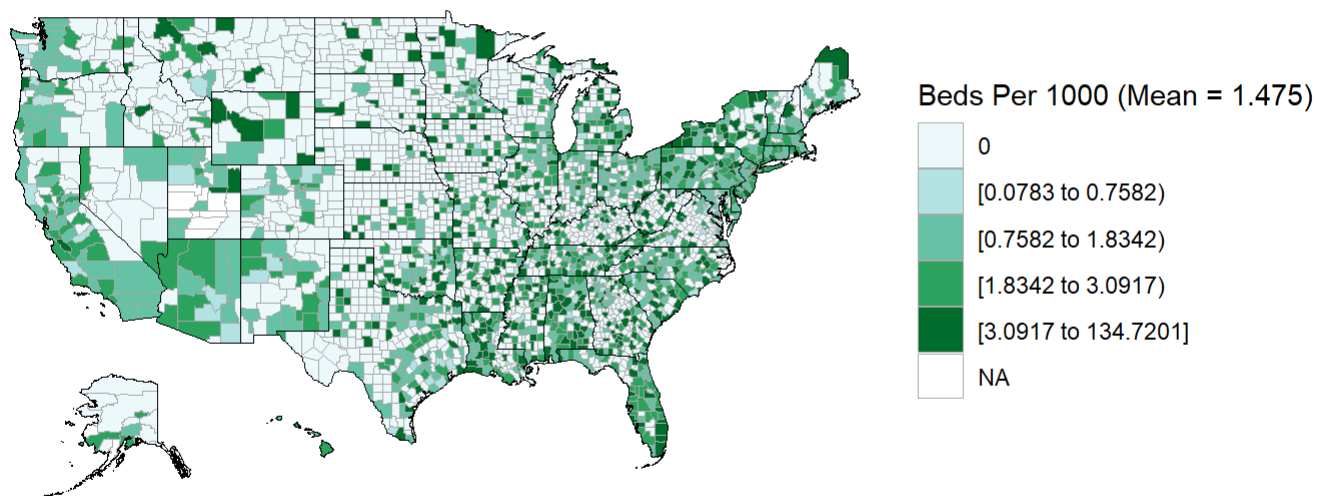
```
choro_beds = CountyChoropleth$new(beds_df)
```

```
## Warning in super$initialize(map.df, user.df): Your data.frame contains the
## following regions which are not mappable: 46102, 2158
```

```
choro_beds$title = "US Number of Beds Per 1000 by County"
choro_beds$ggplot_scale = scale_fill_brewer(name="Beds Per 1000 (Mean = 1.475)", palette=2, direction=1, drop=FALSE)
choro_beds$render()
```

```
## Warning in self$bind(): The following regions were missing and are being set to
## NA: 25007, 49001, 2105, 49009, 49019, 49023, 46113, 2164, 49039, 49027, 49033,
## 49055, 15005, 49017, 51515, 49015, 49025, 25019, 49029, 49031, 2230, 2270
```

## US Number of Beds Per 1000 by County



```
choro_beds
```

```

## <CountyChoropleth>
##   Inherits from: <USACHoropleth>
##   Public:
##     add_state_outline: TRUE
##     bind: function ()
##     choropleth.df: data.frame
##     clip: function ()
##     clone: function (deep = FALSE)
##     discretize: function ()
##     format_levels: function (x, nsep = " to ")
##     get_bounding_box: function (long_margin_percent, lat_margin_percent)
##     get_choropleth_as_polygon: function (alpha)
##     get_max_lat: function ()
##     get_max_long: function ()
##     get_min_lat: function ()
##     get_min_long: function ()
##     get_reference_map: function ()
##     get_scale: function ()
##     get_x_scale: function ()
##     get_y_scale: function ()
##     get_zoom: function ()
##     ggplot_polygon: LayerInstance, Layer, ggproto, gg
##     ggplot_scale: ScaleDiscrete, Scale, ggproto, gg
##     ggplot_sf: list
##     initialize: function (user.df)
##     legend:
##     map.df: data.frame
##     prepare_map: function ()
##     projection: CoordQuickmap, CoordCartesian, Coord, ggproto, gg
##     projection_sf: CoordSf, CoordCartesian, Coord, ggproto, gg
##     render: function ()
##     render_helper: function (choropleth.df, scale_name, theme)
##     render_state_outline: function (states)
##     render_with_reference_map: function (alpha = 0.5)
##     set_num_colors: function (num_colors)
##     set_zoom: function (zoom)
##     theme_clean: function ()
##     theme_inset: function ()
##     title: US Number of Beds Per 1000 by County
##     user.df: data.frame
##     warn: TRUE
##   Private:
##     has_invalid_regions: FALSE
##     num_colors: 7
##     zoom: arizona arkansas louisiana minnesota mississippi montana ...

```

```
#Median household income choropleth
```

```
# Load in the csv
```

```
houses_Data_full <- read.csv("C:/Users/Temi/Downloads/median_house_income.csv")
```

```
houses_df <- data.frame(houses_Data_full)
```

```
colnames(houses_df) <- c("region","value") #rename columns as desired
```

```
#mean(houses_df[["value"]])
```

```
choro_houses = CountyChoropleth$new(houses_df)
```

```
## Warning in super$initialize(map.df, user.df): Your data.frame contains the  
## following regions which are not mappable: 0, 1000, 2000, 2158, 2201, 2232, 2280,  
## 4000, 5000, 6000, 8000, 9000, 10000, 11000, 12000, 13000, 15000, 16000, 17000,  
## 18000, 19000, 20000, 21000, 22000, 23000, 24000, 25000, 26000, 27000, 28000,  
## 29000, 30000, 31000, 32000, 33000, 34000, 35000, 36000, 37000, 38000, 39000,  
## 40000, 41000, 42000, 44000, 45000, 46000, 46102, 47000, 48000, 49000, 50000,  
## 51000, 53000, 54000, 55000, 56000
```

```
choro_houses$title = "Median Household Income by County"
```

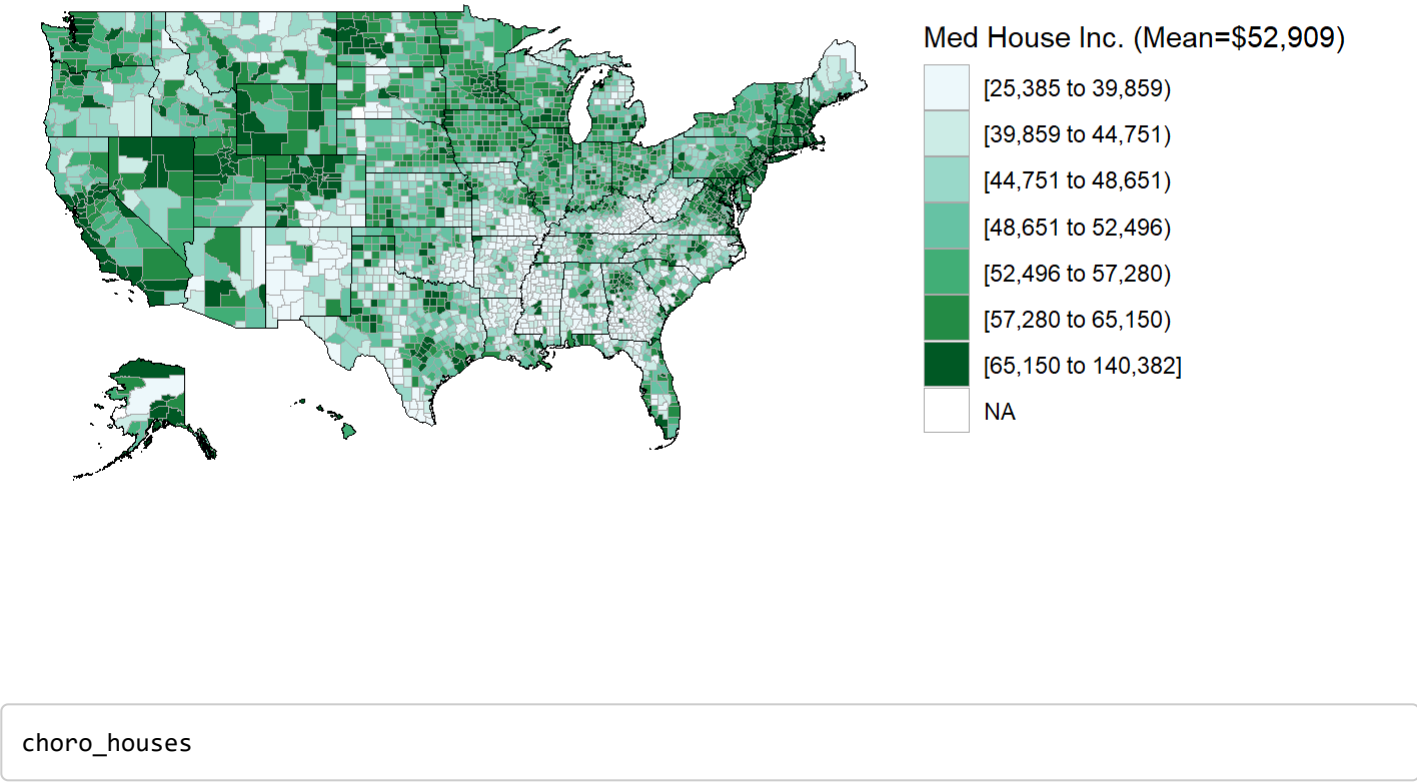
```
choro_houses$ggplot_scale = scale_fill_brewer(name="Med House Inc. (Mean=$52,909)", palette=2, d  
irection=1, drop=FALSE)
```

```
choro_houses$render()
```

```
## Warning in self$bind(): The following regions were missing and are being set to  
## NA: 46113, 15005, 51515, 2270
```



Median Household Income by County



```

## <CountyChoropleth>
##   Inherits from: <USACHoropleth>
##   Public:
##     add_state_outline: TRUE
##     bind: function ()
##     choropleth.df: data.frame
##     clip: function ()
##     clone: function (deep = FALSE)
##     discretize: function ()
##     format_levels: function (x, nsep = " to ")
##     get_bounding_box: function (long_margin_percent, lat_margin_percent)
##     get_choropleth_as_polygon: function (alpha)
##     get_max_lat: function ()
##     get_max_long: function ()
##     get_min_lat: function ()
##     get_min_long: function ()
##     get_reference_map: function ()
##     get_scale: function ()
##     get_x_scale: function ()
##     get_y_scale: function ()
##     get_zoom: function ()
##     ggplot_polygon: LayerInstance, Layer, ggproto, gg
##     ggplot_scale: ScaleDiscrete, Scale, ggproto, gg
##     ggplot_sf: list
##     initialize: function (user.df)
##     legend:
##     map.df: data.frame
##     prepare_map: function ()
##     projection: CoordQuickmap, CoordCartesian, Coord, ggproto, gg
##     projection_sf: CoordSf, CoordCartesian, Coord, ggproto, gg
##     render: function ()
##     render_helper: function (choropleth.df, scale_name, theme)
##     render_state_outline: function (states)
##     render_with_reference_map: function (alpha = 0.5)
##     set_num_colors: function (num_colors)
##     set_zoom: function (zoom)
##     theme_clean: function ()
##     theme_inset: function ()
##     title: Median Household Income by County
##     user.df: data.frame
##     warn: TRUE
##   Private:
##     has_invalid_regions: FALSE
##     num_colors: 7
##     zoom: arizona arkansas louisiana minnesota mississippi montana ...

```