EDA Final Report Spring 2022

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Reminders for knitting commands in code chunks - can delete when we're done

- Knitting commands in code chunks:
- include = FALSE code is run, but neither code nor results appear in knitted file
- echo = FALSE code not included in knitted file, but results are
- eval = FALSE code is not run in the knitted file
- message = FALSE messages do not appear in knitted file
- warning = FALSE warnings do not appear...
- fig.cap = "..." adds a caption to graphical results

1. Introduction

1.1 Context

Waste diversion comes with global benefits including a decrease in

global warming potential (GWP). However, waste diversion stands to especially benefit those populations living closest to landfills by decreasing local green house gas emissions and other hazards such as odor, smoke, noise, and

water contamination. This project aims to identify which populations live closest to construction and demolition landfills in North Carolina and therefore which populations stand to benefit the most from waste diversion in the construction industry. The focus on the construction industry was inspired by one of the group member's master's project which is focused on circularity and waste diversion in the construction industry.

1.2 Research Question

Are construction and demolition landfills in North Carolina disproportionately more common in low income counties and/or counties with high minority populations?

1.3 Rational for Data

what's the difference between this and section 2?

2 Dataset Information

2.1 Source and Content of Data

#######does this also count as table with dataset structure? Meghan askin John on 4/1

Dataset Names	Relevant Information	Source
Site Waste Facility	Lists all landfills in NC and includes landfill type and address.	NC DEQ https: //deq.nc.gov /about/divis ions/waste- management /solid-waste- section/solid- waste-facili ty-lists-pres entations- and-annual- reports/soli d-waste- facility-lists
CDC Social Vulnerability	Contains estimates of poverty and minority data by county.	Agency for Toxic Substances and Disease Registry https://www. atsdr.cdc.go v/placeand health/svi/d ocumentati on/SVI_doc umentation
USA Counties Shape File	Spatial data frame that will establish the map of NC.	_2018.html US Census https://www. census.gov/g eographies /mapping-fil es/time-seri es/geo/carto- boundary- file.html

2.2 Wrangling Process

SVI Variable Name	Variable Description
E_TOTPOP E_POV E_MINRTY	Population estimate,2014-2018 ACS Persons below poverty estimate,2014-2018 ACS Minority (all persons except white, non-Hispanic)estimate,2014-2018 ACS

#import SVI tract-level data and change FIPS from character to factor
svi2018_nc_tract_st <-st_read('./Data/Spatial/NorthCarolinaTract/SVI2018_NORTHCAROLINA_tract.shp')</pre>

^{##} Reading layer `SVI2018_NORTHCAROLINA_tract' from data source

```
`Z:\ENV872\ENV872-SeylerHyyppa_Final\Data\Spatial\NorthCarolinaTract\SVI2018_NORTHCAROLINA_tract.s
    using driver `ESRI Shapefile'
##
## Simple feature collection with 2192 features and 126 fields
## Geometry type: MULTIPOLYGON
## Dimension:
                  XY
## Bounding box: xmin: -84.32187 ymin: 33.84232 xmax: -75.46062 ymax: 36.58812
## Geodetic CRS: NAD83
svi2018 nc tract st$FIPS<-as.factor(svi2018 nc tract st$FIPS)
#mapview(svi2018_nc_tract_st)
#import and select columns of interest from SVI county data and change FIPS from character to factor
svi2018_nc_raw <- read.csv(</pre>
  'https://svi.cdc.gov/Documents/Data/2018_SVI_Data/CSV/States_Counties/NorthCarolina_COUNTY.csv',
  colClasses = c('FIPS' = 'factor')) %>%
  select(COUNTY, FIPS, LOCATION, E_TOTPOP, E_POV, E_MINRTY)
```

3 Exploratory Analysis

relocate(Percent_POV, .before = FIPS)

```
(Rubric: flow between text and visualization is cohesive & relevant exploratory information is visualized)
```

```
#check structure
str(svi2018 nc raw)
                   100 obs. of 6 variables:
## 'data.frame':
## $ COUNTY : chr "Currituck" "Dare" "Haywood" "Clay" ...
             : Factor w/ 100 levels "37001", "37003",...: 27 28 44 22 90 88 15 55 85 57 ...
## $ LOCATION: chr "Currituck County, North Carolina" "Dare County, North Carolina" "Haywood County,
## $ E_TOTPOP: int 25796 35741 60433 10813 226694 33513 10447 81441 45905 34410 ...
             : int 2562 2929 8304 1700 19921 4776 1172 11593 6166 5679 ...
## $ E_MINRTY: int 3304 4447 4300 680 62132 3249 2047 12168 4022 3684 ...
#check colnames
colnames(svi2018_nc_raw)
## [1] "COUNTY"
                  "FIPS"
                             "LOCATION" "E_TOTPOP" "E_POV"
                                                              "E MINRTY"
#investigate what location column includes
glimpse(svi2018_nc_raw$LOCATION)
## chr [1:100] "Currituck County, North Carolina" ...
#create percent poverty and minority values by county to explore which county's have the highest percen
povdividedbytotal_col<-(svi2018_nc_raw$E_POV/svi2018_nc_raw$E_TOTPOP)*100
minrtydividedbytotal_col<-(svi2018_nc_raw$E_MINRTY/svi2018_nc_raw$E_T0TP0P)*100
#add the percentage columns to the raw data
svi2018_nc_processed<-svi2018_nc_raw%>%
  add_column(Percent_POV = povdividedbytotal_col)%>%
  add_column(Percent_MINRTY = minrtydividedbytotal_col)
svi2018_nc_poverty_top10 <- svi2018_nc_processed %>%
   arrange(desc(Percent_POV))%>%
   slice(1:10)%>%
```

```
svi2018_nc_minrty_top10 <- svi2018_nc_processed %>%
    arrange(desc(Percent_MINRTY))%>%
    slice(1:10)%>%
  relocate(Percent MINRTY, .before = FIPS)
#create percent poverty and minority values by county to explore which tracts have the highest minority
povdividedbytotal tract col<-(svi2018 nc tract st$E POV/svi2018 nc tract st$E TOTPOP)*100
minrtydividedbytotal_tract_col<-(svi2018_nc_tract_st$E_MINRTY/svi2018_nc_tract_st$E_T0TP0P)*100
svi2018_nc_tract_st<-svi2018_nc_tract_st%>%
  add_column(Percent_POV = povdividedbytotal_tract_col)%>%
  add_column(Percent_MINRTY = minrtydividedbytotal_tract_col)
svi2018_nc_tract_st<-svi2018_nc_tract_st%>%
  select(COUNTY, FIPS, LOCATION, E_TOTPOP, E_POV, E_MINRTY, Percent_POV, Percent_MINRTY)
svi2018_nc_tract_st_top10 <- svi2018_nc_tract_st %>%
   arrange(desc(Percent_POV))%>%
    slice(1:10)%>%
   relocate(Percent_POV, .before = FIPS)
svi2018_nc_tract_st_top10 <- svi2018_nc_tract_st %>%
    arrange(desc(Percent MINRTY))%>%
    slice(1:10)%>%
  relocate(Percent_MINRTY, .before = FIPS)
knitr::kable(head(svi2018 nc poverty top10[1:10,1:2]),
             "simple",
             col.names = c("County", "Poverty Percentage"),
             align = 'c',
             caption = "Counties by Highest Poverty Percentage in North Carolina"
```

Table 3: Counties by Highest Poverty Percentage in North Carolina

County	Poverty Percentage
Robeson	27.35571
Jones	26.05467
Scotland	25.60830
Bladen	25.60542
Halifax	24.51630
Alleghany	24.35979

Table 4: Counties by Highest Percentage of Minority Populations in North Carolina

County	Minority Percentage
Robeson	74.51177
Hertford	66.55488
Bertie	65.71472
Edgecombe	63.63534
Warren	61.68322
Halifax	61.46472

```
poverty_plot<-svi2018_nc_processed%>%
  arrange(Percent_POV)%>%
  mutate(COUNTY=factor(COUNTY, COUNTY))%>%
    ggplot(aes(x=COUNTY, y=Percent_POV)) +
      geom point(color="lightgreen") +
     geom_segment( aes(x=COUNTY, xend=COUNTY, y=0, yend=Percent_POV))+
      coord flip()+
      ggtitle("Percentage of Poverty by County in North Carolina") +
     xlab("County Name")+
     ylab("Poverty Population Percentage")+
      theme minimal()+
      theme(
        axis.text = element_text(size = 5, face='bold', angle = 30, hjust = 1, vjust =0.5) ,
        panel.grid.major.y = element_blank(),
       panel.border = element_blank(),
       axis.ticks.y = element_blank(),
  )
poverty_plot
minority_plot<-svi2018_nc_processed%>%
  arrange(Percent_MINRTY)%>%
  mutate(COUNTY=factor(COUNTY, COUNTY))%>%
    ggplot(aes(x=COUNTY, y=Percent_MINRTY)) +
      geom_point(color="69b3a2") +
     geom_segment( aes(x=COUNTY, xend=COUNTY, y=0, yend=Percent_MINRTY))+
      coord_flip()+
      ggtitle("Percentage of Minority Populations by County in North Carolina") +
     xlab("County Name")+
     ylab("Minority Population Percentage")+
      theme minimal()+
      theme(
        axis.text = element_text(size = 5, face='bold'),
       panel.grid.major.y = element_blank(),
        panel.border = element_blank(),
        axis.ticks.y = element_blank(),
        plot.subtitle = element_text("By Reino Hyyppa and Meghan Seyler"),
  )
minority_plot
```

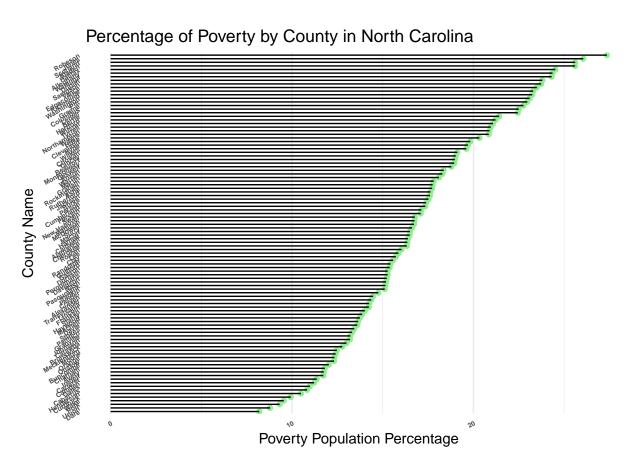


Figure 1: By Meghan Seyler and Reino Hyyppa

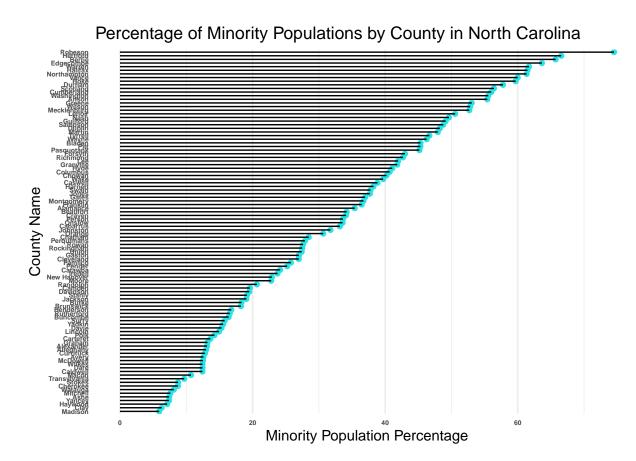


Figure 2: By Meghan Seyler and Reino Hyyppa