Final Project: Walkability and Public Health in the US

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Contents

Objective

The objective is to quantify the causal effect that the "walkability" of a region has on the public health indicators: obesity and physical activity. The original data comes from two sources: 1. The U.S. Chronic Disease Indicators provides reported cases of a set of 124 indicators that are important to public health, and the geographic location of the case. 2. The Walkability Index quantifies every Census 2019 block group's relative "Walkability" as defined by the EPA based on characteristics such as easy walking access to public transit, jobs, stores and services. Quantifying the causal effect of walkability on public health can help policy makers understand how community planning measures that may improve or degrade the walkability of the region will impact public health.

The appendix of this document describes the pre-processing methodology that was used combine the two data sets to enable the quantitative analysis. Because the pre-processing methodology can take an hour or more to execute, we exported the pre-processed data and made it available for download in a publicly accessible location. The beginning of this document imports the pre-processed data and the rest of the analysis is done based on the pre-processed data.

Load necessariy libararies

```r
rm(list=ls())

options(repos = list(CRAN="http://cran.rstudio.com/"))

if (!require('NHANES')) install.packages('NHANES')
library('openxlsx')

if (!require('ggplot2')) install.packages('ggplot2')
library('ggplot2')

if (!require('dplyr')) install.packages('dplyr')
library('dplyr')

if (!require('GGally')) install.packages('GGally')
library('GGally')

if (!require('tableone')) install.packages('tableone')
library(tableone)

if (!require('pROC')) install.packages('pROC')
library(pROC)

if (!require('tidyr')) install.packages('tidyr')
library(tidyr)

if (!require('tidycensus')) install.packages('tidycensus')
library(tidycensus)

if (!require('tigris')) install.packages('tigris')
library(tigris)

if (!require('sf')) install.packages('sf')
library(sf)
```

```r
if (!require('stringr')) install.packages('stringr')
library(stringr)

if (!require('dplyr')) install.packages('dplyr')
library(dplyr)
```

Load the data

Download the data which has already undergone the pre-processing methodology described in the appendix. WARNING: this may take several minutes. To avoid unnecessary downloads, the commands are commented out. Un-comment and execute the commands to download the data.

```r
#download.file("https://walkabilityandhealth.blob.core.windows.net/walkabilityandhealth/disease_with_wa
#unzip("disease_with_walkability.zip", "disease_with_walkability.csv")
```

```r
disease_with_walkability <- read.csv("disease_with_walkability.csv")
```

Shape the data set for our analysis purposes

The walkability data has observations with information about a BlockGroup. BlockGroup is a geographic unit used by the US Census Bureau and is a subdivision of a census tract, which in turn is a subdivision of a county. Block groups usually contain between 600 and 3000 people and are the smallest standardized unit of geography for which the Walkability score is measured. All of our analysis will be based on block group as the observation unit.

The disease indicator data has a column for "Question" which contains the details of the disease indicator that was measured. Of the 203 total questions we have narrowed down to 12 that will be used in our analysis. Questions were selected which have the same unit of measure - Crude Prevalence - which means that the value is the percentage of the overall population. For simplicity we have also selected the more general questions rather than inter-sectional questions. For example we chose "Arthritis among adults aged >= 18 years" rather than "Arthritis among adults aged >= 18 years who have heart disease". The result of the selection process, along with how we intend to use each variable in our analysis, is in the table below:

Topic	Question	QuestionID	Intended Usage
Nutrition, Physical Activity and Weight Status	Overweight or obesity among adults aged >= 18 years	NPAW2_1	Dependent Var
Nutrition, Physical Activity and Weight Status	Meeting aerobic physical activity guidelines for substantial health benefits among adults aged >= 18 years	NPAW11_1	Dependent var
Alcohol	Heavy drinking among adults aged >= 18 years	ALC5_1	Independent Var
Arthritis	Arthritis among adults aged >= 18 years	ART1_1	Independent var
Asthma	Current asthma prevalence among adults aged >= 18 years	AST1_1	Independent var

Topic	Question	QuestionID	Intended Usage
Chronic Obstructive Pulmonary Disease	Prevalence of chronic obstructive pulmonary disease among adults >= 18	COPD2_0	Independent var
Oral Health	Visits to dentist or dental clinic among adults aged >= 18 years	ORH1_1	Independent var
Overarching Conditions	High school completion among adults aged 18-24 years	OVC2_1	Independent var
Overarching Conditions	Current lack of health insurance among adults aged 18-64 years	OVC1_1	Independent var
Tobacco	Current smoking among adults aged >= 18 years	TOB1_2	Independent var
Tobacco	Current smokeless tobacco use among adults aged >= 18 years	TOB2_2	Independent var
Chronic Kidney Disease	Prevalence of chronic kidney disease among adults aged >= 18 years	CKD3_0	Independent var

```r
# filter down to just the 12 selected questions
disease_with_walkability_filtered <- filter(disease_with_walkability, DataValueType == "Crude Prevalence
  StratificationCategory1 == "Overall" & !is.na(NatWalkInd))
filtered_qids <- c("NPAW2_1", "NPAW11_1", "ALC5_1", "ART1_1", "AST1_1", "COPD2_0", "ORH1_1", "OVC2_1", "
disease_with_walkability_filtered <- disease_with_walkability_filtered[disease_with_walkability_filtered

# reshape the data by grouping by all the unique properties per block group, and expanding
# columns with the result of each of the relevant 12 questions for that observation.
# for now we will also keep some descriptive variables (like LocationAbbr)
# which may come in handy for visual data exploration
collapsed_cols = c("YearStart", "LocationAbbr", "LocationDesc", "STATEFP", "COUNTYFP", "TRACTCE", "BLKGI

disease_with_walkability_collapsed <- disease_with_walkability_filtered %>%
  pivot_wider(id_cols = collapsed_cols, names_from = c("QuestionID"), values_from = DataValueAlt)
```

```
## Warning: Using an external vector in selections was deprecated in tidyselect 1.1.0.
## i Please use `all_of()` or `any_of()` instead.
##    # Was:
##    data %>% select(collapsed_cols)
##
##    # Now:
##    data %>% select(all_of(collapsed_cols))
##
## See <https://tidyselect.r-lib.org/reference/faq-external-vector.html>.
## This warning is displayed once every 8 hours.
## Call `lifecycle::last_lifecycle_warnings()` to see where this warning was
## generated.
```

```
# rename the question columns to something easier to read
disease_with_walkability_collapsed <- disease_with_walkability_collapsed %>%
  rename("Overweight" = "NPAW2_1") %>%
  rename("Active" = "NPAW11_1") %>%
  rename("Alcohol" = "ALC5_1") %>%
  rename("Arthritis" = "ART1_1") %>%
  rename("Asthma" = "AST1_1") %>%
  rename("COPD" = "COPD2_0") %>%
  rename("Dentist" = "ORH1_1") %>%
  rename("HighSchool" = "OVC2_1") %>%
  rename("NoInsurance" = "OVC1_1") %>%
  rename("Smoking" = "TOB1_2") %>%
  rename("Vapeing" = "TOB2_2") %>%
  rename("KidneyDisease" = "CKD3_0")
```

Next we will convert our treatment variable, NatWalkInd to binary. Our strategy will be to select the bottom 40% least walkable block groups and consider these "not walkable" and the top 40% most walkable block groups will be considered "walkable." The middle 20% will not be used

```
nwi40 <- quantile(disease_with_walkability_collapsed$NatWalkInd, .40)
nwi60 <- quantile(disease_with_walkability_collapsed$NatWalkInd, .60)
disease_with_walkability_collapsed = filter(disease_with_walkability_collapsed, NatWalkInd < nwi40 | Nat
disease_with_walkability_collapsed$Walkable <- ifelse(disease_with_walkability_collapsed$NatWalkInd >= n
# rename the dataframe to a shorter name
dww <- disease_with_walkability_collapsed
```

Understand the variables in the dataset

The table below describes the variables that are used in this analysis, including the variables that contain the values of the questions we selected. The "Usage In This Analysis" column categorizes how these will be used in analysis.

Variable Name	Variable Description	Usage In This Analysis
Walkable	Binary variable, 1 if the block is walkable, 0 otherwise	Treatment Variable
Overweight	Percentage of the population overweight or obese	Dependent Variable
Active	Percentage of the population that meets physical activity guidelines	Dependent Variable
R_PCTLOWWAGE	Percentage of the population that makes less than $1250/month	Independent Variable
HighSchool	Percentage of the population ages 18-24 who have completed high school	Independent Variable
Alcohol	Percentage of the population with high alcohol use	Independent Variable
Arthritis	Percentage of the population with arthritis	Independent Variable
Asthma	Percentage of the population with asthma	Independent Variable
KidneyDisease	Percentage of the population with chronic kidney disease	Independent Variable
Vapeing	Percentage of the population using smokeless tobacco	Independent Variable
Smoking	Percentage of the population that smokes	Independent Variable
COPD	Percentage of the population with Chronic Obstructive Pulmonary Disease	Independent Variable

Variable Name	Variable Description	Usage In This Analysis
NoInsurance	Percentage of the population without health care coverage	Independent Variable
Dentist	Percentage of the population with dentist visits	Independent Variable

Get familiar with the data using summary statistics

The first thing we will note is that what started as a very large data set with almost a million observations has diminished down to a relatively small sample size (318 observations) with all of the necessary filtering and aggregation that was done. We will need to do the best we can with it. Due to the small sample size, propensity score matching may not be a viable option, and generally we need to take care with the conclusions we draw from the analysis.

```
str(dww)
```

```
## tibble [318 x 23] (S3: tbl_df/tbl/data.frame)
## $ YearStart   : int [1:318] 2012 2013 2010 2014 2012 2011 2017 2015 2014 2011 ...
## $ LocationAbbr : chr [1:318] "MI" "WI" "NJ" "KS" ...
## $ LocationDesc : chr [1:318] "Michigan" "Wisconsin" "New Jersey" "Kansas" ...
## $ STATEFP     : int [1:318] 26 55 34 20 41 5 34 44 66 9 ...
## $ COUNTYFP    : int [1:318] 39 141 29 159 69 119 29 3 10 7 ...
## $ TRACTCE     : int [1:318] 960200 11000 717101 967200 960100 4400 717101 20300 952900 541600 ...
## $ BLKGRPCE    : int [1:318] 2 5 1 1 2 1 1 3 6 1 ...
## $ GEOID       : num [1:318] 2.60e+11 5.51e+11 3.40e+11 2.02e+11 4.11e+11 ...
## $ R_PCTLOWWAGE : num [1:318] 0.258 0.253 0.22 0.337 0.384 ...
## $ NatWalkInd  : num [1:318] 8.17 11.33 6.5 12.33 5.5 ...
## $ HighSchool  : num [1:318] 86.1 87.5 86.7 87.3 87.4 84.5 89.2 90.2 NA 85.6 ...
## $ Alcohol     : num [1:318] 6.1 NA NA 5.1 NA 6.1 NA NA 8.7 6.6 ...
## $ Arthritis   : num [1:318] 31.8 NA NA 25.4 NA 28.7 NA NA 15.7 22.5 ...
## $ Asthma      : num [1:318] 10.5 NA NA 8.7 NA 9.5 NA NA 5.6 9.9 ...
## $ KidneyDisease: num [1:318] 3.4 NA NA 2.6 NA 3 NA NA 4.2 1.9 ...
## $ Overweight  : num [1:318] 65.6 NA NA 66 NA 64.9 NA NA 63.4 59.6 ...
## $ Vapeing     : num [1:318] 3.9 NA NA 5.7 NA 7.1 NA NA 6.6 1.5 ...
## $ Smoking     : num [1:318] 23.3 NA NA 18.1 NA 27 NA NA 29.2 17.1 ...
## $ COPD        : num [1:318] 7.4 NA NA 6.6 NA 8 NA NA 3.2 6.1 ...
## $ Active      : num [1:318] NA NA NA NA NA NA NA NA NA NA ...
## $ NoInsurance : num [1:318] 16.5 NA NA 17.5 NA 29.1 NA NA 26.6 14.7 ...
## $ Dentist     : num [1:318] 68 NA NA 67.3 NA NA NA NA 54 NA ...
## $ Walkable    : num [1:318] 1 0 1 0 1 0 1 0 1 0 ...
```

TODO: Insert rest of paper here

Appendix

Original data pre-processing methodology

As described in the objective section, the original data came from two sources. The disease indicators data contains location information in the form of latitude and longitude. The walkability data contains location information in the form of Federal census location codes (FIPS codes). The pre-processing technique below was used to convert the latitude and longitude to FIPS codes, and then perform a join operation utilizing

the FIPS codes. The resulting data is the original disease indicators data, augmented with the walkability information for the location corresponding to the original latitude and longitude.

In other words, for every row in the disease indicators data set, the corresponding walkability information for the region was added to that row. All of the commands are commented out to prevent them from being executed on knit since they take a long time to run.

```
#download.file("https://edg.epa.gov/EPADataCommons/public/OA/EPA_SmartLocationDatabase_V3_Jan_2021_Fina
#download.file("https://data.cdc.gov/api/views/g4ie-h725/rows.csv?accessType=DOWNLOAD", destfile="disea
```

Download the raw data

```
#walkability <- read.csv("walkability.csv")
## some of the disease data has no GeoLocation, which we cannot use for our analysis, so filter those o
#disease <- filter(read.csv("diseaseindicators.csv"), GeoLocation != "")
```

Load the data into R

```
## Extract the latitude and longitude values from the GeoLocation column using str_extract_all()
#geo_df <- str_extract_all(disease$GeoLocation, "-?[0-9]+\\.[0-9]+")

## Convert the extracted values to numeric and assign them to the corresponding latitude and longitude
#disease$lat <- as.numeric(sapply(geo_df, function(x) x[2]))
#disease$long <- as.numeric(sapply(geo_df, function(x) x[1]))
```

Extract the latitude and longitude into separate columns

Fetch the geographic information required to map latitude and logitude to FIPS blocks   The tigris library provides a function "block_groups" which returns geographic information about every FIPS block. This geographic information can be used to convert latitude and longitude to FIPS block. The following code downloads all of the block_groups for every block in the walkability data set.

```
## create data frame for block_groups data
#allblockgroups <- data.frame(matrix(ncol=6, nrow=0))
#colnames(allblockgroups) <- c('STATEFP', 'COUNTYFP', 'TRACTCE', 'BLKGRPCE', 'GEOID', 'geometry')

## get block geography data for each state in the walkability dataset
#stateCodes <- data.frame(unique(walkability$STATEFP))
#for (i in 1:nrow(stateCodes)) {
#  stateCode=stateCodes[[1]][i]
#  counties = distinct(filter(walkability, STATEFP == stateCode), COUNTYFP)$COUNTYFP
#  new_blocks <- block_groups(state=stateCodes[[1]][i], counties) %>%
#    select(STATEFP, COUNTYFP, TRACTCE, BLKGRPCE, GEOID, geometry)
#  allblockgroups <- rbind(allblockgroups, new_blocks)
#}
```

```
#my_points <- data.frame(
#  x = disease$lat,
#  y = disease$long
#) %>%
#  st_as_sf(coords = c("y", "x"),
#     crs = st_crs(allblockgroups))

#my_points_blocks <- st_join(my_points, allblockgroups)
#disease$STATEFP = as.integer(my_points_blocks$STATEFP)
#disease$COUNTYFP = as.integer(my_points_blocks$COUNTYFP)
#disease$TRACTCE = as.integer(my_points_blocks$TRACTCE)
#disease$BLKGRPCE = as.integer(my_points_blocks$BLKGRPCE)
#disease$GEOID = as.numeric(my_points_blocks$GEOID)
```

Use block geographies to convert longitude and latitude to FIPS blocks

```
# Join the disease data with the walkability data
#disease_with_walkability <- left_join(disease, walkability,
#                                 by = c("STATEFP", "COUNTYFP", "TRACTCE", "BLKGRPCE"))
```

Join the disease indicators and walkability data sets based on FIPS blocks

```
#write.csv(disease_with_walkability, file = "disease_with_walkability.csv")
```

Export the joined data to be used for further processing later.