

Reproduction of Chakraborty 2021: An intracategorical analysis of COVID-19 and people with disabilities

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Rpr-Reproduction of Social Inequities in the distribution of COVID-19: An intra-categorical analysis of people with disabilities in the U.S.

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Abstract

Chakraborty (2021) investigates the relationships between COVID-19 rates and demographic characteristics of people with disabilities by county in the lower 48 states. The study aims to examine public concern that persons with disabilities (PwDs) face disproportionate challenges due to COVID-19. To investigate this, Chakraborty examines the statistical relationship between confirmed county-level COVID-19 case rates and county-level socio-demographic and disability variables. Specifically, Chakraborty tests county-level bivariate correlations between COVID-19 incidence against the percentage of disability and socio-demographic category, with a separate hypothesis and model for each subcategory within disability, race, ethnicity, age, and biological sex. To control for differences between states and geographic clusters of COVID-19 outbreaks, Chakraborty uses five generalized estimating equation (GEE) models to predict the relationship and significance between COVID-19 incidence and disability subgroups within each socio-demographic category while considering inter-county spatial clusters. Chakraborty (2021) finds significant positive relationships between COVID-19 rates and socially vulnerable demographic categories of race, ethnicity, poverty, age, and biological sex.

This reproduction study is motivated by expanding the potential impact of Chakraborty's study for policy, research, and teaching purposes. Measuring the relationship between COVID-19 incidence and socio-demographic and disability characteristics can provide important information for public health policy-making and resource allocation. A fully reproducible study will increase the accessibility, transparency, and potential impact of Chakraborty's (2021) study by publishing a compendium complete with metadata, data, and code. This will allow other researchers to review, extend, and modify the study and will allow students of geography and spatial epidemiology to learn from the study design and methods.

In this reproduction, we will attempt to identically reproduce all of the results from the original study. This will include the map of county level distribution of COVID-19 incidence rates (Fig. 1), the summary

statistics for disability and sociodemographic variables and bivariate correlations with county-level COVID-19 incidence rate (Table 1), and the GEE models for predicting COVID-19 county-level incidence rate (Table 2). A successful reproduction should be able to generate identical results as published by Chakraborty (2021).

The replication study data and code will be made available in a GitHub repository to the greatest extent that licensing and file sizes permit. The repository will be made public at github.com/HEGSRR/RPr-Chakraborty2021.

Chakraborty, J. 2021. Social inequities in the distribution of COVID-19: An intra-categorical analysis of people with disabilities in the U.S. *Disability and Health Journal* 14:1-5. DOI:[10.1016/j.dhjo.2020.101007](DOI:%5B10.1016/j.dhjo.2020.101007%5D)

Keywords

COVID-19; Disability; Intersectionality; Race/ethnicity; Poverty; Reproducibility

Study Design

The reproduction study will try to implement the original study as closely as possible to reproduce the map of county level distribution of COVID-19 incidence rate, the summary statistics and bivariate correlation for disability characteristics and COVID-19 incidence, and the generalized estimating equations. Our two confirmatory hypotheses are that we will be able to exactly reproduce Chakraborty's results as presented in table 1 and table 2 of Chakraborty (2021). Stated as null hypotheses:

H1: There is a less than perfect match between Chakraborty's bivariate correlation coefficient for each disability/sociodemographic variable and COVID-19 incidence rate and our bivariate correlation coefficient for each disability/sociodemographic variable and COVID-19 incidence rate.

H2: There is a less than perfect match between Chakraborty's beta coefficient for the GEE of each disability/sociodemographic variable and our beta coefficient for the GEE of each disability/sociodemographic variable.

There are multiple models being tested within each of the two hypotheses. That is, H1 and H2 both encompass five models, including one for each dimension of socio-demographics: race, ethnicity, poverty status, age, and biological sex.

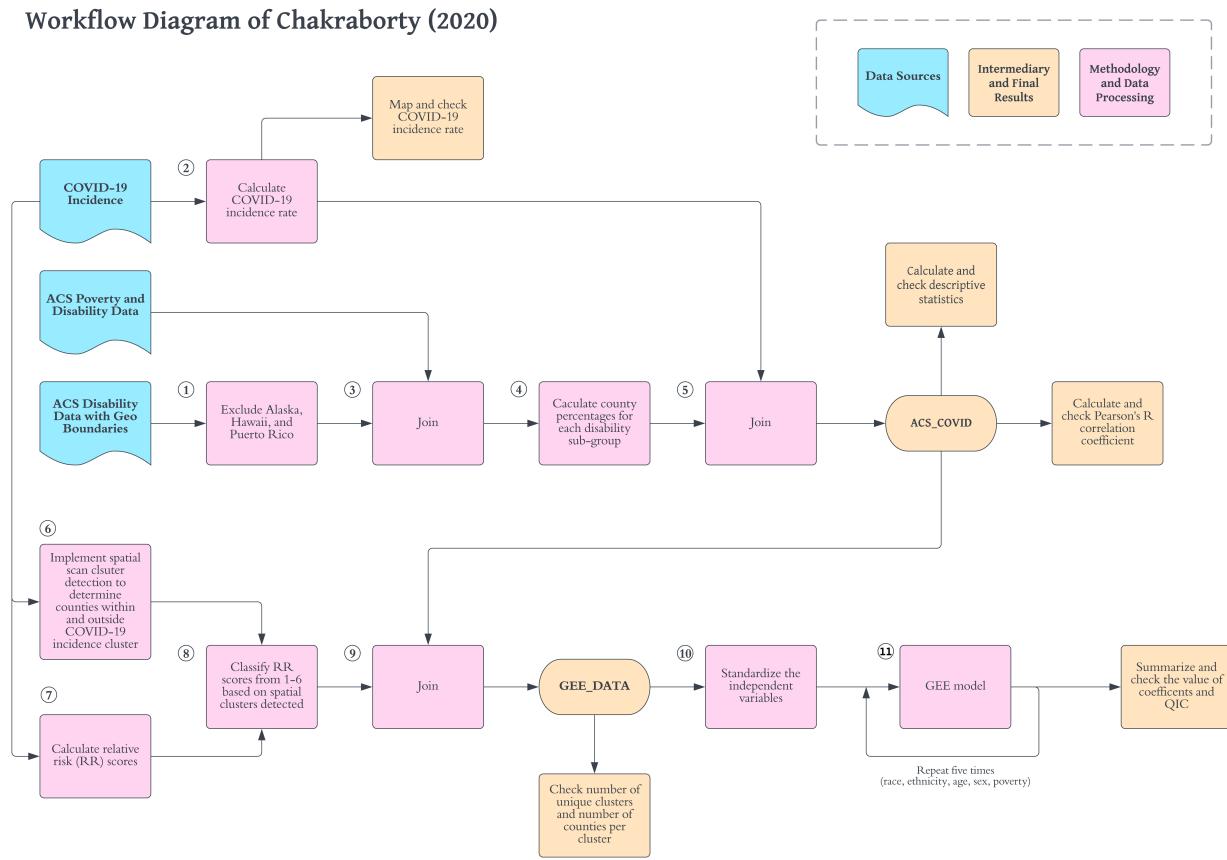
Original study design

The original study is **observational**, with the **exploratory** objective of determining “whether COVID-19 incidence is significantly greater in counties containing higher percentages of socio-demographically disadvantaged [people with disabilities], based on their race, ethnicity, poverty status, age, and biological sex” (Chakraborty 2021). This exploratory objective is broken down into five implicit hypotheses that each of the demographic characteristics of people with disabilities is associated with higher COVID-19 incidence rates.

The **spatial extent** of the study are the 49 contiguous states in the U.S. The **spatial scale** of the analysis is at the county level. Both COVID-19 incidence rates and demographic variables are all measured at the county level. The **temporal extent** of the COVID-19 data ranges from 1/22/2020 (when John Hopkins began collecting the data) to 8/1/2020 (when the data was retrieved for the original study). The data on disability and sociodemographic characteristics come from the U.S. Census American Community Survey (ACS) five-year estimates for 2018 (2014-2018).

There is no **randomization** in the original study.

Workflow Diagram of Chakraborty (2020)



Computational environment

The study was originally conducted using SaTScan software (unspecified version) to implement the Kulldorff spatial scan statistic. Other software are not specified in the publication; however data files and communication with the author show that spatial analysis and mapping was conducted in ArcGIS and generalized estimating equation (GEE) models were calculated in SPSS.

This reproduction study uses R, including the SpatialEpi package for the Kulldorff spatial scan statistics and the geepack package for GEE models.

Data

American Community Survey American Community Survey (ACS) data for sociodemographic sub-categories of people with disabilities can be accessed by using the `tidycensus` package to query the Census API. This requires an API key which can be acquired at api.census.gov/data/key_signup.html

The original study extent is the lower 48 states and Washington D.C. Therefore, Alaska, Hawai'i and Puerto Rico are removed from the data (workflow diagram step 1). Data on people with disabilities in poverty is derived from a different census table (C18130) than data on people with disabilities and age, race, ethnicity, age, and biological sex (S1810). Therefore, join the poverty data to the other data using the GEOFID (workflow diagram step 3).

Save the raw ACS data to `data/raw/public/acs.gpkg`

Load the raw ACS data. Optionally, begin processing here.

Calculate independent socio-demographic variables of people with disabilities as percentages for each sub-category of disability (race, ethnicity, poverty, age, and biological sex) and remove raw census data from the data frame (workflow diagram step 4). Reproject the data into an Albers equal area conic projection.

COVID-19 rates Data on COVID-19 rates from the Johns Hopkins University dashboard have been provided directly with the research compendium because the data is no longer available online in the state in which it was downloaded on August 1, 2020. The dashboard and cumulative counts of COVID-19 cases and deaths were continually updated, so an exact reproduction required communication with the original author, Jayajit Chakraborty, for assistance with provision of data from August 1, 2020.

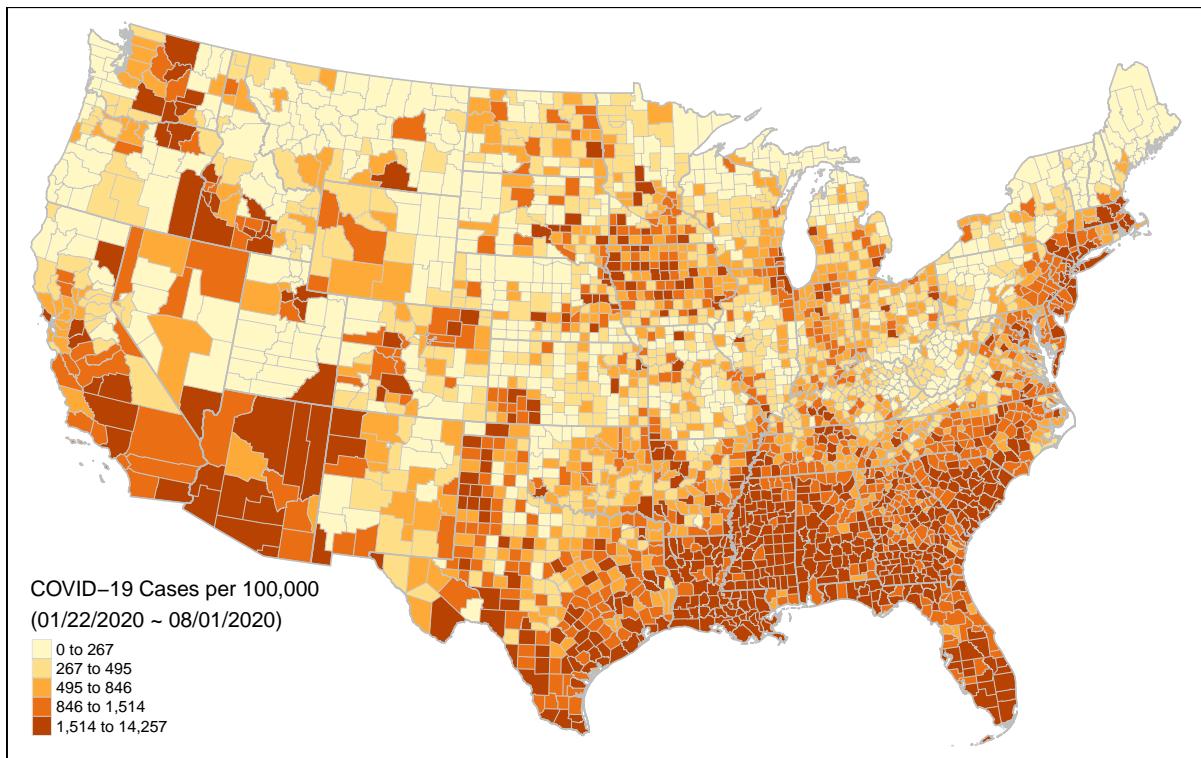
Calculate the COVID incidence rate as the cases per 100,000 people (workflow step 2). *Unplanned Deviation* Initially the descriptive statistics for the COVID rate were slightly different, but we have resolved the difference by rounding the rate to 0 decimal places.

Join dependent COVID data to independent ACS sociodemographic data.

Missing Data There is one county with missing disability and poverty data. This was not mentioned in the original study or our pre-analyis plan. However, we replace the missing data with zeros, producing results identical to Chakraborty's.

```
## Simple feature collection with 1 feature and 23 fields
## Geometry type: MULTIPOLYGON
## Dimension: XY
## Bounding box: xmin: -1032914 ymin: 1477939 xmax: -849865.1 ymax: 1611186
## Projected CRS: NAD83 / Conus Albers
## # A tibble: 1 x 24
##   geoid statefp county county_st covid_rate dis_pct white_pct black_pct
##   <chr>  <chr>    <chr>      <dbl>    <dbl>    <dbl>    <dbl>
## 1 35039  35      Rio Arriba Rio Arriba Co~    751.    16.1    10.8   0.0384
## # i 16 more variables: native_pct <dbl>, asian_pct <dbl>, other_pct <dbl>,
## # non_hisp_white_pct <dbl>, hisp_pct <dbl>, non_hisp_non_white_pct <dbl>,
## # bpov_pct <dbl>, apov_pct <dbl>, pct_5_17 <dbl>, pct_18_34 <dbl>,
## # pct_35_64 <dbl>, pct_65_74 <dbl>, pct_75 <dbl>, male_pct <dbl>,
## # female_pct <dbl>, geom <MULTIPOLYGON [m]>
```

Map Disability and COVID-19 Incidence Map the county level distribution of COVID-19 incidence rates, comparing to Figure 1 of the original study.

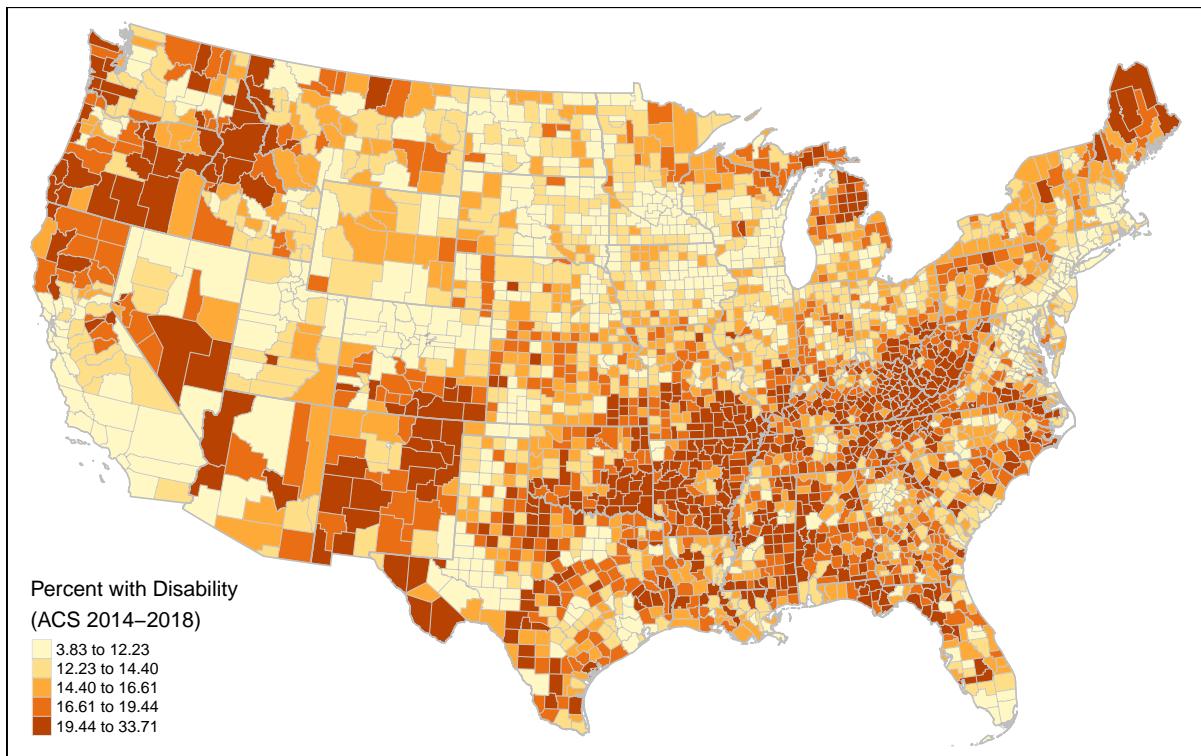


```
## Map saved to C:\GitHub\HEGSRR\RPr-Chakraborty-2021\results\figures\covid_rates.png
```

```
## Resolution: 2647.584 by 1665.669 pixels
```

```
## Size: 8.82528 by 5.552232 inches (300 dpi)
```

In a planned deviation from the original study, we also map the spatial distribution of disability rates.



```
## Map saved to C:\GitHub\HEGSRR\RPr-Chakraborty-2021\results\figures\disability_rates.png
## Resolution: 2647.584 by 1665.669 pixels
## Size: 8.82528 by 5.552232 inches (300 dpi)
```

Descriptive Statistics Calculate descriptive statistics for dependent covid rate and independent socio-demographic characteristics, reproducing the min, max, mean, and SD columns of Table 1. In addition to the original study, also calculate the Shapiro Wilk test for normality.

	min	max	mean	SD	ShapiroWilk	p
## covid_rate	0.00	14257.17	966.90	1003.96	0.74	0
## dis_pct	3.83	33.71	15.95	4.40	0.98	0
## white_pct	0.85	33.26	13.55	4.63	0.98	0
## black_pct	0.00	20.70	1.48	2.66	0.61	0
## native_pct	0.00	13.74	0.28	0.94	0.28	0
## asian_pct	0.00	3.45	0.09	0.18	0.51	0
## other_pct	0.00	15.24	0.55	0.65	0.57	0
## non_hisp_white_pct	0.10	33.16	12.84	4.81	0.99	0
## hisp_pct	0.00	25.26	0.99	2.15	0.42	0
## non_hisp_non_white_pct	0.00	20.93	2.13	2.75	0.70	0
## bpov_pct	0.00	14.97	3.57	1.85	0.93	0
## apov_pct	0.00	27.30	12.48	3.06	0.99	0
## pct_5_17	0.00	5.08	1.03	0.48	0.95	0

```

## pct_18_34          0.00    5.59   1.56    0.67    0.96 0
## pct_35_64          1.01   18.36   6.35    2.30    0.96 0
## pct_65_74          0.00   12.73   3.09    1.16    0.95 0
## pct_75             0.00   11.13   3.87    1.19    0.97 0
## male_pct           1.30   18.19   8.06    2.37    0.98 0
## female_pct         1.91   19.94   7.90    2.26    0.98 0

```

Compare reproduced descriptive statistics to original descriptive statistics by subtracting the reproduced statistics from the original study statistics. Identical results will result in zero.

```

##               min   max  mean    SD
## covid_rate      0 0.17 -0.1 -0.04
## dis_pct         0 0.00  0.0  0.00
## white_pct       0 0.00  0.0  0.00
## black_pct       0 0.00  0.0  0.00
## native_pct      0 0.00  0.0  0.00
## asian_pct       0 0.00  0.0  0.00
## other_pct       0 0.00  0.0  0.00
## non_hisp_white_pct 0 0.00  0.0  0.00
## hisp_pct        0 0.00  0.0  0.00
## non_hisp_non_white_pct 0 0.00  0.0  0.00
## bpov_pct        0 0.00  0.0  0.00
## apov_pct        0 0.00  0.0  0.00
## pct_5_17         0 0.00  0.0  0.00
## pct_18_34         0 0.00  0.0  0.00
## pct_35_64         0 0.00  0.0  0.00
## pct_65_74         0 0.00  0.0  0.00
## pct_75             0 0.00  0.0  0.00
## male_pct          0 0.00  0.0  0.00
## female_pct        0 0.00  0.0  0.00

```

The descriptive statistics are identical except for the precision for the descriptive statistics of the COVID incidence rate.

Analytical Methods

Bivariate Parametric Correlation Analysis Calculate Pearson's R Correlation Coefficient of each independent variable and the COVID-19 incidence rate, reproducing the Pearson's R column of Table 1. These results are identical in direction and significance to Chakraborty's, but differ slightly in magnitude.

```

##               variable      r      t      p
## 1             dis_pct -0.060  3.350 0.000
## 2             white_pct -0.332 19.612 0.000
## 3             black_pct  0.460 28.847 0.000
## 4             native_pct  0.019  1.072 0.142
## 5             asian_pct  0.094  5.272 0.000
## 6             other_pct  0.026  1.460 0.072
## 7             non_hisp_white_pct -0.361 21.545 0.000
## 8             hisp_pct  0.119  6.686 0.000
## 9             non_hisp_non_white_pct  0.442 27.429 0.000
## 10            bpov_pct  0.106  5.914 0.000
## 11            apov_pct -0.151  8.513 0.000

```

```

## 12      pct_5_17  0.084  4.688 0.000
## 13      pct_18_34  0.063  3.493 0.000
## 14      pct_35_64 -0.008  0.460 0.323
## 15      pct_65_74 -0.091  5.113 0.000
## 16      pct_75 -0.186 10.541 0.000
## 17      male_pct -0.134  7.519 0.000
## 18      female_pct  0.023  1.305 0.096

```

Compare the reproduced Pearson's r correlation coefficients to the original study's Pearson's r correlation coefficients.

variable	or_r	or_r_stars	rp_r	rp_r_stars	rp_rdiff	rp_r_starsdiff
dis_pct	-0.056	2	-0.060	2	-0.004	0
white_pct	-0.326	2	-0.332	2	-0.006	0
black_pct	0.456	2	0.460	2	0.004	0
native_pct	0.020	0	0.019	0	-0.001	0
asian_pct	0.097	2	0.094	2	-0.003	0
other_pct	0.028	0	0.026	0	-0.002	0
non_hisp_white_pct	-0.355	2	-0.361	2	-0.006	0
hisp_pct	0.119	2	0.119	2	0.000	0
non_hisp_non_white_pct	0.439	2	0.442	2	0.003	0
bpov_pct	0.108	2	0.106	2	-0.002	0
apov_pct	-0.146	2	-0.151	2	-0.005	0
pct_5_17	0.083	2	0.084	2	0.001	0
pct_18_34	0.066	1	0.063	2	-0.003	1
pct_35_64	-0.005	0	-0.008	0	-0.003	0
pct_65_74	-0.089	2	-0.091	2	-0.002	0
pct_75	-0.181	2	-0.186	2	-0.005	0
male_pct	-0.131	2	-0.134	2	-0.003	0
female_pct	0.028	0	0.023	0	-0.005	0

The reproduced Pearson's r coefficients are very similar to the original study within a range 0.006. *Unplanned Deviation* We should expect identical results for this correlation test, so we loaded the original author's data from `Aug1GEEdata.csv` to re-test the statistic.

or_variable	unplanned_r	variable	or_r	diff
PerDisable	-0.056	dis_pct	-0.056	0
PD_White	-0.326	white_pct	-0.326	0
PD_Black	0.456	black_pct	0.456	0
PD_Native	0.020	native_pct	0.020	0
PD_Asian	0.097	asian_pct	0.097	0
PD_OthRac	0.028	other_pct	0.028	0
PD_NHwhite	-0.355	non_hisp_white_pct	-0.355	0
PD_Hispani	0.119	hisp_pct	0.119	0
PD_NHoth	0.439	non_hisp_non_white_pct	0.439	0
PDisBpov	0.108	bpov_pct	0.108	0
PDisApov	-0.146	apov_pct	-0.146	0
PD_age5to17	0.083	pct_5_17	0.083	0
PDage18to34	0.066	pct_18_34	0.066	0
PDage35to64	-0.005	pct_35_64	-0.005	0
PDage65to74	-0.089	pct_65_74	-0.089	0
PDage75	-0.181	pct_75	-0.181	0

or_variable	unplanned_r	variable	or_r	diff
PD_Male	-0.131	male_pct	-0.131	0
PD_Female	0.028	female_pct	0.028	0

The author's original data produces coefficients identical to the original publication! Is it possible that some of the data values have been transposed to different counties, such that the descriptive statistics are all consistent but the correlation coefficients are in error? *Deviation* We re-calculate the COVID-19 incidence rate with the original author's data and select for unequal results.

```
##   COUNTY_FIPS Countyname Total_POP Cases Incidence recalc_incidence
## 1      1115  St. Clair     88690  1151   1349.52      1297.78
## 2      1117    Shelby    215707  2911   1297.78      1349.52
## 3      5123 St. Francis    25439  1112    704.16      4371.24
## 4      5125     Saline   121421   855    397.33      704.16
## 5      5127     Scott    10319    41    314.15      397.33
## 6      5129    Searcy     7958    25   1322.08      314.15
## 7      5131 Sebastian   127753  1689   5420.39      1322.08
## 8      5133    Sevier    17139   929    570.08      5420.39
## 9      5135     Sharp    17366    99   4371.24      570.08
## 10     8039     Elbert   26282    85    626.60      323.42
## 11     8041    El Paso   713856  4473   323.42      626.60
## 12     8065      Lake    7824    70    349.85      894.68
## 13     8067 La Plata   56310   197   894.68      349.85
```

We found that 13 counties had incorrect COVID-19 incidence scores, and the scores seem to be swapped with other counties, such that the overall descriptive statistics were accurate but the correlation coefficients were inaccurate.

Bivariate Nonparametric Correlation Analysis Calculate Spearman's Rho Correlation Coefficients, deviating from the original study and using a non-parametric correlation test because the variables do not have normal distributions (see Shapiro-Wilk test results above).

Compare the Spearman's *rho* correlation coefficients to the reproduced Pearson's *r* correlation coefficients.

variable	or_r	or_r_star	p_r	rp_r_star	p_r_star	p_r_star	rdiff	rp_r_star	diff	rp_rho_star	p_rho_star	diff	rp_rho_star	diff
dis_pct	-	2	-	2	-	0	-	2	-0.057	0				
	0.056		0.060		0.004		0.113							
white_pct	-	2	-	2	-	0	-	2	-0.095	0				
	0.326		0.332		0.006		0.421							
black_pct	0.456	2	0.460	2	0.004	0	0.575	2	0.119	0				
native_pct	0.020	0	0.019	0	-	0	-	2	-0.104	2				
					0.001		0.084							
asian_pct	0.097	2	0.094	2	-	0	0.194	2	0.097	0				
					0.003									
other_pct	0.028	0	0.026	0	-	0	0.104	2	0.076	2				
					0.002									
non_hisp_white_pct	2	-	2	-	0	-	2	-0.099	0					
	0.355		0.361		0.006		0.454							
hisp_pct	0.119	2	0.119	2	0.000	0	0.231	2	0.112	0				
non_hisp_non_hisp_pct	0.130	2	0.442	2	0.003	0	0.481	2	0.042	0				

variable	or_r	or_r_stars	p_r	rp_r_stars	p_rdiff	rp_r_starsdiff	diff_rho	rho_stars	p_rho_stars	rho_starsdiff
bpov_pct	0.108	2	0.106	2	-	0	0.062	2	-0.046	0
					0.002					
apov_pct	-	2	-	2	-	0	-	2	-0.059	0
	0.146		0.151		0.005		0.205			
pct_5_17	0.083	2	0.084	2	0.001	0	0.079	2	-0.004	0
pct_18_34	0.066	1	0.063	2	-	1	0.034	1	-0.032	0
					0.003					
pct_35_64	-	0	-	0	-	0	-	0	-0.015	0
	0.005		0.008		0.003		0.020			
pct_65_74	-	2	-	2	-	0	-	2	-0.062	0
	0.089		0.091		0.002		0.151			
pct_75	-	2	-	2	-	0	-	2	-0.104	0
	0.181		0.186		0.005		0.285			
male_pct	-	2	-	2	-	0	-	2	-0.070	0
	0.131		0.134		0.003		0.201			
female_pct	0.028	0	0.023	0	-	0	-	0	-0.042	0
					0.005		0.014			

Kulldorf Spatial Scan Cluster Detection

This accomplishes the step 6 of the workflow diagram

Note that the statistic is a Monte Carlo simulation with 999 iterations. Therefore, if you wish to exactly reproduce the same results as our reproduction attempt, please **do not run this section**. Instead, load the scan results below. This code block can take more than 10-20 minutes to run.

Save scan results

Optionally, load scan results

```
## [1] "Most likely cluster:"
```

```
## $location.IDs.included
## [1] 1824 1835 1797 1818 1825 1749 1854 1742 1837 1747 1838 280 1760 1846 1756
##
## $population
## [1] 16949211
##
## $number.of.cases
## [1] 469091
##
## $expected.cases
## [1] 233805.6
##
## $SMR
## [1] 2.006329
##
## $log.likelihood.ratio
## [1] 97983.07
##
```

```

## $monte.carlo.rank
## [1] 1
##
## $p.value
## [1] 0.001

## [1] "Secondary clusters: 134"

```

Summarize spatial scan clusters by county

This accomplishes the step 7 and 8 of the workflow diagram

Summarize the results of the Kulldorff spatial scan cluster detection by cluster

Summarize the results of the Kulldorff spatial scan cluster detection by county Code each county 0 if it is not in a cluster and 1 if it is in a cluster.

How did the classification work?

```

## Classes of local risk and frequency of counties
## # A tibble: 6 x 2
##   loc_class     n
##       <dbl> <int>
## 1 1     2464
## 2 2     476
## 3 3     124
## 4 4     31
## 5 5     5
## 6 6     8

## Warning: Unknown or uninitialised column: 'cluster'.
## Unknown or uninitialised column: 'cluster'.

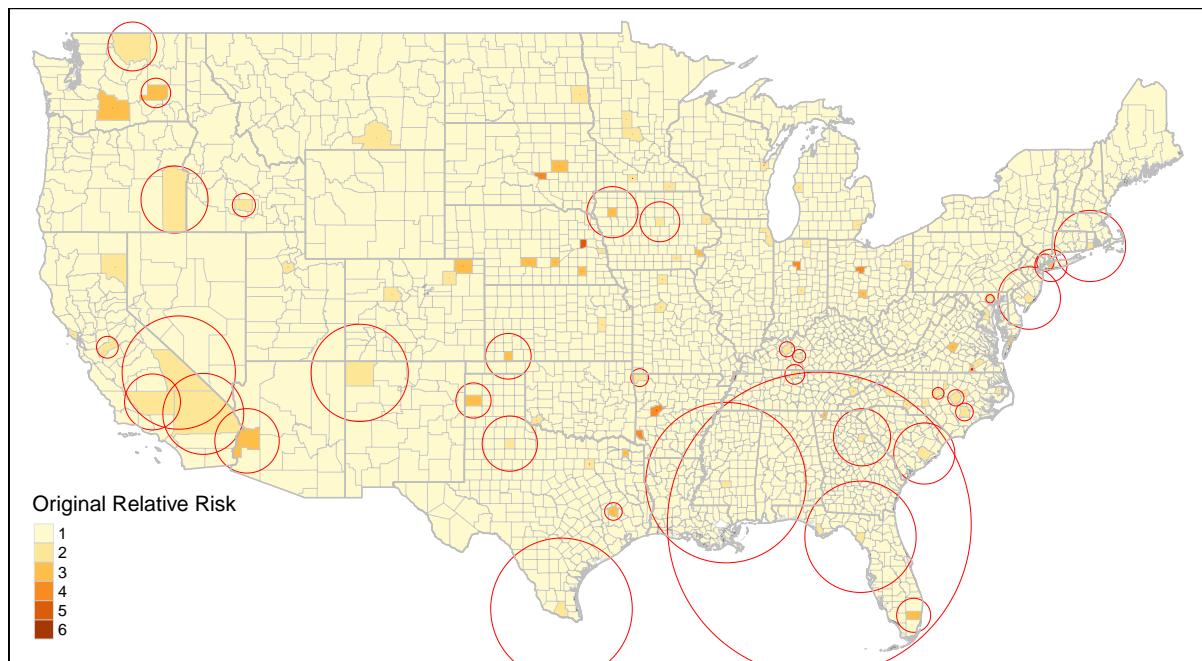
##
## 0 counties lie outside of a cluster, but have local relative risk > 1
##
## 0 counties lie inside of a cluster, but have a local relative risk < 1

## Classes of cluster risk and frequency of counties
## # A tibble: 6 x 2
##   cluster_class     n
##       <dbl> <int>
## 1 1     2170
## 2 2     843
## 3 3     83
## 4 4     9
## 5 5     2
## 6 6     1

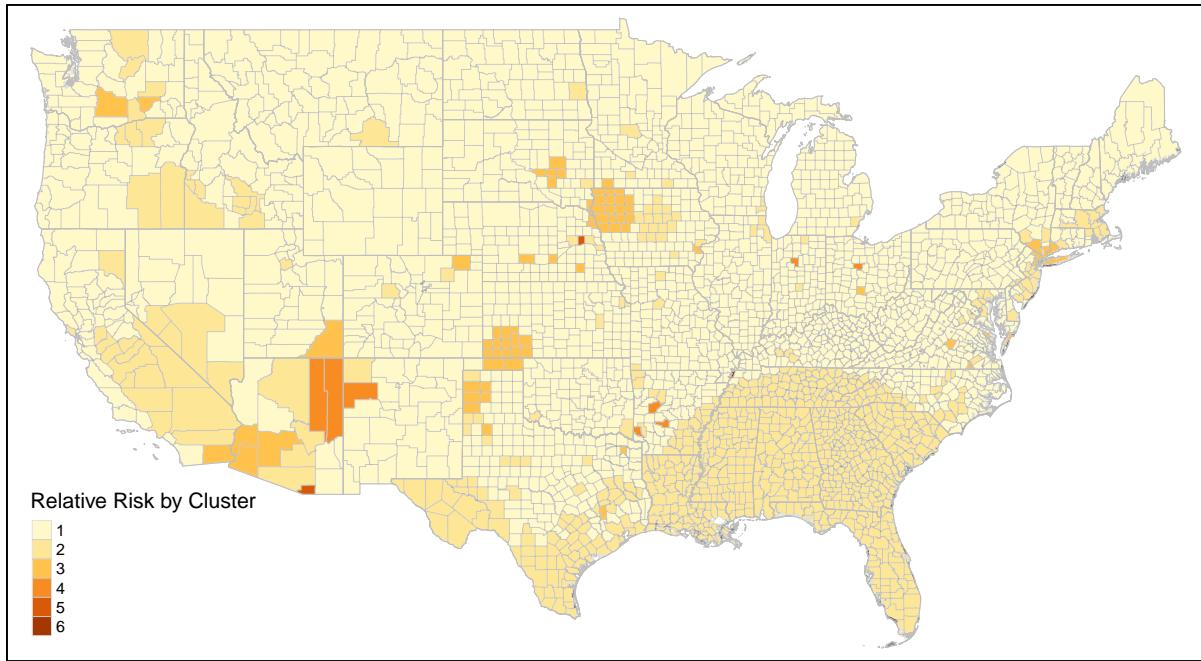
```

Map Relative Risk Scores

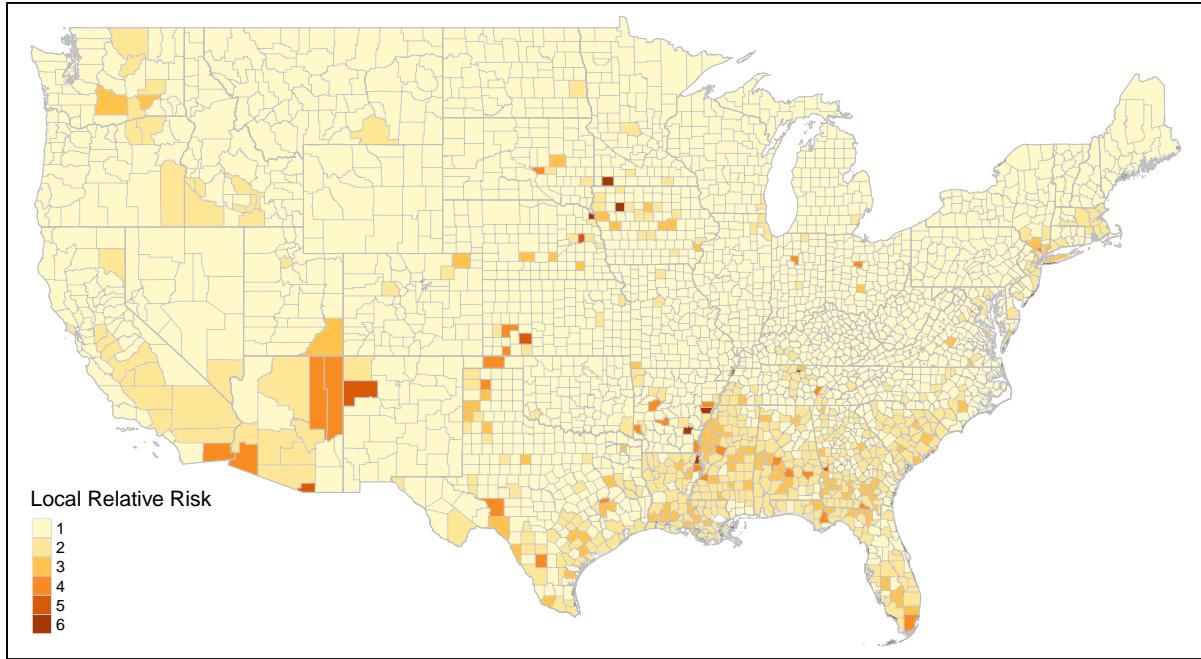
Note that relative risk is > 1 only if the county was in a cluster



```
## Map saved to C:\GitHub\HEGSRR\RPr-Chakraborty-2021\results\figures\rr_original.png
## Resolution: 2837.601 by 1554.129 pixels
## Size: 9.458671 by 5.180432 inches (300 dpi)
```



```
## Map saved to C:\GitHub\HEGSRR\RPr-Chakraborty-2021\results\figures\rr_reproduction_cluster.png
## Resolution: 2837.601 by 1554.129 pixels
## Size: 9.458671 by 5.180432 inches (300 dpi)
```



```
## Map saved to C:\GitHub\HEGSRR\RPr-Chakraborty-2021\results\figures\rr_reproduction_loc.png
## Resolution: 2837.601 by 1554.129 pixels
## Size: 9.458671 by 5.180432 inches (300 dpi)
```

Preprocess data for GEE modelling

This accomplishes the step 9 and 10 of the workflow diagram

Save preprocessed GEE data inputs

Optionally, you may save the preprocessed to `data/raw/public/gee_data.gpkg`

Load preprocessed GEE input data

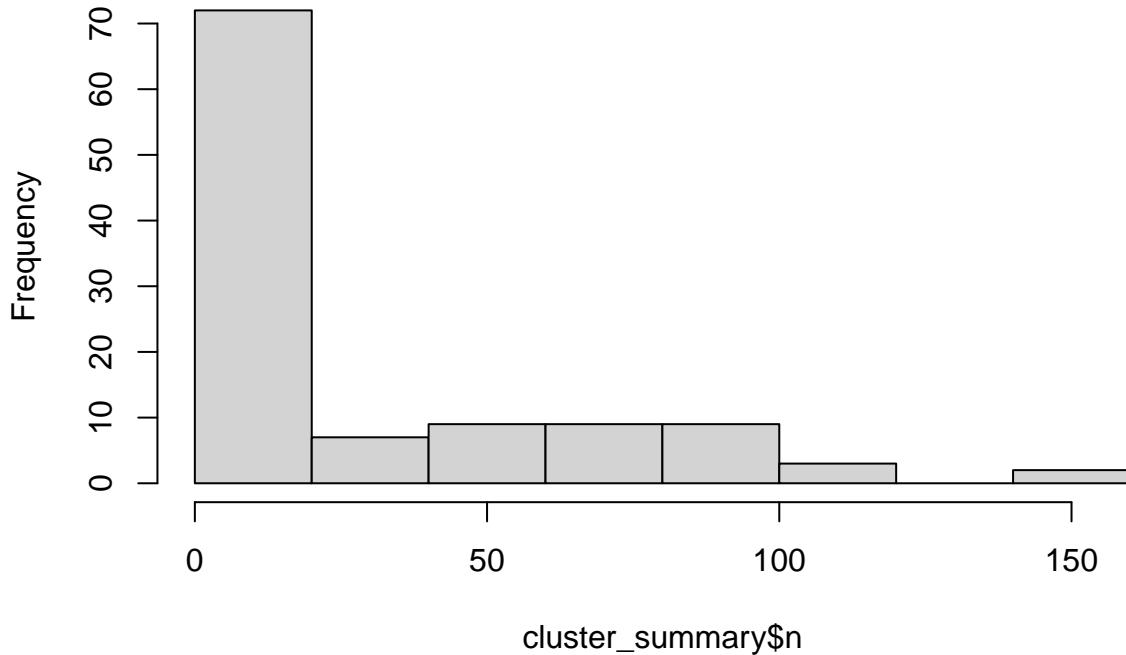
Optionally, you may load the preprocessed data from `data/raw/public/gee_data.gpkg`

Report number of unique clusters and histogram of counties per cluster

```
## 111 unique clusters
```

```
##      Min. 1st Qu. Median      Mean 3rd Qu.      Max.
##      1.00    2.00   7.00    27.56  50.50 159.00
```

Histogram of cluster_summary\$n



GEE Models

This accomplishes the step 11 of the workflow diagram

Generalized Estimating Equation parameters:

“The ‘exchangeable’ correlation matrix was selected for the results reported here, since this specification yielded the best statistical fit based on the QIC (quasi- likelihood under the independence) model criterion.” (Chakraborty 2021, Methods paragraph 5)

“The gamma distribution with logarithmic link function was chosen for all GEEs since this model specification provided the lowest QIC value.” (Chakraborty 2021, Methods paragraph 5)

Useful Reference: <https://data.library.virginia.edu/getting-started-with-generalized-estimating-equations/>

```
##                               Estimate Std. Error t value Pr(>|t|) 
## Race Intercept              6.782    0.018 385.245   0.000
## z_white_pct                -0.214    0.020 -10.619   0.000
## z_black_pct                 0.340    0.019 17.664   0.000
## z_native_pct                0.018    0.018  1.019   0.308
## z_asian_pct                 0.053    0.019  2.810   0.005
## z_other_pct                 0.106    0.018  5.867   0.000
## Ethnicity Intercept          6.773    0.017 391.315   0.000
## z_non_hisp_white_pct       -0.240    0.020 -12.236   0.000
```

```

## z_hisp_pct          0.128      0.019   6.832   0.000
## z_non_hisp_non_white_pct 0.336      0.019  17.896   0.000
## Poverty Status Intercept 6.850      0.019 367.671   0.000
## z_bpov_pct          0.282      0.023  12.167   0.000
## z_apov_pct          -0.319      0.023 -13.754   0.000
## Age Intercept       6.865      0.018 375.694   0.000
## z_pct_5_17           0.079      0.020   3.876   0.000
## z_pct_18_34           0.023      0.022   1.075   0.283
## z_pct_35_64           0.036      0.029   1.223   0.221
## z_pct_65_74           -0.022      0.030  -0.736   0.462
## z_pct_75              -0.203      0.024 -8.619   0.000
## Biological Sex Intercept 6.852      0.018 376.541   0.000
## z_male_pct           -0.464      0.031 -14.860   0.000
## z_female_pct          0.373      0.031  11.957   0.000

##                                     Estimate Std.err   Wald Pr(>|W|)
## Race Intercept                  7.370   0.083 7813.512   0.000
## z_white_pct          -0.163   0.010  275.756   0.000
## z_black_pct           0.104   0.011   88.678   0.000
## z_native_pct          0.036   0.008   21.126   0.000
## z_asian_pct           0.039   0.008   21.766   0.000
## z_other_pct           0.010   0.010   1.029   0.310
## Ethnicity Intercept      7.360   0.083 7769.794   0.000
## z_non_hisp_white_pct  -0.190   0.012  247.675   0.000
## z_hisp_pct             0.005   0.027   0.032   0.857
## z_non_hisp_non_white_pct 0.105   0.011   92.967   0.000
## Poverty Status Intercept 7.382   0.074 9974.920   0.000
## z_bpov_pct             0.109   0.018   35.408   0.000
## z_apov_pct             -0.194   0.014  204.920   0.000
## Age Intercept          7.422   0.077 9253.949   0.000
## z_pct_5_17              0.028   0.010   7.132   0.008
## z_pct_18_34              0.048   0.018   6.945   0.008
## z_pct_35_64              -0.014   0.020   0.481   0.488
## z_pct_65_74              -0.073   0.017  17.382   0.000
## z_pct_75              -0.079   0.013  36.943   0.000
## Biological Sex Intercept 7.421   0.077 9279.249   0.000
## z_male_pct             -0.222   0.016  201.110   0.000
## z_female_pct            0.121   0.017  49.606   0.000

##                                     QIC
## race           3570.703
## ethnicity     3582.909
## poverty_status 3683.829
## age            3586.645
## biological_sex 3562.916

##                                     Estimate Std.err   Wald Pr(>|W|)
## Race Intercept                  6.781   0.018 146425.883   0.000
## ZPD_White           -0.203   0.025   64.795   0.000
## ZPD_Black           0.339   0.016  434.337   0.000
## ZPD_Asian           0.058   0.020   8.286   0.004
## ZPD_Native           0.020   0.024   0.736   0.391
## ZPD_OthRac          0.108   0.017  39.833   0.000

```

```

## Ethnicity Intercept      6.772  0.017 149824.715  0.000
## ZPD_NHwhite            -0.228  0.025    83.830  0.000
## ZPD_Hispani            0.132  0.016    71.424  0.000
## ZPD_NHoth               0.335  0.016   450.155  0.000
## Poverty_Status Intercept 6.849  0.019 134421.024  0.000
## ZPDisBpov              0.283  0.026   117.757  0.000
## ZPDisApov              -0.315  0.032   94.932  0.000
## Age Intercept           6.864  0.018 140695.070  0.000
## ZPD_age5to17            0.077  0.025    9.512  0.002
## ZPDage18to34            0.026  0.031    0.720  0.396
## ZPDage35to64            0.040  0.037    1.160  0.281
## ZPDage65to74            -0.024  0.039    0.386  0.535
## ZPDage75                -0.200  0.030   43.469  0.000
## Biological_Sex Intercept 6.850  0.018 141590.714  0.000
## ZPD_Male                -0.467  0.047   98.128  0.000
## ZPD_Female               0.380  0.046   68.384  0.000

##                               QIC
## race                  6181.412
## ethnicity            6176.208
## poverty_status       6171.740
## age                  6180.967
## biological_sex      6173.250

```