

# Evaluation of COVID-19 Cases and Vaccinations in the State of Georgia, United States: A Spatial Perspective

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## Abstract

This study evaluates the distribution of COVID-19 cases and mass vaccination campaigns from January 2020 to April 2023. There are over 235,000 COVID-19 cases and over 733,000 vaccinations across the 159 counties in the state of Georgia. Data on COVID-19 was acquired from [usafact.org](http://usafact.org) while the vaccination records were obtained from COVID-19 vaccination tracker. The spatial patterns across the counties were analyzed using spatial statistical techniques which include both global and local spatial autocorrelation. The study further evaluates the effect of vaccination and selected socio-economic predictors on COVID-19 cases across the study area. The result of hotspot analysis reveals that the epicenters of COVID-19 are distributed across Cobb, Fulton, Gwinnett, and DeKalb counties. It was also affirmed that the vaccination records followed the same pattern as COVID-19 cases' epicenters. The result of the spatial error model performed well and accounted for a considerable percentage of the regression with an adjusted R squared of 0.68, Akaike Information Criterion (AIC) 387.682 and Breusch-Pagan of 9.8091. ESDA was employed to select the main explanatory variables. The selected variables include vaccination, population density, percentage of people that do not have health insurance, black race, Hispanic and these variables accounted for 68% of the number of COVID-19 cases in the state of Georgia during the study period. The study concludes that both COVID-19 cases and vaccinated individuals have spatial peculiarities across counties in Georgia state. Lastly, socio-economic variables and vaccination are very important to reduce the vulnerability of individuals to COVID-19 disease.

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## Keywords

COVID-19, Vaccination, Spatial Autocorrelation, Georgia, Spatial Pattern, Spatial Regression

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## 1. Introduction

COVID-19 disease popularly referred to as Severe Acute Respiratory Syndrome Coronavirus 2019 (SARS-CoV-19) was announced as a novel global pandemic on March 11, 2020, by the World Health Organization (WHO). This was after the eruption of the disease in Wuhan, China on December 30, 2019. The global and national disruption caused by the transmission of the disease was evident in the economic, social, and political spheres. Since the outbreak of COVID-19 disease in early 2020 in the United States, several attempts have been made to track and reduce the disease transmission [1] [2]. One of the methods is the mass vaccination of individuals across the country. As of May 11, 2023, a total number of 676,728,782 billion doses of COVID-19 have been administered in the United States. Over 42,000 deaths have been attributed to the novel disease [3] as of July 2023. According to [4], massive vaccination is considered as one of the best Non-Pharmaceutical Intervention strategies to tackle both individual and community transmission of the disease.

Since the introduction of vaccines across the United States which were targeted to reduce the basic reproduction ratio ( $R_0$ ) of COVID-19 was high up to 3.8 in March 2020 [5] and the basic reproduction ratio rise to up 8.3 at the end of 2020 [2] [6]. Therefore, a plethora of studies worldwide measures vaccination coverage and accessibility to COVID-19 vaccine centers [7] [8]. Accessibility is defined the relative ease to reach social and economic services from a given geographic location [9]. Indeed, to evaluate COVID-19 cases and vaccinations, COVID-19 vaccination centers should be considered as healthcare services. The spatial distribution of COVID-19 vaccination has been identified as an important investigation that reveals hidden health inequalities and several factors responsible for these inequalities [10]. To reduce the associated problem with COVID-19 vaccination, spatial barriers must be tackled by guaranteeing equitable distribution of medical resources. Studies across several cities like Baltimore, Los Angeles, Michigan, and Chicago to mention a few have revealed the spatial distribution of vaccination and explained the factors responsible for the patterns [10]. It has been affirmed that the periphery and poor areas of cities in Iran had least access to vaccinations services and thereby revealed lower spatial accessibility with people of lower economic status [8]. According to [6], several studies have investigated the spatio-temporal analysis of COVID-19 disease in the first 900 days worldwide [2] [11] [12] Indeed, a plethora of these studies adopted spatial statistics and GIS in their investigations. Studies have necessitated the need to explore the nexus between COVID-19 infections and vaccination cam-

paings [13] [14]. To identify and evaluate the spatial relationship between COVID-19 cases and vaccination rate across counties in Georgia, there is a need to adopt a GIS-based and sophisticated statistical analytical model that will explore the first, second, and third waves of the COVID-19 transmission and how individual responds to vaccination campaigns across Georgia state. Hence, the goal of this study is to provide a framework to monitor and create early warning surveillance on COVID-19 occurrence and vaccination campaigns across counties in Georgia State with a view to improving access to public healthcare during emergencies.

## 2. Methodology

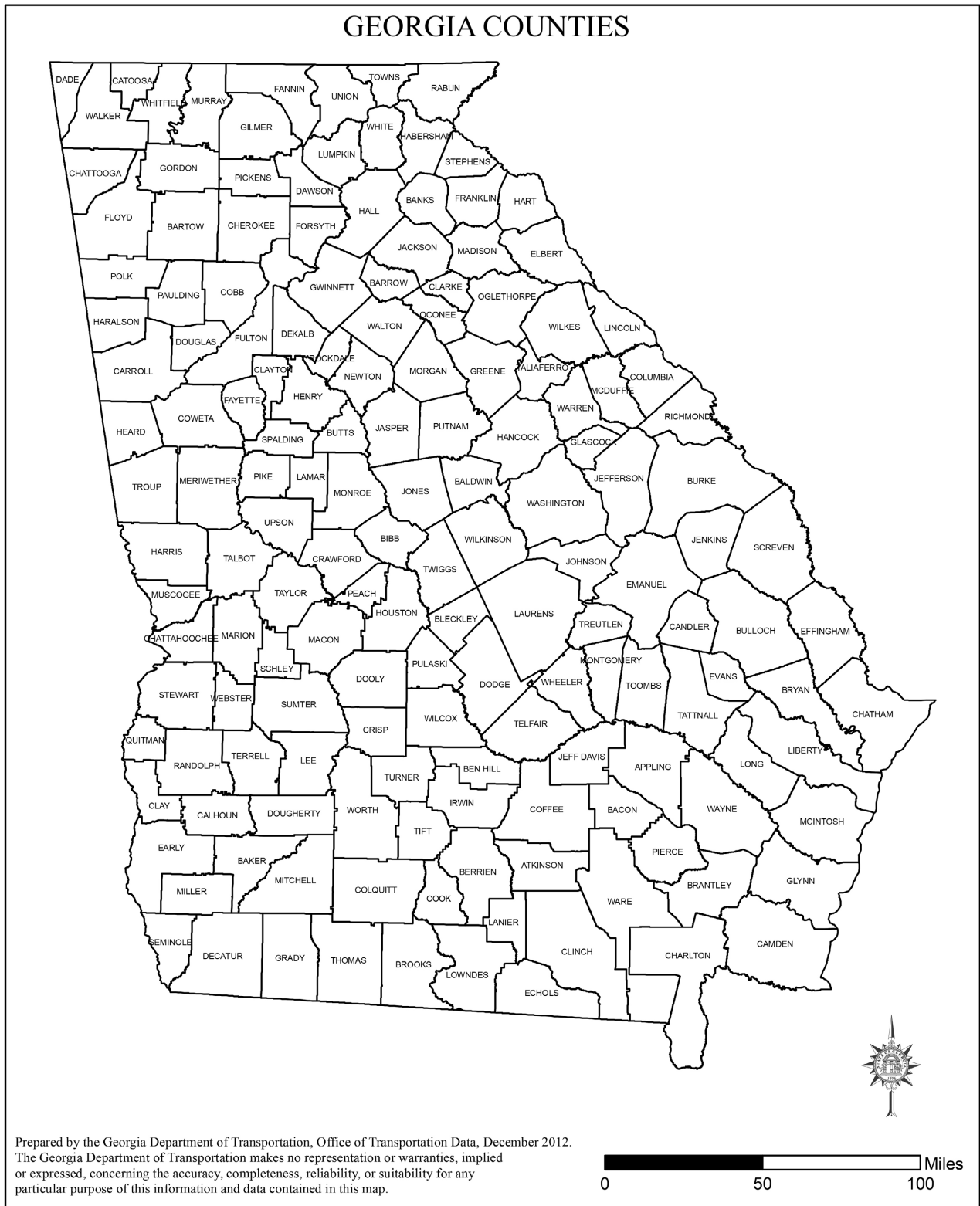
### 2.1. Study Area

The study area for this study comprises of all the counties across Georgia State, in the United States. Georgia is one of the states in the contiguous United States (**Figure 1**) where the occurrence and recurrence of COVID-19 disease have been reported on a large scale. It is considered as one of the fastest growing states in the United States in terms of population [15]. According to [15], Georgia's population increased by 18.3 percent when compared to a national population increase of 9.7 percent between 2000 to 2010. Indeed [16] [17] [18] examined the racial diversity in Georgia and identified the significant growth of "Black belt" counties within the state. This study includes all 159 counties in Georgia State where COVID-19 incidence and mortality were recorded for the study epoch from January 2020 to April 2023.

### 2.2. Data Collection and Preprocessing

Secondary data was the main data type used in this study. The dataset comprises variables of COVID-19 cases, vaccination count, population density, percentage of people with health insurance, and percentage of black people. The COVID-19 case count data was acquired from usafacts dashboard, and the vaccination records were retrieved from COVID-19 vaccination tracker dashboard in the United States. The socio-economic variables were acquired from Emory University COVID-19 Health Equity Interactive Dashboard.

In this study, we acquired COVID-19 disease case count and COVID-19 vaccination from January 2020 to April 2023 across the 159 counties in the state of Georgia. The choice of selecting the period of data collection was to capture the first, second and third waves of COVID-19 disease transmission. The timeframe will also encourage us to investigate how people responded to the disease transmission through vaccination coverage across the study area. Thus, our main goal is to examine the influence of the selected explanatory variables on COVID-19 occurrence and vaccination campaign across the 159 counties in the state of Georgia, United States. Hence, we subjected the data to consistency check and rigorous cleaning. Thereafter, the shapefile of counties in the state of Georgia were built into a geodatabase and spatial attributes were populated in ArcGIS 10.8 environment using counties as the spatial resolution.



**Figure 1.** Map of Georgia showing the counties. Source: Georgia department of transportation [19].

### 2.3. Statistical Models

According to the first law of Geography by Waldo Tobler, “everything is related

to everything else, but near things are more related than distant things” [20]. Due to the forgoing, adding a spatial context in the study of infectious diseases like COVID-19 is imperative. According to recent studies in the field of medical geography, one of the advantages of introducing spatial statistics in disease studies is the ability to check for spatial dependence both communicable and non-communicable diseases in the selected geographic area [1] [2] [6] [21]. In this study, we adopted both global and local regression methods to investigate and identify the spatial patterns of COVID-19 occurrence and vaccination rates. The study further explores the relationships that exist between COVID-19 and explanatory parameters using four different statistical models namely: Global Moran’s I, General G Statistics, Local Moran’s I and Local Geary C.

### 2.3.1. Global Moran’s I Index

Global Moran’s I developed by Patrick Alfred Pierce Moran in 1950 is used to detect the presence of spatial autocorrelation in geographical location as well as test for its significance. The value of the index ranges from  $-1$  to  $+1$ . To compute observed Moran’s I, a spatial matrix is usually used to check if any two counties are neighbors. Binary connectivity matrix is usually used in computing this index. Moran’s I is calculated using the formula below:

$$I = \left( n \sum \sum w_{ij} (x_i - \bar{x})(x_j - \bar{x}) \right) / \left( W \sum (x_i - \bar{x})^2 \right) \quad (1)$$

where  $n$  is the number of counties in Georgia (160),  $(x_i - \bar{x})$  is the deviation from the mean from county  $i$ ,  $w_{ij}$  is the binary connectivity value which is 0 if county  $i$  and county  $j$  are not neighbors but is equal to 1 when county  $i$  and county  $j$  are neighbors,  $(x_j - \bar{x})$  is the deviation from county  $j$ ,  $\bar{x}$  is the average caserate in Georgia,  $(x_i - \bar{x})^2$  is the square of the deviation of each county’s caserate from the mean caserate and  $W$  is either the row sum or column sum of the binary connectivity matrix. The value gotten by the computation of the formula above either positive or negative does not tell the complete story until it is compared with the value of the expected Moran’s I which can be computed with the equation below with  $n$  representing the number of counties in Georgia:

$$E(I) = -1/(n-1) \quad (2)$$

If  $I$  is greater than  $E(I)$ , there is an indication of clustering, if  $I$  is less than  $E(I)$ , there is an indication of dispersion and if  $I$  equals  $E(I)$ , then the observed pattern is random.

### 2.3.2. General G Statistic

The General G Statistic is a statistical model that investigates the degree of clustering that exists among spatial variables. Comparatively, Moran’s I can assess and identify the degree of correlation in the entire areal unit as a single index, and it is unable to tell if there is spatial dependence in counties are due to similarities in high values or low values. As a result of this, the General G Statistic is employed to assess the level of clustering or dispersion across counties in Georgia. The General G statistic is considered as a global statistic of measuring spatial

autocorrelation, thus further explores hot spots or cold spots in the geographic space of study. It can be computed using the formula below:

$$G(d) = \left( \sum w_{ij}(d) x_i x_j \right) / \left( \sum x_i x_j \right) \quad (3)$$

where  $x_i$  and  $x_j$  are two counties in Georgia and  $w_{ij}$  is the weight matrix using an arbitrary distance ( $d$ ). Any two counties within less than or equal to  $d$  are neighbors and as such  $w_{ij}$  is equal to 1. If the distance between the two counties is greater than  $d$ , then that means they are not neighbors and as such,  $w_{ij}$  equals 0.  $G$  statistic is also compared with expected  $G$  statistic to ascertain if there is prevalence of hot spots or cold spots. If  $G(d) > E(G)$ , there is an indication of hot spots but if  $G(d) < E(G)$ , then there is an indication of cold spots. The formula for computing the value of expected  $G$  statistic is given below:

$$E(G) = W / (n(n-1)) \quad (4)$$

$W$  is the row sum or column sum of the binary matrix of distance ( $d$ ) and  $n$  is the number of counties in Georgia.

$$c_i = \sum w_{ij} (z_i - z_j)^2 \quad (5)$$

### 2.3.3. Spatial Lag Model

According to (6), COVID-19 is a spatial disease, whose occurrence varies across space and time. In this study, we employed both Spatial Lag Model (SLM) and Spatial Error Model (SEM) in this study. SLM assumes dependency between the dependent variables and incorporates spatial dependence into the regression model with spatially lagged dependent variable (1, 6). Spatial lag model is presented below:

$$y_i = \beta_0 + x_i \beta + \rho W_i y_i + \varepsilon_i \quad (6)$$

where,

$y_i$  is the dependent variable,  $\rho$  is the spatial autoregressive variable,  $W_i$  is the vector of spatial weight matrix capturing spatial patterns among observations and  $x_i$  is the matrix of explanatory variables.

### 2.3.4. Spatial Error Model

According to [1] [22] expressed Spatial Error Model (SEM) as:

$$y_i = \rho W_i y_i + x_i \beta + \varepsilon_i \quad (7)$$

where the variables are the same as in the SLM above but  $\rho W y$  captures the spatial dependence in the error term.

Six selected regressors (vaccination, black, Hispanic, percentage uninsured, population density and poverty) were included in the models to measure the variations in COVID-19 case rate in the state of Georgia. Both models were analyzed using GeoDa 1.18 software.

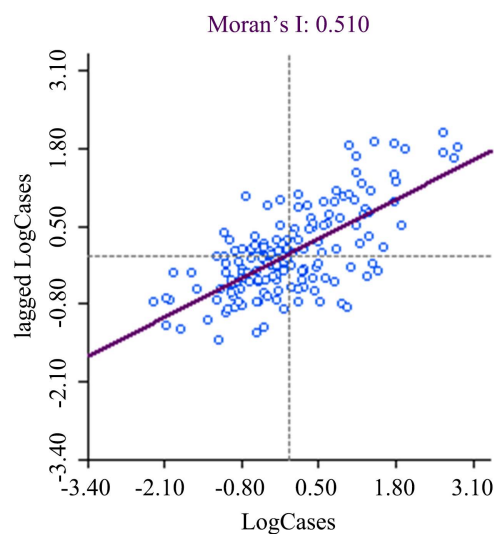
### 2.3.5. Analytical Procedure

To investigate the spatial pattern and spatial dependence characteristics of COVID-19 disease, A Univariate Global Moran's  $I$  was performed using GEODA

1.18 software to test the significance of the statistic. Moran's I index and General G statistics were further explored to diagnose the spatial characteristics. An exploratory spatial analytical procedure was performed to identify and incorporate the actual predictor that explains COVID-19 occurrence across counties in Georgia from January 2020 to April 2023. In this study, COVID-19 case rate was included in the model as the dependent variable while the stepwise regression analysis identified six selected variables as the explanatory variables that were included in the model. A combination of forward selection and backward elimination were employed to identify the most important variables, significantly contributing to the models. These variables are vaccination, % black, % Hispanic, % uninsured, population density and % poverty. In addition, to further evaluate the relationships between selected explanatory variables and the dependent variable, we adopted spatial autoregressive models, SLM and SEM. The evaluation of the models was investigated by comparing the adjusted  $R^2$ , Akaike Information Criterion (AIC), and the spatial characteristics of the coefficients of determination across the study area. A GIS-based hot- and cold-spot investigation was conducted to visually identify the disease's epicenters on the county map for the study periods.

### 3. Results and Discussion

The study explains the spatial distribution of COVID-19 occurrence and vaccination records across the 159 counties in the state of Georgia from three years and four months, capturing 1<sup>st</sup>, 2<sup>nd</sup> and 3<sup>rd</sup> epidemiological waves of the disease across the study area. There are over 235,000 COVID-19 cases and over 733,000 vaccinations across the 159 counties in the state of Georgia during the period of study. As shown in **Figure 2** below, the Global Moran's index for COVID-19 case rate during the study period is 0.510 which shows spatial clustering and is highly significant with a p-value of 0.02217.

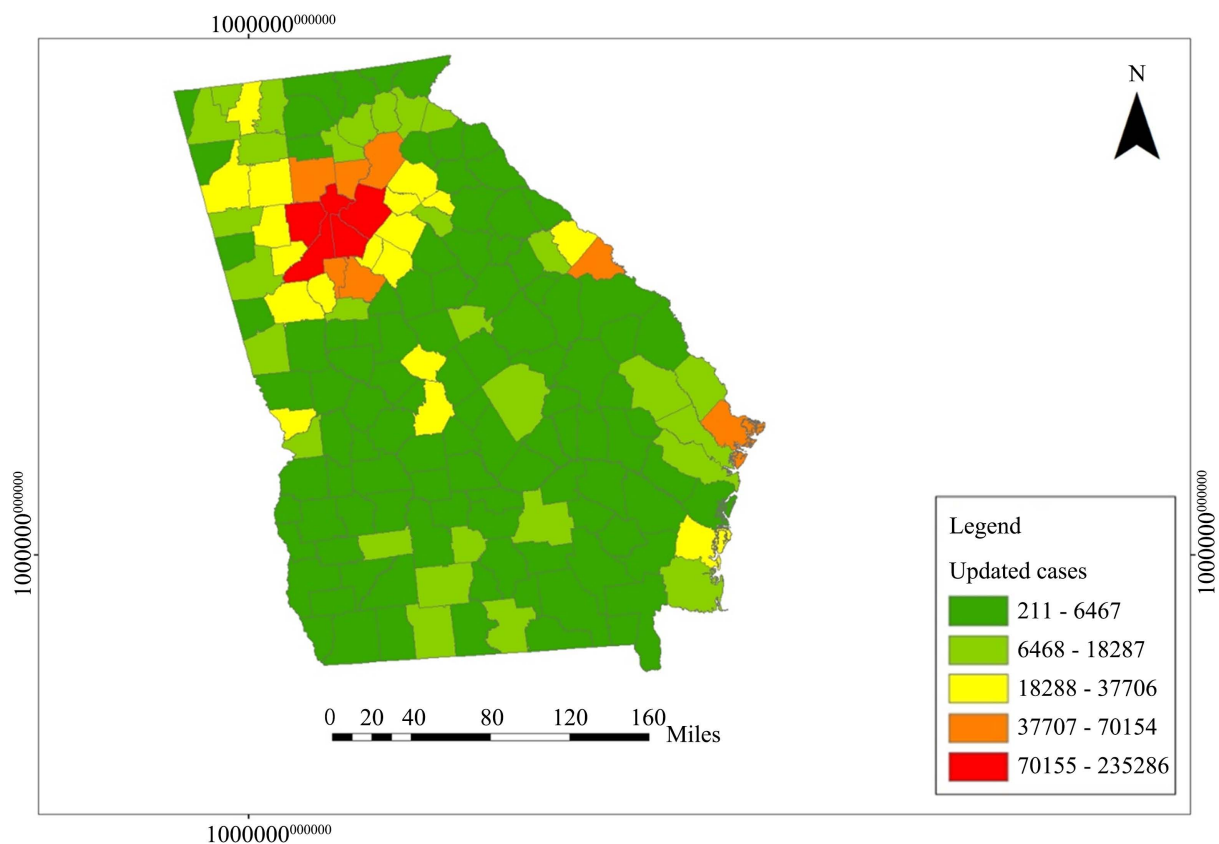


**Figure 2.** Graph showing global Moran's index.



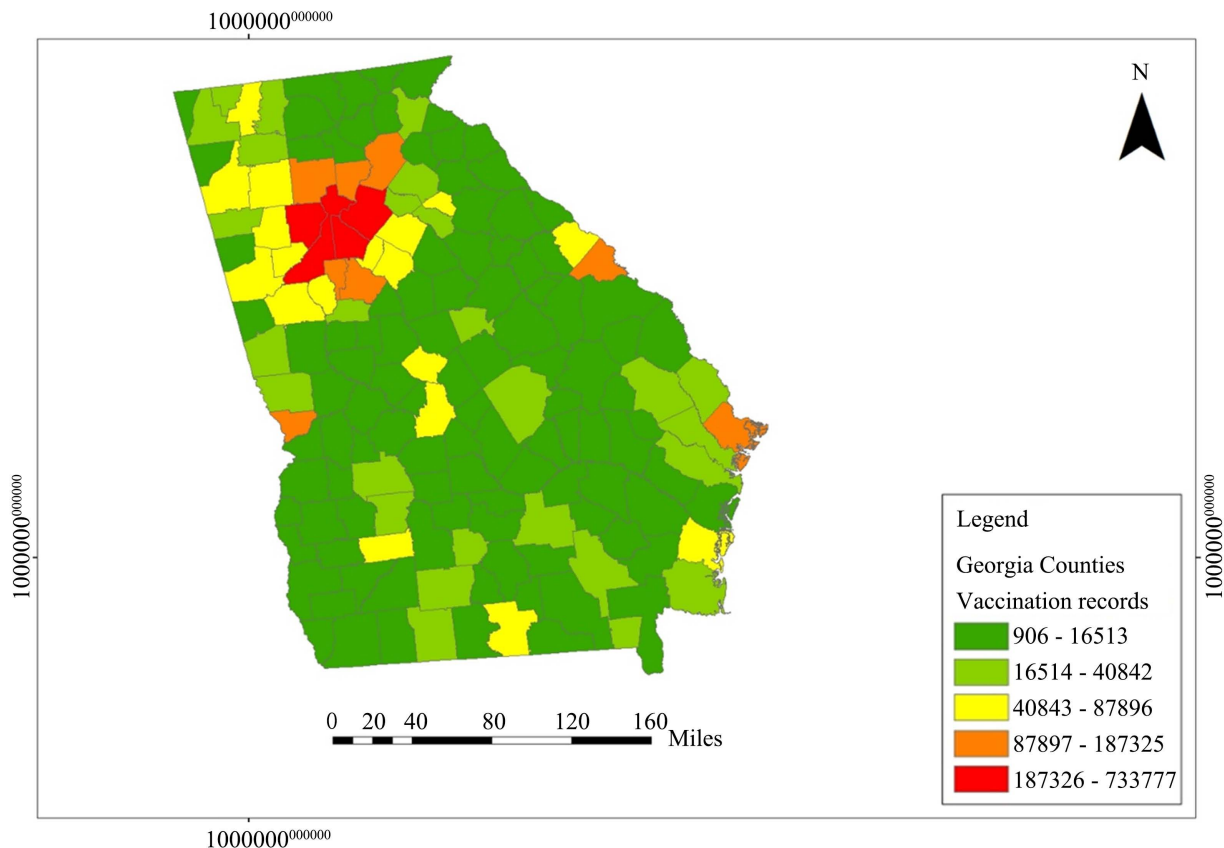
It can be inferred from **Figure 3** that the prevalence of confirmed COVID-19 cases across the counties ranges from 211 to 235,286 from January 2020 to April 2023. It also shows that the most confirmed cases were clustered around the Northwestern counties of the state. The top four counties with the highest reported cases are Fulton, Cobb, DeKalb and Gwinnett with case rate ranging from 70,155 to 235,286. Counties like Cherokee, Forsyth, Hall, Clayton and Henry surrounding the top four counties were also characterized with high case rates when compared to other counties. The prevalence of COVID-19 cases reduces as we move away from the top four counties which is an indication of positive spatial autocorrelation.

**Figure 4** shows a GIS-based map indicating the spatial distribution of vaccination records across counties in Georgia between January 2002 and April 2023. The same pattern described for COVID-19 cases in **Figure 3** is also observable for vaccination cases across the counties in the state of Georgia as shown in **Figure 4**. In this study, we consider the number of people with at least one vaccination across the counties, Fulton, Cobb, DeKalb, and Gwinnett counties had high vaccination records. This observed pattern in vaccination records justifies the high occurrence of COVID-19 in such counties which means that residents protect themselves by their willingness to take vaccines. The vaccination rate also tends to decrease spatially towards the southern part of the state.



**Figure 3.** Spatial distribution of COVID-19 cases.



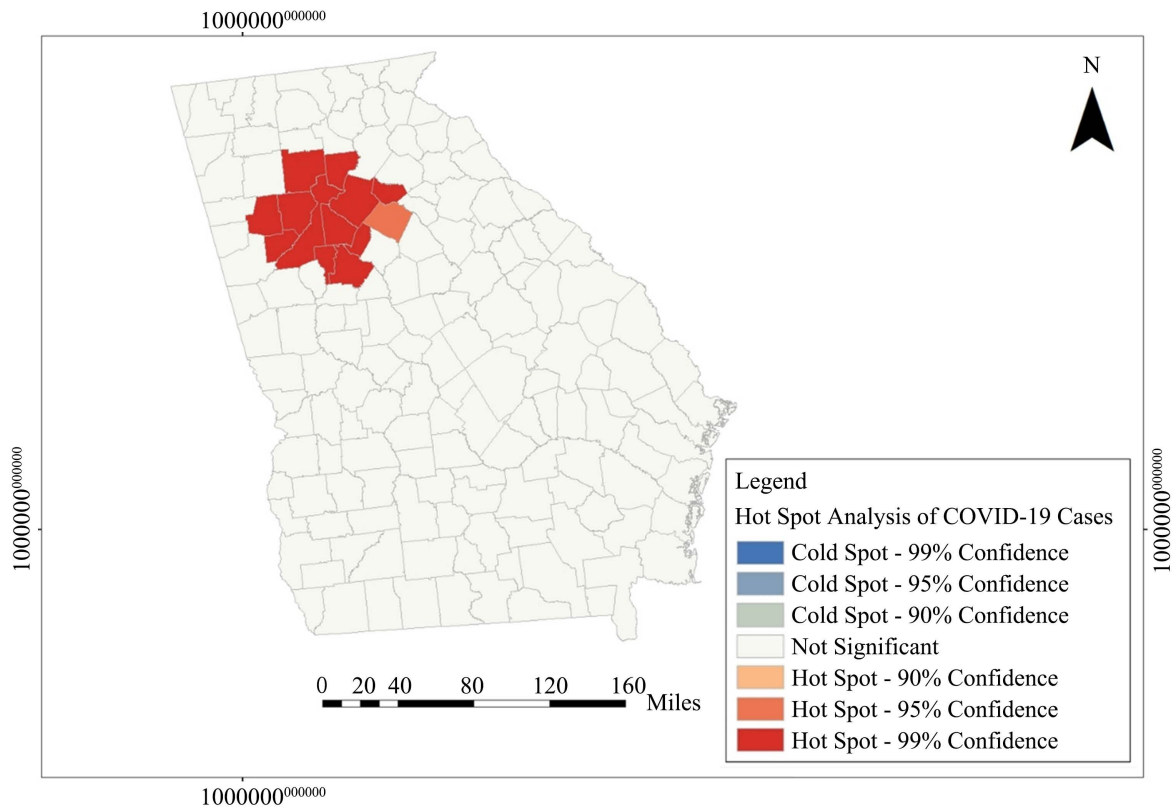


**Figure 4.** Spatial distribution of COVID-19 vaccinations.

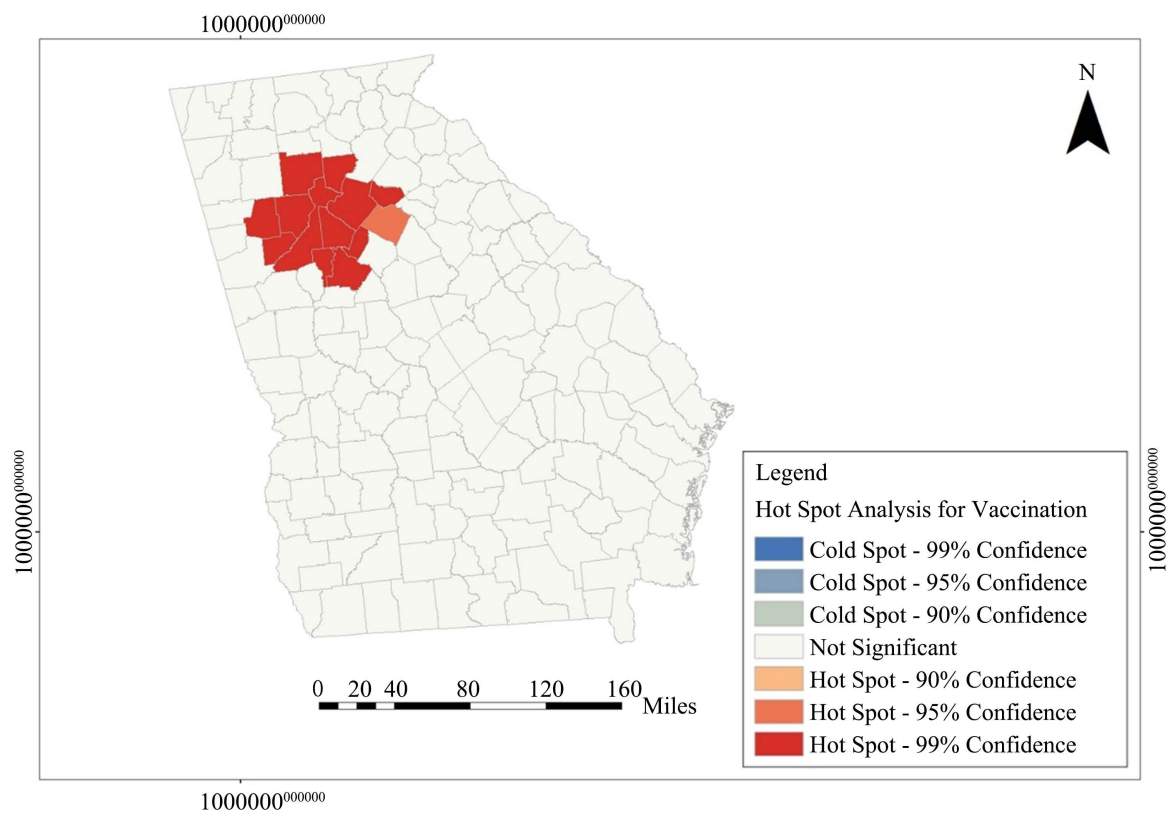
### 3.1. Hot Spot Analysis for COVID-19 Cases for COVID-19 Cases and Vaccination

In cluster studies, hot spot analysis is frequently employed to visualize the regions of statistically significant clusters of high and low occurrence of spatial events. According to [6], the hot spot analysis delineates three zones within the occurrence of an event namely: the hot spot, cold spot, and not significant. In this study, we employ Getis-Ord Hot Spot algorithm in ArcGIS 10.8 to categorize the 159 counties in Georgia into clusters of significantly high, low, and not-significant occurrences of COVID-19 occurrence and vaccination records (**Figure 5**). For the study period, Getis-Ord show similar results for both COVID-19 cases and vaccinations across the 159 counties in the state of Georgia. Indeed, majority of the hot spots are in the northern part of the state with high level of significance ( $p < 0.05$ ) as seen in **Figure 5** and **Figure 6**. A total of twelve counties are within the hot spot significant areas at 95% and one county (Walton) is significant at 90% for both COVID-19 occurrence and vaccination records between January 2020 to April 2023.

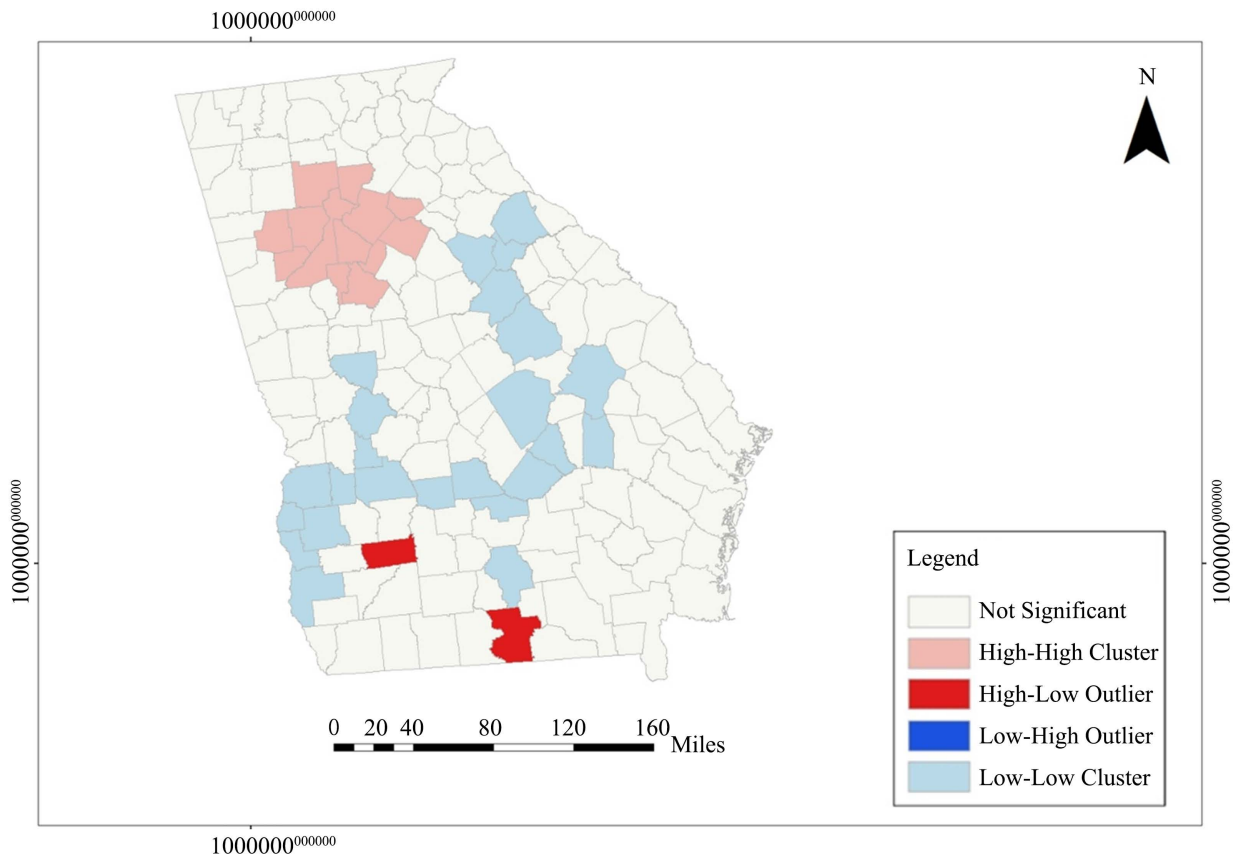
The result of the global clustering for both COVID-19 occurrence and vaccination records were further investigated with a local clustering techniques, with the goal of revealing the local interactions that exists among counties using Cluster and Outlier algorithm. **Figure 7** shows that High-High clustering were



**Figure 5.** Hot spot analysis for COVID-19 cases for counties in the state of Georgia.



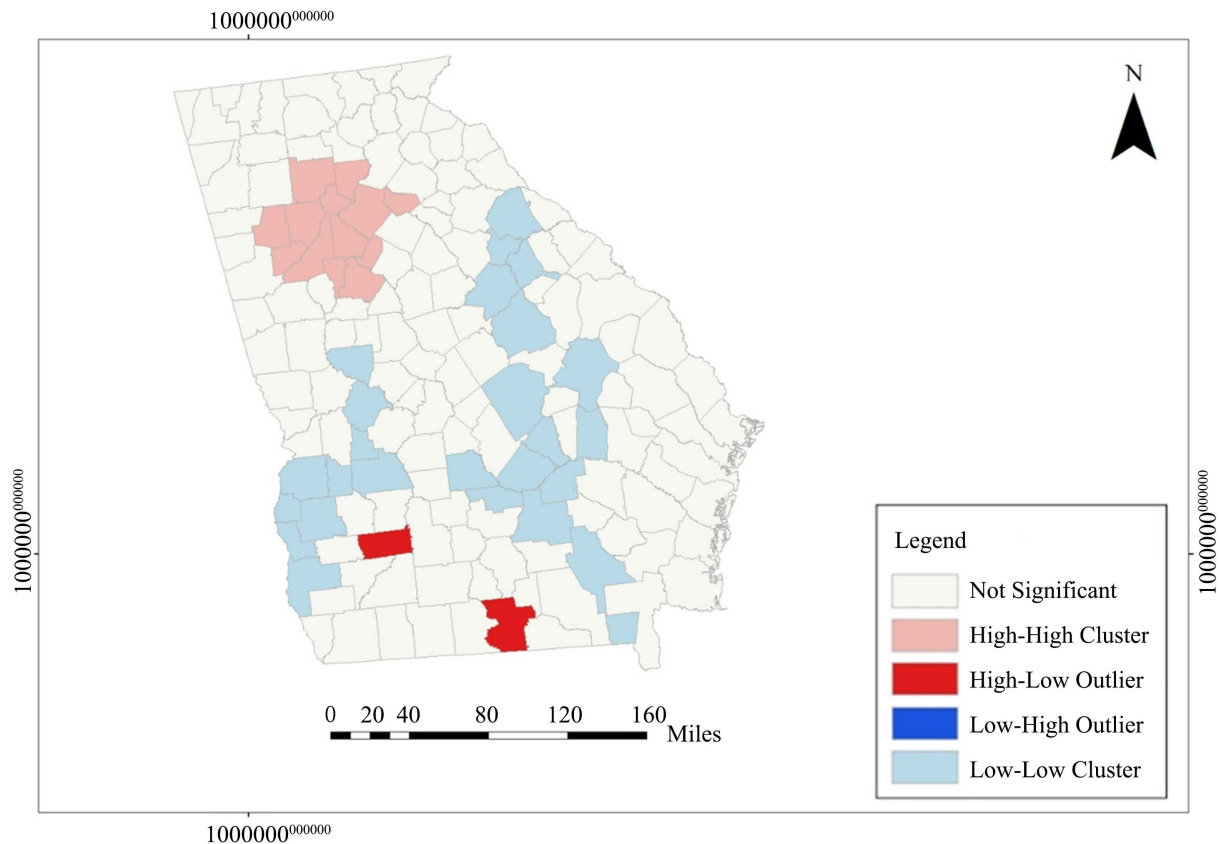
**Figure 6.** Hot spot analysis for COVID-19 Vaccinations for counties in the state of Georgia.



**Figure 7.** Cluster and outlier analysis for COVID-19 cases.

observable in the Northwestern part of the state while there are Low-Low clusters across the other part of the counties. This is indicative of counties with high case rate being close to other counties with high cases and vice versa. Only Dougherty and Lowndes counties have high COVID-19 cases but are surrounded by counties with low COVID-19 cases. The concept of spatial diffusion of diseases by [23] supports these findings by relating this type of diffusion as hierarchical diffusion. Study by [24] also found that disease-causing organisms are transferred across geographic space during migration.

As of April 30, 2023, we also found out that the local clustering investigation as revealed by cluster and outlier algorithm shows that COVID-19 cases and vaccination records indeed revealed the same pattern (**Figure 7** and **Figure 8**). A total of twelve counties showed high-high relationships across counties for both COVID-19 cases and vaccination. This implies that 12 counties; Paulding, Cobb, Fulton, Douglas, Cherokee, Forsyth, Dekalb, Clayton, Henry, Rockdale, Walton, and Barrow with high COVID-19 vaccination are neighboring each other, and they are significant. The implication of this is that they have similar vaccination pattern. Twenty-four (24) counties with low vaccinations are neighboring counties with low vaccinations (Low-Low cluster) and two counties (Dougherty and Lowndes) with high vaccinations are neighbors of counties with low vaccinations rate (dissimilar or High-Low outlier).



**Figure 8.** Cluster and outlier analysis for COVID-19 vaccinations.

### 3.2. Relationship between COVID-19 Cases, Vaccination Records and the Selected Explanatory Variables

The first ESDA and stepwise regression analysis captured six (6) explanatory variables that were included in the models. Hence, we construct our spatial regression models on six explanatory variables, viz: % Black, % Hispanic, population density, % without health insurance, % poverty and vaccination. **Table 1** comparatively presents the results of SLM and SEM of the examined explanatory variables influencing COVID-19 occurrence in the state of Georgia between January 2020 and April 30, 2023. The results from both models SLM and SEM were consistent with R-squared of 65.6% and 67.8%, respectively. The Akaike information Criterion for SEM is smallest (387.682) compared to the SLM (396.382) and as such is the best model to be adopted for this study. SEM shows that the selected variables account for 67.8% change in COVID-19 case rate. Hispanic, population density, percentage of people uninsured and poverty are all statistically significant. Hispanic have a positive relationship with COVID-19. According to [6], in their study to determine socio-economic predictors responsible for COVID-19 mortality in contiguous USA, they found significant relationship between vulnerable populations and COVID-19 mortality. The same relationship was also observed for poverty which is consistent with our findings. When compared to black, for every Hispanic person, the percentage of cases increases.

**Table 1.** Spatial lag and spatial error model of the determinants of COVID-19 cases in the state of Georgia.

Variable	Coefficient		Standard error		Probability	
	SLM	SEM	SLM	SEM	SLM	SEM
CONSTANT	2.19296	0.0419724	2.78282	2.6446	0.43068	0.98734
BLACK	-0.00577089	-0.00760174	0.00543301	0.00502147	0.28815	0.13006
HISPANIC	0.0590393	0.0619819	0.0148703	0.0142549	0.00007***	0.00001***
POPDEN	0.00190637	0.0019823	0.000381477	0.000364716	0.00000***	0.00000***
PCTIC	0.0816211	0.105221	0.0313943	0.0301659	0.00933***	0.00049***
VACCINATION	-1.89255e-07	-2.54081e-07	1.52666e-06	1.47026e-06	0.90134	0.86280
POVERTY	-0.0460838	-0.0419865	0.0150615	0.0139501	0.00222***	0.00261***
R-squared	0.655944	0.677887				
AIC	396.382	387.682				
Breusch-Pagan test	7.9819	9.8091				
Moran's I		0.510				0.02217***

Note: \*\*\*  $p < 0.01$ . POPDEN = Population Density, PCTIC = Percentage uninsured, AIC = Akaike Information Criterion.

The same also applies to population density. If population density increases by one unity, the percentage of COVID-19 case rate increases by 0.1 percent. The percentage of persons without insurance also has a positive relationship with case rate. It is also evident that administration of vaccinations leads to reduction in COVID-19 cases which implies that across space in the state of Georgia, having residents take COVID-19 vaccines was effective in decreasing case rate. The implication of this result is that social determinants of health are key factors in explain the spatial patterns of COVID-19 cases and vaccination is important to reduce vulnerability of individuals to COVID-19 diseases.

In this GIS-based evaluation study, we seek to analyze the influence of socio-demographic and vaccination records on COVID-19 occurrence across counties in the state of Georgia. To achieve this study, we adopted global and local clustering algorithm to investigate COVID-19 cases and vaccination records. In addition, we captured six major explanatory variables through ESDA and included them in the spatial autoregressive model. Our results affirm that the COVID-19 cases and vaccination records vary across space over the study period. The Moran's I index of 0.510 which implies moderate clustering of COVID-19 infections across the 159 counties in Georgia, United states. We further observed that both COVID-19 cases and vaccination are more pronounced across counties located in the northwestern part of the state of Georgia. In addition, this pattern reveals evidence of spatial regime for both COVID-19 cases and vaccination records.

#### 4. Conclusion

In this study, we introduced both global and local clustering algorithms to evaluate the clustering patterns and further explain the relationships that exist be-

tween COVID-19 cases and socio-demographic variables that explain its distributions. The observed spatial pattern shows that the distribution of COVID-19 cases and vaccination records varies spatially across counties in the study area. The northwestern counties of the study area are considered epicenters of COVID-19 cases and vaccination which spreads across 12 counties. The results of the clustering analyses affirmed the effectiveness of the local clustering algorithm over global clustering and provided better means of explaining COVID-19 and vaccination patterns in the study area. The result of the spatial regression analysis indicates that SEM performed better than SLM model while vaccination reduced the COVID-19 case rate in the state of Georgia. Race, population density, poverty, vaccination, and uninsured rate are very important for understanding the spatial variation in COVID-19 cases in the state of Georgia. While researchers are still employing spatial analytical techniques to understand the pattern of COVID-19 case rate and understand the socio/economic and demographic predictors responsible for its prevalence. We believe that in the future, researchers could consider exploring the prevalence of COVID-19 case rate across geographic locations (rural versus urban) and to identify their peculiar predictors driving its prevalence. This will give an even finer understanding of the spatial pattern of COVID-19.

### Conflicts of Interest

The authors declare no conflicts of interest regarding the publication of this paper.

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