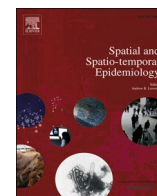




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Using trajectory modeling of spatio-temporal trends to illustrate disparities in COVID-19 death in flint and Genesee County, Michigan

Richard Casey Sadler^{a,*}, Thomas W. Wojciechowski^b, Zachary Buchalski^c, Alan Harris^d, Danielle Lederer^e, Matt Peters^f, Pamela Hackert^g, C. Debra Furr-Holden^h

^a Associate Professor, Michigan State University, Flint, MI, USA

^b Assistant Professor, Michigan State University, East Lansing, MI, USA

^c Data Analyst, Michigan State University, Flint, MI, USA

^d GIS Analyst, Michigan State University, Flint, MI, USA

^e Chief Epidemiologist, Genesee County Health Department, Flint, MI, USA

^f Epidemiologist, Genesee County Health Department, Flint, MI, USA

^g Medical Health Officer, Genesee County Health Department, Flint, MI, USA

^h C.S. Mott Endowed Professor of Public Health, Michigan State University, Flint, MI, USA

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ABSTRACT

COVID-19's rapid onset left many public health entities scrambling. But establishing community-academic partnerships to digest data and create advocacy steps offers an opportunity to link research to action. Here we document disparities in COVID-19 death uncovered during a collaboration between a health department and university research center. We geocoded COVID-19 deaths in Genesee County, Michigan, to model clusters during two waves in spring and fall 2020. We then aggregated these deaths to census block groups, where group-based trajectory modeling identified latent patterns of change and continuity. Linking with socioeconomic data, we identified the most affected communities. We discovered a geographic and racial gap in COVID-19 deaths during the first wave, largely eliminated during the second. Our partnership generated added and immediate value for community partners, including around prevention, testing, treatment, and vaccination. Our identification of the aforementioned racial disparity helped our community nearly eliminate disparities during the second wave.

1. Introduction

Early findings were essential for providing a baseline understanding of socio-ecological risk for COVID-19 death, including neighborhood sociodemographic characteristics. Berenguer et al. (2020) established higher mortality rates among older patients and patients with chronic diseases, with mortality rates defined here as the rate of death due to COVID-19 by those infected. Kim and Bostwick (2020) discovered a high degree of spatial autocorrelation between percent African-American and COVID-19 death rates in Chicago and remarked on how these disparate effects were due to the inherent racial inequality in American society. Andersen et al. (2021) likewise uncovered urban and Black populations as significant predictors of cases and deaths, while (Shim et al., 2020) found that communities with affected hospitals had higher COVID-19 death rates (due, in part, to secondary transmission of the disease to

healthcare workers). Political polarization, meanwhile, has hindered prevention efforts around SARS-CoV-2 transmission in the United States, as many communities have been manipulated into downplaying the severity of the pandemic (Makridis and Rothwell, 2020).

Ample work has already been conducted on the use of spatial tools to model geographic clusters of COVID-19 deaths. Desjardins et al. (2020) were amongst the first to use space-time statistics to monitor the COVID-19 pandemic; they confirmed Detroit and southeast Michigan as one of the earliest hot spots. Urban and Nakada (2020) used various spatial analysis tools to pinpoint clusters in COVID-19 deaths, using their results to remark on the challenges of social distancing in areas marked by socioeconomic vulnerability.

As these findings highlight, spatial tools are essential for understanding determinants of COVID-19 death, especially as more and more findings reveal signature racial and socioeconomic disparities. Even so,

* Corresponding author at: 200 E 1st St Room 337, Flint, MI, 48502 USA.

E-mail address: sadlerr@msu.edu (R.C. Sadler).

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Andersen et al. (2021) recommended more local-level analysis of determinants. Here we take up their recommendation and build on past work on COVID-19 death disparities, exploring racial and sociodemographic correlates of COVID-19 deaths in Flint and Genesee County, Michigan.

Our study sought to identify factors that drove clustering and racial disparities in COVID-19 deaths during different points in the first year of the pandemic in Genesee County, Michigan. Genesee County is the home of Flint, which experienced a water crisis beginning in 2014 as a result of a state-directed infrastructure change that led to a widespread increase of lead in the municipal water system, as well as Legionella contamination (Zahran et al., 2018; Manson et al., 2017; Hanna-Attisha et al., 2016). This environmental injustice on top of years of disinvestment and discrimination has created considerable health disparities (Sadler and Highsmith, 2016), resulting in this area becoming increasingly of interest to public health research. Some conditions for which Flint has disparate health outcomes include blood lead levels, trauma mortality, mental health, food insecurity, and asthma (Hanna-Attisha et al., 2016; Mikhail et al., 2016; Bergmans et al., 2019; Lewis and Sadler, 2021), to name a few. At the outset of the COVID-19 pandemic, Flint and neighboring Detroit represented two of the hardest-hit regions outside of New York City; ongoing water quality concerns have only exacerbated public health concerns (Hyde, 2020). Our analyses therefore sought to identify groupings of communities in Genesee County that demonstrated similar patterns of COVID-19 death risk during the first two waves of the pandemic. We then worked to identify community-level predictors that produced variance in community COVID-19 death risk during these time periods. The potential for racial disparities in community-level deaths were examined while also accounting for variance in gender composition, age composition, and community economic distress; all of which have been shown to potentially demonstrate disparities in COVID-19 outcomes (Ahmed et al., 2020; Gausman and Langer, 2020; Mena et al., 2021). Total number of residents in each census block group (CBG) was also controlled for, as more populous CBGs may have had increased risk for reporting a COVID-19 death simply by virtue of having more residents who may have experienced this outcome.

2. Methods

2.1. Data

Data for this study were provided by the Genesee County Health Department (GCHD) and approved for use by Michigan State University's IRB (STUDY00006123). Deaths stemming from positive COVID-19 diagnoses—based on detecting SARS-CoV-2 RNA in a clinical or autopsy specimen using a molecular amplification test (de Vries et al., 2021; Williamson et al., 2021)—were compiled by the health department and identified by the day the case was diagnosed. A total of 657 COVID-19 deaths were identified in the study period in Genesee County. Our team then geocoded 100% of these deaths to the residential address for initial spatial analyses. CBGs ranged from 0 to 11 COVID-19 deaths within a given testing interval. Data from 3/1/20–1/16/21 were utilized in the analyses. These data were split into two waves (described in Measures section in greater detail). These points were also aggregated to the CBG level (373 areas) for trajectory modeling. CBG aggregation provided the highest resolution for identifying more subtle trends while providing the largest N, linkage of data to census demographic information, and still ensured confidentiality and anonymity. All other data were taken from estimates from the American Community Survey (Manson et al., 2017) or computed from data provided by the GCHD.

All analyses were split into two waves for several reasons. First, the data available to the research team spanned 25 total data points, and nuance was lost when conducting full analyses because of a lull in deaths and cases during summer 2020. Second, and relatedly, COVID-19 testing scope increased a great deal between waves, with three additional testing sites added to Genesee County during this time. Further,

endeavors to improve testing broadly have been undertaken in this time (Eberhardt et al., 2020; Rice et al., 2021). While this is likely to have a greater effect on case counts, identification of cases and linking them to deaths specifically certainly could impact the capacity to attribute deaths to COVID-19 accurately. Finally, we also assessed deaths separately by each wave, as this facilitated determination of whether any identified disparities changed as our understanding of COVID-19 improved and new policy and programming endeavors were undertaken. Decisions like these to delineate data based on testing differences have also been observed in prior work, with research on the HIV pandemic being one prominent example (Johnson et al., 2017).

2.2. Measures

Our dependent variable examined in analyses was a binary variable providing an indication of whether or not a given CBG reported a COVID-19 death during each specified two-week testing intervals. COVID-19 mortality data were tracked beginning 3/1/20 and ending 1/16/21, resulting in a total of 23 testing intervals. Binary variables were used for each two-week testing period which delineated CBGs reporting having a COVID-19 death during that testing period from those who reported no such deaths (0=No; 1=Yes). Given our focus on Black racial disparities in COVID-19 deaths during each case wave, our independent variable was the racial composition of each CBG. This variable provided a proportion of Black residents living in each CBG. We included several additional control variables in analyses to control for potential confounding, including gender, proportion of seniors, and economic distress. Gender composition was a proportion of male residents in each census block group, and was calculated by dividing the number of male residents by the total number of residents living in each CBG. Proportion of senior residents was calculated by dividing the number of residents aged 65 years and older by the total number of residents in each CBG. Economic distress was calculated in an index, and was comprised of a non-weighted sum of z-scores of four census block group-level variables including: percent of households living below the poverty line, unemployed, less than HS education, and single parent households. We also controlled for the total number of residents living in each CBG. We controlled for population to ensure deaths would account for differences in risk based on more or less populated CBGs. The COVID-19 death data were provided by the GCHD and every other variable in the study were taken from the 2019 American Community Survey data.

2.3. Analytic strategy

2.3.1. Group-Based trajectory modeling

Our analytic strategy included several phases. In a preliminary assessment of our COVID-19 death data, we used relative risks (RRs, calculated as the absolute risk among Black residents divided by the absolute risk in all other groups) to identify racial disparities over time in Flint and Genesee County (Schmidt and Kohmann, 2008; Simon, 2001). Our first formal phase utilized group-based trajectory modeling (GBTM) to identify patterns of change and continuity in COVID-19 deaths within each two-week testing interval (Nagin, 2005) ($N = 373$ for each two-week testing interval). This modeling involves the iterative process of fixing of polynomial functions of varying complexity and number to a set of longitudinal outcome data until a set of trajectory groups is identified as providing the best model fit to the data. Polynomial complexity could be any of the following growth patterns for each group: intercept-only, linear, quadratic, or cubic. The method assumes that a set of longitudinal response data is comprised of a mixture of a finite number of groups with census block groups assigned membership to a given group. Group membership is designated based upon maximum likelihood estimation and construction of a likelihood function. Calculation of this likelihood function is critical, as this facilitates identification of the optimum number of groups and their complexity and also how census block groups are assorted across those groups in a

manner that best fits the data. The combinations of individual trajectories are summarized as trajectory groups indexed by j for a given model. The likelihood function is written as a mixture of J conditional likelihoods $P^j(Y^i)$, where $P^j(Y^i)$ is the probability of observing the longitudinal sequence in area i . These conditional likelihoods are defined by the Bernoulli distribution with success probabilities modeled as a polynomial function of degree k . The random selection of a census block group is then denoted by π_j in order to form the unconditional probability of the data: $P(Y_i) = \sum_j \pi_j P^j(Y_i)$. For a given set of j , conditional independence is assumed for the sequential measurements of Y_i across a set of longitudinal responses. This assumption of independence in prior measurements greatly reduces model complexity and provides tractability for modeling, though there remain concerns over how justifiable this assumption is. Nagin (2010) provides additional details on this aspect of model estimation. Nested model fit is ascertained through examination of Bayesian Information Criterion (BIC) statistics (testing of k vs. $k + 1$ groups in a model based on how well the indexing of census block groups into trajectory groups fits to the data overall). BIC is calculated as $BIC = k \ln(n) - 2 \ln(L)$ where L is equal to the maximized value of the likelihood function calculated in the first equation, k is equal to the number of parameters in the model, and n is the sample size. Units of analysis are assigned probabilities of membership to each group in the model and then actually assigned membership to a given trajectory group based on which group they had the highest probability of assignment to. These probabilities are based on each unit's response trajectory across time. In addition to BIC, Nagin (2005) also identified several additional fit criteria that a model should meet to be selected as the best fitting. These include: posterior probabilities of assignment exceeding 0.7 for all groups, average odds of correct classification exceeding 5 for all groups, and 95% confidence intervals that are relatively tightly bound around each identified trajectory group. Two models corresponding to the first and second waves of COVID-19 case surges/deaths are estimated in the analyses.¹ The binary dependent variable of COVID-19 mortality for each CBG during each two-week testing interval were used to identify similarities in patterns among CBG and sort them into trajectory groups in each model. The outcome variables actually assessed in regression analyses are then based on the assignment of CBGs into trajectory groups and looking at how the independent variables impact assignment of CBGs into the COVID-19 mortality trajectory groups.

The first set of GBTM analyses examined the range of COVID-19 death data beginning 3/1/20 and ending 6/20/20. These time points were chosen because testing data first became available on 3/1/20, and because the testing period ending at 6/20/20 represented the lowest case counts observed in these data. At that time, 90% of CBGs reported zero cases. The second set of GBTM analyses examined the time ranging from 8/16/20–1/17/21. The date of 8/16/20 was chosen as a starting point because this was a low point in the summer lull that also began the second wave, where around 70% of CBGs reported zero cases. This percentage of CBGs with zero cases decreased considerably to around 40% at the next testing interval and continued this steady decline through the peak of the second wave. Data tracking for the second wave was terminated on 1/17/21 because case count data saturation was reached at this point, as adding more testing interval data points from the near future beyond this testing interval did not meaningfully alter findings.

¹ The two waves are visually identifiable when examining death count and case count data for both Michigan as a whole and for Genesee County (State of Michigan, 2021). The data explorer tool available through the previous citation allows for identification of trend in deaths across time which clearly indicate a bimodal distribution that provides impetus for the analytic approach chosen wherein individual waves are analyzed.

Table 1

Logistic Regression Model of Covariate Effects on Odds of Assignment to the H1 COVID-19 Death Trajectory Group Relative to Assignment to the L1 Trajectory Group in Odds Ratios (OR) ($N = 373$).

	OR	p-Values	95% Confidence Interval	
Proportion of Black Residents	3.881	.004	1.537	9.797
Proportion of Male Residents	.007	.001	<0.001	.305
Distress Index	1.028	.560	.936	1.130
Proportion of Residents Aged 65 Years or Older	36.365	.026	1.524	867.602
Total Number of Residents	1.001	<0.001	1.000	1.001
Constant	.533	.556	.066	4.331

2.3.2. Logistic regression

The second phase of analyses entailed the use of multivariate regression to understand how the race composition of CBGs influenced odds of assignment to trajectory groups. While the GBTM method is a somewhat inductive process of model identification that may theoretically result in any given number of groups, these analyses indicated that two-group models best fit the data for both the first and second waves. As such, logistic regression was chosen as the modeling choice because binary outcome variables could easily be computed from these trajectory model group assignments. This facilitated more accurate estimation of effects given the departure from normality that binary outcomes entail. This is then calculated as $Y^i \sim \text{Bernoulli}(\mu^i)$ with $\text{logit}(\mu^i) = \beta_0 + \beta_1 x$, with x a matrix containing the intercept and covariates. Model coefficients are displayed as odds ratios (OR). These ORs indicate the predicted difference in the odds of being assigned to the 1 category (high), relative to being assigned to the 0 category (low), based on a one-unit difference in a given independent variable, net of all other covariates. For the main independent race variable, this would then be interpreted concretely as how having a higher or lower proportion of Black residents comprising a given CBG increased or decreased the odds of being assigned to a given Covid-19 deaths trajectory group. Stata/MP 16.1 was utilized to conduct all of the analyses described in this.

2.3.3. Getis-Ord G_i^* Hot Spot analysis

Additionally, reflecting the mapping we provided to the GCHD to aid in response efforts, we used individual point-level data to conduct Getis-Ord G_i^* Hot Spot analyses for each wave. This process uses the presence of death as a weight of 1 and all other cases not resulting in death as a weight of 0, resulting in the identification of significant clusters of COVID-19 death in our study area (signified by the confidence level of hot as well as cold spots). To erase individual points and retain confidentiality, Thiessen polygons were created from these results showing the areas where COVID-19 death was significantly more or less likely.

3. Results

To give us an initial impression of racial and geographic disparities in COVID-19 death, we began our analyses by computing RRs of dying

Table 2

Logistic Regression Model of Covariate Effects on Odds of Assignment to the H2 COVID-19 Death Trajectory Group Relative to Assignment to the L2 Trajectory Group in Odds Ratios (OR) ($N = 373$).

	OR	p-Values	95% Confidence Interval	
Proportion of Black Residents	1.113	.800	.485	2.558
Proportion of Male Residents	1.298	.870	.058	29.201
Distress Index	.952	.252	.876	1.035
Proportion of Residents Aged 65 Years or Older	49.369	.010	2.564	950.737
Total Number of Residents	1.001	<0.001	1.000	1.001
Constant	.215	.111	.032	1.422

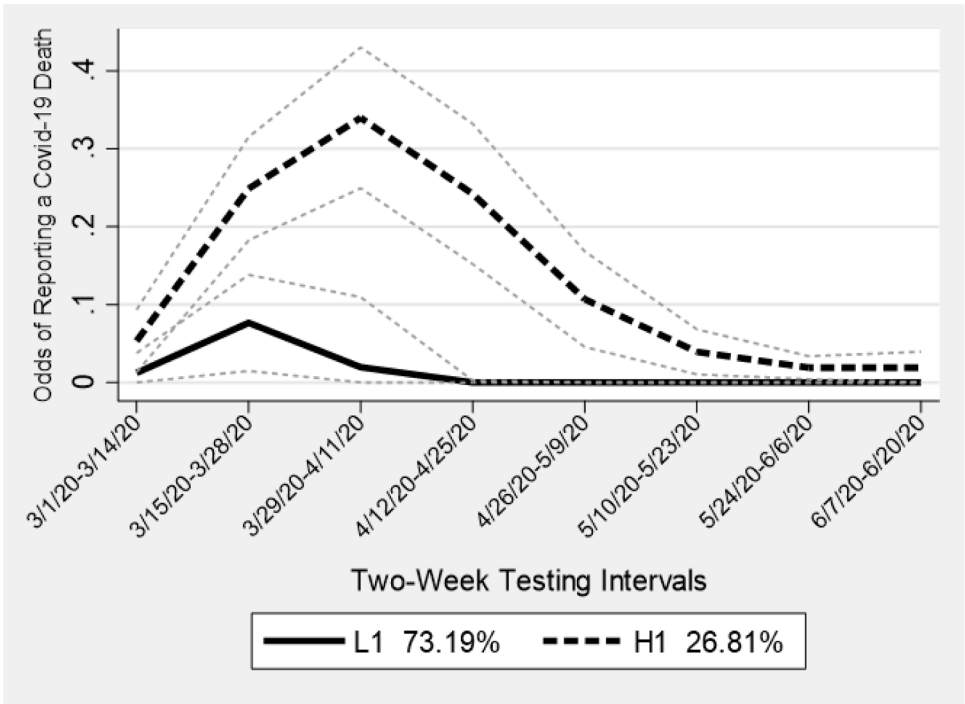


Fig. 1. First Wave COVID-19 Death Trajectory Model Aggregated by Census Block Group.

from COVID-19 by week for African-Americans versus all other races. Supplementary Table 1 shows the RRs for the first wave, with African-Americans having a much higher risk of COVID-19 death throughout that time period in both Flint and Genesee County (an average of between 3 and 4 times higher). Supplementary Table 2 shows the RRs for the second wave. For Genesee County, a slight disparity still persists, with an average RR of 1.34 (not nearly as high as in the first wave), but the City of Flint shows virtually no disparity, with an average RR of 1.01. Supplementary Table 3 provides descriptive data for all variables

included in analyses. Table 1 provides logistic regression estimates for the first wave trajectory model, whereas Table 2 provides these estimates for the second wave trajectory model. The GBTM analyses examining the first wave of data identified a two-group model (Fig. 1). The Y-axis in Fig. 1 represents the odds that a COVID-19 death will be reported by CBGs in each trajectory group during each testing interval. N here will refer to the number of CBGs included in a given group. The two-group model indicated better fit based on BIC compared to the one group and three group models

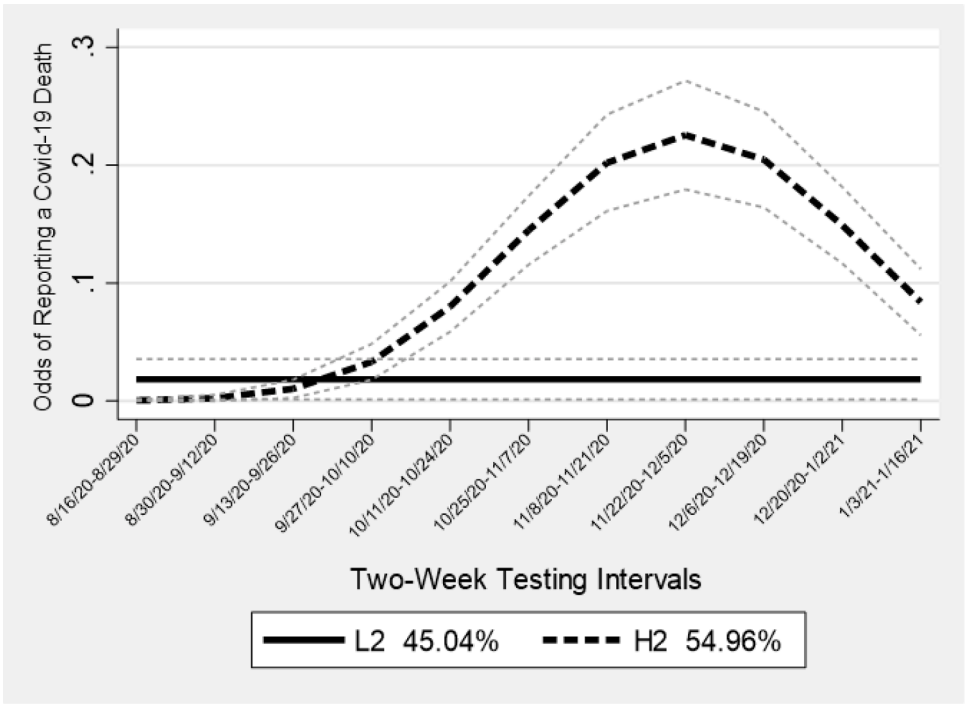


Fig. 2. Second Wave COVID-19 Death Trajectory Model Aggregated by Census Block Group.

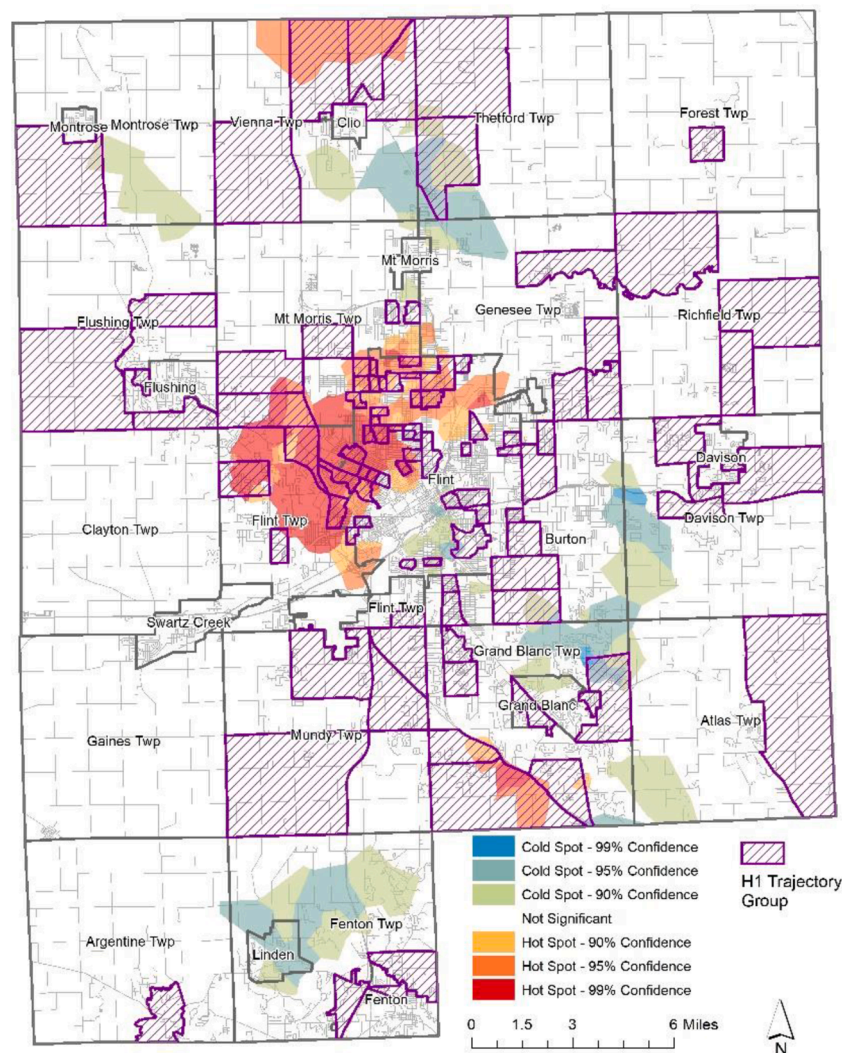


Fig. 3. High Trajectory Groups and Getis-Ord Gi* Hot Spot Analysis Results for COVID-19 Deaths, Genesee County, 3/1/20–6/20/20 (First Wave).

(1=−671.46; 2=−668.42; 3=−677.31). The selected model also provided the best nested model fit based on BIC and also met all other criteria for selection identified by Nagin (2005). To be specific, the chosen model provided adequate fit based on posterior probabilities of assignment exceeding 0.7 for all groups (Group 1: 0.781; Group 2: .930) and 95% confidence intervals were tightly bound around each group, as can be observed in Fig. 1. The first group in the model was characterized by a near zero-death rate across the entire first wave, minus a minor increase early in the first wave. Because of this, this group is described as the First Wave Low or L1 model. 73.19% ($N = 273$) of CBGs were assigned membership to this group and was characterized by a quadratic polynomial function. The other group in the model was characterized by a high spike in odds of reporting a COVID-19 death during a given testing interval and is described as the First Wave High or H1 group. This group had the remaining 26.81% ($N = 100$) of the CBGs assigned membership to it and was characterized by a cubic polynomial function.

Logistic regression analyses conducted on the first wave trajectory groups coded the H1 group in the 1 category and the L1 group in the 0 category. Results indicated that CBGs with a greater proportion of Black residents had higher odds of assignment to the H1 trajectory group ($OR=3.881$). This is to say that, the higher the proportion of Black residents living in a CBG, the higher the odds that CBG would be assigned to the H1 trajectory group. CBGs with more total residents, with a greater proportion of female residents, and a greater proportion of senior residents also had higher odds of assignment to the H1 group.

The GBTM analyses examining the second wave of data identified a two-group model (Fig. 2). The Y-axis in Fig. 2 represents the odds that a COVID-19 death will be reported by CBGs in each trajectory group during each testing interval. The percentage mentioned in the legend corresponds to the percentage of CBGs in a given group. The two-group model indicated better fit based on BIC compared to the one group and three group models (1=−1111.63; 2=−1062.49; 3=−1128.64). The chosen model met Nagin (2005) criteria associated with average odds of correct classification and tightly bound confidence intervals. To be specific, the chosen model provided adequate fit based on posterior probabilities of assignment exceeding 0.7 for all groups (Group 1: 0.784; Group 2: .850) and 95% confidence intervals were tightly bound around each group, as can be observed in Fig. 2. The first group was characterized by near zero COVID-19 death rate during the time period of interest. For this reason, this group is described as the Second Wave Low or L2 group; 45.04% (168 CBGs) of CBGs were assigned membership to this group. This group was characterized by an intercept-only polynomial function. The second group in the model was characterized by a relatively high spike in odds of reporting a COVID-19 death during a given testing interval across the entirety of the second wave. For this reason, this group is described as the Second Wave High or H2 group. This group had the remaining 54.96% (205 CBGs) of CBGs assigned membership to

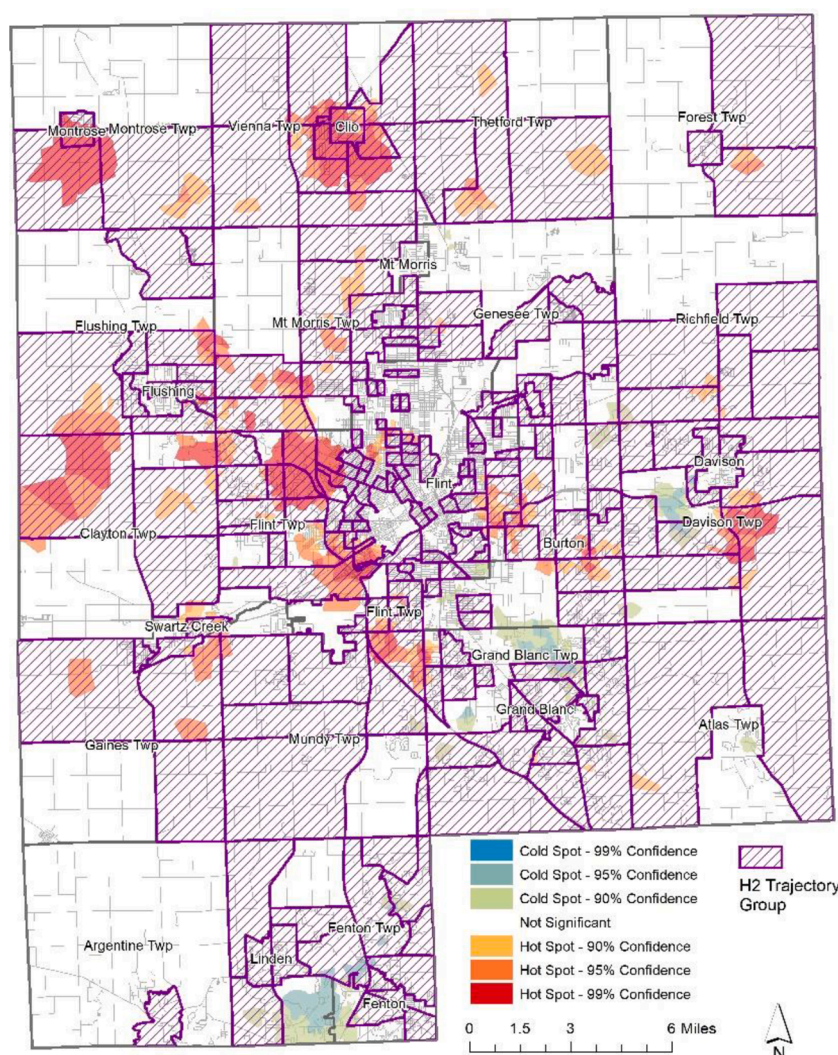


Fig. 4. High Trajectory Groups and Getis-Ord Gi* Hot Spot Analysis Results for COVID-19 Deaths, Genesee County, 8/16/20–1/17/21 (Second Wave).

it and was characterized by a quadratic polynomial function.²

Logistic regression analyses conducted on the second wave trajectory groups coded the H2 group in the 1 category and the L2 group in the 0 category. Results indicated that the ratio of Black residents in a given CBG was not a significant predictor of trajectory group assignment during the second wave. Having more senior residents and having more total residents were both associated with increased odds of assignment to the H2 group during the second wave.

Figs. 3 and 4 illustrate the high groups identified in each of the two waves (in purple outline), as well as the significant cold and hot spots from the Getis-Ord Gi* Hot Spot analyses (in shades of blue and red, respectively). In Fig. 3 (representing the first wave), more of the H1 group can be found in the City of Flint and Flint Township, corresponding closely to the contiguous hot spot. Most of the COVID-19 death

hot spots in the first wave were clustered in this area dominated by poorer and African American residents. In Fig. 4 (representing the second wave), the H2 group is spread throughout the suburbs, with only a single CBG in the City of Flint falling in the H2 group. Generally, COVID-19 death hot spots in the second wave are much more dispersed, including in the suburbs of Montrose, Clio, Flushing, and Davison in addition to Flint Township. This illustrates the data furnished to the GCHD to aid in testing, advocacy, and vaccine decision-making and indicates the utility of the GBTM method for facilitating this endeavor.

3.1. Holistic analysis

Supplementary analyses examined the entirety of the trajectory data in a single model, rather than broken down into waves 1 and 2. Fig. 5 provides visual depiction of the best fitting model. This model was generally consistent with the main analyses, as two groups separately identified the delineated death risk between the two waves (Late Surge, Early Surge). Further consistent with the main analyses, having a greater proportion of Black residents was associated with increased risk of assignment to the Early Surge group and lower risk of assignment to the Late Surge group. Additionally, a Moderate Chronic trajectory group was identified that demonstrated some degree of death risk across the entire study period. The only thing that seemed to distinguish this Moderate Chronic group was having more total residents compared to the Late Surge group.

² The model selected did not fully meet all Nagin (2005) criteria, as posterior odds of probability did not exceed .7 and average odds of correct classification did not exceed 5 for the L2 group. This model, however, was the only option that presented with tightly bound 95% confidence intervals, and also had the best BIC score. For these reasons it was chosen over other very similar models. In terms of substantive differences, there appeared to be none, as the subsequent regression models yielded no differences in how CBG characteristics predicted assignment to trajectory groups regardless of which trajectory model was utilized. This indicates the robustness of these findings.

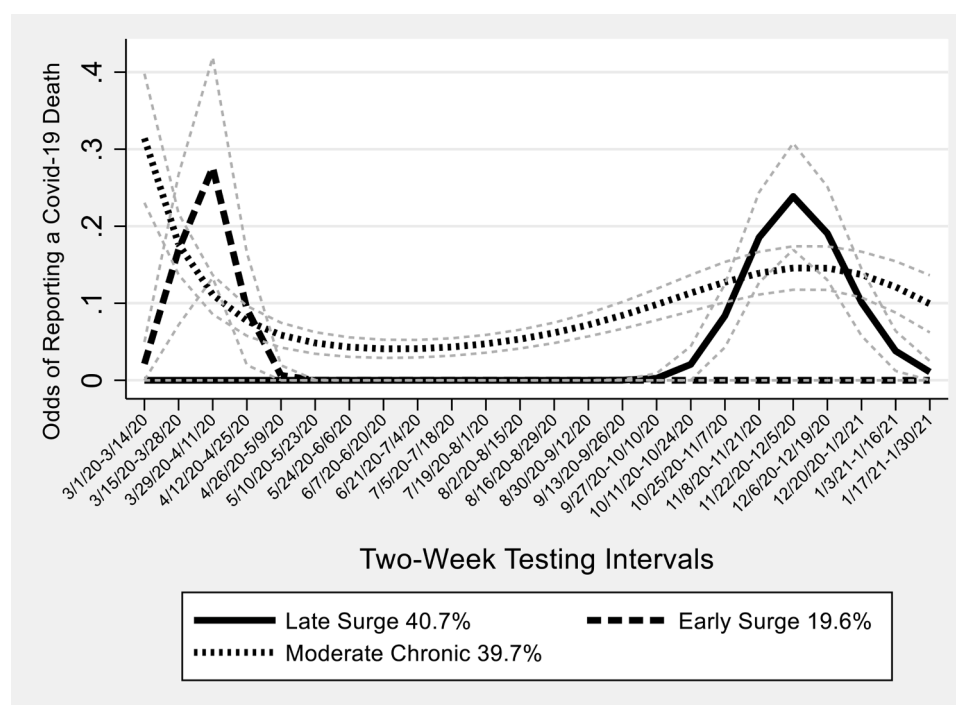


Fig. 5. Full Data COVID-19 Death Trajectory Model Aggregated by Census Block Group.

4. Discussion

Our first major finding—that a racial disparity existed in COVID-19 deaths during the first wave in spring 2020—precipitated the subsequent work identifying latent attributes driving COVID-19 death. Analyses indicated that different community characteristics drove the two waves of COVID-19 deaths observed in Genesee County during the first year of the pandemic. In the first wave (supporting our preliminary results), the highest death rates were seen in the City of Flint and surrounding areas, which are marked by higher socioeconomic distress, and which therefore have a higher vulnerability to severe COVID-19 cases (Sadler and Furr-Holden, 2019; Patel et al., 2020).

Socioeconomic distress was also an important predictor, suggesting that more distressed CBGs were more likely in the H1 group. The disappearance of this pattern in the second wave could have to do with differential adoption of preventive measures taken in these communities versus higher income communities.

The implications of effective public health interventions and prevention strategies can be seen in our work. While predominately African-American communities were more heavily affected during the first wave, the second wave saw much greater spatial dispersion throughout the county, and thus a lower burden on African-American community. Our team established a partnership with the GCHD during the summer of 2020, which included creating a disparities dashboard (GCHD, 2021), holding weekly webinars to disseminate up-to-date and locally relevant information. Given the Flint-focused audience and how this pandemic became politically charged throughout the country, we have reason to believe these efforts helped eliminate the racial disparity in COVID-19 deaths in Genesee County.

These analyses directly informed health department practice in additional ways. Our work was used to develop targeted public health strategies to prevent and reduce COVID-19 transmission and effectively direct allocation of resources in the arenas of community testing and vaccine rollout. Specifically, disparity data and COVID-19 mortality hotspots were factored into the selection of community testing locations and vaccination sites, so that chosen locations would be accessible to communities that were most severely impacted by the pandemic.

GCHD also leveraged the socioeconomic distress metric and COVID death hotspot analyses to enhance their vaccine prioritization methods. At the beginning of the rollout, vaccine quantity was severely limited, and the health department prioritized vaccinations for CBGs with either a) above average socioeconomic distress for the county or b) a significantly high amount of COVID-related deaths relative to the rest of the county.

The immediate availability of this data was an important factor for the vaccine rollout. By the time the state health department provided ZIP code-level Social Vulnerability Index scores to guide vaccine distribution, Genesee County had already identified key vulnerable populations with even higher resolution (SVI can vary greatly between different areas of a single ZIP Code; utilizing smaller distinctions like CBGs can better control for this variation). With the novel dimension of prioritization provided by this paper (which would not have been as readily available to the health department without our partnership), GCHD was able to allocate vaccines in a quick, precise and impactful manner. In general, this work demonstrates that other health departments may stand to benefit from similar partnerships that allow for the integration of data into public health decision processes.

Even so, we acknowledge we cannot identify the exact reasons for the differences in predictors of the H1 and H2 groups between waves. While race and socioeconomic status were predictors, the underlying reasons for these differences are beyond the scope of our study. Relatedly, individual-level data beyond race were not available, thus complicating the implications that may be drawn from these findings. Given the focus of the study at the community-level, however, examination of individual-level predictors of COVID-19 mortality are beyond the scope of this study. As one example, we can consider that more affluent CBGs drove high death risk in the second wave model. In Genesee County, these areas correlate to more conservative-leaning residents; lax social distancing and behavioral differences among residents of these CBGs may have led to higher death counts in the second wave. We continue to advocate for future research to interrogate these issues further so that public health interventions, policy, and outreach can be effectively targeted to reach the most at-risk populations. We also call for future research to take a more direct approach to evaluating the

potential impact that public health interventions and outreach like those in Genesee County may have had on COVID-19 racial disparities in deaths and similar situations in order to determine whether the necessary conditions for causal inference were present/absent.

Supplementary material

Supplementary Table 1: Weekly Relative Risk of COVID-19 Death, African-Americans vs. White/Other Races, 3/1/20–6/20/20 (First Wave)

Supplementary Table 2: Weekly Relative Risk of COVID-19 Death, African-Americans vs. White/Other Races, 8/16/20–1/17/21 (Second Wave)

Supplementary Table 3: Descriptive Statistics for Census Block Groups mmcl.docx

Data Availability

The authors do not have permission to share data.

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Supplementary materials

Supplementary material associated with this article can be found, in the online version, at doi:10.1016/j.sste.2022.100536.

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