

PREVENTING CHRONIC DISEASE

PUBLIC HEALTH RESEARCH, PRACTICE, AND POLICY



Geospatial Perspectives on the Intersection of Chronic Disease and COVID-19

About the Journal

Preventing Chronic Disease (PCD) is a peer-reviewed public health journal sponsored by the Centers for Disease Control and Prevention and authored by experts worldwide. PCD was established in 2004 by the National Center for Chronic Disease Prevention and Health Promotion with a mission to promote dialogue among researchers, practitioners, and policy makers worldwide on the integration and application of research findings and practical experience to improve population health.

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GUEST EDITORIAL

Geospatial Perspectives on the Intersection of Chronic Disease and COVID-19

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PEER REVIEWED

This collection of articles in *Preventing Chronic Disease* (PCD) brings together scientists and practitioners from the breadth of public health and the social sciences to demonstrate how geospatial perspectives can contribute to understanding and addressing the intersection of chronic disease and COVID-19, a respiratory disease caused by the SARS-CoV-2 virus. The COVID-19 pandemic has affected chronic disease in many complex ways. Early in the pandemic, it became clear that people with chronic conditions and those in older age groups were at the highest risk for COVID-19 hospitalization and death (1–3). Racial and ethnic minority populations experienced disproportionately worse health outcomes (4). Pandemic-related disruptions to the health care system and individuals' concerns about health care–related exposures affected chronic disease management: in-person visits for people with chronic conditions declined, supply chain disruptions led to shortages of medications, and the number of cancer screenings, treatments, and surgeries declined in the United States (5–7). More recent evidence suggests that COVID-19 may exacerbate existing chronic diseases and increase the risk of developing new chronic conditions, such as diabetes in adults (8,9), type 1 diabetes in children (10), neurological disorders (11), dementia (12), mental illness (13), and cardiovascular disease (14). In addition, an estimated one-half of COVID-19 survivors worldwide continue to have COVID-related health problems 6 months or more after recovery from the acute infection, making “long COVID” our newest and still largely unresearched chronic disease (15). Finally, social and economic inequities underlie disparities in incidence of both chronic diseases and COVID-19, an intersection that has been labeled a syndemic, defined as the “presence of 2 or more disease states that adversely interact with each other, negatively affecting the mutual course of each disease trajectory, enhancing vulnerabil-

ity, and which are made more deleterious by experienced inequities” (16).

Space and place are key elements of individual and population health — social and environmental determinants of health are embedded within place, and health outcomes and inequities typically exhibit strong geographic variation (17,18). Thus, geospatial perspectives, which address aspects of space and place, play a key role in the public health response to the COVID-19 pandemic and its intersection with chronic disease (19,20). Here, we consider geospatial perspectives to include the broad swath of geospatial data, analytical techniques, and technologies encompassed in the field of geographic information science and technology (GIS&T) (21). Geospatial data on disease incidence and mortality, available at the individual address level or aggregated to small areas, allow us to understand the geographic distribution of COVID-19 and the chronic disease burden and their spatial coincidence with other measures. Geospatial data can also capture community-level socioeconomic characteristics, such as indicators of race, ethnicity, and class, which serve to illuminate interrelated disparities in the incidence of COVID-19 and chronic disease.

Geospatial analytical techniques support the investigation of ecological and individual-level associations among chronic diseases and COVID-19 outcomes. These techniques include mapping and computational and statistical methods adapted explicitly for spatial data analysis, such as geographically weighted regression. Incorporating geospatial data about environmental characteristics and human dynamics, such as local climate and human mobility patterns, can inform analyses of how individual and environmental characteristics interact to produce population-level outcomes of COVID-19 and chronic disease. Geospatial technologies, such as GPS (global positioning systems), satellite remote sensing, and geographic information systems (GIS) software, provide the technological infrastructure to collect and integrate these geospatial data, apply these geospatial analytical techniques, and publicly disseminate data and information through web-based mapping and geospatial data dashboards.

In this collection, the commentary by Smith and Mennis provides an overview of the role of GIS&T in responding to the COVID-19



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pandemic, emphasizing the use of geospatial technologies for collecting data on disease prevalence, analyzing the spread of infection, communicating with the public, and optimizing the distribution of resources (22). The article is enlightening in depicting the use of GIS&T in the initial phase of the pandemic, when geospatial data and analyses were key to understanding the spread and transmission of the disease and the efficacy of nonpharmaceutical interventions, such as business closures and government directives that limited social gatherings.

Other contributions in this collection highlight how the authors used GIS&T to inform chronic disease and COVID-19–related policies, interventions, and public health communications. Foraker et al illustrate one such approach for leveraging GIS&T to support spatially directed interventions by developing a custom geospatial software application for visualizing the locations of COVID-19 cases at the individual residence level (23). This interactive mapping application can target public health responses to emerging disease hotspots and highlights the challenge to regional analyses of residential address-level data, which are typically restricted to authorized public health officials within a single jurisdiction. The research brief by Moise describes a spatial interpolation method that disaggregates zip code–level rates of COVID-19 to the census block group–level to facilitate the use of consistent, small-area spatial support when measuring associations with selected measures of social determinants of health (24).

Many of the contributions in this PCD collection focus on how GIS&T can be used to investigate the association between community attributes and health disparities, measures of social determinants of health, or risk factors related to chronic disease and COVID-19 outcomes. For example, the GIS Snapshots article by DuClos et al reports on a web browser–based software application that displays choropleth maps of chronic disease–related risk factors, hospitalizations, mortality, and the Economic Hardship Index at the county and zip code levels (25). This tool was designed to inform COVID-19 preparedness and response efforts at the local level by identifying communities particularly vulnerable to COVID-19. This map application provides an example of how state and local health departments work to provide access to substate-level data on chronic disease.

Two articles in this PCD collection examined whether the prevalence of a chronic disease geographically coincides with the prevalence of COVID-19. In research by Embury et al, subcounty data from San Diego County, California (which includes urban and rural areas), were used to explore whether spatial modeling of chronic disease rates and selected social determinants of health measures could identify communities most vulnerable to COVID-19 (26). The authors divided data on the pandemic into 5 time frames and examined how relationships between social determinants of

health, chronic disease, and COVID-19 changed over time. Jansen et al tested whether the prevalence of respiratory illness was associated with COVID-19 mortality rates among older adults in Connecticut and Rhode Island (27). Educational attainment decreased the strength of the association, demonstrating that our understanding of COVID-19 outcomes can be improved by accounting for selected social determinants of health.

The pandemic’s impact on food supply and affordability, concurrent with rising unemployment and mobility restrictions, made food access difficult for many households. Lowery et al used mapping to illustrate how the closure of food stores accepting Supplemental Nutrition Assistance Program (SNAP) via electronic benefits transfer (EBT) during the pandemic reduced food access within walking distance in a community in San Diego, California, where food insecurity was prevalent before the pandemic (28). Alternatively, Beese et al showed that food access for SNAP participants in Washington State during the pandemic was enhanced by expanding food delivery services (29). Their maps showed that online food delivery services by grocery stores accepting SNAP via EBT increased substantially during the pandemic, enhancing food access for many low-income communities in the state. However, certain barriers to online delivery services, such as lack of broadband access, remain a challenge, particularly in rural areas.

Other research in this PCD collection focuses on the use of GIS&T to assess factors associated with the efficacy of pharmaceutical and nonpharmaceutical interventions to reduce transmission of SARS CoV-2 infection. In their GIS Snapshots article, Michaels et al found a significant positive correlation between household internet access and COVID-19 vaccination rates at the zip code–level in New York City and used bivariate choropleth mapping to display the areas most at risk of COVID-19 and those with the lowest levels of vaccination and internet access (30). When the analysis was conducted, many vaccine providers in New York City were offering only online systems to schedule appointments. The article highlights the importance of considering the digital health divide in addressing chronic disease, COVID-19, and health inequities.

Li et al leveraged a large, commercial geospatial data set of mobility data collected from GPS-enabled mobile phones in a national-level analysis of the association of COVID-19 outcomes with decreases in travel to common activity space locations, such as work and shopping (31). This research incorporated time lags in tests of association to investigate whether stay-at-home directives, business closures, and related policies that restricted mobility successfully reduced COVID-19 prevalence. Results showed a strong association between reductions in mobility to certain locations, such as workplaces, and declines in infection rates, particularly in urb-

an areas, and demonstrated the efficacy of stay-at-home directives in the early stages of the pandemic.

This PCD collection demonstrates the diverse ways that GIS&T can support research and policy at the intersection of COVID-19 and chronic disease, including 1) the role of social and environmental determinants of health, 2) pharmaceutical and nonpharmaceutical interventions to mitigate the impact of the pandemic, and 3) data and information dissemination for public health practitioners and the public. However, we acknowledge certain limitations of the collection. These articles mainly focus on the early phases of the pandemic; many were written before the Delta and Omicron waves. Little attention was paid to areas of the US that, as of the time of this writing in May 2022, have had the highest rates of COVID-19 mortality, such as the Southeast, regions with high levels of social vulnerability, and rural areas (32). In addition, the collection does not consider the role of GIS&T in preventing or mitigating future waves of COVID-19 or the impact that COVID-19 may have on future geographic patterns of chronic disease. Furthermore, only one article in this collection was authored by practitioners at a public health agency (25), limiting our understanding of how geospatial perspectives on COVID-19 and chronic disease were deployed on the ground during the pandemic.

One important lesson of the COVID-19 pandemic is that the public health community cannot afford to continue regarding infectious disease and chronic disease as separate entities. Public health leaders have noted that “[a] challenge related to long-term COVID-19 sequelae is that we do not know yet the extent that COVID-19 exacerbates chronic disease, causes chronic disease, or will be determined a chronic disease unto itself” (33). Given the emerging evidence that COVID-19 not only exacerbates preexisting chronic disease but may also be a risk factor for developing heart disease, type 1 diabetes among children, depression, and other chronic diseases, geospatial approaches should be employed to identify areas of high rates of COVID-19 incidence that can be targeted for chronic disease surveillance, prevention, and the provision of health services.

We recognize that prevention and control of COVID-19 depend on prevention and management of chronic disease and vice versa, and the level of success in both depends on addressing the structural inequities in economic opportunity, racial and ethnic segregation, and resource accessibility that act as distal forces on more proximal social and environmental determinants of health, such as those associated with individual health behaviors. These structural mechanisms that affect health outcomes typically materialize in differences observed among places and regions. Geospatial approaches are thus critical for ecological analyses of disease incidence rates and for capturing and analyzing data on the structural social and environmental exposures that are key to understanding

how COVID-19 and chronic disease intersect to produce individual health outcomes.

Another lesson from the COVID-19 pandemic is the need for interdisciplinary collaboration across the fields of public health, social science, and GIS&T and across teaching, research, and practice. Only 3 articles in this collection represent collaborations between epidemiologists or other public health professionals and geographers, who often serve as key GIS&T personnel in universities (22,26,31). We recommend that medical and public health investigators include GIS&T experts on their research teams, because they can enhance the translation of complex health findings by contributing to geospatial data acquisition and analytical plans adapted for geospatial data analysis during the earliest phases of research design. These experts can also identify geospatial data policies that may affect health studies, including the US Census Bureau’s 2020 Census differential privacy algorithm (34) or requirements for the maintenance of individual privacy in health research (35). GIS&T experts can also provide insights into how the axiomatic properties of spatial data (36) affect inferential statistical analyses, including violations of statistical independence (37), how the choice of geographic aggregation method can produce different results (the modifiable areal unit problem) (38), that statistical significance of coefficients often varies from place to place (spatial heterogeneity) (39), and the impact of data uncertainty on health studies (40–42).

The small number of collaborative articles in this collection also highlights the need for higher education to be an agent of change for building these collaborative networks. Academic public health programs can enhance the capacity for GIS&T in public health practice by partnering with the academic units within their institutions that already have GIS&T expertise. Graduates from such programs will be more employable in public health fields than graduates trained in GIS&T or public health alone. From a practitioner perspective, epidemiologists working in state and local health departments can benefit from continued and rigorous GIS&T training and resources, such as the Building GIS Capacity for Chronic Disease Surveillance program at the Centers for Disease Control and Prevention (43).

The most powerful contribution that GIS&T scientists can make in a rapidly changing public health environment is to use sound geospatial methods in the service of generating evidence-based public health policies. To ensure the choice of appropriate public health research questions and concordant analytical designs, GIS&T scientists should collaborate with public health researchers and be aware of how issues of health disparities and legacies of discrimination in health care (44) can affect geospatial health research designs and analyses. For example, nearly 23% of states reported that data on race and ethnicity were incomplete for COVID-19

cases in the early part of the pandemic, making it difficult to measure the pandemic's impact on racial and minority populations (45). Qualitative geospatial techniques, such as those using georeferenced narrative data, can also play a central role in eliciting the lived experience of disenfranchised people and in examining how concentrated social and economic disadvantage, collective efficacy, exposure to violence, and other community-level characteristics shape individual health behaviors and outcomes that produce observed population-level health inequities (46).

Finally, we note that the pandemic has shed light on the need to strengthen national public health data infrastructures that support the integration of chronic and infectious disease data across various government agencies and facilitate public health data dissemination and communication for researchers, policy makers, and the public (47,48). This PCD collection highlights the critical need for incorporating a geospatial perspective into such efforts beyond the multiplicity of ad hoc mapping dashboards that have popped up over the past 2 years. Enhancing knowledge of cartography and interactive geospatial data visualization among software developers in the public health community is key to ensuring such tools are effective for science communication and assisting in public health intervention and prevention efforts.

In addition, eliminating barriers to the routine collection, geocoding, and sharing of residential address-level data in public health surveillance systems would provide more actionable data in this pandemic and the next. More broadly, the integration of geospatial perspectives into national public health data infrastructure initiatives to support future research on the intersection of chronic and infectious diseases can benefit from the experience of similar US government data infrastructure projects related to disaster and emergency response, where GIS&T plays a key role (49), such as The National Map (50), and the Disaster Risk Resilience Initiative (51). Data infrastructure development efforts should also be mindful of the confidentiality requirements for personal health information and incorporate recent developments in “geomasking,” which aims to preserve the anonymity of georeferenced observations, because location-based health data can potentially reveal personally identifiable information, even when aggregated over small areas (46). Some of these proposed efforts may present valuable opportunities for the new Center for Forecasting and Outbreak Analytics, launched by the Centers for Disease Control and Prevention in April 2022.

The public health community is only beginning to understand the profound and ongoing consequences of the interaction of chronic disease and COVID-19. This collection highlights the important role of GIS&T in understanding the social and environmental determinants of health that underlie inequities in infectious and chronic disease risk factors, ultimately producing the health dis-

parities observed in outcomes from the intersection of COVID-19 and chronic disease. Interdisciplinary and collaborative efforts to expand geospatial perspectives in chronic disease prevention and treatment are crucial for responding to COVID-19 and future pandemics.

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COMMENTARY

Incorporating Geographic Information Science and Technology in Response to the COVID-19 Pandemic

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PEER REVIEWED

Summary

What is already known about this topic?

Incorporating geographic information science and technology (GIS&T) into COVID-19 pandemic surveillance, modeling, and response enhances understanding and control of the disease.

What is added by this report?

Applications of GIS&T include developing spatial data infrastructures for surveillance and data sharing, incorporating mobility data in infectious disease forecasting, using geospatial technologies for digital contact tracing, integrating geographic data in COVID-19 modeling, investigating geographic social vulnerabilities and health disparities, and communicating the status of the disease or status of facilities for return-to-normal operations.

What are the implications for public health practice?

Protections for individual privacy and close collaboration among the fields of geography, medicine, public health, and public policy to use GIS&T are imperative.

Abstract

Incorporating geographic information science and technology (GIS&T) into COVID-19 pandemic surveillance, modeling, and response enhances understanding and control of the disease. Applications of GIS&T include 1) developing spatial data infrastructures for surveillance and data sharing, 2) incorporating mobility data in infectious disease forecasting, 3) using geospatial technologies for digital contact tracing, 4) integrating geographic data in COVID-19 modeling, 5) investigating geographic social vulnerabilities and health disparities, and 6) communicating the status of the disease or status of facilities for return-to-normal operations.

Locations and availability of personal protective equipment, ventilators, hospital beds, and other items can be optimized with the use of GIS&T. Challenges include protection of individual privacy and civil liberties and closer collaboration among the fields of geography, medicine, public health, and public policy.

Introduction

The spread of infectious disease is inherently a spatial process; therefore, geospatial data, technologies, and analytical methods play a critical role in understanding and responding to the coronavirus disease 2019 (COVID-19) pandemic. Geographic information science and technology (GIS&T) is the academic field centered on geospatial data and analysis. The field encompasses geographic information systems (GIS), spatial statistics and visualization, and location-based data derived from global navigation satellite systems (GNSS, eg, global positioning systems [GPS]) and remotely sensed imagery. Opportunities for incorporating GIS&T into COVID-19 pandemic surveillance, modeling, and response include 1) developing spatial data infrastructures (SDI) for surveillance and data sharing, 2) incorporating mobility data in infectious disease forecasting, 3) using geospatial technologies for digital contact tracing, 4) integrating geographic data in COVID-19 modeling, 5) investigating geographic health disparities and social vulnerabilities, and 6) communicating the status of the disease or status of facilities for return-to-normal operations. Locations and availability of personal protective equipment, ventilators, hospital beds, and other items can be optimized with the use of GIS&T.

Developing Spatial Data Infrastructures for COVID-19 Surveillance and Data Sharing

Current surveillance of COVID-19 at the national and global levels is built on lessons learned from maintaining previously developed databases of contamination and disease, such as FluNet



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on the mobility, purchasing, and web browsing behaviors of individuals and other relevant place-based and georeferenced data that may be useful in understanding disease dynamics. In addition, responding to a rapidly evolving health crisis such as the COVID-19 pandemic requires pipelines for supplying health and related data in near real time, which presents challenges. Finally, privacy protection for individuals is paramount in developing useful SDIs for pandemic response. As with the US NSDI, initiative and management at the federal level is likely necessary to develop an SDI for pandemic response.

Incorporating Population and Mobility Data in COVID-19 Forecasting

Along with handwashing and social distancing, perhaps the foremost mitigation strategy for reducing person-to-person contact and transmission of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) in the absence of pharmaceutical intervention is regulation restricting mobility (ie, human movement and travel behavior). Consequently, one key role for geospatial technologies in responding to the COVID-19 pandemic is monitoring population distribution and mobility through the use of social media and location-tracking applications embedded in mobile telephones that employ GNSS, cell phone tower connections, and/or wireless connections (9). Several corporate location-data collectors and vendors have released spatially aggregated COVID-19 pandemic-related data on population mobility. These data have been widely used by the popular media to report on the effects of jurisdictional stay-at-home orders on population mobility and by researchers to analyze the efficacy of population mobility change for altering disease dynamics (10).

Modeling population distribution and mobility has a long history in GIS&T and focuses on fine-scale estimations of population distribution and mobility (11,12), most recently by using mobile telephone-based location data (13,14). The scholarly response to the pandemic marks a major advance in the incorporation of fine-resolution data on population and individual mobility from geospatial technologies to understand disease dynamics and formulate effective intervention strategies. Because questions remain about the best way to measure and collect data on individual mobility, provide such data to researchers, and incorporate such mobility measures into infectious disease models, the COVID-19 pandemic provides an opportunity for testing methods for using such data to evaluate and forecast the effects of nonpharmaceutical interventions that restrict mobility. However, current legal frameworks and practices for preserving the privacy of individuals are obstacles to widespread adoption.

Using Geospatial Technologies for Digital Contact Tracing

Monitoring mobility at the individual level, in addition to the population level, has also emerged as an important use of geospatial technologies, particularly in its application to digital contact tracing. Conventional contact tracing, involving identifying, contacting, and encouraging quarantine for the people with whom an infected person has had close contact to mitigate disease transmission, is labor intensive. The process can be made more efficient and scaled up to large populations by exploiting individual digital mobility data, as well as data indicating proximity among mobile telephones using Bluetooth or related technologies, to computationally show close proximity among individuals (15). Such location data can be combined with health and other data that might indicate vulnerability to infection or disease. Individuals can then be contacted and given quarantine instructions automatically through mobile telephone text messages, or their future behavior may even be monitored to encourage or enforce quarantine. Such procedures have been used to some degree, in combination with population mobility restrictions, in an attempt to reduce SARS-CoV-2 transmission in China, Israel, Singapore, and South Korea, among other nations, and developments for digital contact tracing technologies by the largest international technology companies continue (16).

Advances in GIS&T have been made in modeling the geographic trajectories of individuals throughout their daily lives, their interactions with other people, and their immediate environment using geographic and computational constructs such as activity space and space-time prisms (17–20). However, to leverage this body of research for digital contact tracing, progress needs to be made in developing, testing, and implementing digital contact tracing applications, including evaluations of behavioral compliance, efficacy, and scaling. Additionally, this approach raises concerns about confidentiality and civil liberties that need to be addressed before widespread adoption (21).

Integrating Geographic Data in COVID-19 Modeling

A strength of GIS is the ability to integrate diverse spatial data sets based on georeferencing, facilitating the integration of health data with contextual characteristics. Descriptive modeling research that leverages this capability has examined the spatial associations of COVID-19 with socioeconomic and environmental characteristics. This research found, for example, that lower income and income inequality (22), higher temperature and humidity (23), exposure to fine particulate air pollution (24), and mobility and transportation

networks (25,26) were associated with a higher prevalence of COVID-19 cases or mortality. GIS&T also offers approaches to investigating statistical spatial effects and spatial heterogeneity, such as spatial autoregressive models and geographically weighted regression, to account for modeling geographic processes such as spatial diffusion and the variation in relationships among variables over space (27,28). Recent research leveraged these approaches in demonstrating the spatial heterogeneity in the relationships among observed COVID-19 cases and mortality with georeferenced socioeconomic and environmental variables (22,29,30) and found that the influence of area-based socioeconomic status, pre-existing health conditions, and environmental characteristics on disease transmission may vary from place to place.

Computational infectious disease models are widely used to predict or forecast the spread of COVID-19 disease and the effects of intervention strategies. Predictive modeling approaches can be generally categorized as SEIR/SIR (susceptible, exposed, infected, and removed/recovered) (31), agent-based (32), or statistical modeling (33). Such modeling approaches are inherently geographic in the sense that they make predictions for certain areas or regions, although only some models contain an explicit spatial interaction component or forecast the spatial variation in disease incidence over small areas. Explicitly incorporating a spatial component into infectious disease models attempts to account for 1) place-based contextual mechanisms of infection or disease related to the socioeconomic, built, or natural environments, such as air pollution or type of employment, 2) spatial heterogeneity in the drivers of disease transmission, for example, where certain socioeconomic characteristics may be associated with disease prevalence in one region but not in another as a result of regional differences in culture or behavioral norms, and 3) transportation networks or patterns of human mobility to better account for disease transmission dynamics (34,35). Such approaches have been extended to modeling the spread of COVID-19, providing evidence that restrictions on mobility have mitigated the spread of COVID-19 in different parts of the world and aided in forecasts of disease diffusion under various scenarios of mobility restriction (36,37).

Spatial transportation and mobility data can play an important role in forecasting disease prevalence, where, for example, the effect of nonpharmaceutical interventions (eg, restrictions on mobility) on city-level transmission of COVID-19 in China was analyzed using mobility data harvested from mobile telephone location-based services. This method allows one to parameterize the local contact rate and forecast the geographic distribution of disease prevalence under different intervention timing scenarios (37). Related approaches to modeling the spread of COVID-19 also incorporated airline transportation networks (38) and were extended to other

countries with extensive COVID-19 outbreaks, such as Italy (36), providing substantial evidence that restrictions on mobility have mitigated the spread of COVID-19 in different parts of the world.

Investigating Geographic Health Disparities of the COVID-19 Pandemic

Indices of social vulnerability are place-based variables that incorporate factors such as race/ethnicity and socioeconomic status to encode the vulnerability to adverse health outcomes and other types of hazards (39). Community social vulnerability, along with health care resources, plays an important role in predicting health care capacity in responding to the COVID-19 pandemic (40). Social vulnerability can interact with pre-existing medical conditions and access to medical resources, such as prescription drugs, to produce inequities in COVID-19 outcomes (41). People with underlying medical conditions, such as asthma, obesity, and diabetes, as well as people who are immunocompromised or aged 65 or older are at higher risk of serious consequences from SARS-CoV-2 infection than their healthier or younger counterparts. Because such medical conditions are often concentrated geographically and among certain demographic groups, understanding the spatial and demographic distribution of these conditions is critical to investigating health disparities associated with COVID-19. For example, COVID-19 morbidity and mortality are higher among African American and Hispanic people than among non-Hispanic white people (42). Such racial/ethnic disparities highlight the importance of efficient collection of socioeconomic, demographic, and other data among people with COVID-19.

Resources for investigating COVID-19-related social disparities include publicly available data on COVID-19 cases by small areas, such as zip codes (43), although such data are not widely available at a national level. The same issue exists for fine spatial resolution data on social vulnerability. The Public Health Disparities Geocoding Project at the Harvard T.H. Chan School of Public Health seeks to address this latter shortcoming (44). Researchers should understand the geographic and historical background of discrimination and resource deprivation that may produce place-based social vulnerabilities, to avoid stigmatizing or placing blame on certain communities. An understanding of the social determinants and structural forces, such as food insecurity, housing insecurity, and disparities in educational or health care infrastructure, that can influence health outcomes such as obesity, hypertension, and certain types of cancer, is important.

The multidimensional social, economic, and health consequences of the COVID-19 pandemic are geographically inequitable: some places and populations have greater social, economic, health and other effects than other places and populations. Beyond the need

to identify such factors as lack of access to resources or the prevalence of pre-existing health conditions is the need to recognize and understand the mechanisms of vulnerability that have been in place and led to the exacerbation of the COVID-19 crisis in some communities. Community recovery from the COVID-19 pandemic requires incorporation of social, economic, and health components and an emphasis on investigating how place shapes the uneven effect of COVID-19.

Implications for Public Health

We have outlined how GIS&T can be used for understanding and responding to the COVID-19 pandemic and future infectious disease epidemics and pandemics. Central to this understanding and response is a commitment for the use of GIS and geospatial technologies as the platform for collecting, integrating, and analyzing georeferenced data on the locations and characteristics of individuals and the spatial distribution of socioeconomic, health, and built and natural environmental characteristics. Geospatial resources for COVID-19 response are available through several organizations, including the University Consortium for Geographic Information Science (www.ucgis.org/covid-19-resources), the OGC (www.ogc.org/resources-for-COVID-19-from-ogc), and the National Alliance for Public Safety GIS Foundation (www.napsgfoundation.org/resources/covid-19).

Leveraging GIS&T for responding to the COVID-19 pandemic requires a close and extensive collaboration between researchers in the fields of geography, medicine, public health, and public policy. The field of GIS&T has a long history of research in data synthesis, statistical modeling, and computational simulation for spatial data and applications. Recognizing that GIS&T is a theoretical and scientific approach rather than simply a set of analytical tools will facilitate transdisciplinary collaboration. Advances in preserving individual privacy and civil liberties in the age of big spatial data, where geospatial technologies generate massive repositories of individual-level data on movement, health, and behavior widely available, are also necessary. These advances will likely require enhanced government regulations, corporate policies, and technological innovations in data sharing and privacy protection.

The COVID-19 pandemic is still in the beginning phase, and the research community is continuing to learn and revise the best way to respond to this global public health crisis. Geospatial data, methods, and technologies have a crucial role to play in understanding and responding to the pandemic, and the lessons learned on the use of GIS&T for pandemic response at this time should enhance preparedness and response for future public health crises.

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ORIGINAL RESEARCH

Enabling Hotspot Detection and Public Health Response to the COVID-19 Pandemic

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PEER REVIEWED

Summary**What is known on this topic?**

Having detailed geographic information on patients affected by the COVID-19 pandemic would allow public health professionals to tailor their efforts and improve future outcomes.

What is added by this report?

We built a real-time, interactive, street-level visualization of patients with a COVID-19–positive test to show emerging patterns in relation to disease prevalence and demographic characteristics of patients.

What are the implications for public health practice?

We expect this tool to aid public health professionals in mapping disease cases with more granularity and gaining real-time insight into COVID-19 hotspot development.

Abstract

Introduction

Public-facing maps of COVID-19 cases, hospital admissions, and deaths are commonly displayed at the state, county, and zip code levels, and low case counts are suppressed to protect confidentiality. Public health authorities are tasked with case identification, contact tracing, and canvassing for educational purposes during a pandemic. Given limited resources, authorities would benefit from the ability to tailor their efforts to a particular neighborhood or congregate living facility.

Methods

We describe the methods of building a real-time visualization of patients with COVID-19–positive tests, which facilitates timely public health response to the pandemic. We developed an interactive street-level visualization that shows new cases developing over time and resolving after 14 days of infection. Our source data included patient demographics (ie, age, race and ethnicity, and sex), street address of residence, respiratory test results, and date of test.

Results

We used colored dots to represent infections. The resulting animation shows where new cases developed in the region and how patterns changed over the course of the pandemic. Users can enlarge specific areas of the map and see street-level detail on residential location of each case and can select from demographic overlays and contour mapping options to see high-level patterns and associations with demographics and chronic disease prevalence as they emerge.

Conclusions

Before the development of this tool, local public health departments in our region did not have a means to map cases of disease to the street level and gain real-time insights into the underlying population where hotspots had developed. For privacy reasons, this tool is password-protected and not available to the public. We expect this tool to prove useful to public health departments as they navigate not only COVID-19 pandemic outcomes but also other public health threats, including chronic diseases and communicable disease outbreaks.

Introduction

Public-facing maps of COVID-19 cases, hospital admissions, deaths, and vaccination rates are commonly displayed at the state, county, and zip code levels, and low case counts are suppressed to protect confidentiality (1). Although state laws and public health departmental regulations vary, a standard approach is used to suppress case counts of fewer than 10 (2). Geographically, this approach applies to areas smaller than a county (ie, zip codes and US



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Census tracts), and case counts are not typically suppressed at the county or state level.

An exception to this rule can be made if data are to be used for quality improvement purposes. Public health departments may prepare reports for internal use that do not suppress case counts. However, such reports cannot be publicly disclosed without approval from a public health authority. Small case counts may be released during a public health emergency, in which, for example, a threat of person-to-person transmission of a communicable disease exists and action must be taken to protect public health.

Public health authorities at the local, regional, and state levels are tasked with case identification, contact tracing, and canvassing for educational purposes during a pandemic. Such authorities have been asked to track vaccination implementation geographically to help ensure equitable distribution of vaccines. Given limited resources, conducting these activities across an entire jurisdiction (ie, a county) or zip code area can be daunting. Rather than being assigned to a high-risk zip code in which to perform public health activities associated with the pandemic, authorities would benefit from the ability to tailor their efforts to a particular neighborhood or congregate living facility.

To address the immediate needs of public health authorities to effectively respond to hotspots of infection in real time, we developed an interactive street-level visualization that shows new cases developing over time and resolving after 14 days of infection. The Health Insurance Portability and Accountability Act (HIPAA) considers residential address to be a direct identifier that must be removed for data to be considered de-identified (3). Thus, access to the identifiable data and visualizations must be restricted to authorized personnel who are proficient data stewards, especially given that such data could be used in harmful ways (4). For privacy reasons, this tool is password-protected and not available to the public. In this article, we describe the methods of building a real-time visualization of patients with COVID-19–positive tests, which facilitates timely public health response to the pandemic.

Methods

We programmed the disease visualization tool using Data-Driven Documents (D³, version 6, d3js.org). We chose D³ for its flexibility and ability to create an animated, interactive map. Our source data for the visualization included patient demographics (ie, age, race and ethnicity, and sex), street address of residence, respiratory test results for influenza and SARS-CoV-2, and date of test. Our case data were provided by regional health systems (5). Project source code is available at <https://github.com/i2-wustl/visualization-ui>.

Additional data that could easily be linked and integrated by zip code included that from the US Census Bureau's decennial census or estimates from the American Community Survey (6) to provide sociodemographic and socioeconomic context to the visualization, as well as county-level data on prevalence of chronic disease from the Behavioral Risk Factor Surveillance System (7). We also enabled the use of cancer surveillance and diabetes data, of most interest to stakeholders in our region. Although our goal was to present data at a more granular geographic level, many publicly available sources of data limit our ability to present data at smaller units of geography (ie, US Census tract or block group).

Two-dimensional density plots of case counts were computed using kernel density estimation with empirically chosen values for bandwidth and cell size for each zoom level. The resulting visualization was optimized to balance visual comprehension, aesthetics, and computational performance. The density is presented as cases per square kilometer (cases/km²) around the census tract centroid. We preprocessed the residential address data using ArcGIS version 10.8.1 (Esri), yielding longitude and latitude coordinates for each record.

For the publication figures, locations underwent 2 masking steps that are described by Haley et al (8). First, a uniform random perturbation was applied in which we added random numbers between -0.01 and 0.01 to each point's latitude and longitude, which corresponds to approximately 1.7 km^2 . Next, we performed point aggregation in which each point's latitude and longitude were rounded to the nearest 0.01 km^2 , corresponding to an approximately 0.85 km^2 -spaced grid. However, the points are not shuffled in the tool when authorized users are logged in.

Results

The resulting visualization (Figure 1) used colored dots to represent influenza (purple) and SARS-CoV-2 (red) infections. Each dot corresponded to a positive case. Fourteen days after the date of the respiratory test, we considered the case resolved and removed the dot from the visualization. The visualization is activated with a play button and can be paused, rewind, or fast-forwarded to a specific date. The resulting animation shows where new cases developed in the region and how patterns changed over the course of the pandemic. Blue dots corresponded to a hospital (dark blue) or testing site (light blue). The screen shot of the animation shown in Figure 1 has case coordinates shuffled for privacy protection.

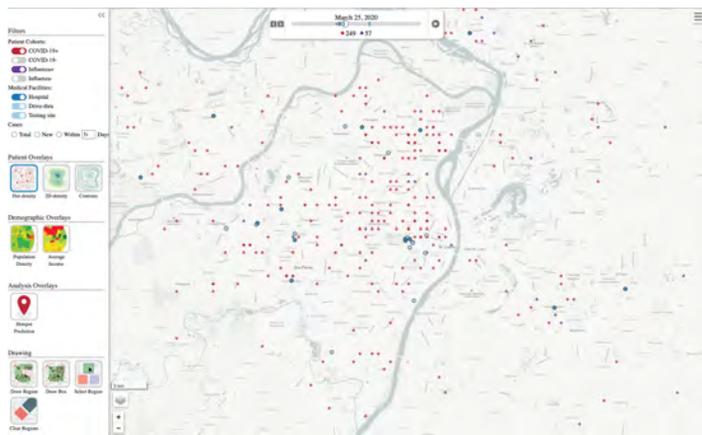


Figure 1. Screenshot of an animation of the disease visualization tool, showing influenza (purple dots) and SARS-CoV-2 (red dots) infections developing and resolving over time. Dark blue dots correspond to hospitals, and light blue dots correspond to testing sites. Case coordinates are shuffled for privacy protection.

The display of case coordinates as well as hospitals and testing sites can be switched on and off (left margin of the visualization) to see only cases of COVID-19 or influenza, for example. Of note, the design of the application is flexible to incorporate other types of health outcomes such as admissions, deaths, and vaccinations. Layers can be added (left margin of the visualization) to show prevalence of chronic disease, sociodemographic characteristics, or socioeconomic characteristics of the zip code or county across the region.

Another view of the visualization (Figure 2) uses a heatmap to show how the density of cases per population changes over time. Darker shades correspond to a higher density of cases. As in Figure 1, we resolved cases after 14 days, and the visualization is set in motion with a play button and can be paused, rewound, or fast-forwarded to a specific date. The resulting animation shows where hotspots of COVID-19 developed in the region and how patterns changed over the course of the pandemic. The screen shot of the animation, shown in Figure 2, is based on Figure 1, which had case coordinates shuffled for privacy protection.

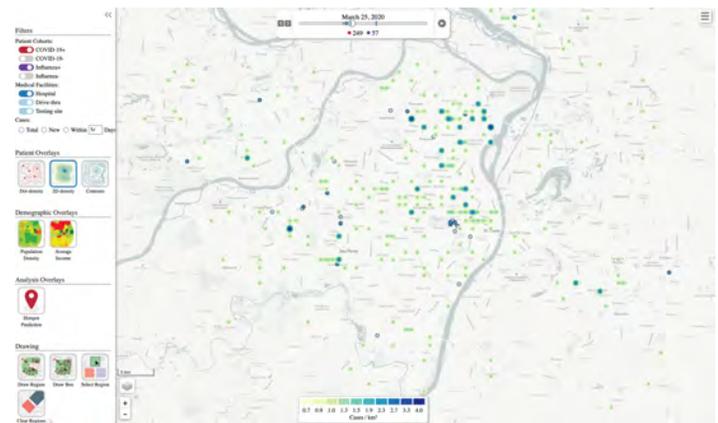


Figure 2. Screenshot of a heatmap animation of the disease visualization tool, showing respiratory virus infection (ie, influenza or SARS-CoV-2) hotspots developing and resolving over time. Case coordinates are shuffled for privacy protection.

We created a secure, password-protected web portal by which approved users can access the application. Users are able to enlarge specific areas of the map and see detail on street-level residential location of each outcome. Tools can be programmed to allow users to select from demographic overlays and contour mapping options to see high-level patterns and associations as they emerge. Additional functionality allows the user to select specific areas on the map to find out more about the demographic distribution of age, race and ethnicity, and sex among outcomes in a particular geographic area.

Conclusion

Our efforts are critical given that the COVID-19 pandemic and other public health threats are not respectful of geopolitical boundaries. Publicly available and easily sharable data at the zip code, county, and state levels are not sufficient to enable a precise public health pandemic response. We demonstrated that an open-source solution can be applied to support public health authorities in conducting their case identification and contact tracing activities in the midst of a crisis.

Before the development of this tool, local public health departments did not have a means to map cases of disease to the street level and gain real-time insights into the underlying population where hotspots had developed. The data visualization tool we created addresses this gap and is expected to provide the necessary data-driven insights that will facilitate a timely public health response to the pandemic.

Feasibility assessments should be conducted to evaluate whether the tool meets the needs of the end users and to ensure that sufficient resources are available to act on the disease hotspots that are

detected by the tool. Following implementation of the data visualization tool, its utility should be assessed to determine if additional functionality is needed or if the tool can be expanded or in some cases simplified to meet the demands of stakeholders during a pandemic.

A strength of our visualization is that it can be programmed to display other types of public health and COVID-19 outcomes such as hospital admissions, deaths, and vaccinations. We created a lightweight, secure application to address the immediate needs of our region in terms of case identification and contact tracing. We expect this tool to prove useful to public health departments as they navigate not only the COVID-19 pandemic but also other public health threats and communicable disease outbreaks.

Realizing the potential benefits of mapping infections to the street level requires attending to legal issues and ethical responsibilities and mitigating potential risks. Tracking infection at this level of granularity could infringe on individual rights to privacy and confidentiality, which must be balanced by the benefits of this activity for public good (9). As previously stated, HIPAA specifies residential address as a direct identifier (3), and only authorized personnel should have access (4). Data accuracy and validation must be addressed for the tool to realize its intended utility (10). Given that many data sets are incomplete and that data sharing among institutions remains a challenge, this should be monitored going forward (5). Public health practitioners should evaluate for benefits and harms to safeguard trustworthiness, while being mindful that harms could be unevenly distributed among different communities (11).

In conclusion, we aim to share these insights in support of a precision public health approach to an ongoing pandemic. This tool could also be scaled in response to other health outcome tracking needs. Legal and ethical considerations must be aligned with this effort to ensure that data are accessed and used appropriately while protecting privacy and confidentiality.

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RESEARCH BRIEF

Variation in Risk of COVID-19 Infection and Predictors of Social Determinants of Health in Miami–Dade County, Florida

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Summary**What is already known about this subject?**

Coronavirus disease 2019 (COVID-19) continues to have a disproportionate impact on certain populations in the United States, particularly racial and ethnic minorities and people with underlying medical conditions.

What is added by this report?

By August 19, 2020, Miami–Dade County accounted for 25% of all new COVID-19 cases reported in Florida. The positive association between a social disadvantage index and COVID-19 rates reflects the localized social networks and neighborhood social disadvantage. In addition, in Miami–Dade County, Florida, COVID-19 is localized to specific geographic areas.

What are the implications for public health practice?

COVID-19 infections are associated with socioeconomically vulnerable groups or areas, indicating a need for place-based and policy-level strategies or social protection policies that protect vulnerable social groups (eg, children, older adults, and single parent households).

Abstract

Miami–Dade County zip code–level (N = 91 zip codes) coronavirus disease 2019 (COVID-19) cases (N = 89,556 as of July 21, 2020) reported from the Florida Department of Health were used to estimate rates of COVID-19 per 1,000 population at the census block group level (N = 1,594 study block groups). To identify associations between rates of COVID-19 infections and multidimensional indexes of social determinants of health (SDOH) across Miami–Dade County, Florida, I applied a global model (ordinary least squares) and a local regression model (geographically weighted regression). Findings indicated that a social disadvant-

age index positively affected COVID-19 infection rates, whereas a socioeconomic status and opportunity index and a convergence of vulnerability index had an inverse but significant connection to COVID-19 infection rates over the study area. Rates of COVID-19 infections were localized to specific geographic areas and ranged from 0 to 60.75 per 1,000 population per square mile.

Objective

By August 19, 2020, Miami–Dade County accounted for 25% (148,093) of all new coronavirus disease 2019 (COVID-19) cases (N = 584,047) reported in Florida (1). Of particular concern is COVID-19's effect on vulnerable populations, such as minorities and people with chronic disease, and its linkage to social determinants of health (SDOH) (2,3). According to Healthy People 2030, SDOH (poverty, unequal access to health care, lack of education, and social conditions) affects a wide range of health, functioning, and quality of life outcomes (4). The SDOH also exacerbate health outcomes for vulnerable populations (5–7). The Centers for Diseases Control and Prevention reported that almost all people (94%) who died of COVID-19 in the United States had at least 1 underlying medical condition (8). A recent study also found overlaps in rates of COVID-19 infection and chronic disease (9). Therefore, finding effective ways to recognize the features that influence disadvantaged populations during a pandemic and to intervene is a persistent problem facing public health. The objective of this study is to quantify different SDOH indexes, examine the measures of these indexes on rates of COVID-19 infections, and determine the spatial variation in COVID-19 risk across census block groups in Miami–Dade County, Florida.

Methods

Confirmed data on the number of COVID-19 cases at the zip code level (N = 91 Miami–Dade County zip codes) as of July 21, 2020, were obtained from the Florida Department of Health COVID-19 Data and Surveillance Dashboard (1). COVID-19 data are reported only at large geographic levels (city, zip code, or county),



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which can mask small area variations (10) such as those occurring at the census block group level where improvements in health outcomes are most needed. Therefore, I used areal interpolation, a kriging-based disaggregation technique. A major advantage of areal interpolation is that it estimates data across different spatial aggregation units (eg, zip codes) and across units missing data (eg, census block groups) to produce a smoothed surface map of COVID-19 infection rates (11). I used the following parameters: a spherical model, a lag distance of 1,000 meters, and I limited the number of block groups in the prediction to 4 neighbors. The predicted data fit best when the model type was K-Bessel and the number of lags was 12, and all other inputs were set to default. Rates of COVID-19 infections per zip code per 1,000 population were calculated before areal interpolation.

Census block group level indicators were obtained from the US American Community Survey (ACS) 5-year estimates (2014–2018) (12). The 15 measures of social and neighborhood factors commonly reported as influencing health outcomes and common to several SDOH frameworks (12) were reduced to 3 indexes by using a principal components analysis (PCA) interpreted as signs of socioeconomic status and opportunity index (SESOP), social disadvantage index (SDI), and convergence of vulnerability index (CVI) (Table). The benefit of PCA is that it produces a new set of uncorrelated measures as a linear grouping of the initial measures and describes as much of the initial variation as possible. Contrary to a similar index construction study (13), this study's results were not consistent with a hypothesis of equal significance of measures in the indexes (eg, predefined measure set). Such measures, for example, did not adequately represent SES for the study area.

The eigenvalue for the SESOP was 6.266, and it explained 41.8% of the variance. The eigenvalue for the SDI was 1.83, and for the CVI was 1.61. The SDI and CVI indexes explained 12.2% and 10.7% of the variance, respectively. To determine the dominant measures in each principal component, the cutoff measure loading of 0.30 for the component was used, which is common practice in the literature. Quintiles maps were generated by using the ArcGIS software version 10.5 (Esri) to visualize census block group level COVID-19 infection rates compared with zip code-level rates (Figure 1) and composite measures (Figure 2). I used ordinary least squares (OLS) for global regression rather than geographically weighted regression (GWR) by using the MGWR version 2.2 software (Microsoft Corp) to identify associations between rates of COVID-19 infections and the SDOH multidimensional indexes across Miami–Dade County, Florida. The model was set as $\text{COVID-19 rates} = \beta_0 + \beta_1 \text{SESOP} + \beta_2 \text{SDI} + \beta_3 \text{CVI} + \epsilon$. β_0 and β_1 were the regression coefficients and ϵ was the model random

error. The Akaike information criterion (AIC) was used to assess goodness of fit between the 2 models.

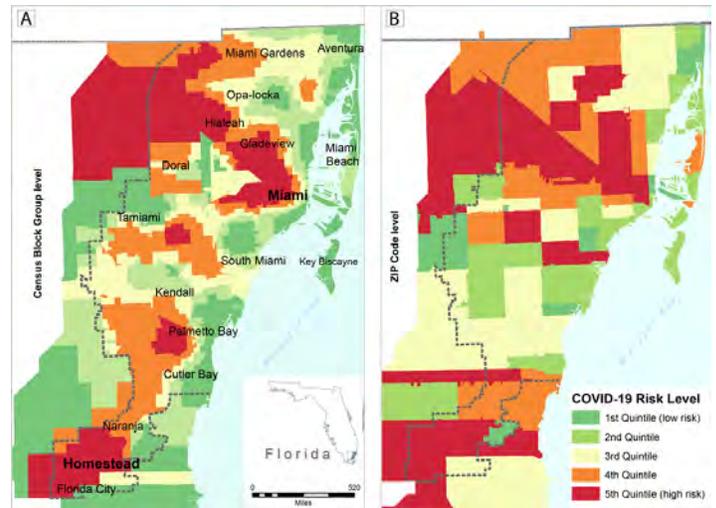


Figure 1. Map A shows estimated census block group level COVID-19 rates per 1,000 population for Miami–Dade County, Florida (generated with areal interpolation) based on zip code level rates. Map B is the same map as A but at a larger geographic area of zip codes. Data are for the 89,556 confirmed cases of COVID-19 reported as of July 21, 2020, in the Florida Department of Health COVID-19 Data and Surveillance Dashboard. Maps show rates (by quintiles) per 1,000 population.

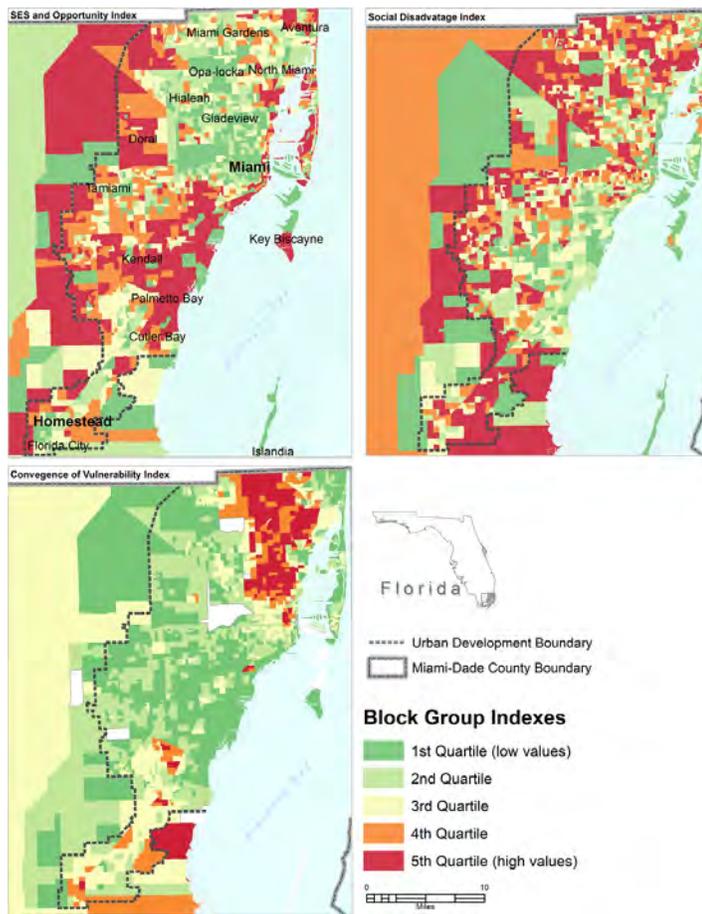


Figure 2. Maps of selected composite measures of 3 social determinants of health indexes for census block groups in Miami–Dade County, Florida: socioeconomic status and opportunity index, social disadvantage index, and convergence of vulnerability index. Abbreviation: SES, socioeconomic status.

Results

A total of 89,556 confirmed COVID-19 cases were reported in Miami–Dade County during the study period. The social disadvantage index was a better predictor of COVID-19 infections ($F_{2, 1,584} = 75.83; P < .001$) compared to the SESOI or the CVI, which suggests a need for policy-level strategies or social protection systems for vulnerable social groups (eg, children, older adults, single parent households). When comparing the OLS model with GWR AIC values, the AIC values show that both models perform roughly the same (GWR, 4,326.972 vs OLS, 4,327.199; adjusted R^2 , 0.120 vs 0.122), with the GWR model being slightly favored. Therefore, reported results are from the global model, which show that a 1-unit increase in social disadvantage is associated with a 0.279% increase in the rates of COVID-19 ($P < .001$). In contrast, the SESOI and convergence of vulnerability index had a negative

relationship with rates of COVID-19 infection. The SDI has more spatial heterogeneity than the SESOI or the CVI (Figure 2). Rates of COVID-19 infections were localized to specific Miami–Dade census block groups and ranged from 0 to 60.75 per 1,000 population per square mile.

Discussion

With the increasing number of COVID-19 cases in Miami–Dade County (from 62,430 cases on July 21, 2020, to 164,299 on September 15, 2020), a central focus of public health efforts should be limiting fatalities. In addition, exploring the heterogeneity of spatial relationships could provide more insights into place-based and policy-level strategies that protect vulnerable social groups. A limitation of this study is its reliance on the Florida Department of Health COVID-19 Dashboard; therefore, the reported cases may be an underestimation. Regardless, the methods used in this study demonstrate that geospatial analyses are powerful tools for estimating health events.

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Table

Table. Component Loadings for the 15 Census Block Group Measures Included in 3 SDOH Components, Miami–Dade County, Florida, 2020

Measure	SES and SESOI	Social Disadvantage Index	Convergence of Vulnerability Index
Component variance ^a	41.78	12.2	10.7
No vehicle	.839	—	—
Renter	.803	—	—
Rent burden	.793	—	—
Limited English proficiency ^b	.679	.570	—
Median household income	-.675	—	—
Living in poverty	.586	—	.544
People with disabilities	.478	—	.436
Crowding	—	—	—
Single parent–headed households	—	.885	—
Households with children aged <18 y	—	.742	.464
Households with one or more people aged ≥65	—	.725	—
No high school diploma	—	.628	—
Uninsured people	.439	.529	.518
Race/ethnicity (all people except non-Hispanic White)	—	—	.862
Unemployed, aged ≥16	—	—	.720

Abbreviation: SDOH, social determinants of health; SES, socioeconomic status; SESOI, socioeconomic status opportunity index; —, excluded low values (below 0.30).

^a Values are percentage variance. Extraction method: principal component analysis. Rotation method: Varimax with Kaiser Normalization (rotation converged in 6 iterations). Data source: US Census American Community Survey 5-year Estimates (2014–2018) (12). The 3 components reflect the convergence of predisposing, enabling, and need attributes of COVID-19 infection risk across census block groups in Miami–Dade County. SES and Opportunity Index include socioeconomic measures of poverty, income, person with limited English proficiency, and physical measures of housing characteristics (eg, renters, rent burden, and crowding) including vehicle access that have been linked to distinct health behaviors and outcomes. The Social Disadvantage Index includes demographic measures of socioeconomically vulnerable groups or areas with a high percentage of people with limited English proficiency, single parent households, households with children aged younger than 18 years, older adults (aged ≥65 y), people with less than a high school education, and uninsured people, which reflect localized social networks and neighborhood social disadvantage. The Convergence of Vulnerability Index includes measures of service environment or areas with a high proportion of people living in poverty, people with disabilities, children aged younger than 18 years, uninsured people, people with minority status, and unemployed people aged 16 or older. These measures compound already poor health profiles of vulnerable groups, increasing their risk of morbidity and mortality from COVID-19.

^b Limited English proficiency crossed the SES and Opportunity Index and the Social Disadvantage Index. Living in poverty and people with disability crossed the SES and Opportunity Index and Convergence of Vulnerability Index. Households with children aged 18 years or younger crossed both the Social Disadvantage Index and the Convergence of Vulnerability Index. Uninsured people crossed all indexes.

GIS SNAPSHOTS

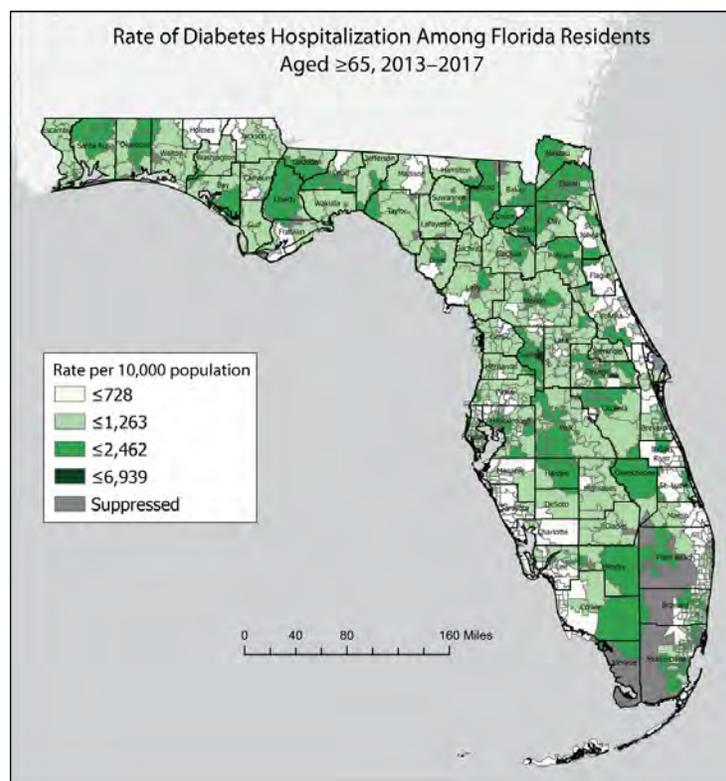
Mapping Chronic Disease Risk Factors With ArcGIS Online in Support of COVID-19 Response in Florida

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PEER REVIEWED



Static display of spatial variability in diabetes, which may increase the risk of severe illness from COVID-19, by Florida zip code and county. In the corresponding interactive map (<https://arcg.is/1D0Lz4>), 16 measures of chronic disease–related morbidity, mortality, and population health were aggregated to 5-year rates and stratified by age. The map application is used by local county health departments to inform COVID-19 response and identify communities at increased risk of COVID-19. Data on zip codes with <5 health events or <20 residents were suppressed.



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Background

The public health emergency caused by COVID-19 demonstrated that some populations are at increased risk of complications from COVID-19 infection and are at higher risk of death (1). The Florida Department of Health (FDOH) Environmental Public Health Tracking (EPHT) Program and Division of Public Health Statistics and Performance Management collaborated to create a Florida mapping resource to illustrate county and subcounty variability in chronic conditions and related factors that may increase the risk of severe illness from COVID-19. The degree of risk of COVID-19 varies by geography in Florida, and this variability has implications for public health practice as the state seeks to control the pandemic and limit severe health outcomes.

Florida is home to more than 21 million residents from diverse racial/ethnic and cultural backgrounds, approximately 20% of whom are adults aged 65 or older. The proportion of Florida's older population grew more rapidly than any other age group in the past decade (2). Older adults and people of any age with underlying medical conditions appear to be at higher risk for developing severe illness from COVID-19 than their younger and less medically compromised counterparts (3–5). Cardiovascular conditions, respiratory complications, and diabetes make up a substantial proportion of health conditions and contributing causes in deaths involving COVID-19 (6).

The aims of our mapping project were to describe the spatial variability in populations at particular risk of COVID-19, illustrate patterns of chronic disease at the county and subcounty level, and communicate this information to county health departments and other community members in Florida. Our goal is to reduce severe illness and premature death resulting from COVID-19 among Florida residents and visitors.

We used measures of illness and death resulting from cardiovascular conditions, respiratory conditions, diabetes, and cancer as indicators of increased risk (7–12). We also used county prevalence estimates of chronic disease–related risk factors (tobacco use and obesity) and zip code calculations of economic hardship. We included economic hardship because it is associated with lower rates of health insurance and reduced access to health care services, both of which could lead to COVID-19 complications (5,12).

Data and Methods

We used 4 data sources for our map. We obtained hospitalization records from the Florida Agency for Health Care Administration to capture data on chronic disease–related morbidity, death data from the FDOH Bureau of Vital Statistics, and data on chronic disease–related risk factors from the 2016 Florida Behavioral Risk Factor Surveillance System (BRFSS) (13). In addition, we calcu-

lated the Economic Hardship Index (EHI) by using variables from the 2014–2018 American Community Survey (14). We developed 16 subcounty measures from the hospitalization and death data and aggregated these data to 5-year rates according to zip code. We also mapped the EHI according to zip code. We mapped BRFSS data at the county level, the smallest level of geography available for this data set. We stratified all measures, except EHI, by age to illustrate increases in risk by age. We developed a web-based mapping application in ArcGIS Online and linked this application to existing web data portals at floridatracking.com (the EPHT portal) and FLHealthCHARTS.com. Because we derived the data measures from different sources, we developed a user guide and linked it to the ArcGIS mapping application. This user guide discusses data limitations and the need to interpret data with caution at the subcounty level because of small population sizes. To promote the new mapping application, we added prominent links to the EPHT portal and FLHealthCHARTS.com, which is the most widely used publicly available FDOH data repository and query system (with thousands of visitors per day).

Highlights

The output of this mapping project is a publicly available online interactive map (<https://arcg.is/1D0Lz4>) that depicts 5-year trends at the zip code and county levels in Florida. This ArcGIS Online application allows users to easily visualize geographic areas at increased risk of COVID-19. The following indicators of risk of COVID-19 are included on the mapping website: hospitalization and death rates resulting from cardiovascular conditions, respiratory conditions, diabetes, and cancer; the prevalence of tobacco use and obesity; and economic hardship scores.

Action

The ArcGIS Online interactive map went live in April 2020 and increased access to data measures for chronic conditions and related risk factors that could lead to COVID-19 complications. The use of zip code geography provides for community-level input on populations disproportionately affected by severe outcomes of COVID-19. The mapping application is used by the public and by the state health office and local county health departments to speak with communities about COVID-19 response and to identify areas of Florida at greatest risk for severe outcomes of COVID-19. In addition, the map informed hospital demand planning for the FDOH Bureau of Preparedness and Response, as concerns grew about exceeding hospital bed capacity in Florida. As of February 2021, the map had more than 4,500 views. Other public health programs could use our mapping application as a template for developing a similar application.

Acknowledgments

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ORIGINAL RESEARCH

A Spatio-Demographic Perspective on the Role of Social Determinants of Health and Chronic Disease in Determining a Population's Vulnerability to COVID-19

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PEER REVIEWED

Summary**What is already known on this topic?**

Social determinants of health are positively correlated with prevalence of both COVID-19 and chronic disease. Communities characterized by low socioeconomic status and high chronic disease rates may be vulnerable to COVID-19.

What is added by this report?

Socioeconomic variables identified as potential social determinants of health contextualize COVID-19 health disparities by race and ethnicity. Spatial models of chronic disease and COVID-19 highlight the spatial variability of COVID-19 population vulnerability.

What are the implications for public health practice?

Through insight into socioeconomic conditions and chronic disease distribution, demonstrated spatial approaches support equitable COVID-19 responses at the community level.

Abstract

Introduction

During the COVID-19 pandemic, health and social inequities placed racial and ethnic minority groups at increased risk of severe illness. Our objective was to investigate this health disparity by analyzing the relationship between potential social determinants of health (SDOH), COVID-19, and chronic disease in the spatial context of San Diego County, California.

Methods

We identified potential SDOH from a Pearson correlation analysis between socioeconomic variables and COVID-19 case rates during 5 pandemic stages, from March 31, 2020, to April 3, 2021. We used ridge regression to model chronic disease hospitalization and death rates by using the selected socioeconomic variables. Through the lens of COVID-19 and chronic disease, we identified vulnerable communities by using spatial methods, including Global Moran I spatial autocorrelation, local bivariate relationship analysis, and geographically weighted regression.

Results

In the Pearson correlation analysis, we identified 26 socioeconomic variables as potential SDOH because of their significance ($P \leq .05$) in relation to COVID-19 case rates. Of the analyzed chronic disease rates, ridge regression most accurately modeled rates of diabetes age-adjusted death ($R^2 = 0.903$) and age-adjusted hospitalization for hypertensive disease (hypertension, hypertensive heart disease, hypertensive chronic kidney disease, and hypertensive encephalopathy) ($R^2 = 0.952$). COVID-19 and chronic disease rates exhibited positive spatial autocorrelation ($0.304 \leq I \leq 0.561$, $3.092 \leq Z \leq 6.548$, $0.001 \leq P \leq .002$), thereby justifying spatial models to highlight communities that are vulnerable to COVID-19.

Conclusion

Novel spatial analysis methods reveal relationships between SDOH, COVID-19, and chronic disease that are intuitive and easily communicated to public health decision makers and practitioners. Observable disparity patterns between urban and rural areas and between affluent and low-income communities establish the need for spatially differentiated COVID-19 response approaches to achieve health equity.



The opinions expressed by authors contributing to this journal do not necessarily reflect the opinions of the U.S. Department of Health and Human Services, the Public Health Service, the Centers for Disease Control and Prevention, or the authors' affiliated institutions.

Introduction

As the novel coronavirus spread throughout the US in early 2020, reports of health disparity challenged claims that COVID-19 was society's "great equalizer" (1,2). As of September 2021, non-Hispanic Black Americans, non-Hispanic American Indians, and Hispanic Americans experienced higher rates of COVID-19 infection (1.1, 1.7, 1.9 times higher, respectively), hospitalization (2.8, 3.5, 2.8 times higher, respectively), and death (2.0, 2.4, 2.3 times higher, respectively) than non-Hispanic White Americans (3). This observed health disparity stems from widespread structural discrimination and its effects on people of color.

Social determinants of health (SDOH) are socio-environmental conditions that dictate how people live and age, whereas differences in these conditions define socioeconomic status (SES) (4). Low SES is directly linked to poor health outcomes for communicable and noncommunicable diseases alike (5,6). In a study of COVID-19 outcomes in a New York City hospital, Black and Hispanic patients were more likely than White patients to present with comorbidities, such as cardiovascular disease or diabetes, that were strongly associated with mortality (7). Dr Anthony Fauci, the immunologist leading the US COVID-19 response, said that the comorbidities that negatively affect COVID-19 outcomes "relate to the social determinants of health dating back to disadvantageous conditions that some people of color find themselves in from birth" (8). Existing research confirms the associations between the disproportionate impact of COVID-19 and chronic disease in socially disadvantaged communities (6,9,10). The compounding effect of low SES, comorbidities, and COVID-19 demands immediate action to support communities vulnerable to COVID-19.

Our goal was to classify the relationships between COVID-19, chronic disease, and socioeconomic variables to promote localized public health policies. We used a spatially explicit modeling approach to meet our 2 study objectives: 1) to determine which socioeconomic variables, correlated with COVID-19 and chronic disease rates, are potential SDOH, and 2) whether spatial modeling of chronic disease rates can identify communities most vulnerable to COVID-19.

Methods

Study area

Our research area was San Diego County, a culturally diverse area well suited to investigation of the various effects of socioeconomic factors and chronic disease on population vulnerability to COVID-19. The county is located in southwestern California

along the US–Mexico border. Its western portion is largely urban and densely populated, and its eastern portion lightly populated and rural. The county is divided into 41 subregional areas (SRAs), a geographic division frequently used to report COVID-19 and other health-related data.

Data collection

We obtained data sets from the San Diego County Open Data Portal (11), aggregated to SRAs, containing 2017 rates for hospitalization, emergency department discharge, and death per 100,000 residents for coronary heart disease (CHD), diabetes, hypertensive diseases (hypertension, hypertensive heart disease, hypertensive chronic kidney disease, and hypertensive encephalopathy), mental illness, and pulmonary disease. We included mental illness in our study because of the toll that COVID-19 has had on mental health (12) and because of the association between mental illness, other chronic diseases, and low SES (13,14).

Socioeconomic data related to age, race and ethnicity, language, housing, income, education, and employment were retrieved from the San Diego Association of Governments (SANDAG) Data Surfer (15) and the US Census Bureau's application programming interface (16). Data were then normalized by SRA population size or number of households. Along with socioeconomic variables, we included 4 health care access variables: health care clinics per SRA population, health care clinics per SRA square mile, hospitals per SRA population, and hospitals per SRA square mile. We calculated values for these health care access variables by using GIS analysis in ArcGIS Pro (Esri) and spatial data from SANDAG.

The County of San Diego Health and Human Services Agency provided COVID-19 rates (17) and aggregated most of the rates to SRA. However, confirmed case rates had zip code aggregations. We converted these confirmed case rates (per 100,000 residents) to the SRA extent with a 2019 population-based crosswalk from SANDAG that used dasymetric techniques to determine the proportion of residents in each zip code that live within the boundaries of an SRA. A similar crosswalk was used to aggregate the US Census Bureau socioeconomic data from census tract to SRA.

Characterization of COVID-19 pandemic stages

We considered 5 pandemic stages in our analysis to better understand the relationships evolving over time between COVID-19, chronic disease, and socioeconomic variables. On the basis of COVID-19 case trends in San Diego County (7-day averages), we divided the pandemic into 5 distinct stages over an approximate 12-month period, from March 31, 2020, through April 3, 2021

(18): March 31, 2020, to June 24, 2020 (Stage 1, 85 days); June 25, 2020, to August 18, 2020 (Stage 2, 54 days); August 19, 2020, to October 31, 2020 (Stage 3, 73 days); November 1, 2020, to January 23, 2021 (Stage 4, 83 days); and January 24, 2021, to April 3, 2021 (Stage 5, 69 days) (Figure 1).

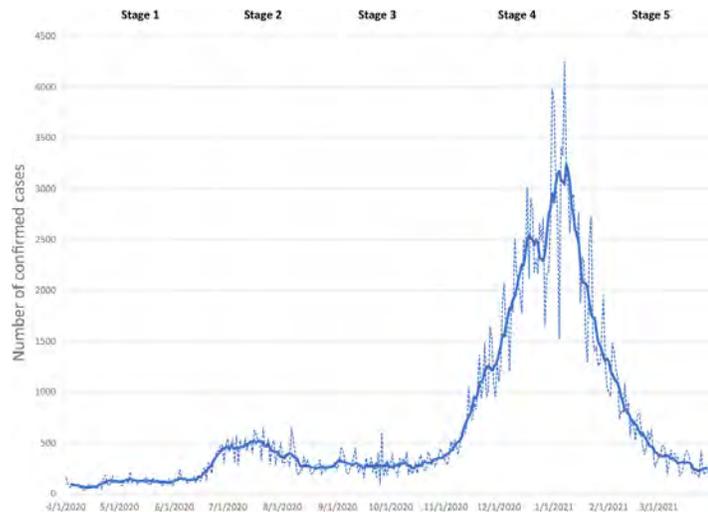


Figure 1. Trends in confirmed cases of COVID-19 over time, San Diego County, California, March 31, 2020, to April 3, 2021. The graph illustrates how the number of county-wide confirmed cases varied during the study period. Observed confirmed case trends were used to define 5 pandemic stages: March 31, 2020, to June 24, 2020 (Stage 1, 85 days); June 25, 2020, to August 18, 2020 (Stage 2, 54 days); August 19, 2020, to October 31, 2020 (Stage 3, 73 days); November 1, 2020, to January 23, 2021 (Stage 4, 83 days); and January 24, 2021, to April 3, 2021 (Stage 5, 69 days).

During Stage 1, the March 19, 2020, California stay-at-home order along with local restrictions enacted from March 29 through April 4, 2020 (eg, regarding face coverings, cruise ships) kept COVID-19 rates low and stable (19). Stage 2 covered San Diego County’s first wave of increased COVID-19 rates, which followed the reopening of many of the county’s businesses, between June 13 and June 25, 2020 (the indoor operation of some business sectors reclosed on July 3, 2020) (19). Stage 3 was a period of relative stability in response to additional public health restrictions that followed the first wave. Stage 4 was characterized by a second wave of dramatic rate surges, possibly related to gatherings for the 2020 Presidential election and winter holidays. A regional stay-at-home order began on December 6, 2020, and continued through January 25, 2021 (19). Stage 5 was marked by steadily decreasing rates as the holiday season ended and county residents were vaccinated. By March 5, 2021, 1 million vaccines had been administered (19). Throughout all stages, COVID-19 confirmed case rates were highest in SRAs located in the southern portion of the

county (Figure 2). Although the pandemic continues, we stopped our analysis at the end of Stage 5 to analyze and interpret existing data.

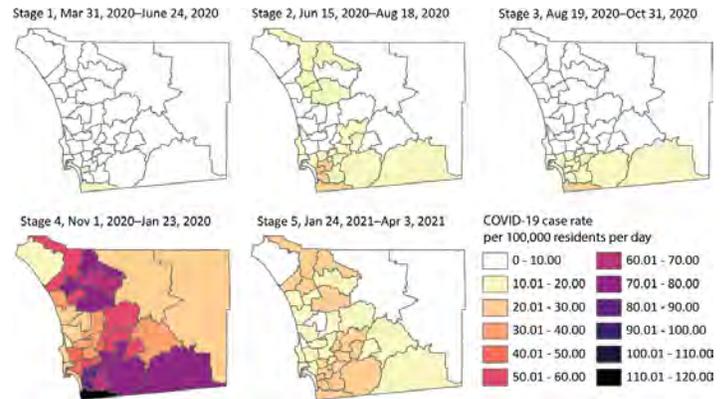


Figure 2. Spatial distribution of confirmed cases of COVID-19 by subregional area, San Diego County, California, March 31, 2020, to April 3, 2021. Maps show the spatial distribution of average daily COVID-19 case rates by subregional area for each of the 5 pandemic stages. Stages were determined by 7-day average case trends. All rates are per 100,000 residents.

Statistical methods

To address our first objective — to determine which socioeconomic variables, correlated with COVID-19 and chronic disease rates, were potential SDOH — we analyzed Pearson correlation coefficients, calculated with the SciPy Python package (SciPy–Python), to determine a set of potential SDOH from significant socioeconomic variables to the average confirmed daily COVID-19 case rates across the 5 pandemic stages. Socioeconomic variables were chosen for further analysis if the Pearson correlation *P* values were less than or equal to 0.05 for all stages, with 2 exceptions for variables with *P* values equal to 0.07 during 1 or 2 of the stages. The Pearson correlation coefficient is commonly used in medical research to test the strength of linear relationships between 2 variables (20). Next, we identified potentially meaningful relationships between COVID-19 and chronic disease comorbidities through a data-driven review of their Pearson correlation coefficients (18). We considered COVID-19 in the contexts of confirmed cases (total, and by race or ethnicity), total hospitalizations, and total deaths across the pandemic stages. For consistency, we selected a minimum of 1 rate, age-adjusted hospitalizations, for each of the chronic diseases.

To assess our potential SDOH, we conducted ridge regression analysis using a Python package, scikit-learn (Python), to evaluate how well the selected socioeconomic variables depicted actual distribution of COVID-19 and chronic disease. Ridge regression, a variant of linear regression, performs model regularization with a

tuning parameter (α) and assigns coefficients to the explanatory variables to minimize the effects of the multicollinearity that is common among sociodemographic indicators (21). We chose the chronic disease rates with the most accurate ridge regression models for spatial analysis of COVID-19 case rates.

For our second objective, to determine whether spatial modeling of chronic disease rates can identify communities most vulnerable to COVID-19, we used 3 spatial techniques to model COVID-19 case rates and find vulnerable communities. Spatial autocorrelation (Global Moran I) tests of COVID-19 confirmed case rates and chronic disease rates assessed the overall appropriateness of spatial modeling. Spatial autocorrelation indicates the similarity of data values across space for a single variable, gauging whether data are clustered, dispersed, or randomly distributed (22). With local bivariate analysis and geographically weighted regression (GWR) modeling, we investigated the relationships between chronic disease rates (independent) and COVID-19 case rates (dependent). Local bivariate analysis tests for significant relationships between two variables within a spatial neighborhood (23). GWR is a regression technique that considers spatial nonstationarity and variable local relationships in the prediction model (24,25). We used Esri's ArcGIS Pro 2.8 software (Esri) to conduct the study's spatial analysis. Together, we synthesized the collective modeling and analysis results to propose links between COVID-19, chronic disease, and SDOH in the context of San Diego County.

Results

COVID-19 correlations with potential SDOH and chronic disease

From an initial data set of 79 socioeconomic variables, 26 variables were recognized as potential SDOH because of their significant linear relationships ($P \leq .05$) to COVID-19 case rates during all 5 stages (Table 1). Two extra variables were included in the subset because at least 1 P value was significant ($P \leq .05$) during 1 of 5 stages: household income of \$60,000 to \$75,000 during Stages 1 ($P = .07$) and 2 ($P = .07$), and household income above \$200,000 for Stage 5 ($P = .07$). We discovered that some of the variables in the socioeconomic variable subset exhibited multicollinearity, such as English and Spanish as home languages, White and Hispanic race or ethnicity, and various industries of employment.

In preparation for further evaluation of the socioeconomic variable subset, we reviewed Pearson correlation coefficients for 113 chronic disease rates and 85 COVID-19–related rates and identified important relationships between COVID-19 and comorbidities. The analyzed chronic disease rates (total, age-adjusted, by sex,

by race or ethnicity, by age group) included hospitalizations, emergency department discharges, and deaths related to CHD, diabetes, hypertensive disease, mental illness, and pulmonary disease with sample sizes of 30 SRAs or more. Similarly, we considered rates of COVID-19 cases, hospitalizations, and deaths (total, age-adjusted, by sex, by race or ethnicity, by age group) in sample sizes of at least 30 SRAs. Ten of the most highly correlated rates, with at least 1 for each chronic disease, were selected for regression modeling: CHD age-adjusted hospitalization, diabetes age-adjusted hospitalization, diabetes age-adjusted death, diabetes hospitalization among patients aged 65 years or older, diabetes emergency department discharge among patients aged 65 years or older, age-adjusted hospitalization for people with hypertensive disease, hospitalization of Hispanic patients with hypertensive disease, mental illness age-adjusted hospitalization, pulmonary disease age-adjusted hospitalization, and pulmonary disease hospitalization of patients aged 65 years or older (Table 2).

In general, highly positive correlations were observed for chronic disease and COVID-19 rates. Key temporal patterns included:

- Decreasing correlation coefficients between COVID-19 case rates among Hispanic residents and age-adjusted hospitalizations for CHD (Stage 1: $r = 0.80$, $P \leq .001$; Stage 5: $r = 0.66$, $P \leq .001$), age-adjusted hospitalizations for diabetes (Stage 1: $r = 0.79$, $P \leq .001$; Stage 5: $r = 0.70$, $P \leq .001$), hospitalizations for diabetes among residents aged 65 years or older (Stage 1: $r = 0.93$, $P \leq .001$; Stage 5: $r = 0.74$, $P \leq .001$), and age-adjusted hospitalizations for hypertensive disease (Stage 1: $r = 0.86$, $P \leq .001$; Stage 5: $r = 0.61$, $P \leq .001$)
- High coefficients between COVID-19 death rates and diabetes death rates (eg, Stage 5, $r = 0.86$, $P \leq .001$), emergency department discharges for patients aged 65 or older with diabetes (eg, Stage 5, $r = 0.87$, $P \leq .001$)
- Decreasing correlation coefficients for hypertensive disease hospitalization rate and total COVID-19 case rates for Hispanic patients (Stage 1: $r = 0.89$, $P \leq .001$; Stage 5: $r = 0.79$, $P \leq .001$)
- Increasing correlation coefficients for age-adjusted hospitalizations for mental illness and COVID-19 case rates (Stage 1: $r = 0.36$, $P \leq .03$; Stage 5: $r = 0.58$, $P \leq .001$)
- High correlation coefficients between case rates among Asian residents and age-adjusted hospitalizations for pulmonary disease (eg, Stage 5: $r = 0.89$, $P \leq .001$)
- High correlation coefficients between COVID-19 case rates among Black residents and hospitalizations for pulmonary disease among residents aged 65 years or older (eg, Stage 5: $r = 0.71$, $P \leq .001$)

These findings suggest how the influence of medical comorbidities might have shifted as the pandemic progressed.

Socioeconomic disease models

Ridge regression modeling showed that the potential SDOH most accurately estimated COVID-19 case rates during Stage 1 ($R^2 = 0.893$, root-mean-square deviation [RMSE] = 0.91, $\alpha = 0.01$) and Stage 5 ($R^2 = 0.875$, RMSE = 2.26, $\alpha = 0.01$). Elevated errors and decreased fit correspond to models of pandemic Stage 2 ($R^2 = 0.685$, RMSE = 3.43, $\alpha = 1.0$) and Stage 4 ($R^2 = 0.809$, RMSE = 10.17, $\alpha = 1.0$) while infection rates surged, as well as to the interim period of relative stability (Stage 3, $R^2 = 0.789$, RMSE = 1.94, $\alpha = 0.1$). Ridge regression for the 10 selected chronic disease rates showed that 2 of the rates, diabetes age-adjusted death (diabetes death: $R^2 = 0.903$, RMSE = 3.15, $\alpha = 0.01$) and hypertensive disease age-adjusted hospitalization (hypertensive disease hospitalization: $R^2 = 0.952$, RMSE = 21.10, $\alpha = 0.01$), had R^2 values greater than 0.900. All other chronic disease rates had R^2 values below 0.810.

Although ridge regression's regularization process limits interpretation of the effect of specific socioeconomic variables on the model, coefficients of greater magnitude (positive or negative) relative to the model run can generally be viewed as important in determining rates of COVID-19 and chronic disease. Variables corresponding to English or Spanish as home language and Hispanic ethnicity were consistently assigned coefficients of relatively high magnitude (Table 3).

Spatial analysis of COVID-19 and chronic disease

The COVID-19 case rates in the 5 stages, diabetes deaths, and hypertensive disease hospitalizations exhibited significant positive spatial autocorrelation (Global Moran I) indicating that rates geographically nearby tend to be similar. Of note, the strength of spatial autocorrelation decreased for COVID-19 case rates during pandemic Stage 1 ($I = 0.561$, $z = 6.548$, $P \leq .001$) and Stage 2 ($I = 0.485$, $z = 5.486$, $P \leq .001$) before stabilizing during Stages 3 through 5 ($0.304 \leq I \leq 0.347$, $3.511 \leq z \leq 3.934$, $P \leq .001$). Spatial autocorrelation results for 2017 hypertensive disease hospitalization rates ($I = 0.413$, $z = 4.912$, $P \leq .001$) were greater than those for the 2017 diabetes death rates ($I = 0.345$, $z = 3.092$, $P = .002$). Subsequent spatial analysis determined the accuracy with which the rate of diabetes deaths or hypertensive disease hospitalizations could be independently used to model COVID-19 case rates, thereby avoiding the multicollinearity problems inherent in the selected socioeconomic variables.

Although diabetes death rates were well estimated by ridge regression by using the potential SDOH variables, data were suppressed for most of the lightly populated (rural) SRAs. Spatial analysis with the COVID-19 case rates produced interesting results, such as a linear bivariate relationship during all stages, but the reliabil-

ity of our findings is challenged by the small sample size. Visualization of diabetes deaths and COVID-19 cases with layered quantile classes separated the urban portion of the county into 3 zones: high-high positive correlations to the south, low-low positive correlations in the center, and higher than expected COVID-19 cases in the north. Also, GWR standard residuals depict the emergence of a clear spatial pattern characterized by under-predictions along major transportation corridors to the south, over-predictions in the county's center, and under-predictions in the north.

Hypertensive disease hospitalization rates were available for all SRAs except Camp Pendleton, a military base in the northwest corner of the county. Visualization of the hypertensive disease hospitalization and COVID-19 case rates using layered quantile classification symbology showed a positive correlation, with several exceptions in northern SRAs, where northeast SRAs had higher hypertensive disease hospitalizations and northwest SRAs had higher COVID-19 cases (Figure 3A). The local bivariate analysis confirmed this observation with linear positive relationships that, in southern SRAs, shifted to concave relationships over time (Figure 3B). GWR standard residuals (prediction errors) divided the county into overpredicted SRAs to the east and underpredicted (or accurately predicted) SRAs to the west (Figure 3C). This demarcation roughly matches the county's rural-urban divide, although rural SRAs along the US-Mexico border were also under-predicted.

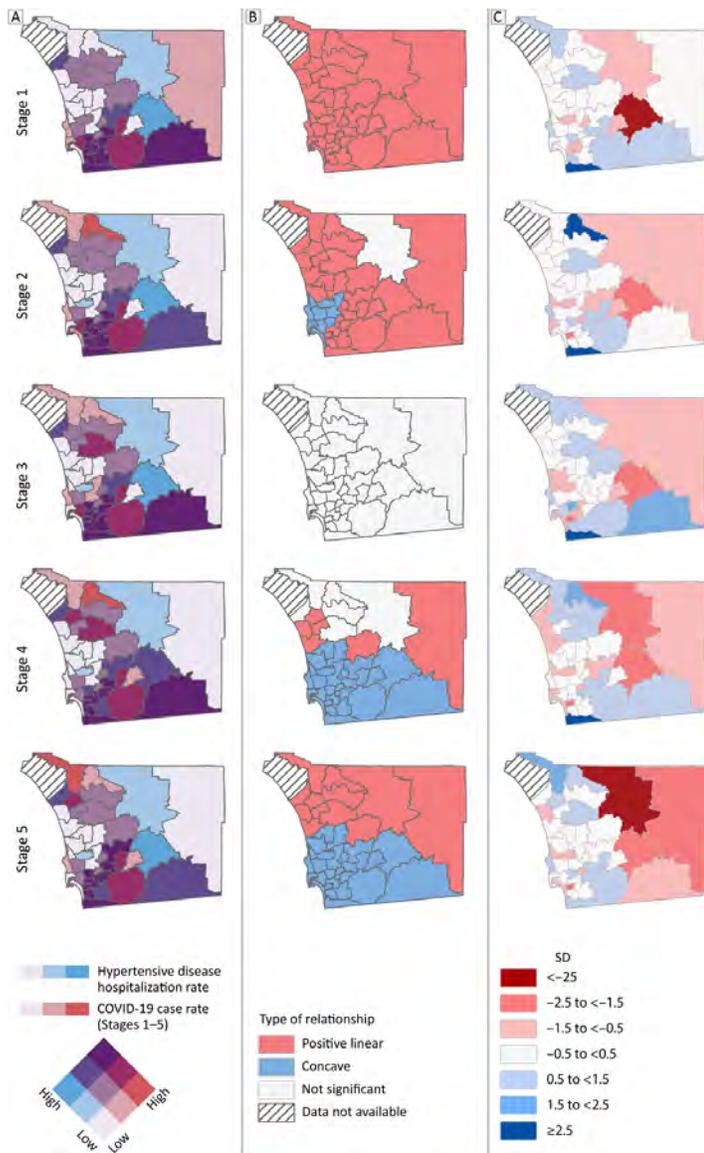


Figure 3. Bivariate visualizations of the age-adjusted hospitalization rate (independent) for hypertensive disease (hypertension, hypertensive heart disease, hypertensive chronic kidney disease, and hypertensive encephalopathy) and the daily average stage case rates (dependent) for COVID-19 in San Diego County subregional areas. Stages were determined by 7-day average case trends: Stage 1: March 31, 2020, to June 24, 2020; Stage 2: June 25, 2020, to August 18, 2020; Stage 3: August 19, 2020, to October 31, 2020; Stage 4: November 1, 2020, to January 23, 2021; and Stage 5: January 24, 2021, to April 3, 2021. Hospitalization rates for hypertensive disease (hypertension, hypertensive heart disease, hypertensive chronic kidney disease, and hypertensive encephalopathy) are for 2017 and consider the annual, age-adjusted rate per 100,000 residents. COVID-19 case rates consider the average daily rates per 100,000 residents for the stage. A. Layered quantile classification method for hypertensive disease hospitalization rates and the COVID-19 case rates. B. Type of local bivariate relationship for hypertensive disease hospitalization rates and COVID-19 case rates (rates not calculated for fewer than 5 events). C. Geographically

weighted regression standardized residuals (prediction errors) as SDs for hypertensive disease hospitalization rates and COVID-19 case rates. Negative SD values indicate overpredicted COVID-19 case rates whereas positive SD values indicate underpredicted COVID-19 case rates.

Discussion

Although the effect of socioeconomic factors on health equity is well established (5,8), spatial approaches are required to respond to known COVID-19 health disparities in regions of varied SES. We analyzed the relationships between socioeconomic variables, COVID-19, and chronic disease rates to identify a set of potential SDOH related to disproportionate disease spread. In a linear ridge regression model, variables across the categories of age, race and ethnicity, language, housing, income, education, and employment provide insight into the distribution of COVID-19. Reported health disparities related to race and ethnicity in San Diego County (27) are contextualized through the selection of related variables (eg, Hispanic ethnicity, Spanish home language) in the potential SDOH subset and their relative coefficient magnitudes during ridge regression. However, the highly related nature of the selected socioeconomic variables, such as high percentage of racial or ethnic minorities in lower-income neighborhoods (28), presents challenges to comprehensive spatial analysis.

As observed by others (7,29,30), people with preexisting chronic health conditions appear to be at increased risk of severe or fatal COVID-19 disease outcomes. As others have shown, in many cases those with an existing condition would not have died in the absence of a COVID-19 infection at the given time point (31). The strong correlations observed in our study are important in considerations related to limiting exposure for people with comorbidities, ensuring prompt vaccination to decrease biological susceptibility and providing prompt treatment if infected.

Because of the importance of comorbidities to COVID-19 outcomes and the observed correlations, we performed spatial modeling (GWR) of COVID-19 rates by using hypertensive disease hospitalization and diabetes death rates as explanatory variables. Not only can these comorbidity rates be well estimated by using the socioeconomic variables chosen to model COVID-19, but they also share similar spatial distributions to COVID-19, as determined through local bivariate analysis. Given these factors, the chronic disease rates should provide reasonable estimates of COVID-19 case rates. The GWR standard residuals indicate SRAs that have higher (underpredictions) or lower (overpredictions) COVID-19 case rates than expected by their comorbidity rates.

We propose that, in certain contexts, the GWR standard residuals highlight communities that are either notably vulnerable (underpredictions) or resilient (overpredictions) to COVID-19. When the

hypertensive disease hospitalization rate is used as the explanatory variable, differences between low- and high-population SRAs become apparent, delineating the county's rural–urban divide. When the diabetes death rate is the explanatory variable, urban subtleties reveal population vulnerabilities that can be further explained by socioeconomic variables and local area knowledge. However, because of suppressed values in the diabetes death rate data set, these findings require further investigation with additional data.

Through a spatial lens, the many interrelated factors that lead to vulnerability to COVID-19 can be better understood and clearly communicated to pandemic response decision makers and other involved planners. Spatially differentiated public health approaches are needed to overcome health disparity. The most effective policies for lightly populated communities will not work in densely populated areas. More importantly, culturally relevant and sensitive policies are needed to address COVID-19 in accordance with community demographics, preferences, and prevailing socioeconomic status. A disproportionately high number of COVID-19 cases in low-income communities might indicate low access to health care, poor communication of public health information, or unsustainable COVID-19 policies.

Our study had limitations. Data limitations posed major challenges. Health data are frequently aggregated to relatively large geographic units (ie, SRAs) and suppressed when rates are below a threshold, which ultimately resulted in a small number of large, varied areas to analyze. COVID-19 data scaled up from the zip code level are susceptible to errors related to the population-based conversion method and modifiable areal unit problem. Findings from our research are applicable only at the level of analysis and cannot be scaled down to make inferences about smaller geographic areas or individuals. Furthermore, because the temporal periods for data about the chronic disease rates (2017, annual) and COVID-19 case rates (2020–2021, 54–85 days) are not the same, uncertainties about variable correlations and temporal dependencies remain. Additional uncertainty relates to health care access in terms of who can, or will, get tested for COVID-19 or seek hospitalization and emergency services for chronic disease.

Limitations also exist in the analysis techniques used for our research. Although ridge regression regularization accommodates multicollinearity, the specific relationships between explanatory and dependent variables become obscured. In addition, our data and results suggest spatial dependency; thus, nonspatial linear models, such as ridge regression, are not reliable because they assume independence of data observations. The algorithms for neighborhood selection and prediction during the local bivariate

analysis and GWR might introduce error due to varied SRA sizes. We expect that access to fine-scale data, enabling analysis with more features, would increase the accuracy of our models and enhance the overall value of the research.

Our analysis demonstrates the value of novel spatially informed approaches to COVID-19 responses and epidemiologic policy. Investigation of potential SDOH provides better understanding of the underlying reasons for COVID-19 and chronic disease distribution patterns. Socioeconomic variable analysis can help decision makers develop relevant pandemic response measures. Location unites different health and socioeconomic variables in support of clear communication about COVID-19, population vulnerability, and public health decisions. Spatial analysis is needed to develop effective policy targeted to diverse communities, such as those found in San Diego County.

Future research is needed to determine causal relationships between potential SDOH, COVID-19, and chronic disease. Access to fine-scale data and additional demographic and health care access variables, either in San Diego County or elsewhere, would permit the detailed analysis required to establish causal relationships between potential SDOH and health data. Our findings provide a basis for hypothesis formation and a framework for ongoing spatial analysis. The heterogenous nature of San Diego County is ideal for investigating how correlations differ across space and inspires ongoing research to address these differences. The promising spatial approaches discussed in this article benefit the continuing development of geographically diverse and socially equitable epidemiologic responses.

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Tables

Table 1. Pearson Correlation Coefficients for Socioeconomic Variables^a and COVID-19 Daily Average Case Rates, by Stage^b, San Diego County Subregional Areas^c, March 31, 2020–April 3, 2021

Socioeconomic variable ^d	Stage 1	Stage 2	Stage 3	Stage 4	Stage 5
Average number of residents per household	0.444 (.004)	0.495 (.001)	0.412 (.007)	0.593 (<.001)	0.576 (<.001)
Education					
Below 9th grade	0.712 (<.001)	0.688 (<.001)	0.743 (<.001)	0.731 (<.001)	0.651 (<.001)
Bachelor’s degree or higher	−0.530 (<.001)	−0.537 (<.001)	−0.499 (<.001)	−0.680 (<.001)	−0.604 (<.001)
Master’s degree	−0.492 (.001)	−0.495 (<.001)	−0.463 (.002)	−0.625 (<.001)	−0.574 (<.001)
Health clinics per square mile^e	0.614 (<.001)	0.545 (<.001)	0.553 (<.001)	0.356 (.02)	0.451 (.003)
Language spoken at home					
English	−0.804 (<.001)	−0.717 (<.001)	−0.734 (<.001)	−0.632 (<.001)	−0.582 (<.001)
Spanish	0.859 (<.001)	0.797 (<.001)	0.833 (<.001)	0.773 (<.001)	0.677 (<.001)
Other Indo-European language	−0.380 (.01)	−0.425 (.006)	−0.377 (.02)	−0.528 (<.001)	−0.466 (.002)
Annual household income, \$					
Household income below the federal poverty level	0.556 (<.001)	0.434 (.005)	0.548 (<.001)	0.418 (.006)	0.305 (.05)
60,000–75,000 ^f	0.285 (.07)	0.433 (.005)	0.290 (.07)	0.426 (.005)	0.587 (<.001)
>200,000 ^f	−0.398 (.01)	−0.318 (.04)	−0.330 (.04)	−0.362 (.02)	−0.289 (.07)
<15,000	0.550 (<.001)	0.483 (.001)	0.543 (<.001)	0.424 (.006)	0.328 (.04)
Households receiving cash or food assistance	0.725 (<.001)	0.665 (<.001)	0.585 (<.001)	0.630 (<.001)	0.642 (<.001)
Foreign-born residents	0.584 (<.001)	0.518 (<.001)	0.527 (<.001)	0.421 (.006)	0.393 (.01)
Households with married parents of children aged <18 years	−0.590 (<.001)	−0.544 (<.001)	−0.550 (<.001)	−0.518 (<.001)	−0.550 (<.001)
Residents with physical disability	0.507 (<.001)	0.436 (.004)	0.500 (<.001)	0.586 (<.001)	0.562 (<.001)
Residents aged 0–9 years	0.508 (<.001)	0.563 (<.001)	0.582 (<.001)	0.636 (<.001)	0.626 (<.001)
Race or ethnicity					
Hispanic	0.823 (<.001)	0.808 (<.001)	0.833 (<.001)	0.806 (<.001)	0.703 (<.001)
White	−0.765 (<.001)	−0.740 (<.001)	−0.720 (<.001)	−0.648 (<.001)	−0.602 (<.001)
Other	−0.408 (.008)	−0.422 (.006)	−0.415 (.007)	−0.569 (<.001)	−0.455 (.003)
Households with ≥1 rooms per person	−0.710 (<.001)	−0.715 (<.001)	−0.700 (<.001)	−0.677 (<.001)	−0.640 (<.001)
Uninsured residents	0.511 (<.001)	0.699 (<.001)	0.638 (<.001)	0.652 (<.001)	0.686 (<.001)
Employment, by industry					
Management, business, science, arts	−0.564 (<.001)	−0.500 (<.001)	−0.497 (<.001)	−0.649 (<.001)	−0.564 (<.001)
Manufacturing, transportation	0.571 (<.001)	0.681 (<.001)	0.661 (<.001)	0.744 (<.001)	0.749 (<.001)

^a 2019 American Community Survey 5-year estimates (16) unless otherwise noted.

^b COVID-19 rates per 100,000 residents. Stages were determined by 7-day average case trends (1–5): March 31, 2020, to June 24, 2020 (Stage 1); June 25, 2020, to August 18, 2020 (Stage 2); August 19, 2020, to October 31, 2020 (Stage 3); November 1, 2020, to January 23, 2021 (Stage 4); and January 24, 2021, to April 3, 2021 (Stage 5).

^c San Diego County is divided into 41 subregional areas (SRAs), a geographic division frequently used to report COVID-19 and other health-related data.

^d Selected from an initial data set of 79 socioeconomic variables recognized as potential social determinants of health because of their significant linear relationships ($P \leq .05$) to COVID-19 case rates during all 5 pandemic stages. Values are $r(P)$ and are per 100,000.

^e Values were determined by using spatial data from the San Diego Association of Governments and GIS analysis (26).

^f Variable included with $P > .05$ was due to significance ($P > .05$) during other pandemic stages.

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Table 1. Pearson Correlation Coefficients for Socioeconomic Variables^a and COVID-19 Daily Average Case Rates, by Stage^b, San Diego County Subregional Areas^c, March 31, 2020–April 3, 2021

Socioeconomic variable ^d	Stage 1	Stage 2	Stage 3	Stage 4	Stage 5
Service	0.611 (<.001)	0.506 (<.001)	0.521 (<.001)	0.553 (<.001)	0.486 (.001)
Management and administration, professional, science, waste management services	-0.449 (.003)	-0.438 (.004)	-0.392 (.011)	-0.593 (<.001)	-0.507 (<.001)

^a 2019 American Community Survey 5-year estimates (16) unless otherwise noted.

^b COVID-19 rates per 100,000 residents. Stages were determined by 7-day average case trends (1–5): March 31, 2020, to June 24, 2020 (Stage 1); June 25, 2020, to August 18, 2020 (Stage 2); August 19, 2020, to October 31, 2020 (Stage 3); November 1, 2020, to January 23, 2021 (Stage 4); and January 24, 2021, to April 3, 2021 (Stage 5).

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^d Selected from an initial data set of 79 socioeconomic variables recognized as potential social determinants of health because of their significant linear relationships ($P \leq .05$) to COVID-19 case rates during all 5 pandemic stages. Values are $r(P)$ and are per 100,000.

^e Values were determined by using spatial data from the San Diego Association of Governments and GIS analysis (26).

^f Variable included with $P > .05$ was due to significance ($P > .05$) during other pandemic stages.

Table 2. Pearson Correlation Coefficients for 2017 Chronic Disease Rates and COVID-19 Cumulative Case Rates, by Stage^a, San Diego County Subregional Areas^b, March 31, 2020–April 3, 2021

Chronic disease rates ^c	Stage 1	Stage 2	Stage 3	Stage 4	Stage 5
Coronary heart disease, age-adjusted hospitalizations	0.792 (<.001)	0.746 (<.001)	0.719 (<.001)	0.745 (<.001)	0.748 (<.001)
Diabetes, age-adjusted hospitalizations	0.695 (<.001)	0.712 (<.001)	0.690 (<.001)	0.773 (<.001)	0.786 (<.001)
Diabetes, age-adjusted deaths	0.825 (<.001)	0.838 (<.001)	0.806 (<.001)	0.819 (<.001)	0.824 (<.001)
Diabetes, hospitalizations, patients aged ≥65 years	0.933 (<.001)	0.924 (<.001)	0.889 (<.001)	0.877 (<.001)	0.876 (<.001)
Diabetes, emergency department discharges, patients aged ≥65 years	0.822 (<.001)	0.798 (<.001)	0.760 (<.001)	0.749 (<.001)	0.749 (<.001)
Hypertensive diseases (hypertension, hypertensive heart disease, hypertensive chronic kidney disease, and hypertensive encephalopathy), age-adjusted hospitalizations	0.823 (<.001)	0.781 (<.001)	0.750 (<.001)	0.710 (<.001)	0.712 (<.001)
Hypertensive diseases, hospitalizations of Hispanic residents	0.887 (<.001)	0.867 (<.001)	0.833 (<.001)	0.793 (<.001)	0.790 (<.001)
Mental illness, age-adjusted hospitalizations	0.354 (.03)	0.411 (.008)	0.447 (.004)	0.571 (<.001)	0.578 (<.001)
Pulmonary disease, age-adjusted hospitalizations	0.680 (<.001)	0.657 (<.001)	0.651 (<.001)	0.704 (<.001)	0.706 (<.001)
Pulmonary disease hospitalizations, patients aged ≥65 years	0.779 (<.001)	0.771 (<.001)	0.754 (<.001)	0.810 (<.001)	0.814 (<.001)

^a COVID-19 rates per 100,000 residents. Stages were determined by 7-day average case trends (1–5): March 31, 2020, to June 24, 2020 (Stage 1); June 25, 2020, to August 18, 2020 (Stage 2); August 19, 2020, to October 31, 2020 (Stage 3); November 1, 2020, to January 23, 2021 (Stage 4); and January 24, 2021, to April 3, 2021 (Stage 5).

^b San Diego County is divided into 41 subregional areas (SRAs), a geographic division frequently used to report COVID-19 and other health-related data.

^c All rates are per 100,000 residents. Values are *r* (*P* value).

Table 3. Ridge Regression Model Coefficients for COVID-19 Daily Average Case Rates by Stage^a, Diabetes Age-Adjusted Death Rate^b, and Hypertensive Disease Hospitalization Rate^b, San Diego County Subregional Areas^c, March 31, 2020–April 3, 2021

Socioeconomic variable ^d	Stage 1	Stage 2	Stage 3	Stage 4	Stage 5	Diabetes deaths	Hypertensive disease hospitalizations
Average number of residents per household	0.32	2.45	0.48	15.65	7.64	7.48	65.29
Education							
Below 9th grade	-11.75	-0.11	0.57	0.89	0.83	-2.02	-1,756.88
Bachelor's degree	-6.19	-0.42	-1.36	-3.39	-19.34	-17.08	725.68
Master's degree	-3.90	-0.02	-1.41	-0.75	-14.34	-6.19	-502.36
Health clinics per square mile ^e	0.26	1.13	1.00	-11.54	0.30	4.75	63.04
Language spoken at home							
English	-12.42	-1.81	-2.95	-3.76	-12.72	-16.87	132.43
Spanish	12.43	2.72	8.25	7.80	8.22	-9.77	803.00
Other Indo-European language	-0.03	-0.39	-0.56	-0.96	8.59	3.68	-731.42
Annual household income, \$							
Below the federal poverty rate	2.76	-0.62	2.92	-1.34	-1.53	-12.91	-518.46
<15,000	5.61	0.11	2.09	-0.14	1.96	-3.67	561.30
60,000–75,000	3.95	0.51	0.73	1.38	36.42	21.29	-386.59
>200,000	2.97	0.99	2.56	3.24	23.98	-12.98	-428.05
Households receiving cash or food assistance, per 100,000	9.30	0.33	-2.63	-1.37	-1.43	28.82	248.10
Foreign-born residents	-7.52	0.21	-2.94	0.58	-5.96	-32.69	-210.04
Households with married parents of children aged <18 years	0.58	-0.18	2.15	-0.36	-26.78	13.95	275.00
Resident with physical disability	0.32	0.91	0.70	6.24	0.88	3.97	35.86
Residents aged 0–9 years	-5.01	0.14	0.18	1.31	17.13	-11.52	-179.35
Race or ethnicity							
Hispanic	-3.00	2.75	8.33	7.66	-1.39	-15.47	-896.04
White	2.62	-2.29	0.49	-1.24	16.73	-22.86	-522.40
Other	0.23	0.00	0.05	-0.01	1.09	0.15	-48.32
Households with ≥1 rooms per person	0.03	-0.53	-0.17	-2.25	-0.07	-1.11	-9.77
Uninsured	-7.17	0.88	1.05	1.59	20.78	-4.46	602.68
Employment, by industry							
Management, business, science, arts	5.88	1.71	5.95	0.91	27.65	26.45	-794.44
Manufacturing, transportation	2.40	0.61	3.77	2.01	17.01	4.43	114.61

^a COVID-19 rates per 100,000 residents. Stages were determined by 7-day average case trends (1–5): March 31, 2020, to June 24, 2020 (Stage 1); June 25, 2020, to August 18, 2020 (Stage 2); August 19, 2020, to October 31, 2020 (Stage 3); November 1, 2020, to January 23, 2021 (Stage 4); and January 24, 2021, to April 3, 2021 (Stage 5).

^b Chronic disease rate for 2017 per 100,000 residents. Hypertensive disease includes hypertension, hypertensive heart disease, hypertensive chronic kidney disease, and hypertensive encephalopathy.

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Table 3. Ridge Regression Model Coefficients for COVID-19 Daily Average Case Rates by Stage^a, Diabetes Age-Adjusted Death Rate^b, and Hypertensive Disease Hospitalization Rate^b, San Diego County Subregional Areas^c, March 31, 2020–April 3, 2021

Socioeconomic variable ^d	Stage 1	Stage 2	Stage 3	Stage 4	Stage 5	Diabetes deaths	Hypertensive disease hospitalizations
Service	2.51	-0.61	-2.16	-1.27	11.86	-19.62	-128.65
Management and administration, professional, science, waste management services	9.67	0.46	3.27	0.46	10.39	14.19	687.10

^a COVID-19 rates per 100,000 residents. Stages were determined by 7-day average case trends (1–5): March 31, 2020, to June 24, 2020 (Stage 1); June 25, 2020, to August 18, 2020 (Stage 2); August 19, 2020, to October 31, 2020 (Stage 3); November 1, 2020, to January 23, 2021 (Stage 4); and January 24, 2021, to April 3, 2021 (Stage 5).

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^e Values were determined by using spatial data from the San Diego Association of Governments and GIS analysis (26).

ORIGINAL RESEARCH

The Town-Level Prevalence of Chronic Lung Conditions and Death From COVID-19 Among Older Adults in Connecticut and Rhode Island

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PEER REVIEWED

Summary**What is already known on this topic?**

Chronic lung diseases, such as chronic obstructive pulmonary disease (COPD) and asthma, are among the top preexisting conditions identified by the Centers for Disease Control and Prevention that increase the risk for severe COVID-19 illness and death.

What is added by this report?

Town-level factors (African American race and Hispanic ethnicity, age ≥ 65 y, and low educational attainment) were significant predictors of COVID-19 death rates, adding to the current understanding of the impact of social determinants of health on outcomes.

What are the implications for public health practice?

Public health policy makers could focus on communities reporting high rates of chronic lung conditions among the older adult population to provide more testing and access to vaccinations.

Abstract

Introduction

As of November 2021, older adults (aged ≥ 65 y) accounted for 81% of all deaths from COVID-19 in the US. Chronic lung diseases increase the risk for severe COVID-19 illness and death. The aim of this research was to examine the association between town-level rates of asthma and chronic obstructive pulmonary disease (COPD) and deaths from COVID-19 in 208 towns in Connecticut and Rhode Island.

Methods

We conducted a multistep analysis to examine the association between town-level chronic lung conditions and death from COVID-19. Pairwise correlations were estimated and bivariate maps were created to assess the relationship between COVID-19 deaths per 100,000 people and 1) asthma prevalence and 2) COPD prevalence among adults aged 65 years or older. We used multiple linear regression models to examine whether chronic lung conditions and other town-level factors were associated with COVID-19 death rates in Connecticut and Rhode Island.

Results

Initial bivariate correlation and mapping analyses suggested positive correlations between asthma and COPD prevalence and COVID-19 death rates. However, after controlling for town-level factors associated with chronic lung conditions and COVID-19 death rates, multiple linear regression models did not support an association, but town-level factors (African American race and Hispanic ethnicity, age ≥ 65 y, and low educational attainment) were significant predictors of COVID-19 death rates.

Conclusion

We found significant associations between town-level factors and COVID-19, adding to the current understanding of the impact of social determinants of health on outcomes.

Introduction

As of November 2021, 81% of all US deaths caused by COVID-19 occurred among people aged 65 years or older (1). Chronic lung diseases, such as asthma and chronic obstructive pulmonary disease (COPD), are among the top preexisting conditions that increase the risk for severe COVID-19 illness and death (2). Patients with preexisting lung conditions, including asthma and COPD, are more likely than people without these conditions to be hospitalized and die of COVID-19 (3–6). Even after controlling for sex, race and ethnicity, body mass index, and 10 prevalent co-



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morbidities, a study found that people with chronic lung conditions were significantly more likely to be admitted to intensive care units, require mechanical ventilation, and die of COVID-19 (3). Although the association between chronic lung conditions and COVID-19 has been established at the individual level (3–6), information about town-level associations is lacking. Thus, the objective of this study was to examine this town-level association measured by the prevalence of asthma and COPD among the population aged 65 years or older per town in Connecticut and Rhode Island.

We addressed the following research questions: 1) Are town-level prevalence rates of asthma and COPD among adults aged 65 years or older associated with town-level COVID-19 death rates? 2) After controlling for other confounding town-level factors associated with the study variables, is there an association between the town-level prevalence of chronic lung conditions among adults aged 65 years or older and COVID-19 death rates?

Connecticut and Rhode Island have higher rates of asthma and similar rates of COPD compared with average rates among the US population aged 65 years or older (7). Additionally, more than 90% of COVID-19 deaths in these 2 states have been among adults aged 60 years or older (8,9), making this study population an appropriate sample to investigate the association between rates of chronic lung conditions and COVID-19 death rates.

Methods

We used data from several publicly available data sets: the Connecticut Department of Public Health and Office of Policy and Management (8), the Rhode Island Department of Public Health (9), the 2021 Connecticut Healthy Aging Data Report (HADR) (10), the 2020 Rhode Island HADR (11), and the US Census Bureau's 2014–2018 American Community Survey (12). Institutional review board approval was not required because no individual-level data were used.

Measures

COVID-19 deaths. The outcome of interest was the total number of COVID-19 deaths from March 2020 through October 7, 2021, for each reported geographic unit (towns and cities; hereinafter, towns) in Rhode Island ($n = 39$) and Connecticut ($n = 169$). We obtained these data from the Connecticut Open Data Portal (8) and the Rhode Island Department of Health (9). If a town reported fewer than 5 deaths but more than 0 deaths, the data were suppressed for reasons of confidentiality (9); data for 6 towns in Rhode Island were suppressed. Because each of these towns reported 1 to 4 deaths, we recoded them as having 1 death to represent

towns with *any* reported deaths to distinguish them from towns with *no* deaths. We calculated population-adjusted COVID-19 death rates to account for differences in the population size of each town ($N = 208$ towns; total population range, 827–179,435).

Chronic lung conditions. Chronic disease measures reported in the HADR were obtained and estimated from the annual summaries of Medicare claims of beneficiaries aged 65 years or older in the 2016–2017 Medicare Beneficiary Summary Files (13). The HADR calculates chronic condition prevalence rates through clinical algorithms applied to individual Medicare fee-for-service claims (13,14). If a beneficiary 65 years or older in 2017 *ever* met the claims-based diagnostic criteria for asthma or COPD since 1999, they were considered *ever* diagnosed with the chronic condition. Criteria were having at least 1 Medicare claim for an inpatient, skilled nursing facility, or home health care or at least 2 hospital outpatient or Part B Medicare claims with appropriate diagnosis codes during a 1-year period. Thus, the prevalence rates of chronic conditions reported in the HADR may be slightly higher than the current prevalence rates among beneficiaries reported by other Centers for Medicare & Medicaid Services sources, because the HADR includes beneficiaries who were *ever* diagnosed since 1999 (14).

The asthma measure was coded as the prevalence rate of asthma among residents 65 years or older who *ever* met diagnostic criteria (14). COPD is a group of lung diseases that includes emphysema and chronic bronchitis, characterized by causing airflow blockage and breathing-related problems (15). The COPD measure was coded as the prevalence rate of COPD among residents 65 years or older who *ever* met diagnostic criteria (14).

Covariates. We obtained data on all covariates from the 2021 Connecticut HADR (10), the 2020 Rhode Island HADR (11), and the 2014–2018 American Community Survey (12). Previous research (16,17) identified factors associated with high COVID-19 death rates at the town and county levels. At the town level, increased household size and proportion of non-US-born residents and African Americans independently predicted increased COVID-19 death rates (16). County-level factors associated with increased COVID-19 infection and death were increases in household size and proportion of non-US-born residents, African American residents, low educational attainment, and the proportion of all commuters using public transportation (17). Thus, to account for potential confounding factors associated with town-level COVID-19 death rates, we included the following covariates: the average household size in each town, the percentage of the town population aged 65 years or older that was African American or Hispanic, the percentage of the town population aged 65 years or older that had less than a high school diploma, the percentage of all commuters using public transportation, and the proportion of

non-US-born residents. In addition, poverty, obesity, smoking, and proportion of African Americans are community-level risk factors associated with asthma prevalence (18). Therefore, we added the following covariates: among residents aged 65 years or older, the percentage living in poverty, the percentage with obesity, and the percentage with tobacco use disorder. Finally, rurality was identified as a community-level factor associated with COPD (19); therefore, we included rural status as a covariate.

The HADRs include more than 190 indicators drawn from more than 20 data sources and reported at local levels (ie, zip codes, neighborhoods, towns, cities) (20). The HADR recodes and categorizes the race and ethnicity of the state population aged 65 years or older as White, African American, Asian, “other” race, and Hispanic/Latino. The HADR defines “other” race as persons reporting their race as Native Hawaiian or Other Pacific Islander, American Indian or Alaskan Native, other tribal entities, 2 or more races, or any other category not captured in previous categories (14). Educational attainment of the state population aged 65 years or older was coded into less than a high school diploma or GED (General Educational Development), high school diploma or some college, college degree, and graduate or professional degree. The percentage of the state’s population 65 years or older living in poverty is defined by the American Community Survey as the percentage of people aged 65 years or older reporting an annual household income at or below the federal poverty level. The average household size is defined by the American Community Survey as the average number of persons per household. We obtained data on the non-US-born population from the 2014–2018 American Community Survey (12); we recoded these data as the percentage per town. We obtained data on the rate of a town’s population that commutes to work and the percentage of all commuters using public transportation from the 2014–2018 American Community Survey (12). Town prevalence of obesity and tobacco use disorder among the population aged 65 years or older was obtained from the 2016–2017 Master Beneficiary Summary File (9) and coded as the prevalence rate among residents 65 years or older who ever met the diagnostic criteria (14). Towns were considered rural if they were inside a rural county as defined by the Office of Management and Budget (21).

Analytic strategy

We combined data on all towns in both states for a total study sample of 208 towns. We conducted a multistep analysis to examine the association between the independent variables (town-level prevalence of asthma and COPD) and the dependent variable, COVID-19 death rates. First, we conducted pairwise correlations between the rate of COVID-19 deaths per 100,000 people and 1) asthma prevalence and 2) COPD prevalence. We calculated tertiles of asthma prevalence, COPD prevalence, and the population-

adjusted COVID-19 death rates to represent low, medium, and high rates for asthma (low, 9.5%–12.8%; medium, 12.9%–14.71%; high, 14.72%–19.1%); for COPD (low, 11.1%–18.9%; medium, 19.0%–22.8%; high, 22.9%–33.7%); and COVID-19 death rate per 100,000 people (low, 0–101.8; medium, 103.2–237.8; high, 239.3–1,694.7). Next, we created 2 bivariate choropleth maps in ArcMap version 10.8.2 (Esri) to visualize the intersection of low, medium, and high levels of asthma, COPD, and COVID-19 death rates. Finally, to account for confounding factors influencing COVID-19 death rates and chronic lung conditions at the town level, we estimated a series of multiple linear regression models. We used the variance inflation factor (VIF) before estimating the linear regression models to test for multicollinearity among the study variables. The VIF for all study variables was less than 4.07, below the standard threshold of less than 10, suggesting that study variables were not significantly correlated with one another. In preliminary analyses (Models 1 and 2), we examined the main effects of the independent variables (the prevalence of asthma and the prevalence of COPD in the population aged ≥ 65 y) separately. Model 3 estimated the main effects of both chronic lung conditions together. Model 4 estimated the main effect of asthma alone on COVID-19 death rates controlling for factors found in previous literature to predict county-level COVID-19 (16,17) and asthma (18). Finally, Model 5 added in the main effect of COPD and rural status as a covariate to Model 4. We conducted all statistical analyses in Stata version 17 (Stata-Corp LLC). *P* values of $\leq .05$ were considered significant.

Results

Across all towns in both states, the average rate of COVID-19 deaths per 100,000 people was 200.2 deaths per town (Table 1). The prevalence of asthma was 13.8%, and the prevalence of COPD was 21.2%. The average town population was 22,299 people and 3,662 people aged 65 years or older. Most of the overall sample was White (93.9%) and had attained some college (53.5%). Of the population aged 65 years or older, 23.5% had obesity and 10.1% had tobacco use disorder. In addition, 11.5% of the overall sample were not US born, 2.5% commuted to work using public transportation, and 6.0% of the population aged 65 years or older were living in poverty. The average household size was 2.5 people per home and did not differ across the 2 states. Finally, 19.7% of the overall sample lived in rural counties; 24.3% of the sample in Connecticut lived in rural counties, whereas Rhode Island had no rural counties ($P < .001$ for difference between 2 states).

Overall, the Connecticut sample was slightly more diverse, healthier, and wealthier than the Rhode Island sample. Connecticut had an average of 196.9 deaths per 100,000 people from COVID-19

per town (vs 214.4 in Rhode Island and 200.2 overall). In bivariate analyses, we found a significant difference in the prevalence of asthma among adults aged 65 years or older by state (Connecticut, 13.7%; Rhode Island, 14.5%) and in the overall sample (13.8%). Compared with Rhode Island, Connecticut had a lower rate of COPD (20.9%) and a higher rate of people aged 65 years or older with a graduate or professional degree (18.1%). The average town population aged 65 years or older in Connecticut (n = 3,477) was lower than in Rhode Island (n = 4,467) and overall (n = 3,662). We found a significant difference between states for rates of obesity and poverty; among residents aged 65 years or older, Connecticut had a lower prevalence of obesity (22.3%) and a lower rate of residents aged 65 years or older living in poverty (5.3%). Finally, Connecticut had a lower rate of non-US-born residents (9.0%).

Rhode Island had a higher prevalence than Connecticut of asthma (14.5%), COPD (22.2%), and obesity (28.3%) among people aged 65 years or older. Towns in Rhode Island had worse health, were poorer, older, and less educated than towns in Connecticut. In Rhode Island, of the population aged 65 years or older, 8.7% lived in poverty and 16.3% had less than a high school diploma. Finally, Rhode Island had more than twice as many non-US-born residents as Connecticut (22.4% vs 9.0%).

We found significant correlations between town-level asthma prevalence among people aged 65 years or older and rate of COVID-19 deaths per 100,000 people ($r[206] = 0.15$; $P = .03$) and town-level COPD prevalence among residents aged 65 years or older and rate of COVID-19 deaths per 100,000 people ($r[206] = 0.15$; $P = .03$). Medium and high rates of chronic lung conditions and COVID-19 overlapped mainly in southwestern, central, and eastern Connecticut and in central and northern Rhode Island (Figure 1 and Figure 2).

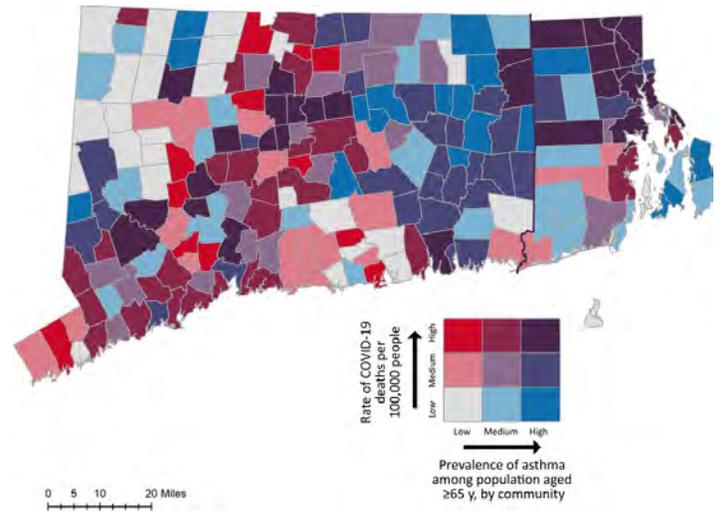


Figure 1. Town-level prevalence of asthma among population aged 65 years or older and COVID-19 death rates per 100,000 people, Connecticut and Rhode Island. Data sources: Connecticut Department of Public Health (8), Rhode Island Department of Public Health (9), HealthyAgingDataReports.org (10,11), CT DEEP GIS (22), and RIGIS (23).

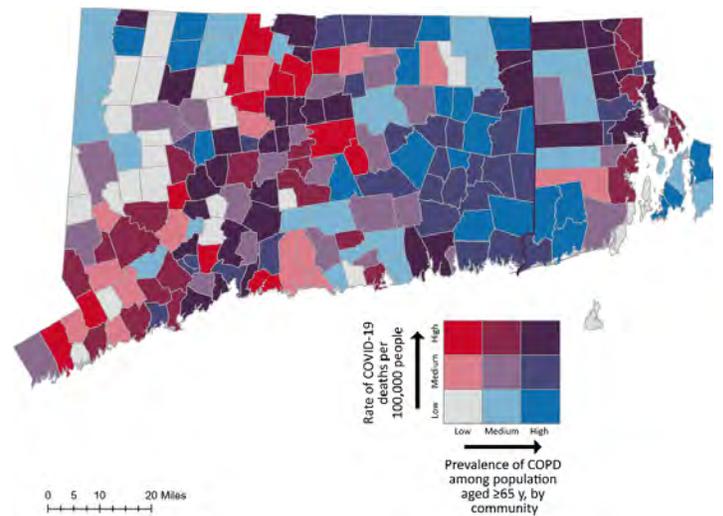


Figure 2. Town-level prevalence of COPD among population aged 65 years or older and COVID-19 death rates per 100,000 people, Connecticut and Rhode Island. Data sources: Connecticut Department of Public Health (8), Rhode Island Department of Public Health (9), HealthyAgingDataReports.org (10,11), CT DEEP GIS (22), and RIGIS (23).

In Model 1, the main effect of town-level prevalence of asthma among residents aged 65 years or older was significant, and the model positively predicted COVID-19 death rates ($\beta = 0.15$, SE, 619.02; 95% CI, 111.79–2,552.62; $P = .03$). Model 2 found a significant, positive association between town-level prevalence of

COPD among residents aged 65 years or older and COVID-19 death rates per 100,000 people ($\beta = 0.15$; SE, 298.12; 95% CI, 48.78–1,224.3; $P = .03$). In Model 3, the significant effect disappeared (Table 2). Model 4 did not demonstrate a significant main effect for asthma ($\beta = 0.02$; SE, 860.31; 95% CI, –1,525.4 to 1,868.2; $P = .84$), but it did show a positive, significant effect in towns with a higher percentage of African American residents aged 65 years or older ($\beta = 0.23$; SE, 254.11; 95% CI, 191.86–1,194.26; $P = .01$) and residents aged 65 years or older without a high school diploma ($\beta = 0.42$; SE, 285.49; 95% CI, 454.55–1,580.72; $P = .001$). Model 5 also did not find a significant main effect between asthma ($\beta = 0.04$; SE, 893.12; 95% CI, 1,436.41–2,086.86; $P = .72$) or COPD ($\beta = 0.02$; SE, 568.27; 95% CI, –1,036.83 to 1,204.94; $P = .99$) and COVID-19 death rates, but multiple covariates had significant effects. Like Model 4, Model 5 showed that towns with a higher percentage of African American residents aged 65 years or older ($\beta = 0.19$; SE, 249.18; 95% CI, 83.8–1,066.8; $P = .02$) and residents aged 65 years or older without a high school diploma ($\beta = 0.45$; SE, 278.98; 95% CI, 529.06–1,629.6; $P = .001$), reported positive associations with COVID-19 death rates. In Model 5, which added COPD, a negative, significant effect was found for the Hispanic population aged 65 years or older ($\beta = -0.23$; SE, 407.43; 95% CI, –1,652.8 to –45.52; $P = .04$) and the population living in rural areas ($\beta = -0.13$; SE, 809.17; 95% CI, –184.92 to –55.95; $P = <.001$). These findings suggest that in our sample, as rurality and the percentage of residents who are Hispanic increased, COVID-19 death rates decreased.

Discussion

This study advanced the research by examining the association between town-level chronic lung conditions and mortality from COVID-19. First, pairwise correlations and bivariate mapping suggested an association between town-level chronic lung conditions (asthma, COPD) and death from COVID-19. The bivariate maps demonstrated multiple clusters in Connecticut and Rhode Island where the prevalence of asthma and COPD among residents aged 65 years or older overlapped with the rate of COVID-19 deaths at the town level. In a comparison of our bivariate maps and maps of variables from the 2021 Connecticut (10) and 2020 Rhode Island HADRs (11), the clusters in southwestern and central Connecticut in both maps are in an area of Connecticut with high proportions of people who are aged 65 years or older, African American, or Hispanic, or have low income and low educational attainment. Additionally, eastern Connecticut is largely rural and has high rates of asthma, COPD, obesity, tobacco use disorder, and older adults living in poverty. Northern Rhode Island also has high proportions of people aged 65 years or older, African American, or Hispanic, or who have low income, obesity, or

low educational attainment (10,11). Although our bivariate maps demonstrated an association, a comparison of these maps with other maps of variables in the 2021 Connecticut and 2020 Rhode Island HADRs (10,11) showed that this association may be driven by other town-level factors.

In Model 4, although we found no significant effect for asthma prevalence predicting COVID-19 death rates among the population aged 65 years or older, the percentage of the population that was African American and aged 65 years or older and the population with less than a high school education had a positive, significant association with COVID-19 death rates. Furthermore, towns with a high proportion of older adults with low educational attainment were also more likely than towns without these characteristics to report higher rates of COVID-19 death rates. A previous study (17) also found that less than a high school education independently predicted at the county level a higher rate of COVID-19 deaths per 100,000 people across the US. Our study also found this effect at the town level among the population aged 65 years or older, underlining the robustness of this association. Thus, this finding suggests that towns with large populations of older adults with low levels of education are especially vulnerable to death from COVID-19.

The final model included both chronic lung conditions and rurality as the final covariate. Although we found no significant main effects, we found that the following covariates were significantly associated with COVID-19 death rates: percentage of population that was African American or Hispanic, aged 65 years or older, or had less than a high school education; average household size; and rurality. The positive, significant association between the African American population aged 65 years or older and mortality was slightly reduced, but the association became slightly stronger between the population that was aged 65 years or older with less than a high school education and COVID-19 death rates. Furthermore, we found a negative, significant effect between 1) the association between rurality and COVID-19 death rates and 2) the Hispanic population aged 65 years or older and mortality. These data suggest that rural towns and towns with large populations of Hispanic people aged 65 years or older had lower rates of COVID-19 deaths per 100,000 people than urban towns without large populations of Hispanic people aged 65 years or older. This finding is confounding because CDC reports that African American and Hispanic people are 1.9 and 2.1 times, respectively, more likely than White people to die of COVID-19 (24). Yet, the “Hispanic paradox” (25) indicates that although older Hispanic people are not healthier than older non-Hispanic people, they have lower rates of mortality and the highest life expectancy in the US (26). Future research could examine this relationship more closely. Finally, our study found that living in a rural county protected against COVID-

19 death rates in Connecticut. However, previous research found that rurality is associated with higher rates of COVID-19 deaths at the county level (27). Our study used a population-adjusted indicator of COVID-19 death rates; only 2 counties in our sample were defined as rural, and both were in Connecticut. Population density may affect the transmission of highly contagious airborne viruses, and living in urban, densely populated areas may increase the everyday risk of COVID-19 exposure (28).

This study has several potential limitations. Although we found that more than 90% of COVID-19 deaths in Connecticut and Rhode Island were among the population aged 60 years or older, the measures of chronic conditions and population characteristics used represented the population aged 65 years or older, and the COVID-19 death rates data were reported for all ages in these states; thus, the age groups do not align exactly across data sources. Additionally, the research design was cross-sectional, so causation could not be determined. Furthermore, this study examined only asthma and COPD; perhaps the study of other common chronic lung conditions would show different results.

Our research fills a gap in the knowledge base of the association between town-level rates of asthma and COPD among older adults and COVID-19 death rates. Our analysis did not find that the prevalence rates of asthma and COPD among the population aged 65 years or older predicted COVID-19 death rates. Yet it did find significant associations between town-level factors and COVID-19 death rates, adding to the knowledge base indicating that large proportions of racial and ethnic minority groups and low educational attainment among the population aged 65 years or older are significant predictors of town rates of COVID-19 deaths.

Future research could examine how demographic indicators most relevant to older adults are associated with COVID-19 death rates at the town level and whether the indicators found for the overall population are the same for the older adult population. Finally, this research identified communities in Connecticut and Rhode Island at the highest risk for hospitalization and mortality from COVID-19. These communities would benefit from additional policy efforts that promote and provide COVID-19 testing and access to vaccination.

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Tables

Table 1. Descriptive Statistics for Study Sample and Bivariate Analyses, by State, Study of Town-Level Prevalence of Chronic Lung Conditions and Death From COVID-19 Among Older Adults in Connecticut and Rhode Island

Factor	Both states	Connecticut	Rhode Island	t Statistic
No. of communities	208	169	39	—
Variable				
Population aged ≥65 y with asthma, %	13.8	13.7	14.5	-2.29 ^a
Population aged ≥65 y with COPD, %	21.2	20.9	22.2	-1.69
COVID-19 death rates per 100,000 people	200.2	196.9	214.4	-0.53
Characteristic				
Total population, no. (SD)	22,299 (26,832)	21,192 (25,564)	27,093 (31,679)	-1.24
Population aged ≥65 y, no. (SD)	3,662 (3,591)	3,477 (3,463)	4,467 (4,051)	1.56
Race and ethnicity of population aged ≥65 y, %				
African American	2.9	3.2	1.7	1.40
Asian	1.5	1.6	1.1	1.70
Hispanic/Latino	2.9	2.9	2.8	0.11
Other ^b	1.6	1.5	2.1	-1.17
White	93.9	93.6	95.2	-1.05
Education of population aged ≥65 y, %				
Less than high school diploma	12.3	11.4	16.3	-3.68 ^c
High school diploma or some college	53.5	53.9	51.7	1.23
College degree	16.5	16.6	16.3	0.11
Graduate or professional degree	17.7	18.1	15.7	1.73
Population aged ≥65 y with obesity, % ^d	23.5	22.3	28.3	-7.66 ^c
Population aged ≥65 y with tobacco use disorder, % ^d	10.1	10.1	10.4	-0.56
Population aged ≥65 y living at or below federal poverty level, %	6.0	5.3	8.7	-5.26 ^c
Population not US born, %	11.5	9.0	22.4	-3.39 ^c
Commute to work using public transportation	2.5	2.7	1.7	1.47
Average household size (SD)	2.5 (0.2)	2.5 (0.2)	2.5 (0.2)	1.92
Rural ^e	19.7	24.3	0	3.52 ^c

Abbreviation: —, does not apply; COPD, chronic obstructive pulmonary disease.

^a $P < .05$.

^b Other race is defined in the Health Aging Data Report as Native Hawaiian or Other Pacific Islander, American Indian or Alaskan Native, and other tribal entries, ≥2 races, or any other race not represented in previous categories (10,11).

^c $P < .001$.

^d Prevalence of the condition is defined as being ever diagnosed with the condition in the Medicare Beneficiary Summary File since 1999 (13,14).

^e Living in a town in a rural county as defined by the Office of Management and Budget (21).

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Table 2. Results of Multiple Linear Regression for Association Between Town-Level Chronic Lung Conditions and Rate of COVID-19 Death Rates per 100,000 People, Connecticut and Rhode Island

Variable	Model 3, ^a β (SE) [95% CI]	Model 4, ^b β (SE) [95% CI]	P value	Model 5, ^c β (SE) [95% CI]	P value
Main effects					
Prevalence of asthma among population aged ≥ 65 y ^d	0.09 (807.37) [-769.22 to 2,414.39]	0.02 (860.31) [-1,525.4 to 1,868.2]	.84	0.04 (893.12) [1,436.41 to 2,086.86]	.72
Prevalence of COPD among population aged ≥ 65 y ^d	0.09 (388.77) [-384.22 to 1,148.77]	—	—	0.02 (568.27) [-1,036.83 to 1,204.94]	.99
Covariates					
Percentage of residents aged ≥ 65 y that are African American	—	0.23 (254.11) [191.86 to 1,194.26]	.01	0.19 (249.18) [83.8 to 1,066.8]	.02
Percentage of population aged ≥ 65 y that are Hispanic	—	-0.19 (411.05) [-1,524.17 to 97.28]	—	-0.23 (407.43) [-1,652.8 to -45.52]	.04
Percentage of population aged ≥ 65 y without a high school diploma	—	0.42 (285.49) [454.55 to 1,580.72]	.001	0.45 (278.98) [529.06 to 1,629.6]	.001
Prevalence of obesity among population aged ≥ 65 y ^d	—	0.13 (376.24) [-246.84 to 1,237.28]	—	—	—
Prevalence of tobacco use disorder among population aged ≥ 65 y ^d	—	-0.17 (649.65) [-2,403.74 to 158.89]	—	-0.14 (809.17) [-2,464.49 to 727.64]	—
Percentage of population aged ≥ 65 y living at or below federal poverty level	—	-0.15 (523.69) [-1,795.81 to 269.96]	—	-0.15 (512.76) [-1,731.98 to 290.8]	—
Percentage of population not US born	—	-0.07 (0.56) [-1.63 to 0.57]	—	-0.09 (0.54) [-1.81 to 0.34]	—
Commute to work using public transportation	—	-0.09 (3.22) [-10.44 to 2.27]	—	-0.06 (3.17) [-9.24 to 3.26]	—
Average household size	—	-0.14 (68.97) [-264.59 to 7.48]	—	-0.17 (67.43) [-288.81 to -22.81]	.02
Rural ^e	—	—	—	-0.13 (809.17) [-184.92 to -55.95]	<.001

Abbreviations: —, does not apply; COPD, chronic obstructive pulmonary disease.

^a Model 3: Constant = 5.44; adjusted R^2 = 0.02.

^b Model 4: Constant = 435.81; adjusted R^2 = 0.11.

^c Model 5: Constant = 537.6; adjusted R^2 = 0.16.

^d Prevalence of the condition is defined as being ever diagnosed with the condition in the Medicare Beneficiary Summary File since 1999 (13,14).

^e Living in a town in a rural county as defined by the Office of Management and Budget (21).

GIS SNAPSHOTS

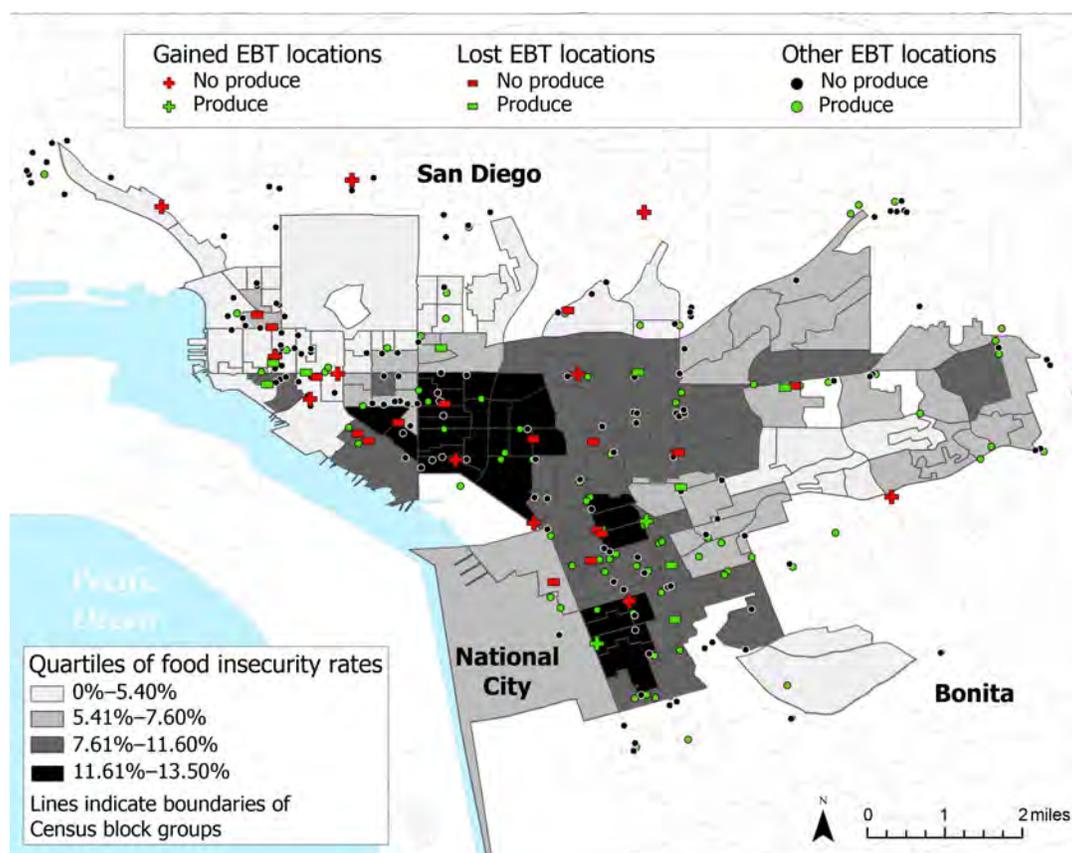
Mapping EBT Store Closures During the COVID-19 Pandemic in a Low-Income, Food-Insecure Community in San Diego

Bryce C. Lowery, PhD¹; Madison R.E. Swayne, PhD²; Iana Castro, PhD³; Jessica Embury, BS⁴

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Changes in access to EBT food retailers in Promise Zone communities before (2019) and during (2021) the COVID-19 pandemic, San Diego. Food insecurity rates in 2018 obtained from the California Health Interview Survey AskCHIS Neighborhood Edition (1). EBT store locations obtained from US Department of Agriculture SNAP Retailer Database (2) for July 23, 2019, and July 23, 2021. Abbreviations: EBT, electronic benefits transfer; SNAP, Supplemental Nutrition Assistance Program.



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Background

Access to food retailers that accept electronic benefits transfer (EBT) can help reduce nutritional inequalities among low-income individuals and families experiencing food insecurity. According to the US Department of Agriculture (USDA), nearly all recipients of the Supplemental Nutrition Assistance Program (SNAP) receive benefits via EBT rather than via paper vouchers (3). The transition from physical vouchers to EBT improved enrollment by reducing the stigma associated with paper vouchers and streamlining the process for distribution of benefits (4). Food retailers that accept EBT may be spatially dispersed in ways that make it difficult for low-income residents to access nutritional resources needed to lead a healthy life (5). Proximity to stores that accept EBT supports food security in communities coping with the challenges of poverty.

The COVID-19 pandemic disproportionately affects low-income communities experiencing food insecurity because of 1) the increased risk for infection among people coping with conditions associated with food insecurity and 2) the effects of the pandemic on physical and financial access to sources of nutrition. The pandemic has increased rates of food insecurity (6) by affecting the supply of food and the capacity of individuals to afford food (7,8). People experiencing poverty are at increased risk for COVID-19 (9), and conditions typically associated with food insecurity, such as obesity, diabetes, and cardiovascular disease, are contributors to intensive care admission and in-hospital mortality among patients diagnosed with COVID-19 (10).

The pandemic instigated an economic downturn that shuttered many businesses that provide food, closed schools where children ate, and left many without jobs. During the first month of the pandemic, approximately 30% of US children, particularly those in low-income and racial and ethnic minority groups, experienced household food insecurity (11). In San Diego, the pandemic has had a similar impact: 44% of Black and Hispanic/Latine residents have experienced food insecurity, compared with 25% of the overall population (12). Nationwide, communities responded to these changes; 17% more families applied for SNAP (13) to help mitigate food inaccessibility and unaffordability (14). EBT programs, like Pandemic-EBT, were created to help families purchase food, and evidence suggests that these programs reduced food hardship (6). However, the availability of stores that accept EBT and changes to these stores during the pandemic have not been described in detail.

We expand existing research on food insecurity to explore changes in the availability of stores that accept EBT during the pandemic, including grocery stores and small food retailers like convenience

stores and small markets. Our objective was to identify how the availability of stores that accept EBT payments, authorized by SNAP, changed in an area of San Diego County with long-standing patterns of food insecurity.

Data and Methods

Our study area included 159 low-income census block groups (CBGs) in 4 zip codes in the federally designated San Diego Promise Zone (92101, 92102, 92113, 92114) and 1 zip code from National City (91950), an adjacent neighborhood. Promise Zones are designated by the US Department of Housing and Urban Development (15) as areas that receive special assistance for community revitalization. This study area comprised 15.5 square miles, approximately 279,511 people, and some of San Diego's most food-insecure zip codes (12,16). We overlaid 2021 land-use data from the San Diego Association of Governments in each CBG. We included CBGs that contain any amount of residential land use, including single family and multifamily.

We downloaded the location of stores that accepted EBT payments from the USDA's online SNAP Retailer Locator tool (2) on July 23, 2019, and 2 years later, on July 23, 2021. Stores on the EBT list for San Diego County include large-scale supermarkets, small-scale local grocers, specialty markets (eg, bakery, butcher), convenience stores, gas station markets, and liquor stores. We coded each EBT store according to the presence of fresh produce reported previously (17) and locations serviced by BrightSide Produce (www.brightside.sdsu.edu), an initiative designed to support the availability of fruits and vegetables at small markets, convenience stores, and liquor stores that accept EBTs.

We mapped EBT retailer locations and spatially joined them to the 2019 CBG boundaries using ArcGIS Pro version 2.8 (Esri). We used buffer analysis to compute the number of EBT retailers within a ½-mile walking distance (18) of the boundary of each CBG in 2019 and again in 2021 to examine changes after the COVID-19 shutdown. The map of EBT retailers across both periods was overlaid with census tract-level data on food insecurity (proportion of adults aged ≥18 y who are low income and food insecure) obtained from the 2018 California Health Interview Survey AskCHIS Neighborhood Edition online data platform (1); we matched these data to CBG geographies. We used additional CBG-level data from the 2019 American Community Survey (16) to estimate median household income, poverty, education, vehicle ownership, and race and ethnicity. Maps were exported and rendered in Adobe Illustrator 2021. We used Mann-Whitney non-parametric tests to explore differences between each socioeconomic variable retrieved from the US Census for CBGs that lost EBT access and those that gained EBT access. The number of CBGs

that gained access to stores that accept EBT with fresh produce was too small to compare (via statistical testing) with the number of CBGs that lost stores that accept EBT with fresh produce, so we reported descriptive statistics only.

Highlights

The study area comprised 200 EBT stores on July 23, 2019; by July 23, 2021, twenty-three stores had been removed from San Diego County's EBT list and 7 stores had been added, resulting in 184 stores (a net loss of 16 [−8.0%] stores). The 23 stores that either closed or stopped accepting EBT were 1 full-service supermarket, 3 bakeries, 3 produce outlets, 1 ice cream shop, 1 pharmacy, 11 convenience stores, 1 gas station, 1 fish market, and a food delivery service. Stores added to the EBT list included 6 convenience stores and 1 pharmacy; the full-service supermarket was not replaced. In 2019, 128 (64.0%) stores offered produce, and in 2021, 121 (65.7%) offered produce (including 2 of 7 new stores). Seven of the 23 closed stores had offered fruits and vegetables. Although fewer stores in 2021 accepted EBT, the percentage of stores that offered produce was similar.

Two-thirds of CBGs (105 of 159; 66.0%) lost access to 1 or more (range, 1–6) EBT stores within ½ mile, and 13 (8.2%) CBGs gained 1 EBT store (Table). Over time, the average number of EBT stores accessible within ½ mile declined by 1.2 stores on average across all CBGs. Mann–Whitney nonparametric tests suggested that the CBGs that lost EBT access, compared with CBGs that gained EBT access, had significantly lower median incomes ($U = 377.0$, $P = .01$), higher poverty rates ($U = 431.5$, $P = .03$), lower high school graduation rates ($U = 422.0$, $P = .02$), a higher proportion of households with no vehicle ($U = 430.5$, $P = .03$), larger Hispanic/Latine populations ($U = 361.0$, $P = .006$), and higher food insecurity rates ($U = 424.0$, $P = .03$). Although we could not use statistical testing, we observed that CBGs that lost EBT stores that carried fresh produce were more varied in socioeconomic composition and experienced lower rates of food security than CBGs that gained fresh produce access.

Action

The loss of EBT stores during the pandemic affected food access to a greater degree among residents in communities experiencing hardships (eg, financial insecurity, lack of vehicle) than in communities experiencing these hardships to a lesser degree. Mapping and monitoring of food insecurity in neighborhoods of concern is crucial as the pandemic continues. Challenges not studied here may affect the number of EBT stores residents can access. As federal income assistance wanes, the demand for food outlets that accept EBT will likely increase. Research on local food landscapes

should consider these changing contexts in neighborhoods of long-standing food insecurity. Measures of food retail choice should consider small food retailers, like the ones studied here, along with supermarkets and grocery stores.

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Table

Table. Sociodemographic and Health Characteristics of Census Block Groups (CBGs) in the San Diego Promise Zone and CBGs Inside the Promise Zone That Experienced a Change in EBT (Electronic Benefits Transfer) Access From 2019 to 2021^a

Determinant	All CBGs in Promise Zone (N = 159)	Gained EBT access (n = 13)	Lost EBT access (n = 105)	Gained EBT access with fresh produce (n = 5)	Lost EBT access with fresh produce (n = 63)
Mean change in EBT access	-1.2	1	-2.0	1	-1.4
Total population	279,511	19,364	186,801	14,310	117,430
% Households <200% of federal poverty level	18.0	13.3	20.7	15.1	17.1
Average median annual household income, \$	58,660	74,694	54,202	43,338	59,415
% Adult population (age ≥18 y) with high school diploma	77.1	82.7	52.4	54.4	67.6
% Low-income adults (≥18 y) experiencing food insecurity	7.7	5.1	8.1	10.0	6.8
% Population that does not have a vehicle	12.6	6.4	14.8	5.4	16.0
% Population that is Hispanic/Latine	54.3	38.2	57.0	59.2	48.5
% Population that is Black	11.0	13.9	9.6	8.5	11.5

^a Data sources: data on EBT store locations from US Department of Agriculture SNAP Retailer Database (2); data on total population, households <200% federal poverty level; median household income, education, vehicle ownership, and race and ethnicity from the 2019 American Community Survey (16); data on food insecurity from UCLA Center for Health Policy Research (1).

GIS SNAPSHOTS

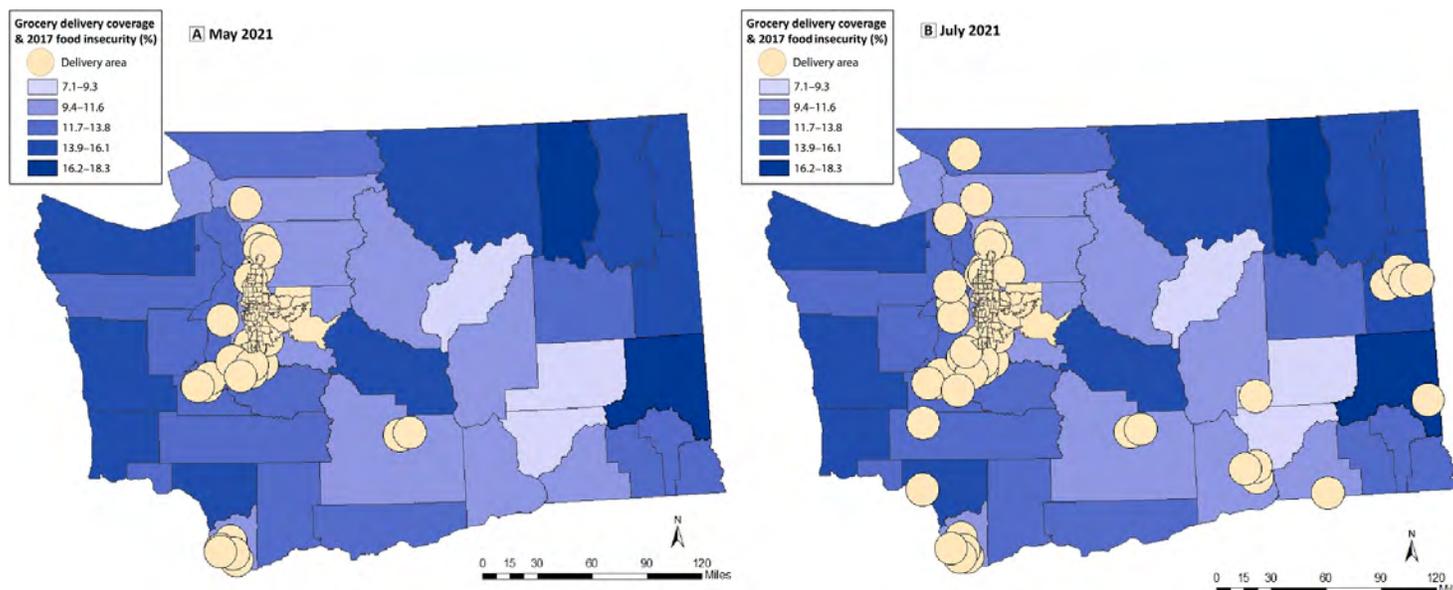
Expansion of Grocery Delivery and Access for Washington SNAP Participants During the COVID-19 Pandemic

Shawna Beese, MBA, BSN, RN^{1,2}; Ofer Amram, PhD, MSc³; Acacia Corylus, MPH, RD²; Janessa M. Graves, PhD, MPH¹; Julie Postma, PhD, RN¹; Pablo Monsivais, PhD, MPH³

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Online grocery delivery access for Washington State Supplemental Nutrition Assistance Program (SNAP) beneficiaries increased between May and July 2021, during the COVID-19 pandemic. The 2017 food insecurity rates spotlight the counties most vulnerable to food insecurity. Sources: Walmart delivery data, <https://www.walmart.com/store/directory>; Amazon delivery data, <https://www.amazon.com>; SNAP benefit data, <https://www.ers.usda.gov/data-products/food-access-research-atlas/download-the-data>; Washington 2010 census tract shapefile, <https://ofm.wa.gov/washington-data-research/population-demographics/gis-data/census-geographic-files>.



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Background

The COVID-19 pandemic ushered in an unprecedented food security crisis that will have long-term health effects (1). As society shut down to slow the spread of SARS-CoV-2, the interruptions tested the limits of our current food supply chain to meet supply and demand (2). Exigencies on our food system, particularly safety-net resources like food banks, increased by 50% nationwide (1). Inequities in access to healthy food became magnified, exacerbating disparities that existed before the pandemic, such as increased risk of food insecurity for people without college degrees and unemployed people (3).

The pandemic generated shifts toward home-based meal preparation and online grocery purchases with home delivery (4,5). State-level pilot programs for online grocery purchase and home delivery for Supplemental Nutrition Assistance Program (SNAP) beneficiaries were already mandated by the 2014 Farm Bill (6), but the pandemic accelerated these initiatives. Modernization of SNAP mirrors efforts spurred on by the pandemic, including national vendors' investments in online grocery delivery infrastructure and expanded delivery services (2). Because of the rapid responses on behalf of private and governmental entities, evaluation of access to delivery services and beneficiary awareness of new online delivery services availability was needed.

The purpose of this GIS Snapshot was to present the results of a geospatial assessment of access to online grocery purchase and home delivery for SNAP beneficiaries in Washington State. A secondary aim of this study was to identify potentially vulnerable populations resulting from the current level of access.

Data Sources and Map Logistics

We mapped the online grocery purchase and delivery coverage for SNAP recipients for Washington State in May 2021 and July 2021. Data sources included the GIS (geographic information system) census tract shapefile from the Washington Office of Financial Management (7). Census tract-level SNAP household data were obtained from the 2015 American Community Survey (ACS), accessed from the US Department of Agriculture Food Environment Atlas website (8).

The approved SNAP Electronic Benefits Transfer (EBT) delivery vendors were confirmed on the Food and Nutrition Service website in May 2021 and July 2021 (9). In July 2021, the 2 approved SNAP EBT online vendors were Amazon and Walmart delivery centers. One other retailer with a single location was also approved for online purchases, but this retailer did not have wide-

spread delivery services, so its 1,530-person catchment was not included. The final analysis and reporting of the evaluation are at the county level.

We used ArcMAP Desktop version 10.8 (Esri) to overlay census tract data with the number of SNAP household units per census tract and the delivery areas of participating vendors. Each census tract was also identified as urban or rural; areas with populations under 2,500 people were classified rural and those with 2,500 people or more were classified urban (10). Delivery areas for Walmart were created with a 9-mile buffer around georeferenced Walmart distribution outlet points for Walmart. We selected a 9-mile radius based on Walmart's delivery area, confirmed on their website in July 2021 and by telephone during confirmation calls to each store (11). The delivery area for Amazon Fresh was created using zip code polygons. All zip codes of the Amazon Fresh delivery services were confirmed on the Amazon Fresh website in July 2021 (12). The number of SNAP households was spatially analyzed by census tract population-weighted centroids within the defined delivery area boundaries.

We mapped the 2017 food insecurity rates by using a choropleth (shaded enumeration of prevalence rates) by county (13). Equal interval data breaks were used to categorize the food insecurity rates, expressed in percentages (13). The data sources for the 2017 food insecurity rates were from the Hunger in Washington website (14). The overall prevalence of food insecurity in Washington State was 11.5% and ranged from 7.1% (Franklin County) to 18.3% (Whitman County) (14).

Highlights

According to 2015 American Community Survey data, 376,467 (11.8%) Washington households were receiving SNAP benefits. In July 2021, during our final analysis, 298,839 (79.4) households receiving SNAP benefits had access to online grocery purchases and delivery (Table). The number of Washington State residents receiving food assistance increased during the COVID-19 pandemic. According to Washington State Economic Services Administration reporting, the number of people on food assistance increased by 16% from September 2019 to July 2020, as reported through management accountability and performance statistics (Economic Services Administration, Management Accountability and Performance Statistics [ESA/EMAPS], the state SNAP client eligibility system).

A preliminary survey conducted in May 2021 confirmed that most online grocery delivery access was concentrated in the Puget Sound region, the state's largest metropolitan area. In July 2021, Walmart launched a delivery service expansion into other urban areas of the state. The expansion increased access from 169,507

(45.0%) of SNAP households statewide in May 2021 to 261,752 (69.5%) of SNAP households statewide. The July 2021 Walmart expansion substantially increased access to home delivery of groceries for Washington State by offering access to areas beyond the Puget Sound region and outlying communities of Vancouver and Yakima. In July 2021, administrative data from the ESA/EMAPS indicated that 2.3% of SNAP benefits were redeemed with online retailers.

Rural counties that were previously designated as food insecure continue to lack access to home delivery. Most households receiving SNAP were included in the new delivery coverage from Walmart's expansion. However, Walmart's expansion of online delivery services is concentrated in more densely populated areas of the state. The 2017 food insecurity rates indicate some of these counties without online delivery access, especially the northeastern Washington counties and the counties along the western coastline, are also food insecure (14).

Action

Our analyses show the expansion of online grocery delivery serving SNAP recipients in Washington State. However, gaps in broadband coverage and lack of home computer technology may still serve as potential barriers to online purchases for rural populations in the state (15,16).

Using administrative data for geographic assessment to quantify access to online grocery delivery services was an essential step, but our analyses did not include assessment of other food assets such as food retail locations, food banks, pantries, and mobile markets (17,18). On the basis of the geographic assessment presented here, next steps include community-based approaches that allow for broader inventory of local food assets, which may be important for food access, particularly in communities with limited online grocery delivery. This involves asset-based inquiry to ground realities from rural food system leaders seeking innovative strategies to provide efficient and equitable solutions for food delivery.

Program administrators and municipal policy makers can use these maps to target underserved areas and strategize building partnerships with local vendors such as farmer's co-ops and regional-based grocery outlets to fill the delivery needs for rural areas.

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Table

Table. Washington State Supplemental Nutrition Assistance Program Online Grocery Delivery Access, May–July 2021

County	Number of households in county in 2015	Number of households with SNAP benefits in 2015	Number (%) of households with SNAP benefits with online delivery access
Adams	6,443	1,265	962 (76.0)
Asotin	9,989	1,782	—
Benton	73,896	10,176	8,992 (88.4)
Chelan	36,890	3,161	—
Clallam	36,526	4,860	—
Clark	175,854	25,515	24,652 (96.6)
Columbia	2,156	352	—
Cowlitz	44,178	8,908	7,280 (81.7)
Douglas	16,592	2,280	—
Ferry	4,485	728	—
Franklin	27,035	5,073	4,291 (84.6)
Garfield	1,245	95	—
Grant	36,385	6,434	—
Grays Harbor	35,816	5,901	—
Island	41,239	3,161	2,251 (71.2)
Jefferson	18,257	1,773	—
King	900,236	86,369	86,019 (99.6)
Kitsap	110,715	12,208	11,996 (98.3)
Kittitas	23,054	2,431	—
Klickitat	10,181	1,205	—
Lewis	34,759	6,373	3,381 (53.1)
Lincoln	5,962	484	—
Mason	33,172	4,103	—
Okanogan	22,901	3,328	—
Pacific	16,036	1,940	—
Pend Oreille	8,163	1,215	—

Abbreviation: —, no delivery available; SNAP, Supplemental Nutrition Assistance Program.

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(continued)

Table. Washington State Supplemental Nutrition Assistance Program Online Grocery Delivery Access, May–July 2021

County	Number of households in county in 2015	Number of households with SNAP benefits in 2015	Number (%) of households with SNAP benefits with online delivery access
Pierce	339,501	44,959	43,334 (96.4)
San Juan	13,908	619	–
Skagit	52,846	7,445	5,439 (73.1)
Skamania	5,777	727	–
Snohomish	302,639	33,385	31,871 (95.5)
Spokane	210,709	33,984	31,890 (93.8)
Stevens	21,524	3,485	–
Thurston	113,750	12,767	11,656 (91.3)
Wahkiakum	2,118	322	–
Walla Walla	24,346	3,556	3,355 (94.3)
Whatcom	94,338	12,460	8,360 (67.1)
Whitman	20,381	1,844	1,252 (67.9)
Yakima	87,809	19,794	11,858 (59.9)
Washington State total	Not applicable	376,467	298,839 (79.4)

Abbreviation: –, no delivery available; SNAP, Supplemental Nutrition Assistance Program.

Sources:

Amazon. Amazon Fresh delivery [interactive database]. <https://www.amazon.com>. Accessed July 20, 2021.

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GIS SNAPSHOTS

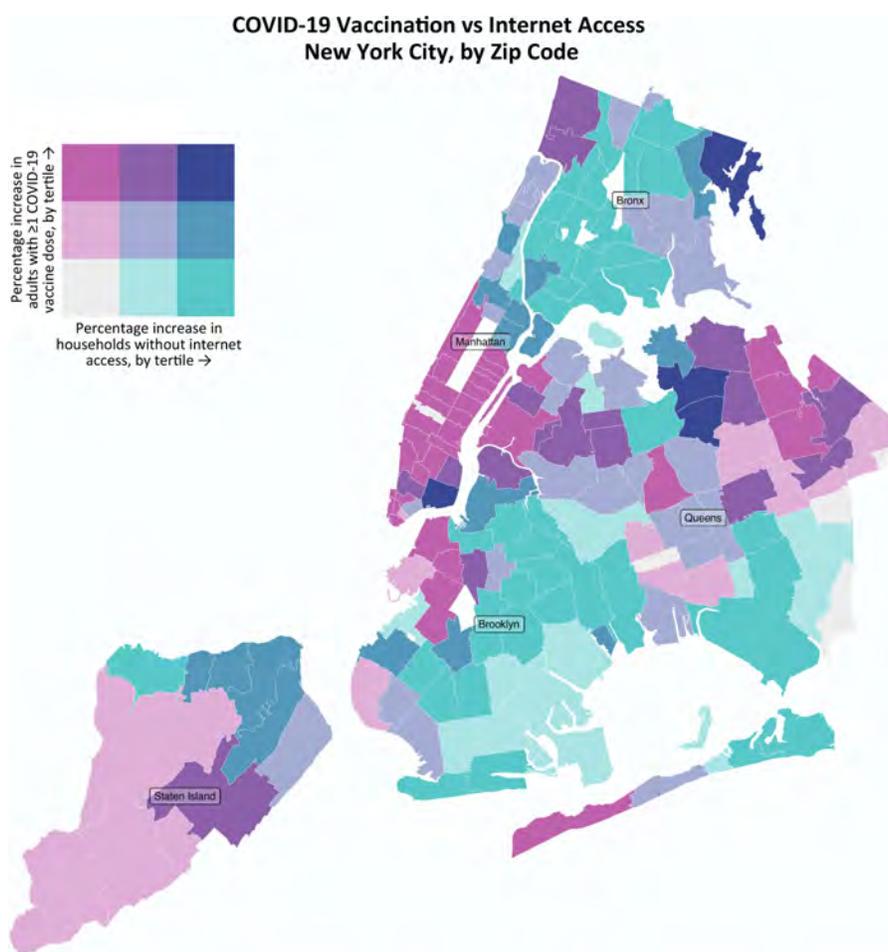
Disparities in Internet Access and COVID-19 Vaccination in New York City

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A bivariate choropleth map that visualizes zip code-level data on household internet access and COVID-19 vaccination in New York City. The map identifies zip codes where the greatest disparities exist. Most disparities are in the Bronx and Brooklyn. This information could be used to place appointment-free vaccination sites in the short term and augment digital education and broadband internet access in the long term. Data on internet access were retrieved from NYC Open Data on April 7, 2021. Vaccination data were retrieved from the New York City Department of Health and Mental Hygiene on April 7, 2021.



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Background

Although COVID-19 is a communicable disease, for many people it could also be a chronic disease (1). In New York City, COVID-19 has had a greater effect on older populations, people living in the outer boroughs of the city's 5 boroughs (eg, the Bronx, Brooklyn, and Queens, compared with Manhattan), people living in poverty, and racial/ethnic minority populations (2). The availability of a COVID-19 vaccine can lessen the effect of the disease on these populations. As of this writing (April 15, 2021), people in New York City had to schedule an appointment to be vaccinated (3), with certain exceptions (4). Many New Yorkers who wanted to be vaccinated were not able to secure appointments, in part because the supply of COVID-19 vaccine was limited (5). Many public health and health care providers use online systems to schedule appointments; as a result, lack of internet access has been suggested as a potential barrier to vaccination (6). We created a map to visualize the community-level distribution of household internet access and COVID-19 vaccination in New York City.

Data and Methods

We obtained estimates of the percentage of households lacking internet access, by zip code, from NYC Open Data (7). Data on internet access were collected by the 2018 5-year American Community Survey. According to NYC Open Data, the American Community Survey frames this question as having "No access to the internet at this house, apartment, or mobile home."

We obtained data on zip code-level percentages of adult residents who received at least 1 COVID-19 vaccine dose from the New York City Department of Health and Mental Hygiene website (8). The vaccination data were obtained from the Citywide Immunization Registry. According to the source data table, "People with at least one dose have received at least one dose of two-dose vaccine series or a single dose shot."

We calculated via simple linear regression the association between the percentage of households without internet access and the percentage of adult residents with at least 1 COVID-19 vaccine dose. Internet access and vaccination data were available for all populated ($n = 177$) modified zip code tabulation areas in New York City (9). We then classified zip codes into 3 internet-access quantiles (tertiles) and 3 COVID-19 vaccination quantiles and visualized them via a bivariate choropleth map (10). We developed the map in R version 4.0.4 (R Foundation for Statistical Computing) by using the tidyverse (11), sf (12), biscale (13), and cowplot (14) packages. All data were retrieved on April 7, 2021.

Highlights

Among zip codes in New York City, the median percentage of households without internet access was 15.5% (SD, 6.7%), ranging from 0% (zip code 10282, Battery Park City, Manhattan) to 32.4% (zip code 10454, Mott Haven/Port Morris, the Bronx). The median percentage of adults that received at least 1 dose of COVID-19 vaccine was 38.2% (SD, 10.0%), ranging from 21.9% (zip code 11691, Edgemere/Far Rockaway, Queens) to 75.0% (zip code 11697, Breezy Point, Queens). In the simple linear regression model, the percentage of households without internet access was negatively associated with the percentage of adult residents who received at least 1 dose of COVID-19 vaccine ($\beta = -0.92$; 95 CI, -1.09 to -0.75 ; intercept = 53.7%; $P < .001$, adjusted $R^2 = 0.38$) (Figure). Most disparities were in the Bronx and Brooklyn.

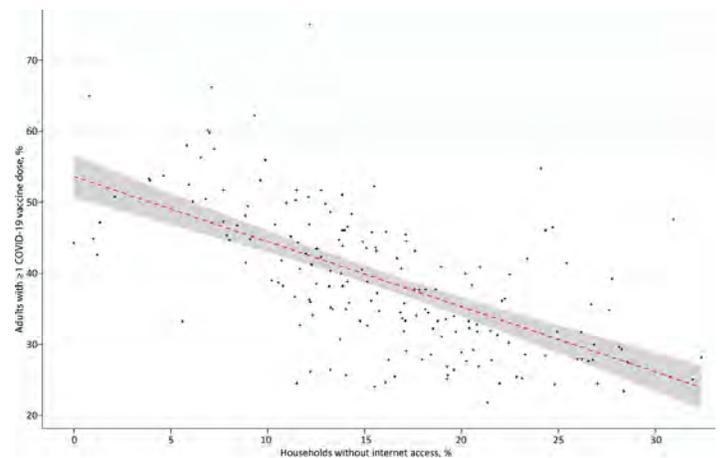


Figure. Association in New York City, at the zip code level, between the percentage of households without internet access and the percentage of adult residents with at least 1 COVID-19 vaccine dose. Each point represents 1 zip code. The dashed line represents a simple linear regression model, and the shaded area indicates 95% CIs. Linear regression summary: $\beta = -0.92$; 95 CI, -1.09 to -0.75 ; intercept = 53.7%; $P < .001$; adjusted $R^2 = 0.38$. Data sources: New York City Department of Health and Mental Hygiene (8), NYC Open Data (7). Data retrieved on April 7, 2021.

Action

COVID-19 vaccination was significantly associated with household internet access in New York City at the zip code level. Although this association neither implies nor precludes causation, and does not control for possible confounders, it is consistent with the hypothesis that lack of internet access is a barrier to vaccination. Internet access is a known social determinant of health (15).

Disparities in internet access exist across multiple socioeconomic dimensions and disproportionately affect low-income neighbor-

hoods (16). A digital health divide in the older population has been widely documented (17). A study published in 2021 suggested that the digital health divide is associated with age, education, income, and race/ethnicity (18).

To facilitate equitable and efficient COVID-19 vaccine uptake in New York City, public health officials should establish appointment-free vaccination sites, work with other agencies and organizations to advocate for legal and policy approaches that increase internet access (19), and increase access to in-person and telephone-based services that provide assistance with vaccine appointment scheduling, especially in zip codes with low rates of internet access. Our map can be used to inform the placement of such interventions. Because most disparities in internet access and vaccination were in zip codes in the Bronx and Brooklyn, appropriate partners for public health officials in these areas include the offices of the borough president, the borough-based New York City Department of Health and Mental Hygiene Neighborhood Health Action Centers, and borough-wide community-based organizations. More generally, we recommend that bivariate mapping be considered when selecting methods for comparing geographic distributions of health determinants and health outcomes.

The availability and accessibility of COVID-19 vaccine in New York City has continued to improve. After this writing, home-based vaccination, appointment-free walk-up vaccination sites, mobile vaccination sites, and pop-up vaccination sites were established (20).

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GIS SNAPSHOTS

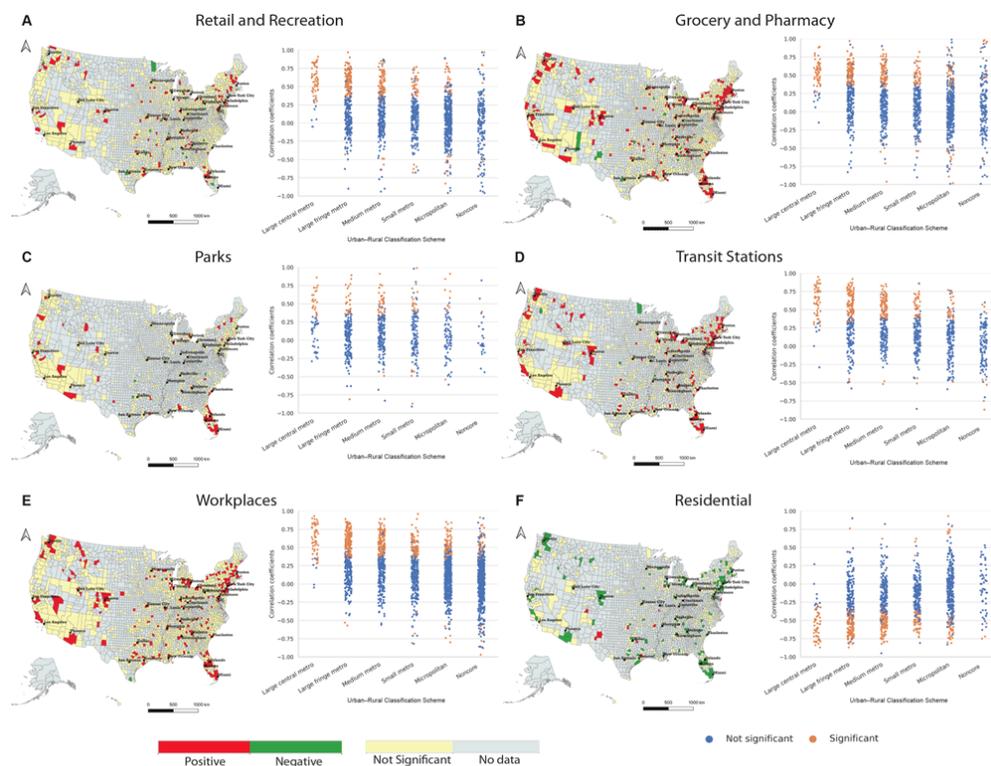
Association Between Population Mobility Reductions and New COVID-19 Diagnoses in the United States Along the Urban–Rural Gradient, February–April, 2020

Xiaojiang Li, PhD, MS¹; Abby E. Rudolph, MPH, PhD²; Jeremy Mennis, MS, PhD¹

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Source: Mobility data are from the Google Community Mobility Report and confirmed COVID-19 case data are from the New York Times, Inc. Urban-rural classification data are from the National Center for Health Statistics.

Spatial distribution of the correlation between change in mobility and percentage increase in new COVID-19 cases 11 days later, from February 15 through April 26, 2020, by US county. Correlations are mapped for visits to 6 different types of places and plotted within 6 different urban–rural classifications. Significance is $P < .05$. A decrease in visits to places outside the home, and an increase in time spent at home, are associated with reduced rates of new COVID-19 cases 11 days later in most counties, suggesting that restrictions on mobility can mitigate COVID-19 transmission. The association is stronger in more urban counties, suggesting that mobility restrictions may be most effective in urban areas. Abbreviation: metro, metropolitan.



The opinions expressed by authors contributing to this journal do not necessarily reflect the opinions of the U.S. Department of Health and Human Services, the Public Health Service, the Centers for Disease Control and Prevention, or the authors' affiliated institutions.

Background

As of July 31, 2020, more than 17 million confirmed novel coronavirus disease 2019 (COVID-19) cases had occurred worldwide with more than 668,000 COVID-19–related deaths (1). More than 4.4 million cases and 151,000 deaths occurred in the United States (2). Pre-existing conditions such as asthma and other respiratory conditions, diabetes, and heart disease are associated with COVID-19 illness severity (3), as is race/ethnicity (4), and chronic health problems may persist among survivors (5). Mitigating the COVID-19 pandemic thus has profound implications for chronic disease prevention and outcomes, health disparities, and overall population health.

The basic reproduction number for an infection, R_0 , is influenced by 3 factors: the probability of infection per contact between an infected and a susceptible individual, the average rate of contact between susceptible and infected individuals, and the average duration of infectiousness. In the absence of pharmaceutical interventions, behavioral interventions that reduce contact rates can reduce viral transmission. In response to the COVID-19 pandemic, state and local governments initially required nonessential businesses, schools, places of worship, restaurants, and bars to close; banned large gatherings; and issued stay-at-home directives to promote social (physical) distancing and reduce contact rates. Investigating the relationship between changes in mobility and future changes in the rate of new COVID-19 diagnoses can reveal the effect of these measures on disease transmission (6,7). We mapped the county-level association between changes in population mobility, derived from location histories captured by GPS embedded in mobile phones (8), and the rate of new confirmed COVID-19 cases 11 days later across the United States. We examined the variation across the urban-to-rural gradient, given differences in population density, travel behaviors, the prevalence of COVID-19, and time since the first case was diagnosed in rural versus urban counties (9).

Data and Methods

County-level daily mobility data for February 15 through April 26, 2020, were obtained from Google’s Community Mobility Report, which comprises aggregated and anonymized data from Google users who turned on the “location history” setting on their cellular telephone (10,11). The data set included 6 location categories, determined by the different types of places encoded within Google Maps: retail and recreation, grocery and pharmacy, parks, transit stations, workplaces, and residential. Daily changes in mobility were measured relative to the median value of travel for the corresponding location type and day of the week from January 3, 2020, through February 6, 2020. County-level daily mobility

change was correlated with the daily county growth rate of COVID-19 cases (12) 11 days later (to account for the average incubation period [13]) plus the time delay between testing and state reporting (14), beginning on the day the first confirmed COVID-19 case was reported in each county. A catplot was used to visualize the distribution of the county-level correlation coefficients and their significance for mobility to each location type, stratified by the 6-level urban–rural classification scheme from the National Center for Health Statistics: large central metropolitan, large fringe metropolitan, medium metropolitan, small metropolitan, micropolitan, or noncore county (15). We repeated the analysis by using a 5-day time lag to test the sensitivity of our results.

Highlights

We plotted the spatial distributions of the correlation coefficients and attendant catplots for each location type. The maps show that retail and recreation, grocery and pharmacy, parks, transit stations, and workplaces generally have significant and positive correlations — a decrease in visits to these locations is associated with a reduced rate of new COVID-19 cases 11 days later. Conversely, an increase in the amount of time spent in residential locations was significantly negatively correlated with an increase in the rate of new COVID-19 diagnoses in most observed counties — staying at home is associated with a slowed growth rate.

Geographic variation is substantial, however, where, in many rural counties, the correlation is not significant. This is illustrated further by the catplots, where for all location types, significant correlations are more likely to occur in urban counties. Indeed, most noncore counties (the most rural) show no significant correlations between change in mobility and the rate of new diagnoses, whereas most large central metropolitan counties show significant correlations for all location types (except parks). Results using the 5-day time lag were consistent with the results presented here.

We acknowledge certain limitations, including extensive missing county mobility data, and that other factors can influence disease transmission and reported cases (eg, testing practices, disease burden, population density, prevalence of chronic health conditions, age distributions, the population living in congregate settings). Additionally, these results reflect cases detected in the United States between February and April, when most states and counties had a combination of stay-at-home directives and business/school closures, and when cases were concentrated in a few urban areas, particularly New York City. In a post-hoc analysis we repeated the analysis by using a February 15 through June 19, 2020, study period. The resulting analogous urban–rural graphs for workplaces and residential places show that the association of mobility reductions with COVID-19 cases we observed for the initial study peri-

od dissipates to some extent, particularly in more rural areas (Figure). Notably, May 2020 was a period of decline in COVID-19 cases in the United States; the initial disease hotspots were cooling, and many states began to phase out mobility-reducing directives. This was followed in June by a rapid increase in COVID-19 cases in Florida, Arizona, and other states that did not act aggressively to reduce mobility and encourage wearing masks, with some states reinstating mobility reduction directives in response.

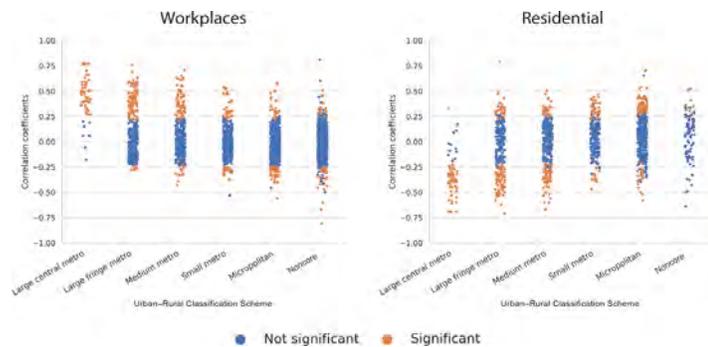


Figure. Post-hoc analysis of correlation between change in mobility and percentage increase in new COVID-19 cases 11 days later for February 15 through June 19, 2020, by US county. Correlations are shown for visits to workplaces and residential places and plotted within 6 different urban–rural classifications. Mobility data are from the Google Community Mobility Report, and confirmed COVID-19 case data are from the New York Times, Inc. Urban–rural classification data are from the National Center for Health Statistics. Significance is $P < .05$. The extended study period shows that the association between mobility change and new COVID-19 cases weakened somewhat as compared to the initial study period, particularly in more rural counties, reflecting the changing geographic pattern of disease dynamics occurring in May and June 2020. Abbreviation: metro, metropolitan.

Action

Although our findings should not be interpreted as a predictive model, these results provide evidence that reductions in population mobility may act to constrain the growth rate in COVID-19 cases, particularly in urban settings, though it is unclear whether the urban–rural differences we observed during the initial rise in COVID-19 cases in the United States will continue in the future, given the changing geography of the pandemic and differences in mitigation approaches used across the country.

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