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Clio Hancock March 25, 2022

Close Quarters: An Investigation of Neighborhood Effects and SARS-CoV-2 in Chicago

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An abstract of
a thesis submitted to the Faculty of Emory College of Arts and Sciences
of Emory University in partial fulfillment
of the requirements of the degree of
Bachelor of Science with Honors

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Abstract

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The unequal impact of SARS-CoV-2 on minority communities across the United States is undeniable, with different disciplines proposing theories to understand the origins of these inequalities. Here I investigate individual behavioral predictors of SARS-CoV-2 exposure and zip code-level predictors of infection in a large COVID-19 seroprevalence study in Chicago, IL (N=7,058), conducted June-November 2020. Participants provided self-collected finger stick dried blood samples which were analyzed for the presence of antibodies against the receptor binding domain of SARS-CoV-2. Seropositivity was modeled as a function of individual variables with multilevel logistic regressions. Results show that age and household density were individual-level variables significantly associated with the odds of seropositivity. Individuals who were over 60 (OR: 0.62, 95% CI: 0.43, 0.90) had lower odds of seropositivity. Those living in a household with more than five people (OR: 2.85, 95% CI: 1.69, 4.80) had a higher chance of seropositivity. After controlling for individual-level variables, a Community COVID-19 Vulnerability Index (CCVI) was constructed to help explain the context of the zip codes being studied. This index used American Community Survey data to rank Chicago's 57 zip codes based on variables in three risk factor categories: socioeconomic, epidemiological and occupational risk factors. Univariate regression showed that Low CCVI was significantly associated with lower chances of seropositivity (OR: 0.68, 95% CI: 0.54, 0.86), but CCVI was not significant when individual-level factors were controlled for. Spatial analysis also found clustering of COVID-19 positivity and of the CCVI throughout the city of Chicago. The Moran's I–a measure of spatial autocorrelation–of COVID-19 rates was 0.19 ($p = 0.008$) and the Moran's I of CCVI Ranking was 0.67 ($p = 2.6 \times 10^{-15}$). These data show that COVID-19 infections are not distributed evenly across the city, and that individual-level factors are significant predictors of SARS-CoV-2 exposure. As more infectious SARS-CoV-2 variants take hold, this analysis may help to understand the complex factors that contribute to infection.

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Acknowledgements

I would like to thank Dr. McDade for his help in sparking this project and Dr. Hadley for all his help in trouble-shooting code and reading drafts of the thesis. I would also like to thank my committee members Dr. McQuade and Dr. Rao for their insights through the research and writing process. Finally, huge thanks to my parents and my teammates for their patience and support as I wrangled R code ☺.

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Introduction

Before 2020, most people had only experienced pandemics through textbooks and Hollywood screens. Outbreaks such as SARS (2003) and H1N1 (2009) sounded the alarm for the possibility of a highly infectious respiratory disease outbreak, but in many countries, these diseases did little to raise awareness about their dangers. The SARS-CoV-2 outbreak revealed lapses in global pandemic readiness. As the coronavirus spread across the world, the unequal burden of disease quickly became apparent. In the United States, minority populations, which are often correlated with socioeconomic status, were hospitalized with COVID-19 at higher rates than the general population. Compared to White individuals, the risk of COVID-19 related hospitalization was 3.06 times higher for Latino and 2.85 times higher for Black/African American individuals (Acosta et al.). Further, COVID-19 mortality was impacted by race/ethnicity, age and comorbidities such as obesity. In the city of Chicago, Black residents account for 31% of the population, but in the early months of the pandemic, they made up 42% of COVID-19 related mortality (Scannell Bryan et al.). This mortality disparity has led to an unequal burden of disease, resulting in increased sequalae and years of life lost in minority communities.

SARS-CoV-2, the virus that causes COVID-19, is readily transmitted through close social contact. Risk of infection is influenced by both individual and community-level factors. The influence of place on health has been well-established through the works of neighborhood effects studies. These studies focus on community-level metrics that assess the physical environment, the social environment or the economic environment to understand the potential mechanisms in which health can be impacted by everyday surroundings (Renalds et al.). Most of these studies have focused on non-communicable diseases and disorders, since these conditions make up the majority of public health focus. However, there exists very little information on infectious diseases, due in part to relatively low levels of morbidity and mortality in the United States. This has left a gap in the literature that this thesis investigates. By better understanding the interplay of "place" and infectious diseases epidemiology, more effective interventions can be made to prevent the spread of COVID-19 and future infectious respiratory diseases. **This thesis will investigate how individual- and community-level risk factors influenced the chances of contracting SARS-CoV-2 in the city of Chicago during the first wave of the COVID-19 pandemic.**

This thesis will start by examining the research that has been done on the biological and social impacts of SARS-CoV-2, as well as establishing the impacts of neighborhood effects studies on general public health, and finally putting these concepts together to see how SARS-CoV-2 risk factors have played out in the city of Chicago's COVID-19 outbreak. There will then be a brief overview of study design, a summary of key results, and a discussion to contextualize the main findings.

Background

Section I: The Biological and Social Impacts of SARS-CoV-2

Virus Emergence and History

Coronavirus disease 2019 (COVID-19) is the disease resulting from infection with the virus severe acute respiratory syndrome coronavirus 2, or SARS-CoV-2. This novel coronavirus was initially reported in Wuhan, China in late 2019 (Timeline WHO). Hospitals in Wuhan began reporting mysterious cases of pneumonia and early contact tracing linked the outbreak to a live animal "wet market" in Wuhan (Worobey). First categorized as viral pneumonia of an unknown source, early genetic sequencing of the virus indicated it was a novel coronavirus (Zhu et al.).

The coronavirus was initially called “2019-nCoV”, and was genetically similar to previous coronaviruses including Severe Acute Respiratory Syndrome (SARS), with bats as the suspected zoonotic host (Singhal).

Coronaviruses are RNA viruses with distinctive spike proteins found in humans, animals and birds (Singhal; Zhu). There are seven unique coronaviruses known to infect humans–four of which cause the common cold, and the other three being highly infectious and zoonotic in origin. The common cold coronaviruses are 229E, OC43, NL63, and HKU1, and are known to cause cough, fatigue and congestion frequently in the population (Singhal). The three highly infectious zoonotic coronaviruses include SARS-CoV-2, SARS and MERS (“Middle East Respiratory Syndrome”). SARS first emerged from China in 2003 and quickly spread to several Asian countries, the United States and Canada. Its mortality of 9.6% is higher than that of COVID-19’s 6.8%, although the COVID mortality estimates vary widely across time and location of study (Lu et al.). MERS is an even-deadlier syndrome resulting from the MERS-CoV virus, with a mortality of 35.5% (Lu et al.).

The base reproduction number, R_0, is a common measure used to demonstrate the infectiousness of a disease. This number articulates how many future infections stem from a single infected individual. If R_0 is greater than 1, cases are likely to multiply, implying a more infectious disease. If R_0 is less than one, an infectious pathogen will likely die out (Delamater et al.). Current estimates place the SARS-CoV-2 R_0 around 2 or 3, with higher R_0 values for more contagious variants like Delta (5 and 7) and Omicron (as high as 10) (CDC, Burki). This number is similar to the R_0 of 3 for the SARS-CoV. MERS-Co-V’s R_0 is much lower, with values less than 1 (Lu et al.). To provide further context, the endemic seasonal influenza has an R_0 of around 1.28, making it less contagious than any of the coronaviruses in question (Biggerstaff et al.).

COVID-19 Clinical Presentation

Soon after viral characterization, a diagnostic real-time polymerase chain reaction (PCR) test was developed to test for 2019-nCoV nucleic acids (C. Huang et al.). Many of the early patients seeking medical treatment had fevers and difficulty breathing. Severe COVID-19 cases first presented as viral pneumonia, confirmed by chest x-ray imaging (P. Huang et al.). Chest scans were diagnosed by identifying increased opacity and shadows in the lungs. Laboratory tests of COVID-19 patients also showed decreased white blood cell count and increased levels of C-reactive protein, a pro-inflammatory marker. Both of these clinical diagnoses are consistent with standard pneumonia, making it difficult to distinguish without a PCR or antibody test (Zhao et al.). Extreme cases of SARS-CoV-2 infection result in organ damage, ARDS (Acute Respiratory Distress Syndrome), acute respiratory injury, renal injuries, and septic shock (Chen et al.). This multisystem organ damage is likely due to an immune response known as a ‘cytokine storm’. In these cases, the immune system response to SARS-CoV-2 is highly aggressive, flooding the body with pro-inflammatory signaling molecules such as IL-1, IL-6 and TNF-α. This massive inflammatory response can cause lung injury and increases physiological vulnerability to the virus (Ragab et al.).

With increasing testing capabilities, a wider range of COVID-19 symptoms emerged as individuals with less severe illness were tested and confirmed COVID-19 positive. Typically, symptomatic COVID-19 cases are mild, with symptoms of fever, respiratory symptoms, fatigue, muscle aches, loss of taste or smell, sore throat, congestion, nausea or diarrhea. These symptoms appear anywhere from two to fourteen days after infection, with most individuals reporting symptoms in five days (Wu and Corum).

In the weeks following the initial spread of SARS-CoV-2 in Wuhan and beyond, it was determined that as many as 35% of COVID-19 cases were asymptomatic, meaning over a third of individuals were infected without showing noticeable symptoms (Sah et al.). Asymptomatic infections have been found with a number of other prominent viruses such as Ebola, dengue and polio, and researchers believe that this type of infection may be a common mechanism used by viruses to spread undetected (Zhang).

Asymptomatic infection allows for the virus to reside in the host for long periods of time and provides ample opportunity for the virus to spread to new hosts. The robustness of a host's immune system seems to be linked to whether an infection is asymptomatic or symptomatic (Zhang). Age is an important predictor of immune function, which matches evidence from 2020 that children and young adults are more likely to report asymptomatic COVID-19 than the elderly (Sah et al.).

Both SARS-CoV-2 infection and severity of COVID-19 are influenced by the health and genetics of the host. In a comparison of the genomes of early COVID-19 patients and controls, 13 genes of interest were identified. Of these 13 genes, they found that 4 genes affect host predisposition to SARS-CoV-2 infection, while the other 9 genes are associated with COVID-19 severity (Asgari and Pousaz).

The presence of other diseases may impact SARS-CoV-2 infection chances due to differences in receptor expression. The SARS-CoV-2 virus uses Angiotensin-Converting Enzyme 2 (ACE2) receptors as the entry point into cells (Samavati and Uhal). These are receptors found all over the body but are found in greater concentrations in the lungs, kidneys, intestines and brain (Roca-Ho et al.). Researchers have found that certain diseases result in the upregulation of ACE2 receptors, creating more entry points into cells, thus increasing the risk of

SARS-CoV-2 infection. These conditions include diabetes, hypertension, chronic lung disease and liver disease (Sriramula et al., Rao et al., Crackower et al., Mak et al.).

The severity of COVID-19 can be also augmented by these pre-existing health conditions. Any diseases that impact immune system function leave the host at greater risk for severe COVID-19 infection (Ejaz et al.). These conditions include cancer, cardiothoracic diseases, renal or liver diseases and obesity. Pregnancy has also been associated with greater risk of severe COVID-19 infection ("People with Certain Medical Conditions").

The recovery period for COVID-19 appears to be linked to the severity of infection. In a follow-up study of adults who contracted SARS-CoV-2 between April and June 2020, one in five had not returned to their previous health levels 2-3 weeks after their test (Tenforde). Individuals reported having a cough, fatigue and shortness of breath. In some cases, individuals can suffer from "long COVID-19", prolonged duration of symptoms beyond the initial infection. In a 2020 study of individuals tracking their COVID-19 symptoms on a mobile app, 4.5% had symptoms longer than 8 weeks and 2.3% for longer than 12 weeks. The "long COVID" symptoms include headaches, difficulty breathing and a loss of smell or taste (Sudre et al.). In patients who had more severe SARS-CoV-2 infection, the prolonged symptoms can include the introduction of autoimmune conditions (CDC). Analysis of plasma donated from COVID-19 positive patients has shown the presence of auto-antibodies, which are key indicators of autoimmune disease (Wang et al.).

Mechanisms of Viral Transmission

The SARS-CoV-2 virus acts primarily on the respiratory system, meaning that it is spread through contact with an infected individual's respiratory fluids. This contact can happen through inhalation of airborne particles or through the contact of fluid with unprotected mucous membranes.

Aerosolized respiratory particles are produced from speaking, singing, exercise, and coughing. These particles can remain in the air for anywhere between seconds and hours, depending on the size. The risk of infection via inhalation is related to the proximity, time elapsed between exhalation and inhalation, and overall ventilation in an area. It has been shown that social distancing (staying at least six feet apart), masking and increased ventilation have helped reduce respiratory transmission (CDC).

Mucous membranes have also emerged as a mode of transmission of SARS-CoV-2, either through direct or indirect contact (Dawood). Relevant mucous membranes include the mouth, nose, eyes (Britannica). Covering these areas with masking and shielding can reduce the chance of direct contact between infected particles and mucous membranes (Dawood). Another preventative method is hand-washing, which can remove the pathway from infected surfaces to mucous membranes via manual touching of the membranes (CDC).

The viral load of an infected individual, or the amount of virus present in the bloodstream, impacts the transmissibility and severity of the disease. The amount of virus in an individual’s body peaks right before symptom onset, meaning that an infected individual is most contagious during the days leading up to symptom presentation (Wu and Corum). The high contagion during asymptomatic infection is part of what enables SARS-CoV-2 to spread so easily and rapidly. It is believed that the majority of SARS-CoV-2 transmission events happen through “silent transmission”, happening while the carrier is either asymptomatic or presymptomatic (Moghadas et al.). Greater viral loads have also been associated with more severe COVID-19 sickness and higher rates of mortality. This was determined by testing the plasma of COVID-19 positive hospitalized individuals and COVID-19 positive non-hospitalized patients, and presents a possible measure for quantifying the severity of disease (Fajnzylber et al.).

Antibody Surveillance

Antibodies are the immune system's form of defense against foreign pathogens–viral, bacterial or otherwise. As part of the body's adaptive immune system, B cells produce antibodies that are highly specific to one particular antigen (Graham). When a new antigen is encountered, antibodies work to neutralize the threat, storing the antigen information to prevent infection upon further exposures ("Immunoglobulins").

SARS-CoV-2 antibodies have been studied extensively in hopes of developing additional testing, surveillance, and vaccination methods for the virus. Three major categories of antibodies are present in the immune response following SARS-CoV-2 infection: total antibody, IgM and IgG. IgM is the initial response to a foreign antigen and provides short-term protection. Following the body's quick response, IgG antibodies are produced to counter the specific antigen. These antibodies remain present in the blood for a much longer duration following infection, protecting the body from re-infection. The majority of antibodies in the blood are IgG, although IgM antibodies can be traceable in a short period following infection ("Immunoglobulins"). Antibodies are first detectable about 10 days after infection (Xiao et al.).

SARS-CoV-2 antibodies can target one of two SARS-CoV-2 antigens, either the nucleocapsid protein or the spike protein of the coronavirus. The nucleocapsid, or the N protein, is the most abundant viral protein. It is related to the virus' RNA binding and dimerization (Smits et al.). The spike protein (S protein) holds the Receptor Binding Domain (RBD) that is responsible for the viral binding to susceptible cells. Neutralizing antibodies primarily work against the SARS-CoV-2 by binding to the RBD, preventing infection ("Serology Surveillance"). The IgG antibodies for both spike and nucleocapsid proteins are detectable for months following infection. Their presence means that individuals infected with SARS-CoV-2 have significant levels of neutralizing antibodies, likely preventing reinfection for several months (McDade et al.). Despite this natural protection, there have been cases of re-infection, which has become more common with the emergence of variants (Stokel-Walker).

SARS-CoV-2 antibody levels are related to the severity of COVID-19 illness. In a 2020 study, individuals with asymptomatic or mild COVID-19 symptoms had lower or undetectable levels of neutralizing antibodies (Milani et al.). Individuals with more severe infections had a stronger antibody response (Rijkers et al.).

Antibodies are typically measured in an individual's blood with an Enzyme-Linked Immunosorbent Assay (ELISA), which uses a capture antigen to bind any antibodies present in the sample. These trapped antibodies can then be quantified based on a color change reaction catalyzed by an enzyme ("ELISA Assays"). Because IgG antibodies remain in circulation much longer than IgM antibodies, most seroprevalence ELISAs only measure IgG. The capture antigen can either be the nucleocapsid or the spike protein, depending on which antibody is being measured (McDade et al.).

Serosurveillance helps to distinguish between SARS-CoV-2 viral exposure and COVID-19 infection. Viral exposure does not always fully develop into a COVID-19 infection and can only be detected using antibody testing. Antibody testing is beneficial for understanding general population immunity (Brown and Walensky). On the other hand, the more typical clinical presentation of COVID-19 is detected using PCR testing or antigen testing (Ciotti et al.). Antibody testing helps to capture a more complete representation of infections by detecting asymptomatic cases and accounting for any individuals who may not have sought medical care or testing when infected (“Serology Surveillance”). Current seroprevalence estimates from nationwide testing show that as much as 33.5% of the American population may have detectable antibodies (CDC).

Pandemic-Related Inequalities

In the early weeks of the COVID-19 pandemic, it was suggested that the virus was a ‘Great Equalizer’, infecting people regardless of race, gender and socioeconomic status (Mein). It became quickly apparent that this virus, like past pandemics, has unequal incidence and mortality across different demographics (Karmakar et al.; CDC).

It is important to note that the factors that impact SARS-CoV-2 infection are not the same as those that impact severity or mortality of COVID-19. Each of the factors discussed may impact infection, mortality, or both. Due to the nature of this thesis, both of these outcomes will be discussed, but the main focus will be on the factors impacting SARS-CoV-2 infection.

Many of the early COVID-19 outbreaks in the United States arose from institutionalized housing environments, such as nursing homes or long-term care facilities (Boodman and Branswell). This trend has persisted through several COVID-19 waves and as of June 1, 2021, one-third of COVID-19 deaths in the United States were related to long-term care facilities. Nursing homes and other long-term care facilities have augmented SARS-CoV-2 infection risk due to high living density and the frequent contact between staff and residents, reducing their ability to social distance. Beyond a risk of infection, the population in these settings typically has an increased risk of comorbidities, which increases the chance of severe illness or mortality from COVID-19 (The New York Times).

In addition to the elderly, minority populations carried a disproportionate burden of disease in the early months of the pandemic. Compared to white populations, Black and Hispanic communities had higher prevalence, hospitalization and mortality ratios, amounting to a higher burden of disease (Mude et al.). Past and present discriminatory practices have led to racial differences in neighborhood locations and conditions, access to healthcare, health status, and socioeconomic status, all of which are thought to impact the rates of COVID-19 morbidity and mortality (“Community Work and School”).

These disparities are likely the manifestations of both pre-existing individual and social inequalities. However, it remains difficult to understand the interplay of individual and community-level factors in SARS-CoV-2 infections. **This thesis will examine how these factors relate to SARS-CoV-2 infection in hopes of untangling these complex threads of influence.** Many of the possible mechanisms of inequality presented here are based upon recent COVID-19 data paired with pre-pandemic socioeconomic data, or are based upon theoretical frameworks of disease transmission. While this is a good starting point, stronger inferences can be drawn from data that represents the current population. This work takes advantage of the SCAN dataset, which captured the current status of individual participants during the pandemic, providing better context for conditions of infection.

Potential Individual-Level Predictors of SARS-CoV-2 Infection

Healthcare Access

In the case of a respiratory pandemic with potentially severe symptoms and both acute and long-term impacts, access to necessary medical care is an important factor when assessing the risks of COVID-19 mortality (Blumenshine et al.). Minority populations may not have access to a primary care provider or a healthcare facility due to location, due to a lack of health insurance, or due to deliberate avoidance of the healthcare system (Szczepura). Accessibility to healthcare in urban Detroit was measured using the two-step floating catchment area method (2SFSA), which is based on demand for and distance to a healthcare service. Residents in the central parts of Detroit, which were majority Black residents, had much lower primary and specialty healthcare access compared to those in the majority white suburbs of the city (Dai). Spatial analysis of COVID-19 rates in Los Angeles between 3/1/20 and 6/30/20 found that areas with higher percentages of uninsured individuals had positivity rates of greater than 5% (Vijayan et al.). Undocumented populations also faced barriers to seeking medical care for COVID-19, putting them at an increased risk for severe illness or death (Page et al.).

Health Status

Both SARS-CoV-2 infection and COVID-19 severity have been linked to the presence of several pre-existing diseases, including diabetes, obesity, chronic cardiothoracic, renal and liver diseases. Almost all of these conditions have racial disparities in which Black and Hispanic populations are more likely to have these conditions, and in some cases, are more likely to develop them at a younger age (Price et al.). In a spring 2020 study of COVID-19 patients, Black and Hispanic patients were more likely to have multiple comorbidities and more likely to test positive for COVID-19 than white patients. When these comorbidities were controlled for, the mortality gap between racial groups diminished, suggesting that pre-existing health conditions are strongly related to the dangers of serious illness and death from COVID-19 (Kabarriti et al.).

Socioeconomic Status

Studies have also shown that lower income has been related to higher rates of SARS-CoV-2 infection as well as COVID-19 mortality. Decades of discriminatory practices have resulted in an income and wealth gap between white and minority populations in the United

States. In 2019, the average income for a white individual was $42,106, but only $24,509 for a Black individual and $22,002 for a Hispanic individual (“S1902”). A lower income often signals less economic flexibility, impacting an individuals’ ability to take necessary COVID-19 preventative behaviors (“Community Work and School”). Poorer individuals are more likely to work essential jobs, which presents barriers to effective social distancing (Chen and Krieger). Additionally, studies in the favelas of Brazil showed that the public health measures of handwashing and masking may be unrealistic in areas of extreme poverty due to a lack of resources (de Oliveria and de Aguiar Arantes). In the first wave of the pandemic, multiple studies of American cities found poverty to be a significant predictor of SARS-CoV-2 infection, COVID-19 related hospitalizations, and death (Vijayan et al. and Wadhera et al.). While conclusions about the uptake of behavioral COVID-19 interventions such as masking and hand-washing are necessary to assess their true effectiveness, very few studies have collected data on specific COVID-19 related behavioral changes because of the rapid emergence and evolution of the pandemic. The SCAN dataset offers an advantage in these circumstances, with data from the first wave of the COVID-19 pandemic on participants’ perceived behavioral changes.

As much of the United States initiated stay-at-home orders for the early stages of COVID-19, racial disparities were further exacerbated due to working conditions. While white collar professions were able to shift to a virtual work-from-home model, those deemed essential workers continued to report for jobs in person. Essential workers are defined as healthcare and non-healthcare workers whose jobs are essential for sustaining societal basic functions. This category includes workers from the healthcare, food production, transportation and manufacturing industries (“Categories of Essential Workers”). Pre-pandemic data shows that 30% white laborers were able to work from home, while only 20% of Black and 16% of

Hispanic workers could. This trend persisted through the pandemic, with Black workers once again more likely to be in-person during the pandemic than white workers (Rogers et al.).

Many essential healthcare workers dealt with COVID-19 positive individuals on a daily basis, often without proper protective equipment, putting them in direct risk for greater SARS-CoV-2 exposure (Jacobs et al.). Even for those not in healthcare settings, working in-person and using transportation to get to work were found to be risk factors for SARS-CoV-2 infection, putting minority workers at a disadvantage compared to those who could remain in the safety of their homes during the early months of the pandemic (van Holm et al.).

Increased rates of severe COVID-19 sickness or mortality were also found among essential worker populations. A study of U.K. healthcare workers conducted from March to July of 2020 found that they were seven times more likely to develop severe COVID-19 than non-essential workers, while social/education workers and other essential workers also had a significantly higher chance of developing severe COVID-19 (Mutambudzi et al.).

Living Conditions

Residential segregation, whether through legal or economic means, has resulted in an unequal spatial distribution of minorities in cities. As a result, minority populations are more likely to live in crowded housing, situated in neighborhoods that lack access to basic services like transportation, health clinics and healthy food sources (Samuels-Kalow et al.). This marginalization also results in negative health outcomes, higher residential segregation has been linked to higher rates of obesity and worse mental health outcomes (Chang et al.; Lee). Crowded living accommodations, both informal and formal, have also been found to increase the chances of SARS-CoV-2 infections (von Seidlein et al.; Anderson et al.). Further, pre-pandemic investigation of housing showed that African American families were the most likely to be homeless. Whether considered “sheltered” or “unsheltered”, those without permanent residence face considerate barriers to remaining healthy in a pandemic. Sheltered homeless individuals may live in crowded shelters, making it more difficult to socially distance, while unsheltered individuals also lack necessary access to healthcare, testing and vaccination (“Fact Sheet–Population At-Risk”).

Another consequence of crowded housing is intergenerational cohabitation, which can introduce the possibility of SARS-CoV-2 transmission from younger, healthier individuals to older family members who may be at higher risk for serious illness (Stokes and Patterson). Intergenerational cohabitation is practiced more among Asian, Black and Hispanic populations than white populations (Cohn and Passel).

Contrary to initial impressions of the pandemic, COVID-19 has not impacted communities equally. Instead, it has mirrored society’s pre-existing patterns of inequality, often along racial and socioeconomic lines. These risk factors for infection and mortality have been measured and hypothesized using a combination of pre- and mid-pandemic data. Given the dramatic changes in individual socioeconomic and health status over the past two years, it is crucial that these predictors are assessed in the context in which they occurred. The individual-level observations in the SCAN dataset includes variables such as Race/Ethnicity, Age, Crowding, Work Conditions, Interactions, Insurance, and Prevention Net, which all describe individual-level risk factors for SARS-CoV-2 infection, will help to decipher how these potential predictors may truly impact individuals in the context of the pandemic.

Section II: Neighborhood Effects and Health

Studies of “place” or “neighborhood effects” acknowledge the phenomenon that the environment in which an individual resides can have a strong impact on both behaviors and health outcomes. The theoretical basis for neighborhood effects studies comes from the field of social epidemiology and specifically the ecosocial theory of health, which has exploded in popularity alongside these studies. The ecosocial theory of health acknowledges that a wide range of upstream factors beyond biological characteristics can influence individual health outcomes (Krieger). These factors include individual and community behaviors, environmental conditions and policy or cultural determinants. The interactions between these factors can have a strong impact on individual and population health (Corburn). Neighborhood effects studies have further established that people influence place, and places influence people (Cummins et al.). Ranging from changes in individual smoking behavior to the economic factors controlling the availability of fresh food, neighborhoods and their residents are shaped in tandem. This results in complex systems in which neighborhood conditions often mediate individual health outcomes (Diez Roux et al.). Studies at the population level have both public health and policy implications. The insight that health is impacted by more than just individual factors has resulted in a broadening of what is considered public health policy. Because of the importance of the built environment in neighborhood effects, sectors of city planning such as transportation and housing are now often regarded as key elements of public health (Diez Roux and Mair). These studies can provide health, behavioral and structural insights that can be invaluable for place-specific health and behavioral interventions.

Due to the nature of these studies, most are cross-sectional observational studies that measure neighborhood characteristics and health outcomes at one point in time, making it difficult to study and prove causality. Longitudinal controlled studies, the most effective method for studying correlation, have not yet been widely adopted as a feasible format for studying neighborhood effects.

The question of how best to measure a neighborhood has dominated social epidemiological studies. Across neighborhood effects studies, there are two main approaches used to describe neighborhood conditions. Some studies use the physical surroundings as a neighborhood predictor, looking at variables like walkability, safety, housing density and land use mix (Arcaya). These built environment variables can be determined based on participant-based surveys or through geospatial analysis with technologies like GIS. Participant interviews access the unique knowledge of community residents by asking them to rate specific aspects of their environment through phone or in-person surveys. GIS software can be used to identify physical characteristics of an area, such as housing density, green space and major landmarks from satellite images or maps (Mujahid et al.). Neighborhood conditions can also be approximated using indices of advantage and disadvantage, which are typically indicative of socioeconomic status. These indices can contain community-level information on educational attainment, poverty, unemployment, crowded housing and single-parent households (Messer et al.). One version of this used heavily around the recent COVID-19 pandemic is a vulnerability index.

Vulnerability indices are typically used in the context of a natural disasters such as hurricanes, flooding or in this case, a pandemic (CDC/ATSDR). Vulnerability is a measure of how susceptible a *community* is to negative consequences following a disaster. The CDC maintains such an index, the social vulnerability index (SVI), which measures socioeconomic and environmental variables to understand how much support a community will likely need following a crisis. The index categories include socioeconomic status, race and ethnicity, household composition and transportation access (CDC/ATSDR). These indices have been adapted to measure the impacts of COVID-19 on the community level, adding factors like comorbidity status, essential worker percentages, hospital capacity and population density (Gaynor and Wilson, Amram et al.). These COVID-19 Community Vulnerability Indices (CCVI) are a useful adaptation of previously existing community-level metrics for disaster recovery. A higher CCVI ranking indicates more social vulnerability, which results in higher COVID-19 incidence and mortality (Karmakar et al.). I chose to use this type of index in my research because it provided a clear way to capture the neighborhood conditions as they related to chances of contracting SARS-CoV-2.

Health and Place Theory

How might where one lives impact their health above and beyond their individual level characteristics? The influence of place on health has been hypothesized to act through several different mechanisms. One's neighborhood can impact their social networks, their immediate residential environment and their extended community environment. All of these spheres of living can exert different influences on individuals, creating possibility for these neighborhood effects.

Social Cohesion/Collective Efficacy

Some studies have found that social cohesion is essential in protecting especially vulnerable residents from detriments in physical or mental health. Collective efficacy is a term coined by Robert Sampson pertaining to the safety or quality of a community. Sampson establishes the concept that when everyone in a community is united together through common norms or beliefs, there is greater effort made to undertake actions to improve neighborhood conditions or safety (Sampson). In turn, this can foster a safer, more positive community environment, which can have positive health outcomes.

A robust social network is particularly important in supporting the physical and mental health of elderly populations (Rowe and Kahn). These populations often have reduced mobility and constricted social networks, making it increasingly important that they have community level support systems to minimize accidents and general decline (Levasseur et al.). An analysis of social structures and the 1994 Chicago heat wave found that this extreme event had impacts on the community-level and that collective efficacy seemed to buffer against mortality in the months surrounding the heat wave, but not during the actual event (Browning et al.).

Further, a commonly-observed health phenomenon, the Immigrant Health Paradox, highlights the importance of social structure and health outcomes. In this phenomenon, immigrant populations have better health and lower mortality than ethnically comparable populations (Markides and Rote). It is theorized that this is due to the protective effects of strong social networks found in immigrant communities, and this effect diminishes with more time spent in the United States (Anderson et al.).

The impact of social networks on infectious disease transmission has been studied in the context of tuberculosis. It was theorized that a lack of social cohesion promotes ‘negative’ behaviors such as alcohol and drug use that put an individual at higher risk for tuberculosis infection than others (Acevedo-Garcia). More specifically to SARS-CoV-2 infection rates, Jaspal and Breakwell found that social support, measured as how much help participants would receive during times of strain, was positively associated with perceived risk of COVID-19, and therefore with increased preventative behaviors. Further, they found that another indicator of social support, neighborhood identification, was associated with higher rates of COVID-19 testing and vaccination, presenting an important avenue of exploration as the challenges of vaccination continue in the United States (Jaspal and Breakwell). Neighborhood identification is a measure of how much individuals report that their neighborhood is tied to their identity, which is assessed through feelings of fulfillment, happiness and belonging (Fong et al.).

Household Crowding

Household crowding is measured by the U.S. Census as a residence with more than one individual per room. Crowded households have strong racial and sociodemographic patterning, with poorer individuals more likely to reside in a crowded household (Blake et al.). Living in crowded households has been linked to poorer health and educational outcomes in children and adolescents (Martens et al.).

Crowded households have also been linked to increased transmission of respiratory illnesses. Tuberculosis is an infectious pathogen that is spread primarily through aerosolized droplets, similar to the current COVID-19 pandemic. Acevedo-Garcia’s theoretical framework for the racial differences in tuberculosis indicated that past practices of segregation have resulted increased housing density, which has the potential to increase transmissibility of a respiratory illness like tuberculosis.

Resource Access

The conditions of a neighborhood influence the opportunities available to its residents. Among the most impactful to health are access to food, healthcare, transportation. These elements are important in terms of both SARS-CoV-2 infection and COVID-19 disease severity. The well-known phenomenon of ‘food deserts’ arise from a lack of affordable healthy food sources , which can limit community residents’ nutritional choices (Sadler et al.). Nutrition is directly impactful to many aspects of health, as poor nutrition can result in obesity, or more advanced metabolic conditions such as diabetes. Diabetes and obesity are both considered comorbidities for COVID-19, increasing risk of serious illness upon infection ("People with Certain Medical Conditions"). Proper immune system function also requires a delicate balance of macro and micronutrients, and dietary imbalances can be detrimental to its function, therefore making it more susceptible to infection (Childs et al.).

Access to healthcare is also essential in both long-term and acute health scenarios. Individuals of lower socioeconomic status are more likely to have difficulty accessing health resources, due to transportation or economic barriers, as mentioned in Section I. However, studies have shown that this patterning also exists on the neighborhood scale, irrespective of individual characteristics. There are four hypothesized mechanisms in which a neighborhood can have insufficient healthcare access–through social networks, community health norms, social capital and healthcare resources (Prentice).

Transportation access is another resource that is influential in the health and well-being of residents. An important aspect of transportation with health implications is the walkability of a community. Communities with pedestrian or bicycle access are more likely to support activity of residents, whether for leisure or for utilitarian physical activity. A more active lifestyle has a myriad of positive health benefits, including a reduced chance of developing non-communicable diseases. Therefore, neighborhoods that foster walkability have the potential to indirectly decrease severity of COVID-19 by keeping their residents healthier in the first place (Adlakha and Sallis).

While public transportation is often imperfect, serving some communities while isolating others, it is often the only option when economic constraints prevent the use of personal transportation. A key element in a community's ability to respond to disaster is transportation access (CDC/ATSDR). However, more reliance on public transportation may be detrimental to community health in the context of the COVID-19 pandemic. Although many major cities experienced precipitous drops in ridership of public trains and buses, many essential workers and low-income individuals were left without a choice for transportation (Gold et al.). The lack of social distancing and ventilation on trains and buses present possible mechanisms of SARS-CoV-2 transmission (Stabley and Ramachandran). The connections between COVID-19 and transportation may extend past public services. A study of Chicago neighborhoods found that for neighborhoods where residents lacked their own transportation and relied on carpooling, COVID-19 mortality rates were higher (Scannell Bryan et al.).

A neighborhood's social or physical infrastructure can have direct implications on how residents can access necessary resources, or on their chances of contracting and suffering from illness.

Population Density

The impact of population density on community health during the COVID-19 pandemic is one of the most divided issues in the literature. Historical and practical perspectives on a respiratory pandemic have indicated that population density is an important factor in the spread of disease. However, current literature is divided on the impact of density.

Retrospective models of the 1918 influenza pandemic in India have shown that population density was impactful in mortality rates. There was a significant difference in influenza mortality between the high and low-density areas, showing that above 175 people per square mile, the influenza had a greater impact on the population (Chandra et al.). Models of SARS-CoV-2 transmissibility also have shown that increasing population density results in an increased R_0, which suggests that population density is key in sustaining an outbreak due to increased contacts between individuals (Sy et al.).

However, actual studies of COVID-19 in dense cities have shown conflicting results. In a nationwide study based on March-June 2020 COVID-19 rates, population density, measured in people/km^2, has been shown to increase SARS-CoV-2 transmission (Chen and Li). Other studies have shown that higher density neighborhoods in Chicago actually corresponded to lower rates of SARS-CoV-2 transmission (Scannell Bryan et al.). This counterintuitive mechanism may be due to the greater impact that social distancing efforts have on denser areas, or due to greater preventative behavior adherence by residents (Hsu).

As shown in this review, there are multiple pathways, some at the individual-level and others at the community-level, that influence SARS-CoV-2 exposure and COVID-19 infection (**Figure 1**).

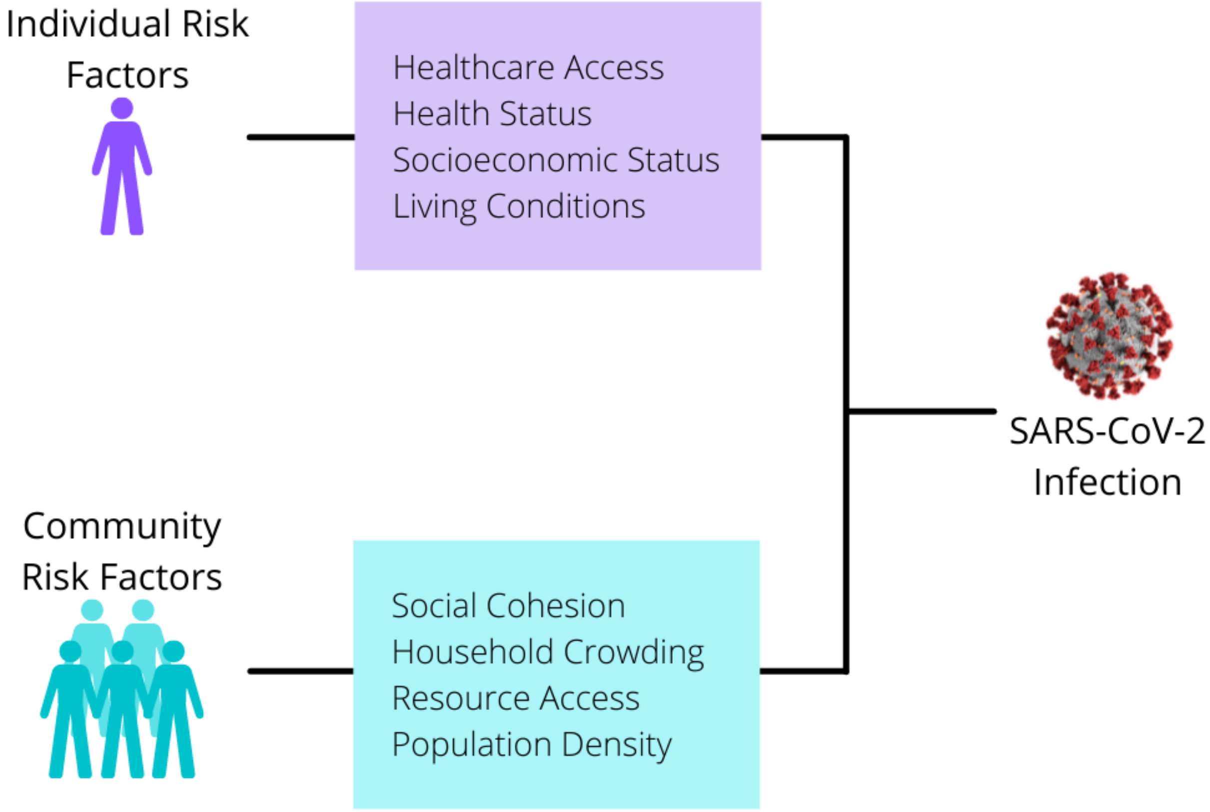


Figure 1: Risk Factors for SARS-CoV-2 Infection. *This figure summarizes the individual- and community-level risk factors detailed in this literature review.*

Health Outcomes and Place

Neighborhood effects studies have traditionally focused on noncommunicable diseases and mental health. Common health outcomes or behaviors for neighborhood effects studies include mental health, obesity, physical activity, pregnancy, respiratory conditions (such as asthma) or mortality.

In a review of studies focused on depression in neighborhoods, Kim notes that social disorder seems to be related to higher depressive rate, likely due to the additional stress and lack of support networks in a struggling community. Further, he concludes that socioeconomic status seems to be protective against depression, which has a strong community-level patterning (Kim).

Mental health is often measured through participant-based surveys, not unlike the SCAN data. Variables in SCAN dataset like Worry Health and Worry Financial assessed participants' concern about the impact of COVID-19 on their health and financial situation on a Likert scale provide a valuable glimpse into the emotional status of participants. Although this study does not capture clinical aspects of mental health, it is important to measure emotions or attitudes in order to better understand the strain experienced by members of a population.

Obesity is often studied on the community level using BMI values. Researchers found that physical or social disorder moderated the impacts of racial isolation on female obesity. Physical disorder was measured using housing authority data to create an index of housing density, housing quality and residential housing prices. Social disorder was measured using crime rates from the Philadelphia Police Department. The researchers found that individual-level predictors of obesity were less significant upon the addition of neighborhood-level conditions, but there remained disparities between white, Hispanic and Black women (Chang et al.).

Christian et al. measured parental attitudes towards their child's independent mobility. These survey results were matched with physical and social environment descriptors to understand how freely children could move between school, home and other destinations. It was found that child mobility depended on the perceived safety of travel and on community-wide parental norms. Child mobility is an important aspect to development, helping with social and cognitive development (Christian et al.). All-cause mortality was also found to be related to neighborhood characteristics such as socioeconomic status, population density and social cohesion (Meijer et al.).

Asthma is a health outcome related to the current COVID-19 pandemic as a potential risk factor for severe illness. In a study of Chicago it was found that both individual and community level factors were associated with asthma or difficulty breathing. Individual factors were measured through the Metropolitan Chicago Information Center Metro Survey, which contained questions on race, age, gender, smoking behaviors and obesity. Neighborhood conditions were measured using U.S. Census data on socioeconomic disadvantage as well as the Project on Human Development in Chicago Neighborhoods Community Survey, which included participant assessments of the levels of physical and social disorder in 343 Chicago neighborhood clusters (“Project on Human Development”). Gender, smoking and obesity were individually significant while collective efficacy was found to reduce chances of asthma (Cagney and Browning).

Far less common are neighborhood effects studies looking at infectious diseases, reflecting a smaller infectious disease burden in developed countries. There have been several studies examining the impact of segregation on neighborhood conditions and the spread of infectious diseases like tuberculosis and chlamydia. As mentioned above, Acevedo-Garcia’s work on tuberculosis in African American communities showed that past practices of segregation resulted in a concentration of disadvantage, which was directly related to higher rates of tuberculosis. In another study focused on infectious diseases, adolescents were tested for chlamydia, along with a screener for individual sexual behaviors and mental health conditions. In that study, neighborhood level poverty was related to an increased risk of contracting chlamydia, regardless of individual risk factors like increased sexual activity and depression (Ford and Browning).

In light of the COVID-19 pandemic, it is clear that infectious disease does spread unequally through communities, but there is a dearth of studies that assess both the individual and community risk factors of COVID-19. This presents an opportunity for further exploration, which this thesis aims to do. Community-level infectious diseases studies have not yet examined the impact of other neighborhood conditions beyond that of racial segregation. This leaves much to be desired, as there are other environmental variables that may impact a community's vulnerability to COVID-19. I will examine sociodemographic, epidemiological and occupational community-level variables using American Community Survey and Chicago Health Atlas data to better understand how these factors compare to the individual level risk factors detailed by SCAN survey responses.

Section III: City of Chicago and COVID-19 Impacts

The City of Chicago

The City of Chicago is the third largest city in the United States, with just under 3 million residents ("Facts & Statistics"). The racial makeup of Chicago is 33.3% non-Hispanic White, 29.6% Black and 28.8% Hispanic or Latinx (U.S. Census Bureau). Chicago, while racially diverse, is one of the most highly segregated cities in the United States. Using an Index of Dissimilarity, a statistic commonly used to describe segregation between two ethnic or racial groups, Chicago received a score of 82.5 for White-Black segregation. This is larger than every other major American city, including New York (81.4), Boston, (69.2), Los Angeles (66.9) and Dallas (66.1) ("Residential Segregation").

Due in part to the influential "Chicago School" of thought founded at the nearby University of Chicago, Chicago has been a case study for urban sociology focusing on the social and economic impact of living within a segregated metropolis. The prevailing theories from this school of thought have revolved around the importance of social "order" and connectivity, often with respect to crime.

Many of the neighborhood effects studies done in Chicago have focused on different interventions for crime and poverty, such as the Moving to Opportunity program, which helped move families in the experimental group out of poor neighborhoods (Moving HUD). This study showed the influence of neighborhood conditions on outcomes like economic mobility and crime rates ("Neighborhood Effects" Sampson).

Another landmark neighborhood effects study in Chicago, the Project on Human Development in Chicago Neighborhoods (PHDCN) took a multi-faceted approach to study the impact of neighborhood conditions on child development. This project consisted of community surveys, which assessed the social cohesion of communities by asking residents to detail the hierarchical structure of their social networks, systematic observations, in which sampled city blocks were videotaped and analyzed for key environmental characteristics, and a longitudinal cohort study of children and their caretakers to measure metrics of health and social structures over time. This project represented a massive undertaking to understand both the social and physical manifestations of the construct of a community. It was found that social networks remain essential to city life and behavior, even as these networks grow and change in an era of increasing digitization (Sampson). While focused heavily on social measurements such as crime, safety and belonging, the PHDCN also helped to demonstrate detrimental health impacts of social disorder.

The longitudinal cohort component of PHCDN was evaluated to understand how health perception was related to neighborhood deprivation. Children between ages of 11 and 12 were asked "How do you perceive your health?", and it was determined that lower socioeconomic deprivation and better neighborhood perception was related to a more positive perception of health from an early age (Drukker et al.). Beyond perceptions, actual health differences were identified in Chicago. One study using PHDCN data as the reference for neighborhood conditions found that lower collective efficacy and a more pronounced “broken windows” effect (environmental cues of social disorder) mediated mortality due to cardiovascular disease (Cohen et al.).

Factors such as social cohesion, socioeconomic status and resource access can be analyzed to better understand the community-level factors that influence COVID-19 disparities in the city of Chicago. By utilizing U.S. Census data and Chicago Health Atlas data, measures of deprivation in neighborhoods will be approximated using a COVID-19 Community Vulnerability Index. This will help to contextualize health outcomes similarly, by adding important socioeconomic context to SARS-CoV-2 infection rates.

Chicago COVID Response

Based on population-level data on SARS-CoV-2 infections and COVID-19 mortality, there have been several analyses that dig into the root causes of such differences. Since the beginning of March 2020, there have been over 2.8 million confirmed COVID-19 cases and 30,000 deaths in Illinois (“Illinois Data”). As the largest city in Illinois, Chicago has had significant COVID-19 burden, with 538,000 confirmed cases and 7,000 associated deaths as of January 28, 2022.

Chicago was the site of some of the first COVID-19 cases in the United States in the winter months of 2020. The first few cases were related to individuals traveling from Wuhan, while later cases demonstrated some of the first known examples of community transmission in the United States (“Illinois Coronavirus”). As COVID-19 cases began to grow more rapidly, Illinois Governor J.B. Pritzker declared all of Illinois to be in a “disaster area”, essentially indicating a State of Emergency. Eleven days later, Gov. Pritzker declared a stay-at-home order, which lasted over two months from March 20 until May 29, 2020 ("Executive Order 2020-10"). On the municipal level, the City of Chicago followed all statewide social distancing orders. Further steps were taken to reduce crowding in the city by closing parks and paths around the city, including the 606, a walking and bicycling path along the Northwest side of the city, and the Lakefront Trail, which stretches 18 miles along the shores of Lake Michigan ("COVID-19 Orders"). In the summer months of 2020, some restrictions, including the stay-at-home order were cautiously rolled back as the city saw declining case rates.

Most of these restrictions were reinstated in the winter of 2020 as cases began to climb once again. During this nationwide "Second Wave" of COVID-19 infections, the City of Chicago experienced its greatest burden of COVID-19 cases thus far, with over 2,000 cases per day at its peak in November 2020 (Chicago Tribune). This spike in cases prompted a re-issuing of curfews, business restrictions and finally, the stay-at-home order. The emergency use authorization of COVID-19 vaccines in late December of 2020 helped to reduce daily caseload over the next three months ("Illinois Data").

Spatial Disparities

As a whole, Chicago has been heavily impacted by COVID-19, both medically and economically. However, these impacts have not been uniformly distributed across the city. Analysis of COVID-19 cases from March to July of 2020 has shown that minority populations were disproportionately impacted–both in terms of infection and mortality. The racial and ethnic population proportions are not equally reflected in SARS-CoV-2 infection or COVID-19 mortality. Understanding the processes that produce these inequalities is a goal of much work, and indeed is the overall aim of this thesis.

Data from the first months of the pandemic showed that the Black non-Hispanic population was overrepresented in COVID-19 cases and deaths, making up 45% of cases and 56% of deaths despite totaling only 30% of the population (Kim and Bostwick). Other racial or ethnic populations were underrepresented in these totals, with White non-Hispanic people accounting for 20% of cases and 16% of deaths (Kim and Bostwick).

Pierce et al. used Years of Potential Life Lost (YPLL), another metric to understand unequal disease burden, to estimate the impacts of COVID-19 mortality across Chicago at the census tract level. Once again, the burden of disease was not distributed equally. Hispanic populations had the highest YPLL score, with 811 years lost per 100,000 residents, followed by non-Hispanic Black populations with 559 years lost and non-Hispanic White populations with 312 years lost (Pierce et al.).

Throughout the pandemic, those in nursing homes and other institutionalized settings were at an increased risk of infection due to crowding. Early deaths showed that White non-Hispanic individuals had higher mortality rates in institutionalized settings. This likely reflects the baseline demographic disparity of nursing homes and long-term care facilities in the United States, which are upwards of 80% White non-Hispanic but underscores the idea that individuals living in dense areas might be at elevated risk of and beyond their individual behaviors ("Fast Stats").

Spatially, due in part to the highly segregated nature of Chicago, there were clear clusters of COVID-19 cases throughout the city. Matching the demographic distribution across Chicago (**Figure 2**), COVID-19 hot spots were concentrated in the South and West sides of the city. These areas are predominantly Hispanic and Black. The downtown as well as surrounding suburban zip codes had much lower rates of COVID-19 at the beginning of the pandemic and are majority White (Kim and Bostwick). In the ensuing waves of COVID-19, the nationwide trend of infections shifted out of cities and into suburban and rural areas (Cuadros et al.).

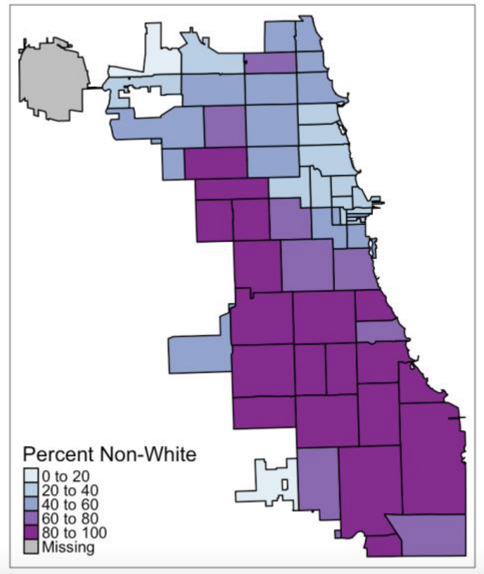


Figure 2: Percentage of non-White Residents in Each Zip Code. *This figure uses data from the ACS Demographic and Housing Estimates ("DP05"). The number of non-Hispanic White residents was extracted, then subtracted from the total population in each zip code to yield the number of non-White residents. This was turned into a percentage by dividing by the total number of residents in each zip code.*

Several Chicago-specific studies focused on measures of segregation as their independent variable for COVID-19 outcomes by using racial demographic percentages or vulnerability indices. In addition to standard sociodemographic measures, studies looked at health variables that were thought to be related to COVID-19 severity, such as obesity, diabetes and cardiothoracic disease. The final major category of variables were those related to the social risk factors of COVID-19. Measures of household environment, social distancing capabilities and essential worker populations were included to estimate how much a community could abide by public health guidance to avoid infection (Anderson et al.; Scannell Bryan et al.; Kim and Bostwick).

Kim and Bostwick investigated the social vulnerability and health risk factors of different Chicago community areas to determine the differences in disease burden across the city. They used American Community Survey (ACS) 5-year estimates and Chicago Health Atlas data to estimate how these factors impacted COVID-19 mortality. They discovered that there was a spatial clustering of social vulnerability and comorbidities, and that African American communities bore the brunt of this disadvantage, which was also evident in a higher COVID-19 mortality in African Americans than in other races. They concluded that “traditional public health variables” like population density, age, crowding and housing quality, were significant and associated with COVID-19 infections in the expected direction, however, they did not eliminate the significance of segregation (Kim and Bostwick).

Scannell Bryan et al. also investigated Chicago’s COVID-19 mortality, although they did so at the census tract level (a more granular approach than the community areas). They considered 33 neighborhood characteristics that estimated risk of both SARS-CoV-2 infection and COVID-19 mortality. Using Poisson and regularized linear regressions, they found that COVID-19 mortality was increased in neighborhoods with greater barriers to public health measures like social distancing. They also found that the associations between neighborhood conditions and race varied, with the neighborhood context being the most impactful for white residents. Neighborhood context summarized 33 census tract level characteristics, belonging to categories of SARS-CoV-2 infection risk, COVID-19 mortality risks and structural inequalities (Scannell Bryan et al.).

Anderson et al. assessed SARS-CoV-2 infection rather than COVID-19 mortality, and did so through the lens of segregation. They focused solely on the demographics of different zip codes to understand how segregation scores were related to SARS-CoV-2 infection. They found that greater segregation was related to higher rates of SARS-CoV-2 infection (Anderson et al.).

These studies showed that measures of segregation and economic vulnerability were often the strongest predictors of SARS-CoV-2 infection and COVID-19 mortality, and were better predictors than individual-level variables like age, sex and education level. All of these studies focused solely on community-level data, either at the zip code, community area or census tract level. This geographic focus provided a strong basis against which to compare indices and COVID-19 distribution, but these papers often cited a lack of behavioral metrics as one of their limitations. In this thesis, I intend to use individual-level observations about SARS-CoV-2 infection and personal behavioral changes to compare to the zip code-level, or community effects, of COVID-19. Variables were selected based on my current understanding of the pandemic as well as prior research and theory on infectious disease epidemiology and the role of "place" in the patterning of health outcomes. **This study will investigate how much individual-level factors predict SARS-CoV-2 infection as opposed to the typical neighborhood effects measure of community-level factors.**

Methods

The database used in this thesis is from the Screening for Coronavirus Antibodies in Neighborhoods (SCAN) study, conducted by Northwestern University. The principle investigators are Thom McDade Ph.D., Richard T'Aquila M.D., Elizabeth McNally M.D. Ph.D., Brian Mustanski Ph.D., and Alexis Demonbreun Ph.D.. The study originally started as a comparative study between neighboring zip codes with a large difference in COVID-19 rates, but was later expanded beyond the initial ten Chicago zip codes to encompass the entire city ("Screening for Coronavirus Antibodies in Neighborhoods"). Potential participants were informed of the study through social, broadcast, and print media, then filled out a web-based screener form that recorded basic demographic and consent information, as well as zip code. Participants were invited based on demographic criteria and given a questionnaire and mailed a dried blood spot (DBS) kit to test for receptor binding domain (RBD) SARS-CoV-2 antibodies. Samples were collected between June 24 and September 6, 2020. These antibodies were then measured using an ELISA to identify and quantify the amount of IgG antibody present in the sample, using the methods created and validated by McDade et al.. Participant samples for this study were collected between June and September 2020. The SCAN dataset included 7,058 individuals from 192 zip codes. From these data, mixed model linear regressions were applied, with a random effects term for zip codes, to better understand the impact of different individual and zip code-level factors on SARS-CoV-2 seroprevalence.

For each respondent, I selected information on their age, gender, self-reported racial/ethnic classification, their living status, occupational information, transportation behaviors, the occupation of those in their household, any self-reported comorbidities and self-reported COVID-19 prevention behaviors. At the zip code level, I selected a series of variables that describe the community vulnerability. These variables were composed into indices that describe the zip code’s socioeconomic status, the household composition and disability rates. These indices, along with percentage of essential workers, percentage of senior residents, mobility rates, percentage of residents without a primary-care physician and residents with at least one comorbidity, were combined into a COVID-19 Community Vulnerability Index (CCVI), based on the CCVI developed by Surgo Ventures (“Bringing Greater Precision”).

The outcome of interest was SARS-CoV-2 infection, measured based on the result of the SARS-CoV-2 IgG RBD assay. Positive results from these assays indicate previous SARS-CoV-2 exposure. This variable, COVID Result, had binary outcomes based on the experimentally measured antibody concentration from each participants' DBS sample. The antibody concentrations were measured to extremely high sensitivity and with a cutoff of 0.40 μg/mL used to identify seropositivity (McDade et al.). It was coded with a 1 for those above the cutoff were considered seropositive, with measurable amounts of IgG antibodies, and 0 for those below the cutoff.

Age was recorded based on the reported birth dates of individuals and the date of survey, the resulting variable was a continuous variable accurate to five decimal places. This variable was then sorted into five levels of a factor variable based on the age categorization used in Demonbreun et al.'s paper on the SCAN dataset: "Age 18-29", "Age 30-39", "Age 40-49", "Age 50-59" and "Age 60+". Gender was coded as 1 for man, 2 for woman and 3 for gender non-conforming. For those who chose "3", a follow-up question asked about the sex assigned to that individual at birth. Race/Ethnicity of participants were recorded in separate questions, respondents were able to choose multiple options to best reflect their racial and ethnic identity. These were coded into eight categories, non-Hispanic American Indian/Alaska Native, non-Hispanic Asian, non-Hispanic Black or African American, non-Hispanic Native Hawaiian/Pacific Islander, non-Hispanic White, Hispanic/Latinx, non-Hispanic Other and Multiracial. All non-Hispanic categories were coded to ensure that the respondent had reported a race as well as the ethnicity option "not of Hispanic, Latino or Spanish origin". The "Hispanic/Latinx" category included those who reported a race of "White" and an ethnicity option. All possible combinations of race and ethnicity were recorded in separate binary variables. For each participant, there combinations were tallied to determine whether an individual had selected multiple races or multiple ethnicities. The "Multiracial" category was created based on responses that selected multiple races. Initial analyses were carried out with all factors of this variable, however, due to convergence issues with the multivariate models, the variable was modified to add the extremely small categories of non-Hispanic Native Hawaiian/Pacific Islander and non-Hispanic American Indian/Alaska Native into non-Hispanic Other.

Living Status of participants was based on their description of their permanent housing situation, the options included “House/Townhouse”, “Shelter”, “Apartment/Condo”, “Dormitory”, “Assisted Living Facility”, “Skilled Nursing Facility”, “No consistent residence” or “Other”. This variable was recoded into a factor variable because it initially had numeric character. Crowding was a continuous variable based on how many people shared the participant’s kitchen and living space. Responses ranged from 1 (participant lived by themselves) to 6 (six or more people including the participant), and were further categorized into “Alone”, “1-2”, “3-4” and “5 or more”.

The occupational information of participants was recorded in the form of several variables: Work Now, Work Flex, Work Remote and Work Type. In Work Now, individuals reported whether they were currently employed or unemployed. This variable was coded such that 1 was employed and 0 was unemployed. In Work Flex, individuals reported to what degree they were encouraged to take sick days when ill. This variable was recoded as a factor, 1 corresponded to those who could take paid sick days, 2 corresponded to those who could take unpaid sick days and 3 corresponded to those who could not take days off work. Work Remote was a variable that asked participants to record how much of their work they could complete remotely or from home. 1 corresponded to all work, 2 corresponded to some work and 3 corresponded to no work. In Work Type, individuals who self-identified as essential workers selected the category of occupation that best matched their job. Due to the dwindling sample sizes with the Work Remote and Work Type variables, a new variable was created to encompass all employment possibilities. This variable, Work Conditions, had four levels, “Unemployed”, “Work From Home”, “Healthcare”, “Non-Healthcare”. If participants indicated they were not currently working in Work Now, they were “Unemployed”. If participants indicated that they were employed and that they did all their work remotely in Work Remote, they were “Work From Home”, if they did not work remotely, they were classified into either “Healthcare” or “Non-Healthcare” based on their Work Type answer. The Work Close variable evaluated participants who said they worked in-person to some extent, participants were asked if they worked in close proximity to others, 1 indicated they did and 0 indicated they did not.

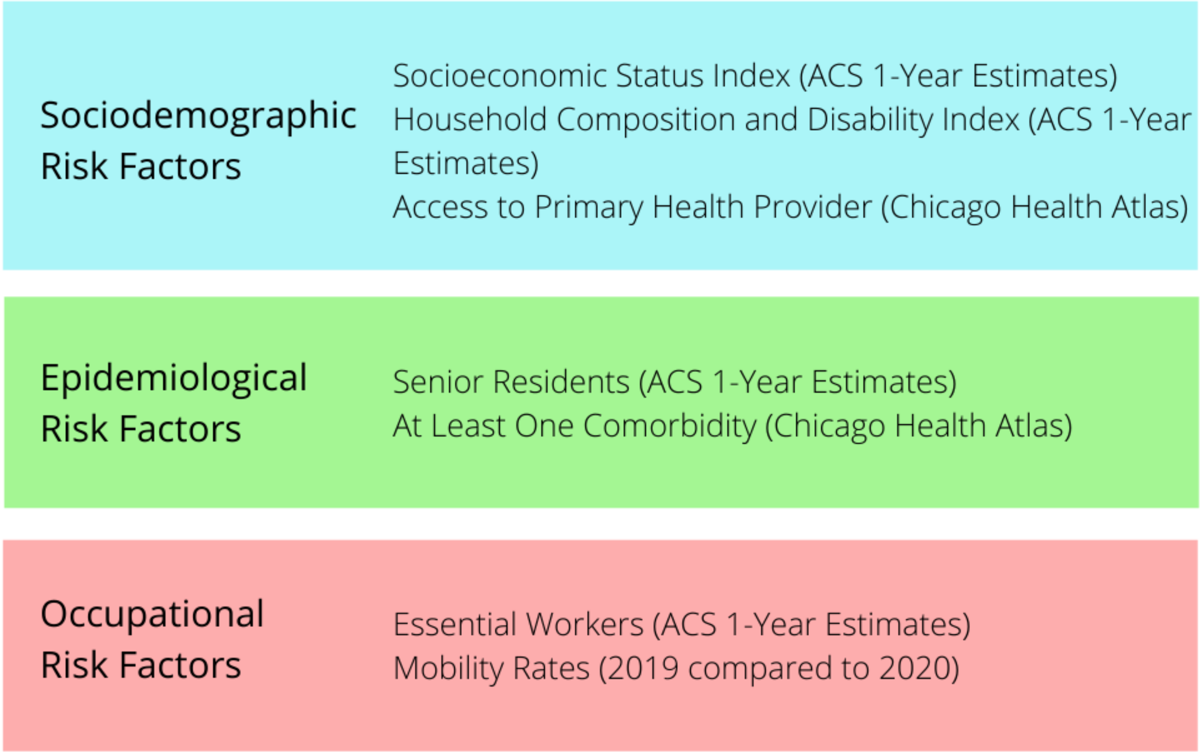
Transportation Behavior described the type of commute taken by participants who worked in person. It was a factor variable consisting of five different modes of transportation, with options for “”Public transportation”, “Personal motorized vehicle”, “Ride share or carpool”, “Walked or used a bicycle”, “Worked Remotely”, “Some other method”. Household Work was a numerical variable that assessed how many members of the participants’ household worked in close contact with other people or in healthcare settings. It was converted into categories of “No One”, “1-2 People” and “3+ People”.

Participants reported whether they had ever been diagnosed with a series of conditions, understood to be COVID-19 comorbidities. This was represented in a series of dichotomous variables, one per condition. I constructed an additional dichotomous variable, Comorbidities, which entered a 1 for those who had any comorbid conditions, and a 0 for those who had none. Insurance was a dichotomous variable based on whether a participant had reported being insured, 1 represented those with insurance and 0 represented those without insurance.

The final category of variables related to the self-reported COVID-19 prevention or avoidance behaviors of participants. The first of these, Interactions, asked participants to rate how much they had reduced their social interactions with others in the pandemic. Responses were on a Likert scale with five options each corresponding to a numeric value: “Not at all” (1), “A little bit” (2), “Somewhat” (3), “Quite a bit” (4), and “Extremely” (5). Prevention Behaviors was a series of eight dichotomous variables that each detailed a certain COVID-19 preventative behavior. These variables included the “Increased Hand-washing”, “Social Distancing”, “Self-Isolation”, “Covering my nose and mouth in public”, “Avoid Public Transportation”, “Avoid Traveling”, “Other” and “None of the above”. I created a Net Preventative Behaviors variable, where each participants responses were tallied to create a numeric variable ranging from 0 to 7, with higher scores indicating a respondent had enacted more preventative behaviors. Venues was series of dichotomous variables that described venues that a participant may have visited since March 1, 2020, including “Doctor’s room/clinic”, “Emergency department”, “School/University”, “Assisted living home/retirement community”, “Transport”, “Concert venue/movie theater/conference”, “Office/workplace”, “Religious space”, “Other public venue”, “None of the above”. The next variable, School Exposure, detailed the potential exposure due to others in the participants’ household attending some form of in-person school. The Crowding variable was used to determine whether the participant lived alone or not, if their response to Crowding was 1, they were considered “Alone”. The House School variable categorized participants based on household school attendance. Participants were asked if any other members of their household had attended in-person school since August 1, 2020, if participants answered 0, they were considered “Not in School”. If they answered 1, they were considered in school, which was further sorted into categories of “PreK/Daycare”, “K-12” and “College” based on participants' reporting of what category of school was being attended in-person. Overall, there were five levels to the School Exposure variable, "Alone", "Not in School", "Pre K", "K-12" and "College".

For one of the key variables, Crowding, there were 847 missing values due to "NA" or "0" responses. Because of a high rate of missing data, an additional dichotomous variable was created to test if these responses were missing at random or not. Using the base R function "is.na", a dichotomous Crowd Test variable was created. If a participant indicated an "NA" value for Crowding, Crowd Test was given a value of 1. If they answered a numeric value for Crowding, Crowd Test took on a value of 0. From this binary variable, t-tests and Chi-squared tests were run on several key variables: "Race/Ethnicity", "CCVI Score", "Work Conditions" and "COVID Result", to determine if there is a significant difference in the characteristics of participants who answered or left blank the question of household crowding. A two-sample t-test was applied to CCVI Score and Crowd Test, to determine if there was a significant difference in the mean of those with and without answers to Crowding. With a p-value of less than 2.2×10^{-16}, the difference in CCVI Score was significant. Further, Chi-squared tests were applied to the variables Race/Ethnicity, Work Conditions and COVID Result. For Race/Ethnicity, the command "simulate.p.value" was used in order to increase the accuracy of the test because of low sample values among less common ethnicities. The X^2 value was 18.85 with a p-value of 0.01, indicating significant differences between different racial/ethnic categories. For Work Conditions, the X^2 value was 11.03 with a p-value 0.01, indicating significant differences in whether Crowding was answered across occupational categories. For COVID Result, the X^2 value was 0.05, with a p-value of 0.82, indicating that there was not a significant difference in COVID seropositivity based on those missing Crowding values and those not. Overall, these results show that data were not missing in a random fashion, but were instead related to differences in race/ethnicity, working conditions and vulnerability scores.

The next step was to build an index that indicated levels of COVID-19 vulnerability at the zip code level to compare to these individual variables and potentially further explain variability in SARS-CoV-2 infections. Several studies have looked at a COVID-19 Community Vulnerability Index (CCVI) as a way to combine health and socioeconomic factors to understand how an area can handle the economic and physical strain of the pandemic (Tiwari). The City of Chicago Department of Health and Human Services developed a Chicago-specific CCVI that presented data at the Community Area level, with the intent of estimating the impact of COVID-19 to evaluate barriers to vaccination (“Chicago CCVI”). This index was created at the community area rather than the zip code level and contained variables about COVID-19 rates and mortality which presented a tautological conflict if used in this thesis. Chicago has 77 community areas, the boundaries of which were created in the 1920s by University of Chicago demographers (“Neighborhoods and Community Areas”). These community areas are not superimposable on zip codes, making it difficult to overlay the City’s version of the index on SCAN data. Additionally, in an index meant to measure the potential vulnerability to COVID-19, the index included current COVID-19 incidence, hospitalizations and mortality measures, all of which were removed in my version of the index to prevent redundancy. An overview of the CCVI is contained in **Figure 3**.



Sociodemographic Risk Factors	Socioeconomic Status Index (ACS 1-Year Estimates) Household Composition and Disability Index (ACS 1-Year Estimates) Access to Primary Health Provider (Chicago Health Atlas)
Epidemiological Risk Factors	Senior Residents (ACS 1-Year Estimates) At Least One Comorbidity (Chicago Health Atlas)
Occupational Risk Factors	Essential Workers (ACS 1-Year Estimates) Mobility Rates (2019 compared to 2020)

Figure 3: Overview of CCVI Components. *This figure provides a breakdown of the main risk factors covered by the index, the variables in each of the risk categories and the data sources of the variables.*

The first category of variables approximated the socioeconomic status of each zip code. It was composed of a Poverty, an Unemployment, an Income Level, a Less than High School Diploma and a Health Insurance variable. All of the variables were taken from the 2019 ACS 1-Year Estimate Data Profiles, provided by the U.S. Census. Poverty, Unemployment, Income Level and Health Insurance all came from the "Selected Economic Characteristics" table, while Less than High School Diploma came from "Selected Social Characteristics" ("DP03", "DP02"). The Poverty variable was defined as the percentage of families in the given zip code below the poverty line. The Unemployment variable was the percentage of civilians above the age of 16 who identified as unemployed. The Income Level variable was the mean per capita income based on 2019 inflation-adjusted dollars, based on the "Mean Income in the Past 12 Months" table (“S1902”). The Health Insurance variable was percentage of the noninstitutionalized civilian population that was uninsured. The Less than High School Diploma variable was a combination of the percentage of those with less than 9th grade education and those with 9th-12th grade education but without a diploma.

These variables were then compiled into a Socioeconomic Status Index (SESI) using the simple aggregative method, where each variable was weighted equally. Each Census variable was downloaded for every zip code in the United States due to limitations in the API functionality. From the nationwide dataset, the results were filtered down to Chicago’s zip codes. The values were then ranked, using the function “dense_rank”, with the higher percentages receiving a higher rank and lower percentages receiving a lower rank. The exception to this was the income variable, which was inverted, with higher income ranked lower. This was inverted because greater scores for the index were meant to represent greater socioeconomic vulnerability. For each zip code, the rankings were added together to create a composite value, and then re-ranked. Each variable was equally weighted. This index could take on values from 1 to 57, with higher scores indicating greater neighborhood socioeconomic vulnerability.

The second category of variables described the household and disability status in each zip code. The variables included Group Quarters, Under 18 Population, Single Parents, Disabled Population and Community Crowding. The Group Quarters variable came from the ACS Detail Table “Group Quarters Population” and was the estimate of total group quarters population (“B26001”). This estimate was converted into a percentage by dividing by the total population in each zip code. The Under 18 Population came from the “ACS Housing and Demographics Estimates” table and was a percentage of total population (“DP05”). The Single Parents variable was made by combining two variables from the “Selected Social Characteristics” table, the percentage of homes with a male householder only, and the percentage of homes with a female householder only (“DP02”). These percentages were added together, resulting in the overall Single Parents variable. The Disabled Population variable also came from “Selected Social Characteristics” and was the percentage of civilian non-institutionalized population with a disability (“DP02”). The Community Crowding variable was created based off of the U.S. Census definition of a crowded household, more than one person per room (“Historical Census”). This was done by taking the occupied housing unit variables from “Selected Housing Characteristics”, then dividing by the population in the zip code (“DP04”). Then, the percentage of housing 1.00 or less was subtracted from total occupied housing, resulting in the percentage of housing with more than 1.00 people per room, or Community Crowding.

The same procedure as above was followed for creating the Household Composition and Disability Index (HCDI). The variables were pulled at the zip code level, then ranked, with highest values or percentages receiving a higher ranking. These rankings were then added to a composite value which was re-ranked, with each variable weighted equally. This index once again took on values ranging from 1 to 57, with higher rankings corresponding to greater household and disability vulnerability.

Occupational risk factors were expressed by the variable Essential Workers, which was the percentage of essential workers in each zip code. The occupation categories were found by determining the US Bureau of Labor Statistics Occupation Code for each essential profession (“SOC System”). The essential worker categories included “education, training and library” (SOC 25-0000), “healthcare practitioner and technical workers” (SOC 29-0000), “protective service” (SOC 33-0000), “food prep and serving related” (SOC 35-0000), “personal care and service” (SOC 39-0000), “farming, fishing and forestry” (SOC 45-0000), “production” (SOC 51-

0000) and “transportation and material moving” (SOC 53-0000). Each of these categories were downloaded from the US Census’ Detail Table “Sex by Occupation for the Civilian Employed Population 16 Years and Over” (“S2401”). Each occupation was downloaded as a percentage of female and male workers separately due to data availability. The male and female percentages were then added together to get total percentage for each occupation. The final step included compiling every essential category together to get the overall percentage of zip code residents who worked in essential jobs.

The Senior Residents variable was the percentage of zip code residents aged 65+. This was created by compiling several age categories from the US Census “ACS Demographic and Housing Estimates” table (“DP05”). The variables “65-75”, “75-85” and “85+” were downloaded, which represented estimates of each population range in the zip code. These numbers were combined to create an estimate of the 65+ population, then divided by the total zip code population for the Senior Residents variable.

Mobility was a variable taken directly from the Chicago Department of Public Health CCVI, it was provided from the company BlueDot, whose Outbreak Intelligence Platform provided mobility rates as a ratio between 2019 and 2020 (“Chicago COVID-19”). These mobility rates were the percentage of mobile phone check-ins that were within a close range of a residents’ home (“Helping Chicago”). Mobility rates were given as rankings of each community area, with the greatest reduction in mobility representing a lower ranking. I then converted these rankings to zip code using a weighted percentage of the community area’s population in each zip code, based on population distribution from the 2010 US Census (Paral).

The Without Primary Care Provider and 1+ Comorbidity variables were derived from the Chicago Health Atlas website. These variables came from the Healthy Chicago Survey, which is an annual survey from the Chicago Department of Public Health (“Healthy Chicago”). Without Primary Care Provider was the percentage of residents without access to a primary care provider. The Chicago Health Atlas variable gave the percentage of adults in each community area that could identify one person who was their personal doctor or health care provider (“Chicago Health Atlas”). This percentage was subtracted from 100 in order to get the percentage of adults without a primary care provider. The data was originally for community areas, so it was converted into zip codes using the same weighted average method as above to get the final Without Primary Care Provider variable. 1+ Comorbidity variable was the percentage of residents that had at least one of three possible health indicators. The conditions: Smoking, Obesity and Diabetes, were downloaded as percentages at the community area level from the Chicago Health Atlas. These three health indicators were equally weighted and averaged to create an overall percentage of residents with at least one of the conditions. Due to a high number of missing values across the three indicators, especially among the diabetes rates, the 1+ Comorbidity variable was coded to average across the categories available. This meant that the weighted average was either across two or three health indicators, depending on the data availability. Finally, this variable was converted from community area to zip code using the population distribution method above.

In order to create the final COVID-19 Community Vulnerability Index (CCVI), the SESI, the HCDI, and the Essential Workers, Senior Residents, Mobility, Without Primary Care Provider, 1+ Comorbidity variables were compiled, with equal weights. The rankings across each variable were averaged to create a “Risk Factor Average”. This was then ranked again, using “dense_rank” so that those with a higher “Risk Factor Average” had a higher CCVI Rank than those without. This CCVI Rank was further categorized into “High”, “Medium” and “Low” categories using the following cutoffs: “Low” was zip codes ranked 1-18, “Medium” was zip codes ranked 19-36, and “High” ranked 37-54, this categorical variable was called CCVI Categories. This summary index therefore represents a broad, place-based assessment of vulnerability based on sociodemographic and epidemiological risk factors for SARS-CoV-2 infection and COVID-19 mortality at the zip code level for Chicago.

Statistical Analyses

Cronbach’s alpha tests were run to determine the reliability of the CCVI, this was done by measuring the alpha of the smaller indices (SESI and HDCI), as well as of the overall CCVI. Logistic regressions were run to further elucidate what factors influence an individual’s chances of contracting SARS-CoV-2. Due to the fact that respondents were nested within differing zip codes, multi-level mixed regression models were used, with a varying intercept for each distinct zip code. All regressions were binary, reflecting the COVID Result response variable. Individual logistic regression models were run first to identify variables of interest and to gauge their statistical significance. Variables with a statistically significant result ($p < 0.05$) were then put into a series of multivariable models. Models were built starting from a baseline logistic regression (containing only the random effects variable) and individually-significant variables were added systematically to assess how the significance of specific factors changed with the addition of new risk factors. The models were built with individual-level variables from the SCAN dataset first and community-level CCVI Categories added to the final iteration. Individual-level variables were included based on their significance in univariate logistic regression testing. These models were run to understand the cumulative effects of individual and community variables on SARS-CoV-2 infection. P-values were used to assess the statistical significance of the relationships in the model, whereas R^2 and AIC (Akaike Information Criterion) values were used to estimate the predictive power of the regressions. R^2 is used to estimate how well the model fits the data and can be further separated into conditional and marginal R^2, conditional R^2 defines the total explanatory power of the model (both fixed and random effects) while the marginal R^2 defines the explanatory power of *only* the fixed effects portion of the model.

Spatial analysis was done on the SCAN dataset and the CCVI to determine if there was significant spatial clustering and to further specify the locations of any hot or cold spots. When working with spatial data, a different statistical approach must be taken. In a non-spatial context, most statistical models assume a normal and independent distribution of independent variables unless statistical tests prove that this is beyond chance. However, with spatial data, as has been shown repeatedly in social science studies, there exists inherent geographic clustering of these values that make it more difficult to analyze statistically. It cannot always be assumed that variables are randomly distributed across space. For example, population density does not vary randomly across the United States, rather, there are clusters of high density population along the Eastern seaboard and throughout the Midwest. This is due to sociopolitical processes and the geographic variation that has dictated the spread of the United States population. On a more granular level, segregation has also resulted in the unequal distribution of minority populations throughout American cities, meaning that racial distribution does not occur randomly throughout a city, but rather in population clusters that have largely remained consistent since the end of legal segregation.

In order to understand the spatial distribution of variables, spatial autocorrelation (or spatial dependence) tests can be run to understand how the errors of variables located near each other are related (Cromley and McLafferty 65). Spatial clusters can be measured at three levels, using global, local or focused methods. Global methods of spatial autocorrelation are used to determine whether there is any spatial clustering of a variable at all. This method does not provide any information about the clusters but simply indicates the presence. Local methods of spatial autocorrelation identify the locations of these clusters in a given space. Finally, focused methods of spatial correlation look at how data cluster around a specific point. These are often used in public health settings to identify health outcomes relating to a specific environmental hazard (Cromley and McLafferty 158-159). These methods can be further broken into field-based and object-based methods. In this thesis, field-based methods were used exclusively.

Three methods of spatial autocorrelation were used–Global Moran's I, Local Moran's I, and Getis and Ord's G_i*. Global Moran's I is a way to estimate the global autocorrelation, Local Moran's I is an adaptation of the global statistic to understand the clustering in space. G_i* is used to further investigate local clustering by classifying hot and cold spots based on clustering of similar or dissimilar values.

Moran's I can be thought of as a correlation coefficient that compares between a variable in one spatial location and the composite values of that same variable in neighboring spaces. To find this statistic, a variable is plotted against its "lagged" values, which are those surrounding the geography of question. The resulting plot is fitted with an ordinary least squares regression, resulting in a correlation coefficient (Gimond). The significance of this number can be assessed with the resulting p-value from the regression, although Monte Carlo tests are sometimes used to estimate significance (Lansley and Cheshire). Local Moran's I is adapted from this global measure, using the statistic I_i, and can be plotted to show which areas contribute to more spatial autocorrelation than others. The G_i* statistic can be used to further understand the nature of the spatial clustering. It weights areas based on their proximity, then compares corresponding values. When the G_i^* statistic is positive, it indicates high values of the variable are clustered together and when it is negative it indicates low values of the variable are clustered (Cromley and McLafferty 161-162). These values can be interpreted as hot spots and cold spots.

These three methods were used to assess the spatial clustering at the zip code level of CCVI Category, CCVI Rank, COVID Result and Comorbidities. Because these statistical tests were done at the zip code level, a new data frame was made that contained the variable Case Rate and Comorb Rate. The Case Rate variable was the sum of all the COVID-19 Results in SCAN that were positive (1), divided by the total number of observations in that zip code, the resulting value was tested using Global Moran's I. The next variable tested was CCVI, this was examined both in the continuous form of Rank (1-57) and in the Category form (Low, Medium, High). The factor CCVI Category was converted to a numeric variable for the test, with 1 corresponding to "Low", 2 corresponding to "Medium" and 3 corresponding to "High". The final variable tested for spatial correlation was Comorb Rate, this was similarly derived from the Comorbidities variable and was determined by totaling the number of individuals with Comorbidities and then dividing by the total number of observations.

First, the neighbors of each zip code, in the form of a spatial polygon, were determined. This was done using the function "poly2nb" and the command "queen = FALSE". This command designates neighbors based on neighboring edges or vertices rather than sharing an entire border, expanding the definition of proximity ("Contiguity Based Spatial Weights"). After the neighbors have been designated, a Global Moran's test was run using the function "moran.test". A Local Moran's was also run to find the more specific locations of clustering, greater values of the I_i statistic correspond to greater clustering of values. The final statistical test was the Getis-Ord G_i statistic, which requires the distance-based definition of neighbors. This was set using the function “dnearneigh”, and manually adjusting the size of the search radius until every region had a defined nearest neighbor. As shown in **Figure 4**, this process honed in on the value 17,800 m (or 17.8 km), as the lowest possible radius while still preventing empty neighbor sets.

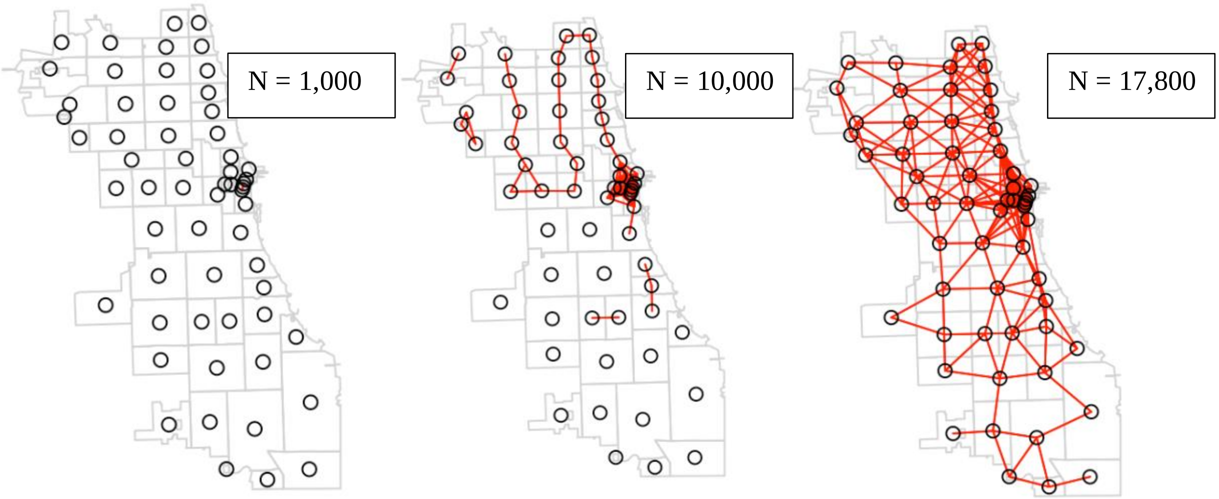


Figure 4: G_i* Nearest Neighbors Definition. *This figure visually shows the different parameters that were tested in order to determine the lowest radius at which every zip code had a neighbor based on distance rather than shared borders.*

All statistical analysis was carried out using the software R (R Core Team). The R package “glmer” was used to handle the multi-level effects of individual-level observations with a zip code differentiation (Bates). The R package “spdep” was used for the spatial autocorrelation calculations (Bivand and Wong). This study was exempt from institutional review board approval at Emory University due to the deidentified nature of the data.

Results

Overview of Study Participants

Of all potential participants invited to take the survey, 75.9% completed the survey and 73.0% of those invited collected and submitted DBS samples. The following values are summarized in **Table 1**. The mean age of the SCAN sample was 40.3 years old (SD = 13.0), with an IQR of 18.2 years. The sample is made up of 1,816 (44.3%) men, 2,264 (55.2%) women and 18 (0.4%) gender non-conforming individuals. Based on the Race/Ethnicity variable, the data were comprised of 2,086 non-Hispanic White (44.2%), 794 Hispanic/Latinx (16.8%), 729 non-Hispanic Asian (15.5%), 624 Multiracial (13.2%), 416 non-Hispanic Black/African American (8.8%), 50 non-Hispanic Other (1.1%), 14 (0.3%) non-Hispanic Native Hawaiian/Pacific Islander and 4 non-Hispanic American Indian/Alaskan Native individuals (0.1%). Due to convergences issues with multivariate regressions, non-Hispanic Native Hawaiian/Pacific Islander and non-Hispanic American Indian/Alaska Native categories were combined into non-Hispanic Other, resulting in a final count of 68 non-Hispanic other participants (1.4%).

The Living Status variable showed that two main forms of residence were highly favored. 1,800 participants (38.2%) said they lived in a home/townhome, and 2,905 participants (61.6%) said they lived in an apartment or condo. The remaining options showed that 1 person resided in a shelter, 4 people in dormitories, 1 participant in assisted living, and the remaining 4 lived in other situations.

For Crowding, it was found that 2,057 people (45.2%) lived alone, followed by 996 participants (21.9%) who lived with one person, 851 participants (18.7%) who lived with two people, 400 participants (8.8%) who lived with three people, 151 participants (3.3%) living with four people, and 97 participants (2.1%) who lived with five or more people. As mentioned, the high number of missing values for this variable necessitated further statistical testing to determine if these values were missing at random. There were significant differences between the study sample who answered the question and those who left it blank.

The following values are summarized in **Table 3**. The Work Now variable showed that 3,726 participants (79.0%) were currently employed, while 991 participants (21.0%) were unemployed at the time of survey. The Work Flex variable showed that, of those currently working, 2,815 (75.7%) were able to take paid sick days if needed, 640 participants (17.2%) could take unpaid sick days, 180 participants (4.8%) could not take sick days, and 83 participants (2.2%) worked multiple jobs with different conditions. The Work Remote variable indicated that, of those currently working, 1,992 individuals (53.6%) could do all their work remotely, 827 individuals (22.2%) could do some work remotely and 898 individuals (24.2%) could not do any of their work remotely. The Work Close variable showed that 1,273 of participants (73.7%) who were in-person also worked in close proximity to others, while 454 (26.3%) did not. The Work Type variable categorized the occupation category of those who could not work entirely remotely. 463 of these individuals (26.9%) worked in Healthcare, 105 (6.1%) worked in Essential Retail, 87 (5.0%) worked in Restaurant services, 45 (2.6%) worked in Food Production, 38 (2.2%) worked in Trade services, 52 (3.0%) worked in Construction, 72 (4.2%) worked in Social Services, 32 (1.9%) worked in Media, 93 (5.4%) worked in First Responder/Emergency, 109 (6.3%) worked in Public Services, 38 (2.2%) worked in Transportation Services and 22 (1.3%) worked in Mail/Delivery, and 711 (41.2%) worked in Other categories. The Work Conditions variable condensed all of these findings into four categories: 1,145 were unemployed (20.7%), 2,316 worked from home (41.8%), 545 worked in healthcare (9.8%) and the remaining 1,537 worked in other jobs (27.7%).

Transportation Behavior showed that 1,230 participants (71.3%) used a personal car or vehicle to commute, 244 participants (14.2%) walked or rode a bicycle, 192 participants (11.1%) used public transportation, 42 participants (2.4%) used rideshare and 16 participants (0.9%) used other methods. Household Work indicated that 2,507 participants (64.8%) had no others in their homes who worked in healthcare, 1,301 participants (33.7%) had one or two individuals in their homes who worked in healthcare, and 58 participants (1.5%) had more than two individuals in their homes who worked in healthcare.

The Comorbidities variable divided those with and without COVID-19 comorbid conditions, 1,318 participants (28.5%) had at least one comorbidity and 3,314 participants (71.5%) had no comorbidities. Specifically, 335 participants (7.2%) had chronic lung disease, 153 participants (3.3%) had diabetes mellitus, 84 participants (1.8%) had cardiovascular disease, 15 participants (0.3%) had chronic renal disease, 12 participants (0.3%) had chronic liver disease, 33 participants (0.8%) had HIV/AIDS, 61 participants (1.3%) were otherwise immunocompromised, 42 participants (0.9%) had a neurological impairment, 35 participants (0.8%) were currently pregnant, 669 participants (14.4%) had other chronic illnesses, and 260 participants (5.6%) had high blood pressure. 4,462 participants (94.7%) had insurance and 252 (5.3%) were uninsured under the Insurance variable.

Preventative Behaviors

The following descriptive statistics are summarized in **Table 4**. The Interactions variable–which assessed how much participants had reduced their social interactions due to the pandemic–showed that 1,910 participants (40.5%) extremely reduced their interactions with others as a result of the COVID-19 pandemic, 2,164 participants (45.9%) reduced their interactions quite a bit, 479 participants (10.2%) reduced their interactions somewhat, 135 participants (2.9%) only reduced their interactions somewhat, and 29 participants (0.6%) did not reduce their interactions at all. As for Prevention Behaviors, 4,611 participants (97.8%) increased their handwashing, 4,609 participants (97.7%) increased their social distancing, 1,559 participants (33.1%) self-isolated, 4,661 participants (98.8%) used masking in public spaces, 3,835 participants (81.3%) avoided public transportation, 3,422 participants (72.6%) avoided all traveling, 202 participants (4.3%) took other precautions and 3 participants (0.1%) did not undertake any preventative behaviors at all. As for Net Preventative Behaviors, participants took on average 4.86 preventative behaviors (SD = 1.02). For Venues, 2,981 participants (63.3%) visited the doctor's office since March 2020, 521 participants (11.1%) visited a Hospital's Emergency room, 991 participants (21.0%) visited a school or university, 180 participants (3.8%) visited an assisted living community, 1,826 participants (38.8%) used some mode of transportation, 274 participants (5.8%) attended a large gathering such as a conference or concert, 2,438 participants (51.8%) visited an office or workplace, 441 participants (9.4%) visited a religious space, 1,412 participants (30.0%) visited some other venue or gathering, and 321 participants (6.8%) did not visit any such venue.

The School Exposure variable showed that 1,112 participants (45.7%) of the sample lived alone, 1,138 participants (46.4%) lived with someone who was not attending school in-person, 37 participants (1.5%) lived with someone attending in-person PreK or Daycare, 90 participants (3.7%) lived with someone attending in-person grades K-12, and 66 participants (2.7%) lived with someone attending in-person college.

Overview of Seroprevalence

Out of the 192 zip codes represented in the SCAN dataset, 173 were located in Illinois (6,876 participants) and 58 were located inside the City of Chicago (5,668 participants). From these 5,668 participants, only 4,717 had SARS-CoV-2 antibody results. **Figure 5** shows the distribution of SCAN participants across the City of Chicago and **Figure S1** shows the distribution of SCAN participants across the greater Chicago area. The most observations were found in zip code 60643, with 352 participants. The least represented zip code was 60603, with only two participants. The average number of participants in each zip code was 103.

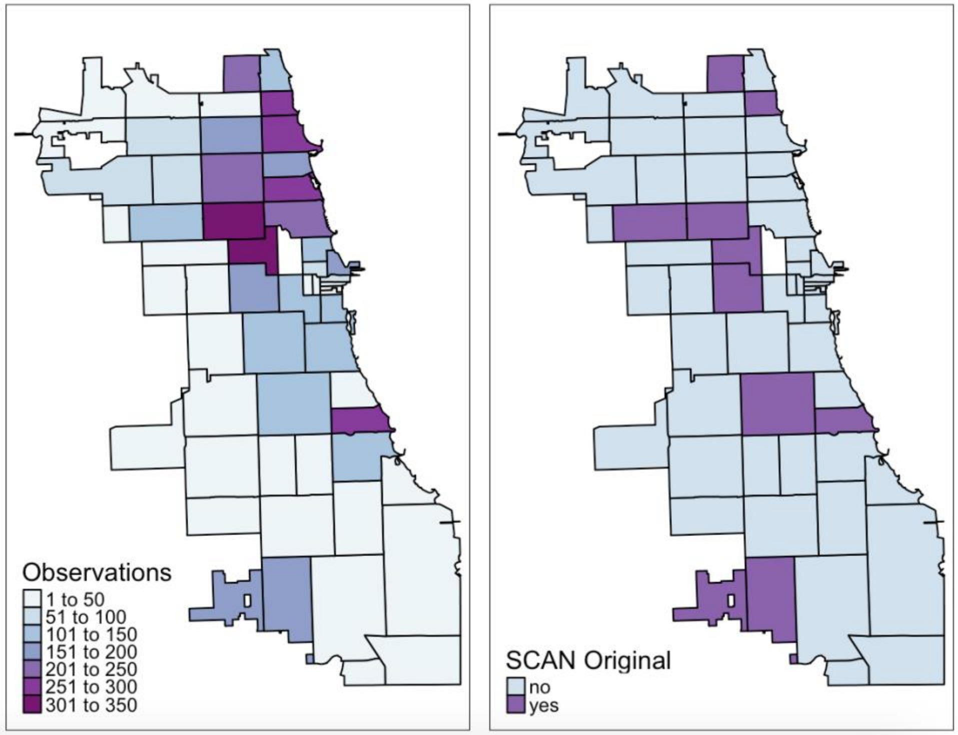


Figure 5: Zip code Distribution of SCAN participants. *The map on the left shows the distribution of the SCAN dataset by zip code. The original sampling for SCAN focused on 5 pairs of adjacent zip codes with very different COVID-19 case rates, these original 10 zip codes are shown in the map on the right.*

Of the 4,717 SCAN participants who had data on antibody levels, 859 (18.2%) of the sample tested positive for anti-RBD IgG SARS-CoV-2 antibodies. Meaningful seropositivity was defined as having antibody levels greater than 0.40 μg/mL. 3,858 (81.9%) of the participants were considered seronegative (antibody levels below 0.40 μg/mL). Of these seropositive participants who reported their gender, 337 (46.4%) were men and 388 (53.4%) were women, one participant was gender non-conforming (0.1%). Overall, 18.6% of men were seropositive and 17.1% of women were seropositive. The average age of COVID-19 positive participants was 39 (SD = 12.50), with the oldest COVID-19 positive participant being 93 and the youngest being 18. The Race/Ethnicity breakdown of COVID-19 positive participants was as follows: 292 participants (34%) were non-Hispanic White, 182 (21%) were Hispanic/Latinx, 140 (16%) were Multiracial, 139 (16%) were non-Hispanic Asian, 94 (11%) were non-Hispanic African American, 9 (1%) identified as non-Hispanic Other, 2 (0.2%) were non-Hispanic Native Hawaiian/Pacific Islander and 1 (0.1%) was non-Hispanic American Indian/Alaska Native.

The sample's SARS-CoV-2 seroprevalence also varied widely by zip code, as shown in **Figure 6**. The zip code with the highest COVID-19 rate was 60628, 43% of participants surveyed had SARS-CoV-2 antibodies. The zip code with the lowest COVID-19 rate was 60602, where none of the participants had SARS-CoV-2 antibodies.

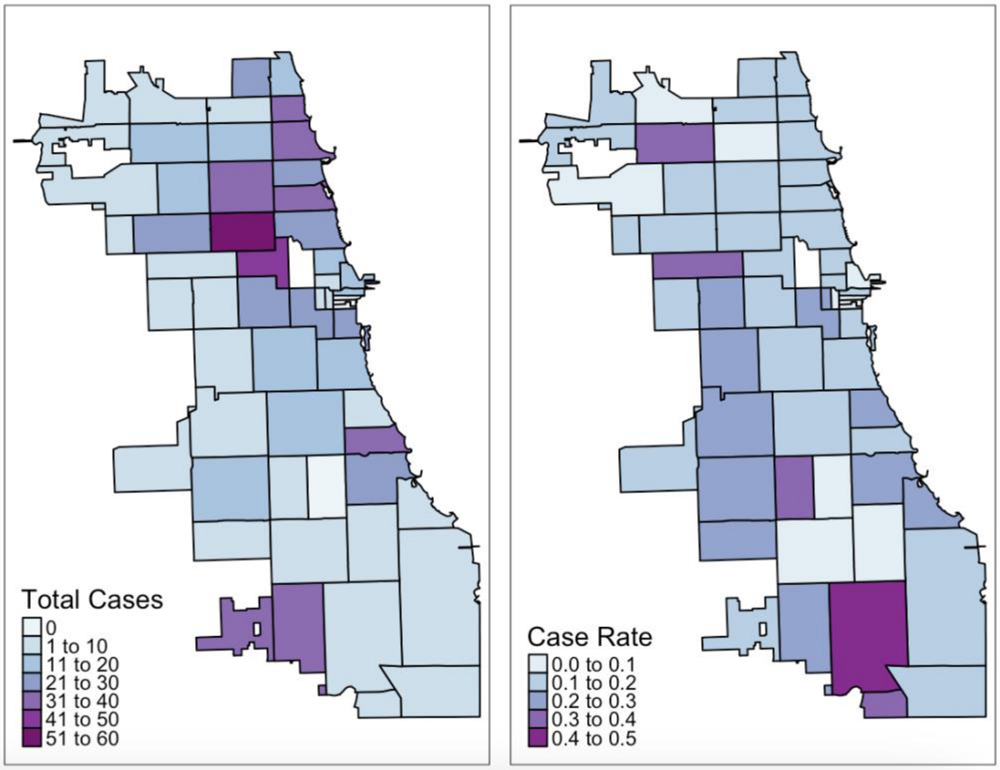


Figure 6: Seroprevalence Distribution of SCAN Participants. *The map on the left shows the COVID-19 total cases across the zip codes of Chicago. The map on the right shows the Case Rate (the number of positive COVID results divided by the total number of observations in each zip code) across Chicago zip codes.*

Community COVID-19 Vulnerability Index (CCVI)

The CCVI ranged from 1 to 57, ranking all the City of Chicago zip codes, with the exception of 60666, with was eliminated due to lack of health and mobility data (this zip code is the location of Chicago O'Hare International Airport). The zip code with the lowest CCVI ranking was 60604, located in "The Loop", a wealthy residential and business district. The highest CCVI ranking (57) was 60632, located on the Southwest side of the city. There were 20 zip codes categorized with a "Low" CCVI ranking, 19 zip codes categorized with a "Medium" ranking, and 18 zip codes with a "High" ranking. These rankings vary by place across the city (**Figure 7**), most "Low" ranked zip codes were located across the North side of the city, along

Lake Michigan. The "High" CCVI zip codes were similarly concentrated in the South and West portions of the city. The "Medium" ranked zip codes were more distributed across the city, some located in the Northwest and some throughout the Southside.

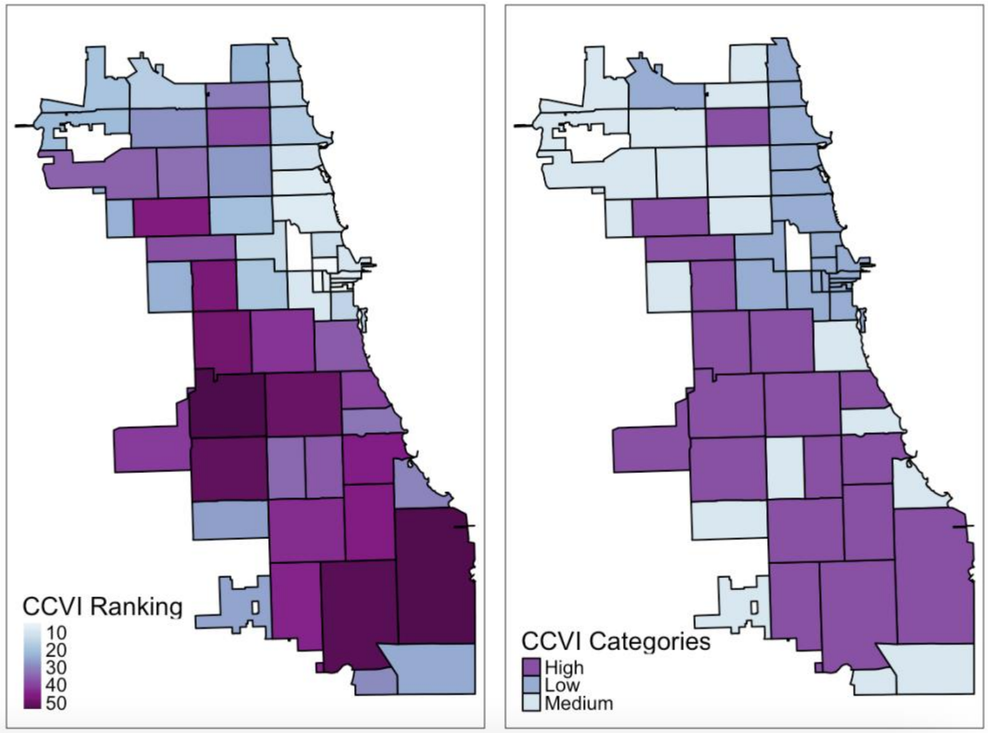


Figure 7: CCVI Ranking and Category by Chicago zip code. *This figure shows the spatial distribution of community vulnerability as measured by the CCVI. ZIP codes were ranked from 1-57 based on their composite scores across different categories in the CCVI. They were then categorized based on their ranking into "Low" (1-18), "Medium" (19-36) and "High" (37-54).*

Cronbach's alpha was used to determine the correlations of variables contained in the CCVI index. First, the SESI and HDCI were tested to determine the correlation of the variables contained within each index. The Cronbach's alpha value for SESI was 0.91 (95% CI: 0.87, 0.95). This value indicates strong average inter-variable correlation within the index, meaning that the index is effectively measuring the same concept, which here is outlined as socioeconomic status. For the HDCI, the Cronbach's alpha value was 0.69 (95% CI: 0.59, 0.79). While not as high as the SESI, it still indicates strong average inter-variable correlation. This index is effectively measuring a single construct, interpreted here as household composition and disability status. Overall, these two indices, along with the variables Essential Workers, Senior Residents, Mobility, Without Primary Care Provider and 1+ Comorbidity, made up the CCVI. The Cronbach's alpha of the entire CCVI was 0.87 (95% CI: 0.82, 0.92), indicating a strong average inter-variable correlation. This index contained both strong inter and intra-index correlation, helping to measure community vulnerability in the context of COVID-19.

Spatial Correlation Results

The following variables were tested for spatial correlation to understand the clustering of the dependent variable and the CCVI. Each of the variables tested was found to have significant spatial clustering. The first variable tested was COVID-19 Result. Because these are tested at the zip code level, a new data frame was made that contained the variable Case Rate. The Case Rate geographic distribution is shown in **Figure 8**. The Global Moran's I statistic value was 0.19 (p-value = 0.008) and was considered significant, resulting in moderate spatial clustering overall. G_i statistic calculations show a range from -2.72 to 3.46. Negative values indicate clustering of low values (cold spots) and positive values indicate clustering of high values (hot spots). Cold spots appear in the downtown areas of Chicago, while hot spots of infection appear in the South and West sides of the city.

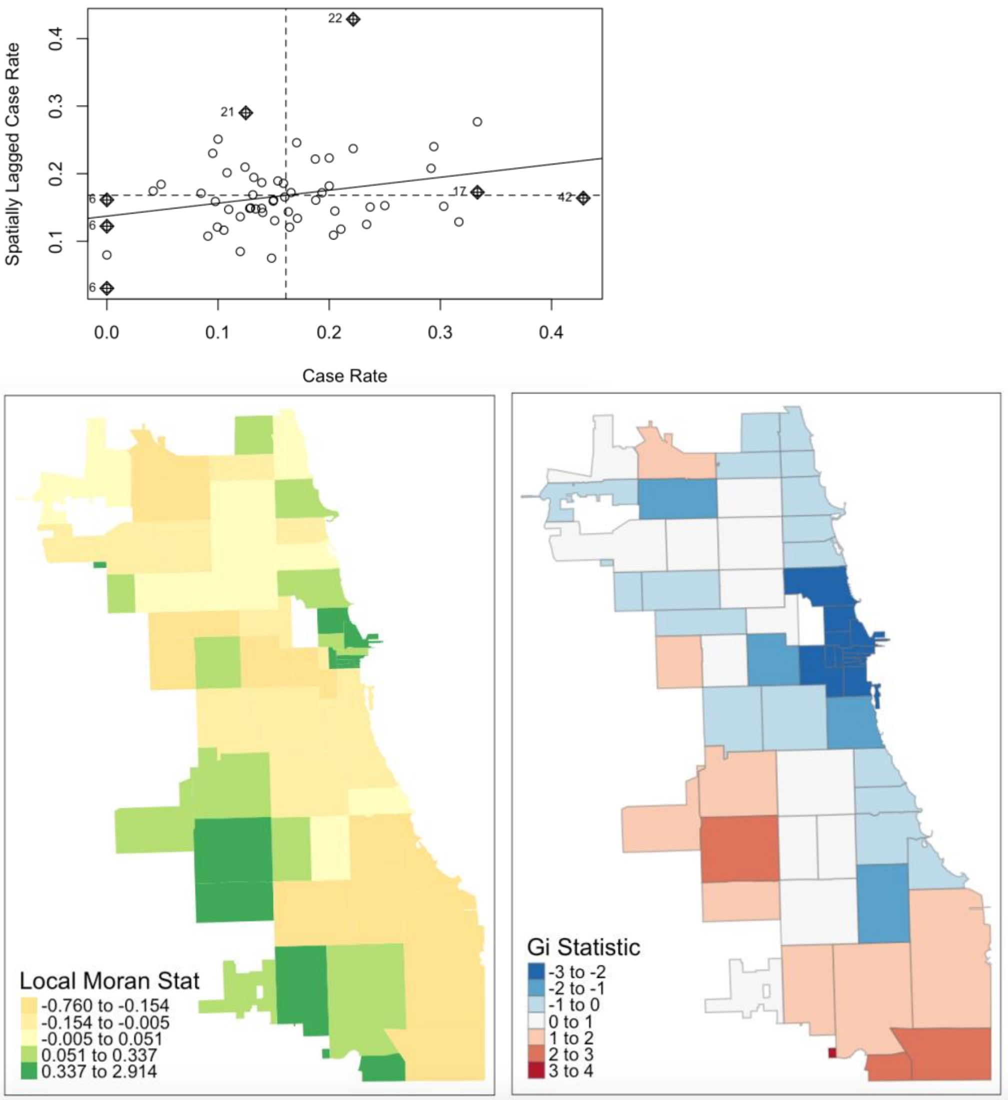


Figure 8: Spatial Clustering of SARS-CoV-2 antibodies in the SCAN data. *The Local Moran's I plot shows the COVID Case Rate plotted against the spatially lagged Case Rates (the average of neighboring ZIP codes), the slope of this OLS-fitted line is 0.19, indicating that there is moderate but significant spatial clustering of these values, which is also depicted in the map on the left. The Gi statistic plot on the right shows the clustered hot spots and cold spots across the SCAN ZIP codes.*

The next variable tested was the CCVI, this was examined both in the continuous form of Rank (1-57) and in the Category form (Low, Medium, High). The geographic distribution of CCVI Rank is shown in **Figure 9**. Both of these versions of the CCVI variable showed statistically significant spatial clustering, with the Moran's I statistic of 0.67 for Rank (p-value =

2.6E-15) and the value of 0.55 for Category (p-value = 4.6E-11). The spatial distribution of this variable was similar to the COVID Results, the G_i ranged from -5.45 to 3.07. The map showed cold spots downtown and hot spots across the South side of the city.

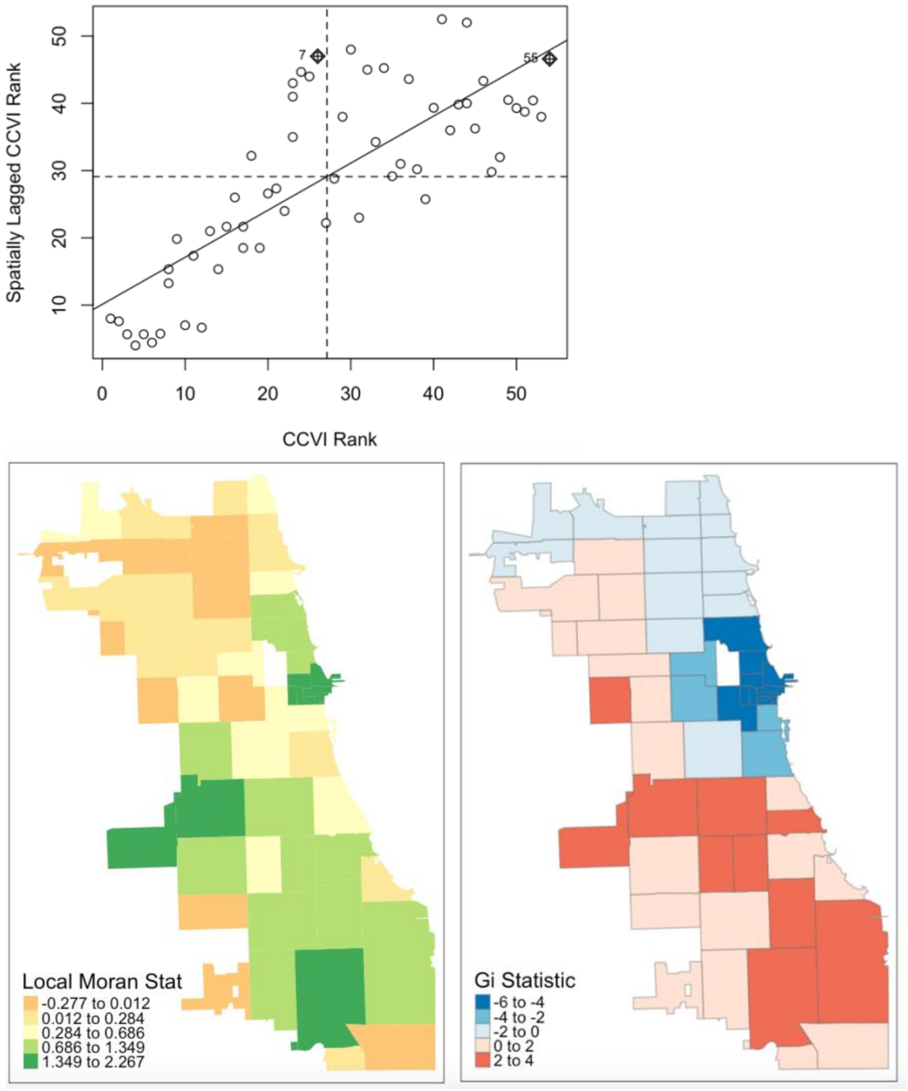


Figure 9: Spatial Clustering of CCVI Rankings in SCAN data. *This Local Moran's I plot shows the CCVI plotted against the spatially lagged CCVI (the average of neighboring ZIP codes), the slope of this OLS-fitted line is 0.67, indicating that there is strong spatial clustering of these values, shown visually in the map on the left. Green areas indicate areas of data clustering, these values are further expanded upon in the map on the right. This Gi statistic plot shows the clustered hot spots and cold spots across the SCAN ZIP codes.*

The Comorb Rate variable’s geographic distribution is shown in **Figure 10**. This variable also had significant rates of spatial clustering, the Moran’s I statistic was 0.30 (p-value = 5.7E-5). The Gi values ranged from -2.45 to 4.41, and showed a cold spot on the North side of the city and a hot spot on the South side.

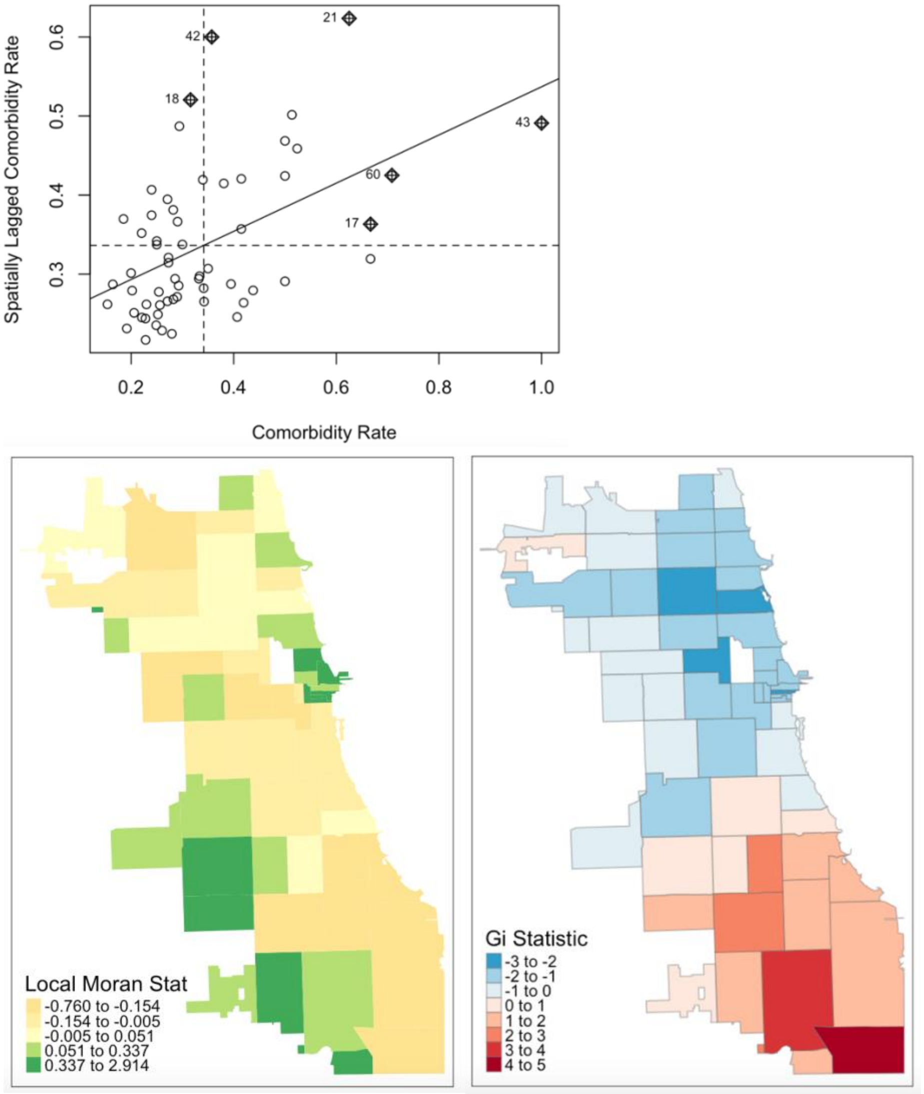


Figure 10: Spatial Clustering of Comorbidities in SCAN data. *The Global Moran’s I plot shows the CCVI plotted against the spatially lagged CCVI 0.67 (the average of neighboring ZIP codes), the slope of this OLS-fitted line is 0.30, indicating that there is moderate yet significant spatial clustering of these values, shown also on the map on the left. Green areas indicate areas of data clustering, these values are further expanded upon in the map on the right. This* G_i *statistic plot shows the clustered hot spots and cold spots across the SCAN ZIP codes.*

Univariate Regressions

Univariate logistic regressions were first conducted between all variables and seropositivity to determine if the independent variables significantly predicted the presence of SARS-CoV-2 antibodies in individual respondents. These regressions were all mixed models, with zip code as the random effects variable. The results of all univariate regressions are summarized in **Table 5**.

The age of participants (Age) did significantly predict the presence of SARS-CoV-2 antibodies. Overall, 19.7% of individuals aged 18-29, 18.0% of individuals aged 30-39, 18.9% of individuals aged 40-49, 19.6% of individuals aged 50-59 and 13.1% of individuals older than 60 years old had SARS-CoV-2 antibodies. Individuals over the age of 60 years had significantly lower predicted SARS-CoV-2 antibodies (OR: 0.60, 95% CI: 0.45, 0.82) compared to individuals between the ages of 18 and 29. Compared to individuals 18-29, those between 30 and 39 years old (OR: 0.90, 95% CI: 0.73, 1.09), between 40 and 49 years old (OR: 0.92, 95% CI: 0.74, 1.16), and between 50 and 59 years old (OR: 0.97, 95% CI: 0.75, 1.26) did not have a significantly higher chance of SARS-CoV-2 antibodies. Because of the overall significance, this variable was retained for further models.

The self-reported gender of participants (Gender) did not significantly predict having SARS-CoV-2 antibodies. 18.6% of men, 17.1% of women and 5.6% of gender non-conforming participants had antibodies. Women (OR: 0.90, 95% CI: 0.76, 1.06) did not have a significant difference in antibody rates compared to men. This variable was not retained for further models.

The race or ethnicity of participants (Race/Ethnicity) was a significant predictor of SARS-CoV-2 antibodies. Across racial and ethnic categories, 14.0% of Non-Hispanic White participants, 22.9% of Hispanic/Latinx participants, 22.4% of Multiracial participants, 19.1% of

Non-Hispanic Asian participants, 22.6% of Non-Hispanic Black/African American participants and 17.6% of Non-Hispanic “other” participants had antibodies. Non-Hispanic Whites had significantly lower prevalence of SARS-CoV-2 antibodies (OR: 0.68, 95% CI: 0.54, 0.85) compared to non-Hispanic Asian participants. Multiracial participants (OR: 1.21, 95% CI: 0.92, 1.58), Hispanic/Latinx participants (OR: 1.23, 95% CI: 0.96, 1.59), non-Hispanic Black/African American participants (OR: 1.19, 95% CI: 0.88, 1.61) or non-Hispanic Other-identified participants (OR: 0.92, 95% CI: 0.48, 1.76) did not have significant differences in SARS-CoV-2 antibodies from the non-Hispanic Asian participants. Because of overall significance, this variable was retained for further models.

The type of home that participants resided in (Living Status) was not a significant predictor of SARS-CoV-2 antibodies. The prevalence across Living Status categories was as follows, 17.5% of participants living in apartments had antibodies, 19.4% of participants living in a house had SARS-CoV-2 antibodies, while 20% of participants living in “other” accommodations had antibodies. COVID-19 risk was not associated with living in an apartment or condo (OR: 0.93, 95% CI: 0.79, 1.11) nor was it associated with “other” living arrangements (OR: 1.11, 95% CI: 0.23, 5.30) compared to the rates of those living in a house. Since this variable lacked significance, it was not retained for further study.

The number of people living in a household (Crowding) was overall a significant predictor of SARS-CoV-2 antibodies. 15.7% of participants living alone had antibodies, while 19.1% of participants living with 1-2 others, 20.5% of participants living with 3-4 others and 41.4% of participants living with 5 or more had antibodies. Each level of this variable corresponded to a significantly higher SARS-CoV-2 antibody rate than those participants without any others in their household. Individuals living with 1-2 others in their household were more likely to be infected than those living alone (OR: 1.25, 95% CI: 1.04, 1.50), as were those living with 3-4 people (OR: 1.35, 95% CI: 1.04, 1.76) or 5 or more (OR: 3.70, 95% CI: 2.23, 6.09). This variable was significant and was retained for further models.

The occupational conditions of participants (Work Conditions) was not associated with risk of SARS-CoV-2 infection. For the prevalence of antibodies, 18.4% of participants who were unemployed, 16.8% of participants who worked from home, 21.8% of participants who worked in healthcare and 19.2% of participants who worked in other occupations had antibodies. Those individuals who worked from home (OR: 0.90, 95% CI: 0.74, 1.10), in healthcare (OR: 1.24, 95% CI: 0.95, 1.64) and in another occupation (OR: 1.04, 95% CI: 0.84, 1.29) had no significant difference in risks of infection compared to those who were unemployed, so the variable was not retained for further analysis.

Beyond the occupational conditions of the participant, the occupational conditions of those in their household (Household Work) was a significant predictor of SARS-CoV-2 antibodies. 16.7% of participants who had no one working outside the home in healthcare had antibodies, compared to 20.3% of participants with 1-2 people in their household and 31.0% of people who more than 3 people in their household in healthcare. Those who had 1-2 people in their household working in healthcare (OR: 1.25, 95% CI: 1.05, 1.48) as well as those with more than three people in their house working in healthcare (OR: 2.12, 95% CI: 1.20, 3.78) had significantly higher chances of SARS-CoV-2 infection compared to those who had no one in their household working in healthcare. Due to the significance of this variable, it was retained for further models.

The number of comorbidities (Comorbidities) that an individual had was not significant in predicting SARS-CoV-2 antibodies (OR: 0.90, 95% CI: 0.76, 1.07). Of individuals who had at least one comorbidity, 17.1% of them had antibodies, compared to 18.5% of individuals with no comorbidities. The presence of specific individual comorbidities, including chronic lung diseases, diabetes, cardiovascular disease, chronic renal disease, chronic liver disease, HIV/AIDS, or “other” immunocompromised conditions, neurological or neurodevelopment conditions, pregnancy and high blood pressure, were also insignificant for infection. This variable was not kept in further models.

Individual insurance status (Insurance) was statistically associated with increased odds of being infected with SARS-CoV-2. 17.9% of insured participants had antibodies, compared to 23.8% of uninsured participants. Those with insurance (OR: 0.71, 95% CI: 0.52, 0.95) were significantly more likely to avoid SARS-CoV-2 infection than those who were uninsured. The Insurance variable was retained for further analysis.

The degree to which participants reduced their social interactions during the pandemic (Interactions) was not sufficient to significantly predicting SARS-CoV-2 antibodies. 13.8% of participants who did not reduce their interactions at all had antibodies. 23.0% of participants who reduced interactions by “A Little Bit” had antibodies. 19.0% of participants who “Somewhat” reduced their interactions had antibodies. 18.3% of participants who reduced interactions “Quite a Bit” had antibodies and finally, 17.6% of participants who “Extremely” reduced interactions had antibodies. Scored on a scale from 1 to 5, a change in interactions (OR: 0.95, 95% CI: 0.87, 1.05) was not sufficient to significantly predict the chances of contracting SARS-CoV-2. The regression was also run treating Interactions as a factor variable and the results were not significant. The Interactions variable was not included for subsequent models.

The number of preventative behaviors taken by an individual (Net Preventative Behaviors) to avoid COVID-19 was significant in predicting the presence of SARS-CoV-2 antibodies. The antibody prevalence in individuals based on the number of behaviors taken was as follows: 28.6% for one behavior, 21.0% for two behaviors, 21.0% for three behaviors, 18.8% for four behaviors, 17.7% for five behaviors, 17.3% for six behaviors and 17.0% for all seven behaviors. More preventative behaviors taken significantly lowered the chance of having antibodies (OR: 0.92, 95% CI: 0.86, 0.99). However, no one behavior, such as "Social Distancing" or "Avoiding Public Transportation", was individually significant (Prevention Behaviors). A Cronbach's alpha test was run to further investigate the correlation between individual behaviors, the resulting value was 0.42 (95% CI: 0.39, 0.44), showing that there was not very good inter-item correlation. Because of the overall significance, Net Preventative Behaviors was retained for further models.

The types of public spaces attended by participants between March 1, 2020 and the time of survey (Venues) was a significant predictor of SARS-CoV-2 antibodies. 17.7% of participants who went to the Doctor's Office, 22.1% of participants who went to the Emergency Room, 20.0% of participants who went to School, 22.2% of participants who visited an Assisted Living community, 18.4% of participants who took Transportation, 15.3% of participants who attended a Concert, 18.0% of participants who went into an Office, 22.2% of participants who went to a Religious Space, 17.6% of participants who went to another venue and 21.2% of participants who went to None of the possible venues had SARS-CoV-2 antibodies. Going to the Emergency Room (OR: 1.31, 95% CI: 1.07, 1.67) and or visiting a Religious Space (OR: 1.31, 95% CI: 1.03, 1.68) were both significant predictors of having COVID-19 antibodies, while visits to the doctor's office (OR: 0.93, 95% CI: 0.80, 1.10), to a school (OR: 1.16, 95% CI: 0.98, 1.39), to an assisted living community (OR: 1.11, 95% CI: 0.85, 1.77), using some form of transportation (OR: 1.09, 95% CI: 0.93, 1.29), a concert venue (OR: 0.81, 95% CI: 0.57, 1.13), to an office or workplace (OR: 0.99, 95% CI: 0.85, 1.16), visiting another public venue (OR: 0.95, 95% CI: 0.80, 1.13) and not visiting any venues (OR: 1.31, 95% CI: 0.95, 1.83) were all insignificant. Because of the significance of several levels of this variable, it was retained for use in further models.

Whether participants' household members attended school in the fall of 2020 (School Exposure) was not significant in predicting SARS-CoV-2 antibodies. 16.1% of participants who lived alone had antibodies, 17.7% of participants who had no one in-person at school had antibodies, 13.5% of participants who had a child in PreK had antibodies, 16.7% of participants who had a child in K-12 had antibodies and 22.7% of participants who lived with someone in college had antibodies. Those who had no children attend in-person school (OR: 1.07, 95% CI: 0.85, 1.35), those with children in daycare or PreK (OR: 0.75, 95% CI: 0.28, 1.96), those with children in K-12 (OR: 0.96, 95% CI: 0.54, 1.74) and those with children or cohabitants in College (OR: 1.46, 95% CI: 0.79, 2.68) did not have a greater chance of having SARS-CoV-2 antibodies compared to participants who lived alone. Because of this, the School Exposure variable was not retained for further analysis.

Univariate analysis of the measures of COVID-19 vulnerability (CCVI Category) showed was significant in predicting SARS-CoV-2 antibodies. 16.2% of participants residing in "Low" CCVI zip codes had antibodies, compared to 19.0% of "Medium" zip code inhabitants and 21.7% of "High" zip code inhabitants. Those in "Low" CCVI zip codes had a significantly lower chance of having antibodies (OR: 0.68, 95% CI: 0.54, 0.86), while those in "Medium" CCVI zip codes did not have a significant difference in antibodies (OR: 0.85, 95% CI: 0.66, 1.08) compared to those living in "High" zip codes.

Multivariate Analysis

Following the identification of significant variables, a series of multivariate binomial mixed models were built in order to understand how the variance in SARS-CoV-2 antibodies changed with the addition of different individual and community-level variables. In total, there were eight models and a baseline model. The first seven models included individual-level variables from SCAN, and the eighth and final model included the community-level CCVI categories. The predictive power of these models were measured using conditional and marginal R^2 as well as the AIC values. Higher R^2 values and lower AIC values correspond to a better fit. The results of all stages of the multivariate regressions are shown in **Table 6**.

The base model (Base a) did not include any independent variables, only the random intercept term of Zip Code. The marginal R^2 value was 0.00, while the conditional R^2 value was 0.016, indicating that the total explanatory power of this model was incredibly weak, with nothing relating to the fixed effects variables, which is logical because there are no fixed effects variables in this baseline model.

The eighth model (8a) included the following variables: Race, Age, Crowding, Household Work, Insurance, Venues, Prevention Net and CCVI Category. Race was a significant variable, with non-Hispanic White individuals (OR: 0.76, 95% CI: 0.58, 0.99) having significantly lower rates of SARS-CoV-2 antibodies than non-Hispanic Asian participants. The other racial/ethnic categories were not significant predictors of antibody status (Black or African American OR: 1.28, 95% CI: 0.90, 1.82; Hispanic/Latinx OR: 1.22, 95% CI: 0.91, 1.63; non-Hispanic Other OR: 0.88, 95% CI: 0.41, 1.88; and Multiracial OR: 1.18, 95% CI: 0.87, 1.60). Those who were above the age of 60 (OR: 0.67, 95% CI: 0.47, 0.97) had significantly lower chances of having SARS-CoV-2 antibodies compared to the comparison groups of people aged 18-29. The other age categories were insignificant (Ages 30-39 OR: 0.96, 95% CI: 0.76, 1.21;

Ages 40-49 OR: 0.95, 95% CI: 0.73, 1.24; Ages 50-59 OR: 1.05, 95% CI: 0.78, 1.41). Those who lived in crowded households, sharing their common spaces with five or more people (OR: 2.74, 95% CI: 1.62, 4.63) had significantly higher chances of having antibodies than those who lived alone. Those who shared their home with one to two others (OR: 1.1, 95% CI: 0.91, 1.33) or three to four others (OR: 1.33, 95% CI: 0.72, 2.46) did not have a significantly lower chance of having SARS-CoV-2 antibodies compared to those who lived alone. The occupation of others in the household did not have a significant impact in this model. Compared to those who had no one in their household working in healthcare, those who had one or two in their household (OR: 1.15, 95% CI: 0.96, 1.37) and those who had three or more in their household (OR: 1.33, 95% CI: 0.72, 2.46) did not have a significantly different rate of antibodies. Those who had health insurance (OR: 0.83, 95% CI: 0.58, 1.19) did not have a significantly different chance of having SARS-CoV-2 antibodies. None of the possible venues visited during spring/summer of 2020 impacted participants chances of having antibodies (Doctor's office OR: 1, 95% CI: 0.82, 1.20; Emergency department OR: 1.28, 95% CI: 1, 1.64; School/university OR: 1.05, 95% CI: 0.85, 1.30; Assisted living/retirement community OR: 1.25, 95% CI: 0.83, 1.88; Transportation OR: 1.11, 95% CI: 0.91, 1.34; Concert venue OR: 0.77, 95% CI: 0.51, 1.16; Office/workplace OR: 1.02; 95% CI: 0.85, 1.22; Religious spaces OR: 1.23, 95% CI: 0.94, 1.62; other public venue OR: 0.93, 95% CI: 0.77, 1.13; No venues OR: 1.39, 95% CI: 0.97, 2.00). The net number of preventative behaviors taken was not significant (OR: 0.92, 95% CI: 0.85, 1.00), neither were the low or medium CCVI categories (Low OR: 0.80, 95% CI: 0.63, 1.01; Medium OR: 0.96, 95% CI: 0.76, 1.21) compared to high CCVI, both with p values just above the 0.05 cutoff for significance. The marginal R^2 value was 0.047, while the conditional R^2 value was 0.049. The R^2 decreased with each addition of variable to the model, showing that each variable helped to better predict the patterns of COVID-19 infection. Further, the AIC values can be tracked across each model, showing that they overall decreased moving from the baseline to the final Reg 8a, indicating a better fit with the addition of variables. The predictive power of these models remain very low, as indicated by R^2 values less than 0.20 throughout each iteration, indicating very weak fit of the models. With observations ranging from 2-352 per zip code, I initially hypothesized that this low predictive power was due to the variation from zip codes with a small number of observations. In order to further explore this, the SCAN dataset was filtered from the 57 zip codes down to only those zip codes with more than 50 observations (35 total zip codes). I ran the regressions with these zip codes as the random effects groupings, and this did not improve the predictive power or fit of the regression. Finally, the 57 zip codes were filtered down to only the 10 zip codes included in the original SCAN data collection, once again, the results did not improve.

Discussion

The overall aim of this thesis was to investigate the individual and community level factors related to SARS-CoV-2 infection to better understand the relationship between individual and "place" in an infectious diseases context. This was done by analyzing the survey responses from SCAN participants to understand individual circumstances and how they impacted the chance of having detectable SARS-CoV-2 antibodies. These SARS-CoV-2 antibodies were measured using a DBS kit mailed to participants, and were considered to be indicative of past infection. Next, a Community COVID-19 Vulnerability Index (CCVI) was built from ACS and Chicago Health Atlas data. This was used to score the estimated zip code level vulnerability to COVID-19. These individual and community factors were tested in mixed level models that took into account the zip code-level clustering in the sample. **Overall, I found that individual-level**

risk factors were significant predictors of SARS-CoV-2 antibodies. This thesis had the advantage of using individual-level data to supplement the previous findings based on COVID-19 testing and mortality data, this individual-level data provided up-to-date information about changing circumstances of the pandemic, relating to employment, crowding, prevention behaviors taken and other pertinent variables.

Seroprevalence

The SCAN dataset seroprevalence was 18.2%, indicating that almost one in five study participants had meaningful rates of SARS-CoV-2 antibodies. This indicates one of the strengths of this thesis, the use of the antibody surveillance method helped to capture a wider range of the population with COVID-19 than other measures such as test positivity or mortality rates. There are a number of reasons that this seroprevalence is drastically higher than the test positivity rate, city residents may not seek out a test because of concerns of availability, cost or transportation barriers to accessing testing, or due to asymptomatic presentation of COVID-19. These results show that a far greater proportion of City of Chicago residents were likely infected with SARS-CoV-2 than previously believed. This adds to a growing understanding among epidemiologists and public health experts that the true numbers of SARS-CoV-2 infections may be as much as ten times what is reported (Reese et al., Havers et al.).

Population Comparisons

The SCAN dataset was comprised of 42.6% non-Hispanic White, 17.2% Hispanic/Latinx, 15.3% non-Hispanic Asian, 14% Multiracial, 9.3% non-Hispanic African American, 1.1% non-Hispanic Other, 0.3% non-Hispanic Native Hawaiian/Pacific Islander and 0.1% non-Hispanic American Indian/Alaskan Native. The City of Chicago overall is 33.3% non-Hispanic White, 28.8% Hispanic/Latinx, 2.8% Multiracial, 6.6% Asian, 29.6% African American, 0.0% Native

Hawaiian/Pacific Islander and 0.3% American Indian/Alaskan Native ("US Census Bureau QuickFacts"). This shows that this sample overrepresents non-Hispanic White, Hispanic/Latinx, Multiracial and Asian populations while dramatically under-representing the African American population. The original SCAN data analysis did not include sample weights, so none were present here (Demonbreun et al.). Based on these percentages, these results may not be entirely generalizable to the larger population but they still provide important insights into the social mechanisms of SARS-CoV-2 infection.

Preventative Behaviors

Many participants did take preventative behaviors, following public health expert guidance in an effort to avoid contracting COVID-19. Unfortunately, these behaviors were not significant in changing the odds of SARS-CoV-2 infection. There were gendered differences in preventative behaviors, with women taking significantly more preventative behaviors on average than men in the sample (p-value = 1.28×10^{-6}). The SCAN survey also asked individuals to rate their concern about how COVID-19 would impact their health or their financial situation in the variables Worry Health and Worry Financial. Individuals who were more worried about the impacts of COVID-19 on their health (OR: 1.04, 95% CI: 1.02, 1.06) or their finances (OR: 1.22, 95% CI: 1.19, 1.25) took significantly more preventative behaviors than those who were less worried. Despite individual sentiments about COVID-19, these actions did little to impact their actual chances of disease.

Neither Interactions, which measured how much participants reduced their social interactions, nor Net Preventative Behaviors, which was the sum of COVID-19 avoidance behaviors taken, were significant in reducing the chances of having SARS-CoV-2 antibodies. This shows that individual conditions may prompt certain preventative actions, but these actions do not have significant influence on the actual outcome of contracting COVID-19. Interestingly, there was also a low Cronbach's alpha score between the individual preventative behaviors taken, meaning that there was low average correlation between COVID-19 avoidance behaviors in this sample.

In an approach that is contradictory to the very nature of an infectious disease, much of the American pandemic response has focused on the individuality of fighting COVID-19. From the beginning, the response to the pandemic was focused on smaller entities. States were forced to find ventilators, lacking a cohesive movement from the federal government. Healthcare workers were forced to crowdsource necessary personal protective equipment on their own. It was the general public's own responsibility to stay at home, regardless of individual economic circumstances. This approach of American individuality was echoed even from the most powerful public health experts. Following the relaxation of the CDC's guidance on masking for vaccinated people, CDC director Dr. Rochelle Walensky tweeted "Your health is in your hands" (Walensky). President Biden has also emphasized the importance of getting vaccinated, ultimately ending with the messaging "The choice is yours" ("Remarks by President Biden"). These results highlight the dissonance in an individual approach to fighting a global pandemic. Despite individual concern and actions, people must rely on those around them to behave in a similar manner in order to reduce the chances of spreading SARS-CoV-2. The burden of individual responsibility also unfairly impacts those who *cannot* take necessary steps and places blame rather than offering supplemental support. As the preventative behaviors shift from social distancing to vaccination, the same group of individuals are left behind. As put by Ed Yong, "Predictably, the new pockets of … vulnerability map onto old pockets of *social* vulnerability".

The attendance of participants in certain venues was also a significant predictor of SARS-CoV-2 infection. The venues of concern included the hospital emergency rooms and religious spaces, which both had significant odds ratios. Emergency room attendance may have been a risk factor for COVID-19 due to increased chances of exposure. Throughout the pandemic, many hospitals have been at full capacity due to an influx of critically ill COVID-19 patients. This has resulted in widespread impacts in the healthcare system, including delaying or slowing down necessary non-COVID-19 procedures. News reports have shown that with the most recent COVIID-19 Omicron variant, emergency room wait times have increased, possibly increasing an exposure window for those in attendance (Eldridge). Religious spaces have also been identified as risk factors for COVID-19 in the literature, due to the extended close proximity of participants and the potential increased viral transmission related to singing or speaking (Quadri). Two variables showed that school attendance does not seem to be a significant predictor of SARS-CoV-2 antibodies (Venues and School Exposure). This has been a topic of heated debate since the early days of the pandemic, with school closures often being one of the public health measures used in areas of high SARS-CoV-2 transmission. Although children typically have milder COVID-19 cases, they are still susceptible to infection and schools have been identified as areas of outbreaks (CDC).

CCVI Results

The results of the CCVI Cronbach's Alpha testing show that overall, the variables have strong correlation. This supports the construction of the index and indicates that the variables are all measuring the same underlying construct, which is interpreted here community vulnerability. There was slightly more variability in correlation coefficients within the individual HDCI, an index with the CCVI. The HDCI had some strong, moderate and weak positive relationships, but also some negative correlations. Surprisingly, one of the negative correlations occurred between percentage of residents in Group Quarters and percentage of Crowding. Group Quarters are defined by the US Census as “all people not living in housing units”, which can be categorized into institutional and non-institutional quarters (“Group Quarters”). The nature of these living situations is that multiple individuals may live in a single room or cell (in the case of correctional facilities). This indicates that there may be imperfections in the measurement of Community Crowding, which was found by dividing the number of housing units by the population of the zip code. Issues may have arisen because those in group quarters are not counted in the “housing units”.

Spatial Clustering

This thesis also highlights the importance of place in the context of health, especially in a respiratory pandemic like COVID-19. COVID-19 positivity rates varied widely throughout the city, mirroring the established patterns of vulnerability and racial segregation documented in other Chicago-based studies (Kim and Bostwick). Further, the Global Moran’s and G_i of COVID-19 Case Rates per zip code of the SCAN data show that these cases have significant spatial clustering across the city. The significance of the Global Moran’s statistic for both CCVI Rank and CCVI Category indicates the index does have spatial clustering on the zip code level. The spatial clustering of the Comorb Rate variable also shows some patterning across the city, which indicates differing health status based on location. This is once again supports Kim and Bostwick’s work that found a spatial clustering of both social vulnerability and health risk factors.

Univariate Regressions

Sociodemographic variables such as Age and Race/Ethnicity were found to be significant predictors of past or current SARS-CoV-2 infection (through investigation into SARS-CoV-2 antibodies), which is line with the existing literature that identifies Age as a risk factor and finds Race/Ethnicity to be related to several upstream factors that increase the likelihood of SARS-CoV-2 infection and COVID-19 mortality ("Community Work and School"). Only one participant in this study lived in an assisted living facility, which was identified earlier as a potential mechanism of increased SARS-CoV-2 transmission among older adults. This low rate of assisted living inhabitants may show how older adults living independently are able to take further precautions to significantly reduce their chance of SARS-CoV-2 infection. Further, Gender was not found to be a significant predictor of SARS-CoV-2 infection, which is a concept still being debated in the literature (Jin et al., Yuan et al.).

The amount of people living in a household was found to be significant, but the type of residence was not. While the actual physical structure may have no direct impact on SARS-CoV-2 infection, the *number* of people living the household increases contact, potential exposure, and makes it more difficult to safely quarantine if a house member is exposed or contracts SARS-CoV-2. This echoes the call of researchers to focus more on specific measures rather than the overall density variable due to the better specificity of the variable in explaining COVID-19 risk factors (Hsu). Another analysis of SARS-CoV-2 rates at the zip code-level showed that in both Chicago and New York city, household size was more influential than population density in predicting exposure rates (Maroko et al.).

There were mixed results relating to participant occupation and SARS-CoV-2 antibodies. Participants' occupations (Working Conditions) were not found to be significant, but exposure to members of the household working in healthcare (Household Work) was significant. This was contrary to previous studies that have shown that working in-person has increased SARS-CoV-2 infection rates (van Holm et al.). However, the Household Work variable offers a unique lens into the widespread impacts of essential work outside of the household. Although one's own occupation was not an important predictor, the occupations of those around them may have meant an indirect avenue for increased SARS-CoV-2 exposure. This further highlights the importance of the housing context on COVID-19 risks.

The presence of participant comorbidities were not significant in predicting SARS-CoV-2 infection. While comorbidities have been extensively studied for their poor outcomes relating to COVID-19 morbidity and mortality, they may also impact initial infection through their increased expression of ACE2 receptors or impairment of immune system function (Ejaz et al.).

Having health insurance was a significant predictor of lower rates of SARS-CoV-2 antibodies. Those who were uninsured were more likely to have SARS-CoV-2 antibodies. This result may be due to other surrounding socioeconomic conditions that are highly correlated with insurance rates. The Cronbach's alpha test on the SESI demonstrated that there was strong inter-variable correlation between insurance rates, poverty rates, average income and unemployment rates. These conditions may make it more difficult for individuals to work remotely or adhere to other disease prevention behaviors such as social distancing.

Multivariate Analysis

The multivariate model offered further investigation into the above variables. The fully constructed model showed that those who were older (Age 60+) and participants who identified as non-Hispanic white had lower chances of antibodies, while living in a household with more than five others (Crowding 5+) was positively associated with SARS-CoV-2 antibodies. The multivariate regression showed results consistent with other COVID-19 studies focused in

Chicago, as both Race and Community Vulnerability were significant predictors of having SARS-CoV-2 antibodies.

This emphasizes the importance of community-level interventions that provide solutions to upstream determinants of health such as improving socioeconomic conditions of a neighborhood, improving access to resources and healthcare and community-based social relationship building to improve collective efficacy.

COVID-19 Morbidity and Mortality

Due to the nature of the seroprevalence surveillance data collected in SCAN, only observations about the prevalence of SARS-CoV-2 infection were made. However, with an estimated case fatality rate of 6% as of May 20, 2020, COVID-19 mortality remains a major area of focus and of concern (“Cumulative Case Fatality Rate”). Based on the City of Chicago COVID-19 mortality data through the end of 2020, spatial autocorrelation was carried out to determine any clustering of mortality in order to compare to the infection data (“Latest Data”). Based on the mapping of G_i* values, hot spots were found across the South side of the city (**Figure 10**). From my analysis of SARS-CoV-2 antibody hot spots, both the Southwest and Southeast sides of the city were also identified as areas with high infection rates. I also determined that downtown Chicago represented a low clustering of COVID-19 mortality, which lined up with my analysis of SARS-CoV-2 antibodies. As established earlier, there can be slightly different factors impacting SARS-CoV-2 infection and COVID-19 mortality, however it does seem logical that areas with the highest SARS-CoV-2 antibodies would also have higher mortality.

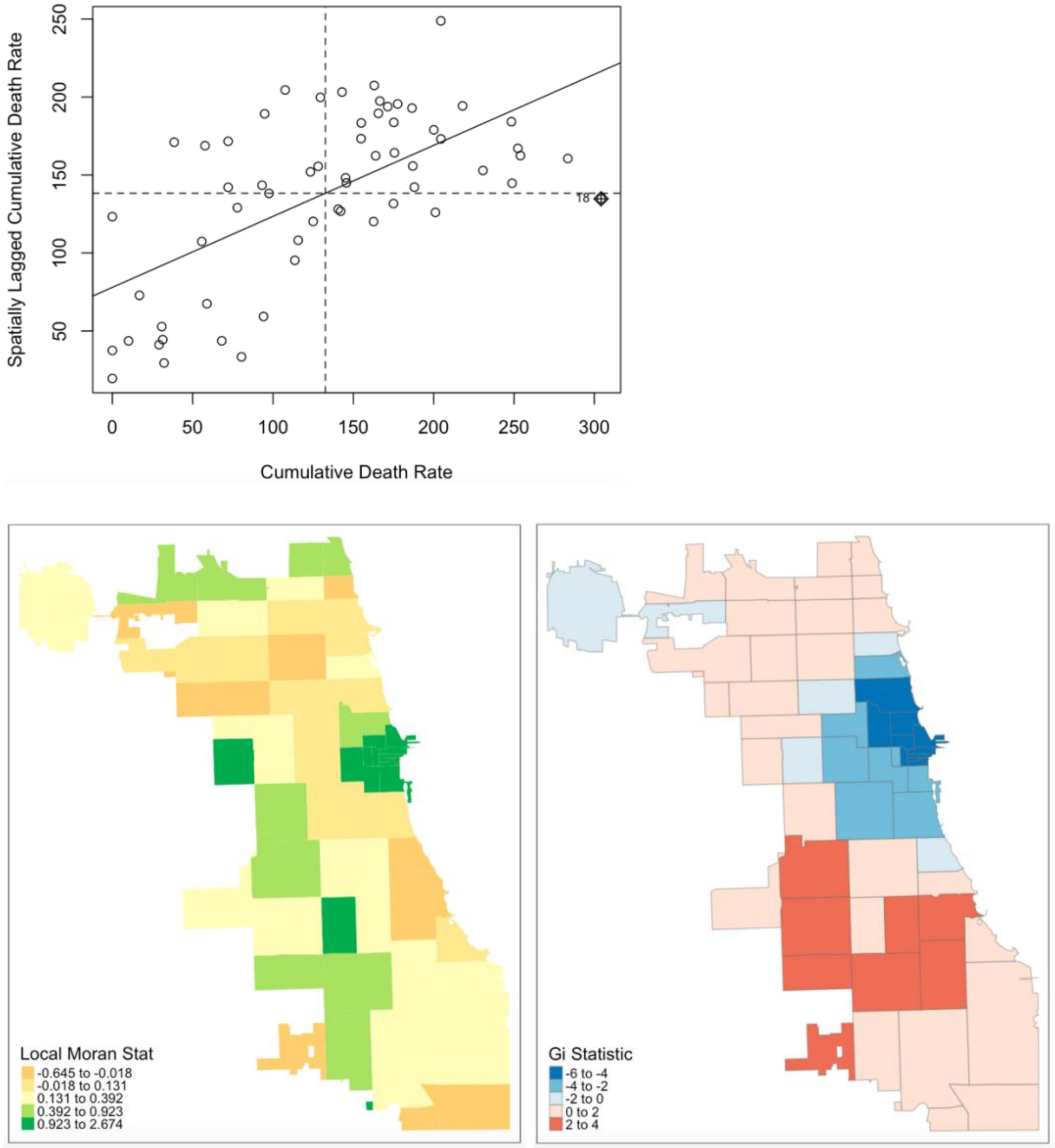


Figure 11: Spatial Clustering of City of Chicago Mortality Data. *The Global Moran's I plot shows the cumulative COVID-19 mortality rate plotted against the spatially lagged mortality rate (average of neighboring zip codes), the slope of this OLS-fitted line is 0.46, indicating that there is moderate yet significant spatial clustering of these values. The map on the left shows the areas of Chicago that contributed significantly to overall spatial autocorrelation in the sample. Green areas indicate areas of data clustering, these values are further expanded upon in the map on the right. This* G_i *statistic plot shows the clustered hot spots and cold spots across the entire city of Chicago.*

Limitations

While this thesis offers an exciting new perspective through individual-level observations based on SARS-CoV-2 antibodies, there are several limitations. One of the primary limitations is a common challenge with neighborhood effects studies, the Modifiable Areal Unit Problem (MAUP). Since this study relies on zip code level data, any geographic analysis is limited to the arbitrary boundaries, rather than actual natural groupings of people (Arcaya et al.). Data at the community area or census tract level would provide higher definition and present smaller, and potentially more accurate groupings of people. The selection of variables for the univariate regressions was done largely based on pre-established trends from the literature, but there is a chance of subjectivity when they are picked out manually.

The large amount of missing data from a key variable, Crowding, presents a major limitation to this experiment. As shown earlier, the study population that answered this question was statistically significantly different from the population who left the question blank. Further, the low predictive power of the models means that future relationships between variables cannot be elucidated with more certainty.

The limited time frame of this study also constrains these results to the initial wave of COVID-19. Due to the number of increasingly infectious strains such as Delta and Omicron, the dynamics of SARS-CoV-2 transmission may be different, potentially influencing some of the factors that were considered significant in this thesis. Finally, the CCVI was constructed based on variables considered representative of vulnerability. However, for variables such as those contained in the Socioeconomic Status Index, there is debate over the accuracy with which they actually predict socioeconomic conditions (Braveman et al.). With more time, validation could be performed by applying City of Chicago COVID-19 testing data to the CCVI to see how well the index actually predicts the burden of disease.

Future Directions

In the future, symptoms and the influence of diagnosis within the surveyed household may be interesting to investigate. Additionally, the potential interactions between individual- and community-level variables could be investigated further by running separate models based on the CCVI categories to see if there are differences in interactions between high, medium and low vulnerability zip codes. Finally, future iterations of data collection on these participants could provide useful temporal perspective on the continuously changing landscape of COVID-19, with variants and changing general attitudes towards masking.

Conclusion

Overall, this thesis shows that elements of individual behaviors and of community conditions are influential in the chances of contracting SARS-CoV-2. The spread of COVID-19 through much of the country, but in this case Chicago, has not been equal in terms of geography, sociodemographic or economic status. This thesis shows that there is clustering of SARS-CoV-2 infection rates across Chicago that closely mirrors the spatial clustering of COVID-19 vulnerability. The public health response to COVID-19 has already been hampered by such variabilities across space, and this goes to show that both individual and community interventions are important for effectively fighting the spread of SARS-CoV-2. By harnessing insights on factors such as behavioral changes, housing density and occupational conditions, structural improvements can be made so that humans can continue to exist in conjunction with their surroundings.

The pandemic has changed the nature of the social interactions and dynamics central to our existence, resulting in widespread impacts beyond that of a viral infection. Anthropology has always helped to explain the existence of human connection and meaning making, and this pandemic provided a natural experiment in which to investigate the impacts of a sudden shock to global systems. This thesis attempted to further investigate the interplay of individual and “place”, both socially and physically.

As variants progress, the severity of COVID-19 has decreased and the possibility of a shift from pandemic to endemic is becoming a reality. It remains critical to address the structural elements in our society that have been the source of pandemic inequalities–elements such as job, housing and social equity–along with health concerns such as the comorbidities that lead to poorer COVID-19 outcomes among some populations. As society makes this transition from pandemic to endemic, the steps taken towards equality will have lasting impacts and will shape the narrative of future disease outbreaks.

Tables

Table 1: SCAN Descriptives

Table 1 SCAN Descriptives n = 4,717	n	%
Total	4717	100
Gender		
Man	1,816	44.3
Woman	2,264	55.2
Gender Non-Conforming	18	0.4
Age		
Average	40.3	IQR: 18.2
18-29	1,082	23
30-39	1,599	34
40-49	938	20
50-59	586	12.4
60+	502	10.6
Race/Ethnicity		
Hispanic/Latinx	794	16.8
Multiracial	624	13.2
NH Asian	729	15.5
NH Black/African American	416	8.8
NH White	2,086	44.2
NH Other TOTAL	68	1.4
NH Other	50	1.1
NH Native Hawaiian/Pacific Islander	14	0.3
NH American Indian/Alaska Native	4	0.1
Living Status		
House/townhouse	1,800	38.2
Shelter	1	0.02
Apartment/Condo	2,905	61.6
Dormitory	4	0.08
Assisted Living Facility	1	0.02
Skilled Nursing Facility	0	0
No Consistent Primary Address	0	0
Other	4	0.08
Comorbidities		
At least 1	1,318	28.5
No comorbidities	3,314	71.5
Chronic lung disease	335	7.2
Diabetes mellitus	153	3.3
Cardiovascular disease	84	1.8
Chronic renal disease	15	0.3
Chronic liver disease	12	0.3
HIV/AIDS	33	0.8
Other Immunocompromised condition	61	1.3
Neurologic/neurodevelopmental	42	0.9
Pregnant	35	0.8
Other chronic	669	14.4
High blood pressure	260	5.6

Table 2: SCAN Seroprevalence

Table 2 SCAN Seroprevalence n = 4,717	Seropositive		Seronegative		Total	
	n	%	n	%	n	%
Total	859	18.2	3,858	81.8	4,717	100
Gender						
Man	337	18.6	1,479	81.4	1,816	100
Woman	388	17.1	1,876	82.9	2,264	100
Gender Non-Conforming	1	5.6	17	94.4	18	100
Age						
18-29	213	19.7	869	80.3	1,082	100
30-39	288	18	1,311	82	1,599	100
40-49	177	18.9	761	81.1	938	100
50-59	115	19.6	471	80.4	586	100
60+	66	13.1	436	86.9	502	100
Race/Ethnicity						
Hispanic/Latinx	182	22.9	612	77.1	794	100
Multiracial	140	22.4	484	77.6	624	100
NH Asian	139	19.1	590	80.9	729	100
NH Black/African American	94	22.6	322	77.4	416	100
NH White	292	14	1,794	86	2,086	100
NH Other	12	17.6	56	82.4	68	100
CCVI Category						
Low	368	16.2	1,901	83.8	2,269	100
Medium	279	19	1,191	81	1470	100
High	212	21.7	766	78.3	978	100

Table 3: SCAN Working Conditions Descriptives

Table 3 SCAN Working Conditions Descriptives		
n = 4,717	n	%
Work Now		
Employed	3,726	79
Unemployed	991	21
Work Flex		
Paid Sick Days	2,815	75.7
Unpaid Sick Days	640	17.2
No Sick Days	180	4.8
Different Conditions for Multiple Jobs	83	2.2
Work Remote		
Completely Remote	1,992	53.6
Partially Remote	827	22.2
None Remote	898	24.2
Work Close		
Close Proximity to Others	1,273	73.7
Not Close Proximity	454	26.3
Work Type		
Healthcare or public health operations	463	26.9
Essential retail services	105	6.1
Restaurant service	87	5
Food and beverage production	45	2.6
Trade services	38	2.2
Construction	52	3
Charitable and social services	72	4.2
Media	32	1.9
First responder/emergency	93	5.4
Public services	109	6.3
Transportation services	38	2.2
Mail and delivery services	22	1.3
Other	711	41.2
Work Conditions		
Unemployed	1,145	20.7
Work from home	2,316	41.8
Healthcare	545	9.8
Other work types	1,537	27.7
Transportation Behavior		
Public transportation	192	11.1
Personal motorized vehicle	1,230	71.3
Rideshare	42	2.4
Walk or bicycle	244	14.2
Other	16	0.9
Household Work		
None	2,507	64.8
1-2 in household	1,301	33.7
3+ in household	58	1.5

Table 4: SCAN Preventative Behavior Descriptives

Table 4 SCAN Preventative Behavior Descriptives		
n = 4,717	n	%
Interactions		
Not at all	29	0.6
A little bit	135	2.9
Somewhat	479	10.2
Quite a bit	2,164	45.9
Extremely	1,910	40.5
Prevention Behaviors		
Increased handwashing	4,611	97.8
Increased social distancing	4,609	97.7
Self-isolation	1,559	33.1
Masking	4,661	98.8
Avoid public transportation	3,835	81.3
Avoid traveling	3,422	72.6
Other	202	4.3
None	3	0.1
Net Preventative Behaviors		
Average	4.86	1.02 (SD)
Venues		
Doctor’s room/clinic	2,981	63.3
Emergency department	521	11.1
School/university	991	21
Assisted living home/retirement community	180	3.8
Transport	1,826	38.8
Concert venue	274	5.8
Office/workplace	2,438	51.8
Religious space	441	9.4
Other public venue	1,412	30
None	321	6.8
School Exposure		
Alone	1,112	45.7
No in-person school	1,138	46.4
PreK/Daycare	37	1.5
K-12	90	3.7
College/University	66	2.7

Table 5: Univariate Logistic Regression Results

Table 5 Univariate Logistic Regression Results

Variable	Prevalence n (%)	OR	95% CI	p-value	Marginal R2 / Conditional R2
Age					0.006 / 0.021
18-29	213 (19.7%)	--	--	--	
30-39	288 (18.0%)	0.9	0.73, 1.09	0.28	
40-49	177 (18.9%)	0.92	0.74, 1.16	0.49	
50-59	115 (19.6%)	0.97	0.75, 1.26	0.84	
60+	66 (13.1%)	0.6	0.45, 0.82	0.001**	
Gender					0.003 / 0.020
Man	337 (18.6%)	--	--	--	
Woman	388 (17.1%)	0.9	0.20, 0.27	0.19	
Race/Ethnicity					0.021 / 0.032
Non-Hispanic Asian	139 (19.1%)	--	--	--	
Hispanic/Latinx	182 (22.9%)	1.23	0.96, 1.59	0.11	
Non-Hispanic White	292 (14.0%)	0.68	0.54, 0.85	0.001**	
Multiracial	140 (22.4%)	1.21	0.92, 1.58	0.17	
Non-Hispanic Black/African American	94 (22.6%)	1.19	0.88, 1.62	0.26	
Non-Hispanic Other	12 (17.6%)	0.92	0.48, 1.76	0.8	
Living Status					0.000 / 0.006
House/townhouse	350 (19.4%)	--	--	--	
Apartment/condo	507 (17.5%)	0.93	0.79, 1.11	0.43	
Other	2 (20%)	1.11	0.23, 5.30	0.89	
Crowding					0.012 / 0.019
Alone	278 (15.7%)	--	--	--	
1-2 others	301 (19.1%)	1.25	1.04, 1.50	0.02*	
3-4 others	94 (20.5%)	1.35	1.04, 1.76	0.03*	
5+ others	29 (41.4%)	3.7	2.23, 6.09	2.84E-7***	
Work Conditions					0.003 / 0.017
Unemployed	182 (18.4%)	--	--	--	
Work from home	334 (16.8%)	0.9	0.74, 1.10	0.32	
Healthcare	101 (21.8%)	1.24	0.95, 1.64	0.12	
Other work types	242 (19.2%)	1.04	0.84, 1.29	0.71	
Household Work					0.005 / 0.016
None	419 (16.7%)	--	--	--	
1-2 in household	264 (20.3%)	1.25	1.05, 1.48	0.01*	
3+ in household	18 (31.0%)	2.12	1.20, 3.78	0.01*	
Comorbidities					0.001 / 0.014
No comorbidities	612 (18.5%)	--	--	--	
At least 1	225 (17.1%)	0.9	0.76, 1.07	0.25	
Insurance					0.002 / 0.017
Uninsured	60 (23.8%)	--	--	--	
Insured	799 (17.9%)	0.71	0.52, 0.95	0.02*	
Interactions					0.001 / 0.016
Continuous 1-5		0.95	0.87, 1.05	0.32	
Not at all	4 (13.8%)	--	--	--	
A little bit	31 (23.0%)	1.81	0.58, 5.60	0.3	
Somewhat	91 (19.0%)	1.43	0.49, 4.23	0.52	
Quite a bit	397 (18.3%)	1.39	0.48, 4.03	0.54	
Extremely	336 (17.6%)	1.33	0.46, 3.86	0.6	
Net Preventative Behaviors					0.002 / 0.018
Continuous 1-7		0.92	0.86, 0.99	0.03*	
Prevention Behaviors					0.032 / 0.045
Increased hand-washing	834 (18.1%)	0.83	0.51, 1.36	0.47	
Social distancing	830 (18.0%)	0.72	0.45, 1.17	0.19	
Self-isolation	296 (19.0%)	1.11	0.95, 1.31	0.18	
Masking	843 (18.1%)	0.66	0.35, 1.25	0.2	
Avoid public transportation	681 (17.8%)	0.97	0.79, 1.19	0.75	
Avoid traveling	595 (17.4%)	0.85	0.71, 1.01	0.07	
Other	29 (14.4%)	0.76	0.51, 1.14	0.19	
Venues					0.008 / 0.022
Doctor’s room/clinic	529 (17.7%)	0.93	0.80, 1.10	0.42	
Emergency department	115 (22.1%)	1.31	1.07, 1.67	0.01*	
School/university	198 (20.0%)	1.1	0.98, 1.39	0.12	
Assisted living home/retirement community	40 (22.2%)	1.11	0.85, 1.77	0.27	
Transport	336 (18.4%)	1.09	0.93, 1.29	0.3	
Concert venue	42 (15.3%)	0.81	0.57, 1.29	0.22	
Office/workplace	439 (18.0%)	0.99	0.85, 1.16	0.89	
Religious space	98 (22.2%)	1.31	1.03, 1.68	0.03*	
Other public venue	248 (17.6%)	0.95	0.80, 1.13	0.55	
None	68 (21.2%)	1.31	0.95, 1.83	0.1	
School Exposure					0.002 / 0.024
Alone	181 (16.1%)	--	--	--	
No in-person school	201 (17.7%)	1.07	0.85, 1.35	0.55	
PreK/Daycare	5 (13.5%)	0.75	0.28, 1.96	0.55	
K-12	15 (16.7%)	0.96	0.54, 1.74	0.91	
College/University	15 (22.7%)	1.46	0.79, 2.68	0.22	
CCVI Category					0.007 / 0.015
High	212 (21.7%)	--	--	--	
Medium	279 (19.0%)	0.85	0.66, 1.08	0.19	
Low	368 (16.2%)	0.68	0.54, 0.86	0.001**	

Table 6: Multivariate Logistic Regression Results

Table 6: Multivariate Regression

	Base Model a			Reg 1a			Reg 2a			Reg 3a			Reg 4a			Reg 5a			Reg 6a			Reg 7a			Reg 8a		
Predictors	*Odds Ratios*	*CI*	*p*	*Odds Ratios*	*CI*	*p*	*Odds Ratios*	*CI*	*p*	*Odds Ratios*	*CI*	*p*	*Odds Ratios*	*CI*	*p*	*Odds Ratios*	*CI*	*p*	*Odds Ratios*	*CI*	*p*	*Odds Ratios*	*CI*	*p*	*Odds Ratios*	*CI*	*p*
Intercept	0.23	0.20 – 0.25	**<0.001**	0.24	0.20 – 0.30	**<0.001**	0.25	0.20 – 0.32	**<0.001**	0.2	0.15 – 0.27	**<0.001**	0.19	0.14 – 0.25	**<0.001**	0.24	0.15 – 0.37	**<0.001**	0.22	0.13 – 0.34	**<0.001**	0.32	0.17 – 0.61	**<0.001**	0.37	0.19 – 0.71	**0.003**
Race																											
NH Asian																											
NH Black or African American				1.19	0.88 – 1.61	0.26	1.23	0.91 – 1.68	0.184	1.43	1.01 – 2.02	**0.045**	1.41	1.00 – 2.00	0.05	1.41	0.99 – 1.99	0.054	1.38	0.98 – 1.96	0.069	1.36	0.96 – 1.92	0.086	1.28	0.90 – 1.82	0.176
NH White				0.68	0.54 – 0.85	**0.001**	0.7	0.55 – 0.88	**0.002**	0.79	0.61 – 1.02	0.07	0.79	0.61 – 1.02	0.069	0.79	0.61 – 1.02	0.071	0.78	0.60 – 1.02	0.067	0.77	0.59 – 1.00	0.051	0.76	0.58 – 0.99	**0.038**
Hispanic/Latinx				1.23	0.96 – 1.59	0.106	1.25	0.97 – 1.61	0.084	1.33	1.00 – 1.77	**0.048**	1.31	0.99 – 1.75	0.059	1.3	0.98 – 1.73	0.069	1.29	0.97 – 1.71	0.083	1.26	0.95 – 1.69	0.109	1.22	0.91 – 1.63	0.179
NH Other				0.92	0.48 – 1.76	0.798	0.93	0.48 – 1.78	0.821	0.97	0.46 – 2.06	0.939	0.97	0.46 – 2.06	0.947	0.97	0.46 – 2.06	0.945	0.93	0.44 – 1.97	0.84	0.89	0.42 – 1.90	0.762	0.88	0.41 – 1.88	0.743
Multiracial				1.21	0.92 – 1.58	0.166	1.21	0.93 – 1.58	0.163	1.3	0.96 – 1.75	0.089	1.28	0.95 – 1.73	0.106	1.26	0.93 – 1.70	0.134	1.23	0.91 – 1.67	0.179	1.22	0.90 – 1.66	0.197	1.18	0.87 – 1.60	0.299
Age																											
18-29																											
30-39							0.94	0.77 – 1.14	0.516	0.95	0.76 – 1.18	0.623	0.95	0.76 – 1.19	0.673	0.96	0.77 – 1.20	0.724	0.97	0.77 – 1.22	0.78	0.96	0.77 – 1.21	0.751	0.96	0.76 – 1.21	0.74
40-49							0.96	0.77 – 1.21	0.741	0.92	0.72 – 1.19	0.548	0.94	0.73 – 1.22	0.645	0.95	0.74 – 1.23	0.706	0.96	0.74 – 1.25	0.785	0.95	0.73 – 1.24	0.725	0.95	0.73 – 1.24	0.708
50-59							1.05	0.81 – 1.36	0.735	1.05	0.78 – 1.40	0.756	1.05	0.78 – 1.40	0.751	1.06	0.79 – 1.41	0.703	1.06	0.79 – 1.43	0.685	1.06	0.79 – 1.42	0.7	1.05	0.78 – 1.41	0.742
60+							0.67	0.49 – 0.91	**0.011**	0.68	0.48 – 0.97	**0.031**	0.69	0.48 – 0.97	**0.036**	0.7	0.49 – 0.99	**0.045**	0.7	0.49 – 1.01	0.056	0.69	0.48 – 0.99	**0.044**	0.67	0.47 – 0.97	**0.035**
Crowding																											
Alone																											
1-2 Others										1.19	0.99 – 1.43	0.07	1.17	0.97 – 1.41	0.099	1.16	0.96 – 1.40	0.114	1.13	0.94 – 1.37	0.202	1.13	0.93 – 1.36	0.227	1.1	0.91 – 1.33	0.325
4-5 Others										1.23	0.94 – 1.62	0.136	1.17	0.88 – 1.55	0.272	1.16	0.88 – 1.54	0.294	1.13	0.85 – 1.51	0.392	1.12	0.84 – 1.49	0.439	1.09	0.82 – 1.44	0.574
6+ Others										3.35	2.02 – 5.55	**<0.001**	3.14	1.88 – 5.23	**<0.001**	3.1	1.86 – 5.18	**<0.001**	2.88	1.71 – 4.85	**<0.001**	2.87	1.70 – 4.85	**<0.001**	2.74	1.62 – 4.63	**<0.001**
Household Work																											
None																											
1-2 in Household													1.17	0.98 – 1.40	0.078	1.16	0.98 – 1.39	0.091	1.16	0.97 – 1.39	0.101	1.16	0.97 – 1.38	0.107	1.15	0.96 – 1.37	0.135
3+ in Household													1.47	0.80 – 2.69	0.21	1.46	0.80 – 2.68	0.217	1.42	0.77 – 2.61	0.257	1.39	0.75 – 2.56	0.291	1.33	0.72 – 2.46	0.358
Insurance																											
Insurance																0.8	0.56 – 1.13	0.206	0.8	0.57 – 1.15	0.228	0.82	0.58 – 1.18	0.287	0.83	0.58 – 1.19	0.313
Venues																											
Doctor's Office																			0.99	0.81 – 1.19	0.88	0.99	0.82 – 1.20	0.903	1	0.82 – 1.20	0.963
Emergency Department																			1.28	1.00 – 1.64	0.053	1.28	1.00 – 1.65	0.051	1.28	1.00 – 1.64	0.054
School/university																			1.07	0.87 – 1.31	0.533	1.07	0.87 – 1.31	0.541	1.05	0.85 – 1.30	0.63
Assisted living/retirement community																			1.27	0.85 – 1.90	0.251	1.26	0.84 – 1.89	0.271	1.25	0.83 – 1.88	0.282
Transport																			1.12	0.92 – 1.35	0.255	1.08	0.89 – 1.31	0.424	1.11	0.91 – 1.34	0.306
Concert venue																			0.76	0.50 – 1.15	0.197	0.76	0.50 – 1.15	0.201	0.77	0.51 – 1.16	0.215
Office/workplace																			1.03	0.86 – 1.23	0.773	1.02	0.85 – 1.22	0.812	1.02	0.85 – 1.22	0.831
Religious Spaces																			1.28	0.98 – 1.68	0.075	1.24	0.95 – 1.63	0.12	1.23	0.94 – 1.62	0.134
Other public venue																			0.93	0.77 – 1.13	0.461	0.93	0.77 – 1.13	0.46	0.93	0.77 – 1.13	0.477
No Venues																			1.36	0.94 – 1.95	0.1	1.37	0.95 – 1.97	0.093	1.39	0.97 – 2.00	0.076
Prevention Net																											
Prevention Net																						0.92	0.85 – 1.01	0.066	0.92	0.85 – 1.00	0.065
CCVI Category																											
High CCVI																											
Low CCVI																									0.8	0.63 – 1.01	0.066
Medium CCVI																									0.96	0.76 – 1.21	0.708

Random Effects									
σ^2	3.29	3.29	3.29	3.29	3.29	3.29	3.29	3.29	3.29
τ_{00} zipcode_repeat1	0.05	0.04	0.04	0.02	0.01	0.01	0.01	0.01	0.01
ICC	0.02	0.01	0.01	0.01	0	0	0	0	0
N zipcode_repeat1	57	57	57	57	57	57	57	57	57
Observations	4717	4717	4707	3863	3859	3856	3851	3850	3850
Marginal R^2 / Conditional R^2	0.000 / 0.016	0.021 / 0.032	0.026 / 0.037	0.034 / 0.039	0.036 / 0.040	0.036 / 0.040	0.043 / 0.047	0.045 / 0.048	0.047 / 0.049
AIC	4474.841	4437.026	4432.182	3617.998	3612.992	3612.693	3614.133	3609.704	3609.623
AICc	4474.844	4437.05	4432.238	3618.107	3613.133	3612.852	3614.529	3610.129	3610.11

Supplementary Figure

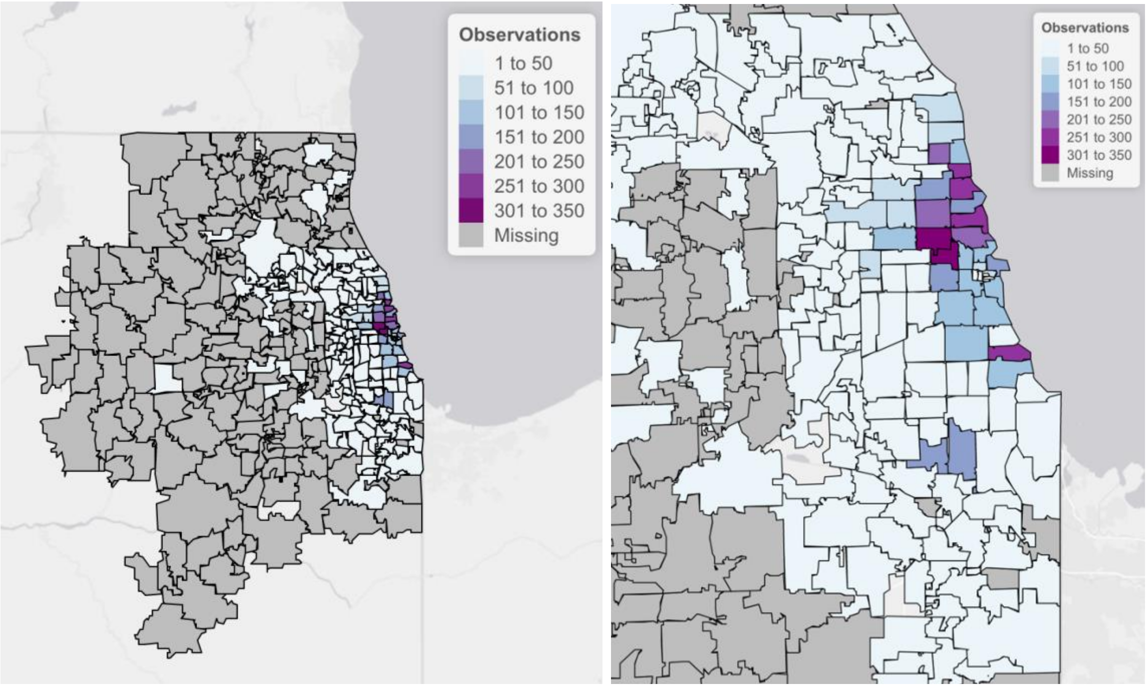


Figure 12: Distribution of SCAN participant zip codes across Northeastern Illinois. *This map provides zoomed-out views of the range of participant zip codes in SCAN. Any zip codes outside of Chicago's 57 were not included for analysis.*

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