A Replication of DiMaggio et al. (2020) in Phoenix, AZ

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Original submission: Dec 15, 2021
Peer-review received: Apr 23, 2022
Revision submitted: May 18, 2022
Accepted for publication: May 23, 2022

Abstract. This research replicates in Phoenix, Arizona a study originally conducted by DiMaggio et al. (2020) that investigated the associations between positive COVID-19 tests and demographic, socioeconomic, and racial characteristics in New York City at the ZIP Code Tabulation Area level. We extend that work through a conceptual replication that introduces covariates appropriate to Phoenix, AZ. Our direct replication, which focuses on that city's first wave of COVID-19 (May 31, 2020 to August 1, 2020), demonstrates that the framework used by DiMaggio et al. can be transferred across cities, but also identifies specification decisions that need careful consideration. Our conceptual replication identifies the proportion of Hispanic residents, rather than that of Black/African American residents, to be a key predictor of positive COVID-19 testing. This finding sheds light on the dynamics of race during the pandemic.

1 Introduction

Facing the novel threat of COVID-19, scientists have produced a deluge of research that medical professionals, government officials, and policymakers have continually used to revise their response to the pandemic. To make informed decisions, those responsible for pandemic response must know more than the results of recent COVID-19 research; they must also know how reliable those results are, and whether the results obtained at one location and time are likely to hold in a different location and at a different time. One way to establish the generalizability of research findings is by conducting independent replications of prior work. However, the need to rapidly respond to COVID-19 runs counter to the cautious and often time-consuming re-evaluation of the emerging body of evidence about this disease via replication. Failing to thoroughly evaluate COVID-19 research, which was produced and published on an accelerated time frame, has the potential to both short-circuit the accumulation of scientific evidence and impair decision-making, possibly on a global scale. Without assessing the reliability of COVID-19 research, we also risk fueling public skepticism of this work and the policies it supports.

We begin to address this gap in the literature by replicating the work of DiMaggio et al. (1) in Phoenix, Arizona. By replicating DiMaggio et al., we establish whether the same socioeconomic factors are associated with positive COVID-19 tests in New York as in Phoenix. We also assess whether areas of elevated COVID-19 risk existed in Phoenix during the pandemic's first wave. More broadly, our replication allows us to check the specification of the original analyses and, by documenting and openly sharing our approach and procedures, provide a model that others can follow when replicating geographic analyses of COVID-19.

We selected DiMaggio et al. as the basis of our replication for four reasons. First, the study addresses key research questions at the center of many geographic studies of COVID-19: (a) Do areas of unusually elevated COVID-19 incidence exist? (b) Where are those areas located? and (c) What are the ecological risk factors associated with elevated incidence of COVID-19? Second, the analysis is conducted at the Zip Code Tabulation Area (ZCTA) level, which is a more informative spatial scale than the county-level analyses common in the COVID-19 literature (2; 3; 4). More broadly, the type of data used in the original study, an area-based aggregate measure of disease occurrence, is commonly used in epidemiological analysis which makes our research design and analytical approach of interest across a large number of studies. Third, the authors' finding that the presence of Black/African American residents is strongly associated with the rate of positive COVID-19 tests in New York City addresses frequently investigated questions about the role of race in the pandemic (5; 6; 7; 8). While multiple studies identify a statistical association between race and COVID-19 at the neighborhood level (9; 10), further investigations into how these associations vary from place to place, or across different racial and ethnic compositions, remain underexplored. Fourth, as a practical matter, we selected DiMaggio et al. because the authors made their data and analytical code available.

We selected Phoenix, AZ as the site of our replication for three reasons. First, following the initial COVID-19 outbreak in New York City that was modeled by DiMaggio et al. (1), the Phoenix metropolitan area quickly became the next epicenter of the pandemic in the U.S. Given that a central motivation of our analysis was to assess whether the original analyses of DiMaggio et al. can be used to inform decision-making in other locations, examining the next epicenter addresses this question while also helping to control for other factors that might change with time. Second, unlike New York City, Phoenix is characterized by a sprawling and low-rise pattern of urban development and a different demographic mix. Only 5 percent of Phoenix residents are Black/African American compared with 23 percent of New York City residents. Conversely, non-white Hispanic residents represent 31 percent of Phoenix residents, but only 12 percent of New York

City residents. Finally, Phoenix is one of the few cities in the country where COVID-19 testing data is available for the first wave of the pandemic at the ZCTA level, which allows us to use the same spatial scale as used by DiMaggio et al.

The remainder of this paper is organized into five sections. In the following section, we briefly introduce the data analyses and the key findings of DiMaggio et al. (1). In the third section, we present our data and detail how our approach deviates from that of the original. In the fourth section, we present our results. The fifth section presents a discussion of those results, before we present our principal conclusions and avenues for future work in the final section.

2 Statistical Analyses and Findings of DiMaggio et al. (2020)

DiMaggio et al. (1) analyzed the association between positive COVID-19 test counts and population-level estimates of demographic, socioeconomic, and health variables at the ZCTA level in New York City during the first wave of the COVID-19 pandemic (April 3 to April 22, 2020). Applying a Poisson model estimated using a Bayesian statistical framework, the final model estimated the risk of positive COVID-19 tests (θ_i) via an intercept (β_0); ZCTA-level predictors for race, age, housing density, health factors (heart disease, COPD) ($\beta_j x_i^T$), a set of spatially unstructured random effect terms (υ_i), and a set of spatially structured random effect terms (η_i). An offset that measures the total number of tests in each ZCTA was also included. The spatially structured random effect terms were assigned via the intrinsic conditional autoregressive prior proposed by Besag et al. (11). The model, as presented by the authors, is shown below. Complete model details are available in the original paper and the code used to fit the model was made available as an electronic supplement.

$$\begin{aligned} Y &\sim \text{Pois}(\lambda_i = E_i \cdot \theta_i) \\ \log \theta_i &= \beta_0 + \beta x_i^T + \upsilon_i + \eta_i + (\text{offset}) \\ \upsilon_i &\sim N(0, \tau_\upsilon) \\ \eta_i &\sim N(\bar{\eta_\rho}, \tau_\eta / \eta_\rho). \end{aligned}$$

The authors' primary conclusions were that areas with large proportions of Black/African American population were at significantly higher risk for COVID-19. The authors also estimated the degree to which residual spatial clustering of positive COVID-19 cases was explained by within- and between-ZCTA variability and concluded that about one-third was attributed to between-ZCTA spatial structure.

3 Data and Approach to Replication

3.1 Data

We obtained weekly data on the number of COVID-19 cases and the percent of positive COVID-19 tests for all ZCTAs located within Maricopa County, AZ (12; 13). Maricopa County includes the greater Phoenix metropolitan area. Using this information, we estimated the total number of COVID-19 tests conducted in each ZCTA per week by dividing the number of positive tests by the percent positivity rate. To be consistent with DiMaggio et al. (1), we restricted our analysis to the weeks immediately preceding and following the first peak of COVID-19 cases in Phoenix and, as such, aggregated the total number of cases and tests from May 31, 2020 to August 1, 2020 at the ZCTA level. To limit the influence of outlying areas, we additionally restricted our study area to

ZCTAs that were (a) fully contained within Maricopa County, (b) had more than 10,000 residents and (c) had more than 500 persons per square mile (Supplement B.1). Our final sample included 100 ZCTAs.

Data on the sociodemographic and health composition of each ZCTA were obtained from the 2019 American Community Survey 5-Year Estimates (14) and the Centers for Disease Control and Prevention Places Data File (15). Consistent with DiMaggio et al., information on the percentage of the population who were non-Hispanic Black, over the age of 65, or had chronic obstructive pulmonary disease (COPD) were included in the analysis as was household density per square mile. Additional characteristics, including the percent of individuals who speak a language other than English, percent Hispanic, percent receiving public assistance, percent with heart disease, median household income, and population density, were also considered.

3.2 Replications of DiMaggio et al. (2021)

Adopting the statistical framework used in the original analysis, we conducted two replication analyses. First, we repeated the authors original analysis in as close a manner as possible via a direct replication (16) in Phoenix. Two direct replication sub-analyses were considered. Both sub-analyses maintained the functional form, specification, and computational implementation of the original model. Both sub-analyses also removed heart disease as a predictor variable due to strong collinearity with COPD and percentage of the population age 65 or older, and used the ACS 2019 5-year estimates for our predictor variables as opposed to the 2010 Census data used by the original authors. The two sub-analyses were differentiated by the inclusion/exclusion of the offset term for the total number of tests. Our first direct replication included the offset as per the original model code. The second direct replication excluded the offset.

The second replication analysis was a conceptual replication (16) of DiMaggio et al. that tested the same fundamental hypothesis of the original study, but adopted a model specification that considered conditions specific to Phoenix. For this replication, we added two predictors to the model - percent Hispanic and median household income.

Following DiMaggio et al. we estimated the direct replication models within R using the INLA package (17). We estimated our conceptual replication within R, but used the STAN package (18). We opted to use STAN because it allowed us to clearly specify how the offset term functioned within the model. The full details of our statistical models are available in electronic Supplements A-B.2. The data and code to reproduce both replications are available as part of an Open Science Framework Repository at `https://osf.io/n32ge/`, as are project-level metadata explaining our analytical process.

Together these two replications allowed us to investigate two questions: (1) Can the model specification adopted by DiMaggio et al. be used to describe the pattern of positive COVID-19 tests in a new geographic context? and (2) Do the same factors appear to be predictors of the number of positive tests in these two communities? To answer the second question, we calculated the degree to which the 95% uncertainty intervals for the parameters common to DiMaggio et al. and this study were overlapping.

4 Results

4.1 Descriptive statistics

Over the time frame described in Section 3.1, the mean number of COVID-19 tests per ZCTA In Phoenix was 5841.40 (95% CI 5383.40, 6299.40) and the mean number of positive COVID-19 tests

per ZCTA was 998.96 (95% CI 871.75, 1126.17). The positive test data are skewed in the opposite direction of DiMaggio et al. DiMaggio et al., indicating that most ZCTAs had low numbers of positive tests while a few ZCTAs had high numbers of positive tests (Fig. 1).

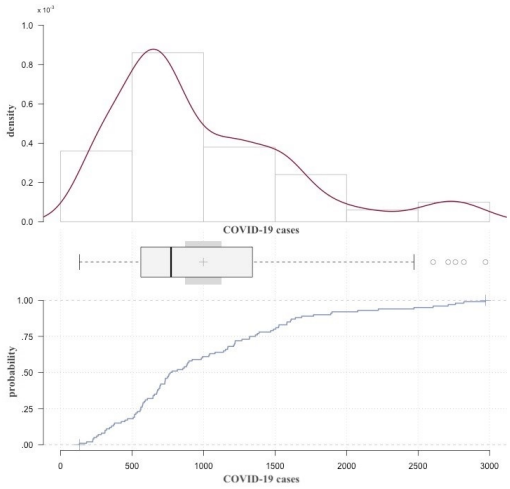

Figure 1: Total positive COVID-19 tests at the ZCTA level. Phoenix, AZ; May 31, 2020 to August 1, 2020. The observed density of positive tests (top) and cumulative probability of positive tests (bottom)

4.2 Replication models

Before attempting either of our replications, we first constructed an aspatial regression model (Supplement B.2) to confirm the need for a spatial model in Phoenix. An analysis of the aspatial model residuals indicated the presence of spatial autocorrelation in the dataset ($Moran's I = 0.354$, pseudo-p $= 5.81^{-9}$) and the need for a spatial model.

Our first direct replication (Fig. 2, red), which included COPD, the proportion of Black/African American residents, housing density, age greater than 65 produced extremely large credible intervals. This model replicated the code of DiMaggio et al., where the offset term was specified within the function specifying the Besag-York-Mollié (BYM) prior. In the second direct replication (Fig. 2, green), we removed the offset term from the model. This reduced the size of the credible intervals to an interpretable range. The difference in the credible intervals produced by these two specifications likely indicates some problem with the handling of the offset term as applied to the Phoenix context. Our exploration of this issue is presented in the discussion. For the second replication, we observed directional effects consistent with DiMaggio et al. except in the case of the proportion of residents over 65. Our estimates for the proportion of Black/African American, COPD, and housing density all fell within the 95% credible intervals of the original authors, although there may be issues with these credible intervals in the original studies, as discussed below.

In the conceptual replication (Table 1), we expanded the predictor set to include the proportion of Hispanic residents and the median income of each ZCTA. We also added the log-transformed total number of tests a as the model intercept as and specified the intercept in the conventional location. This model identified the proportion of Hispanic residents as the only positive predictor of COVID-19 cases at the 95% credible thresholds. Median income and the proportion of residents older than 65 were the only other predictors associated with COVID-19 cases with a probability

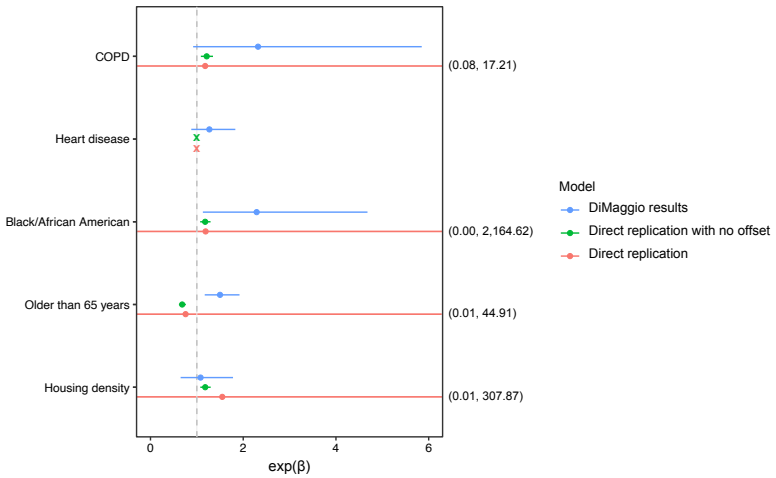

Figure 2: Posterior means (points) and 95% uncertainty intervals (horizontal lines) of the coefficients from DiMaggio et al. (blue), the direct replication (red), and the direct replication excluding the offset term (green). The replications are based on data for Phoenix, AZ Zip Code Tabulation Areas, May 31, 2020 to August 1, 2020. The hashed vertical line indicates a relative risk of 1. The uncertainty intervals for the direct replication with the offset are noted.

greater than chance (more than 50% of the posterior probability of the coefficient estimate greater than 1). Both variables were negative predictors of COVID-19 cases.

Table 1: Results of the conceptual replication of DiMaggio et al. in Phoenix, AZ, May 31, 2020 to August 1, 2020.

Parameter	Median	2.5%	97.5%
Intercept	0.15	0.15	0.16
COPD	0.98	0.89	1.08
Proportion Black	1.02	0.93	1.11
Older than 65	0.95	0.85	1.05
Housing Density	1.01	0.95	1.08
Proportion Hispanic	1.24	1.09	1.40
Median Income	0.93	0.83	1.04
υ_i	0.09	0.05	0.13
η_i	0.06	0.04	0.08

We use the mean coefficient estimates and the percent overlap between the 95% credible intervals of our conceptual replication and DiMaggio et al. to assess the similarity in predictor associations with the number of positive COVID-19 tests in Phoenix and New York City (Table 2). The direction of the median estimates were consistent for the proportion of Black/African American residents and housing density, but were inconsistent for COPD and the proportion of residents over the age of 65. Only the proportion Black/African American residents and age greater than 65 were unambiguous predictors of positive COVID-19 test counts in the original analysis of DiMaggio et al. In our conceptual replication, age greater than 65 was associated with negative test counts, with an estimated median association outside the credible interval of the original authors. In Phoenix, the proportion of Black/African American residents, which was the strongest positive predictor in New York City, shares the direction of the median estimate of association, but shares less than 1%

of its credible interval with the original study.

Table 2: Comparison of the median parameter estimates of the conceptual replication with the estimates and credible intervals of DiMaggio et al.

Parameter	Medians Share Direction	Median Located in Original Interval	Proportion Within Original Interval
COPD	No	Inside	89.81%
Proportion Black	Yes	Outside	0.83%
Older than 65	No	Outside	0.00%
Housing density	Yes	Inside	100.00%

In the conceptual replication, the residual risk, after controlling for the predictors in the model, was primarily explained by between-ZCTA spatial structure - $VPC = 0.59$. Following DiMaggio et al., we calculated and mapped (Fig. 3) the spatial risk estimate for each ZCTA as the sum of the unstructured and spatially structured variance components of our conceptual replication. ZCTAs with the highest residual risk were concentrated in the center of our study region, in communities near Glendale and Sun City West. In contrast, ZCTAs in outer-ring suburbs, such as Fountain Hills and Chandler, exhibited the lowest levels of residual risk.

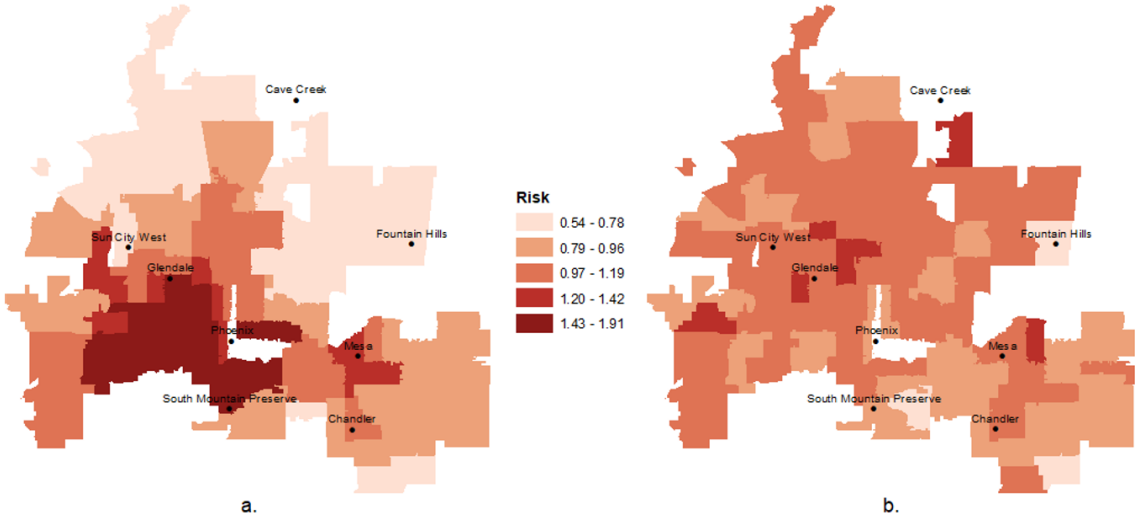

Figure 3: Quintile map of (a) COVID-19 risk due to the predictor variables and (b) Residual risk (sum of unstructured and spatially structured random effect terms) for the conceptual replication of DiMaggio et al. in Phoenix, AZ; May 31, 2020 to August 1, 2020.

5 Discussion

This work adds to our knowledge of COVID-19 in two ways. First, our replications demonstrate that some associations between neighborhood-level predictors and COVID-19 positive test counts do not remain constant across locations, indicating these relationships are likely sensitive to geographic context. Our findings suggest that racial associations with COVID-19 cases may be among those sensitive to context. County-, neighborhood-, and individual-level analyses have all demonstrated

associations between the percentage of residents from different minority groups and confirmed COVID-19 cases and deaths (5; 6; 19; 20). However, the majority of those studies do not consider if and how these results may be sensitive to the study context. Our conceptual replication of DiMaggio et al. allows us to make such comparisons within a consistent statistical framework.

We find that the proportion of Black/African American residents in a ZCTA in Phoenix was not a positive predictor of COVID-19 cases as it was in New York City. Instead, the strongest predictor of positive COVID-19 tests in Phoenix was the proportion of Hispanic residents in a ZCTA. Collectively, these neighborhood-level estimates suggest that the proportion of non-white residents in a neighborhood is likely an important predictor of positive COVID-19 test counts, however the specific racial and ethnic groups that face greater risk likely depends on context. This finding raises intriguing questions about the transmission and detection of SARS-CoV-2 in different community settings. Published individual-level analyses of COVID-19 morbidity and case severity reinforce the idea that Black and Hispanic patients are more likely to test positive for COVID-19 (21; 22; 23). However, discrepancies in this same literature suggest that the condition of patients when they present for hospitalization, if they present at all, determines mortality more so than minority status. Those studies suggest it is a lack of access to care or decision to delay care among minority communities that is responsible for higher mortality in these communities. While our neighborhood-level estimates of case counts cannot measure mortality, our results reinforce the idea that it may not be minority status alone that associates these groups with COVID risk, but rather the systemic disadvantages closely linked with minority status and specific regional histories of inequality.

The observed difference in racial parameter estimates also sheds light on a speculation by DiMaggio et al. that disparities in COVID-19 case counts may be affected by the size of the racial population and how well established those communities are in a city. Black/African Americans represent a far smaller percentage of the Phoenix population than Hispanic residents. Being dispersed across Phoenix, the experiences of Hispanic residents have a greater opportunity to be captured by the Phoenix model, and to influence locations through the effect of the model's spatial prior. Inversely, we suspect that the lack of association between the proportion of Black/African American residents and COVID-19 cases in Phoenix may be the product of the relatively small number of Black residents in Phoenix and their spatial concentration in a small number of densely populated areas.

Second, our replications allowed us to gain greater insight into the modeling process used by DiMaggio et al. and to examine conceptual and methodological questions that other researchers will likely encounter should they attempt similar replications. Our direct replications of DiMaggio et al. revealed questions about how the authors handled the model offset in their original analysis. We discovered that the authors used the total number of tests as the offset rather than the log transformed number of tests, and that the authors specified the offset terms as an argument within the INLA function for the BYM prior distribution. When we replicated this model code in Phoenix, our model produced extremely large credible intervals which likely indicate a problem in the code; one that may only become evident when comparing the results of the same model fit to different data and using different software packages. This reinforces the importance of ensuring that all statistical models are tested for sensitivity to different assumptions and parameterizations, particularly when models are not explicitly defined by the researchers.

Our work also highlights the importance of carefully considering the spatial structure of the location being studied and how that structure is reflected in the data analysis. New York City's pattern of dense urban development generally creates ZCTAs with consistent size, density, and number of neighbors whereas Phoenix has a sprawled urban development pattern that leads to variation in ZCTA size, density, and number of adjacent ZCTAs. This variation is important when

modeling COVID-19 case counts using the Bayesian framework employed in this study because it can influence both coefficient and error estimates. We attempted to control for these effects by focusing our analysis on the core of the Phoenix metropolitan statistical area. Even so, the majority of the residual variance of our conceptual replication was explained by spatial structure. This result is likely the product of the true influence of the spatial structure of Phoenix and the strength of the BYM prior relative to the sample size. Future replications should similarly consider to what extent their estimates may be influenced by spatial structure before making comparisons across regions.

While our findings are suggestive, like DiMaggio et al. they provide a fractured view of the disease processes at work in a community. Our analyses are subject to the uncertainties in our data and model building process. First, our models likely have a degree of measurement error associated with our limited and varying capacity to gather information about COVID-19 prevalence early in the pandemic. The capacity to test for and identify positive COVID-19 cases was limited during the pandemic, particularly during the first wave, and our testing capacity was also regionally varied. Even within cities, the centralization of testing likely created accessibility issues that may have led to non-random testing across population groups. These concerns may be somewhat lessened for Phoenix, as the first wave modelled here occurred after earlier waves in coastal cities, which gave the city time to set-up testing facilities. Second, like other ecological analyses of COVID-19, our models may not capture changes in residence that occurred during regional crests in the pandemic. Our analyses rely on recent ACS estimates, but these data may not capture portions of the Phoenix population that were particularly dynamic during the time period studied. Specifically, Phoenix is a destination for a large retired population that regularly exits the city at the time of our analysis. These caveats should be considered alongside the other temporary migrations out of many cities during the pandemic.

6 Conclusion and Future Work

In this paper, we demonstrate that the neighborhood-level predictors of positive COVID-19 test counts in New York City modelled by DiMaggio et al. during the first wave of the pandemic remained associated with positive test counts in Phoenix, AZ. Our analyses did not replicate the primary association observed by DiMaggio et al., that neighborhoods with higher proportions of Black/African American residents were at a non-random elevated risk for COVID-19 when accounting for other predictors. Instead, we find that, in Phoenix, AZ it is neighborhoods with higher proportions of Hispanic residents that are at elevated risk. This finding is important because it suggests race and the size of a region's racial minority group may be a proxy for the disadvantages these groups face, which may be the true driver of elevated risk of COVID-19. Our analyses also demonstrate that the modeling framework adopted by DiMaggio et al. can be transferred across locations, but needs some modification to local contexts. Replicating the original analyses also allowed us to identify specification decisions that need careful consideration when interpreting or expanding upon the original results.

We see three avenues to directly extend this work. First, our Phoenix model estimates residual spatial risk for each ZCTA and the associations between the predictor variables and positive COVID-19 testing under the constraints imposed by our model specification. That specification was developed based on a review of the existing COVID-19 literature and an examination of how local public officials responded to the pandemic during the study period. As our understanding of SARS-CoV-2 and its variants evolves, it will be appropriate to revisit and adjust this model. While we believe the strength of the relationships observed during the first wave of the pandemic makes

the model robust to specification changes that would extend from changes in the model, we also believe that the model should be adjusted for cross-sectional studies of future waves or longitudinal analyses of the entire pandemic.

Second, our model of Phoenix could be further refined to explore temporal and spatial-temporal variation in COVID cases (see 24). Phoenix has experienced three distinct waves of COVID-19 infection during the pandemic as of December 2021. In this paper, we establish a positive association between the proportion of Hispanic residents in a ZCTA and COVID-19 case rate, however, we have not explored whether this association, or others, change over time or space. National scale tracking of racial case rates (25) suggests that different ethnic groups have experienced peaks in cases at different points in the pandemic. Exploring whether these shifts exist in Phoenix and what their spatial patterns are could provide lessons on how to plan for the future SARS-CoV-2 variants, for example, by finding that the proportion of Black/African American residents had stronger associations with COVID-19 during early stages of the pandemic whereas the proportion of Hispanic residents had stronger associations with COVID-19 during latter stages.

Third, our model could be placed in a hierarchical framework that extends across multiple cities. This approach would extend the single replication logic used here to many locations and provide more complete evidence for the consistency of COVID-19 predictors both within- and between-urban areas. Such a model could include urban hotspots of COVID-19 and be used to estimate local (city-specific) and global (common to multiple cities) relationships between race and COVID-19 incidence across space and time. Such an analysis would also serve as a counterpoint and corrective to early national scale ecological analyses of associations between COVID-19 cases and socio-demographics conducted at the county scale that failed to account for the reality that COVID cases are often concentrated in specific urban neighborhoods. Many of those studies may have erroneous conclusions because they fail to account for population density and build their spatial relationship structures at a scale that is not directly relevant to disease transmission. One restriction on such an analysis remains the availability of COVID-19 case data at fine geographic scales (e.g., finer than counties).

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Funding

This material is based on work supported by the National Science Foundation under Grant No. (**BCS-2049837**), a fellowship awarded to **Kedron** under Grant No. (**OAC-1743184**), and a Graduate Research Fellowship awarded to **Hoffman** under Grant No. (**026257-001**).

CRediT Statement

Kedron led project administration, conceptualization, and writing, and co-led methodological development with Quick. **Quick** also co-led analysis with Bardin and contributed to writing and code review. **Bardin** led code development (R) and data curation, co-led data analysis, and contributed to conceptualization, and writing. **Hoffman** led code development (Python) and contributed to conceptualization, data analysis, and writing. **Sachdeva** led mapping, reviewed code, and contributed to conceptualization, data analysis, and writing. **Holler** reviewed the manuscript, contributed to the organization of the Github repository.

A Statistical Framework and Model Details

The count of positive COVID-19 tests in ZCTA i is denoted as Y_i (i = 1, ..., 100) and is modelled using a Poisson likelihood where E_i is a known offset that measures the total number of tests in ZCTA i and θ_i is the unknown COVID-19 positive test rate. Following DiMaggio et al. (1), $\log(\theta_i)$ is modeled as the sum of an intercept (β_0), a set of regression coefficients and predictor variables ($X_i^\intercal \beta$), and two sets of random effect terms that capture the residual COVID-19 risk that is explained by within-ZCTA variability (υ_i) and between-ZCTA spatially structured variability (η_i). The sum of υ_i and η_i is known as the BYM prior (11). For interpretation, $\exp(\beta_0)$ represents the average positive COVID-19 test rate in the study region, the β_j's quantify the association between COVID-19 case rates and each predictor variable, and the sum of υ_i and η_i represent the residual COVID-19 rates not modeled by the intercept or predictor variables.

The intercept and coefficients were assigned vague normal prior distributions. The η_i's were modeled via an intrinsic conditional autoregressive prior distribution ($\eta_i \sim N(\bar{\eta_\rho}, \tau_\eta/\eta_\rho)$), which assumes that nearby regions may have similar COVID-19 positive test rate. A first-order Queen adjacency matrix was used to specify the spatial structure. The υ_i's were modeled via independent normal distributions ($\upsilon_i \sim N(0, \tau_\upsilon)$), which assumes no correlation between nearby ZCTAs. The precisions on these components were assigned the following priors:

$$\tau_\upsilon \sim \Gamma(3.2761, 1.81)$$
$$\tau_\eta \sim \Gamma(1, 1).$$

The results of the model were similar under alternative prior distributions.

Our model is:

$$Y_i \overset{\text{iid}}{\sim} \text{Poisson}(E_i \cdot \theta_i)$$
$$\log \theta_i = \beta_0 + X_i^\intercal \beta + \upsilon_i + \eta_i$$
$$\upsilon_i \sim N(0, \tau_\upsilon)$$
$$\eta_i \sim N(\bar{\eta_\rho}, \tau_\eta/\eta_\rho).$$

Symbol	Dimension	Description
Y	$n \times 1$	Case counts in each area
X	$n \times k$	Design matrix of k covariates
E	$n \times 1$	Total number of positive COVID-19 tests
β_0	scalar	Model intercept
β	$k \times 1$	Vector of parameters
θ	$n \times 1$	Positive COVID-19 test rates in each area
υ	$n \times 1$	Unstructured random effects
η	$n \times 1$	Spatially structured random effects
τ_υ	scalar	Precision for υ
τ_η	scalar	Precision for η

Table S1: Symbols and dimensions for the model. Here, n is the number of ZCTAs and k is the number of predictor variables.

In this model, the offset allows us to account for the total number of tests in an area. Importantly, the covariates of this model are not restricted to the population of people who got tested. By incorporating this fixed factor into the rate of the Poisson variable, we restrict the inference to the population that got tested.

B Analytical Setup

B.1 Removal of Low Population and Low Density Areas

Unlike New York City, Phoenix is characterized by sprawling development pattern made up of ZCTAs of varying size and population density. Peripheral ZCTAs with low population densities experienced the pandemic differently and, during the period we examined, reported small case counts. To align the context of our analysis with that of DiMaggio et al., we removed ZCTAs with populations of 10,000 people or fewer and ZCTAs with population densities of 500 people per square mile or less (Fig. 4).

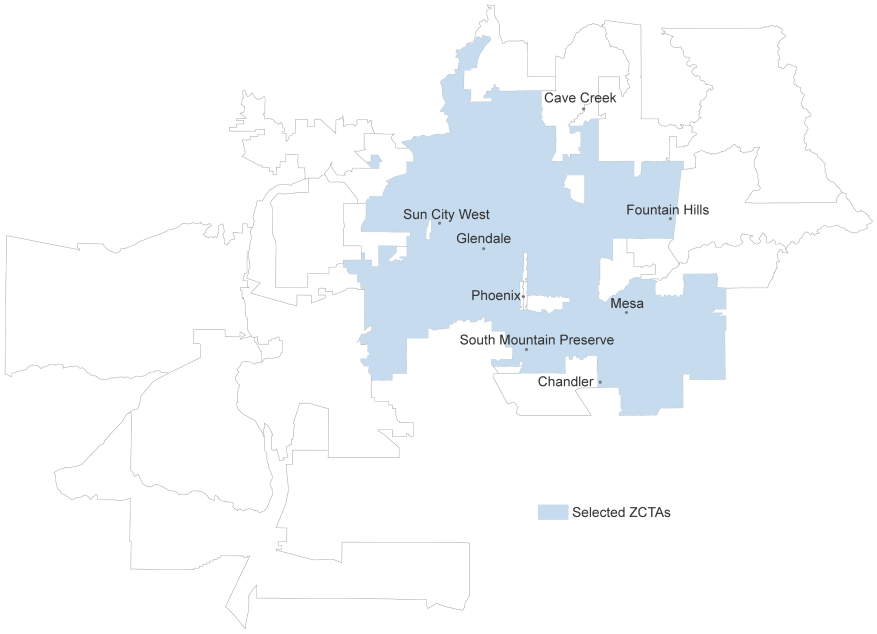

Figure 4: ZCTAs selected by the selection criteria described in Section B.1.

B.2 Aspatial Replication

To begin our analysis, we conducted an aspatial regression using the covariates for COPD, percent black people, percent 65 and older, and housing density. The aspatial model took the same form as the model presented in Section A with no spatially structured random effects term. A map of the spatially unstructured residuals are shown in Fig. 5. The residuals have a global Moran's I of 0.354, indicating the presence of spatial autocorrelation and suggesting the need for a spatial model.

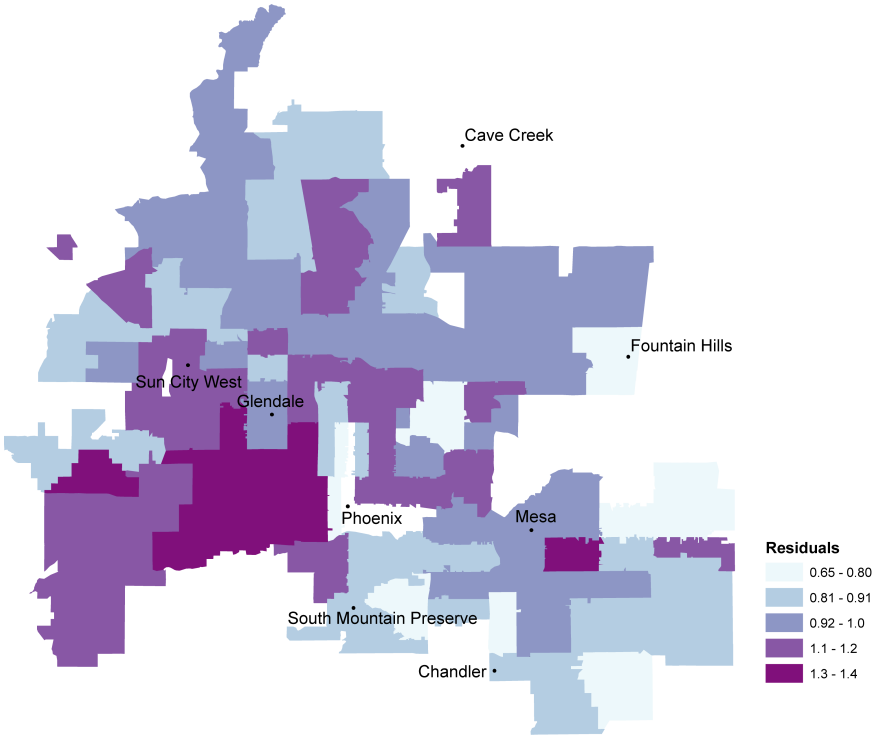

Figure 5: Residual from aspatial model of positive COVID-19 test counts. Replication performed on data from Phoenix, AZ Zip Code Tabulation Areas, May 31, 2020 to August 1, 2020.