Statistical implications of endogeneity induced by residential segregation in small-area modelling of health inequities

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Health inequities are commonly assessed by health departments to identify social groups disproportionately and unfairly burdened by disease and by academic researchers to understand how social, economic, and environmental inequities across privileged vs. marginalized groups manifest as health inequities. Small-area health data for racialized social groups are often utilized for this purpose, and generalized linear models (GLM) or generalized linear mixed models (GLMM) are employed to estimate the extant health inequities. Here we explore how residential segregation combined with social group differences in on-average individual risk can lead to model misspecification and contradictory findings from the standard GLM and GLMM approaches, owing largely to particular type of endogeneity induced in the GLMM. To our knowledge this issue has not been noted previously in the literature. We illustrate this phenomenon in simulated data and in real census tract premature mortality data from Massachusetts for the Black and white non-Hispanic populations. We also propose an alternative model specification to eliminate this issue and obtain additional insights into factors driving racialized health inequities.

Keywords: small-area analysis; generalized linear mixed models; disease mapping; endogeneity; health inequities; racial segregation

# 1. Introduction

Modeling of small area disease/health event rates has long been critical to quantifying health inequities-- that is, unjust, unnecessary, and in principle preventable differences in health status across social groups (Braveman and Gruskin 2003; Whitehead 1992) -- and to informing public health policies seeking to eliminate these inequities. Health departments employ such models to identify social groups disproportionately and unfairly burdened by disease and likely to benefit from public health interventions and resources (Association of State and Territorial Health Officials 2021; National Association of County Health Officials 2021). Academic researchers also model disease rates to investigate how social, economic, and environmental inequities across privileged vs. marginalized groups manifest as health inequities and how risk patterns and inequities vary over space (Beckfield 2018; Berkman, Kawachi, and Glymour 2014). Small-area disease rates for social groups, e.g. racialized or economic groups, are often utilized for this purpose, and either generalized linear models (GLM) or generalized linear mixed models (GLMM) for count/rate outcomes are employed to estimate the extant health inequities (Burton et al. 2010; Chen 2013; Massachusetts Department of Public Health 2010).

Under the usual modeling assumptions, the standard log-linear GLM and GLMM used to model inequities estimate the same marginal rate ratio comparing health outcomes across social groups (Demidenko 2007; Young et al. 2007; Zhang et al. 2012). In academic research, GLMMs, also known as disease mapping models, are often preferred due to their ability to estimate inequity measures with a marginal interpretation while accounting for correlation in small-area data and allowing for estimation of smoothed rates for small areas where observed rates may be noisy. However, GLMMs may not estimate marginal parameters if the data violate key modeling assumptions. Endogeneity in the form of correlation between covariates and areal-level random effects in a GLMM can compromise the marginal interpretations of parameters in the log-linear GLMM (Bates et al. 2014; Mundlak 1978; Neuhaus and McCulloch 2006).

Although impacts of such endogeneity in multilevel model frameworks have been well-studied, to our knowledge little to no work has focused on the implications for disease mapping models for health inequity research. We find that residential segregation combined with social group differences in on-average individual risk give rise to small-area data that induce endogeneity due to correlation between *the offset* and random effects in disease mapping models. To our knowledge, this specific form of endogeneity has not been discussed in the statistical literature. This study examines – and demonstrates – how such endogeneity leads to model misspecification and contradictory findings from the GLM and GLMM approaches.

Specifically, using the example of racialized health inequities, we demonstrate how racialized residential segregation combined with baseline on-average racialized differences in health outcomes, conditions which frequently co-occur, lead to endogeneity and contradictory inequity estimates from the GLM and GLMM. We evaluate the magnitude and implications of these discrepancies in real data and in simulations, and we propose an alternative model specification that we term the “individual and neighborhood inequities” model (INE). This alternative formulation eliminates this problem and can provide greater insights into the factors driving health inequities.

In Section 2, we motivate this work by describing census tract (CT) premature mortality rate data for two racialized social groups in Massachusetts (MA), as defined by the US census: the Black population and the white non-Hispanic population (WNH) (US Census Bureau 2017, 2020). In Section 3, we mathematically formalize the GLM and GLMM approaches and examine how small-area disease/health event data stratified by racialized group can induce endogeneity. In Section 4, we evaluate the impact these issues can have using simulated data. In Section 5, we demonstrate this phenomenon in a health inequity analysis using the MA premature mortality data. We conclude with a discussion in Section 6.

# 2. Motivating data

To motivate this work, we introduce the data we use to investigate inequities in CT-level premature mortality (death before age 65) in the Black and WNH populations in MA. CTs are small administrative units defined by the US Census Bureau, which are designed with a target of having each one include roughly 4,000 residents (US Census Bureau 2019). They are commonly used to investigate spatial patterns in public health (Hund et al. 2012; Krieger et al. 2005; Lawson 2013). Premature mortality is a widely used population health indicator known to manifest strong social gradients, making it an appropriate choice for studying health inequities. It also has the advantage of being unaffected by misclassification of cause of death (Chen et al. 2006; Krieger et al. 2017, 2020).

We obtained records for all premature deaths in MA during 2008-2012 from the MA Department of Health (55*,*836 total premature deaths). We geocoded the residential address at death to the corresponding CT, with only 0.4% of deaths unable to be geocoded at that level of precision. We extracted the US census race-, age- and sex-stratified population sizes, as categorized with US census terminology, for each CT from the 2010 decennial census using the R package tidycensus (Walker 2020). We then multiplied each population count by five to obtain the at-risk person-years corresponding to our five years of mortality data. Our study included all MA CTs with non-zero Black and WNH populations, totaling *N* = 1*,* 465 CTs (99.1% of MA’s 1,478 CTs in 2010).

Let index CT and index racialized group within CT so that is the observed count of premature deaths in racialized group within CT . We constructed standardized mortality rates (SMRs) using the indirect standardization approach (Chen 2013). CT and racialized group-specific expected premature death counts are calculated to serve as a denominator (or offset in statistical modeling) to account for differential at-risk person-time and age and sex compositions. Briefly, the state of MA was used as the reference population, and we computed the state age and sex stratum-specific premature mortality rates from our data. Within a given CT and racialized group, we obtained the expected count for each age/sex stratum by multiplying the stratum’s person-years by its rate in the reference population. We then summed the age/sex specific expected counts for the CT and racialized group to obtain the final expected premature mortality count. We denote the expected count for racialized group in CT by .

The SMR is then given by . Figure 1 shows the distributions of the CT racialized group-specific 5-year expected counts and SMRs. To illustrate the racialized segregation and the concentration of the Black population in a small number of CTs, Figure 2 shows the CT expected count of premature mortality for Black and WNH populations in MA, and a magnified view of the city of Boston. The maps of expected counts for the Black and WNH populations appear nearly inverted. They also demonstrate the sparsity of Black persons, and the ubiquity of WNH persons, across most of the state. In MA, the average number of CT expected Black premature deaths for 2008-2012 was 2.20, and 54% of CTs had less than 1 expected Black premature mortality case over the 5-year period. Boston was more diverse, with an average of 6.50 expected Black premature deaths per CT and only 28% of Boston CTs having less than one expected Black premature death.

# 3. Methods

We focus on two traditional approaches to health inequity analysis using small-area data: GLMs, also called aggregated analyses, and GLMMs, also called disease mapping models, both of which we describe in detail below. Although we motivate this work using an analysis of Black vs. WNH health inequities, these approaches can be used for any small-area-based health inequity analysis, and for general exposition, we refer to two social groups: privileged and marginalized (e.g., WNH and Black populations).

A standard GLM specification for estimating health inequities across the study population’s social groups is

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|  |  | (1) |

where denotes the indicator of social group (marginalized =1, privileged = 0). and are the CT- and group-specific event counts and expected event counts, described in Section 2. This model is often estimated assuming a Poisson likelihood, although more flexible approaches such as the quasi-Poisson or the negative binomial distribution are also common. The rate ratio (RR) for comparing the CT-level rate of the health event in the marginalized vs. privileged population is .

The GLM approach assumes that the independent unit of analysis is the CT- and social group-specific rate, however, the independence assumption is likely to be violated, as the rates of a health outcome in marginalized and privileged populations in the same neighborhoods are almost certain to be correlated. In spite of its over-simplified specification, the GLM approach retains relevance because RR from the GLM can be shown to be equivalent to that obtained from an aggregated social group inequity analysis. The aggregated approach, often used by state health departments to monitor health inequities, aggregates incidence data from the entire state to generate a state-wide age-adjusted RR comparing the marginalized and privileged groups (Massachusetts Department of Public Health 2010).

The GLMM model extends the GLM approach by including random effects, often with a spatial correlation structure, in the Poisson regression model, in addition to the social group indicator fixed effect which is used to estimate the RR (Chen 2013; Kiang et al. 2019). In addition to estimating the overall RR, this model enables estimation of smoothed area-specific incidence/mortality rates, which can be used to further investigate spatial patterns in risk. A standard GLMM specification for estimating health inequities is

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|  |  | (2) |

where is a CT-specific random intercept. In the standard mixed model framework, the are assumed to be i.i.d. Normal, i.e., . In addition to accounting for correlation in social group-specific health event rates from the same CT, the random effect can also be conceived as capturing some unmeasured CT-level factors that drive baseline rates. The spatial version of this model for areal data generally specifies a conditionally auto-regressive (CAR) structure on the , which further allows for correlation in the health outcomes of spatially proximate CTs. CAR structures are described in detail by (Schmidt and Nobre 2018). Previous work has described conditions that can lead to discrepancies in fixed effect estimates from spatial and non-spatial mixed models (Hodges and Reich 2010; Reich, Hodges, and Zadnik 2006). In this work, in order to isolate the impact of endogeneity resulting from residential segregation, we focus here on the non-spatial GLMM, but the issues we illustrate here would extend to spatial analogues.

In general cases, the fixed effects from GLMs and GLMMs are not directly comparable, as GLM parameters represent marginal associations while GLMM parameters represent conditional ones. However, under standard assumptions, a log-linear GLMM with a Normally distributed random intercept is a well-documented special case in which the parameters in the two models coincide (Demidenko 2007; Young et al. 2007; Zhang et al. 2012). This is apparent once one integrates over the random effects in the GLMM, which yields

Thus, the marginal mean structure for this GLMM is equivalent to the GLM mean structure, with the exception of the constant multiplicative term . While this term causes the intercepts from the two models to differ by , the marginal RR for social group remains . This feature of a log-linear GLMM with a random intercept, namely its ability to estimate marginal fixed effect parameters while also accounting for complex correlation structures and allowing for estimation of area-specific smoothed rates, makes it an appealing and popular choice for disease mapping.

## 3.1 Endogeneity

As shown above, and should agree when the true data are generated from equation (1) or (2). However, we do not expect that these are the true, “causal” data generating mechanisms for complex health outcomes like premature mortality. Note that the goal of statistical modeling in the context of health inequities research is to accurately describe and understand patterns of unequal risk experienced by historically disadvantaged populations as defined by, for example, racialized group. Researchers may also want to explore the mechanisms by which these inequities arise, e.g., by including additional variables such as individual or neighborhood socioeconomic or environmental exposures in statistical models, without necessarily making causal claims about “the effect of race”. Although building a causal model may not be the goal of inequity analyses, certain types of model misspecification and violations of assumptions can impact model performance and interpretability of the results.

In biostatistics, one often overlooked assumption of the GLMM is that the random effects generating the data, the in our notation, are uncorrelated with the fixed predictors on the right-hand side of the model. In the economics literature, correlation between random terms and fixed terms on the right-hand side of a regression model is generally referred to as the problem of *endogeneity*. GLMMs assuming i.i.d. Normal random effects suffer from model misspecification in the context of endogeneity arising due to correlation between covariates and random effects, which has been widely discussed in the literature (Bates et al. 2014; Mundlak 1978; Neuhaus and McCulloch 2006). Because endogeneity is a very general term, perhaps most often referring to omitted variable bias in causal inference settings (where the omitted variables are confounders of the “causal” effect of an exposure of interest), we explicitly clarify here that our use of the term endogeneity throughout this paper refers to model misspecification arising from correlation between a fixed covariate and a random term in a non-causal setting.

Critically, when a fixed effect term is correlated with the random effect, fixed effect parameters in the properly-specified GLMM have a conditional, rather than marginal, interpretation, even in the special case of the log-linear model with a random intercept. Moreover, some literature on this topic suggests that, when a standard GLMM with i.i.d. random effects is erroneously specified and fit in the presence of this type of endogeneity, fixed effect parameter estimates are largely insensitive to the model misspecification (Neuhaus and McCulloch 2006), meaning that bias of the conditional effect estimator under endogeneity is typically small.

While the RR estimator from the GLMM estimates the conditional association parameter in the presence of endogeneity, the RR estimator from the GLM estimates the marginal association. Thus, endogeneity can lead to discrepancies between the GLM and GLMM inequity estimates. In the following section, we describe how endogeneity can arise in health inequity models due to correlation between the offset and the random intercept.

## 3.2 Racialized segregation and baseline health differences

Here we demonstrate how the combination of racialized segregation and higher baseline rates of disease and mortality in neighborhoods whose residents are predominantly persons of color, conditions that commonly co-occur in practice, induce a unique type of endogeneity. Although the concepts in this section are general, we will connect them to our motivating data example for clarity. In our context, strong racialized segregation generally manifests as homogeneity in the racialized composition of CT residents. CT expected event counts in Black and WNH groups, and respectively, will be negatively correlated in the presence of racialized residential segregation, with the magnitude of the correlation reflecting the degree of CT segregation. Moreover, if Black populations comprise a small portion of the study area’s total population and reside largely in a small number of neighborhoods, as in MA (Figure 2), may be very small in most neighborhoods, resulting in unstable and zero-heavy CT-level rates of the outcome for Black populations.

In the US, racialized residential segregation is often accompanied by the residents’ greater exposure to community disinvestment and environmental hazards, as well as household- and individual-level exposures to racial discrimination and economic deprivation, together potentially increasing risk of poor health status among all persons living in this neighborhood (Duncan and Kawachi 2018; Roux and Mair 2010). These higher baseline rates of the health outcome of interest in neighborhoods whose residents are predominantly people of color-- in our example, Black-- can be considered in the context of a GLMM-type data generating mechanism (equation 2) as higher values of the random effect, , occurring in CTwith high Black population size/expected counts, . This leads to a setting in which is positively correlated with and negatively correlated with —an endogeneity problem arising from correlation between a random effect and a fixed *offset*. Although the offset is in essence just a special type of fixed covariate, to our knowledge it has never before been identified as a source of endogeneity. Note that, in this scenario, has no association with , since each CT, , has exactly one count with and one withby design. Nonetheless, the endogeneity introduced by the correlation between and (and ) creates a scenario in which the marginal and conditional associations between and differ, and the GLM and GLMM RRs diverge, even for a model with log link.

Further insight into this phenomenon can be obtained by deriving the closed form estimators of the coefficients in the Poisson GLM and a simplified analogue of the Poisson GLMM. First, note that the GLM we have specified is a saturated model, so that the estimator of when using a Poisson distribution takes the form

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|  |  | (3) |

This confirms that the RR from the GLM is equivalent to the RR from an aggregated analysis, as stated in Section 1. Now, in order to develop closed-form expressions that highlight the impact of endogeneity, for the moment assume the random effects in the GLMM model are a priori known constants. In this case the can be absorbed into the offset term and the model is again a saturated model with closed form estimator of

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|  |  | (4) |

Because this model explicitly adjusts for the , has a conditional interpretation. From these closed form estimators, we can see that if for some constant , then and reduce to the same expression. When is a constant proportion of across areas, this indicates the absence of racialized residential segregation, and in this setting, the marginal and conditional inequity RR parameters will coincide.

However, when there is both racialized residential segregation, , and baseline heterogeneity in rates of the outcome across areas, , equations (3) and (4) are not equal. Thus, the marginal and conditional estimates will, in general, be different. To gain further insight, we now equivalently write equation (4) as

where the can be thought of as weights. This “weighted” expression makes clear that when the are large for large (i.e., co-occurence of racialized residential segregation and higher baseline health risk in predominately Black communities), the conditional estimator up-weights the Black expected counts in the denominator that are the largest, and down-weights the WNH counts in the numerator that are the largest. Comparing this to the estimator in equation (3), which takes the same form but with weights , and assuming a positive marginal association, we see that . Thus, the marginal estimate will be larger than the conditional estimate in the presence of racialized residential segregation and higher baseline risks in predominately Black communities. This suggests that the health inequity estimate from the GLMM will be an underestimate of the marginal association.

Our MA premature mortality data illustrate this phenomenon (Figure 3). In the left panel, the CT observed vs expected counts are plotted for Black and WNH populations, and a steeper positive relationship on average for the Black population is evident by the corresponding regression lines. In the right panel, we multiply the expected counts for each racialized group by the total-CT baseline mortality rate, which we call the “adjusted expected premature mortality”. After this adjustment, a steeper relationship on average for the WNH population emerges. The left panel roughly corresponds to the Black vs WNH relationship detected by the GLM and the right panel to the relationship detected by the GLMM. We delve deeper into this issue below with pseudo-simulated data and provide results for the MA premature mortality data.

## 3.3 Separating neighborhood racialized composition from individual membership in racialized groups in health inequities modelling: the “individual and neighborhood inequities” model

The phenomenon described above leads to a GLM RR estimate that reflects the marginal comparison of Black vs. WNH premature mortality across all CTs, while

the GLMM RR estimate more closely approximates a conditional comparison of Black vs. WNH premature mortality within a given CT. Thus, the GLMM RR is effectively comparing mortality rates for Black vs. WNH individuals living in the same neighborhood. As discussed above, the goal of small area health inequity modeling is, in general, not to estimate the causal effect on the outcome of an individual belonging to a specified social group(s), but rather to understand how an accumulation social factors results in social group inequities in the occurrence (e.g., incidence) of adverse health events. Thus, the GLMM may be “adjusting away” the association of interest in disease mapping studies of health inequities.

Because the GLMM may implicitly separate the neighborhood-level social group associations (random effect) from the individual-level social group associations (fixed effects), we suggest explicitly disentangling these factors in the models through the use of additional area-level fixed effects. In particular, we recommend the following modified GLMM model specification:

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|  |  | (5) |

where is, say, the percent Black in CT . Here, is the multiplicative change in premature mortality risk corresponding to a one-unit increase in a CT’s percent black residents. The term is the multiplicative association between premature mortality and racialized group within a CT, conditional on the CT’s racialized composition. Analogously, can be included as a covariate in the GLM model.

This alternative modeling approach, which we call *the individual and neighborhood inequities (INE) model*, has several implications. First, including in the GLMM should reduce or eliminate the endogeneity issue. Thus, if is included in both the GLM and GLMM, they should produce similar RR estimates. However, including explicitly separates the association between neighborhood social group composition and health from the association between individual membership in the social group and health, conditioning each association on the other. In many contexts, separating these associations may provide additional insights into the social factors that lead to inequities. Moreover, the modified GLMM can still provide smoothed small- area estimates of incidence rates or rate ratios, which are often a target of inference in the GLMM approach. If, however, interest lies in a simple RR to compare overall disease incidence across racialized groups, the standard GLM specification in equation (1) or a generalized estimating equations (GEE) approach, which may produce more accurate uncertainty estimates, will be most appropriate. Although they are not commonly used in this context, in our simulations and data analysis below, we fit GEE models as a comparator for the GLMs and GLMMs.

# 4. Simulations

This simulation study was conducted in R (R Core Team 2020), and fully reproducible code is provided in the online Supplementary Materials and on the first author’s Github site. To illustrate how racialized residential segregation and differing baseline health event rates impact common models for racialized health inequity analyses, we simulate CT-level racialized group-specific data reflecting various combinations of these features. Following the GLMM notation above, CT event counts are generated as , with

As detailed below, four different mean structures are created by altering the specification of the baseline rates, and the expected counts . All simulations have CTs, corresponding to the number of MA CTs in our study.

**Simulation 1: Racialized residential segregation, common baseline rate across CTs.** The CT- specific Black and WNH expected counts are negatively correlated. The expected counts are taken from real MA CT-level data, to simulate a realistic degree of racialized residential segregation and low percentages of Black populations in many CTs. A common baseline rate is achieved by setting .

**Simulation 2: No racialized residential segregation, differing baseline rates across CTs.**  is randomly generated to create differing CT baseline event rates. Expected counts do not differ by racialized group within a CT, i.e., , to represent a setting with no racialized residential segregation. We generate .

**Simulation 3: Racialized residential segregation, differing baseline rates across CTs. CT baseline rates are independent from race-specific expected counts.**  is randomly generated. The CT-specific Black and WNH expected counts are negatively correlated. The expected counts are again taken from real MA CT-level data.

**Simulation 4: Racialized residential segregation, differing baseline rates across CTs. CT baseline rates are positively associated with Black expected counts and negatively associated with WNH expected counts.** Expected counts are taken from real MA CT-level data. We let where and is the centered/scaled WNH expected count. This leads to a correlation of -0.36 between (the baseline rate) and the WNH expected count, and a correlation of 0.16 between and the Black expected count. This simulation corresponds to the structure anticipated in real health data from segregated areas.

In simulations 1-3, where the coefficient parameters have marginal interpretations, we fix *β*0 = 0*.*02 and *β*1 = 0*.*32. In simulation 4, where the parameters have a conditional interpretation, we let *β*0 = 0*.*03 and *β*1 = −0*.*07. Where applicable, and . We generate 200 datasets for each of the four simulation scenarios. To each dataset, we fit a Poisson and negative binomial GLM (equation 1), a Poisson and negative binomial GLMM (equation 2), and a GEE model with a Poisson-like quasi-likelihood and exchangeable working correlation structure. We report the bias in the estimated Black vs. WNH RR from each model in Figure 4, and the 95% confidence interval coverage probabilities for the RR from each model in Table S.1 of the Supplementary Materials.

As evidenced by the results for Simulations 1-3, all models yield unbiased estimates of the RR in settings with racialized residential segregation alone or differing CT baseline rates alone, or when both segregation and differing baseline rates are present but are uncorrelated. In Simulation 4, the scenario in which the baseline rates and racialized group-specific expected counts are correlated, endogeneity yields discrepancies between the GLM and GLMM RR estimates. The GLMM estimate approximates the conditional association, while the Poisson GLM estimates the marginal association. The GEE estimates fall between the true marginal and conditional, although closer to the marginal.

In Simulation 4, we also fit the INE models, i.e., including both an individual and neighborhood fixed effect for racialized group as in equation (5). The results, in Figure 5, show that the GLM, GLMM, and GEE estimates now largely agree.

# 5. Analysis of Massachusetts Premature Mortality Data

We now illustrate this phenomenon by investigating Black vs. WNH inequities in premature mortality in MA using the CT level data described in Section 2. We also conduct secondary analyses restricted to the Boston area, since a large majority of the state’s Black population lives in Boston. The standard GLM and GLMM models fit to these data are specified as in equations (1) and (2), respectively, using both Poisson and negative Binomial likelihoods. The GEE models use the GLM mean structure with a Poisson-like quasi-likelihood and exchangeable working correlation structure. The INE models build on the standard models by adding CT proportion Black (centered and scaled) as a covariate. Each model type is fit to the CT data from the entire state of MA and, separately, to the Boston CTs only. All analyses were performed in R using the lme4, MASS, and geepack packages (Bates et al. 2015; Halekoh, Højsgaard, and Yan 2006; Venables and Ripley 2002).

The MA results mimic the findings from simulated data, i.e., the standard GLMs suggests that members of the Black compared to WNH population experience substantially higher rates of premature mortality, while the standard GLMMs find the opposite (Table 1). The GEE results fall between the GLM and GLMM results, though closer to those of the GLM. In contrast, the results of the INE GLMs, GLMMs, and GEE generally agree. Specifically, they suggest that CT proportion Black is associated with significantly higher rates of premature mortality after conditioning on individual membership in the specified racialized groups, while individual-level measures of being a member of the Black population is associated with lower premature mortality rates after conditioning on CT racialized composition.

In 2010, Boston was 24% Black, as compared to 7% Black in MA. However, as shown in Figure 2, Boston’s CTs are highly segregated, in relation to the Black and WNH populations, resulting in CT compositions that are primarily of one or the other racialized group. In the analyses restricted to Boston (Table 2), inference from the standard GLMs and GLMMs agree that members of the Black population experience higher rates of premature mortality. However, the GLMM point estimates are substantially smaller than the GLM estimates, suggesting that endogeneity may still be impacting these analyses. Additionally, most of the INE models for Boston indicate that after conditioning on CT proportion Black, individuals categorized as Black have a higher risk of premature mortality, in contrast to the findings for MA overall. Hence, in Boston, both individual-level measures of membership in the Black population and neighborhood proportion Black contribute jointly to racialized inequities in premature mortality.

# 6. Discussion

In this paper, we report that the commonly co-occurring conditions of racialized residential segregation and baseline health differences among individuals residing in neighborhoods whose residents are either predominantly WNH or predominantly Black can lead to divergent results in GLM and GLMM approaches often used to analyze racialized health inequities. This divergence occurs due to endogeneity induced by correlation between the offset and the random intercept in the GLMM, and can occur even for models with a log link, for which the literature largely notes that marginal and conditional parameters coincide. In this case, regression coefficients in the log-linear GLM have conditional interpretation, while the GLM coefficients represent marginal associations. We demonstrate this phenomenon both in pseudo-simulated data and in real CT premature mortality data from MA. We also show that explicitly modeling separate, conditional associations between individual membership in racialized social groups and health outcomes, and between neighborhood racialized composition and health outcomes, may reduce endogeneity issues in the models and may provide important insights into factors driving health inequities.

Critically, our findings suggest that the ability to estimate marginal association parameters, one of the most appealing features of log-linear GLMMs popular for disease mapping, may often be compromised in the presence of highly segregated study regions and heterogeneous area-level rates that are correlated with the area’s social group composition. In practice, health inequity estimates from standard GLMMs stratified by racialized group may reflect inequities after conditioning on neighborhood, i.e., effectively comparing disease/mortality across racialized groups living in the same neighborhood. Moreover, we have shown that the combination of racialized residential segregation and differences in baseline event rates in predominately WNH vs. Black neighborhoods results in GLMM effect estimates that are typically lower than their marginal counterparts. Thus, past analyses that estimated racialized health inequities using the GLMM approach may have underestimated the magnitude of marginal health inequities.

We note that previous literature has emphasized the importance of explicitly considering area-level social context when analyzing how individual-level membership in a social group is associated with an outcome (Subramanian et al. 2009). Failure to do so can lead to what is known as the “individualistic fallacy”. On the basis of this literature and our findings here, we recommend use of the INE model we have proposed in future small area health analysis employing data on both individual membership in privileged versus marginalized groups and residential segregation in relation to these groups, whether these social groups are defined in relation to racialized groups, economic groups, or other social groups reflecting inequitable social relationships (Beckfield 2018; Berkman et al. 2014; Krieger 2020). While the INE model is simple and straightforward, we note that more complex GLMM specifications that relax assumptions of the standard GLMM, such as the shared component model which allows for separate spatially correlated random effects across groups (Kiang et al. 2019), are likely to be suitable alternative approaches for dealing with the endogeneity problem.

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Table 1. MA Premature Mortality Fixed Effect Estimates (95% CI)

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  |  | P-GLM | P-GLMM | NB-GLM | NB-GLMM | GEE |
| Standard Model | Intercept | 1.02 (1.01,1.03) | 1.03 (1.00,1.06) | 1.15 (1.12,1.18) | 1.03 (1.01,1.06) | 1.02 (0.99,1.04) |
| Black RR | 1.37 (1.33,1.42) | 0.92 (0.88,0.95) | 1.13 (1.07,1.19) | 0.93 (0.89,0.96) | 1.26 (1.19,1.33) |
| INE Model | Intercept | 1.06 (1.05,1.07) | 1.04 (1.02,1.07) | 1.15 (1.12,1.18) | 1.04 (1.02,1.07) | 1.06 (1.03,1.08) |
| Individual Black RR | 0.89 (0.85,0.92) | 0.85 (0.82,0.88) | 0.98 (0.93,1.04) | 0.86 (0.82,0.89) | 0.82 (0.76,0.87) |
| CT Proportion Black RR | 1.20 (1.19,1.22) | 1.26 (1.23,1.29) | 1.22 (1.2,1.25) | 1.25 (1.22,1.29) | 1.22 (1.19,1.25) |

Table 2. Boston Premature Mortality Fixed Effect Estimates (95% CI)

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  |  | P-GLM | P-GLMM | NB-GLM | NB-GLMM | GEE |
| Standard Model | Intercept | 1.17 (1.12,1.21) | 1.16 (1.07,1.26) | 1.32 (1.21,1.45) | 1.17 (1.08,1.26) | 1.16 (1.06,1.28) |
| Black RR | 1.52 (1.43,1.61) | 1.22 (1.12,1.32) | 1.36 (1.19,1.56) | 1.24 (1.14,1.35) | 1.51 (1.35,1.69) |
| INE Model | Intercept | 1.14 (1.09,1.18) | 1.04 (0.95,1.13) | 1.19 (1.09,1.3) | 1.04 (0.96,1.13) | 1.13 (1.03,1.24) |
| Individual Black RR | 1.21 (1.11,1.31) | 1.11 (1.02,1.21) | 1.22 (1.06,1.39) | 1.13 (1.03,1.24) | 1.20 (1.05,1.39) |
| CT Proportion Black RR | 1.07 (1.05,1.09) | 1.12 (1.08,1.16) | 1.11 (1.07,1.14) | 1.12 (1.08,1.16) | 1.07 (1.04,1.10) |



Figure 1. Racialized group-stratified histograms of CT 5-year expected premature mortality counts (left) and SMRs (right) in Massachusetts.

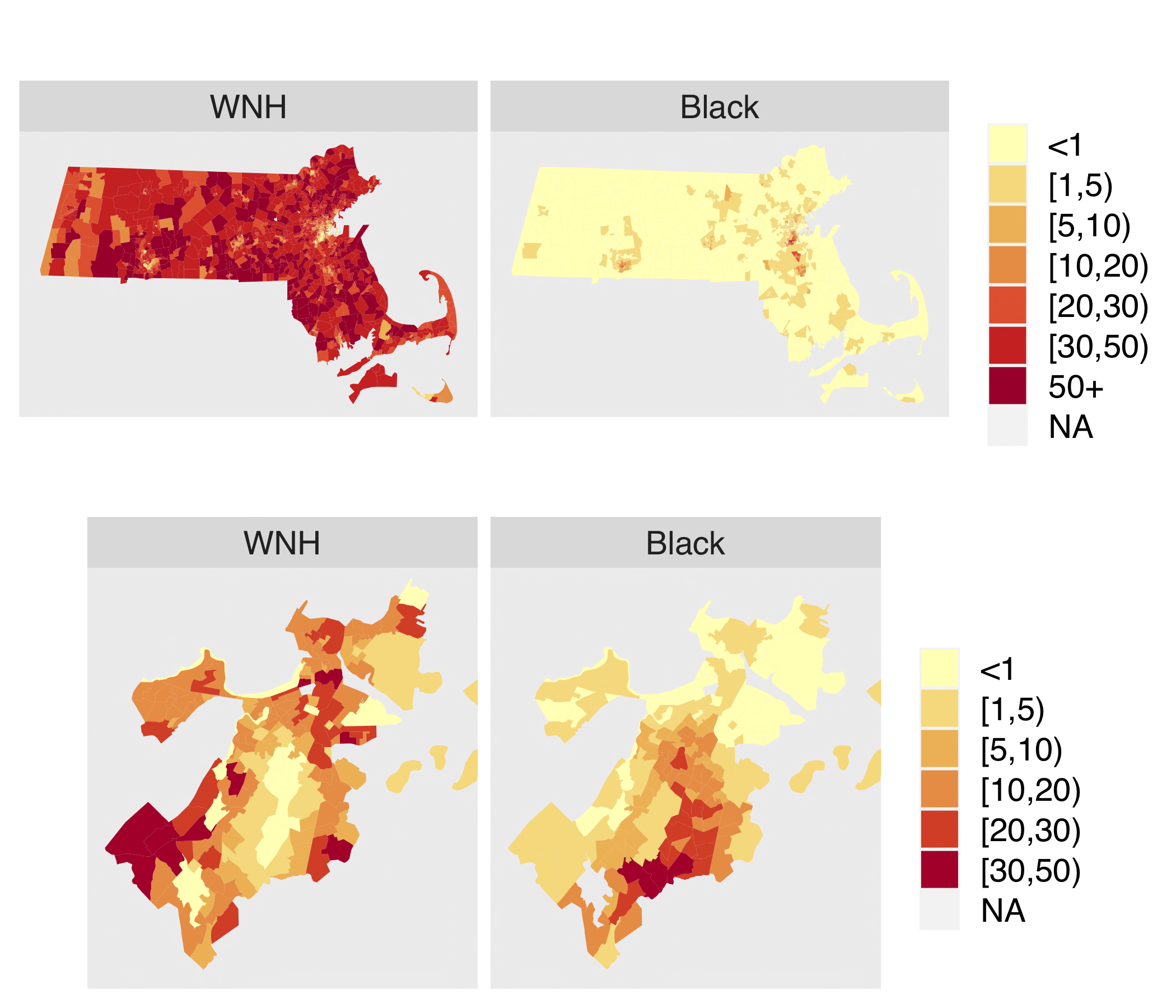


Figure 2. CT expected premature mortality counts by racialized group for MA (top panel) and Boston (bottom panel).



Figure 3. MA CT observed vs expected premature mortality counts for Black vs. WNH populations. In the left panel, raw expected counts are used and in the right panel, the raw expected counts are adjusted by the CT baseline mortality rate.



Figure 4. Simulation Results. Black vs. WNH RR estimates from the Poisson GLM and GLMM, the GEE, and the Negative Binomial GLM and GLMM fit to simulated data for each of the four simulation scenarios. True marginal RR used to generate the data is indicated by the black horizontal line and true conditional RR is indicated by the red horizontal line.



Figure 5. Simulation Results. RR estimates from the INE model specification of the Poisson GLM and GLMM, the GEE, and the Negative Binomial GLM and GLMM fit to simulated data. The left panel shows estimates of the RRs for the individual Black indicator and the right panel shows estimates of the RRs for CT proportion Black.

**Supplementary Material**

Table S.1. 95% confidence interval coverage percentages for simulations.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Simulation | P-GLM | P-GLMM | NB-GLM | NB-GLMM | GEE |
| 1 | 94.5 | 94.5 | 94.5 | 94.5 | 94.5 |
| 2 | 94.5 | 55.5 | 98.5 | 94.5 | 94.0 |
| 3 | 85.0 | 96.0 | 99.5 | 96.0 | 99.5 |
| 4 | 95.5 | 0.0 | 0.0 | 0.0 | 58.0 |