Accounting for migration in spatiotemporal models of county-level health

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## Abstract

Although the relationship between place and health is well studied and measured, typical place-based measures of health are static, representing a single point in time without accounting for movement or mobility. Among the well-established understanding that place influences health is the understanding that place differentially impacts some groups of people more than others. What remains unknown is to what extent population migration explains place-based health and health disparities. Thus, there is a critical need to measure the degree to which county-level patterns in health factors and outcomes can be attributed to county-level patterns in mobility. Without such knowledge, we are unable to fully capture the complexities of county-level health, limiting our ability to inform local policy making.

This paper aims to provide understanding of the mechanisms by which mobility may be related to place-based health disparities so that local decision-makers may account for patterns in mobility when creating policy towards improved health for all people in all places. In this paper, we quantify and devise techniques for quantifying the relationship between county-level mobility and county-level health. Understanding rural-urban mobility patterns is a necessary first step towards understanding place-based health disparities.

## Introduction

We are still discovering how changes in our geographical location relate to our health. Geographical changes can happen *to* a person, by either staying in a geographical location that changes around them or moving to a new location. They can also happen *by* a person: when individuals move, not only do they experience a change in location, but they take their sociodemographic identities, income, health, employment, and education with them. As a result, the place they are leaving and the place they are arriving changes, if only slightly. In aggregate, composition changes at a geographic location could potentially change the health of the population as a whole. In this paper, we explore methods for accounting for composition changes due to migration when measuring average health outcomes across U.S. counties.

Measuring health outcomes has been important for guiding effective policy-making. The idea is to identify potential factors that may influence health so that policy-makers can design precise, well-founded strategies. In this regard, it is important for policy-makers to separate changes in average health outcomes that stem from the built environment as opposed to the composition of the population itself. If the built environment is the cause, enhancing access to parks, medical facilities, and public transport might be a solution. If, however, composition changes are the cause, policy-makers may want to learn about their the new residents. This insight will allow for a more tailored approach to meet their specific needs, such as providing affordable housing for low-income families. County-level data and analyses have been valuable tools in gaining this insight, serving to inform local policies on how to raise the average health of a county or reduce disparities within a county . This approach has proven especially valuable in the face of challenges like the COVID pandemic, where local entities like health departments, school boards, and faith-based organizations played a pivotal role in responding to public health needs based on county data.

Traditional approaches to county-level analyses of health involve autoregressive models that account for variation across space and time. The application of autoregressive models at the county level has seen various implementations, such as a county’s relative position and historical mortality rates for forecasting future mortality rates (Tse Chuan Yang, Jensen, and Haran 2011), or estimating mortality rates that adjusts for county-level information on income and employment, population density and rurality, and race/ethnicity (“An Application of Spatially Autoregressive Models to the Study of US County Mortality Rates - Sparks - 2010 - Population, Space and Place - Wiley Online Library,” n.d.). Similarly, during the early stages of the COVID-19 pandemic, a spatial autoregressive model was utilized to assess the relationships between county-level COVID-19 mortality rates and county-level sociodemographic characteristics (Fielding-Miller, Sundaram, and Brouwer 2020). This modeling approach has also been applied to age-group and country-level data to explain cohort effects within countries(Li, Lu, and Lyu 2021), and more recently, to enhance the estimation of country-level life expectancy, particularly for younger demographics, with improved efficiency and accuracy (Shi 2021).

These modeling approaches, however, overlook the aspect of migration.  An important consideration is how much of the variation in a county’s average health outcomes could be attributed to the movement of individuals between regions. As a first hypothesis, we might anticipate that a person moving from a region with better (worse) average health outcomes to one with worse (better) average outcomes would increase (decrease) the average health outcomes of their destination, however slightly. If this is true, then models that ignore this source of variation may incorrectly attribute a change in average health outcomes to other factors, such as the built environment.

A major drawback with this first hypothesis is that it assumes that when a person moves from one place to another, their health status is representative of the average health status of the place they are coming from. In other words, movers are neither more nor less likely to be healthier than the general population of their original location, making their health outcomes comparable to the average health outcomes of that area. Previous research suggests this assumption is not accurate, indicating that the health of migrants often differs from the average health of their origin in addition to the average health of their destination.

To start, migration can have a direct impact on the health of the individual moving. For example, relocation from rural areas to urban areas has been associated with increased risk of cardiovascular disease in some populations (Miranda, Gilman, and Smeeth 2011). Similarly, relocation to high-income countries has been associated with adverse cardiovascular health effects (Agyemang and Born 2019). Several studies have found that rates of cardiovascular disease are higher among migrants than among their peers who did not migrate(Agyemang and Born 2022). For instance, a study of people who migrated to the US from Japan found that Japanese migrants to California had age-adjusted prevalence rates of cardiovascular disease that were more than twice as high as their peers who migrated to Hawaii or did not migrate at all (Marmot et al. 1975). This suggests that the average health of migratory populations becomes more similar to the average health of their destination than that of their origin, possibly because migrants take on the diets, habits, and other health factors of the place to which they relocate.

Another explanation is that people who move are systematically different than people who stay. That is, migration is not random, but selective. According to Lee’s theory (Lee 1966), migration is influenced by “push” factors that compel people to leave their origins, due to hardships like job losses, climate events, or war, and by “pull” factors that attract people to new destinations, often favoring those with high income or education. Consequently, migration typically involves either the most advantaged or the least advantaged individuals. This logic might extend to the health of migrants: only the most and least healthy individuals migrate. For example, when the barriers between origin and destination are particularly high, migrants are often healthier on average than the people living in their destination, because unhealthy people are less likely to move when the barriers are high (Halliday and Kimmitt 2008). In the aforementioned study of migrants from Japan, for instance, it is possible that people who migrated to California were “pushed” to California while people who migrated from Japan to Hawaii were “pulled” to Hawaii.

Because migration is selective, a second hypothesis might be that certain factors about a county help explain the relationship between average health of a county and the average health of the counties from which people are moving.  For example, migrants who move from more resource depleted regions to less resource depleted regions often have better health on average than the population in their destination while migrants who move from less depleted regions to more depleted regions have worse health on average than the population in their destination (Norman, Boyle, and Rees 2005). One specific factor of interest is urbanicity, because, for one reason, urban and rural regions differ in their average health. For instance, higher rates of high quality of life in Finland were found in rural areas but not after controlling for perceived loneliness(Weckroth et al. 2022), and people in urban areas have higher prevalence of both depression and anxiety despite a lower prevalence of other risk factors (Zijlema et al. 2015). For another reason, urban and rural regions differ in ways that relate back to the health of their population, such as access to green space(Tsai et al. 2018); concentration of populations marginalized from resources, crowded living conditions, and air pollution(Ha 2017); access to social organizations(Tse-Chuan Yang 2019), and educational and financial opportunities(Ha 2019). Therefore, if the second hypothesis is true, then we may want to let county factors, like urbanicity, modify how compositional changes due to migration relate to average county health in our modeling.

Still, even if we accounted for county factors, there may still be *unobserved* factors at play. For example, some people may choose to live in urban places and others in rural environments. These choices could be influenced by the past and present sociocultural context of each community which affects who feels welcomed into which communities. Factors such as personality and familial ties play large roles in both health and choice of living location (Chan 1977). Thus, we arrive at a third hypothesis, in which unobserved factors help explain the relationship average health of a county and the health of the counties from which people are moving. If true, then we may want to investigate the potential for unobserved factors to modify how compositional changes due to migration are incorporated into the model.

In this paper, we propose novel extensions of traditional spatiotemporal models to account for compositional changes due to migration. Our broad strategy is to use migration flows in and out of counties to adjust the autoregressive term in the model in a principled way. By way of this strategy, we are able to first, formalize and, then, test three hypotheses:

1. County-to-county migration flows improve the explainability of autoregressive models of county-level health outcomes.
2. The role that county-to-county migration flows plays in county-level health outcomes differs significantly between rural and urban counties.
3. Taking into account unmeasured factors in county-to-county migration flows improves our ability to explain county-level health outcomes as well as the differential role that migration plays in urban versus rural counties.

We note these hypotheses mirror the three broad hypotheses introduced earlier. Using publicly accessible mortality data from CDC WONDER (“CDC WONDER,” n.d.)and county-to-county migration flow data from the IRS (“SOI Tax Stats - Migration Data | Internal Revenue Service,” n.d.), we investigate these hypotheses, focusing specifically on county-level premature age-adjusted mortality and on using Bayesian information criteria (BIC) as a measure of model fit. Through this investigation, we seek to demonstrate our strategy for incorporating migration into spatiotemporal models of average health. Additionally, we seek to determine what our modeling strategies reveal about the relationship between county-to-county migration and county-level premature age-adjusted mortality, especially as it relates to urbanicity and the possible influence of unmeasured factors.

## Methods

#### Data and Variables

All of the data used in these analyses is publicly accessible. We use county-level estimates of premature age-adjusted mortality available through the CDC WONDER Underlying Cause of Death 1999-2020 database(“Underlying Cause of Death, 1999-2020 Request,” n.d.) joined with IRS county-to-county migration flow data(“SOI Tax Stats - Migration Data | Internal Revenue Service,” n.d.).

The outcome of interest is county-level age-adjusted rates of premature mortality We refer the age-adjusted premature mortality rate for each destination county at year as . Premature mortality is defined as any death occurring before age 75. Age-adjusted rates of premature mortality are commonly used as a gold standard when comparing various dimensions of health across counties since death has a clear and common definition (“Self-Rated Health Status as a Health Measure: The Predictive Value of Self-Reported Health Status on the Use of Physician Services and on Mortality in the Working-Age Population” 1997; Jylhä 2009; Olson-Williams 2023), and since premature age-adjusted mortality has important policy and health equity implications and can be used to assess which individuals or groups are likely to live longest and which individuals or groups may be most in need of additional care. For our analyses, we excluded years after and including 2020 because the onset of the pandemic is unrelated to other factors included in our model. Additionally, to match migration data, we excluded years prior to 2011. Therefore, we include premature age-adjusted mortality rates for 8 years total (2011 through 2019) for each destination county .

A necessary baseline explanatory factor is lagged premature age-adjusted mortality, which we refer to as . This is our autoregressive term. In order to predict future age-adjusted rates of premature mortality, we use the age-adjusted premature mortality rate of the prior year for each destination county .

An explanatory factor of interest is urbanicity. To assess urbanicity, we assign each county an urbanicity category based on the 2013 National Center for Health Statistics (NCHS) Urban–Rural Classification Scheme for Counties (Rothwell, Madans, and Arispe, n.d.). To maximize the number of counties per category and improve precision, we chose to use only two urbanization categorizations: urban and rural, where urban includes large central metro, medium metro, and small metro counties, and rural includes micropolitan and noncore counties. We assessed 1948 unique rural counties and 1159 unique urban counties.

The primary explanatory factor of interest is the *migration term* which we refer to as . We calculate for each destination county during each year using the following equation: The migration term accounts for the premature age-adjusted mortality rates of individuals who have moved to a county of interest during a given period. This term is essentially a weighted average of the mortality rates of all of the origin counties for a given destination county . We calculate the following for each change in year and for each destination county :

where is the lagged premature age-adjusted mortality rate of destination county as defined above and is the population under age 75 of an unique destination county at initial year . Both and come from the CDC WONDER Underlying Cause of Death database. The term represents the number of migrants from a unique origin county who migrated to a destination county between year and year . The values of come from IRS migration flow data from 2011 through 2019. We exclude years prior to 2011 because in 2011 the IRS changed their methods to produce migration estimates based on a full year of income tax filings rather than a partial year. Prior to 2011, migration estimates represented between 95 and 98 percent of total annual income tax filings and excluded income taxes filed after September of each calendar year (Pierce 2015); estimates after 2011 include all annual income tax filings collected for each year. Therefore, we have chosen only to include data after the 2011 change in IRS methodology. We have chosen to use IRS rather than ACS estimates of migration because ACS does not publish single year estimates of migration (only five year estimates), we want to emphasize the temporal aspects of migration, necessitating the use of IRS single year estimates.

Since we are particularly interested in spatial trends in premature mortality and migration, we exclude counties from Hawaii and Alaska and include only contiguous counties. Additionally, to avoid systematically excluding counties with small population size and to ensure that we have balanced panel data, we used the mice R package(Buuren and Groothuis-Oudshoorn 2011) to impute lagged premature age-adjusted mortality rates for counties with missing values. There are a total of 3107 US counties included in our analyses.

## Model fitting

Using the data and variables outlined above, we first established a baseline autoregressive spatial error model of county-level premature age-adjusted mortality . The **baseline model** is as follows:

where is the intercept, is a coefficient for the affect of each year on county-level premature age-adjusted mortality , is a coefficient for the effect of lagged premature age-adjusted mortality on predicted premature mortality, is a random intercept for each destination county , and represents an error term accounting for spatial dependencies. We define the equation for spatial dependency as follows:

Thus, the magnitude of spatial dependency results from the product of a scalar , the spatial autoregressive parameter, which is close to 0 when there is no spatial interdependence and increases as spatial interdependence grows, and , a spatial weights matrix with row-standardized weights. We created using the spdep R package (Bivand and Wong 2018) with the “queen” criterion which considers counties that share any point as neighbors. Finally, represents the spatially independent random error term for each county at year .

We created this baseline model and all subsequent models using the splm and splines R packages (2024; Bivand, Millo, and Piras 2021). To establish a model with the most explanatory power, we began by iteratively adding splines with two to five degrees of freedom for the lagged age-adjusted county-level premature mortality rates to capture potential nonlinear trends over time. We compared models using the Bayesian Information Criterion (BIC), which is commonly used to identify models with the greatest explanatory power(Kuha 2004).

Next, we added the migration term to this baseline model. We again attempted to capture nonlinear trends over time by iteratively adding splines with two to five degrees of freedom for the lagged age-adjusted county-level premature mortality rates and the migration term . The addition of this weighted average migration term to our model allows us to implicitly account for between-county selection for migration. However, does not account for within-county selection of migrants. In other words, our best guess for the mortality rate of migrants is exactly the mortality rate of their original county; meanwhile, some counties are more likely to be destinations for migration than others.

To determine whether the role that county-to-county migration flows play in county-level health outcomes differs significantly between rural and urban counties (Hypothesis 2), we added a factor term for urbanicity including interaction terms between urbanicity and and urbanicity and . We again compared these models using BIC while iteratively adding splines with two to five degrees of freedom for migration and lagged premature mortality. We chose a final model for our simulation of health-related selection based on BIC score and stability. This model is as follows:

where (in addition to the terms defined in our baseline model) is a binary indicator variable equal to 1 for rural destination counties and 0 for urban destination counties, is a natural spline transformation of the lagged premature age-adjusted mortality rate with 2 degrees of freedom, and is a natural spline transformation of the migration term with 2 degrees of freedom.

Finally, to determine whether taking into account unmeasured factors in county-to-county migration flows improves our ability to explain county-level health outcomes (Hypothesis 3), we added parameters and to the premature mortality rate of each origin and each destination within our equation for the migration term. We call this new **simulated migration term .** The equation for is shown below:

We use to simulate within-county selection for migration: when the parameter is subtracted (ie decreased mortality rate), we simulate migration by individuals who are healthier than the average of their origin . When the parameter is added (ie increased mortality rate), we simulate migration by individuals who are unhealthier than the average of their origin . Likewise, when the parameter is subtracted (ie decreased mortality rate), we simulate migration by individuals who are healthier than the average of their destination . When the parameter is added (i.e., increased mortality rate), we simulate migration by individuals who are unhealthier than the average of their origin . We specify that depends on both origin and destination since health related selection for migration is connected to both the origins and the destinations of counties; meanwhile is dependent only upon the health of destination .

Since we are most interested in how the values of and are related to each other, we chose to simplify such that is held constant and only fluctuates. Therefore, we assign the parameter to be the difference between and , thus creating a new equation for in terms of and such that . The value of can be thought of as a modeling term to explain health-related selection bias. Then our equation for becomes:

which can be simplified into the following:

Therefore, using the equation above, we simulate health-related selection occurring as a result of the differences in health between the origin and the destination counties. When is positive, we estimate that the origin is less healthy than the destination. When is negative, we estimate that the origin is healthier than the destination.

To determine which values of best explain trends in county-level premature mortality rates, we replace ([Equation 1](#eq-mig)) with ([Equation 7](#eq-smig_d)) in the model with the most explanatory power, [Equation 4](#eq-forsimulation), as determined in our previous model selection steps. We tested many potential values of . We began by incrementing by 50 from -200 to 200 such that migrants had an estimated premature mortality rate that was between 200 premature deaths per 100,000 population higher and 200 premature deaths per 100,000 population lower than their origin county.

To understand this phenomenon further, we next conducted a grid search to test potential values of when accounting for urbanicity. Specifically, we examined how the values of vary based on the urbanicity of both the origin and destination counties. We defined these variations as follows: for the difference in average health between an urban origin and an urban destination, for the difference in average health between a rural origin and a rural destination, for the difference in average health between a rural origin and an urban destination, and for the difference in average health between an urban origin and a rural destination.

We began with a broad increment of 50, testing values ranging from -200 to 200 premature deaths per 100,000 higher than the destination county, resulting in 6,561 unique sets of . After identifying a range of values that minimized the BIC score, we refined our search. Using a smaller increment of 20, we tested a specific range of values to account for a -140 to 20 difference in age-adjusted premature mortality rates between urban origins and urban destinations. For all other types of migration, we used the same range. Therefore, we tested , , and values with a range of -80 to 80 difference between origin and destination. This resulted in an additional 6,561 unique sets of .

### Results and Conclusions

The tables below present descriptive statistics for ​ (premature age-adjusted mortality rate) and migration rates for each year and categorized by county type (rural, urban). Note that migration rates for the year 2011 are not included. This is because the migration-flow data starts from 2011 to 2012, and these values are shown in the 2012 section of the table, corresponding with the 2012 premature age-adjusted mortality rates.

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After examining the data, our first goal was to establish that our migration term added explainability (as measured by lower BIC scores) to our most basic autoregressive model accounting for spatial error. We observed that models including splines with equal degrees of freedom for both the migration term and the lagged premature mortality rate resulted in consistently lower BIC scores than models with splines with unequal degrees of freedom. The best fitting model in terms of BIC score included splines with four degrees of freedom for both the autoregressive term and our weighted average migration term. This indicates that models incorporating migration had more explanatory power than models that included only the prior year’s average county-level mortality rate.

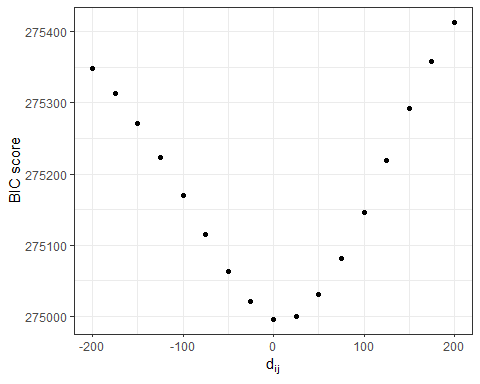
Next, we sought to determine whether our migration term would improve the explainability of our spatiotemporal model, even after accounting for urbanicity. We added interaction terms between urbanicity and lagged premature mortality and urbanicity and migration. After adjusting for urbanicity, we found that the models with the lowest BIC scores included splines with four degrees of freedom each for the migration term and lagged age-adjusted mortality. This further confirmed that the migration term added explainability to our models, even when accounting for urbanicity.

The plot below demonstrates lower BIC scores for models that include the migration term along with an interaction between and urbanicity. The difference in BIC scores between models that include the migration term and those that do not is more pronounced when an interaction term for urbanicity is added. This suggests that the migration term significantly enhances model explainability when accounting for urbanicity, indicating that the relationship between average county-level health and migration may differ substantially across urbanicity levels.

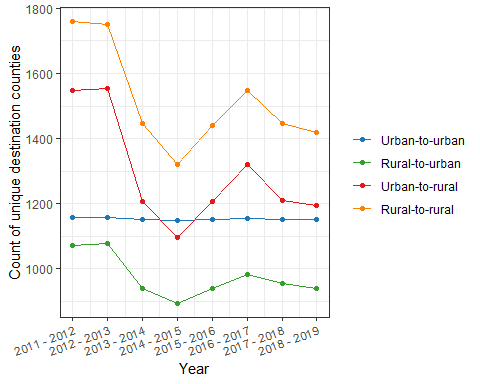
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| Figure 1 |

In the plot above, we see that the difference in the BIC scores of models with splines with two degrees of freedom and models with splines with four degrees of freedom for and is only 6.4. Due to concerns about potential overfitting, and since there appears to be little explainability added by additional degrees of freedom, we chose to use a model with splines with two degrees of freedom for lagged premature mortality rate and migration term, thus, we settled on the model [Equation 4](#eq-forsimulation).

After replacing ([Equation 1](#eq-mig)) with ([Equation 7](#eq-smig_d)) in [Equation 4](#eq-forsimulation), and testing values of between -200 and 200 iterating by 50, we found that the model with the most explanatory power had . As the magnitude of the difference between the health of origin and destination increased, our models had less explanatory power as measured by higher BIC scores. This is shown in the plot below. This suggests that, according to our models, health-related selection for migration may not be important to modelling county-level health when we do not account for urbanicity.



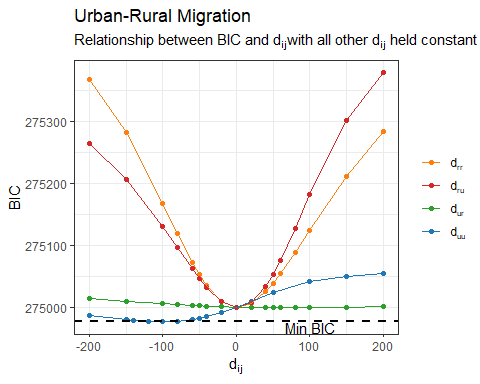
To explore the possibility of health-related selection further, we conducted a second simulation, in which we varied for each possible combination of origin and destination type: rural-to-urban, rural-to-rural, urban-to-rural, and urban-to-urban. In the plot below, we see the number of destination counties for each migration type over time. Notably, the rural-to-rural migration type has the most unique destination counties because there are more rural counties than urban counties. This approach allows us to emphasize all counties, instead of focusing primarily on migration to urban destinations, which is more commonly studied.



In our urbanicity-specific simulation, we started with increments of 50, ranging from -200 to 200, resulting in a total of 6,561 unique sets of . This coarse search identified a minimum BIC score for the set . To verify this minimum and the trends observed in the coarse search, we refined our increment to 20. Specifically, we tested values from -140 to 20 to include the previously identified minimum and the null hypothesis . For other types of migration, represented by , , and we tested a range of -80 to 80 around 0, which was the value producing the minimum BIC score in our coarse search. This refined search resulted in an additional 6,561 unique sets of .

The results of this narrowed search were largely consistent with our coarse search findings, with a minimum BIC score for the set . The plot below illustrates the relationship between BIC scores and ​ for each migration type, while holding other ​ values constant at 0. For migration to rural destinations (orange ​ and red ​), the minimum BIC score occurs when there is no health difference between origin and destination. However, for urban-to-urban migration (blue ​), lower BIC scores are observed when urban origins have lower age-adjusted premature mortality rates than urban destinations, suggesting that movers tend to migrate from healthier urban counties to less healthy urban counties. For rural-to-urban migration, there is some indication that rural origins have higher age-adjusted premature mortality rates compared to their urban destinations, as indicated by the minimum BIC score occurring at . However, the relationship between ​ and BIC score appears to be approximately linear, with all BIC scores remaining close to the minimum, regardless of the value of . Therefore, there is little evidence of health-related selection from rural origins to urban destinations. This is likely because the larger populations in urban counties make their average health less affected by relatively small numbers of migrants from rural counties.

The minimum BIC score occuring at supports the healthy migrant hypothesis, indicating that migrants from urban areas are healthier on average than their urban destinations. Interestingly, although the trends for and are similar, BIC scores are slightly lower for positive values of and slightly higher for negative values of while the pattern in BIC associated with is opposite. This suggests that migrants from rural origins might be slightly less healthy on average compared to their rural destinations, while migrants from urban origins may be slightly healthier on average than their rural destinations. However, since the minimum BIC score occurs when both and are equal to 0, we cannot definitively conclude that health-related factors drive migration from rural to rural or from urban to rural counties. Further detailed analysis focusing specifically on migration to rural destinations could provide deeper insights into these patterns.



### Discussion and Limitations

We consider several pitfalls and alternatives. First, because our migration term is essentially a weighted average of the mortality rates of origin counties, the migration term and lagged mortality rates are highly correlated, resulting in multicollinearity. As a result, we cannot easily interpret the direct effect of the migration term itself. However, its inclusion clearly enhances the model’s overall explanatory power, which is valuable for understanding county-level health.

The use of county-level premature age-adjusted mortality as the outcome of interest offers both strengths and limitations. While this measure allows for comparability across different times and locations and has a robust definition, it does not perfectly align with the demographics of migrating populations. The median age of movers in the US is under 30 years (“S0701: GEOGRAPHIC MOBILITY BY ... - Census Bureau Table,” n.d.), suggesting a potential mismatch since mortality primarily results from chronic diseases with long latency periods. Although previous research indicates that health differences among immigrants can be detected within a relatively short period, applying this to our study assumes similar dynamics for non-infectious diseases (Aart et al. 2017). Nonetheless, county-level measures of premature mortality are widely used as a proxy for overall county health. For example, a 1983 WHO report recommended mortality and morbidity measures to understand health and migration (Gushulak and MacPherson 2006), and length of life measures hold 50% weight in the County Health Rankings Model of place-based health outcomes (“Explore Health Rankings | Rankings Data & Documentation,” n.d.).

Another significant limitation is the reliance on IRS data, which includes only approximately 45% of the total US population (“New Estimates Of How Many Households Pay No Federal Income Tax” 2015; DeSilver 2023). Excluded groups, such as university students, low-income individuals, and informal workers (DeWaard et al. 2022), are systematically missing from our analysis, possibly biasing the results. Despite these limitations, IRS migration data has been used many times in the past to complete complex and accurate analyses of US migration patterns. For instance, IRS migration flow data has been used to estimate the effects of sea-level rise on geographic distribution of the US population (Hauer 2017), measure recovery after Hurricanes Katrina and Rita (Curtis, Fussell, and DeWaard 2015), and assess the economic impacts of migration resulting from environmental hazards (Shumway, Otterstrom, and Glavac 2014).

We attempt to leverage the limitations of the IRS data as a strength in our analyses: because IRS county-to-county migration data includes only individuals who file taxes with the US government both before and after they migrate, we assume that individuals represented in the IRS migration flows data are more homogeneous than migrants excluded from IRS estimates since they may be less likely to have been pushed to migrate by potentially health-related factors such as violence, famine, and corruption than individuals who migrate but are excluded from the IRS data. Therefore, any differences in changes in health between counties may be the result of self-selection by IRS-represented migrants or health-related selection by non-IRS-represented migrants.

Additionally, while the data quality issues identified in the post-2011-2012 IRS migration data are concerning (DeWaard et al. 2022), we believe that the added temporal volatility does not undermine our conclusions. Since our analysis examines the US as a whole and focuses on rural/urban differences, all counties are presumably treated similarly. This uniform treatment across counties suggests that the relative comparisons between rural and urban areas remain valid, and the temporal volatility should not disproportionately affect one type of county over another.

Finally, our data precedes the COVID-19 pandemic, which significantly altered migration patterns and health outcomes. According to the Chicago Federal Reserve Bank, state-to-state moves were 15.1% higher pre-pandemic than during the pandemic (“U.S. Migration Patterns Before and After the Start of the Covid-19 Pandemic - Federal Reserve Bank of Chicago,” n.d.), and rates of domestic migration and international migration decreased in urban counties in 2020 while domestic migration increased in suburban counties in 2020 (“Pandemic Population Change Across Metro America: Accelerated Migration, Less Immigration, Fewer Births and More Deaths,” n.d.). Future studies should consider the pandemic’s impact to provide a more current understanding of migration and health dynamics. Understanding these shifts is crucial for developing policies that address the evolving needs of migrating populations in a post-pandemic world.

### Conclusion

There are many factors that contribute to the health of a place. In our analyses, we have chosen to emphasize the potential impact of migration or movement between places on place-based health. We accounted for intercounty selection for migration (ie some counties are more likely to experience migration than others) using our weighted average migration term and intracounty selection for migration (ie some individuals are more likely to migrate than others) using our simulation. We cannot fully understand county-level health without first understanding county interconnectedness and how it drives place-based health disparities. Recognizing that the United States is heterogeneous and that the mechanisms by which migration may impact health may also be heterogeneous, we attempt to quantify rural-urban differences in the relationship between migration and place-based health. The long-term goal of this work is to contribute to understanding the mechanisms by which mobility may be related to place-based health disparities so that local decision-makers may account for patterns in mobility when creating policy towards improved health for all people in all places. Understanding rural-urban mobility patterns is a necessary first step towards understanding rural-urban health disparities.

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