# Measuring Geographic and Racial Disparities within Counties, An Exploratory Analysis in New York

# Abstract

Appropriate health disparity indices are fundamental to identifying inequities and disparities within geographical areas and are crucial to motivating and informing efforts to reduce and, ultimately, eliminate them. In the absence of publicly accessible and nationally representative individual- or household-level disparity datasets, we proposed approaches to calculate and evaluate county-level disparity indices from tabulated Census Bureau datasets. Using the median household income as an exploratory measure for counties in New York derived from the 2015-2019 5-year American Community Survey, the disparity ratio, Gini index, and Atkinson’s index were calculated using census tract and subpopulation (i.e., race) group data within counties. We evaluated percentage changes and rank order correlations of counties between a census tract, alone, and census tract plus subpopulation model. On average, the census tract model tended to underestimate the level of disparity in a county compared to that from the model with incorporated subpopulation data. The rank order of the three disparity indices was highly correlated with one other and across the two models. The disparity indices were likely penalized by small sizes of counties or subpopulations. Health disparity indices at the county level are urgent population health tools that could connect a missing link in the ongoing efforts to measure and improve community health. Not only calculating disparity indices for each county, but also quantifying the level of disparity as the changes from the census tract model to the subpopulation model would be an informative assessment of the health disparity in counties.

Key words: health disparity; disparity ratio; Gini index; Atkinson’s index; County Health Rankings & Roadmaps, New York

# Introduction

There are stark disparities in health and the factors that influence health between population subgroups in the United States, such as race/ethnicity and socioeconomic status. Many studies at the national, state, and local levels have quantified the variation in health among populations and point to inequitable conditions and outcomes for socially disadvantaged groups. For instance, a recent study documented that not only have the overall trends in the percentage of infants born at low birth weight increased in recent years, but so too have disparities by maternal race and education level.1 Another study reported that the recent trend of mortality fluctuation in the U.S. resulted from mortality disparities among race/ethnicity and age groups.2 These studies imply that because overall population health measures could mask health disparities among subpopulations in communities, it is imperative to simultaneously examine health disparities to identify disadvantages among these subpopulations. However, outside of scientific literature, there is little widely-available data that would allow non-scientific audiences to investigate and understand local health disparities in the context of other community conditions. This is due to a lack of, or inconsistency in, data provision, both across geographic locations and different health-related measures.

Population health improvement platforms across the nation, such as the County Health Rankings & Roadmaps (CHR&R)3,4, are well-positioned to expand upon their current data infrastructure to include more explicit measurement of health disparities in a way that would facilitate meaningful comparisons and advance the understanding and – ideally – the elimination of pervasive health inequities. CHR&R has provided summarized statistics of more than 60 measures covering health outcomes and health factors for the nation’s 3,143 counties annually for more than ten years. Evolving CHR&R and other health platforms to address the goals of the U.S. Department of Health and Human Services’ Public Health 3.0 initiative - that is, leveraging data and resources to address social, environmental, and economic conditions that affect not only overall health but also health equity –could provide communities with actionable information on the state of potential barriers to equitable health for all of their residents.

There are myriad ways to measure health disparities, each with a series of methodological and analytic considerations that are not only tailored to a specific use but also reflect the norms and values of the user.6,7 Although health disparity metrics have been employed by researchers and public health practitioners for years,8,9 there are few examples of their use catered to lay audiences and, to the authors’ knowledge, little or no practical guidance on how to do so most effectively. If publicly-facing health data platforms like CHR&R, for instance, were to incorporate such measures of health disparities into their existing schema and methods of ranking, they would first need to select a subset of measures and then critically evaluate the feasibility of calculating them at the county level for a single health outcome or determinant. Once complete, this information could be used to guide the selection of candidate measures to be developed into a multidimensional measure of health disparities by incorporating multiple health outcomes.

In this paper, we aim to take the first step of calculating county-level disparities indices and assessing their performance using median household income (MHI) as the exploratory health determinant of interest. Specifically, analytic datasets at the household level were generated from overall and race-specific MHI estimates of nationally representative tabulated data. A suite of county-level disparity indices were estimated by census tracts and subpopulations within census tracts from the analytic datasets and then evaluated for agreement using rank order correlations.

# Methods

Data

Data came from the 2015-2019 5-year American Community Survey (ACS), a nationally representative survey conducted by the United States Census Bureau that provides data on the demographic, socioeconomic, and housing characteristics of the U.S. population.[@uscbAmericanCommunitySurveya]

The overall and race-specific MHI and the number of households in each census tract were used to construct analytic datasets of pseudo-populations for calculating disparity indices of counties in the U.S. the measure was selected exploratory because income is one of the most well-estabilished and impactful social determinants of population health.10,11,12,13 For example, in the U.S., the life expectancy of the richest 1% of men was 14.6 years (95% CI, 14.4 to 14.8 years) longer than that of the poorest 1% between 2001 and 2014, and it was 10.1 years (95% CI, 9.9 to 10.3 years) longer for women.[@chettyAssociationIncomeLife2016;@borPopulationHealthEra2017] Furthermore, the procedure for replicating pseudo-populations can be better understood using the MHI measure as an example. The resampling process involves estimating each group’s point estimate a number of times using the point estimate and standard error for each group under a specific distribution, which generates the replicated dataset with a set of resampled estimates.[@HealthyPeopleStatistical2020] When applied to the MHI measure, the dataset can be understood as a pseudo-population with a household as a unit of analysis.

Racial groups were categorized as White, Black, Asian, American Indian and Alaska Native (AIAN), Native Hawaiian and Pacific Islander (NHPI), and a category containing all other racial groups. While data on Hispanic or Latino ethinicty are available from ACS, these data are not separated in the data tables in a way that would allow for a mutually exclusive set of racial groups that were exhaustive of the entire population. Thus, data for all six racial groups included both Hispanic and Latino householders and non-Hispanic and Latino householders.

## Census Tract and Subpopulation Models

This paper proposes constructing pseudo-populations at the household level from tabulated summary statistics to enhance the calculation and assessment of disparity indices of individual- or household-level data. Two pseudo-populations were constructed with a household as a unit of analysis based on the availability of estimates for the overall and race-specific MHI at the census-tract level in the ACS. A census tract model utilized the overall MHI in a census tract as an estimate for each household, whereas the subpopulation model added mutually exclusive race-specific MHI in the census tract. The pseudo-population of the census tract model represents a group of households whose household income is equal to the overall MHI in the census tract, and that of the subpopulation model indicates a group of households whose household income is equal to the race-specific MHI in the census tract. In other words, pseudo-populations in this study are weighted datasets by the number of households in census tracts.

## Disparity Indices

Three common disparity indices, including the disparity ratio, Gini index, and Atkinson’s index, were estimated from pseudo-populations of the census tract and subpopulation models. As indicated by the different definitions, each disparity index captures a unique aspect of disparity.18–21

The disparity ratio, the ratio of any two percentiles, is one of the most common and intuitive indices. For instance, each of the , the , or the ratios indicate where the disproportional distribution disparity is occurring.18,19,22 The ratio index is robust to outliers because it utilizes only two percentile values to capture distributional characteristics. However, it ignores relevant distributional aspects, such as the actual shape of the distribution, potentially mischaracterizing the disparity pattern. The disparity ratio ranges from 1.0 (i.e., no disparity) to any positive value, with larger values indicating higher disparity in communities.

The Gini index is one of the most commonly used disparity indices for income, capturing the average difference between all pairs of incomes in a population.[@lynchIncomeInequalityDeterminant2004a;@lynchIncomeInequalityDeterminant2004] It is based on the ratio of the area under the Lorenz curve (i.e., the observed cumulative distribution) and the area under the diagonal distribution curve. [@lynchIncomeInequalityDeterminant2004a;@lynchIncomeInequalityDeterminant2004]20,23–25 It ranges from 0.0 (i.e., complete equality: every household in a county has the same household income) to 1.0 (i.e., complete inequality: a single household receives all the income in a county), with larger values indicating higher levels of inequality in communities.23[@lynchIncomeInequalityDeterminant2004a;@lynchIncomeInequalityDeterminant2004] The following equation was used to calculate the Gini index for each county, where and are the and household income in a county and is a mean household income.24,25

Another informative disparity index is Atkinson’s index, which captures the degree of disparity to be reduced by an aversion parameter ().20 The magnitude of reflects the degree of aversion to disparity; increasing the magnitude of , Atkinson’s index will be more sensitive to changes in the lower ranked subpopulation in the distribution.20,21 The following equation generalized the Atkinson index () where is the household income in a county and is a mean household income.20,24

This study set the inequality aversion parameter equal to 1.0 (), which is a similar setting to that used in the human development index.9 This index ranges from 0.0 (i.e., exact equality) to 1.0 (i.e., exact inequality). Unlike the Gini index constructed from the difference between two values (i.e., ), Atkinson’s index captures the ratio of each value to the mean (i.e., ).20,21

The percentage changes from the census tract models to the subpopulation models were calculated to quantify the magnitude of change introduced by additional racial heterogeneity.The change in each disparity index between the census tract and subpopulation models represents the amount by which the census tract-level disparity would be reduced if racial disparity within the census tract was eliminated.

Ddisparity are not feasible due to the differences in the metric and interpretation of each disparity index Therefore, Spearman’s rank-order correlation coefficients were calculated to evaluate the comparability and agreement of the rank orders of counties within a state from three disparity indices across two models.

This paper presented results from New York, a state among the worst for within-county income inequality[@ucsbCensusBureauTable2021], but results from other states are available upon request. The 2019 5-year ACS estimates and GIS information were accessed using the Census Bureau application programming interface (API) system.14 R and several , and Spearman’s rank correlation coefficients, and visualize geographic gradients[add R ref]

# Results

Table 1 demonstrates how pseudo-populations for the census tract and subpopulation models were constructed using an example from the most populous census tract in Kings County, New York. A pseudo-population for the census tract model consisted of households with $87,237 as a household income estimate in Census Tract 15. The dataset for the subpopulation model is a collection of a white subpopulation of 1,636 households with a household income of $147,308, a black subpopulation of 1,044 households with a household income of $45,455, an Asian subpopulation of 990 households with a household income of $42,813, and so on. The suppressed numbers of households or MHI estimates were excluded from both models. Figure 1 visualizes the race-specific geographical distributions of household income in New York and Kings County from the replicated household-level datasets.

Three county-level disparity indices of MHI in New York for the census tract and subpopulation models, and the percentage changes between the two models were calculated (Appendix 1). Table 2 summarizes disparity indices of MHI for all counties, the five most populous counties, and tertiles by the number of households. First, for all counties in New York, the average percentage changes of the disparity ratio, Gini, and Atkinson’s index between the census tract and subpopulation models were 0.21%, 2.55%, and 10.60%, respectively. Secondly, in Kings County, the most populous county in New York, the disparity ratio, the Gini index, and Atkinson’s index for the census tract model were 2.03, 0.27, and 0.11, respectively, which increased in the subpopulation model by 19%, 12%, and 23%, respectively. Thirdly, when counties were stratified by the number of census tracts, the average percentage change in Gini and Atkinson’s index between models was the largest in the top tertile, followed by the middle and bottom tertile. Notably, disparity indices in the subpopulation model were smaller than those in the census tract model in some counties (Table 2 and Appendix 1). For instance, in Fulton County, the disparity ratio, Gini, and Atkinson’s index decreased by 1.23%, 3.50%, and 6.35%, respectively, from the census tract to the subpopulation model.

Table 3 summarizes the rank-order coefficient of counties between the three disparity indices across the census tract and subpopulation models. The rank orders of the counties from three disparity indices were highly correlated in both the census tract model (i.e., r > 0.93) and the subpopulation model (i.e., r > 0.93). The agreement of the rank orders from each disparity index between the census tract and subpopulation models was also high (i.e., r > 0.93).

# Discussion

This study utilized an approach for constructing pseudo-populations to calculate a set of county-level disparity indices from MHI using nationally representative ACS datasets, using New York as a case study. Within-county disparities were characterized both as the differences between census tracts (census tract model) and the differences between census tracts accounting for heterogeneity among subpopulations (i.e., racial groups) within tracts (subpopulation model). The agreement of rank orders of individual disparity indices across the census tract and subpopulation models were also calculated to determine if the choice of disparity indices would affect the rank orders of counties.

The magnitudes of the three county-level disparity indices for MHI were generally larger in the subpopulation model than in the census tract model. In the census tract model, where household income only varies by census tracts, disparity indices represent geographic heterogeneity among census tracts within a county. In the subpopulation model, where household income varied by both census tracts and racial subpopulations within a census tract, disparity indices characterize heterogeneity from both geographic and demographic components.

In some counties, however, the percentage changes between the two models were minimal or even negative when a single race dominated most census tracts in a county. For example, the opposite direction of a percentage change was observed in Genesee County and Fulton County, which are similar and comparable in the number of census tracts (i.e., 15 vs. 15) and households (i.e., 22,557 vs. 23,769). Figure 2 visualizes household income distributions by the census tract and subpopulation models for Genesee and Fulton Counties. In Genesee County, race-specific MHI reduced the concentration of households near the mean MHI of each census tract (i.e., census tract-specific MHI) and thus increased the variability of household income within the county. In contrast, in Fulton County, race-specific MHI did not reduce the concentration of households near the mean MHI of each census tract, resulting in a similar household income distribution to that of the census tract model. This situation would be particularly observed when a single race dominated most census tracts in counties, as in Fulton County.

The rank orders from the disparity ratio, Gini, and Atkinson’s index were highly correlated, implying that any choice of disparity index would be expected to provide similar information regarding the level of disparity within counties. Thus, the preference of one disparity index over another for capturing health disparity may be determined by other external factors, such as interpretability and communicability. The disparity ratio is the most intuitive index, being easy to communicate and providing directly interpretable and actionable information. However, it does not capture all distributional characteristics of the measure because it utilizes only two percentile values. On the other hand, while the Gini index or Atkinson’s index may not be directly interpretable and as easily communicated, they capture more of the distributional characteristics than the disparity index.

This study has a few limitations. Firstly, it only evaluated disparities in a single social determinant of population health, MHI. The intention is not to oversimplify the complex nature of population health with a single MHI measure, but rather to provide an easier way to clarify the resampling process. The replication of MHI estimates by the number of households can be seen as creating a pseudo-population with a household as a unit, while the same procedure for most health measures, such as obesity rates, would be seen as a collection of estimates from a resampling process. Another paper that includes a variety of health determinants and outcomes is being prepared[@parkCharacterizingWithincountyHealth2023]. Secondly, geographic dependency, small area estimation, and data suppression are all essential considerations in studies on community health[@zhangMultilevelRegressionPoststratification2014;@zhangValidationMultilevelRegression2015a], but the approach in this study did not take these issues into account. The observed gradients of disparity indices by tertiles indicated that small area estimates are still relevant, and suppressed race-specific MHI and household sizes were excluded from the analysis. Future studies should aim to incorporate these issues during the data replication process.

Despite its limitations, this study is one of the few that utilized pseudo-populations in calculating and evaluating measures of total disparity from tabulated estimates in nationally representative survey datasets. Although measures of total disparity provide an essential context for understanding the decomposition of health disparity measures across a population of individuals or households in a community, they are less informative about systematic disparities in health among subpopulations than measures that include sociodemographic-group disparity.[@gakidouDefiningMeasuringHealth2000;@gakidouMeasuringTotalHealth2002;@harperMethodsMeasuringCancer2010]. Our approach overcame this limitation by employing dedicated pseudo-populations of households with geographic-specific MHI (i.e., the census tract model) and race-geographic-specific MHI (i.e., the subpopulation model), which were used to estimate disparity indices to determine the sources and magnitude of disparities in a county, as well as the agreement of rank orders across disparity indices and models. Further, the approach can be easily applied to other health measures and tabulated nationally representative datasets, providing an opportunity to characterize total disparity in communities even in the absence of datasets at the individual or household level.

## Conclusions

Data-to-action platforms have established a ‘communities matter’ framework using absolute metrics for the population health factors and outcomes from nationally representative datasets. Unfortunately, relative metrics for health disparity in a county that can serve the same purpose have not yet been established. Thus, health disparity indices are urgent population health tools that could connect a missing link in the ongoing efforts to measure and improve community health.

This study proposed an approach to utilize tabulated summary estimates in replicating pseudo-populations to estimate health disparity indices in counties, for both census tract-level and futher subpopulation (i.e., race) level data, and then evaluated the performance of each model in terms of the rank orders of counties. Our approach is immediately applicable to public communication and to intervene in geographic disparities conveyed by inequality across subpopulations. Further studies should aim to fill the gaps in conceptualizing and measuring health disparity and the methodological obstacles due to limited data availability.

Figure 1. Geographic and Racial Disparities in Median Household Income, Kings County, New York

* Overall and Race-specific Median Household Income, the State of New York

A screenshot of a map

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* Overall and Race-specific Median Household Income, Kings County in New York

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Figure 2. Comparison of the Census Tract and Subpopulation Models across Two Similar Counties, Genesee and Fulton County, New York

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Table 1. Median Household Income Estimates for the Census Tract and Subpopulation Models, Kings County, New York

| Census tract | Race | N. of households | MHIa | MHI by racesb |
| --- | --- | --- | --- | --- |
| Census Tract 15 | White | 1,636 | 87,237 | 147,308 |
| Census Tract 15 | Black | 1,044 | 87,237 | 45,455 |
| Census Tract 15 | AIAN | 14 | 87,237 | n.a |
| Census Tract 15 | Asian | 990 | 87,237 | 42,813 |
| Census Tract 15 | NHPI | 13 | 87,237 | n.a |
| Census Tract 15 | Other | 330 | 87,237 | 47,545 |
| aEstimates used for census tract models. | | | | |
| bEstimates used for subpopulation models. | | | | |
| Abbreviations: MHI (Median household income); AIAN (American Indian and Alaska Native); NHPI (Native Hawaiian and Pacific Islander); n.a (not available) | | | | |
| Source: The 2015 - 2019 5-year American Community Survey | | | | |

Table 2. The Changes of Disparity Indices between the Census Tract and Subpopulation Models

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | Census Tract Models | | | Subpopulation Models | | | Change (%) | | |
| Group | Ratio | Gini | Atkinson | Ratio | Gini | Atkinson | Ratio | Gini | Atkinson |
| All Counties | 1.46 | 0.13 | 0.03 | 1.44 | 0.13 | 0.03 | 0.21 | 2.55 | 10.6 |
|  |  |  |  |  |  |  |  |  |  |
| Top 5 populous counties | | | | | | | | | |
| Kings | 2.03 | 0.27 | 0.11 | 2.41 | 0.3 | 0.14 | 19.08 | 12.15 | 23.46 |
| Queens | 1.59 | 0.16 | 0.05 | 1.7 | 0.19 | 0.06 | 6.58 | 15.45 | 32.75 |
| New York | 2.88 | 0.29 | 0.15 | 3.35 | 0.3 | 0.17 | 16.21 | 3.68 | 15.81 |
| Bronx | 2.16 | 0.26 | 0.1 | 2.45 | 0.28 | 0.12 | 13.29 | 9.54 | 21.79 |
| Suffolk | 1.55 | 0.14 | 0.03 | 1.51 | 0.15 | 0.04 | -2.45 | 5.1 | 14.62 |
|  |  |  |  |  |  |  |  |  |  |
| Tertile by the number of census tracts | | | | | | | | | |
| Top | 1.9 | 0.19 | 0.07 | 1.86 | 0.2 | 0.07 | -0.12 | 5.02 | 13.79 |
| Middle | 1.44 | 0.12 | 0.03 | 1.41 | 0.12 | 0.03 | -0.42 | 1.77 | 8.88 |
| Bottom | 1.27 | 0.08 | 0.01 | 1.26 | 0.08 | 0.01 | 0.6 | 1.22 | 3.46 |

Source: Authors' calculations using the 2015 - 2019 5-year American Community Survey

Double-check numbers.

- (percentage changes for each counties; and then calculated the mean of all and each categories; therefore, it is not directly calculated using the values in Table 2)

- Top 5 should have the same values in the table.

- Add two counties as a example

Table 3. The Rank-Order Correlation Coefficients by Disparity Indices and Models

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
|  | | Census Tract Models | | | Subpopulation Models | | |
|  |  | Ratio | Gini | Atkinson | Ratio | Gini | Atkinson |
| Census Tract Model | Ratio |  |  |  |  |  |  |
|  | Gini | 0.95 |  |  |  |  |  |
|  | Atkinson | 0.94 | 0.99 |  |  |  |  |
| Subpopulation Models | Ratio | 0.98 | 0.94 | 0.93 |  |  |  |
|  | Gini | 0.94 | 0.99 | 0.99 | 0.94 |  |  |
|  | Atkinson | 0.93 | 0.98 | 0.99 | 0.93 | 0.99 |  |

Source: Authors' calculations using the 2015 - 2019 5-year American Community Survey

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Appendix 1. The Changes of Disparity Indices between the Census Tract and Subpopulation Models in the State of New York

|  | | | Census Tract Models | | | Subpopulation Models | | | Change (%) | | |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| County | n of tract | n of households | Ratio | Gini | Atkinson | Ratio | Gini | Atkinson | Ratio | Gini | Atkinson |
| Albany | 74 | 126,525 | 1.97 | 0.20 | 0.07 | 2.06 | 0.21 | 0.08 | 4.51 | 5.38 | 15.15 |
| Allegany | 12 | 17,947 | 1.10 | 0.03 | 0.00 | 1.10 | 0.04 | 0.00 | 0.04 | 7.04 | 47.45 |
| Bronx | 326 | 502,569 | 2.16 | 0.26 | 0.10 | 2.45 | 0.28 | 0.12 | 13.29 | 9.54 | 21.79 |
| Broome | 55 | 78,549 | 1.85 | 0.18 | 0.06 | 1.75 | 0.18 | 0.07 | -5.60 | 0.20 | 22.28 |
| Cattaraugus | 20 | 31,779 | 1.21 | 0.10 | 0.02 | 1.26 | 0.10 | 0.02 | 4.12 | 4.71 | 11.76 |
| Cayuga | 19 | 31,221 | 1.64 | 0.15 | 0.04 | 1.68 | 0.14 | 0.04 | 2.74 | -2.34 | -4.42 |
| Chautauqua | 34 | 52,981 | 1.54 | 0.12 | 0.03 | 1.49 | 0.12 | 0.03 | -2.95 | -1.16 | 2.57 |
| Chemung | 21 | 33,989 | 1.80 | 0.18 | 0.06 | 1.77 | 0.19 | 0.07 | -1.41 | 3.04 | 12.75 |
| Chenango | 12 | 20,697 | 1.30 | 0.08 | 0.01 | 1.34 | 0.08 | 0.01 | 2.52 | 4.52 | 10.66 |
| Clinton | 18 | 31,301 | 1.34 | 0.11 | 0.02 | 1.36 | 0.11 | 0.02 | 1.38 | 2.04 | 10.31 |
| Columbia | 21 | 24,966 | 1.37 | 0.11 | 0.02 | 1.41 | 0.12 | 0.03 | 3.51 | 3.69 | 10.54 |
| Cortland | 12 | 17,745 | 1.64 | 0.13 | 0.03 | 1.67 | 0.13 | 0.03 | 1.46 | -5.00 | -8.70 |
| Delaware | 13 | 18,968 | 1.22 | 0.06 | 0.01 | 1.21 | 0.06 | 0.01 | -0.88 | -0.94 | 12.24 |
| Dutchess | 76 | 108,395 | 1.72 | 0.17 | 0.05 | 1.70 | 0.18 | 0.06 | -1.40 | 5.81 | 13.79 |
| Erie | 230 | 389,557 | 2.02 | 0.22 | 0.09 | 1.86 | 0.22 | 0.09 | -7.89 | -0.37 | 3.93 |
| Essex | 13 | 15,790 | 1.23 | 0.06 | 0.01 | 1.14 | 0.05 | 0.00 | -7.05 | -10.29 | -13.05 |
| Franklin | 14 | 19,015 | 1.25 | 0.09 | 0.02 | 1.27 | 0.10 | 0.02 | 1.11 | 6.52 | 14.42 |
| Fulton | 15 | 22,557 | 1.38 | 0.11 | 0.02 | 1.37 | 0.11 | 0.02 | -1.23 | -3.50 | -6.35 |
| Genesee | 15 | 23,759 | 1.36 | 0.09 | 0.02 | 1.37 | 0.11 | 0.02 | 1.08 | 10.89 | 30.63 |
| Greene | 14 | 17,100 | 1.41 | 0.11 | 0.02 | 1.44 | 0.11 | 0.02 | 1.84 | 5.25 | 7.04 |
| Hamilton | 4 | 1,157 | 1.23 | 0.07 | 0.01 | 1.23 | 0.07 | 0.01 | -0.19 | -0.20 | -0.20 |
| Herkimer | 19 | 24,524 | 1.46 | 0.11 | 0.02 | 1.41 | 0.11 | 0.02 | -3.27 | 1.72 | 8.88 |
| Jefferson | 24 | 42,734 | 1.54 | 0.13 | 0.03 | 1.55 | 0.13 | 0.03 | 0.58 | 1.77 | 2.31 |
| Kings | 745 | 956,744 | 2.03 | 0.27 | 0.11 | 2.41 | 0.30 | 0.14 | 19.08 | 12.15 | 23.46 |
| Lewis | 7 | 10,247 | 1.06 | 0.03 | 0.00 | 1.06 | 0.03 | 0.00 | 0.38 | 17.39 | 59.28 |
| Livingston | 13 | 24,176 | 1.46 | 0.10 | 0.02 | 1.38 | 0.10 | 0.02 | -5.65 | -1.84 | -0.17 |
| Madison | 16 | 25,877 | 1.32 | 0.12 | 0.02 | 1.36 | 0.12 | 0.03 | 2.60 | 2.63 | 9.06 |
| Monroe | 188 | 300,960 | 2.11 | 0.23 | 0.09 | 1.97 | 0.23 | 0.10 | -6.55 | 1.35 | 8.21 |
| Montgomery | 16 | 19,660 | 1.74 | 0.14 | 0.04 | 1.75 | 0.15 | 0.05 | 0.69 | 7.43 | 31.73 |
| Nassau | 272 | 443,236 | 1.49 | 0.16 | 0.04 | 1.58 | 0.17 | 0.05 | 5.81 | 8.27 | 22.29 |
| New York | 273 | 751,154 | 2.88 | 0.29 | 0.15 | 3.35 | 0.30 | 0.17 | 16.21 | 3.68 | 15.81 |
| Niagara | 60 | 88,519 | 1.82 | 0.19 | 0.07 | 1.75 | 0.19 | 0.07 | -4.18 | -1.31 | 1.47 |
| Oneida | 68 | 89,705 | 1.90 | 0.19 | 0.07 | 1.77 | 0.18 | 0.07 | -6.65 | -1.83 | -1.54 |
| Onondaga | 138 | 185,134 | 1.87 | 0.22 | 0.09 | 1.90 | 0.22 | 0.09 | 1.41 | 0.84 | 6.58 |
| Ontario | 25 | 44,787 | 1.49 | 0.14 | 0.03 | 1.47 | 0.15 | 0.04 | -1.19 | 2.44 | 8.72 |
| Orange | 79 | 128,016 | 1.90 | 0.19 | 0.07 | 1.88 | 0.20 | 0.07 | -1.36 | 2.94 | 10.73 |
| Orleans | 10 | 16,563 | 1.37 | 0.09 | 0.01 | 1.26 | 0.08 | 0.01 | -8.37 | -2.72 | -5.19 |
| Oswego | 29 | 46,079 | 1.42 | 0.11 | 0.02 | 1.42 | 0.11 | 0.02 | -0.50 | -1.79 | -4.24 |
| Otsego | 16 | 23,400 | 1.13 | 0.08 | 0.02 | 1.15 | 0.08 | 0.02 | 1.08 | 9.39 | 31.59 |
| Putnam | 19 | 34,854 | 1.28 | 0.07 | 0.01 | 1.31 | 0.09 | 0.01 | 1.96 | 22.17 | 76.91 |
| Queens | 640 | 778,846 | 1.59 | 0.16 | 0.05 | 1.70 | 0.19 | 0.06 | 6.58 | 15.45 | 32.75 |
| Rensselaer | 42 | 64,906 | 1.78 | 0.17 | 0.05 | 1.87 | 0.17 | 0.06 | 5.38 | -0.59 | 7.31 |
| Richmond | 106 | 165,824 | 1.49 | 0.16 | 0.06 | 1.49 | 0.17 | 0.07 | -0.12 | 5.99 | 20.18 |
| Rockland | 65 | 100,438 | 2.20 | 0.21 | 0.08 | 2.33 | 0.22 | 0.09 | 5.75 | 5.02 | 12.54 |
| Saratoga | 49 | 94,402 | 1.45 | 0.12 | 0.03 | 1.53 | 0.13 | 0.03 | 5.81 | 6.82 | 12.64 |
| Schenectady | 43 | 54,302 | 1.99 | 0.23 | 0.09 | 1.94 | 0.22 | 0.09 | -2.59 | -0.19 | 2.33 |
| Schoharie | 7 | 12,559 | 1.19 | 0.06 | 0.00 | 1.21 | 0.06 | 0.01 | 1.43 | 16.57 | 108.29 |
| Schuyler | 5 | 7,324 | 1.29 | 0.06 | 0.01 | 1.27 | 0.06 | 0.01 | -1.07 | -3.42 | -5.59 |
| Seneca | 10 | 13,564 | 1.18 | 0.06 | 0.01 | 1.19 | 0.06 | 0.01 | 0.51 | -3.21 | -1.71 |
| St. Lawrence | 26 | 41,928 | 1.37 | 0.11 | 0.02 | 1.37 | 0.12 | 0.02 | -0.37 | 3.63 | 8.80 |
| Steuben | 30 | 39,861 | 1.34 | 0.12 | 0.03 | 1.32 | 0.13 | 0.03 | -1.24 | 1.25 | 12.87 |
| Suffolk | 321 | 488,105 | 1.55 | 0.14 | 0.03 | 1.51 | 0.15 | 0.04 | -2.45 | 5.10 | 14.62 |
| Sullivan | 24 | 28,184 | 1.64 | 0.17 | 0.04 | 1.71 | 0.17 | 0.05 | 3.92 | 2.47 | 13.89 |
| Tioga | 10 | 20,030 | 1.36 | 0.13 | 0.03 | 1.34 | 0.13 | 0.03 | -1.07 | -0.69 | -2.30 |
| Tompkins | 22 | 39,600 | 1.46 | 0.14 | 0.05 | 1.34 | 0.14 | 0.06 | -8.36 | 5.71 | 17.01 |
| Ulster | 47 | 69,320 | 1.54 | 0.13 | 0.03 | 1.45 | 0.14 | 0.04 | -5.80 | 6.62 | 24.27 |
| Warren | 19 | 28,015 | 1.27 | 0.13 | 0.03 | 1.25 | 0.12 | 0.03 | -1.23 | -4.04 | -9.58 |
| Washington | 17 | 24,014 | 1.27 | 0.09 | 0.01 | 1.26 | 0.09 | 0.01 | -0.93 | -4.04 | -7.95 |
| Wayne | 22 | 36,720 | 1.44 | 0.11 | 0.02 | 1.43 | 0.12 | 0.02 | -0.42 | 0.41 | 20.23 |
| Westchester | 209 | 335,775 | 2.28 | 0.27 | 0.11 | 2.40 | 0.28 | 0.13 | 5.15 | 4.46 | 11.77 |
| Wyoming | 11 | 15,917 | 1.18 | 0.07 | 0.01 | 1.22 | 0.07 | 0.01 | 2.75 | -2.60 | -6.41 |
| Yates | 5 | 8,919 | 1.17 | 0.06 | 0.01 | 1.22 | 0.06 | 0.01 | 3.89 | 2.72 | -0.13 |
| Source: Authors' calculations using the 2015 - 2019 5-year American Community Survey | | | | | | | | | | | |