



# The Impact of US County-Level Factors on COVID-19 Morbidity and Mortality

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**Abstract** The effect of socio-economic factors, ethnicity, and other factors, on the morbidity and mortality of COVID-19 at the *sub-population*-level, rather than at the *individual* level, and their temporal dynamics, is only partially understood. Fifty-three county-level features were collected between 4/2020 and 11/2020 from 3,071 US counties from publicly available data of various American government and news websites: ethnicity, socio-economic factors, educational attainment, mask usage, population density, age distribution, COVID-19 morbidity and mortality, presidential election results, and ICU beds. We trained machine learning models that predict COVID-19 mortality and morbidity using county-level features and then performed a SHAP value game theoretic importance analysis of the predictive features for each model. The classifiers produced an AUROC of 0.863 for morbidity prediction and an AUROC of 0.812 for mortality prediction. A SHAP value-based analysis indicated that poverty rate,

obesity rate, mean commute time, and mask usage statistics significantly affected *morbidity* rates, while ethnicity, median income, poverty rate, and education levels heavily influenced *mortality* rates. Surprisingly, the correlation between several of these factors and COVID-19 morbidity and mortality gradually shifted and even reversed during the study period; our analysis suggests that this phenomenon was probably due to COVID-19 being initially associated with more urbanized areas and, then, from 9/2020, with less urbanized ones. Thus, socio-economic features such as ethnicity, education, and economic disparity are the major factors for predicting county-level COVID-19 mortality rates. Between counties, low variance factors (e.g., age) are *not* meaningful predictors. The inversion of some correlations over time can be explained by COVID-19 spreading from urban to rural areas.

**Keywords** Coronavirus · Disparities · Vulnerability · Ethnicity · Socio-economic · Temporal distribution · Urbanity

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Nevo Itzhak and Tomer Shahar contributed equally to this work and should be considered as co-first authors.

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## Introduction

Since December 2019, the novel coronavirus disease 2019 (COVID-19) has spread rapidly around the globe, infecting millions, leading to severe illness, hospitalization, admission to intensive care units (ICUs) [11], and death. In the USA, more than

20 million people have been infected, and some 400,000 died from COVID-19.

Individual patient predictors include age, gender, and ethnicity [10, 12, 17].

However, both infection and death rates vary highly among different countries and regions and are not easy to predict [9].

It is important to comprehend the population-level factors affecting morbidity and mortality due to COVID-19, to better appreciate the effect of various interventions, prepare for expected morbidity and mortality in different regions, and apply the preventive and therapeutic measures most appropriate for each site (e.g., vaccination).

Population density does not seem to be linked with COVID-19 morbidity or mortality in the UASA [6] and China [19] but has been linked in countries such as India [2]. A few studies have found that prolonged exposure to poor air quality may lead to more COVID-19 deaths [21]. Other researchers, such as Chang et al. [7], demonstrated that a small minority of *superspreader* crowded points of interest, such as restaurants and grocery stores, account for a large majority of the infections. Higher infection rates among disadvantaged racial and socio-economic groups seemed to result solely from differences in mobility, due to lack of ability to work from home.

The spread of COVID-19 at the county-level for the USA was also studied by assessing the counties' vulnerability [5, 20] or by assessing the effect of county-level features [15, 16, 18]. Statistical analysis was the popular approach [5, 15, 18]; however, some studies used a machine learning approach [16, 20]. Counties with a larger percentage of racial and ethnic minorities were affected the most [15, 16, 18]. Millett et al. [15] found that counties with a large percentage (greater than 13%) of African Americans accounted for more than half of the cases and deaths nationally. Cahill et al. [5] found that counties with a lower *case fatality rate* (CFR) had a greater proportion of the population reporting having two or more races. However, no significant differences were found between high and low CFR counties with respect to the mean income or poverty rate.

Most studies used a *subset* of the features we are analyzing in the current study; none contain *all* of the ethnicity, socio-economic, epidemiological factors, population density, and population age features, as

well as additional features, such as mask usage and even presidential election results.

Two studies comparable to ours also adopted machine learning approaches. Tiwari et al. [20] built a machine learning model to measure county-level vulnerability and then overlaid the vulnerability map on county-level features, such as on the racial minority population percentage data. Paul et al. [16], like us, examined factors that contribute to COVID-19 prevalence or death rate using machine learning and then an approach inspired by game theory to calculate the features' importance. Unlike us, these authors solved the task using *regression* instead of *classification*.

Our study's goals were:

1. Determine, using a machine learning approach, coupled with a method inspired by game theory, the relative impact of a large number of static factors, such as ethnicity, socio-economic status, and self-reported behavior, on sufficiently accurate machine learning models that we have built, for the prediction of COVID-19 *morbidity* and *mortality* for any county in the USA at any time.
2. Determine how the aforementioned impact varies over *time* and the trends characterizing the varying importance. (Note: we did not try to *predict* any *future* COVID-19 morbidity or mortality rates. Our approach is purely classification-based.)

## Materials and Methods

The USA is comprised of 3,243 counties; we have gathered COVID-19-related data for the 3,071 counties for which all the features were publicly available.

Specifically, we gathered ethnicity, socio-economic (e.g., income, mode of transportation), educational attainment, epidemiological factors, ICU bed availability, mask usage, presidential election results, population density, and age and gender distribution across multiple age groups.

The data were extracted from multiple sources. The full list of data types and of their sources appears in the Supplementary Materials.

Our goal was to assess the relative importance of the features and examine their impact on the classification of each county's morbidity and mortality rates. To do this, we trained two separate classification

models: one for predicting the morbidity rate and one for predicting the mortality rate, in any given county. We treated the task as a *binary classification* problem. A county in the top quartile of morbidity rates (5.8% or higher) was labeled as “high morbidity,” otherwise as “low morbidity.” Similarly, a county in the top quartile of mortality rates (0.1% or higher) received a label of “high mortality,” otherwise “low mortality.”

Morbidity and mortality rates across the USA can be viewed in the Supplementary Materials.

Both COVID-19 morbidity and mortality classification models were induced using a random forest algorithm [4]. We used hyperparameter optimization to fit the best parameters to our model, using a tenfold cross-validation.

The details of inducing the classification model are provided in the Supplementary Materials.

Once the model converged, and we confirmed that it achieved a sufficiently high accuracy score, a *SHapley Additive exPlanations* (SHAP) [13] computation, inspired by an established game theory result that determines the importance of different players in various coalitions, was used to determine the absolute impact (and direction of influence) of different variables on the classification models’ output, through a tenfold cross-validation. A SHAP value computation is highly useful for assigning importance values to a complex classification or prediction model. In general, the SHAP values reveal, in a linear, additive fashion, by how much a given feature changed the model’s prediction, and in which direction.

The details of building the SHAP model are provided in the Supplementary Materials.

## Results

After removing highly correlated features such as the percentage of females and males, the median male age and median total age, and voting statistics for the democratic and liberal parties, the dataset used, representing the integrated data of 3,071 counties, included 53 features. The random forest morbidity and mortality classification models we have built were based on these features.

The model that predicted the morbidity level resulted in an *area under the ROC curve* (AUROC) of 0.863 and an *area under the precision-recall curve*

(AUPRC) of 0.697. (See Supplementary Materials for evaluation metrics’ details.)

The model that predicted the mortality rates resulted in an AUROC of 0.812 and an AUPRC of 0.629.

Thus, we considered both models as sufficiently accurate for the impact weights to be meaningful.

Figure 1 presents the SHAP summary output, which shows the impact of the features on the COVID-19 morbidity (Fig. 1a) and mortality (Fig. 1b) models that were induced, on all of the individual instances of all counties on which the model was tested. The figure sorts the features in a top-down fashion by the absolute sum of the SHAP value magnitudes over all samples and uses the SHAP values to show the distribution of the impacts each feature has on each model output. Only the top twenty features are presented; the rest were less impactful.

The colors correspond to the *value* of each instance of the feature, red being the highest and blue being the lowest. For example, in the case of *mortality* (Fig. 1b), one can see a county with a very *low* percentage (i.e., colored as deep blue) of Caucasian people, which had produced an impact SHAP value of approximately +0.15. Since +0.15 is a (relatively) large and positive value, that feature contributed to a *high* likelihood for that particular county instance being classified by the model as having a “high mortality” label.

Three out of the top five highest impact features within the *morbidity* model (see Fig. 1a) were related to wearing a mask. *Always wearing a mask* correlated *negatively* with morbidity; other mask-wearing modes were correlated positively with it.

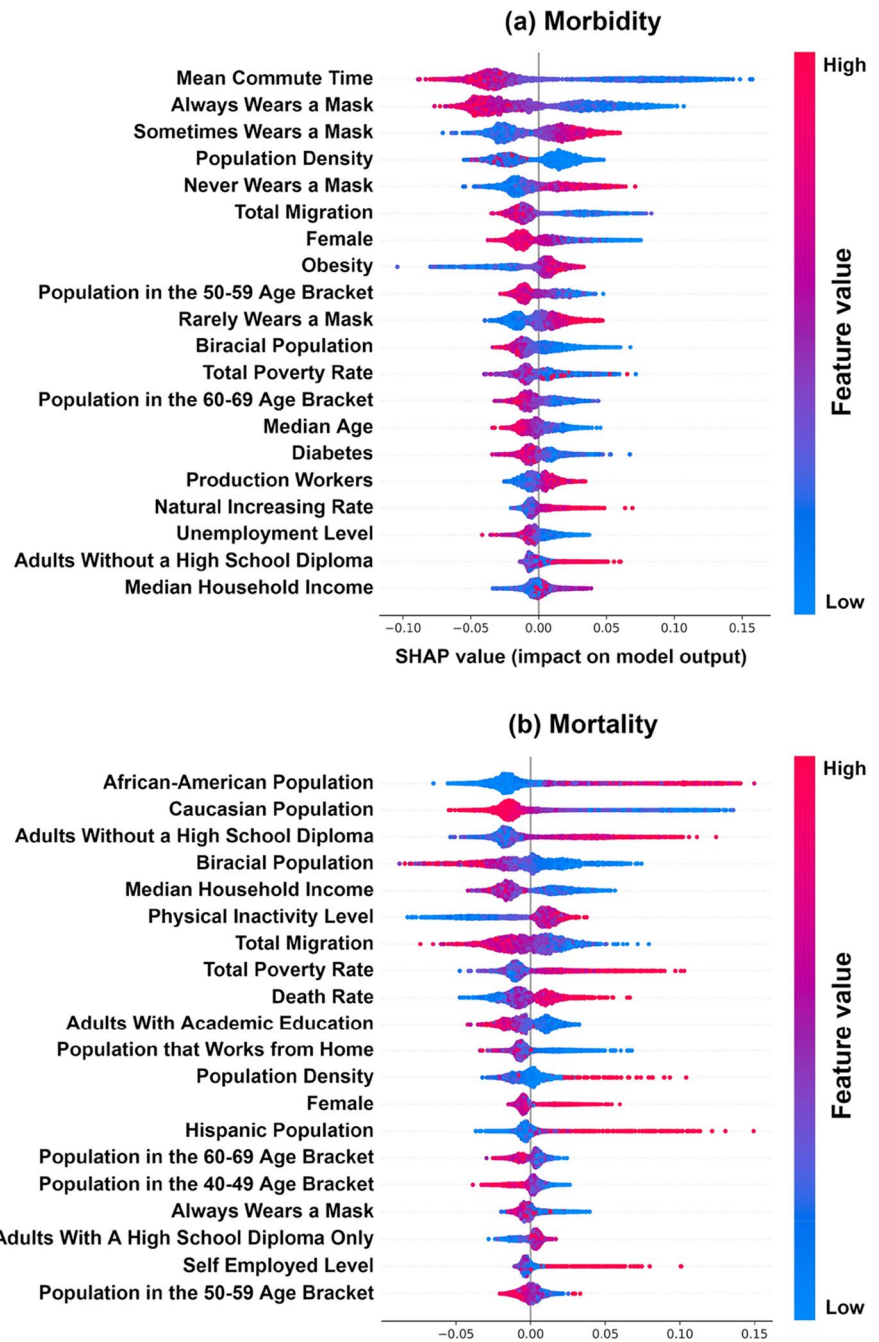
The *mean commute time* had a very high impact on the morbidity model. It was surprisingly *negative*; one would predict that having people travel long distances in public transportation might *increase* COVID-19 cases, as noted in other studies [7].

We shall soon examine such surprising results in more detail.

*Population density*, a feature with a higher value in metropolitan counties and lower for rural ones, also had a surprisingly negative impact on morbidity prediction.

*Total migration* describes how many people entered or left the county in 2019. Like population density, this is a feature associated with larger cities, since they often enjoy positive migration rates

**Fig. 1** SHAP summary output of the morbidity and mortality classification models. SHAP=SHapley Additive exPlanations. SHAP summary output of the COVID-19 morbidity classification model (a) and mortality classification model (b). Features are sorted by the absolute sum of their SHAP magnitude value, the top features being the most impactful



(i.e., more people enter the city than leave). Again, the correlation of lower migration rates with higher morbidity seems initially quite surprising.

The percentage of females in the county had a negative impact, in which *higher* values resulted in *lower* morbidity rates and vice versa.

Obesity had a slightly positive but mostly a large negative impact, on morbidity.

The production-worker percentage, natural increasing [growth] rate (the difference between the birth rate and death rate), and percentage of adults

without a high school diploma positively affected morbidity.

For the COVID-19 *mortality* model (see SHAP summary output in Fig. 1b), the most (positively) impacting feature was the African American percentage.

The *education level* of the county's citizens was an important factor: next to ethnicity, the most (positively) impacting feature was the rate of adults *without* a high school diploma.

Lower median household incomes and lower total migrations had a negative impact on mortality prediction. As in the case of migration, household income tends to be higher in urban counties [3].

Total poverty rates had a strong positive impact on the mortality model, indicating that counties with a higher percentage of poor citizens suffered more deaths.

The *death rate* feature (the proportional mortality rate that the county had experienced in 2019) had a somewhat high impact.

Working from home, always wearing a mask, and population between 4069 had a negative impact on the mortality model; population density, female percentage, and people who are self-employed had a positive impact on it.

Our results suggest a strong influence of ethnicity, socio-economic state, and self-reported mask-wearing, on county morbidity and especially mortality rates.

However, the other, more surprising results suggest the need for examining the data from an additional aspect: *time*.

#### Behavior of Morbidity and Mortality Predictors over Time

Since the beginning of the pandemic, COVID-19 has been suspected to hit harder the lower-income population, and indeed, most of our results confirm this suspicion.

However, when analyzing, using the same computational methodology (machine learning and then calculation of SHAP impact values), the same data types, but at *different time points along 2020*, starting from April 2020, it becomes clear that some features behave similarly even as more data becomes available, while others seem to have an *inverse* impact on morbidity or mortality than the one they started with.

Several socio-economic features, such as total poverty rates or percentage of African Americans in the population, seem to have an essentially similar impact on the model's predictions over time, in this case, a high and positive impact on the morbidity and mortality predictions, respectively.

Other features, however, seem to change over time both their absolute impact and its *direction* of influence (Fig. 2).

The most striking “flipping sides” factor is the *mean commute time* (Fig. 2a) — a feature describing the average time it takes for people to arrive at work. In early August 2020, the value of this feature had a low but positive impact on the number of COVID-19 cases. However, when calculated using data collected up to November 28th, 2020, the correlation is in the opposite direction: now, higher commute times are associated with *lower* morbidity rates), and this feature now provides the highest absolute impact on the morbidity model.

Figure 2a presents the Pearson correlation, over time, between the *mean commute time* feature and the percentage of COVID-19 cases in the county. We can clearly see the positive correlation with COVID-19 cases *until the beginning of September*. It then decreases quickly and flips to actually become negative and even considerably so.

We analyzed similarly all features correlated with morbidity and mortality since April 1st, 2020, until November 28th, 2020. Several of these are exemplified in Fig. 2.

Like the mean commute time, multiple features presented a similar correlation direction (positive or negative) from the April 1st until approximately *September 1st*. Then, numerous features rapidly decreased their correlation with the morbidity outcome, sometimes even completely flipping the correlation's direction.

Other features maintained their consistent impact, though it might have changed its magnitude. For example, the correlation between the percentage of African Americans in a county and the mortality reached its peak during September (+0.5) and by November 28th dropped to +0.3 (Fig. 2f).

Note that the USA experienced a surge of COVID-19 cases around mid-October. Combined with the fact that features altered their correlation only slightly earlier, it is likely that a gradual process occurred, which by September had changed the typical profile of the



**Fig. 2** Pearson correlations between the most impactful features and the percentage of morbidity and mortality. The Pearson correlations between the five most impactful features for each model and the percentage of morbidity (a– e) and mortality (f–j). The features are sorted such that the more impactful ones are higher (i.e., a and f are the most impactful for the morbidity and mortality model, respectively). The correlation is plotted over time, from April 1st until the November 28th

counties that are characterized by relatively high COVID-19 morbidity.

We suspect that this *correlation reversal* is related to how *rural* or *urban* each county is — in the *beginning* of the pandemic, *highly urban* states such as New York and New Jersey bore the brunt of the virus. Later on, less densely populated states such as North Dakota, South Dakota, Iowa, and Nebraska had experienced a rise of COVID-19 cases and were found to have the highest numbers, relative to population size.

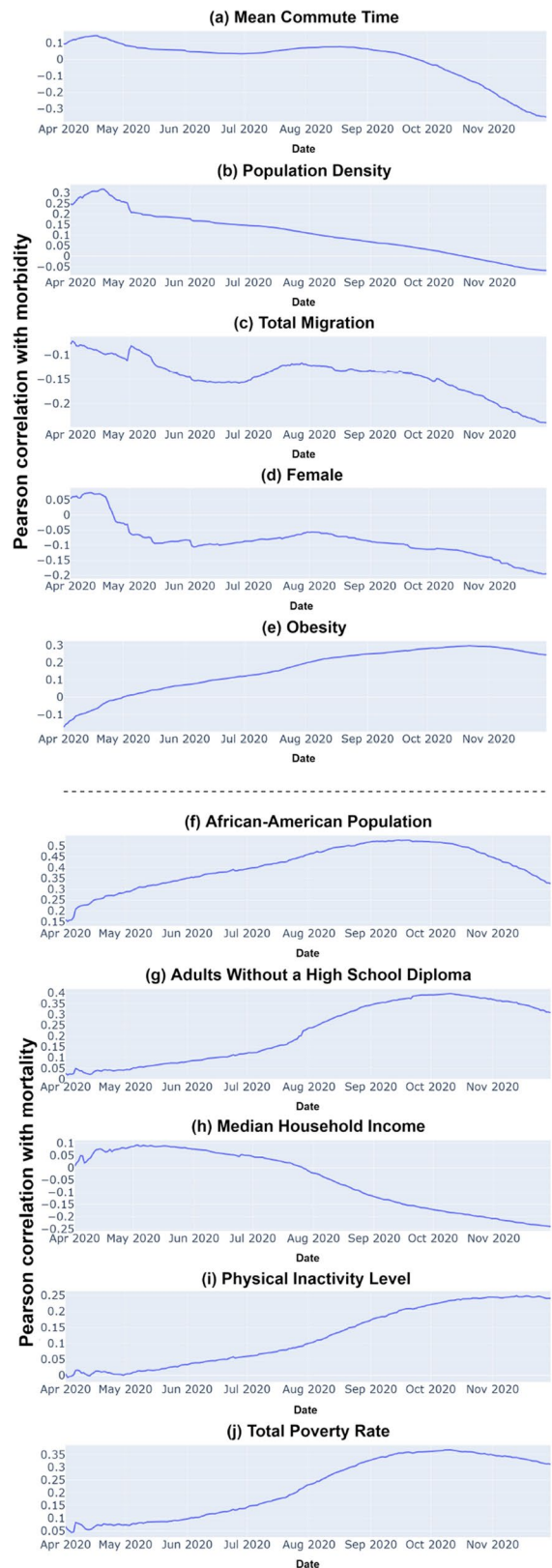
*Urbanity and Ruralness of Affected Counties over Time*

We can test this theory by referring to a classification scheme used by the US Department of Agriculture Economic Research Service (USDA) named *Rural–Urban Continuum Codes* (RUCC) [8]: the USDA assigns each county in the USA an RUCC value from 1 to 9, representing how urban or rural it is based on the county’s own population and the population of adjacent counties. An RUCC of one represents the most “urban” counties (metro areas with a population of 1 million or more); an RUCC of nine represents the most “rural” counties (less than 2,500 population, not adjacent to a metro area). Typically, counties with an RUCC of 1 to 3 are considered metropolitan and comprise approximately 37% of the counties in the USA, while counties with an RUCC of 4 to 9 are considered non-metropolitan and comprise 63% of the counties in the USA.

The total RUCC distribution can be found in the Supplementary Materials.

Our analysis shows that counties in the top quartile of “mean commute time” values have *lower* RUCC values, with a value of one being predominant.

Other features such as “always wear a mask,” which correlated negatively with morbidity, also characterize mostly metropolitan counties, when focusing on the top quartile of their values.



**Fig. 3** Histograms for the RUCC values of the counties with the most COVID19 cases and deaths. RUCC=Rural–Urban Continuum Codes. Histograms for the Rural–Urban Continuum Codes distribution of the counties in the top quartile for the rate of COVID-19 cases (a) and deaths (b). The vertical axis denotes the number of counties and the horizontal axis the RUCC value. Each row represents a different date. Time progresses from top to bottom

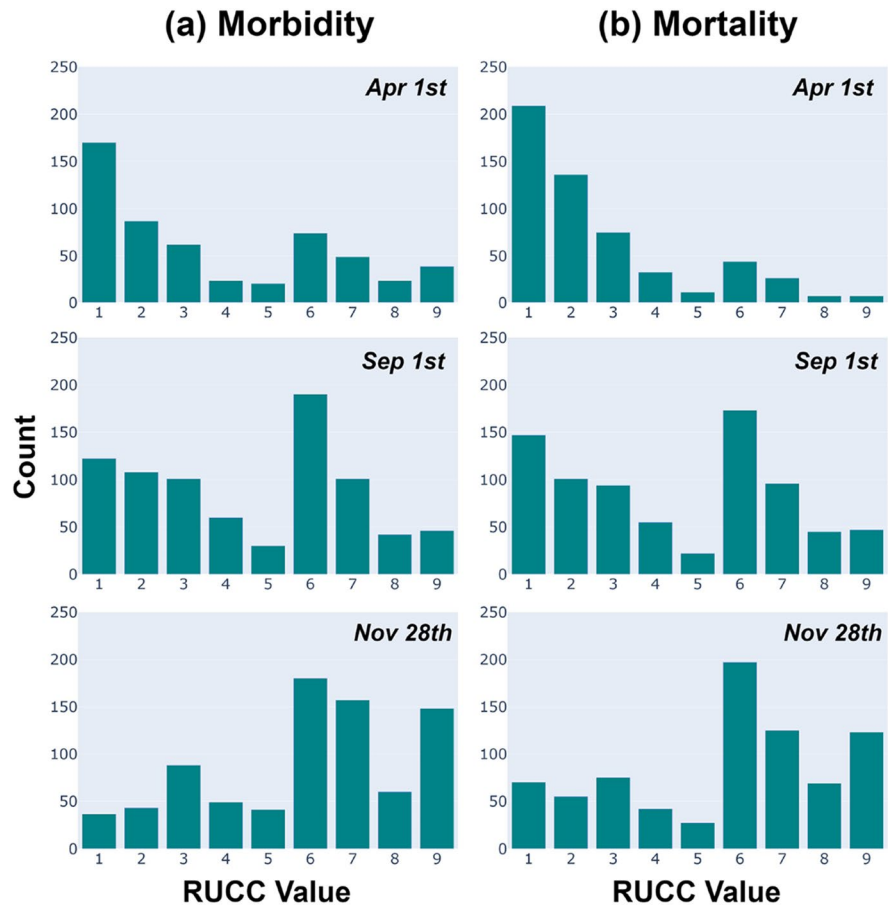


Figure 3 presents from the top-down the distribution, at three different time points (April 1st, September 1st, November 28th), of RUCC values for the counties that are at the top quartile of COVID-19 morbidity (Fig. 3a) and deaths or mortality (Fig. 3b).

During early April, both cases and deaths were highly concentrated at the urban counties. However, as time passes, the counties manifesting both the highest morbidity and mortality rates tend to be the more rural ones. *September 1st is a tipping point in which the sum of the urban counties in the top morbidity and mortality quartiles is similar to that of the rural ones*, and by November 28th, the ratio is much higher for rural counties. Clearly, the COVID-19 “wave” spread from the urban counties towards the rural ones.

## Discussion

We can sum up the results of this study, which includes data up to the end of November 2020, with two main conclusions: (1) *the COVID-19 disease is highly correlated with socio-economic status*.

Wealthier counties with fewer minorities, a higher educated population, and lower overall poverty rates had lower morbidity and especially mortality rates.

These results are in line with previous research [7, 10, 12, 17, 20] using other methods.

(2) *COVID-19 initially affected the most urban areas of the USA and gradually spread, as a wave, to more rural ones, eventually becoming more prevalent there from September onwards*.

It is also worth noting that obesity is less prevalent in metropolitan counties [14]. Even though the

Pearson correlation between obesity and diabetes prevalence is relatively high (0.698), these two features impacted the model differently, possibly due to the low variance in diabetes prevalence ( $5.76 * 10^{-4}$ ) between counties, leading to relatively random results when we computed the diabetes feature's SHAP values for the Morbidity outcome. In contrast, the variance in obesity prevalence was higher ( $2.02 * 10^{-3}$ ), leading to a SHAP value that markedly indicated a rise in Morbidity when obesity prevalence is higher.

These results, through a between-county analysis, confirm in a rather striking fashion previous research that pointed out the discrepancy of mortality rates between different ethnic groups in the USA. As presented in previous studies [15, 18], counties with higher proportions of African American citizens had more COVID-19 cases and deaths. These authors offer multiple explanations and possible reasons for these disparities: occupational type, inadequate access to high-quality medical care, and racial biases in COVID-19 testing and treatment.

Our results suggest that this disparity might well stem from economic reasons.

Several features which are known to increase the mortality from COVID-19 (such as older age, gender, and ICU bed availability) were considered in our study but did *not* appear in the list of highly impacting factors or appeared with a low weight. In particular, the low impact of the *age* or *gender* features on morbidity and mortality in our results might initially seem surprising, considering the well-known association in COVID-19 individual patients between being at an elderly age and suffering the most severe complications and the higher propensity for death in males.

The likely reason for this lack of association in our current study is a *low variance of these features among counties*, as opposed to their high variance among individuals. The Supplemental Materials demonstrate this observation in more detail.

Other features which were taken into account in the model and in the SHAP computation but which did not appear in the top impacting factors list include the presidential election results and the mode of transportation to work.

Note also that COVID-19 morbidity and mortality rates might also be associated with unknown, dynamically changing factors that cannot be easily

measured, such as the number of infected but asymptomatic people in each county.

The results in Fig. 2 and Fig. 3 present the movement over time of the COVID-19 “wave” across the USA. This offers an explanation as to why features such as *mean commute time*, which at the *individual* level increases the probability of being infected by COVID-19, actually resulted, by the end of November 2020, in a *negative* correlation with morbidity levels. This is because when viewing such as feature at a county-level, it is actually strongly correlated with the level of *urbanization* (or ruralness) of the county. And *eventually*, the COVID-19 wave hit the rural counties, regarding both morbidity and mortality.

Note that our results do *not* suggest that there is a clear-cut distinction between the urban and rural counties in terms of the *magnitude* of COVID-19 deaths: for example, the total poverty rate is generally higher in *urban* counties [3]; but nevertheless, over the whole period, it had a high positive impact on the mortality model. This seems quite likely, because poverty is a better, more direct predictor for a county's mortality rate than its level of ruralness or urbanization: Poor people tend to not have access to proper healthcare, whether they live in a sprawling city or in the peripheral countryside.

In addition, the African American population is distributed rather uniformly across counties with respect to their RUCC [1]; thus, the RUCC value of a county is not enough to predict morbidity or mortality rates; as we had demonstrated, its percentage of African American population is the strongest predictor of mortality within our model.

Note also that the data regarding COVID-19 cases and deaths used in this study have been collected up to November 28th, 2020, while the pandemic is still ongoing; new data have become available, and some correlations might have slightly changed.

In addition, all of the county-level features, aside from the mask-wearing survey and the capacity of ICU beds, were extracted before the beginning of the spread of the COVID-19 and might not have captured some rapid changes that might have occurred up to November 28th, 2020.

Finally, all counties were considered equal in the current study, even though their area and population size are different in real life.

In conclusion, our findings might shed some light on (1) why some counties are prone to a relatively



high COVID-19 morbidity or mortality and (2) how that characterization changed over time in the USA.

Better understanding of these factors and their temporal dynamics might assist us in better focusing preventive and therapeutic measures, such as vaccination, at the spots in which these factors are most likely to be of benefit.

Our methodology, which is based on explainable machine learning binary classification models, and exploits game theoretic principles to calculate the impact of multiple factors, can be easily extended to study the spread of other diseases and other countries.

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**Author contribution** N. I., T. S., and R. M. designed the research; N. I. and T. S. performed the research; N. I. and T. S. analyzed the data; N. I., T. S., and Y. S. wrote the paper.

**Data Availability** See supplementary material for more information.

<https://github.com/nytimes/covid-19-data> <https://www.cdc.gov> <https://www.census.gov> <https://townhall.com/>

**Code Availability** Not applicable.

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