

The Influence of Contextual Factors on the Initial Phases of the COVID-19 Outbreak across U.S. Counties

Wolfgang Messner¹ and Sarah Payson¹

¹University of South Carolina

June 12, 2020

Abstract

Background. This study examines the influence of contextual factors on the initial phases of the COVID-19 outbreak across U.S. counties. **Methods.** Contextual factors are simultaneously tested at the county- and state-level with a multilevel linear model using full maximum likelihood. **Results.** The variation between states is substantial and significant ($ICC = 0.243$, $u_0 = 4.50E-04$, $p < 0.001$). At the state-level, the cultural value of collectivism is positively associated with the outbreak rate. At the county-level, the racial and ethnic composition contributes to outbreak differences, affecting Black/African and Asian Americans most. Counties with a higher median age have a stronger outbreak, as do counties with more people below the age of 18. Higher income, education, and personal health are generally associated with a lower outbreak. Obesity is negatively related to the outbreak, in agreement with the value expectancy concepts of the health belief model. Smoking is also negatively related, but only directionally informative. Air pollution is another significant contributor to the outbreak, but population density does not give statistical significance. **Conclusions.** Because of a high variation in contextual factors, policy makers need to target pandemic responses to the smallest subdivision possible, so that countermeasures can be implemented effectively.

Wolfgang Messner Sarah E. Payson

University of South Carolina University of South Carolina

Darla Moore School of Business, University of South Carolina, Columbia, SC, United States

wolfgang.messner@moore.sc.edu; spayson@email.sc.edu

ORCID-ID: <https://orcid.org/0000-0003-3229-6363>

Faculty homepage: https://sc.edu/study/colleges_schools/moore/directory/messner_wolfgang.php

LinkedIn: <https://www.linkedin.com/in/wmessner/>; <https://www.linkedin.com/in/sarahpayson/>

Running title: COVID-19 Outbreak across U.S.

Acknowledgements

We gratefully acknowledge support through the Darla Moore School of Business and the Center for International Business Education and Research (CIBER) at the University of South Carolina.

Human participant protection and data sharing

No humans participated in this study. The original data sources are referenced in the section Methods and in Table 1

The Influence of Contextual Factors on the Initial Phases of the COVID-19 Outbreak across U.S. Counties

Background . This study examines the influence of contextual factors on the initial phases of the COVID-19 outbreak across U.S. counties.

Methods . Contextual factors are simultaneously tested at the county- and state-level with a multilevel linear model using full maximum likelihood.

Results . The variation between states is substantial and significant ($ICC = 0.243$, $u_0 = 4.50E-04$, $p < 0.001$). At the state-level, the cultural value of collectivism is positively associated with the outbreak rate. At the county-level, the racial and ethnic composition contributes to outbreak differences, affecting Black/African and Asian Americans most. Counties with a higher median age have a stronger outbreak, as do counties with more people below the age of 18. Higher income, education, and personal health are generally associated with a lower outbreak. Obesity is negatively related to the outbreak, in agreement with the value expectancy concepts of the health belief model. Smoking is also negatively related, but only directionally informative. Air pollution is another significant contributor to the outbreak, but population density does not give statistical significance.

Conclusions . Because of a high variation in contextual factors, policy makers need to target pandemic responses to the smallest subdivision possible, so that countermeasures can be implemented effectively.

Keywords: COVID-19; Novel coronavirus; Outbreak; Pandemic; Regional differences.

Introduction

First reports of a pneumonia of unknown etiology emerged in Wuhan, China, on December 31, 2019. The extremely contagious virus was identified as severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), and spread quickly beyond Wuhan. In the U.S., the first case of COVID-19, the disease caused by SARS-CoV-2, was reported on January 22, 2020. Despite unprecedented government action, the number of cases in the U.S. grew to over 593000 as of April 14, and crossed one million on April 28.¹

The local press and epidemiological research alike have reported local differences in the outbreak.² A community's susceptibility to any virus is determined by a variety of factors, inter alia, biological determinants, demographic profiles, and socioeconomic characteristics.³ These factors vary significantly across the U.S.; for instance, COVID-19 fatalities in New York, an epicenter of the outbreak in the U.S., disproportionately affect males and people belonging to older age groups, from Black/African and Hispanic ethnicities, and with certain comorbidities.⁴

As of May 09, 2020, more than half of COVID-19 data reported by the Centers for Disease Control and Prevention (CDC) are missing race and ethnicity disaggregation; other individual variables are lacking as well. To understand local differences in the outbreak and risk of contracting COVID-19, we therefore deploy an ecological analysis using contextual factors. A two-level hierarchical linear model with full maximum likelihood allows us to simultaneously test and disentangle county- and state-level effects.

Our study contributes to various strands of current COVID-19 research. First, we note that contextual factors influence the COVID-19 outbreak. Because significant variations in the outbreak exist between states and counties within a state (Figures 1 and 2),² we recommend policy makers to look at pandemics from the smallest subdivision possible for effective implementation of countermeasures and provision of critical resources. Second, we develop an understanding of how regional cultural differences relate to outbreak variations, driven by specific psychological functioning of individuals and the enduring effects of such differences

on political processes, governmental institutions, and public policies.^{5,6} Third, we debunk rumors that a state’s leadership, as expressed by the political party in control or the gender of its governor, has a statistically significant influence on the outbreak.⁷ Fourth, we identify how the virus affects counties differently, depending on their demographic profile. Fifth, while good personal health is generally associated with a lower risk, we identify the prevalence of obesity and smoking in counties to be negatively related with the outbreak. Sixth, while previous studies link air pollution to the death rate, we show that it also contributes to the number of cases.

Methods

We now explain the estimation of the outbreak rate, and the reasons for including certain contextual factors; Table 1 summarizes the data sources.

Outbreak rate

We obtain COVID-19 outbreak data from USA Facts, as of April 14, 2020.¹ Since January 22, this database has aggregated data from the CDC and other public health agencies. The 21 cases on the Grand Princess cruise ship are not attributed to any counties in California. We discard cases only allocated at the state-level due to lack of information. On average, these are only 308 cases per state, but a few states have as many as 4866 (New Jersey), 1300 (both Rhode Island and Georgia), or 1216 (Washington State). Following approaches by the Institute for Health Metrics and Evaluation at the University of Washington⁸ and the COVID-19 Modeling Consortium at the University of Texas at Austin,⁹ we model the outbreak using the exponential growth equation $\frac{dy}{dt} = b y$, where b is a positive constant called the relative growth rate with units of inverse time. Going forward, we simply refer to b as the outbreak rate. The shape of the trends in case counts enables us to see differences between counties.¹⁰ Solutions to this differential equation have the form $y = a e^{bt}$, where a is the initial value of cases y . The doubling time T_d can be calculated as $T_d = \frac{\ln(2)}{b}$. We estimate the outbreak rate for 1987 out of 3142 counties in the 50 U.S. states that have a minimum of 10 reported cases. This is a statistical, but not an epidemiological model, that is, we are neither trying to model infection transmission nor estimate epidemiological parameters, such as the pathogen’s reproductive or attack rate. Instead, we are fitting curves to observed outbreak data at the county level. A change-point analysis using the Fisher discriminant ratio as a kernel function does not show any significant change points in the outbreak, and therefore justifies modeling the COVID-19 outbreak as a phenomenon of unrestricted population growth.¹¹ We cannot forecast outbreak dynamics with this statistical approach, though we do not require extrapolated data in our work.

Cultural values

Culture can be defined as a set of values that are shared in a given social group. While cultural values are often used to distinguish countries,¹² more than 80% of cultural variation resides within countries.¹³ The original North American colonies were settled by people hailing from various countries, who have spread their influence across mutually exclusive areas. Their distinct cultures are still with us today.⁶ Although today’s U.S. states are not strictly synonymous with these cultural areas, there is abundant evidence that political boundaries can serve as useful proxies for culture.¹⁴

One of the most useful constructs to emerge from cultural social psychology is the individualism-collectivism bipolarity. It has proven useful in describing cultural variations in behaviors, attitudes, and values. Briefly, individualism is a preference for a loosely knit social framework, whereas collectivism represents a preference for a tightly knit framework, in which its members are interdependent and expected to look after each other in exchange for unquestioning loyalty. While the majority of research on collectivism involves comparing countries¹², we use an index developed at state-level solely within the U.S.⁵ Previous studies have

shown that the regional prevalence of pathogens and international differences in the COVID-19 outbreak are positively associated with collectivism.^{14,15}

Institutional confounders

In addition to culture, we include various institutional confounders at the state-level, such as the political affiliation of a state's governor, the gender of the governor, and government spending per capita. Government plays a critical role in policy development and implementation, and so state-level differences could influence the outbreak rate.¹⁶

Racial composition

While first systematic reviews about COVID-19 incidences from China relied on ethnically homogenous cohorts^{17,18} ethnically diverse populations, such as in the U.K. and U.S. may exhibit different susceptibility or response to infection because of socioeconomic, cultural, or lifestyle factors, genetic predisposition and pathophysiological differences. Certain vitamin or mineral deficiencies, differences in insulin resistance or vaccination policies in countries of birth may also be contributing factors.¹⁸ We include variables measuring the composition of U.S. counties regarding racial and ethnic groups.

Income and education

Poverty is arguably the greatest risk factor for acquiring and succumbing to disease worldwide, but has historically received less attention from the medical community than genetic or environmental factors. The global HIV crisis brought into sharp relief the vulnerability of financially strapped health systems, and revealed disparities in health outcomes along economic fault lines.¹⁹ We include the median household income to quantify potential economic disparities between U.S. counties. In addition, we measure non-proficiency in English and math performance of students. Lower educational levels may result in a lower aptitude as it relates to understanding and effectively responding to the pandemic.

Other demographics

Age and gender also play a potential role in a population's susceptibility. During the aging process, immune functions decline, rendering the host more vulnerable to certain viruses.²⁰ We use the percentage of population below 18 years of age and their median age to determine potential effect of differences in mobility, response, and lifestyle factors. We also control for the percentage of the population that is female, as one COVID-19 study in Italy showed that about 82% of critically ill people admitted into intensive care were men.²¹

Personal health

Good overall personal health is a general indicator for disease resistance. Additionally, the health belief model suggests that a person's belief in a personal threat of a disease, together with faith in the effectiveness of behavioral recommendations, predicts the likelihood of the person adopting the recommendation.²² We use the percentage of the population that reports insufficient amount of sleep, is obese (as defined by a body mass index above 30), and smokes daily. Given the latter two are publicized risk factors for COVID-19, there is a potential for greater caution following the value-expectancy concepts of the health belief model. Yet, medicinal nicotine has been identified as a potential protective factor against infection by SARS-CoV-2.²³ We also measure the preventable hospitalization rate (that is, the rate of hospital stays for ambulatory-care sensitive conditions) as a potential indicator of poor personal health and the social association rate (that is, the average number of membership associations), which is generally connected with positive mental health and happiness.

External health

Previous studies suggest that exposure to pollution can suppress immune responses and proliferate the transmission of infectious diseases,²⁴ and that the COVID-19 mortality rate is associated with air pollution.²⁵ However, the impact of air pollution on the spread of COVID-19 is not yet known.²⁴ We use the 2014 average daily density of fine particulate matter PM_{2.5} to measure air pollution across U.S. counties, and the percentage of population living in rural areas to account for physical distancing being more prevalent in rural areas. In addition, the food environment index reflects access to grocery stores and healthy foods.

Other confounders

Population density and overcrowding is significant when considering public health crises, facilitating the spread of diseases in developing and developed countries alike.²⁶ As the climate is another highly publicized confounder potentially influencing the COVID-19 transmission rate,²⁷ we also include each county’s average temperature during February and March 2020. To control for the temporality of the outbreak, we bring in a variable representing the number of days between January 01 and the 10th confirmed case reported.

Statistical results

To simultaneously test county- and state-level effects of contextual factors on the outbreak rate with cross-level interactions, we estimate a two-level linear model using full maximum likelihood in HLM 7.03 (Figure 3). This accounts for potential similarities in counties within the same state.²⁴ We center all predictors around the group mean at level 1 and grand mean at level 2.

We first estimate a one-way random effects ANOVA (unconditional model), which has an intraclass correlation coefficient (ICC) of 0.243. That is, more than 24% of the variation in the outbreak rate is between states, and about 76% is within the states and between their counties. The variation between states is statistically significant ($u_0 = 4.50E-04$, $p < 0.001$). We thus deem it prudent to proceed with a multilevel model as follows:

$$\text{Level 1 (counties): Outbreak rate}_{ij} = \beta_{0j} + \beta_{1j} [\text{Black \& African American}] + \beta_{2j} [\text{Native American}] + \beta_{3j} [\text{Asian American}] + \beta_{4j} [\text{Native Hawaiian}] + \beta_{5j} [\text{Hispanic American}] + \beta_{6j} [\text{Household income}] + \beta_{7j} [\text{Nonproficiency in English}] + \beta_{8j} [\text{Math grade}] + \beta_{9j} [\text{Persons under 18 years}] + \beta_{10j} [\text{Median age}] + \beta_{11j} [\text{Female persons}] + \beta_{12j} [\text{Social associations}] + \beta_{13j} [\text{Sleep deprivation}] + \beta_{14j} [\text{Preventable hospitalization}] + \beta_{15j} [\text{Obesity}] + \beta_{16j} [\text{Smoking}] + \beta_{17j} [\text{Air pollution}] + \beta_{18j} [\text{Rural area}] + \beta_{19j} [\text{Food environment}] + \beta_{20j} [\text{Outbreak date}] + \beta_{21j} [\text{Density}] + \beta_{22j} [\text{Temperature}] + r_{ij}$$

$$\text{Level 2 (states): } \beta_{0j} = \gamma_{00} + \gamma_{01} [\text{Party control}] + \gamma_{02} [\text{Gender of governor}] + \gamma_{03} [\text{Government spending}] + \gamma_{04} [\text{Collectivism}] + u_{0j}; \beta_{1j} = \gamma_{10} + u_{1j}; \beta_{2j} = \gamma_{20}; \beta_{3j} = \gamma_{30}; \beta_{4j} = \gamma_{40}; \beta_{5j} = \gamma_{50}; \beta_{6j} = \gamma_{60}; \beta_{7j} = \gamma_{70}; \beta_{8j} = \gamma_{80}; \beta_{9j} = \gamma_{90}; \beta_{10j} = \gamma_{100}; \beta_{11j} = \gamma_{110}; \beta_{12j} = \gamma_{120}; \beta_{13j} = \gamma_{130}; \beta_{14j} = \gamma_{140}; \beta_{15j} = \gamma_{150}; \beta_{16j} = \gamma_{160}; \beta_{17j} = \gamma_{170}; \beta_{18j} = \gamma_{180}; \beta_{19j} = \gamma_{190} + u_{19j}; \beta_{20j} = \gamma_{200} + u_{20j}; \beta_{21j} = \gamma_{21}; \beta_{22j} = \gamma_{22}$$

We provide the inter-item correlation matrix in Table 2, and the results of the multilevel model in Table 3. Additionally, we perform several robustness tests to inform our results.

First, because outbreak rates change over time and their estimation is somewhat sensitive to the starting figure, we alternatively calculate them after 10 and 25 cases in the respective unit, finding a high correlation among the rates. When using the rate after 10 cases, the outbreak date as a control variable changes its sign and loses significance ($p = 0.065$). Notably, the following coefficients gain significance: government spending ($p = 0.064$); temperature ($p = 0.011$). Conversely, the following coefficients lose significance: household income ($p = 0.989$); food environment ($p = 0.144$); density ($p = 0.709$). More importantly, the signs of the coefficients remain the same. The variable outbreak date controls for temporality of the outbreak in the original model (1.912, [1.322; 2.502], $p < 0.001$).

Second, we iteratively include several other contextual variables and logged versions to assess the robustness of the results. But because it is nearly impossible to establish a complete list of confounding variables, we quantify the potential impact of unobserved confounds (Table 3; impact threshold).²⁸ For instance, the necessary impact of such a confound for air pollution would be 0.043, that is, to invalidate the variable’s inference on the outbreak rate, a confounding variable would have to be correlated with both the outbreak rate and air pollution at $\sqrt{0.043} = 0.207$. Next, to alleviate concerns that some counties are omitted from the analysis because they are not yet affected by the virus,²⁴ we ask how many counties would have to be replaced with unobserved cases for which the null hypothesis is true (i.e., a contextual variables has no influence on the outbreak rate) in order to invalidate the inference.²⁸ As Table 3 (confound threshold) shows, 43.962% of the counties would have to be replaced with counties for which the effect is zero in order to invalidate the influence of air pollution. In summary, it can be claimed that the influence of the identified contextual variables on the pandemic is reasonably robust.

Third, a potential omission of relevant variables can lead to multicollinearity issues, which are generally a serious problem in epidemiological studies.²⁹ Even though HLM 7.03 checks for multicollinearity, we conduct several additional diagnostics to eliminate any potential issues. In the inter-item correlation matrix (Table 2), the average (absolute) correlation is 0.172, and the highest correlation is 0.754, which is below the typical cutoff of 0.8. Most high correlations exist between racial composition and income and education. Additionally, we conduct a linear regression analysis at level 1 in IBM SPSS 26 ($R^2 = 0.495$; without variable math grade; pairwise exclusion of missing values), and find that the variable inflation factor (VIF) never exceeds the threshold of 5 (highest being nonproficiency in English, 4.024). The variance-decomposition matrix also does not show any groups of predictors with high values.

Fourth, we rerun our model excluding the 23 counties of the New York metropolitan area. As a COVID-19 hotspot, they could unduly influence our analysis. All signs remain the same, and the following coefficients gain significance: household income ($p = 0.009$); persons under 18 years ($p = 0.038$).

Fifth, because there is no statistically correct choice for centering decisions in multi-level models³⁰, we retest our model with raw values. With the exception of the variable collectivism losing statistical significance ($p = 0.711$), the results are fully consistent with the group- and grand-mean centered predictors in Table 3.

Lastly, we are aware that an accurate estimation and comparison of the outbreak rate across units depends on similar testing strategies, test sensitivities, specificities, and reporting of tests performed vs. individuals tested.^{10,31} Even within the U.S., some states report tests performed and others individuals tested.³¹ The number of tests administered and the number of confirmed cases therefore correlates to varying extents across states.³² By using a multi-level model, we aim to accommodate such differences between states.

Discussion of results

In the absence of national-level data controlled for location and disaggregated by race and ethnicity, demographics, information about comorbidity and other personal health variables, an ecological analysis provides an alternative way of measuring the disproportionate impact of COVID-19 across the U.S. and among segments of Americans. It may be contrary to expectations that the outbreak rate of a new pathogen, which is able to infect virtually anyone, manifests contextual disparities. But for other conditions, such as HIV and cancer, regional health disparities have been reported before,^{33,34} and with the current study we show that contextual factors in the U.S. also create a variation in COVID-19 cases.

Our analysis indicates that higher outbreak rates can be found in U.S. states characterized by a higher cultural value of collectivism (coefficient 0.998, confidence interval [0.351; 1.645], $p = 0.004$). As Table 2 shows, collectivistic values are more prevalent in counties that are warmer (correlation with temperature 0.715, $p < 0.001$) and have a higher percentage of people with a Black/African background (with Black/African American 0.539, $p < 0.001$). This mirrors findings from international cultural research.¹² Conversely, we cannot find any statistical evidence that the government spending, the gender of the governor, or the party

in control would be in any way linked to the outbreak. This certainly debunks myths spread by the popular media.

A disproportionately stronger outbreak of COVID-19 cases can be found in counties with a higher percentage of Black/African (1.158, [0.725; 1.591], $p < 0.001$) and Asian Americans (1.305, [0.166; 2.444], $p = 0.025$), which supports prior infection and mortality studies in the U.S. and U.K.^{18,35} The former counties are also characterized by a higher rate of sleep deprivation (0.568, $p < 0.001$) and warmer temperatures (0.533, $p < 0.001$). The latter have a higher population density (0.553, $p < 0.001$). While we found sleep deprivation to be associated with a higher outbreak rate (1.557; [0.412; 2.702], $p = 0.008$), a positive influence of population density (0.050, [-0.009; 0.109], $p = 0.095$) and temperature (0.301, [-0.518; 1.120], $p = 0.472$) are only directionally informative, but not statistically significant. In the first robustness test, higher average temperatures are positively and significantly related to the outbreak (1.027, [0.235, 1.861], $p = 0.011$), potentially related to more time spent indoor with air conditioning.

Conversely, counties with more Hispanic Americans are less affected by the pandemic, with borderline statistical significance (-0.447, [-0.915; 0.021], $p = 0.061$). We could not find a significant effect for counties with a higher Native American (0.763, [-0.209; 1.735], $p = 0.124$) or Hawaiian population (1.478, [0.506; 2.450], $p = 0.538$) though.

We see that higher income and education levels are associated with a less aggressive outbreak (household income: -3.854, [-7.437; -0.271]; $p = 0.035$; nonproficiency in English: 2.090; [0.547; 3.633]; $p = 0.008$; math grade: -0.002, [-0.004; 0.000]; $p < 0.001$). In counties with a higher household income, the obesity rate and the percentage of smokers tends to be lower (-0.518, $p < 0.001$ and -0.666, $p < 0.001$ respectively). Both are negatively associated with the outbreak rate. The effect of the obesity rate is highly significant (-1.093, [-1.828; -0.358], $p = 0.004$), but the effect of the percentage of smokers is only directionally informative (-0.784, [-3.150; 1.582], $p = 0.516$). Studies report that people with obesity are at increased risk of developing severe COVID-19 symptoms,³⁶ but, to the best of our knowledge, a link to the infection rate has not yet been established. A potential explanation of this is that people with obesity heed the warnings issued by the CDC, and are extra careful in avoiding social contact, in line with the value expectancy concepts of the health belief model.²² Other studies report that smoking or medicinal nicotine might be a protective factor against infection by SARS-CoV-2;²³ our ecological data does not contradict this finding. Many other variables related to good personal health are associated with a slower outbreak (social associations: -2.027, [-2.911; -1.143], $p < 0.001$; sleep deprivation: 1.557, [0.412; 2.702], $p = 0.008$; preventable hospitalization: 0.001, [-0.001; 0.003], $p = 0.207$).

Regarding age-related demographics, we confirm early observations that counties with an older population are more affected by the outbreak, with borderline significance (median age: 0.657, [-0.033; 1.347], $p = 0.062$). Notably, the percentage of persons under 18 years is positively associated with the outbreak rate, again with borderline significance (1.066, [-0.014; 2.146], $p = 0.053$). A possible reason is that younger people physically interact more frequently, closer, and longer with their friends, thus contributing to the spread of the virus. Conversely, we find no effect of differences in gender (0.167, [-0.880; 1.214], $p = 0.755$). None of these demographic variables are strongly correlated with any other variable.

Air pollution is a significant contributor to the outbreak (3.329, [1.465; 5.193], $p < 0.001$), and, concurrently, counties with a rural environment experience a slower outbreak (-0.443, [-0.574; -0.312], $p < 0.001$). This calls for studies linking air pollution to the lethality of COVID-19^{24,25} to include the outbreak rate as a potential confounding variable. Contrariwise, a better food environment is associated with a higher outbreak rate (5.996, [1.286; 10.706], $p = 0.016$). While the food environment index is usually associated with a healthier lifestyle, better access to grocery stores and supermarkets in the vicinity also means more interaction with other people, and thus an increased likelihood of transmission.

As a final point, we want to note that we have presented associations between contextual factors and the COVID-19 outbreak which are consistent with the deliberations leading to our research model. However, these associations, even when statistically significant, are not an inference of causality. Establishing causal

inference is, of course, critical for our understanding of and fight against COVID-19, but this represents a direction for further research using more detailed data at the level of individual patients.

References

1. USA Facts. Coronavirus locations: COVID-19 map by county and state. Available at <https://usafacts.org/visualizations/coronavirus-covid-19-spread-map/>. Accessed 14 April 2020.
2. Messner W, Payson SE. Variation in COVID-19 outbreaks at U.S. state and county levels. medRxiv 2020:1-9.
3. Chen JT, Kahn R, Li R, et al. U.S. county-level characteristics to inform equitable COVID-19 response. medRxiv 2020:1-38.
4. New York State Department of Health. COVID-19 fatalities. Available at <https://covid19tracker.health.ny.gov/views/NYS-COVID19-Tracker/NYSDOHCOVID-19Tracker-Fatalities?%3Aembed=yes&%3Atoolbar=no&%3Atabs=n#/views/NYS%252dCOVID19%25>. Accessed 9 May 2020.
5. Vandello JA, Cohen D. Patterns of individualism and collectivism across the United States. *J Pers Soc Psychol* 1999;77:279-292.
6. Woodard C. *American Nations*. London: Penguin; 2011.
7. Wittenberg-Cox A. What do countries with the best coronavirus responses have in common? Women leaders. *Forbes*. <https://www.forbes.com/sites/avivahwittenbergcox/2020/04/13/what-do-countries-with-the-best-coronavirus-reponses-have-in-common-women-leaders>. Published April 13, 2020. Accessed May 13, 2020.
8. Murray CJ. Forecasting COVID-19 impact on hospital bed-days, ICU-days, ventilator-days and deaths by US state in the next 4 months. medRxiv 2020:1-26.
9. Woody S, Tec M, Dahan M, et al. Projections for first-wave COVID-19 deaths across the U.S. using social-distancing measures derived from mobile phones measures. Available at https://www.tacc.utexas.edu/ut.-covid-19_mortality_forecasting_model_report. Accessed 19 April 2020.
10. Pearce N, Vandenbroucke JP, VanderWeele TJ, Greenland S. Accurate statistics on COVID-19 are essential for policy guidance and decisions. *Am J Public Heal* 2020;April:e1-e3.
11. Texier G, Farouh M, Pellegrin L, et al. Outbreak definition by change point analysis: A tool for public health decision? *BMC Med Inform Decis Mak* 2016;16:1-12.
12. Hofstede G. *Culture's Consequences: Comparing Values, Behaviors, Institutions, and Organizations across Nations*. 2nd ed. Thousand Oaks, CA: Sage; 2001.
13. Kirkman BL, Lowe KB, Gibson CB. A retrospective on Culture's Consequences: The 35-year journey. *J Int Bus Stud* 2017;48:12-29.
14. Fincher CL, Thornhill R, Murray DR, Schaller M. Pathogen prevalence predicts human cross-cultural variability in individualism/collectivism. *Proc R Soc B Biol Sci* 2008;275:1279-1285.
15. Messner W. The institutional and cultural context of cross-national variation in COVID-19 outbreaks. medRxiv 2020:1-13.
16. Adolph C, Amano K, Bang-Jensen B, Fullman N, Wilkerson J. Pandemic politics: Timing state-level social distancing responses to COVID-19. medRxiv 2020:1-19.

17. Li B, Yang J, Zhao F, et al. Prevalence and impact of cardiovascular metabolic diseases on COVID-19 in China. *Clin Res Cardiol* 2020;531-538.
18. Khunti K, Singh AK, Pareek M, Hanif W. Is ethnicity linked to incidence or outcomes of COVID-19? *BMJ* 2020;369:14-15.
19. Alsan MM, Westerhaus M, Herce M, Nakashima K, Farmer PE. Poverty, global health, and infectious disease: Lessons from Haiti and Rwanda. *Infect Dis Clin North Am* 2011;25:611-622.
20. Schoggins JW. A phospholipase linkAGE to SARS susceptibility. *J Exp Med* 2015;212:1755.
21. Grasselli G, Zangrillo A, Zanella A, et al. Baseline characteristics and outcomes of 1591 patients infected with SARS-CoV-2 admitted to ICUs of the Lombardy Region, Italy. *JAMA* 2020;323:1574-1581.
22. Strecher VJ, Rosenstock IM. The health belief model. In: Baum A, Newman S, Weinman J, McManus C, West R, eds. *Cambridge Handbook of Psychology, Health and Medicine*. Cambridge: Cambridge University Press; 1997:113-117.
23. Tindle HA, Newhouse PA, Freiberg MS. Beyond smoking cessation: Investigating medicinal nicotine to prevent and treat COVID-19. *Nicotine Tob Res* 2020:1-2.
24. Wu X, Nethery RC, Sabath MB, Braun D, Dominici F. Exposure to air pollution and COVID-19 mortality in the United States: A nationwide cross-sectional study. *medRxiv* 2020:1-35.
25. Travaglio M, Popovic R, Yu Y, Leal NS, Miguel L. Links between air pollution and COVID-19 in England. *medRxiv* 2020:1-13.
26. Kaneda T, Greenbaum C. How demographic changes make us more vulnerable to pandemics like the Coronavirus. Available at <https://www.prb.org/how-demographic-changes-make-us-more-vulnerable-to-pandemics-like-the-coronavirus/>. Accessed 13 May 2020.
27. Chiyomaru K, Takemoto K. Global COVID-19 transmission rate is influenced by precipitation seasonality and the speed of climate temperature warming. *medRxiv* 2020:1-13.
28. Frank KA. Impact of a confounding variable on a regression coefficient. *Sociol Methods Res* 2000;29:147-194.
29. P. Vatcheva K, Lee M. Multicollinearity in regression analyses conducted in epidemiologic studies. *Epidemiology* 2016;06:1-9.
30. Kreft IGG, de Leeuw J, Aiken LS. The effect of different forms of centering in hierarchical linear models. *Multivariate Behav Res* 1995;30:1-21.
31. Roser M, Ritchi H, Ortiz-Ospina E. Coronavirus disease (COVID-19) - Statistics and research. Available at <https://ourworldindata.org/coronavirus>. Accessed 21 March 2020.
32. Kaashoek J, Santillana M. COVID-19 positive cases, evidence on the time evolution of the epidemic or an indicator of local testing capabilities? A case study in the United States. *SSRN* 2020:1-14.
33. Ransome Y, Kawachi I, Braunstein S, Nash D. Structural inequalities drive late HIV diagnosis: The role of black racial concentration, income inequality, socioeconomic deprivation, and HIV testing. *Heal Place* 2016;42:148-158.
34. Fang CY, Tseng M. Ethnic density and cancer: A review of the evidence. *Cancer* 2018;124:1877-1903.
35. Millett GA, Jones AT, Benkeser D, et al. Assessing differential impacts of COVID-19 on black communities. *medRxiv* 2020:1-26.
36. Stefan N, Birkenfeld AL, Schulze MB, Ludwig DS. Obesity and impaired metabolic health in patients with COVID-19. *Nat Rev Endocrinol* 2020:4-5.

Figure 1: Epidemic days at county level (South Carolina)

Hosted file

image1.emf available at <https://authorea.com/users/332811/articles/459199-the-influence-of-contextual-factors-on-the-initial-phases-of-the-covid-19-outbreak-across-u-s-counties>

The spaghetti lines trace the COVID-19 outbreak in South Carolina (black dashed line) and the counties (straight lines) as a percentage of the cases reported on April 14, 2020. Cases unallocated to a county due to lack of information are included in the state line; counties with less than 20 reported cases are not shown in the diagram.

Figure 2: Variation in outbreak rates at U.S. county level

Hosted file

image2.emf available at <https://authorea.com/users/332811/articles/459199-the-influence-of-contextual-factors-on-the-initial-phases-of-the-covid-19-outbreak-across-u-s-counties>

This geo map reveals a large variation in outbreak rates at U.S. county level (April 14, 2020). Lighter colors signify that the pandemic has a slower relative growth rate, and darker colors point to a faster growth.

Figure 3: Multilevel research model

Hosted file

image3.emf available at <https://authorea.com/users/332811/articles/459199-the-influence-of-contextual-factors-on-the-initial-phases-of-the-covid-19-outbreak-across-u-s-counties>

This figure details the multi-level research model and the variables used at state- and county-level.

Table 1: Variables and descriptive statistics

Variable	Primary source	Secondary source	S
<i>State institutions</i>			
Party control	WIK		
Gender of governor	WIK		
Government spending	SIP	Census Bureau	C
<i>People cultural values</i>			
Collectivism	VAN		
<i>Racial composition</i>			
Black & African American	CHR	Census population est.	C
Native American	CHR	Census population est.	C
Asian American	CHR	Census population est.	C
Native Hawaiian	CHR	Census population est.	C
Hispanic American	CHR	Census population est.	C
<i>Income & education</i>			
Household income	CHR	Small area income and poverty est.	S
Nonproficiency in English	CHR	Census population est.	C
Math grade	CHR	Stanford education data archive	S
<i>Other demographics</i>			
Persons under 18 years	CHR	Census population est.	C
Median age	SCP	American community survey	A
Female persons	CHR	Census population est.	C
<i>Personal health</i>			
Social associations	CHR	County business patterns	C
Sleep deprivation	CHR	Behavioral risk factor surveillance system	B

Variable	Primary source	Secondary source
Preventable hospitalization	CHR	Mapping Medicare disparities tool
Obesity	CHR	United States Diabetes Surveillance System
Smoking	CHR	Behavioral Risk Factor Surveillance System
<i>External health</i>		
Air pollution	CHR	Environmental public health tracking network
Rural area	CHR	Census population est.
Food environment	CHR	USDA food environment atlas; Map the meal gap from Feeding America
<i>Other confounders</i>		
Density	SCP	American community survey
Temperature ^{a)}	NCDC	

This table lists the independent variables at both levels of analysis and their provenance.

Notes: CHR: County health rankings, www.countyhealthrankings.org; SCP: Social Capital Project, <https://www.jec.senate.gov/public/index.cfm/republicans/2018/4/the-geography-of-social-capital-in-america>; NCDC: National Centers for Environment Information, <https://www.ncdc.noaa.gov/cag/county/mapping/1/tavg/202003/2/value>; VAN: Collectivism index proposed by Vandello & Cohen (1997);⁵ WIK: https://en.wikipedia.org/wiki/List_of_United_States_governors.^{a)} The NCDCs do not provide temperature mapping for Hawaii; all Hawaiian counties replaced by historical average data from <http://holiday-weather.com/hawaii/averages>. All websites accessed in May 2020.

Table 2: Inter-item correlation matrix

	b	c	d	e	f	g	h	i	j	k	l	m	n
a	-0.034	-0.251	0.035	0.083	0.048	-0.095	0.011	0.121	-0.106	0.046	-0.007	0.206	-0.088
b		0.052	-0.368	-0.102	0.049	-0.027	-0.024	-0.104	0.003	-0.066	-0.023	0.001	0.079
c			-0.389	-0.200	0.004	0.134	0.007	-0.043	0.269	-0.013	0.004	-0.030	0.054
d				0.539	-0.209	0.045	-0.044	0.051	-0.165	0.013	-0.057	-0.015	-0.094
e					-0.104	0.013	-0.011	-0.127	-0.321	-0.035	-0.002	-0.074	-0.141
f						-0.047	0.015	0.009	-0.095	-0.002	0.004	0.232	-0.110
g							0.060	0.195	0.483	0.221	-0.030	0.049	-0.269
h								0.250	-0.139	0.630	0.755	-0.025	-0.341
i									0.009	0.749	0.254	0.324	-0.398
j										-0.083	-0.201	0.160	-0.031
k											0.699	0.164	-0.470
l												-0.098	-0.339
m													-0.447
	o	p	q	r	s	t	u	v	w	x	y	z	
a	-0.006	-0.083	-0.002	-0.007	0.115	0.028	0.057	0.025	-0.156	0.014	-0.095	0.258	
b	0.014	0.173	-0.178	-0.113	0.108	-0.054	-0.089	0.066	0.017	0.042	-0.062	-0.237	
c	-0.039	0.198	-0.296	-0.133	-0.153	-0.217	-0.292	-0.071	0.214	-0.024	0.129	-0.477	
d	0.128	-0.272	0.557	0.301	0.203	0.138	0.407	-0.030	-0.241	-0.116	0.045	0.715	
e	0.154	-0.123	0.568	0.278	0.404	0.360	0.230	-0.045	-0.442	-0.128	0.119	0.533	
f	-0.034	-0.049	-0.064	0.047	0.076	0.270	-0.219	0.091	-0.105	0.064	-0.047	-0.108	
g	0.058	-0.169	-0.046	-0.137	-0.362	-0.315	0.097	-0.501	0.087	-0.448	0.553	0.033	
h	-0.338	-0.070	-0.228	-0.150	-0.014	0.014	-0.130	-0.033	0.516	-0.064	0.012	-0.018	
i	-0.187	-0.217	-0.159	-0.093	-0.239	-0.234	-0.169	-0.290	0.191	-0.104	0.092	0.237	
j	0.064	-0.051	-0.327	-0.322	-0.518	-0.666	-0.031	-0.384	0.309	-0.353	0.246	-0.276	
k	-0.188	-0.171	-0.235	-0.143	-0.140	-0.109	-0.167	-0.203	0.494	-0.131	0.153	0.116	

	b	c	d	e	f	g	h	i	j	k	l	m	n
l	-0.228	-0.030	-0.283	-0.150	0.004	0.039	-0.166	0.040	0.656	-0.017	-0.015	-0.049	
m	0.138	-0.117	-0.020	0.103	0.144	0.004	0.055	-0.190	-0.063	-0.028	-0.062	0.021	
n	0.079	0.276	-0.046	-0.007	-0.014	-0.118	-0.039	0.440	-0.107	0.239	-0.145	-0.108	
o		0.064	0.118	0.045	0.069	0.037	0.176	-0.156	-0.105	-0.119	0.097	0.080	
p			-0.259	-0.031	0.041	-0.076	-0.092	0.142	0.063	0.206	-0.065	-0.288	
q				0.436	0.456	0.568	0.501	-0.018	-0.510	-0.046	0.098	0.514	
r					0.386	0.433	0.228	0.115	-0.323	0.098	-0.027	0.325	
s						0.611	0.289	0.283	-0.296	0.246	-0.228	0.213	
t							0.227	0.248	-0.372	0.203	-0.118	0.222	
u								-0.114	-0.176	-0.136	0.083	0.340	
v									0.001	0.518	-0.369	-0.064	
w										-0.070	0.029	-0.360	
x											-0.342	-0.107	
y												0.043	
z													

This table shows the inter-item correlations between the variables at both levels of analysis.

Variables: a: Party control; b: Gender of governor; c: Government spending; d: Collectivism; e: Black & African American; f: Native American; g: Asian American; h: Native Hawaiian; i: Hispanic American; j: Household income; k: Nonproficiency in English; l: Math grade; m: Persons under 18 years; n: Median age; o: Female persons; p: Social associations; q: Sleep deprivation; r: Preventable hospitalization; s: Obesity; t: Smoking; u: Air pollution; v: Rural area; w: Food environment; x: Outbreak date; y: Density; z: Temperature.

Table 3: HLM contextual model

Fixed effect	Coefficients ^{a)}	Standard error	Confidence interval	p	Effect size ^{b)}	Reliability
Outbreak rate	154.947	0.003	[148.685; 161.209]	<0.001		0.845
<i>State institutions</i>						
Party control ^{e)}	-2.271	0.006	[-14.382; 9.840]	0.715	-4.542	
Gender of governor ^{f)}	-3.441	0.005	[-15.034; 8.152]	0.564	-8.823	
Government spending	0.820	0.001	[-2.318; 3.958]	0.611	0.314	
<i>People cultural values</i>						
Collectivism	0.998	0.000	[0.351; 1.645]	0.004	0.088	
<i>Racial composition</i>						
Black & African American	1.158	0.000	[0.725; 1.591]	<0.001	0.242	
Collectivism (cross-level)	-0.049	0.000	[-0.088; -0.010]	0.014		
Native American	0.763	0.000	[-0.209; 1.735]	0.124	0.100	
Asian American	1.305	0.001	[0.166; 2.444]	0.025	0.441	
Native Hawaiian	1.478	0.000	[0.506; 2.450]	0.538	1.369	
Hispanic American	-0.447	0.000	[-0.915; 0.021]	0.061	-0.031	
<i>Income & education</i>						
Household income ^{c)}	-3.854	0.002	[-7.437; -0.271]	0.035	-2.733	
Nonproficiency in English	2.090	0.001	[0.547; 3.633]	0.008	0.560	
Math grade ^{d)}	-0.002	0.000	[-0.004; 0.000]	<0.001	0.000	
<i>Other demographics</i>						
Persons under 18 years	1.066	0.001	[-0.014; 2.146]	0.053	0.305	
Median age	0.657	0.000	[-0.033; 1.347]	0.062	0.107	
Female persons	0.167	0.001	[-0.880; 1.214]	0.755	0.054	

Fixed effect	Coefficients ^{a)}	Standard error	Confidence interval	<i>p</i>	Effect size ^{b)}	Reliability
<i>Personal health</i>						
Social associations	-2.027	0.000	[-2.911; -1.143]	<0.001	-0.343	
Sleep deprivation	1.557	0.001	[0.412; 2.702]	0.008	0.363	
Preventable hospitalization	0.001	0.000	[-0.001; 0.003]	0.207	0.000	
Obesity	-1.093	0.000	[-1.828; -0.358]	0.004	-0.243	
Smoking	-0.784	0.001	[-3.150; 1.582]	0.516	-0.221	
<i>External health</i>						
Air pollution	3.329	0.001	[1.465; 5.193]	<0.001	1.707	
Rural area	-0.443	0.000	[-0.574; -0.312]	<0.001	-0.014	
Food environment	5.996	0.002	[1.286; 10.706]	0.016	3.945	0.284
<i>Other confounders</i>						
Outbreak date	1.912	0.000	[1.322; 2.502]	<0.001	0.205	0.622
Density	0.050	0.000	[-0.009; 0.109]	0.095	0.000	
Temperature	0.301	0.000	[-0.518; 1.120]	0.472	0.026	

Random effects	Variance	<i>df</i>	χ^2	<i>p</i>
Variance between state intercepts (τ_{00})	4.00E-04	43	350.334	<0.001
Variance within states (σ^2)	1.26E-03			

This table provides the detailed results for the multi-level linear model. Run-time deletion reduced the number of level-1 records from 3118 to 1438, and level-2 from 50 to 48.

Notes: ^{a)} The coefficients are multiplied with 1000 for more intuitive figures. Ditto for the confidence interval. ^{b)} The effect size is calculated as coefficient / standard deviation, again multiplied with 1000. ^{c)} The variable for household income is divided by 10000. ^{d)} All effects for Math grade are from a separately calculated model because the variable is unavailable for 675 counties across the U.S. Consequently, run-time deletion reduced the number of level-1 records to 1140 and level-2 to 43. This updates some *p*-values, but does not affect the sign of the coefficients. ^{e)} Party control: 0 = Democratic, 1 = Republican. ^{f)} Gender of governor: 0 = male, 1 = female.