A Novel Bayesian Spatial–Temporal Approach to Quantify SARS-CoV-2 Testing Disparities for Small Area Estimation

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See also Vaughan, p. 35, Seewald, p. 37, Wang and Chakraborty, p. 49, and Liu et al., p. 60.

Objectives. To propose a novel Bayesian spatial–temporal approach to identify and quantify severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) testing disparities for small area estimation.

Methods. In step 1, we used a Bayesian inseparable space–time model framework to estimate the testing positivity rate (TPR) at geographically granular areas of the census block groups (CBGs). In step 2, we adopted a rank-based approach to compare the estimated TPR and the testing rate to identify areas with testing deficiency and quantify the number of needed tests. We used weekly SARS-CoV-2 infection and testing surveillance data from Cameron County, Texas, between March 2020 and February 2022 to demonstrate the usefulness of our proposed approach.

Results. We identified the CBGs that had experienced substantial testing deficiency, quantified the number of tests that should have been conducted in these areas, and evaluated the short- and long-term testing disparities.

Conclusions. Our proposed analytical framework offers policymakers and public health practitioners a tool for understanding SARS-CoV-2 testing disparities in geographically small communities. It could also aid COVID-19 response planning and inform intervention programs to improve goal setting and strategy implementation in SARS-CoV-2 testing uptake. (*Am J Public Health*. 2023;113(1):40–48. https://doi.org/10.2105/AJPH.2022.307127)

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Since the COVID-19 pandemic started, a growing body of literature has revealed disparities in severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) testing. For example, minority communities of Blacks and Hispanics had lower testing rates.[1] Language barriers and lack of health insurance have also been identified as barriers to SARS-CoV-2 testing.[2,3] Geographical disparities in SARS-CoV-2 testing have been recognized in many studies.[4,5] SARS-CoV-2 testing rates were lower in rural states and higher in well-off suburbs with predominantly White populations.[6,7] Most studies have adopted an ecological analysis of SARS-CoV-2 testing in US counties to examine testing disparities geographically and the association between testing and various area-level contextual factors. Although many found evidence of testing disparities, they rarely quantified the testing gap; in other words, they rarely answered the question: How many tests should be done to remove the disparity?

One exception is Dryden-Peterson et al.,[8] who proposed a rank-based approach to quantify the number of tests needed by zip code tabulation areas in Massachusetts to bridge the disparities in SARS-CoV-2 testing. This approach makes minimal assumptions about data distribution and other factors contributing to testing and infection patterns (e.g., vaccination and nonpharmaceutical interventions). Moreover, ranks are performed to compare areas relative to each other in the study region, so this approach could be more informative to local public health departments for planning and resource allocation.

Although such a rank-based approach is appealing, some issues are also noted, particularly in the context of small area estimation.[9] First, when the geographic areas are small or the relevant population is small, the observed test positivity rate (TPR)—usually calculated as the ratio of the number of positive cases to the number of tests conducted on a daily or weekly basis—would be highly variable and often as extreme as 0% or 100%. In some situations, such as when there are zero tests performed in a specific area or time frame, it is impossible to accurately estimate the number of positive infections (e.g., TPR would be 0/0 mathematically). Second, from a practical perspective, the rank-based approach to examining testing disparity would be more useful if the assessment could be made prospectively, as opposed to retrospectively. For example, if the testing gap (by rate or by number) could be quantified for the weeks ahead, it could greatly support local health departments and health practitioners in setting goals for resource allocation, community outreach and engagement, and educational programs.

The National Institutes of Health–funded Rapid Acceleration of Diagnostics–Underserved Populations (RADx–UP) projects, which focus on enhancing SARS-CoV-2 testing among health disparate populations, could also benefit from the quantification of testing gaps. Indeed, our motivation for developing the proposed 2-step Bayesian spatial–temporal approach arose from the gaps and limitations related to small geographical areas experienced by authors and key community stakeholders in their practice and research responses to the COVID-19 pandemic.

We illustrate the rank-based algorithm proposed by Dryden-Peterson et al.[8] in detail and demonstrate the issues of directly applying this approach for small area estimation. We apply our approach to SARS-CoV-2 testing and infection surveillance data from Cameron County, Texas, where over 90% of the population is Mexican American.[10] Cameron County is also one of the study sites of an ongoing RADx–UP project.[11]

METHODS

We illustrate the issues of the existing rank-based algorithm in small area estimation and describe our proposed Bayesian spatial–temporal approach.

Rank-Based Approach

To illustrate the algorithm proposed by Dryden-Peterson et al.,[8] we used mock data from Table 1 and adapted values from the actual Cameron County COVID-19 surveillance database between March 2020 and February 2022. Let m_{it} denote the number of SARS-CoV-2 tests reported in area (e.g., zip code tabulation areas) i ($i=1, \cdots, I$) at time point t ($t=1, \cdots, T$), and y_{it} denote the number of detected positive cases. To assess the testing disparity, we needed measures of the testing intensity r_{it} (representing the supply aspect) and the epidemic intensity p_{it} (representing the demand aspect). The observed testing intensity was quantified as the testing rate per 10 000 population, calculated as $\hat{r}_{it} = \left(\frac{m_{it}}{N_{it}}\right) \times 10\,000$, with N_{it} being the population size.

The epidemic intensity is measured by the TPR, calculated as $\hat{p}_{it} = y_{it}/m_{it}$ using the observed testing and case numbers. For a given time point t, we ranked areas in the study region by the testing intensity $\hat{r}_{it}$ (e.g., from the lowest to the highest)

TABLE 1— Mock Data Illustrating the Rank-Based Approach to Assessing the Testing Gap Proposed in Dryden-Peterson et al.[8]

GEOID	Population, No.	Testing Frequency	Testing Rate per 10 000	Rank of Testing Rate	Positive Frequency	TPR	Rank of TPR	Gap Exists?	Testing Gaps, No.
GEO1	1190	20	168.1	5	2	0.10	1	No	0
GEO2	1095	10	91.3	2	2	0.20	2	No	0
GEO3	1000	10	100.0	3	5	0.50	4	Yes	4
GEO4	1200	16	133.3	4	4	0.25	3	No	0
GEO5	880	1	11.4	1	1	1.00	5	Yes	14
GEO6	1790	0	0.0	. . .	0	0	. . .	. . .	. . .

Note. GEOID = geographic ID; TPR = test positivity rate. Testing frequency was the number of tests performed for a given area and time. We calculated TPR as the ratio of the number of cases to the number of tests performed. Positive frequency was the number of tested positive cases for a given area and time. We adopted values in the table from the Cameron County COVID-19 surveillance data between March 2020 and February 2022, with the actual GEOID masked and population size slightly adjusted for privacy purposes. GEO6 presented the case this algorithm could not handle and motivated the Bayesian 2-step approach we propose.

and by the epidemic intensity $\hat{p}_{it}$. Our rationale for the rank-based comparison was that if the supply met the demand, the rank of the supply would match the rank of the demand; otherwise, the rank of the supply would be lower than the rank of the demand. In the context of SARS-CoV-2 testing disparities, an area would be considered to have a testing deficiency if its rank of epidemic intensity (i.e., $\hat{p}_{it}$) was higher than its rank of test intensity (i.e., $\hat{r}_{it}$). We calculated the number of tests needed to remove the deficiency as the additional number of tests required to achieve the matching ranks after accounting for the different population sizes by area.

The algorithm can be seen more clearly using the data in Table 1. We present SARS-CoV-2 testing and case data from 6 census block groups (CBGs) in Cameron County. The observed testing frequency ranged from 0 to 20, and the number of positive cases ranged from 0 to 5. We first calculated the test intensity rates (we used per 10 000 population because the CBG-level population size was small) and the TPRs. For example, for area GEO1, the test intensity rate was 168.1 (calculated as [20/1190] × 10 000), and TPR was 0.1 (2/20). At first, we considered only the areas GEO1–GEO5 because GEO6 presented a special issue that we will describe later.

We ranked the 5 areas respective to the testing rate and TPR from lowest to highest. For area GEO1, because its rank of testing rate (i.e., fifth) was higher than its rank of TPR (i.e., first), there was no testing deficiency. For area GEO5, its rank of testing rate (i.e., first) was lower than that of its TPR (i.e., fifth), and hence there was a testing deficiency. To calculate the needed tests, one would first locate the area with the testing rate rank matching the corresponding TPR. For GEO5 with TPR ranking fifth, we located the area with the testing rate ranking fifth—GEO1—because the testing rate for GEO1 was 168.1 per 10 000 population and so should be the expected testing rate for GEO5. After accounting for the population size in GEO5, the expected test frequency was 168.1 × 880/10 000 = 14.8. The difference between the expected and the observed test frequency was then 14.8 − 1 = 13.8, or 14 tests, rounding up. Therefore, there were testing disparities in GEO5, and 14 additional tests should have been performed to address the deficiency.

Although easily implemented by software such as Excel, this algorithm fails to accommodate the case of GEO6, as it has zero tests and zero cases. On one hand, one may argue that zero cases suggest no expected infection, and hence there was no testing deficiency for this area. On the other hand, one could argue that areas with zero tests indicate the highest testing deficiency and hence should be prioritized for testing. Moreover, for area GEO5, the observed TPR of 100% lacks accuracy because of the small number of tests performed (i.e., 1). These issues motivated our proposed Bayesian 2-step approach.

Proposed Bayesian 2-Step Approach

The 2-step approach we propose addressed the estimation and prediction of testing disparity in the context of small area estimation. It has broader applications beyond COVID-19 testing and could be used as a routine analytical framework for infectious disease surveillance systems.

Proposed 2-step approach. In step 1, we employed the Bayesian inseparable space–time models originally proposed in Knorr-Held,[12] which has been popular in disease-mapping models,[13] including models of COVID-19 outcomes.[14] These models provided the estimated TPR, denoted by p_{it} for area i and time t, with accuracy for small area estimation improved by borrowing information across time and space.[15,16] We assumed the observed number of positive cases Y_{it} to follow a binomial distribution with the parameter p_{it}:

$$(1) \qquad Y_{it} \sim Binom(m_{it},\ p_{it}),$$

where m_{it} denoted the total tests performed in area i and time t. On the logit scale, we decomposed the positive rate p_{it} additively as

$$(2) \qquad \text{logit}(p_{it}) = \mu + \mathbf{X}_{it}\boldsymbol{\beta} + u_i + v_i + \psi_t + \boldsymbol{\gamma}_t + \delta_{it}.$$

Here, $\mathbf{X}_{it}$ denotes a vector of potential risk factors or barriers for area i at time t, which could include area-level characteristics, such as the percentage of the population without health insurance, or the percentage of the population vaccinated—if such data were available. The parameter vector exp($\boldsymbol{\beta}$) estimated the odds ratio of infection associated with those risk factors. The main spatial effect was modeled as the Besag-York-Mollié model,[17] with a structured spatial component $\mathbf{u}$ and an unstructured spatial component $\mathbf{v}$. We assumed the structured component to have an intrinsic conditional autoregressive model and the unstructured component to have a normal distribution $N_I(0, \sigma_v^2\mathbf{I})$, where $\mathbf{I}$ indicates the identity matrix, and σ_v^2 the corresponding variance parameter.

We modeled the main temporal effect additively with a structured temporal effect $\boldsymbol{\psi}$ and an unstructured temporal effect $\boldsymbol{\gamma}$, assuming $\boldsymbol{\psi}$ to have a second-order random walk (to impose temporal smoothing) and $\boldsymbol{\gamma}$ to have a normal distribution: $N_T(0, \sigma_\gamma^2\mathbf{I})$. The space–time interaction term $\boldsymbol{\delta}$ can take 4 different

forms as the product of 1 of the spatial main effects (i.e., **u** and **v**) and 1 of the temporal main effects (i.e., **ψ** and **γ**). More details of the model specification can be found in the supplementary materials (available as a supplement to the online version of this article at http://www.ajph.org). We used a conditional predictive ordinate for model selection.[18] Our main interest was the estimated p_{it} but not the individual spatial or temporal component. The inseparable model provided the smoothing needed for the observed TPR with an extreme value (e.g., 100%); moreover, it allowed our imputation of the TPR for areas with 0 tests performed (i.e., $m_{it}=0$). This can be done by setting the observed Y_{it} to NA and the corresponding m_{it} to 1 when fitting the model. We chose the noninformative priors used previously.[12] We used the posterior mean and the 95% credible intervals (95% CrI) when making our inference of the estimated TPR.

In step 2, we ranked the areas using the estimated TPRs from step 1 and then assessed the testing deficiency and calculated the additionally needed tests in the same way as the rank-based approach.

Prospectively predicting the testing gap using the proposed 2-step approach for testing planning. The Bayesian inseparable space–time models allow short-term prediction of the TPR for future events. We emphasize that the prediction is regarding future events and should not be confused with the fitted values from statistical modeling, which are often called the "predicted values." For example, Lieberman-Cribbin et al.[19] used "prediction" to present the estimated positivity rate from fitting a Poisson regression model, which differed from the prediction we are proposing. The predicted TPRs, denoted by $\tilde{p}_{i,t+1}$ or $\tilde{p}_{i,t+2}$, would be obtained from the Bayesian model in step 1. The testing deficiency would be performed by comparing the ranks using predicted TPRs to the ranks of testing intensity at current time t. Other ways to quantify the infection intensity instead of the TPR, such as case acceleration rates or the "doubling rate" of cases for the past weeks, can also be used in ranking.

We assessed the testing gap in 3 ways, reflecting the immediate, short-term, and long-term disparities. We tested the immediate testing disparity by comparing the predicted TPR $\tilde{p}_{i,t+1}$ at week $t+1$ to the current testing rate $\hat{r}_{it}$ at week t. The rank difference between these 2 rates would give the expected tests and hence the testing deficiency. Because the testing rate often fluctuated every week, we compared the predicted TPR to the average testing rate from the previous month for the short-term testing disparity. Finally, we compared the predicted TPR to the average testing rate across the entire study window (i.e., from the time the pandemic started to the time of analysis) for ranking to obtain the long-term testing disparity.

We implemented the proposed method in R version 3.6.3 and R package INLA (R Foundation for Statistical Computing, Vienna, Austria).[20] R code to implement the proposed approach is available at http://bit.ly/3UPLmLI, along with a simulated data set.

RESULTS

We have demonstrated our proposed 2-step approach to SARS-CoV-2 testing disparities in Cameron County, Texas. Cameron County is located in the Lower Rio Grande Valley in south Texas on the US–Mexico border and is among the poorest of US counties, with more than 30% of its residents living in poverty.[10] The prevalence of several chronic disease conditions that have been identified as comorbidities that increase the risk of COVID-19 infection and severity is also exceptionally high, with type 2 diabetes more than 27% and obesity more than 50%.[21–23] More than 90% of the population is Mexican American,[10] and similar to other minority groups, this population has seen disproportionately high infection and fatality rates since the first local reported cases of COVID-19 on March 18, 2020.

Several COVID-19 mitigation responses led by local public health departments and government–academic partnerships for community-based intervention programs have focused on improving SARS-CoV-2 testing and vaccination in Cameron County. The mitigation strategies targeted small, defined areas of the county where populations with health disparities (e.g., low income, low educational attainment, crowding) reside. When conducting education and outreach (particularly door-to-door) efforts, information about the testing pattern at granular spatial levels such as the CBGs is more desirable. The CBG-level population size was approximately 1900 on average and ranged from 208 to 14 481; the small population size posed special challenges to providing accurate estimates of infection and testing.

A total of 667 052 SARS-CoV-2 testing records were reported in Cameron County between March 18, 2020 and February 10, 2022. Of these, 70 795 (10.6%) were positive. We were able to geocode the majority (89.9%) of the testing records to obtain the corresponding CBG. We included only the polymerase chain reaction (PCR) tests (71.7% of all reported tests) in quantifying the testing gap because SAR-CoV-2 infection was confirmed only by the

PCR test. We included 222 CBGs in our analysis (shown in Section A, available as a supplement to the online version of this article at http://www.ajph.org, for the geography). The data-processing flowchart is presented in Section B (available as a supplement to the online version of this article at http://www.ajph.org). The weekly trend of SARS-CoV-2 infection and testing patterns for Cameron County as a whole had 4 distinctive peaks (shown in Section C, available as a supplement to the online version of this article at http://www.ajph.org). However, we observed substantial variation in both infection and testing rates at the CBG level.

We applied our proposed approach to weekly CBG-level testing data. Based on the conditional predictive ordinate, we considered the Bayesian inseparable model with type II interaction the best, so we used it for inference. Detailed results from all models can be found in Sections E through G (available as a supplement to the online version of this article at http://www.ajph.org). Figure 1 presents the temporal trends of the observed TPRs (black dots) and model-based TPRs (blue line, with 95% CrIs in a lighter shade) from 6 selected CBGs. Areas 1 and 2 represent CBGs with relatively large population sizes (~14 000 and ~13 000, respectively; we do not include the exact population size to avoid identification of specific areas), and the TPRs were fairly stable and followed the overall pattern at the county level. Areas 3 through 6 represented CBGs with much smaller population sizes: from approximately 300 to approximately 1000 individuals. Given the sparse testing data, the observed TPRs fluctuated substantially from week to week, with many extreme values of 0% and 100%. Moreover, these areas also had weeks when no tests were conducted; hence there is no observed TPR (dots not shown).

Our model fitted the observed data very well: for areas with sufficient tests (areas 1 and 2), the fitted lines followed the observed points very closely. For areas with sparse tests (areas 4–6), model-based estimates provided the needed shrinkage on extreme values of the observed TPR, which better reflected the underlying infection trend. Meanwhile, although the model borrowed information across CBGs, it also preserved any local pattern that deviated from the overall county trend (e.g., in area 3). After we obtained the model-based TPR, we calculated the testing deficiency by week for each CBG. Figure 2 presents the number of additional tests needed during the study time frame, in which the county-level TPR was overlaid (red line) with the y-axis scale on the right. Figure 2, panel a, displays the number of CBGs (of the total 222) that we identified as having a testing gap, and panel b presents the variation of additional tests from these CBGs. Throughout the period, 217 of the 222 CBGs experienced testing deficiency at some point. The testing deficiency ranged substantially and differed by waves. Our analysis also suggested that substantial tests should have been performed even during the low infection period (e.g., February–May 2021).

Figure 3 presents the predicted testing disparity by CBG based on the predicted TPR for the week of February 7, 2022, using all observed data from March 18, 2020 through February 7, 2022. For the immediate testing disparity, we used the testing rate from the preceding week (i.e., January 31–February 6, 2022) for testing ranks. For short- and long-term disparities, we used the testing rate from the preceding month (i.e., January 10–February 6, 2022) and the average testing rate across the entire study period (i.e., March 18, 2020–February 6, 2022), respectively. Although the areas with immediate or short-term testing deficiencies tended to have increased infection rates, the areas predicted to have long-term testing disparity tended to be more rural and experienced limited access to care (including COVID-19 testing) even before the COVID-19 pandemic.

DISCUSSION

We have demonstrated our proposed novel Bayesian 2-step approach to identifying SARS-CoV-2 testing disparities and quantifying testing deficiencies in the context of small area estimation. Our analytical framework can provide key information to aid local public health departments in COVID-19 response planning and inform intervention programs, such as RADx–UP, to improve goal setting and strategic implementation of interventions to increase SARS-CoV-2 testing uptake.

Strengths

Our proposed analysis has several advantages over those proposed in other studies for identifying SARS-CoV-2 testing disparities. First, we developed a novel statistical framework and a data-driven approach to understanding testing disparity in the context of small area estimation. To our knowledge, this is the first study to evaluate population-level SARS-CoV-2 testing deficiencies with the spatial granularity of CBGs. Second, we provided a sophisticated spatial–temporal approach to better estimate infection intensity (e.g., TPRs) with sparse or no testing data, so that one can assess testing disparities more accurately. Third, we went beyond the qualitative assessment of

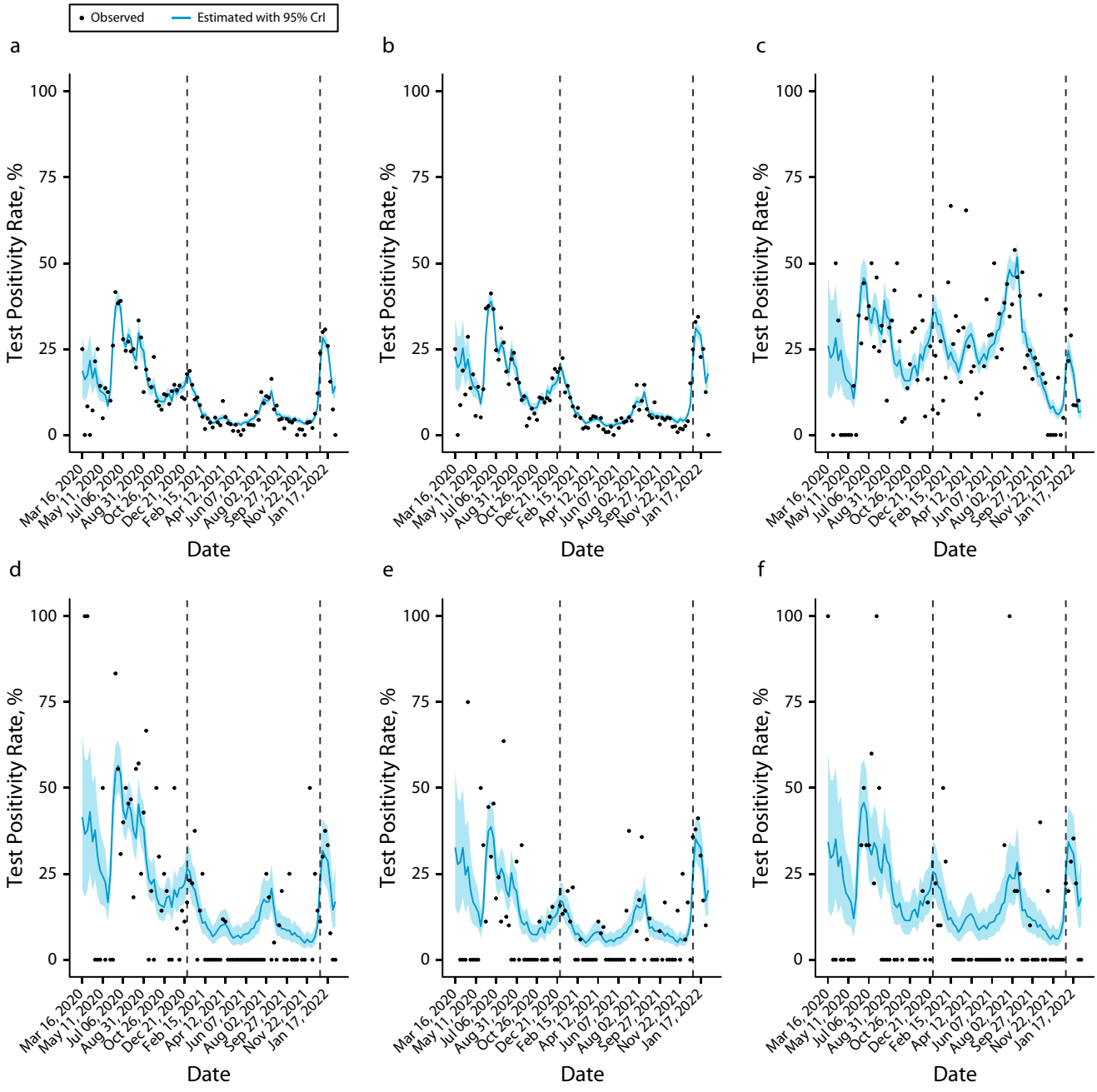

FIGURE 1— Selected Areas With Observed COVID-19 Test Positivity Rate and Model-Based Estimates for (a) Area 1, (b) Area 2, (c) Area 3, (d) Area 4, (e) Area 5, and (f) Area 6: Cameron County, TX, March 2020–February 2022

Note. CBG = census block group; CrI = credible interval; TPR = test positivity rate. TPR is shown by the black dots; 95% credible intervals is shown in the light blue shade. The vertical dashed line represents January 1 of years 2021 and 2022. Areas 1–2 represent CBGs with a relatively larger number of tests, and the fitted lines followed closely with the observed TPRs, with narrow 95% CrIs. For areas with sparse tests (areas 4–6), model-based estimates provided the needed shrinkage, which we obtained by borrowing information across space and time, where the extreme values in observed TPRs were shrunken to the overall average and resembled the general trend at the county level.

whether there are testing gaps. We provided valuable quantification of the additional tests needed. Fourth, our proposed spatial–temporal framework has the flexibility to accommodate the ever-changing dynamics related to COVID-19 when assessing testing disparity, which is particularly important.

The World Health Organization suggests that 10 to 30 tests should be performed for every positive case to control the spread of disease.[24,25] Such simple

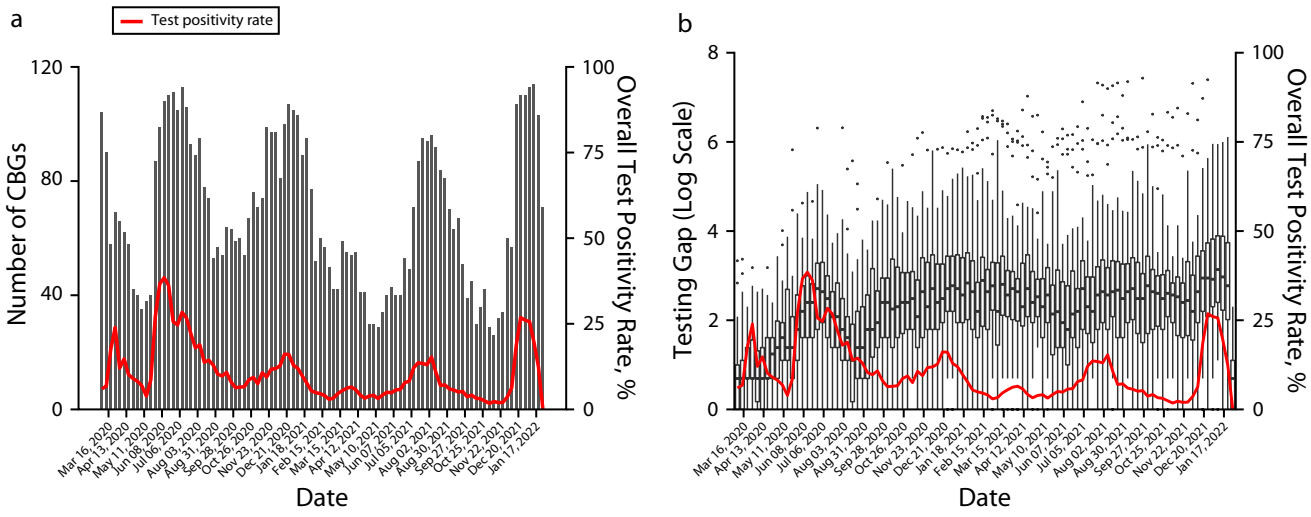

FIGURE 2— Weekly Number of Tests Deficiency by (a) Number of CBGs, and (b) Testing Gap: Cameron County, TX, March 2020–February 2022

Note. CBG = census block group. County-level overall test positivity rate was overlaid as the red line with the y-axis scale on the right. Panel a presents the number of CBGs that were identified with testing deficiency, by each week. Panel b presents the boxplots of the number of needed tests from these CBGs with testing deficiency. For example, 111 CBGs (of the total 222) experienced testing deficiency during the week of July 7, 2020 (panel a); among these CBGs, the additional needed tests had a median value of 410 and ranged from 1 and 548 (panel b).

calculations using the test and case ratio do not account for the changing intensity of the pandemic and may increase testing disparity across demographic subgroups or geographical areas. For example, CBGs that have not received sufficient tests would show lower infection rates, which would suggest even lower testing needs. More importantly, the ability of communities to implement the suggested number of tests depends on the availability of the tests, different tool kits, testing facility capacities, staffing, and many other factors. Finally, by using a Bayesian analytical framework, we were able to predict testing deficiency based on the local testing and infection patterns. This fills an important gap in the current research of SARS-CoV-2 testing disparities, in which testing gaps have always been identified retrospectively.

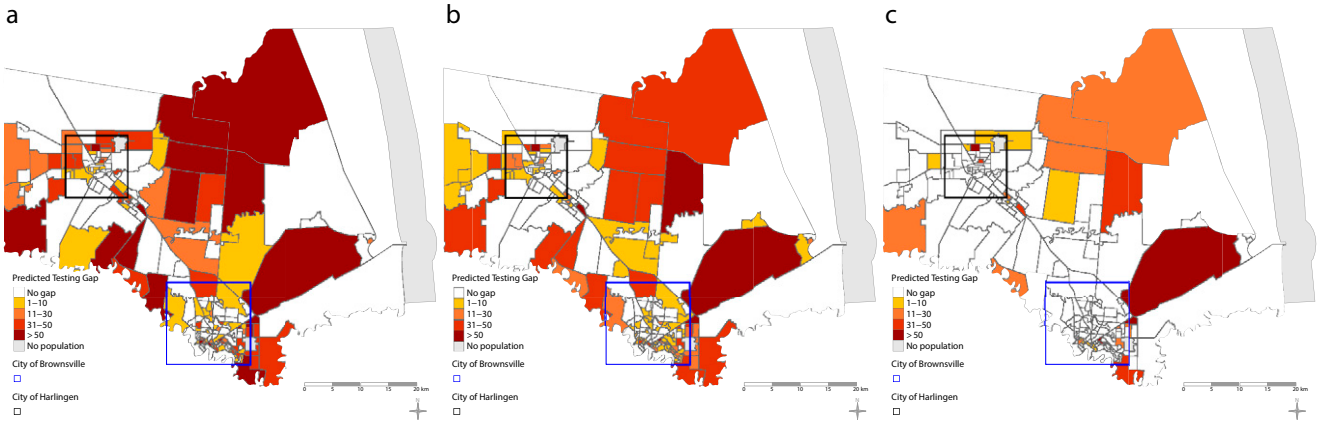

FIGURE 3— Predicted Testing Disparity by Census Block Group for (a) Immediate Testing Deficiency, (b) Short-Term Testing Deficiency, and (c) Long-Term Testing Deficiency: Cameron County, TX, February 7–13, 2022

Note. We used the observations before February 7, 2022, for comparison. Panel a presents the immediate testing deficiency, where testing rate was from the previous week (i.e., January 31–February 6, 2022) when performing the testing ranks. Panels b and c present the short-term testing deficiency using testing data from the previous month (i.e., January 10–February 6, 2022) and long-term testing deficiency using the average testing rate across the entire study period, respectively.

We argue that, in practice, the quantification of testing gap and deficiencies prospectively provides more useful and needed information for COVID-19 response.

Limitations

Our article has some limitations. First, we used only PCR-reported positive tests in our analysis. PCR is the most accurate SARS-CoV-2 testing method and, indeed, was used for the majority of the tests in the SARS-CoV-2 surveillance data used in this analysis. As other over-the-counter tests and testing methods become more available, testing results may not be captured in official epidemiologic surveillance databases, which will affect testing gap assessment. We consider this deficit a reporting issue commonly seen in surveillance systems. Purportedly, if every SARS-CoV-2 test result was captured by a surveillance database, our approach would be able to estimate the testing gap. Second, we were not able to incorporate the SARS-CoV-2 transmission modes and contact-tracing information in quantifying the needed tests, which would be highly informative in identifying who should be tested and where testing might be most convenient. However, as this pandemic has shown, contact-tracing data are extremely challenging to collect[26] and generally have been unavailable for analytical purposes at the population level. Third, about 10% of the testing records could not be geocoded, as they either had missing addresses or used a post office box.

Conclusions

From an implementation science perspective, we believe that our proposed analytical framework offers policymakers and practitioners a tool for understanding SARS-CoV-2 testing disparities in geographically small communities. Local public health officials and practitioners often desire spatial granularity, such as which street blocks they should go to for the community educational program or door-to-door visits to promote COVID-19 testing. Our proposed analytical framework provides a data-driven approach for this decision-making process. Community leaders, with this understanding and the knowledge of which small geographically bounded areas to prioritize, can address testing disparities with coordinated multilevel interventions by enhancing access to testing, improving outreach to assist in education and navigation to testing, and implementing effective large and small media messages to promote testing tailored to the population. Future research on the use of this approach and the derived data to drive these decisions should be rigorously evaluated to determine whether testing gaps across locations are eliminated in health disparate populations. AJPH

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CONTRIBUTORS

C. Bauer conceptualized and designed the analysis. C. Bauer, X. Li, and K. Zhang analyzed the data and wrote the initial draft of the article. M. Lee, E. Guajardo, and B. Reininger acquired the data. M. Lee, S. Fisher-Hoch, J. McCormick, M. E. Fernandez, and B. Reininger revised the article. M. E. Fernandez and B. Reininger acquired financial support for the project. All authors interpreted the results.

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CONFLICTS OF INTEREST

The authors report no conflicts of interest.

HUMAN PARTICIPANT PROTECTION

The University of Texas Health Science Center School of Public Health institutional review board approved this study (no. HSC-SPH-20-1372).

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