No increase in COVID-19 mortality after the 2020 primary elections in the USA*

Eric M. Feltham†‡, Laura Forastiere†§, Marcus Alexander†, Nicholas A. Christakis†∥

†Yale Institute for Network Science, Yale University
‡Department of Sociology, Yale University
§Department of Biostatistics, Yale School of Public Health
∥Department of Statistics and Data Science, Yale University

07 October, 2020

Abstract

We examined the impact of voting on the spread of COVID-19 after the US primary elections held from March 17 to July 11, 2020 (1574 counties across 34 states). We estimated the average effect of treatment on the treated (ATT) using a non-parametric, generalized difference-in-difference estimator with a matching procedure for panel data. Separately, we estimated the time-varying reproduction number ($R_t$) using a semi-mechanistic Bayesian hierarchical model at the state level. We found no evidence of a spike in COVID-19 deaths in the period immediately following the primaries. It is possible that elections can be held safely, without necessarily contributing to spreading the epidemic. Appropriate precautionary measures that enforce physical distancing and mask-wearing are likely needed during general elections, with larger turnout or colder weather.

Introduction

COVID-19, like any serious outbreak of a contagious disease, can place the virtues of public health and civic engagement into direct conflict. Epidemics pose a difficult problem for the democratic process, which relies on elections so that the public may hold their leaders accountable for policies enacted to manage the epidemic in the first place. Even if the will

---

*We thank Benjamin Snyder and Bradley Yam for research assistance. Support for this research was provided by the Robert Wood Johnson Foundation. The views expressed here do not necessarily reflect the views of the Foundation.

†Corresponding Author: Yale Institute for Network Science, 17 Hillhouse Ave, New Haven, CT 06520; eric.feltham@yale.edu
of the majority is aligned with the public interest of most effectively containing, mitigating, and recovering from an epidemic, participation in elections is necessary to translate the majority’s preferences for candidates best deemed capable of fighting the epidemic. But when most citizens vote in-person, participation in elections itself can contribute to worsening the epidemic. Both from a public health perspective and an individual point-of-view, the question arises whether holding elections during an epidemic is safe.

In the Spring of 2020, the United States was in the midst of its Presidential primary elections when the COVID-19 pandemic began. Concerns immediately arose about the potential of in-person voting to lead to a rise in community transmission of the SARS-CoV-2 virus, making elections into potential super-spreader events with adverse consequences of excess, otherwise-preventable deaths in every community, across all US counties, where polling takes place.

Election procedures themselves have also become a partisan issue under COVID-19: with some Democrats attempting to signal a commitment to public health, by avoiding the polls, and some Republicans signaling defiance of COVID-19, by showing up in person. This is further associated with the fact that COVID-19 is viewed in partisan terms by the electorate.

Most saliently, COVID-19 sparked a partisan uproar over postponing primaries and mail-in voting, reaching its zenith with the Wisconsin Supreme Court battle in Wisconsin, where a Republican effort blocked an attempt by Governor Tony Evers, a Democrat, to reschedule the primary election. The decision to hold the election was met with great controversy on the other side of the aisle. By contrast, a number of majority Democratic states successfully moved their primaries. Yet, it is not clear whether community spread of the virus was higher or lower than it would have been on the rescheduled dates.

Troublingly, the discussion so far has occurred in the absence of a comprehensive assessment of the actual risk of voting – with the exception of two prior studies of Wisconsin, which reached conflicting conclusions regarding the impact of in-person voting on the subsequent course of the COVID-19 epidemic in that state. The COVID-19 epidemic thus also highlights the important role of science and transparency for policy-making in a democratic society.

We examined the impact of voting on the spread of COVID-19 after the primary elections for the entire United States. Specifically, our analysis applies two separate statistical approaches to evaluate a possible impact on the course of the epidemic following a primary election with in-person voting.

Modeling the spread of COVID-19 is particularly challenging for two major reasons. The first is the quality of the underlying data. The US has struggled to test an adequate number of individuals, and especially early on, there were not enough tests to adequately track the number of cases. Furthermore, testing relies on the willingness and ability of individuals to get tested and of institutions to test them. As a consequence, to track the course of the epidemic, we examined mortality data, which is the best measure of the impact of COVID-19 currently available. We use county-level daily mortality rates in our matching model, and state-level daily mortality counts for the epidemiological model.

The second issue relates to the fact that many of the available statistical tools make assump-
tions that are not appropriate to modelling the spread of a virus. This difficulty lead us to apply two very recent techniques from statistical and epidemiological modeling which better capture the dynamics of an epidemic. Our first approach applies a non-parametric differences-in-differences estimator for panel data, matching counties with similar socio-demographic characteristics and similar dynamics of the epidemic before the time of the elections. The second approach applies a recent epidemiological model, which models the reproduction rate of COVID-19 over time, relying on daily death counts as a function of model-specified interventions.

With both methods, we find no increase in overall COVID-19 mortality due to in-person voting in the primaries that took place in the spring of 2020 in the USA.

Data

County-level COVID-19 deaths were collected from a repository maintained by *The New York Times* of data from local and state health agencies. We only make use of the COVID-19 death counts, rather than positive test results, as our outcome measure due to (1) limited and changing testing capacity; (2) bias with respect to COVID-19 testing implementation; and (3) the lack of available test data at the county level. We removed observations not linked to any data not attributable to any specific US county. Additionally, we retained observations where the cumulative death counts declined from one day to the next, marking those changes as zero counts. We analyze data from 1574 counties across 34 states, out of 3141 counties in 50 states, from March 01 to August 01, 2020.

We exclude states that had early primary elections, before the material impact of the epidemic; specifically, we exclude California, Texas, and Massachusetts (which held their primaries on March 03). Of course, COVID-19 may have arrived in these states as early as January, prior to the start of the *New York Times* data collection effort. Additionally, we exclude 15 states that did not have COVID-19 data available until after their primary elections were held (AL, AR, ID, ME, MI, MN, MO, MS, NC, ND, OK, TN, TX, VT, and VA – all of these primary elections were held on either March 3 or 10.). Additionally, we make use of county-level demographic data from the American Community Five Year Survey.

Methods

Modelers of COVID-19, and interventions that affect its spread, face a methodological dilemma: whether to apply an epidemiological or an econometric technique. The first faces difficulties with identification, and reliance upon estimated epidemiological parameters that may change as the pandemic unfolds, which is increasing in the complexity of the process model. The second brushes against the limitations of many common statistical approaches (reviewed below).
Matching method

Existing econometric analyses of the impact of non-pharmaceutical interventions on the spread of COVID-19 apply either interrupted time series\textsuperscript{13}, or standard difference-in-differences estimation\textsuperscript{15}. The primary limitation in the use of interrupted time series is that it adopts a linear contagion process, thereby relying on the assumption that, without the intervention, the spread of COVID-19 could have been predicted from the model fit to the process from the pre-intervention period, ruling out other time-varying factors. Specifically, Fowler et al. (2020)\textsuperscript{13} and Hsiang et al. (2020)\textsuperscript{14} estimated fixed-effects models that indirectly account for the contagion process as reduced-form models justified on the assumption that the proportion of susceptibles approaches unity.

However, we do not find this assumption justified in the absence of reliable testing data in the US; while it may be reasonable in a study of the stay-at-home orders, which occurred early in epidemic-time, our study duration ranges from March to August. Additionally, this and many other existing approaches rely on the assumption that cases are log-linear, which induces bias, especially when the mean counts are low and overdispersed, which holds true in our county-level daily death data. Furthermore, our data is strongly zero-inflated, limiting the utility of traditional count models.

To avoid relying on parametric models for the dynamics of COVID-19, the difference-in-differences approach measures the effect of an intervention by comparing the outcome change over time across treatment groups. However, this strategy requires that, in the absence of the intervention, the outcome would have followed the same trend in the treated and control arms. In addition, the standard difference-in-differences technique is used when the intervention occurs for all treated units at a specific time point.

In the wake of these difficulties, we apply a non-parametric, generalized difference-in-differences estimator with a matching procedure for time-series cross-sectional data to estimate the average effect of the treatment on the treated (ATT)\textsuperscript{7}. This approach makes less stringent assumptions than many traditional approaches for the estimation of causal effects with panel data. As opposed to the standard difference-in-differences estimator, this method relies on a parallel trend assumption only after conditioning on both baseline and time-varying covariates before the intervention, including the pre-treatment outcome history.

Given the underlying contagion process, we assume that the primary elections are durable changes: once an election is held, its effect does not reverse at some time after the primary, but rather alters the epidemic trajectory if it has an effect. Under this assumption, our causal effect of interest is the average difference between the treated and control counties in the daily death rate. This can be written as:

\[
\delta(F, L) = E[Y_{i,t+F}(\{X_{i,t+1}\}_{t=1}^{F} = 1, X_{i,t} = 1, X_{i,t-1} = 0, \{X_{i,t-l}\}_{l=2}^{L}) - Y_{i,t+F}(\{X_{i,t+1}\}_{t=1}^{F} = 0, X_{i,t} = 0, X_{i,t-1} = 0, \{X_{i,t-l}\}_{l=2}^{L}) | \{X_{i,t+1}\}_{t=1}^{F} = 1, X_{i,t} = 1, X_{i,t-1} = 0]
\]

where \(F\) is the number of days after the treatment administration for which we estimate the
difference in the potential outcomes. \( F = 0 \) represents the administration of the treatment. \( 1_F \) is a vector of ones, with length equal to the number of leads; \( 0_F \), accordingly, is a vector of zeros. Here, the first term represents the potential outcome in each county, where the election takes place. The second term is the potential outcome without the treatment. \( L \) is the number of periods prior to treatment administration, for which we adjust our estimates.

This approach relies on two key assumptions:

1. Non-interference between units. This method assumes that there is no interference between counties over the study period. This assumption is clearly not justified in general for the spread of COVID-19. However, voting is a fundamentally local activity, and individuals typically do not travel outside of their neighborhood to cast a ballot, let alone across county lines. Furthermore, mobility in the spring and summer of 2020 was below usual levels, in the wake of stay-at-home orders and an increase in the number of individuals who work from home. Consequently, we believe that it is unlikely for an election held in a single county to yield an increase in infections in other counties, over the study follow-up period we consider.

2. Parallel trends, conditional on treatment, covariate and outcome histories for \( L \) days before the day of the elections. This assumption relaxes sequential ignorability – that the treatment assignment is unconfounded, conditional on the covariate and outcome history up to \( t - L \). Instead, it allows for the presence of unobserved confounding variables. The parallel trend assumption holds conditionally on the treatment, covariate, and outcome histories for \( L \) days before treatment administration.

The choice of \( L \) is subject to a bias-variance tradeoff: choosing a longer lag period, on which to match, decreases the bias of the model, insofar as treated and matched counties are increasingly similar with respect to the overall COVID-19 trend. However, a longer lag period leads to greater difficulty in matching, increasing the variance of the estimator. Note that matching on the cumulative death rate implicitly contains information about the whole history of the epidemic trend, adjusting not only for the daily deaths over the lag period, but the total deaths accrued over the reporting window. We feel that this adjustment better matches counties in terms of their COVID-19 trends.

The choice of \( F \) faces similar constraints: we desire a period sufficiently long, after the administration of their “treatment” (the primary election), to capture deaths that are plausibly due to infections contracted on the day of the primary election. However, extrapolation is increasing in \( F \), as other interventions obtain in counties that alter the course of COVID-19. Consequently, we restrict our analysis to an epidemiologically-informed window after the primary election. We capture deaths from first-hand infection on primary day by looking at a period from 13 to 32 days after the primary election in a given county. We choose this window based on epidemiological estimates of the incubation period, and the time from symptom-onset to death\(^8\).

Figure 1 represents this information as the distribution of times from infection to death. We define this quantity as the sum of two, independent, gamma distributions\(^8\):
Figure 1: Distribution of times from infection to death: The shaded region corresponds to the period in which we expect 60% of the deaths to occur for those that die due to infection. The distribution is based on estimates from the epidemiological literature on COVID-19.
\[ \pi \sim \text{Gamma}(5.1, 0.86) + \text{Gamma}(17.8, 0.45) \]

We choose our post-treatment window-of-interest to be bounded by the 20th and 80th percentiles of this distribution, given by 13 and 32 days after the primary election. Consequently, we consider the administration of the treatment to occur 10 days after a primary election; this is the point at which we expect the first deaths from infection on primary day to likely occur. We treat the range from 10 days prior to 10 days after the primary election to be the pre-treatment period for the purpose of matching.

Figure 2 presents the distribution of the treatments over time in the 34 states used in our analyses. While we present county-level data, each primary occurs at the state-level.

Figure 2: Distribution of windows in which we would expect deaths due to a primary election to occur. The red lines represent the date of the primary, in each state. The pink region corresponds to the middle 60% of the distribution of time to death, in each state, after the primary. The blue areas are outside of this window, before and after the primary elections. States that are entirely blue are mail-in or had elections before the onset of COVID-19 in that state. Grey areas in the plots represent periods without COVID-19 death count data, at the county level. This plot displays the total set of states whose counties are used as treated or control units. We notably exclude states with early primaries (CA, MA, and TX) and due to incomplete deaths data in recent history (CT) (since the primary was held on 11 August).
The matching procedure contains two steps: exact matching on the pre-treatment history of each county, and matching refinement from the set of exact matches. That is, if we consider Chippewa County, WI, which held its primary on April 07, we consider the set of counties that have not held their primary before April 07 + 10 + $F$ (we consider the treatment to be administered with a lag of 10 days after the primary election, as discussed below) as possible matches for estimation. This amounts to exact matching on the treatment history in historical time. Our matching period ranges from 20 days before April 07 + 10 days, and we only consider covariate history over this period for possible controls. After exact matching on the treatment history, we conduct matching refinement on a set of county-level time-invariant demographic characteristics, which are relevant to behavior and the spread of COVID-19 in a given county: the percentage African-American, the log median income, the percentage of the population with a bachelor’s degree, the population density, the log of the population, the percentage 65 years of age and above, the unemployment rate, and Trump’s share of the vote in the 2016 General Election. Additionally, to adjust for the features of the epidemic, we adjust for the date of the first reported infection in that county, and one time-varying feature, the cumulative county-level death rate.

We refine the set of potential matches to the five closest matches with respect to Mahalanobis distance:

$$S_{i,t}(i') = \frac{1}{L} \sum_{l=1}^{L} \sqrt{(V_{i,t-l} - V_{i',t-l})^T \Sigma_{i,t-l}^{-1} (V_{i,t-l} - V_{i',t-l})}$$

Where $i' \in M_{i,t}$ is a unit in the set of potential matches to a treated unit $i$, and $V_{i,t'}$ is the set of time-varying covariates for which we adjust in the pre-treatment lag period, and $\Sigma_{i,t'}$ is its sample covariance matrix. Note that the distance is computed for each potential match, for each day in the pre-treatment lag period, which is then averaged over that period (from $t - L$ up to the treatment administration, 10 days after the primary).

Our estimator of the ATT is given by

$$\hat{\delta}(F, L) = \frac{1}{\sum_{i=1}^{N} \sum_{t=L+1}^{T-F} D_{i,t}} + \sum_{i=1}^{N} \sum_{t=L+1}^{T-F} D_{i,t} \{(Y_{i,t+F} - Y_{i,t-1}) - \sum_{i' \in M_{i,t}} w_{i,t}(Y_{i',t+F} - Y_{i',t-1})\}$$

$D_{i,t} = 1$ when a unit-observation changes treatment status at $t - 1$ to $t$, and has $\geq 1$ matched unit. We use the observed history of both the pre-treatment-treated and the pre-treatment-untreated; we match treated counties to untreated counties for estimation of the ATT.

**Epidemiological model**

We modify and apply a recent epidemiological model that uses a Bayesian estimation procedure to estimate the transmissibility and mortality of COVID-19\(^8\). We apply this model to daily COVID-19 death counts aggregated at the state-level, from 01 March 2020 to 21 May 2020.
This model is specifically tailored to model the spread of a virus through a population, and makes direct use of epidemiological parameters, including the distribution of times from infection to death and estimates of the infection fatality rate in order to estimate the reproduction rate backwards, in time, from the observed death count at a given time. We do not rely on this method to infer causal conclusions; instead, we use it as a validation approach for the matching method developed above, and choose it for its strength as a process model of virus transmissibility. We include in this model two interventions that could have had an impact on the spread of COVID-19: the state-level stay-at-home orders, and the primary elections themselves.

We regress the reproduction rate, $R_t$, on binary interventions to infer their impact on the transmissibility of the infection.

$$R_{t,m} = R_{0,m}e^{-\sum_k^{K} \alpha_k I_{k,t,m} - \beta_m I^*_t}$$

Where $I^*_t$ is the indicator for the last intervention that was implemented in state $m$, during the epidemic.

$R_{0,m}$ is the baseline reproduction rate, which is given a prior, as $R_{0,m} \sim N^+(3.28, |\kappa|)$, such that $\kappa \sim N(0, 0.5)$, based on estimates from the literature.

$k$ indexes the interventions, which are the primary-election and the stay-at-home order, so that $K = 2$.

The priors for the effects are given as:

$$\alpha_K \sim \text{Gamma}(1/K, 1) - \frac{\log(1.05)}{K}$$

and

$$\beta_1, ..., \beta_m \sim N(0, \gamma)$$

such that $\gamma \sim N^+(0, 0.2)$, where $m$ indexes each US state included in the model.

However, $R_t$ is a latent quantity, only observable vis-a-vis infections and deaths. Consequently, we model the expected number of infections on day $t$ in $m$:

$$c_{t,m} = (1 - \frac{\sum_{i=1}^{t-1} c_{i,m}}{N_m})R_{t,m} \sum_{\tau=0}^{t-1} c_{\tau,m} g_{t-\tau}$$

The number of infections at $t$ arises from the past infections, weighted by the generation distribution for infections. This term is scaled by two components: the reproduction rate, which tracks the number of secondary infections, and an adjustment factor representing the proportion of susceptibles in $m$. The generation distribution gives the time from an
infection in $i$ to the infection of $i$’s contacts; it is approximated by the estimated serial interval distribution for COVID-19, and is given as $g \sim \text{Gamma}(6.5, 0.62)$.

Additionally, since we only rely on death data, the number of cases is also an unobservable in our application; the cases arise from a model of the daily death counts:

$$d_{t,m} = ifr^* \sum_{\tau=0}^{t-1} c_{\tau,m} \pi^*_{t-\tau,m}$$

The expected number of deaths at $t$ is the sum of previous infections weighted by the probability of death. The probability of death itself is given by the distribution of times from infection to death (used to define the post-treatment window for the matching approach). The infection fatality ratio is taken to be a random quantity: product of the estimated rate in the literature and a normal distribution to capture uncertainty in the estimate:

$$ifr^*_m = ifr^*_m N(1, 0.1)$$

The directly observed daily deaths, $D_{t,m}$ are taken to follow a negative binomial distribution:

$$D_{t,m} \sim \text{Negative Binomial}(d_{t,m}, d_{t,m} + \frac{d_{t,m}^2}{\Psi})$$

with $\Psi \sim N^+(0, 5)$

**Results**

**Matching method**

We observe that the spring 2020 primary elections did not lead to a detectable overall increase in the COVID-19 mortality rate from elections held across the US, through the application of our matching procedure and non-parametric estimation of the ATT over a window in which we expect first-hand deaths to occur from any infection on primary day.

Figure 3 displays the standardized average difference between the treated and control units over the lag window of 20 days. This plot displays the covariate balance before and after matching refinement, using Mahalanobis distance. After refinement, to the closest five counties for each treated unit, we observe moderate imbalance, which improves substantially through matching refinement.

Our matching variables essentially fall into two categories: direct characteristics of the epidemic trend, and county-level demographic features which are relevant insofar as they impact the epidemic. For the former, we match on the cumulative death count and the date of the first reported case. These serve as the most important indicators of a county’s status as an effective counterfactual for some treated county. For the latter, we include (log) population size and population density, which alter how the virus moves through the
Figure 3: Covariate balance on cumulative death rate, date of the first reported case, median income, population size, population density, percentage African-American, percentage with a college degree, Trump’s share of the vote in 2016, and the unemployment rate. All covariates are at the county level. The left-hand-panel displays the balance prior to matching refinement, and the right-hand-panel displays the balance after matching refinement to the five-best matches to each treated county. The plot is in terms of the standardized mean difference between the treated and control units, over a pre-treatment lag period of 20 days (see Supplement for calculation).
population. The other demographic characteristics may be relevant to how people behave, which in turn may affect the spread of the virus: e.g. counties in which Trump had a higher share of the vote may be less likely to practice social distancing; counties with a higher percentage of African-Americans or that are lower in terms of median income may have a greater share of essential workers. Treated counties tend to have lower median income, and a higher proportion of African-Americans. While treated counties tend to be smaller in population, they tend to be denser. The balance plot reveals that both the set of potential matches and the best matches, on average, tend to have a higher cumulative death rate, and a more recent date of first reported case. Nevertheless, the cumulative death rate is relatively stable over the lag window, indicating that the parallel trend assumption seems to hold between the treated and matched control counties. Additionally, we feel that the balance of the remaining variables falls within acceptable range for the purposes of inference.

Using a difference-in-differences estimator, under the assumption of parallel trends conditional on the obtained matched sets, we report a negative and significant ATT in the post-treatment window, presented in Figure 3. If anything, our results are consistent with a (negligibly small) decrease in risk of death after an election is held, on the order of less than 1 in a million fewer deaths.

**Epidemiological model**

We fit this model to states, over time, up to May 21. We observe a moderate impact of the lockdown, and a statistically insignificant and negative estimate of the primary elections. Our model gives common estimates for the overall effect of the stay-at-home orders and the primary elections.

Figure 4 displays results from Florida and Illinois, illustrating the model fit to the daily death count trend for each state, and the inferred reproduction number over the same period. Across all the states, we see well behaved decreases in the estimated contagion of the virus in response to the lockdowns (whether the lockdown occurred before or after the primary election), and no material increase in the estimated contagion with the primary elections.

A variety of further robustness checks are in the SI.

**Discussion**

Valid estimation in this context requires that the treatments themselves are exogenous to the outcome and that there is sufficient variation of the treatment onsets to find a suitable set of matches for each treated unit. The rolling schedule of the primaries, from February to August, helps to satisfy the latter condition. Furthermore, while states are not randomly assigned to election days, and states with later elections may differ in their characteristics from those with earlier elections, we observe sufficient county-level variation on the features of interest to obtain acceptable matching to the treated units. While several states had primaries that were either cancelled or rescheduled due to COVID-19, we feel justified in treating cancelled primaries as control units over those dates. Furthermore, the rescheduled
Figure 4: The average treatment effect on the treated, across all treated counties, from 10 to 36 days after the primary election. The pink region corresponds to the middle 60% of the distribution of times from infection to death (13 to 32 days after the election treatment). The y-axis displays the average daily death rate difference, county-level, in terms of deaths per 1000 people.
Figure 5: Example results from FL and IL. The left-hand side shows the model’s fit to the daily death counts over time. The blue shaded regions show the 95%, 90%, and 50% uncertainty intervals of the model fit. The vertical lines show the primary date, the expected median-time-to-death for an infection on primary day, and the stay-at-home order. The right-hand side show the model estimates for the change in the reproductive rate of COVID-19 over time, as a function of the two interventions. We observe no statistically meaningful effect of the primary intervention, using data from across the US.
primaries were moved to periods in which community spread still obtained, allowing us to use the counties therein as valid treated units.

It is worth stressing that the treated counties have a higher cumulative death rate prior to administration of the election. While it is conceivable that the treated counties tend to reach an inflection point, such that the death rate naturally decreases in those counties not due to the primary, but as a function of the epidemic curve, we doubt this explanation for two reasons: (1) it is unlikely that a sufficient proportion of the population had been converted to infectives over the study period, such that we would observe this decrease, and (2) the ATT represents the average effect across primaries that occur at different times, both in historical time, and with respect to the epidemic trajectory in each county.

While we do not use positive testing data for lack of reliability, we do not adjust for underreporting in the COVID-19 death counts, which increases as we move closer to the current date\textsuperscript{18}. Furthermore, it may be possible that the tendency to classify deaths as COVID-19 fatalities may have changed over the course of the pandemic. Relatedly, the distribution of times from infection to death may have changed over time, as medical professionals increased their facility in managing severe COVID-19 cases. Nonetheless, this worry is eliminated insofar as we expect that the ability of medical professionals to care for COVID-19 patients is unconfounded by the treatment, since we apply exact matching in historical time.

The approach we used for the epidemiological analysis\textsuperscript{8}, which was recently developed, has been criticized for estimating very large reductions in transmissibility due to the implementation of “non-pharmaceutical interventions” (e.g. the stay at home orders), stemming from its heavy reliance on correct model specification for the reproduction rate, which is unlikely to hold given the innumerable range of interventions that may obtain over a period of time in a given area (stay-at-home orders, rallies, protests – any large gathering may be relevant)\textsuperscript{19}. The model has been more directly critiqued as question-begging\textsuperscript{20}, such that the included interventions will absorb natural decreases in the reproduction rate over time, in addition to decreases attributable to concurrent interventions. Consequently, we take this model to be overly liberal insofar as it is more likely to find an effect of a given intervention, which may be attributable to unobserved factors (e.g. changes in mobility). Its failure to show an adverse impact of elections on COVID-19 cases is therefore reassuringly consistent with our matching approach.

Conclusion

We need to interpret these findings with extra caution because the detection and tracking of COVID-19 has been marked by widespread institutional failure. Under a mismanaged public health response, the US has failed to test an adequate number of individuals to track the spread of the virus, and the data are often subject to reporting delays. Additionally, election data is also difficult to access and often disorganized, for instance, with no clearly reliable data on in-person turnout numbers at the county level. Finally, and most importantly, our analysis is ecological\textsuperscript{21}, in the sense that we examine whether primary elections affected the course of the pandemic in a county, not whether, at the individual level, going to the polls affects an individual’s risk of contracting the infection.
The chief mechanism to ensure ballot access during the COVID-19 epidemic has been the expansion of mail-in voting. While previous research has shown that there is no clear partisan bias with respect to the rejection of mail-in ballots, evidence has emerged that mail-in ballots from African-Americans are already being rejected at a higher rate than those from white voters in the 2020 election. While the expansion of mail-in voting – and enfranchisement in general – is clearly laudable, serious worries remain over the capacity of the US Postal Service to handle the massive increase in mail-in votes this November. The Trump administration has already made efforts to undermine the USPS; while those efforts have been blocked by the U.S. District Court for the Eastern District of Washington, the chief judge involved in the ruling, Stanley A. Bastian, noted that the attacks have already likely “irreparably” harmed states’ abilities to handle the election. Beyond this, the USPS has warned 46 states that mail-in ballots may not arrive in time to be counted for the election, effectively disenfranchising an untold number of Americans even if they follow state guidelines regarding mail-in voting procedure.

Hence, in-person voting remains the primary way for the great majority of Americans to have their voices heard. But we emphasize caution over the interpretation of our results.

While we do not find a spike in the mortality rate associated with the primary elections, it is important to note key differences with respect to the safety of voting in-person in the general election in November. Most of the primary elections were held under fair-weather conditions, enabling individuals to wait in long-lines outside, at lower risk of transmission. We believe that the risk will be higher if voters are cramped indoors to avoid cold weather. Additionally, the absolute turnout numbers are much lower in primary elections than in the general election. Given the contentious nature of this election, it may be reasonably expected that above-normal turnout could increase the risk of spreading the virus well-above our findings, perhaps by increasing crowding at the polls. Increasing the number of polling places or expanding polling hours would surely mitigate such a risk. Both the CDC and the International Institute for Democracy and Electoral Assistance have released guidelines on the execution of elections under COVID-19, which the implementation of social distancing strategies to manage the flow of voters, and the use of personal protective equipment.

We further stress that there is no fixed, intrinsic connection between elections and the spread of COVID-19. The outcome hangs on the particular policies and behaviors found at individual voting sites and across the nation as a whole: whether masks are used by poll-workers and voters, and whether individuals are physically distanced while waiting in line. Super-spreader events do happen; a single wedding in Maine has been linked to 270 cases, and eight deaths, enough to fundamentally alter the trajectory of COVID-19 in a state that previously had relatively few deaths and cases. However, most of these events are familial settings associated with close contact and a lack of precautions.

Voting itself is not an intimate activity. People tend to stay apart, and are often in relatively large and well ventilated spaces such as school gymnasiums. People tend to be quiet, or even silent, while voting (loud talking and singing have been associated with viral transmission and outbreaks). Voting may present a similar level of risk to shopping at a grocery store, or waiting in line outside a restaurant for a take-out order.
Supplementary Information

Replication Materials

Replication materials for this paper are available at https://github.com/human-nature-lab/covid-voting-pre-print.

Balance score calculation

The Balance plots present the standardized mean difference between the treated and control units, across all used counties, calculated according to:

\[ B_{it}(j,l) = \frac{V_{i,t-l,j} - \sum_{i' \in M_{i,t}} w_{i,t} V_{i',t-l,j}}{\sqrt{\frac{1}{N_1-1} \sum_{i'=1}^{N_1} \sum_{t'=L+1}^{T-F} D_{i',t'} (V_{i',t'-l,j} - \bar{V}_{t'-l,j})^2}} \]

Where \( N_1 \) is the total number of treated observations, and \( V_{i,t,j} \) represents the jth covariate of unit i at t. \( w_{i,t} \) represents the weight given to match \( i' \) for control unit i, at t.

N.B. that \( w = 0 \) for each \( i' \) that is not a match for the control unit. \( \bar{B}(j,l) \) is simply the average balance over the treated units:

\[ \bar{B}(j,l) = \frac{1}{N_1} \sum_{i=1}^{N} \sum_{t=L+1}^{T-F} D_{i,t} B_{i,t}(j,l) \]

Robustness checks

exclusion of “pre-COVID” states

In our primary analysis, we count Nevada and South Carolina, with primary elections in late February, as untreated states, since their elections were most likely conducted prior to community spread of COVID-19 in these areas. However, we include model estimates that exclude these states from the model, to check the sensitivity of our results to this assumption. Figure S1 displays the results of the estimation procedure after removing the counties in Nevada and South Carolina, Figure S2 displays the resulting covariate balance. We observed that the main results are robust to the removal of these two states.
turnout-stratified analyses

Given that holding a primary election may be viewed merely as an intention to treat, we conducted analysis that stratify by in-person turnout at the county level, based on percentile thresholds on the in-person turnout data available at the county level. The effect of the primary elections on the spread of COVID-19 really regards the presence of individuals physically at the polls, transmitting infection. Caveats apply, as we found discrepancies in reporting this data, obtained directly from state election agencies. We executed a model that (1) excluded all treated counties that fell below the 50th percentile with respect to the aggregate distribution of in-person turnout across all counties included in our data, and (2) a model that excluded treated counties below the 25th percentile. In each case, we
also conducted a “low” turnout analysis, using only treated units that fell below the above thresholds. Turnout does not seem to affect our results.
ATT: treated below 25th percentile

The shaded region corresponds to middle 80% of the time-to-death distribution.
ATT: treated above 25th percentile

The shaded region corresponds to middle 80% of the time-to-death distribution.
Balance: treated below 50th percentile

metric

bacc  cum_death_rte  median_inc_ln  pop_density  trump_share_2016
black  first_case  perc_65_up  pop_in  Urate

type  constant  time-varying
ATT: treated below 50th percentile

The shaded region corresponds to middle 80% of the time-to-death distribution.
ATT: treated above 50th percentile

The shaded region corresponds to middle 80% of the time-to-death distribution.
Epidemiological model-fits by state
Kentucky Mortality

Kentucky Transmission

Daily deaths

Date

Mar 15 Apr 01 Apr 15 May 01 May 15

intervention median time-to-death primary stay at home order

R^c

Mar 15 Apr 01 Apr 15 May 01 May 15
References

1. CNN, A. by H. E. Trump is creating an untraditional partisan divide on vote by mail. CNN (2020).


3. Nam, R. Pandemic sparks partisan brawl over voting by mail. The Hill (2020).


