Evaluation of Effectiveness of Mitigation Strategies for COVID-19 Pandemic

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Introduction

- COVID-19 pandemic is a global health challenge
- States-level responses: **non-pharmaceutical interventions (NPIs)** to mitigate COVID-19
  - Physical distance closures (lockdown): stay-at-home orders; closing of schools, businesses, restaurants, bars; ban visitors to long term care facility
  - Mask mandates
  - Reopening business (e.g., restaurants, bars, retails)

Estimate the Effects of NPIs

- **Process-based infectious disease models** to simulate counterfactual outcomes under interventions (Ferguson et al. 2020)
- **Regression models** to study association between NPIs and outcomes
- **Quasi-experiment designs** for longitudinal (panel) data with staggered adoption of intervention (e.g., lockdown) across states. Often used to study health policies when randomized trials are not feasible

Causal inference methods

- **Difference in difference (DID)** regression, or interrupted time series analysis (e.g., Wing et al. 2018)
- **Synthetic controls** (Abadie et al. 2010): create weights to match pre-treatment period of control units

Our Goals

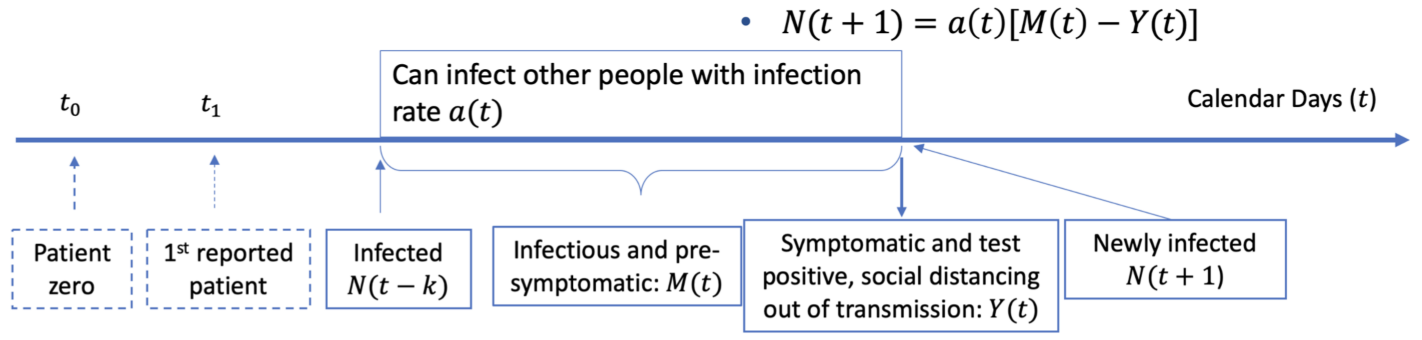
Use **quasi-experiment framework** to account for confounding and estimate **average treatment effect (ATE)** and **heterogeneity of treatment effect (HTE)**

Proposed Method

- **Outcome measures** for COVID-19 transmission
  - Observed cases are subject to high variation/noises
  - Underlying mechanism of disease transmission can be summarized by **effective reproduction number R_t**
  - More meaningful time scale is to match by disease stage: **shift calendar time to time since first reported case**
- **Estimate outcome R_t**

Survival-Convolution Model

- $M(t)=\sum_{k=0}^{\infty} N(t-k)S(k)$
- $Y(t)=\sum_{k=0}^{\infty} N(t-k)[S(k)-S(k+1)]$
- $N(t+1)=a(t)[M(t)-Y(t)]$



$N(t)$: number of new infections on date t; $a(t)$: effective transmission rate, modelled as **non-negative, piece-wise linear functions**; $S(k)$: discrete survival function of time to out of transmission.

Effective reproduction number (R_t): $R_t=\frac{N(t)}{\sum_{k=1}^{C} N(t-k)w(k)}$,

$w(k)$: probability mass function of the serial interval distribution

- **Causal estimand: ATE**

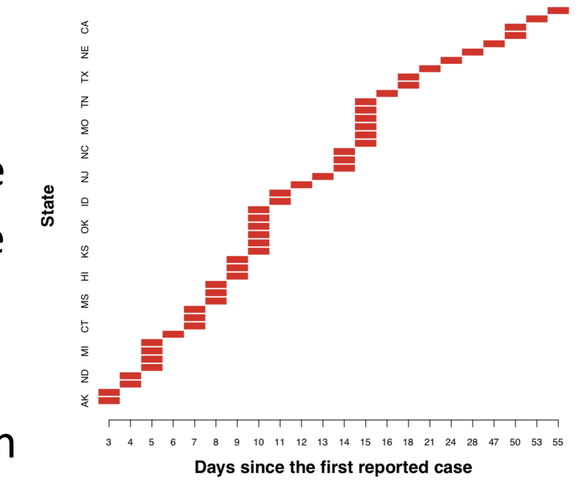
$Y_i^{(1)}(t+\Delta;t)$: potential outcome (change of Rt between t and $(t+\Delta)$) when **intervention of interest is applied at t** and no other interventions in $(t,t+\Delta)$.

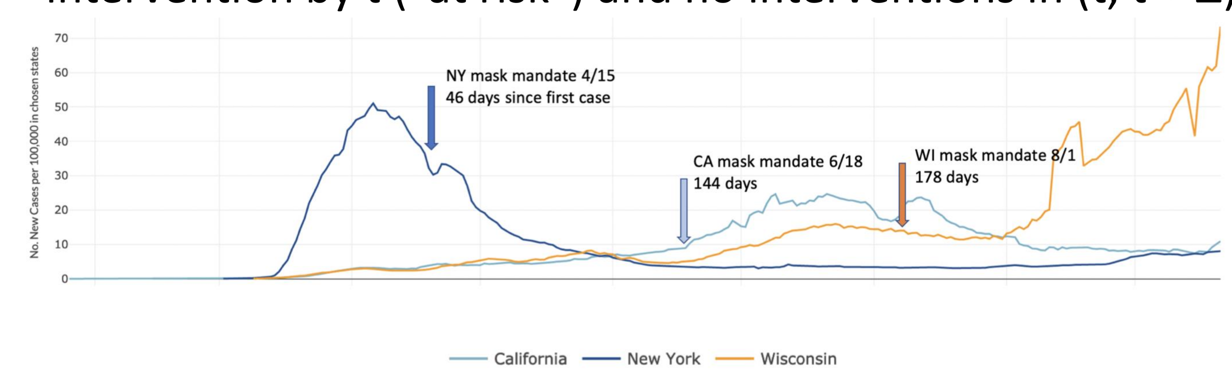
$Y_i^{(0)}(t+\Delta;t)$: potential outcome when **no intervention is applied at time t**, and no other interventions in $(t,t+\Delta)$.

Intervention effect Δ days after t: $\gamma(\Delta,t)=E[Y_i^{(1)}(t+\Delta;t)-Y_i^{(0)}(t+\Delta;t)]$

ATE is defined as $\gamma(\Delta)\equiv\int\gamma(\Delta,t)dF_T(t)$, where $F_T(\cdot)$ is the distribution of the intervention times T_i

- **Assumptions**
  - Stable unit treatment values assumptions (SUTVA)
  - No unmeasured confounder
- **Nested Case-Control Design**
  - Align each state's data according to the time since first reported case so states are more similar in stage of the epidemic.
  - For each state with an intervention, create "control states" as those without an intervention by t ("at risk") and no interventions in (t, t + Δ).





- **Covariates for Propensity Scores**
  - X_i: state-level demographics (e.g., age, race, ethnicity distribution) and social vulnerability index (SVI) variables (available from the CDC).
  - $H_i(t)$: previous week's R_t, new cases, new deaths, testing positivity rate, hospitalizations
- **Estimation Methods**

$\gamma(\Delta,t)=E[\frac{I(T_i=t)}{P(T_i=t|T_i\geq t,H_i(t),X_i)}\{Y_i(t+\Delta;t)\}]-E[\frac{I(T_i=t)}{P(T_i>t|T_i\geq t,H_i(t),X_i)}\{Y_i(t+\Delta;t)\}]$

and ATE is $\gamma(\Delta)\equiv\int\gamma(\Delta,t)dF_T(t)$.

ATE is estimated by **inverse-propensity score weighted DID estimator**, i.e., empirical version of $\gamma(\Delta)$.

Propensity score model: logistic regression of covariates $(H_i(t),X_i)$

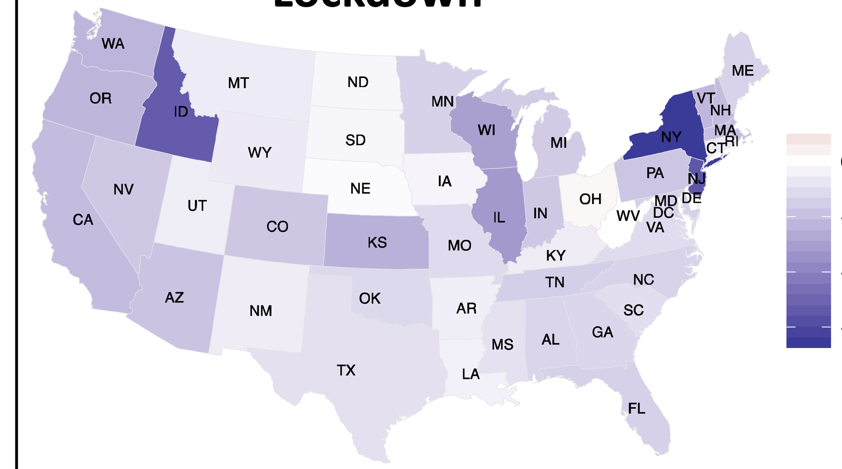
HTE by regression: moderators Z_i, postulate model for the conditional average treatment effects (CATE) $E\left[Y_i^{(1)}(t+\Delta;t)-Y_i^{(0)}(t+\Delta;t)\middle|Z_i\right]=\theta^T Z_i$

The estimator for θ can be obtained by solving estimating equation.

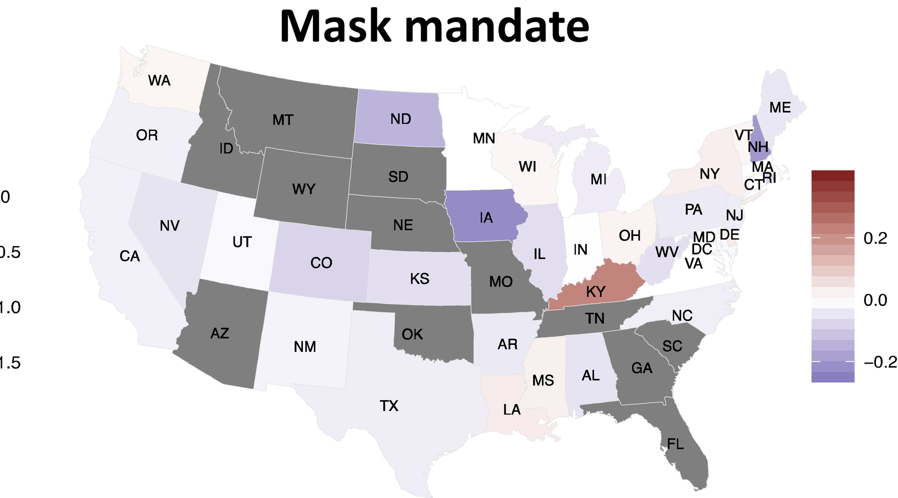
Results

- **Significant covariates in propensity score model**
  - Lockdown: R_t, new cases, new deaths, Latino population size, limited English ability, institutionalized population size
  - Mask mandate: R_t, new cases
  - Reopen business: R_t, mobile home
  - Reopen bars: new cases
- **Observed R_t difference 7-days post-intervention and 1 day before**

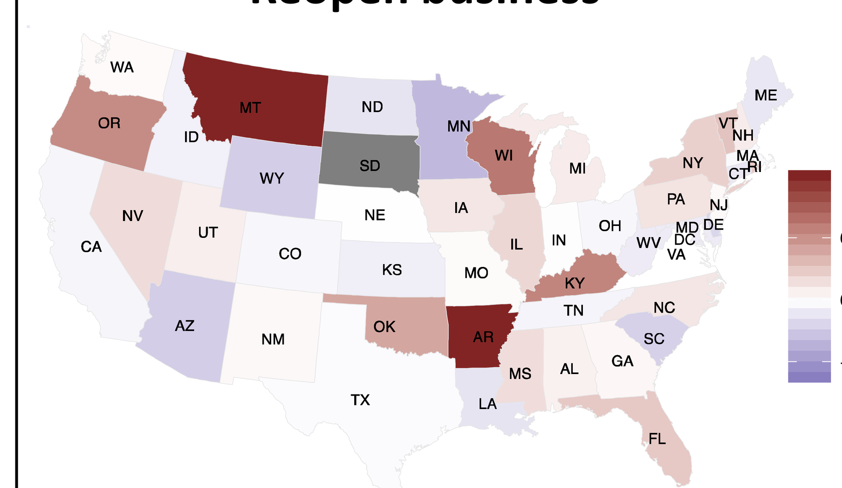
Lockdown



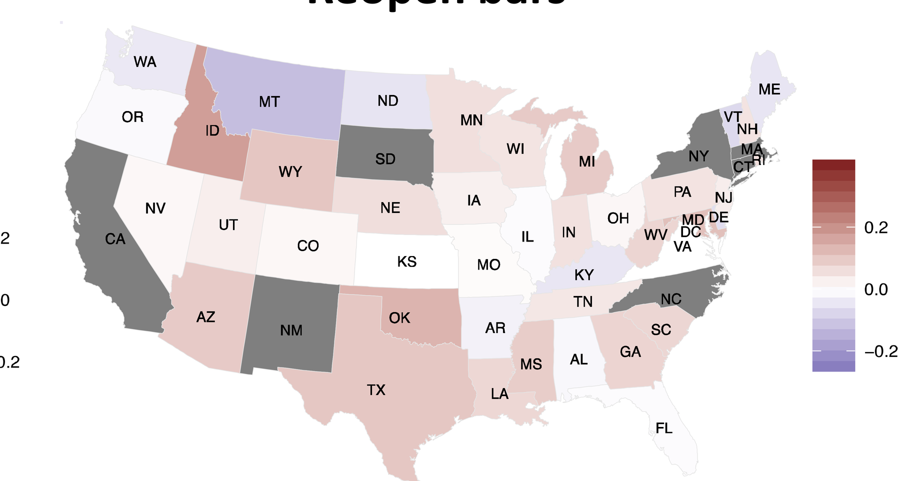
Mask mandate



Reopen business

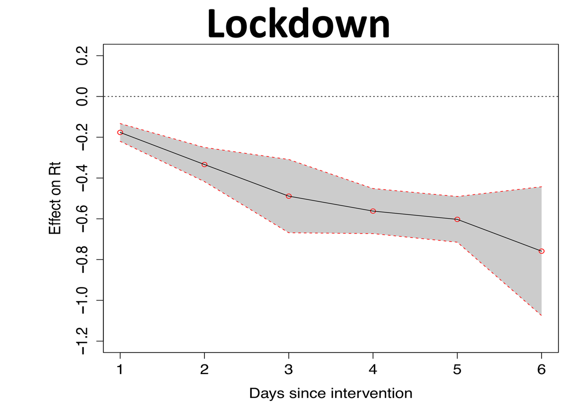


Reopen bars

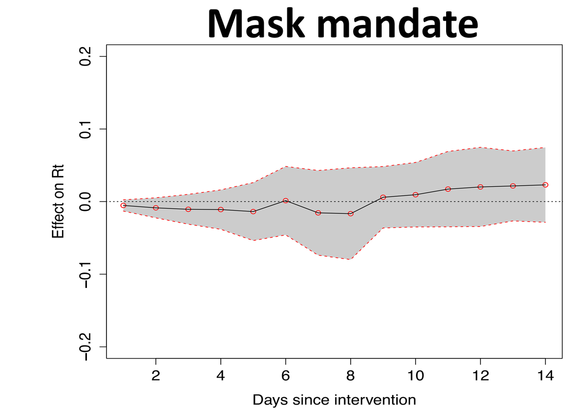


- **ATE with 95% confidence intervals**: **lockdown** and **reopening bars** are significant, while mask mandate is not significant

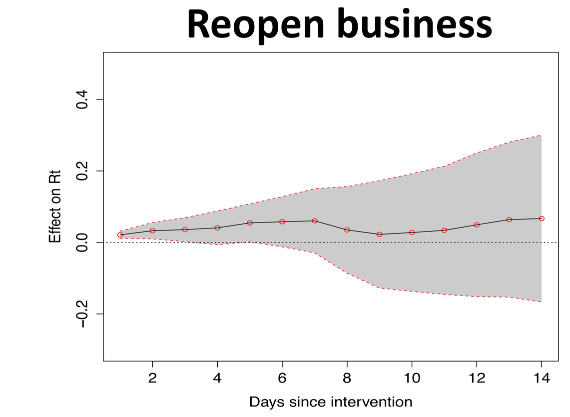
Lockdown



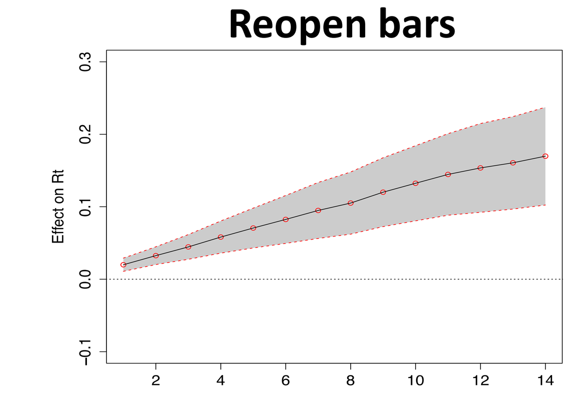
Mask mandate



Reopen business



Reopen bars



- **CATE**: effects are universal (no moderator)

Conclusions

Evaluate ATE and HTE of mitigation strategies for COVID-19

- Difference in R_t as measure of intervention effect
- Construct propensity scores under a nested case-control design and use a weighted DID estimator
- Lockdown has the largest effect on reducing transmission, business re-open does not increase R_t but re-opening bars needs to be carefully planned
- Mask mandate may not be the same as mask wearing behavioral

References

1. Wang Q, Xie S, Wang Y, Zeng D. (2020). Survival-Convolution Models for Predicting COVID-19 Cases and Assessing Effects of Mitigation Strategies. *Frontiers in Public Health*. 8:325. Github site.
2. Xie S, Wang W, Wang Q, Wang Y, Zeng D. (2021). Evaluating Public Health Intervention Strategies for Mitigating COVID-19 Pandemic. Submitted.

We acknowledge the U.S. National Institute of Health grant support (GM124104A1-S1).