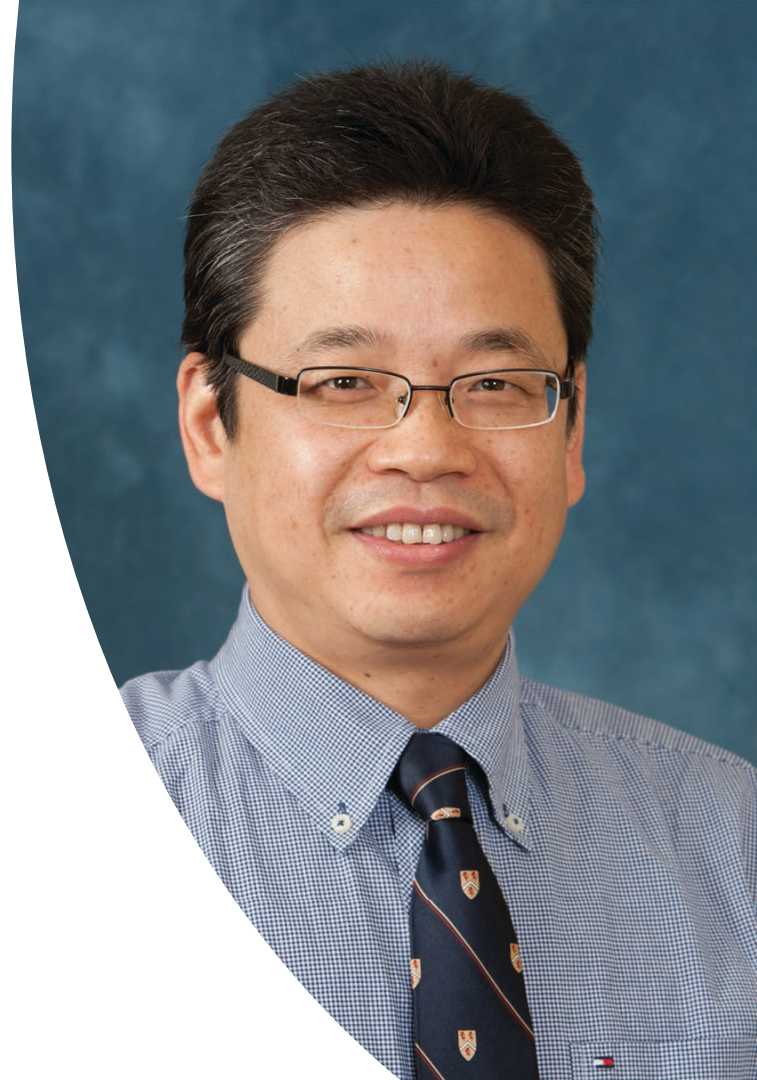


“An Epidemiological Forecast Model to Assess the Effect of Social Distancing on Flattening the Coronavirus Curve in the USA”

Peter Song

Professor and Associate Chair
Department of Biostatistics
School of Public Health
University of Michigan



An Epidemiological Forecast Model to Assess the Effect of Social Distancing on Flattening the Coronavirus Curve in the USA

Peter Song and Song Lab

Department of Biostatistics, University of Michigan

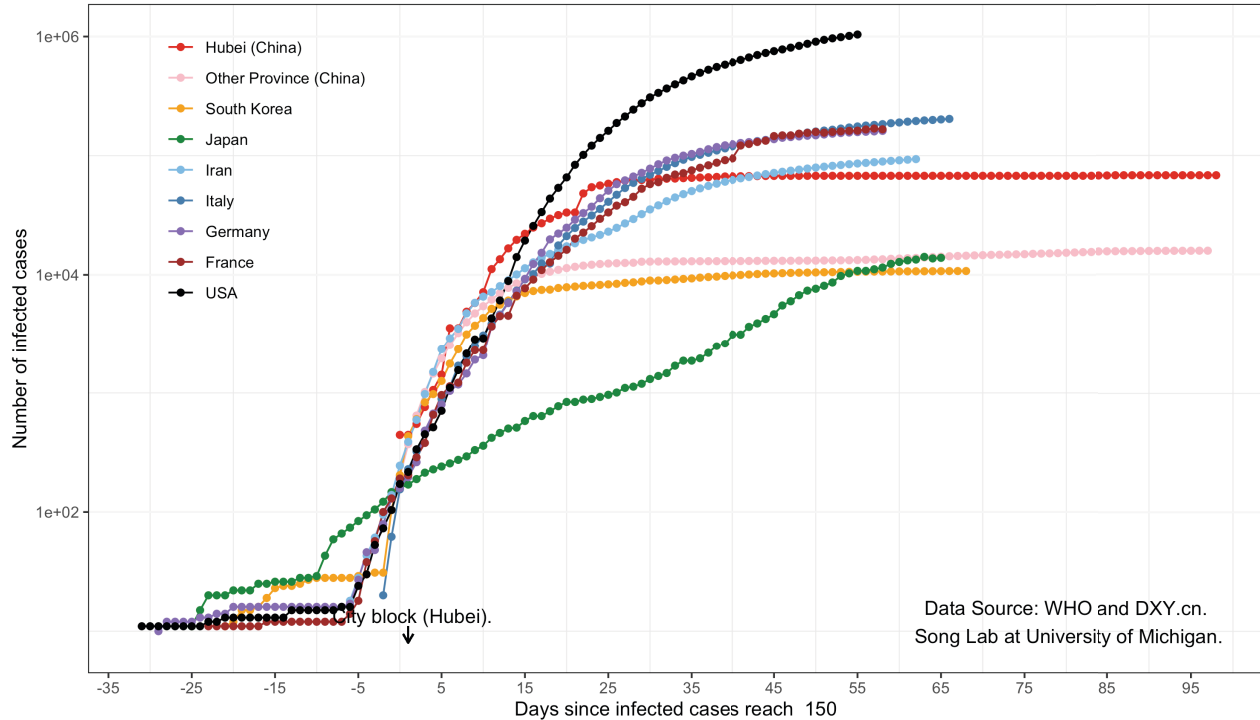
May 1, 2020



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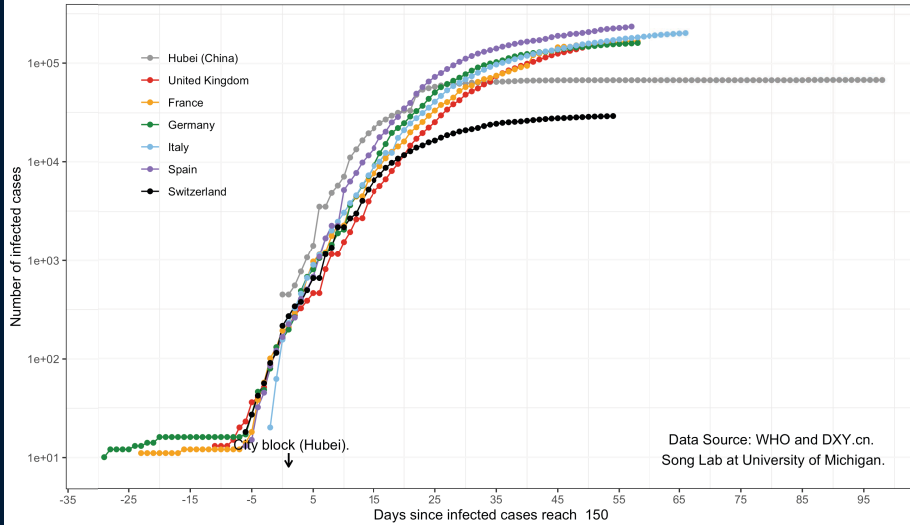
The Outbreak of the COVID-19 in the USA

Cumulative Number of COVID-19 Infections updated on April 29th.

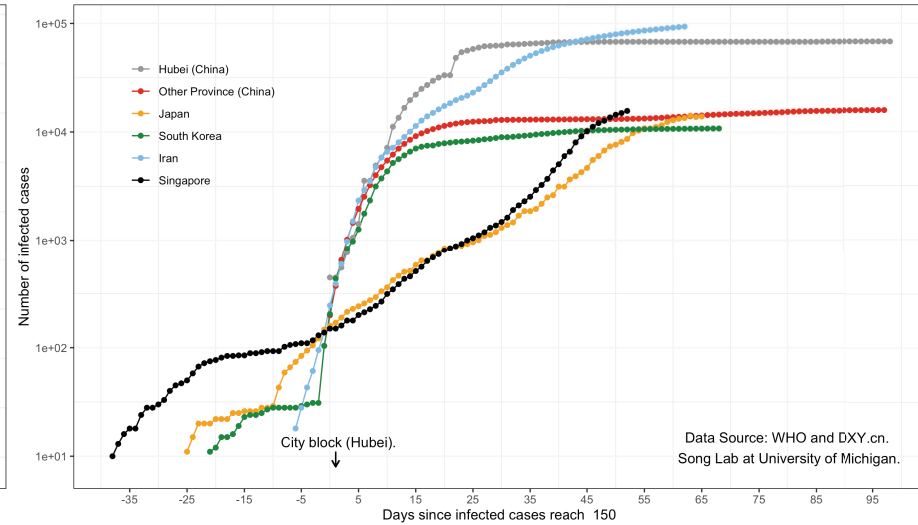


Public Health Intervention Strategies Matter

Cumulative Number of COVID-19 Infections updated on April 29th.



Cumulative Number of COVID-19 Infections updated on April 29th.

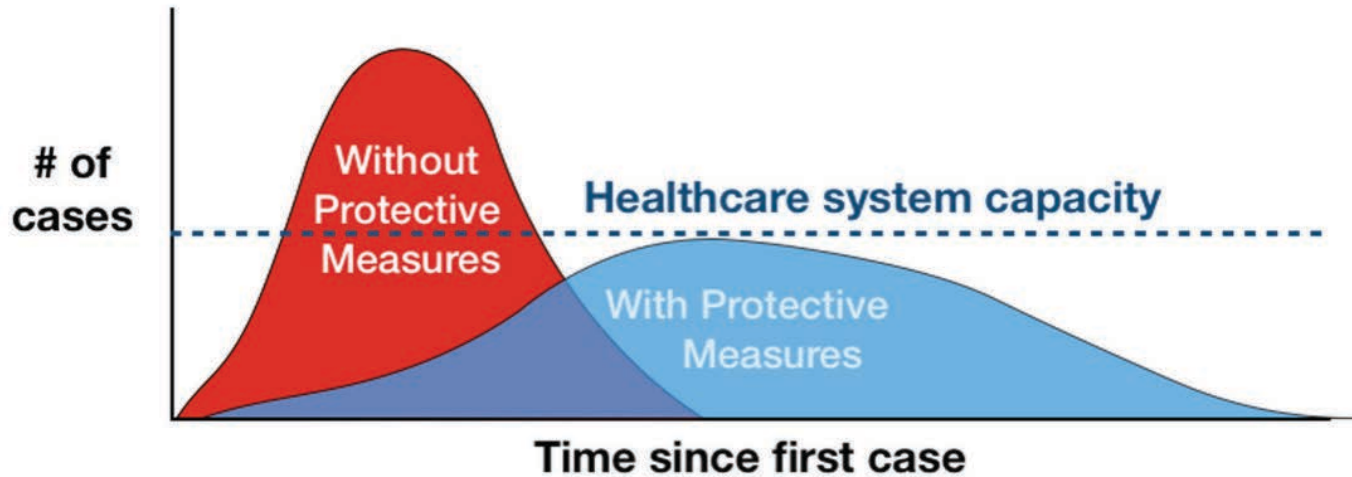


Case Fatality Rate by Country

Continent	County (Area)	Mortality Rate (March 24)
Asia	Hubei, China	7.1%
	Other, China	0.6%
	Japan	2.8%
	South Korea	2.3%
	Iran	6.4%
	Singapore	0.1%
	Europe	United Kingdom
France		18.8%
Germany		4.0%
Italy		13.6%
Spain		11.5%
Switzerland		12.3%
North America	USA	5.9%

Flattening the Coronavirus Curve

One chart explains why slowing the spread of the infection is nearly as important as stopping it.



Adapted from CDC / The Economist

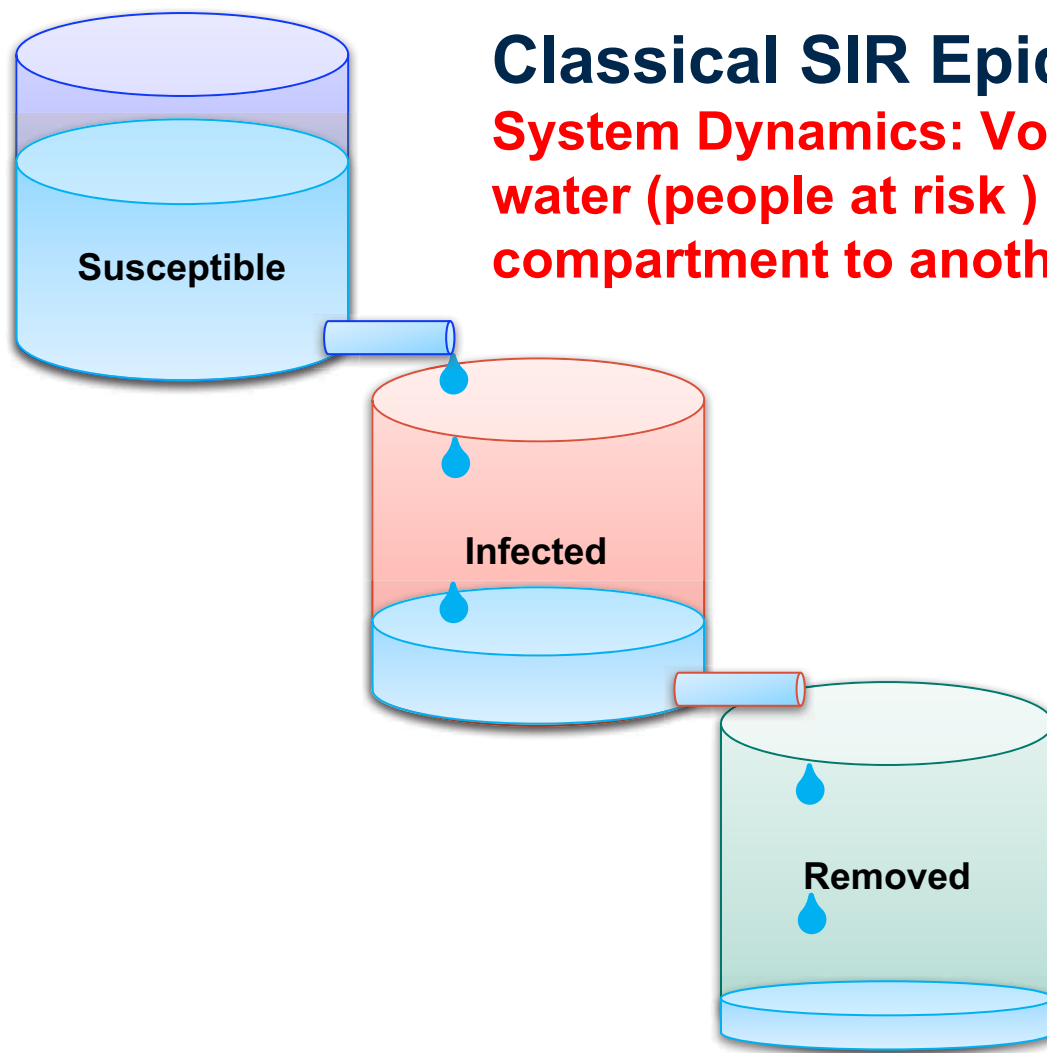
Modeling Is Essential to Project the Future Risk

- **AIM 1:** Build an epidemiological forecast model to assess effect of social distancing on the evolution of the disease in the US.
- **AIM 2:** Build a community-level risk information system that informs people in the US about projected risk score of infection in local areas.



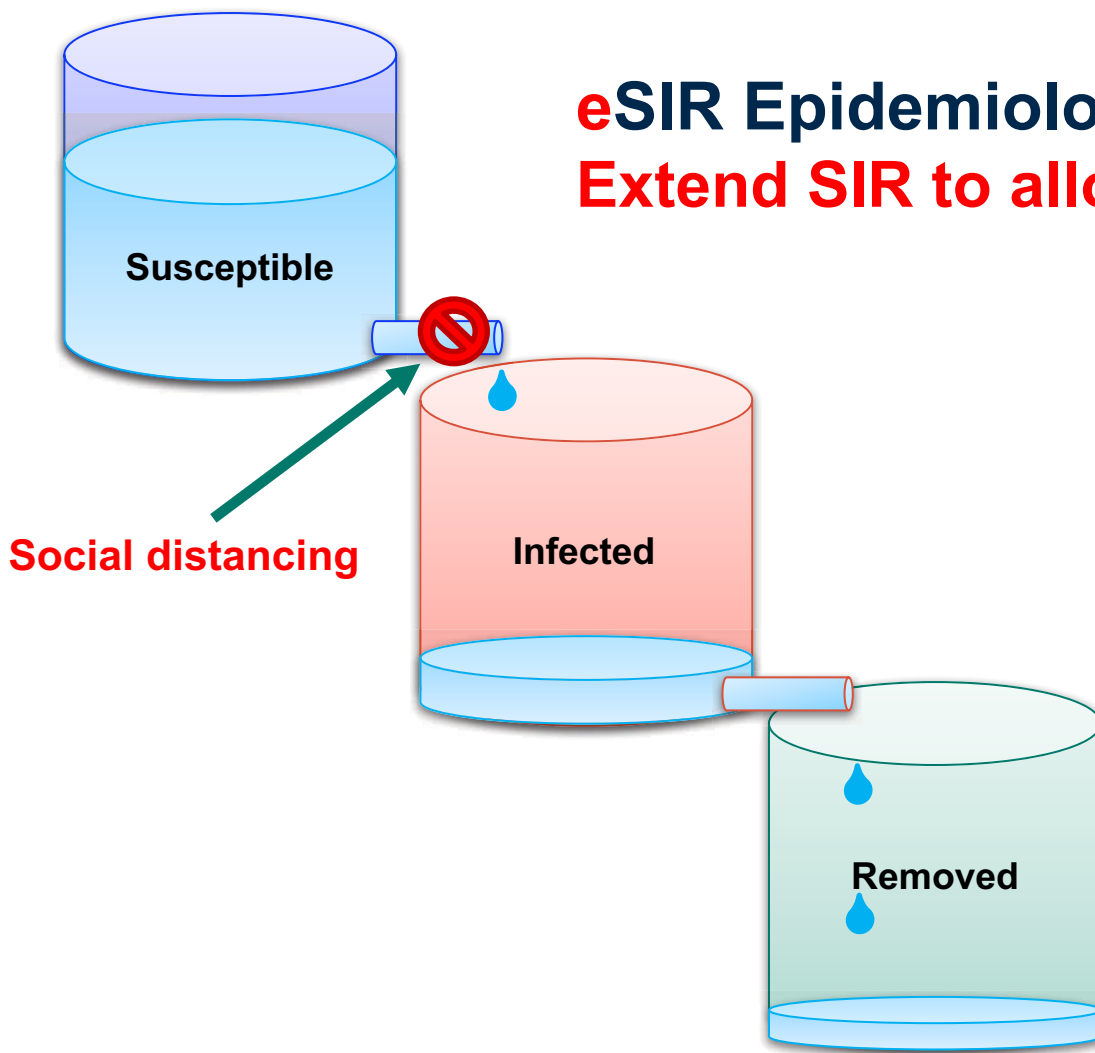
Classical SIR Epidemiological Model:

System Dynamics: Volume and speed of water (people at risk) flow from one compartment to another over time.



eSIR Epidemiological Model

Extend SIR to allow social distancing






















































Public COVID-19 Data From 1Point3Acres

US Cases

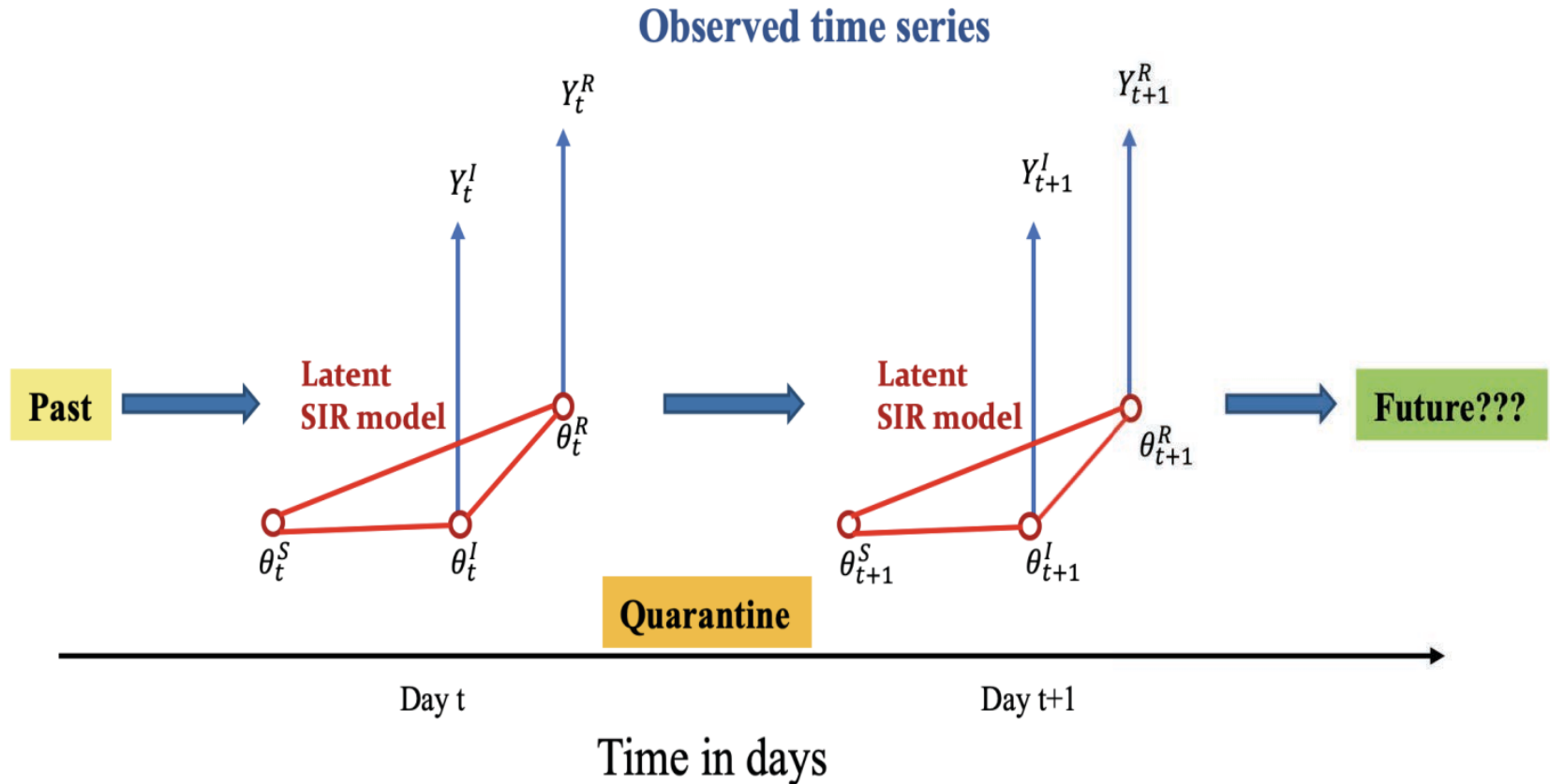
[Reset Map](#)

[Click here to check state level testing data/location](#)

Location	Cases	Deaths	Fatality	Recovered
United States 	+28,452 1,094,347	+2,132 63,737	5.8%	+2,111 128,627
 New York    	+3,957 310,435	+274 23,754	7.7%	+169 33,501
 New Jersey    	+2,287 118,652	+457 7,228	6.1%	730
 Massachusetts    	+1,940 62,205	+157 3,562	5.7%	1,299
 Illinois    	+2,563 52,921	+140 2,355	4.5%	645
 California    	+1,012 49,841	+60 2,016	4%	+7 3,643
 Pennsylvania    	+1,513 47,971	+90 2,475	5.2%	837
 Michigan    	+984 41,379	+120 3,789	9.2%	8,342
 Florida    	+498 33,690	+50 1,268	3.8%	174
 Texas    	+923 28,313	+29 788	2.8%	+26 12,771
 Louisiana    	+342 28,001	+61 1,905	6.8%	



Epidemiological Forecast Model with Social Distancing



eSIR Model with A Disease Transmission Rate Modifier



$$\frac{d\theta_t^S}{dt} = -\beta\pi(t)\theta_t^S\theta_t^I, \quad \frac{d\theta_t^I}{dt} = \beta\pi(t)\theta_t^S\theta_t^I - \gamma\theta_t^I, \quad \frac{d\theta_t^R}{dt} = \gamma\theta_t^I$$

β disease transmission rate

γ removal rate

Basic reproduction number $R_0 = \beta / \gamma$

$\pi(t)$ transmission rate modifier

The manuscript appears in J of Data Sci (Discussion)

[https://www.medrxiv.org/content/10.1101/2020.02.29.20029421v1.
abstract](https://www.medrxiv.org/content/10.1101/2020.02.29.20029421v1.abstract)

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An epidemiological forecast model and software assessing interventions on COVID-19 epidemic in China

 Peter X Song, Lili Wang, Yiwang Zhou, Jie He, Bin Zhu, Fei Wang, Lu Tang, Marisa Eisenberg

doi: <https://doi.org/10.1101/2020.02.29.20029421>

This article is a preprint and has not been peer-reviewed [what does this mean?]. It reports new medical research that has yet to be evaluated and so should *not* be used to guide clinical practice.

Abstract

Info/History

Metrics

 Preview PDF

eSIR R package and R Shiny with details available at Song Lab webpage www.umich.edu/~songlab.

<https://github.com/lilywang1988/eSIR>

R package eSIR: extended state-space SIR epidemiological models

Song Lab 2020-02-29

Purpose

The outbreak of novel Corona Virus disease (a.k.a. COVID-19), originated in Wuhan, the capital of Hubei Province spreads quickly and affects many cities in China as well as many countries in the world. The Chinese government has enforced very stringent quarantine and inspection to prevent the worsening spread of COVID-19. Although various forms of forecast on the turning points of this epidemic within and outside Hubei Province have been published in the media, none of the prediction models has explicitly accounted for the time-varying quarantine protocols. We extended the classical SIR model for infectious disease by incorporating forms of medical isolation (in-home quarantine and hospitalization) in the underlying infectious disease dynamic system. Using the state-space model for both daily infected and hospitalized incidences and MCMC algorithms, we assess the effectiveness of quarantine protocols for confining COVID-19 spread in both Hubei Province and the other regions of China. Both predicted turning points and their credible bands may be obtained from the extended SIR under a given quarantine protocol. R software packages are also made publicly available for interested users.

The standard SIR model has three components: susceptible, infected, and removed (including the recovery and dead). In the following sections, we will introduce the other extended state-space SIR models and their implementation in the package. **All the results provided are based on very short chains.** Please set at least `M=5e5` and `nburnin=2e5` to obtain stable MCMC chains via `rjags`.



$$\frac{d\theta_t^S}{dt} = -\beta\theta_t^S\theta_t^I, \quad \frac{d\theta_t^I}{dt} = \beta\theta_t^S\theta_t^I - \gamma\theta_t^I, \quad \frac{d\theta_t^R}{dt} = \gamma\theta_t^I,$$

<https://umich-biostatistics.shinyapps.io/eSIR/>

Explore eSIR Corona Virus results

State-space SIR models with time-varying quarantine protocols

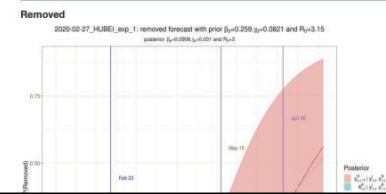
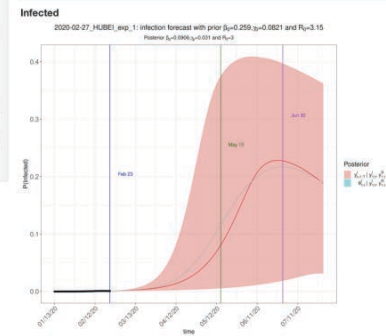
Use the drop-down menus to view model results by day, location, and model.

Select day
2020-02-27

With or without calibration?
 With calibration
 Without calibration

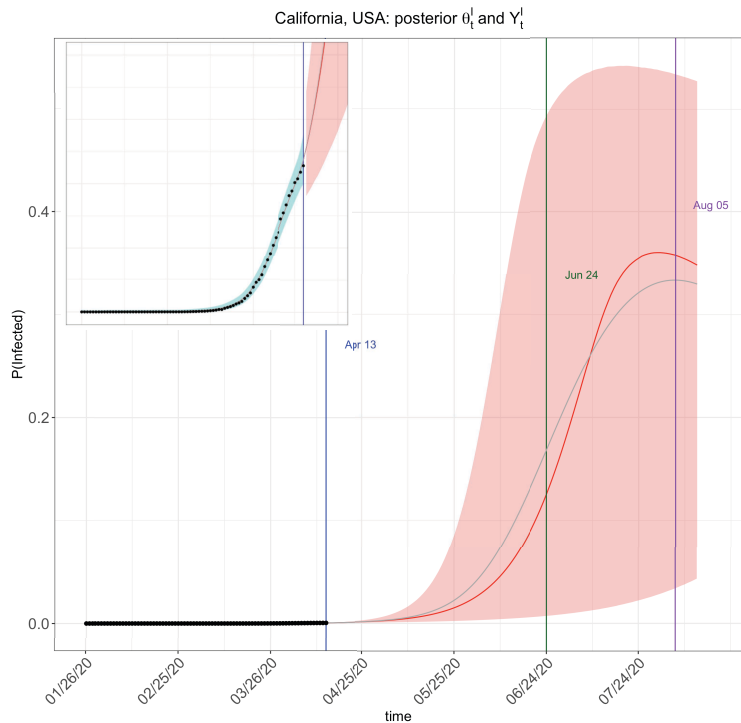
Choose location
Hubei

Choose function
No intervention

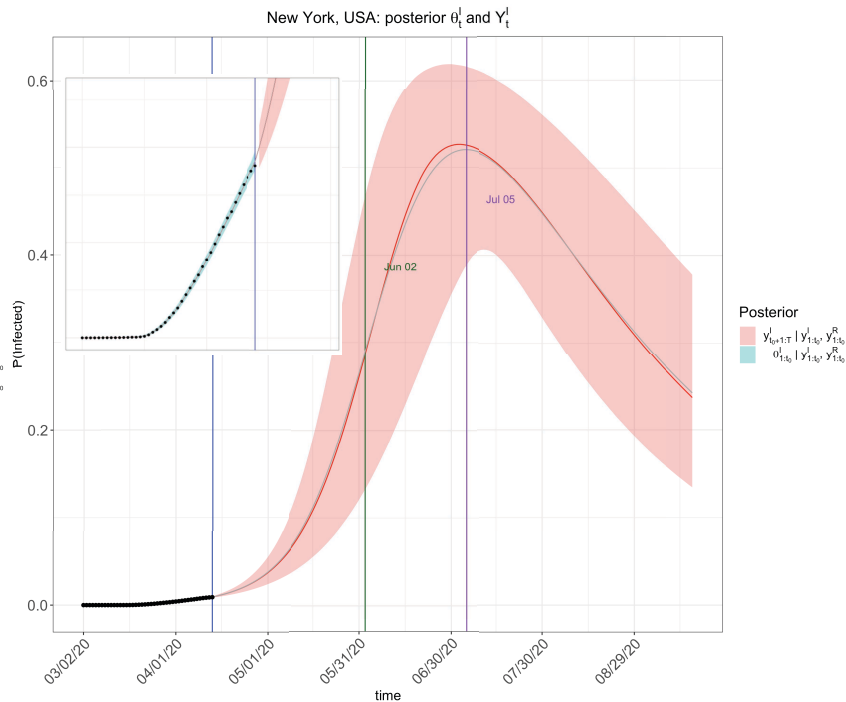


Projected USA Covid-19 Trends with no intervention

California, USA

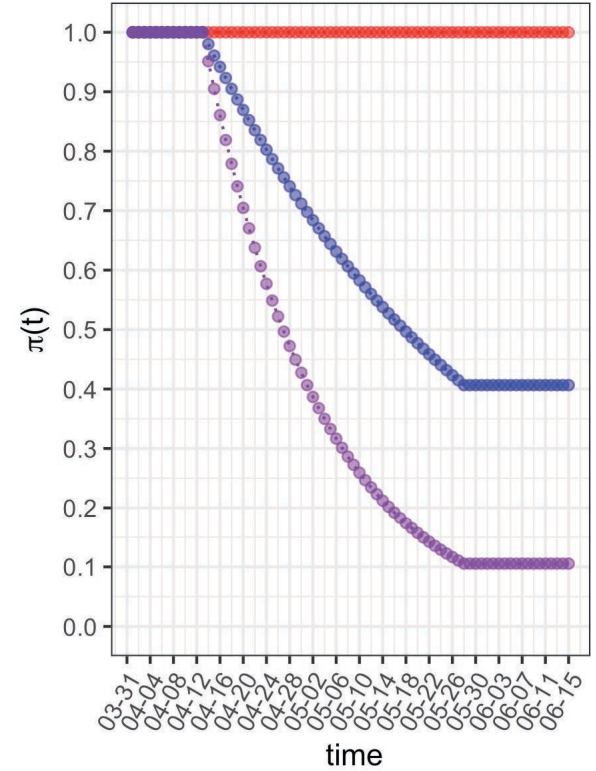
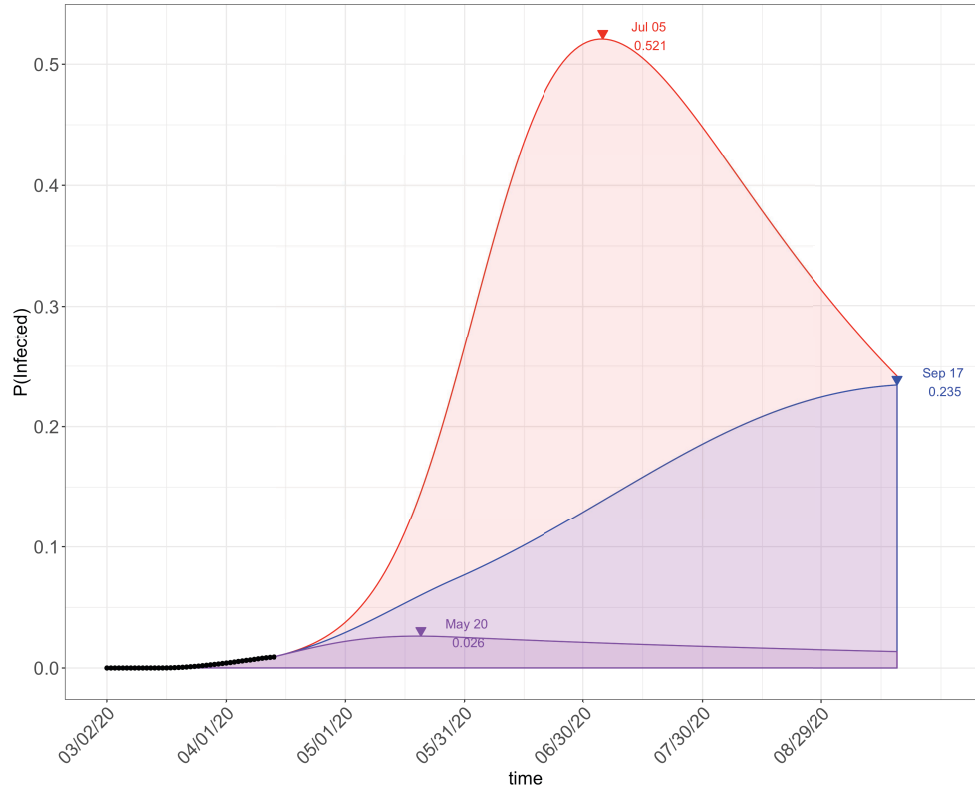


New York, USA



Flattening the Coronavirus Curve

New York State, USA: Posterior Mean Prevalence

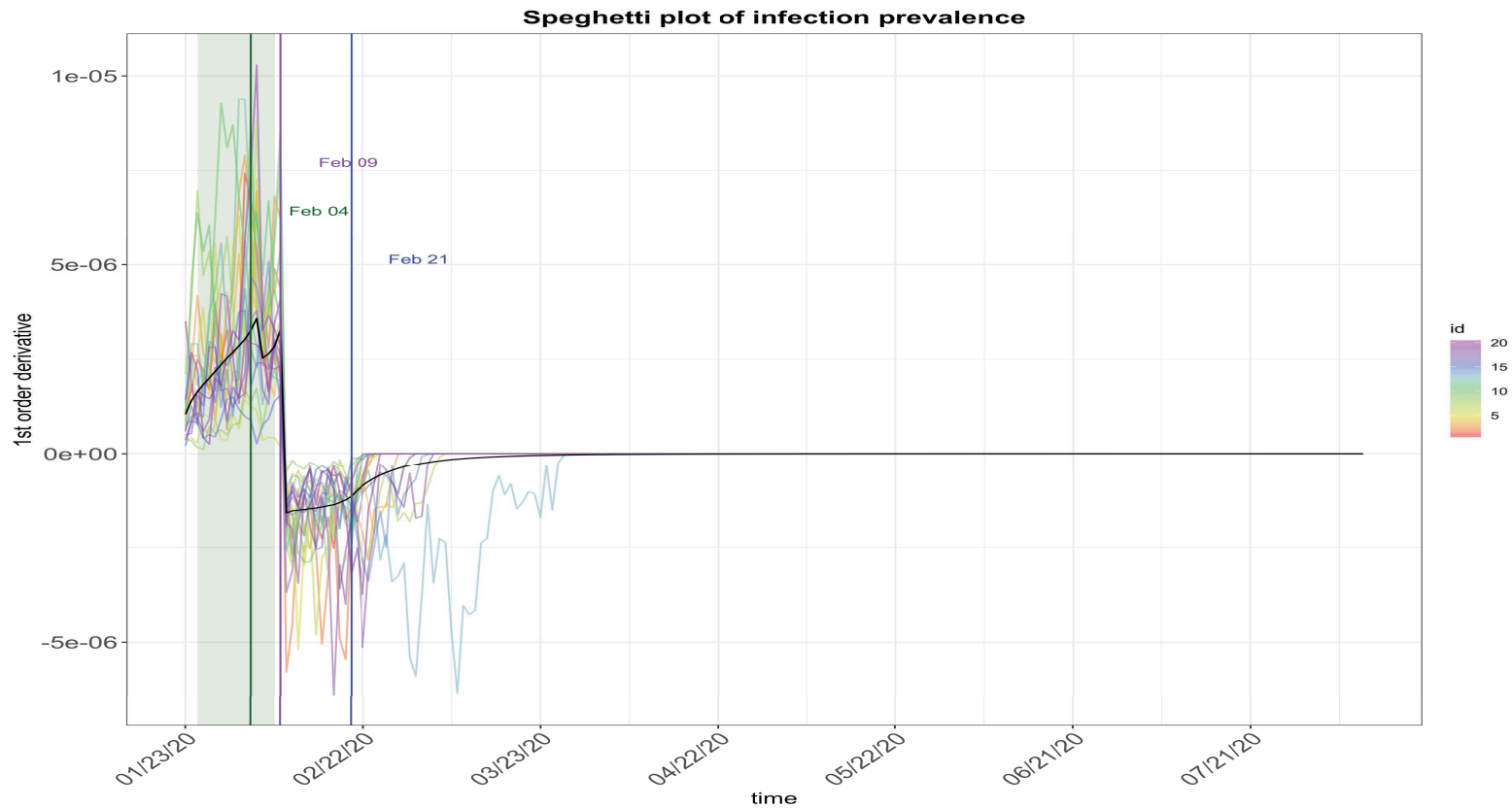


Estimated R0 in USA

State	Estimate	95% CI	
New York	5.87	4.28	7.85
New Jersey	6.29	4.43	8.60
Massachusetts	6.86	4.87	9.39
California	4.29	2.78	6.31
Washington	4.77	3.28	6.74
Michigan	4.26	2.87	6.06

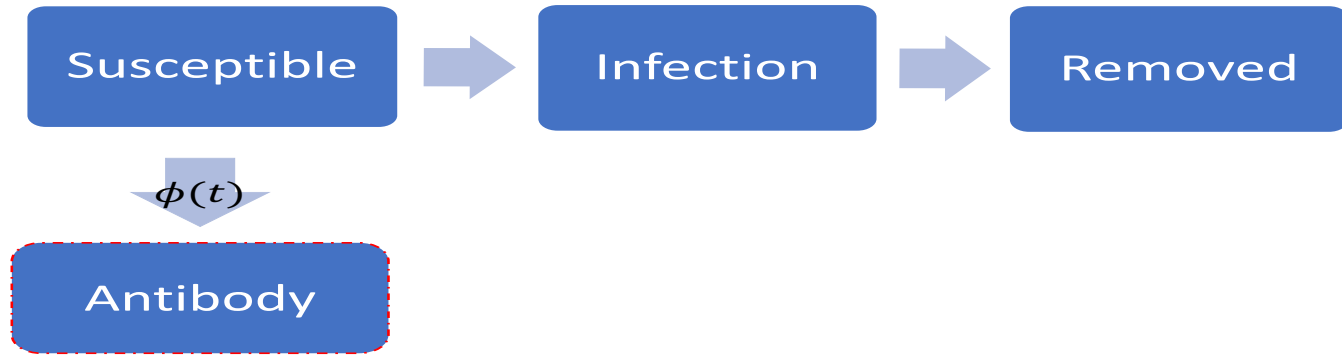
- The East Coast states seem at a relatively earlier stage with a larger productivity than the West Coast
- The removed cases were also underreported, thus R0 might be overestimated

Uncertainty assessed from 200,000 projected curves



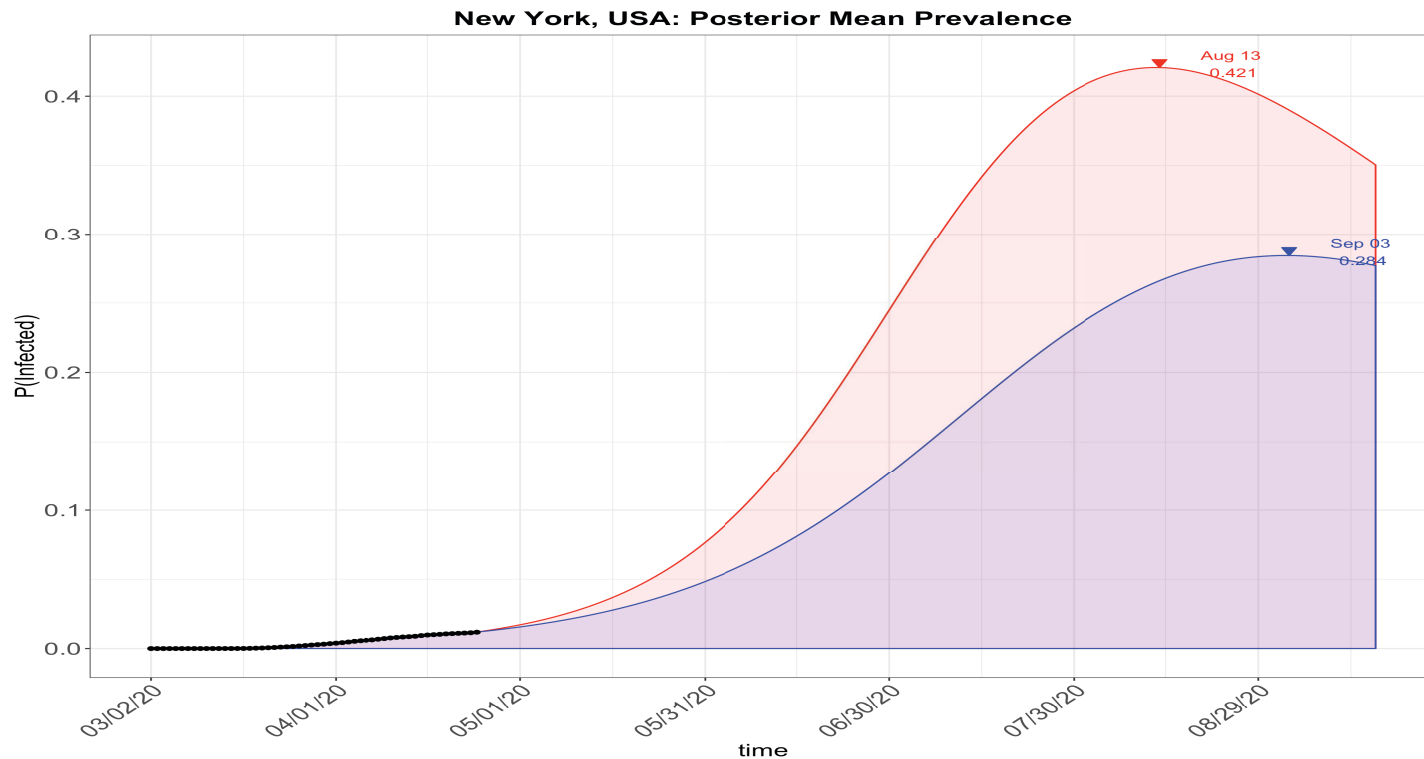
SAIR Model for Herd Immunity: Antibody

ASSUMPTION: people with antibody is immune to the coronavirus.



$$\frac{d\theta_t^A}{dt} = \phi(t)\theta_t^S, \quad \frac{d\theta_t^S}{dt} = -\beta\pi(t)\theta_t^S\theta_t^I - \phi(t)\theta_t^S, \quad \frac{d\theta_t^I}{dt} = \beta\pi(t)\theta_t^S\theta_t^I - \gamma\theta_t^I, \quad \text{and} \quad \frac{d\theta_t^R}{dt} = \gamma\theta_t^I.$$

IF 20% of People in New York had antibody



Epidemiological Forecast Models Can Help

- Statistical forecast models are very powerful to **utilize limited data to learn a complex underlying infectious disease system** developed by epidemiologists, which can help project the evolution of the coronavirus pandemic and quantify risk in the future.
- More importantly this toolbox helps to **evaluate different preventive measures and public health policies** on the mitigation of the infection.
- This model allows us to **assess the likelihood of second outbreak** if the social distancing is relaxed in some regions of the country
- It is important to have better data sources, not only from public database, but also from **extensive surveys on antibody**, to mitigate the underreporting issue in data collection and to make better prediction.
- Better data leads to better projection and thus make better public policies and decisions on both health and economies.



Lan Shi, Msc student @Umich



Fei Wang, PhD @CarGurus



Lu Tang, PhD @Pittsburg



Bin Zhu, PhD @NIH



R0=9



Yiwang Zhou, PhD candidate @Umich



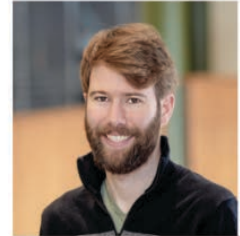
Jie He, PhD @Umich



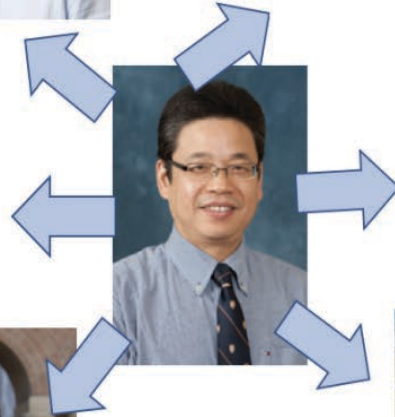
Lili Wang, PhD candidate @Umich



Michael Kleinsasser, Staff @Umich



Daniel Barker, Staff @Umich



Thank You!

Stay Well



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Project 2: Spatiotemporal Prediction Model for County-level COVID-19 Risk in the USA

SIR model:

- Population mixing is strong.
- Concentrations of effected types of population (susceptible, infected, removed) are spatially homogeneous.
- SIR model neglect spatial heterogeneity of the epidemic process.

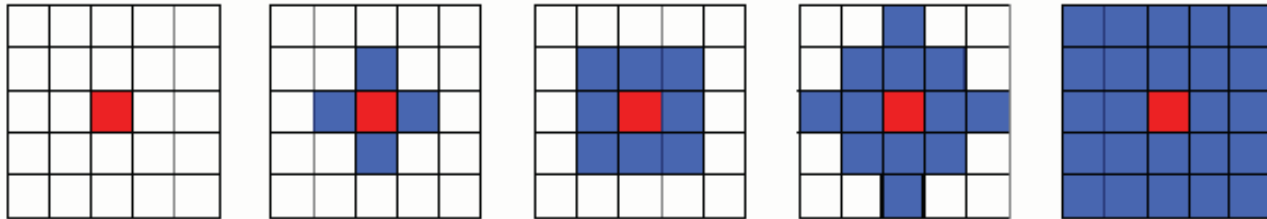
Cellular Automata (CA):

- A model based on interacting particle system.
- Eliminate the shortcoming of SIR model in neglecting spatial heterogeneity.
- Treat individuals in biological populations as discrete entities.

Project 2: Spatiotemporal Prediction Model for County-level COVID-19 Risk in the USA

Cellular Automata (CA)

- A collection of "colored" cells on a grid of specified shape.
- Evolves through a number of discrete time steps according to a set of rules based on the states of neighboring cells.
- The rules are applied iteratively for as many time steps as desired.

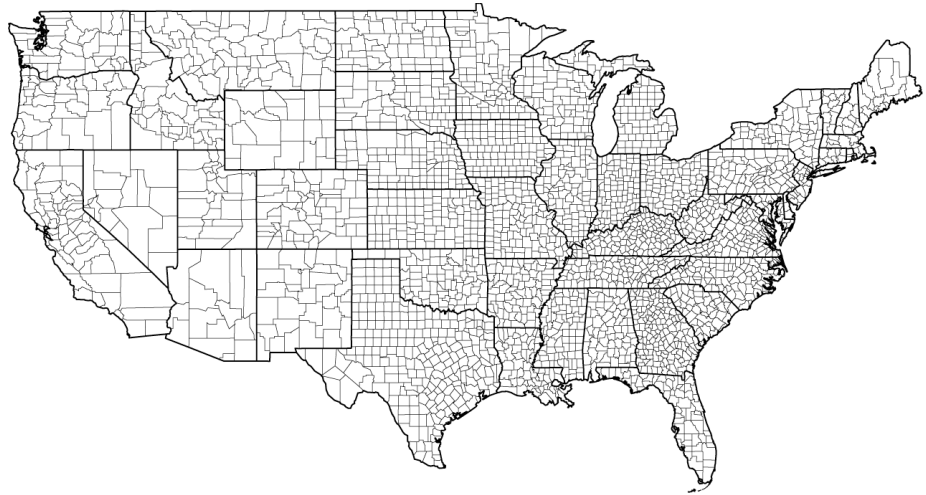


CA neighborhoods: (a) Empty, (b) Von Neumann, (c) Moore, (d) MvonN, (e) Extended.

Project 2: Spatiotemporal Prediction Model for County-level COVID-19 Risk in the USA

CA-SIR model:

- Utilize the CA's strength in spatial modeling combined with the powerful state-space SIR model.
- Make timely and accurate localized predictions of infection spread patterns and infection rates for all 3109 continental US counties.



Prediction equations of CA-SIR model

$$\theta_c^S(t) = \theta_c^S(t-1) - \beta\theta_c^S(t-1)\theta_c^I(t-1) - \beta\theta_c^S(t-1) \sum_{c' \in \mathcal{C}_{-c}} \omega_{cc'}(t) \left\{ \frac{N_{c'}\theta_{c'}^I(t-1)}{N_c} \right\}$$

$$\theta_c^I(t) = (1 - \gamma)\theta_c^I(t-1) + \beta\theta_c^S(t-1)\theta_c^I(t-1) + \beta\theta_c^S(t-1) \sum_{c' \in \mathcal{C}_{-c}} \omega_{cc'}(t) \left\{ \frac{N_{c'}\theta_{c'}^I(t-1)}{N_c} \right\}$$

$$\theta_c^R(t) = \theta_c^R(t-1) + \gamma\theta_c^I(t-1)$$

- $\theta_c^S(t), \theta_c^I(t), \theta_c^R(t)$ are the susceptible, infected and removed prevalence of county c at time t .
- β and γ are the transmission and removal rates that are estimated from the eSIR model.
- $c' \in \mathcal{C}_{-c}$ are all the other counties within the set \mathcal{C} except c .
- N_c is the population of county c .
- $\omega_{cc'}(t) = a(c')\exp\{-d(c, c') + h(t)\}$ is the connectivity-coefficient that quantifies both volume and accessibility from county c to c' ; $a(c')$ is the weight of county c being a transportation/medical center; $d(c, c')$ is the geo-distance between county c and c' ; $h(t)$ is the time of major gatherings.

County-level Risk Prediction

One-day ahead risk prediction

- Let t_0 be the current time (day, today)
- $$\theta_c^I(t_0 + 1) = (1 - \gamma)\theta_c^I(t_0) + \beta\theta_c^S(t_0)\theta_c^I(t_0) + \beta\theta_c^S(t_0) \sum_{c' \in \mathcal{C}_{-c}} \omega_{cc'}(t_0) \left\{ \frac{N_{c'} \theta_{c'}^I(t_0)}{N_c} \right\}$$
- Based on the above equation, we can predict the one-day ahead risk of COVID-19 infection for each county on time $t_0 + 1$.

County-level Risk Prediction

t-day ahead risk prediction

- $$\theta_c^S(t) = \theta_c^S(t-1) - \beta\theta_c^S(t-1)\theta_c^I(t-1) - \beta\theta_c^S(t-1)\sum_{c' \in \mathcal{C}_{-c}} \omega_{cc'}(t) \left\{ \frac{N_{c'}\theta_{c'}^I(t-1)}{N_c} \right\}$$
- $$\theta_c^I(t_0+1) = (1-\gamma)\theta_c^I(t_0) + \beta\theta_c^S(t_0)\theta_c^I(t_0) + \beta\theta_c^S(t_0)\sum_{c' \in \mathcal{C}_{-c}} \omega_{cc'}(t_0) \left\{ \frac{N_{c'}\theta_{c'}^I(t_0)}{N_c} \right\}$$
- $$\theta_c^R(t) = \theta_c^R(t-1) + \gamma\theta_c^I(t-1)$$
- Based on the above equations, we can predict the *t*-day ahead risk of COVID-19 infection for each county on time $t_0 + t$.
- The risk score over a period of *t* days from t_0 is given by:
- $$RS_c(t|t_0) = \theta_c^I(t_0+1) + \{1 - \theta_c^I(t_0+1)\}\theta_c^I(t_0+2) + \{1 - \theta_c^I(t_0+1)\}\{1 - \theta_c^I(t_0+2)\}\theta_c^I(t_0+3) + \dots + \{1 - \theta_c^I(t_0+1)\} \dots \{1 - \theta_c^I(t_0+t-1)\}\theta_c^I(t_0+t)$$

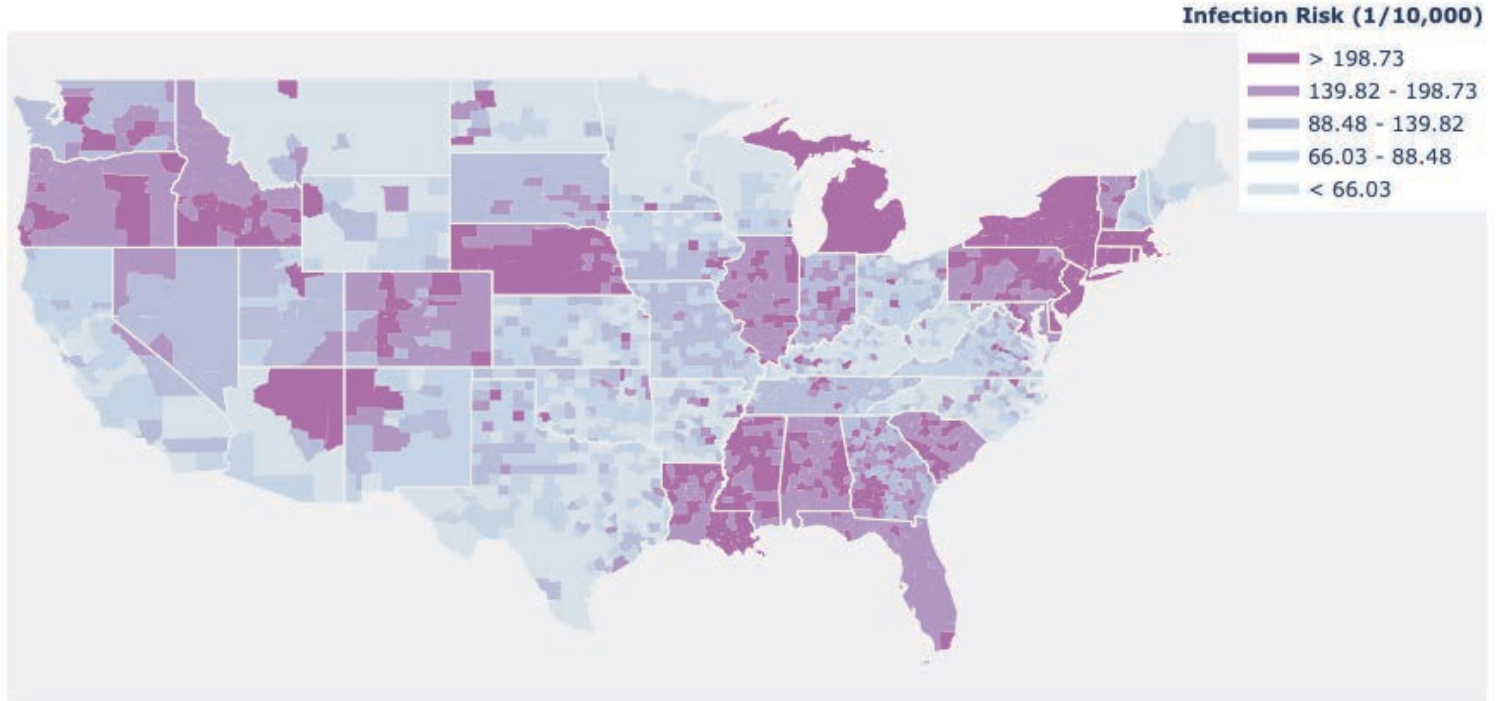
County-level Risk Prediction

Risk prediction of travel

- Let C be a set of counties that a traveler plans to stop by over next t days.
- Suppose the traveler stops at one county per day, denoted as $C = \{c_1, \dots, c_t\}$ with c_j being the county visited on day $t_0 + j, j = 1, \dots, t$.
- The risk score of this travel is given by:
- $$RS(C, t|t_0) = \theta_{c_1}^I(t_0 + 1) + \{1 - \theta_{c_1}^I(t_0 + 1)\}\theta_{c_2}^I(t_0 + 2) + \{1 - \theta_{c_1}^I(t_0 + 1)\}\{1 - \theta_{c_2}^I(t_0 + 2)\}\theta_{c_3}^I(t_0 + 3) + \dots + \{1 - \theta_{c_1}^I(t_0 + 1)\} \dots \{1 - \theta_{c_{t-1}}^I(t_0 + t - 1)\}\theta_{c_t}^I(t_0 + t)$$

County-level Risk Forecast Made on April 14th

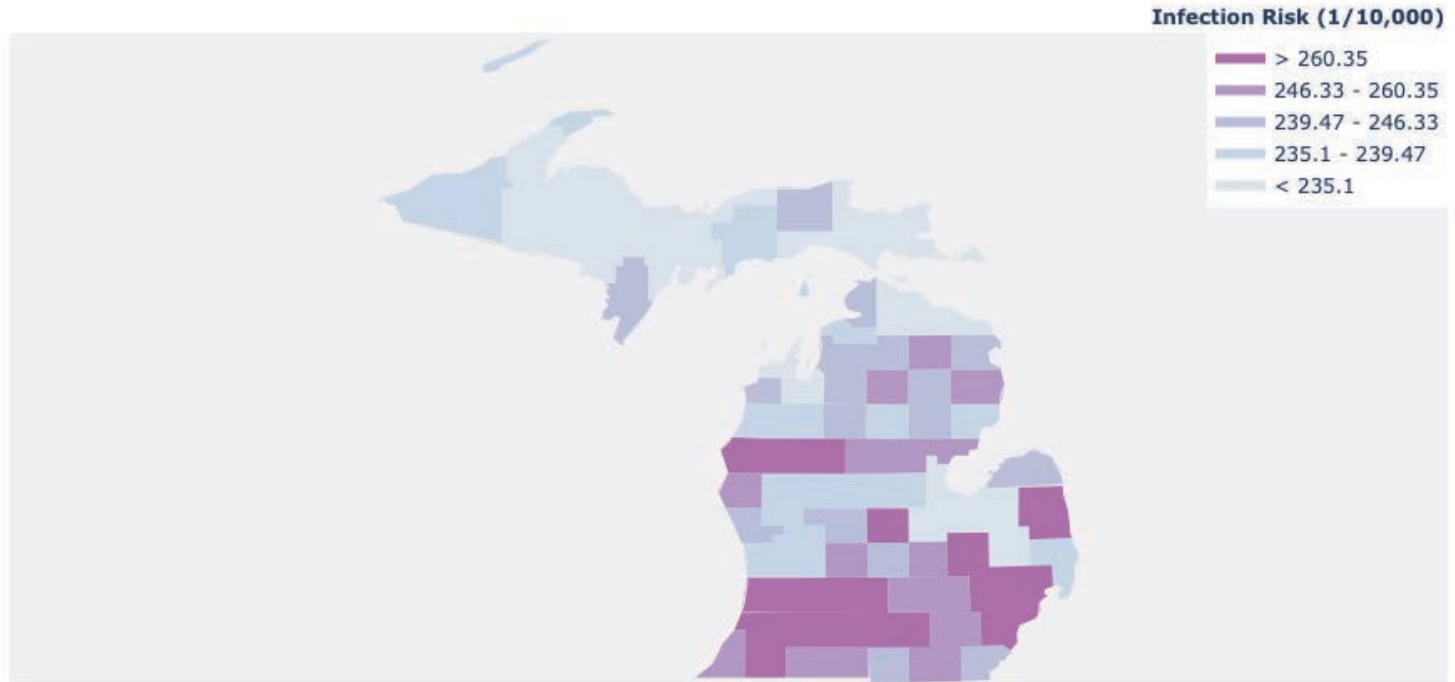
One-week ahead projected risk map



County-level Risk Forecast Made on April 14th

One-week ahead projected risk map for MI

- Wayne county with higher connectivity coefficient since DTW is located there.



County-level Risk Forecast Made on April 14th

Projected risk map for a hypothetical travel

- Ann Arbor (Washtenaw, MI) - Detroit (Wayne, MI) – Chicago (Cook, IL)

