

A Data-driven Approach for Assessing the Impact of Re-opening Order and Non-pharmaceutical Interventions on the Spread of COVID-19 using Time-dependent SEIR Model

Instructor: Jingyi Zheng
Department of Mathematics and Statistics
Auburn University, AL, USA.

Students: Ismail Abdulrashid, Fauziya Yakasai, Yuexin Li

August 21, 2020

Outline

- 1 Background and Objectives
- 2 Mathematical Models
- 3 Proposed SEIR Model
- 4 Methodology
- 5 Numerical Results
- 6 Summary & Conclusion

Background

- The outbreak of COVID-19, caused by a coronavirus called SARS-CoV-2 virus, has been declared a pandemic by the World Health Organization (WHO) in March and rapidly spread to over 100 countries.
- As of May 20, there are over 4.9M cumulative confirmed cases with 324K deaths worldwide.
- Authorities worldwide responded by implementing travel restrictions, lockdowns, workplace hazard controls, and facility closures to stop further spread.
- The pandemic has caused global social and economic disruption, including the largest global recession since the Great Depression and global famines affecting 265 million people.

Objectives

- To design Kermack McKendrick-type SEIR epidemic model for the transmission dynamics and control of COVID-19 in a population.
- To assess the community-wide impact of early implementation of strict lockdown measures in China, Italy and USA.
- To assess the community-wide impact of early lifting of lockdown in the US states of Texas, Iowa and Maryland.

Data Source

- The dataset is acquired from various publicly-available sources, such as the World Health Organization and the John Hopkins' Center for Systems Science and Engineering COVID-19 Dashboard.

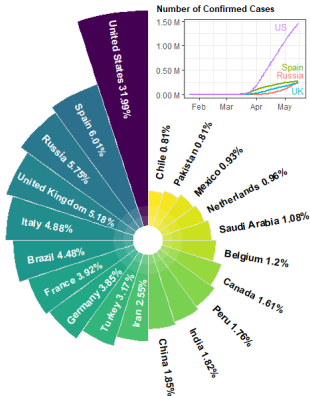
Country	Start date	End date
China	01 – 15 – 2020	05 – 05 – 2020
Italy	02 – 24 – 2020	05 – 03 – 2020
USA	03 – 04 – 2020	05 – 05 – 2020

State	Start date	End date
Maryland	04 – 12 – 2020	05 – 04 – 2020
Iowa	04 – 12 – 2020	05 – 04 – 2020
Texas	04 – 012 – 2020	05 – 04 – 2020

Most Impacted Countries

- As of May 16, the United States, Spain, Russia, and United Kingdom, shared more than 5% of the global cases.

Top 20 Countries Most Impacted by COVID-19



Data Source: nCov2019

Mathematical Models

- Influential in providing deeper understanding on the transmission mechanisms and burden of the ongoing COVID-19 pandemic.
- Contribute to the development of public health policy and understanding.
- Mathematical models of the COVID-19 pandemic can broadly be divided into two type:
 - ① Population-based, SIR (Kermack-McKendrick)- type models, driven by differential equations.
 - ② Agent-based models, in which individuals typically interact on a network structure and exchange infection stochastically.
- Kermack-Mckendrick-type models has been widely adapted to model the transmission dynamics and control of COVID-19 in a population.

An SIR Model for COVID-19 with Undetectable Infected Persons [Yi-Cheng Chen et. al., (2020)]

$$\begin{aligned}\frac{dS}{dt} &= -\frac{\beta(t)S(t)I(t)}{n}, \\ \frac{dI}{dt} &= \frac{\beta(t)S(t)I(t)}{n} - \gamma I(t), \\ \frac{dR}{dt} &= \gamma I(t),\end{aligned}$$

where

$$N(t) = S(t) + I(t) + R(t)$$

- N : Total human population at time t .
- $S(t)$: Populations of individuals who are susceptible at time t .
- $I(t)$: Population of infected individuals at time t .
- $R(t)$: Population of recovered individuals at time t .
- β, γ : Transmission rate (infectious contact rate) & Recovery rate, resp.

Proposed SEIR Model

- Our model assumed existence of latent period prior to the onset of infectiousness, we add one more compartment, exposed (E), in the dynamic model.
- Incubation rate σ , transmission rate β , and recovery rate γ are considered to be time-dependent.
- Our model to include both symptomatic and asymptomatic infectious cases.

Proposed SEIR Model Cont'd

$$\frac{dS}{dt} = \frac{-\beta(t)S(t)I(t)}{N}, \quad (1)$$

$$\frac{dE}{dt} = \frac{\beta(t)S(t)I(t)}{N} - \sigma(t)E(t), \quad (2)$$

$$\frac{dI}{dt} = \sigma(t)E(t) - \gamma(t)I(t), \quad (3)$$

$$\frac{dR}{dt} = \gamma(t)I(t), \quad (4)$$

where

$$S(t) + E(t) + I(t) + R(t) = N(t).$$

- $\sigma(t)$: incubation rate, the rate at which individuals progress to either symptomatic or asymptomatic infectious.

Proposed SEIR Model with Symptomatic and Asymptomatic Persons

$$\frac{dS}{dt} = -\beta(t)(I + \eta A) \frac{S}{N}, \quad (5)$$

$$\frac{dE}{dt} = \beta(t)(I + \eta A) \frac{S}{N} - \sigma E, \quad (6)$$

$$\frac{dI}{dt} = \alpha\sigma E - \gamma_I I, \quad (7)$$

$$\frac{dA}{dt} = (1 - \alpha)\sigma E - \gamma_A A, \quad (8)$$

$$\frac{dR}{dt} = \gamma_I(t)I + \gamma_A(t)A, \quad (9)$$

- η : relative infectiousness of asymptomatic persons (in comparison to symptomatic persons).
- α : fraction of cases that are symptomatic.

Analytical Results

- The basic reproduction number, \mathcal{R}_0 , for the special case of model (5)-(9) when $\beta(t) \equiv \beta_0$, $\gamma_I(t) \equiv \gamma_I$, and $\gamma_A(t) \equiv \gamma_A$ is given as:

$$\mathcal{R}_0 = \frac{\beta_0 \alpha}{\gamma_I} + \frac{\beta_0 \eta (1 - \alpha)}{\gamma_A}.$$

- \mathcal{R}_0 measures the average number of new COVID-19 infections generated by an average infected individual introduced into a population.
- Newly symptomatic infectious person can infect on averaged $\frac{\beta_0}{\gamma_I}$ with probability α . Similarly, the asymptomatic individual can infect on average $\frac{\beta_0}{\gamma_A}$ with probability $(1 - \alpha)$.

Theorem

The disease-free equilibrium DFE: $(S^, E^*, I^*, A^*, R^*) = (N(0), 0, 0, 0)$, of the model (5)-(9) is locally-asymptotically stable if $\mathcal{R}_0 < 1$, and unstable if $\mathcal{R}_0 > 1$.*

- **Epidemiological implication:** Community transmission of COVID-19 can be effectively suppressed in the community if the control and mitigation strategies implemented can bring the reproduction number (\mathcal{R}_0) to a value less than unity.

Tracking $\beta(t)$, $\sigma(t)$, & $\gamma(t)$ Using Ridge Regression

- We track and predict $\beta(t)$, $\sigma(t)$, and $\gamma(t)$ using Finite Impulse Response (FIR) filters in linear systems.
- We use Ridge Regression as our estimation method to solve the following optimization problem:

$$\min_{a_j} \sum_{t=J}^{T-2} (\beta(t) - a_0 - \sum_{j=1}^J a_j \beta(t-j))^2 + \lambda_1 \sum_{j=0}^J a_j^2$$
$$\min_{b_k} \sum_{t=K}^{T-2} (\sigma(t) - b_0 + \sum_{k=1}^K b_k \sigma(t-k))^2 + \lambda_2 \sum_{k=0}^K b_k^2,$$
$$\min_{c_l} \sum_{t=L}^{T-2} (\gamma(t) - c_0 + \sum_{l=1}^L c_l \gamma(t-l))^2 + \lambda_3 \sum_{l=0}^L c_l^2,$$

where λ_1 , λ_2 and λ_3 are the regularization parameters.

Predicting the Number of Exposed $\hat{E}(t)$, Infected $\hat{I}(t)$, and Recovered Persons $\hat{R}(t)$

Algorithm 1: Tracking Discrete Time Time-dependent SEIR Model

input : $\{E(t), I(t), R(t), 0 \leq t \leq T - 1\}$, regularization parameters λ_1, λ_2 and λ_3 , order of autoregressive model J, K, L , prediction window W .

output : $\{\beta(t), \sigma(t), \gamma(t), 0 \leq t \leq T - 2\}$,
 $\{\hat{\beta}(t), \hat{\sigma}(t), \hat{\gamma}(t), 0 \leq t \leq T - 2\}$,
 $\{\hat{E}(t), \hat{I}(t), \hat{R}(t), t \geq T\}$.

- 1 Measure $\{\beta(t), \sigma(t), \gamma(t), 0 \leq t \leq T - 2\}$ using (15), (14), and (13) respectively.
- 2 Train the ridge regression and estimate $\hat{\beta}(T - 1), \hat{\sigma}(T - 1)$ and $\hat{\gamma}(T - 1)$ using (16), (17), and (18).
- 3 Estimate the number of exposed persons $\hat{E}(t)$, infected persons $\hat{I}(t)$ and recovered persons $\hat{R}(t)$ on the next day T using (19), (20) and (21) respectively.
- 4 **While** $T \leq t \leq T + W$ **do**
- 5 Estimate $\hat{\beta}(t), \hat{\sigma}(t)$ and $\hat{\gamma}(t)$ by (13), (14) and (15) respectively.
- 6 Predict $\hat{E}(t + 1), \hat{I}(t + 1)$ and $\hat{R}(t + 1)$ using (19), (20), and (21) respectively.
- 7 **end while**

Prediction Results

Country	Start date	End date	Pred Window	Predicted Cases
China	01/15/20	05/05/20	100	84,413
Italy	02/24/20	05/03/20	100	230,088
USA	03/04/20	05/05/20	100	1,742,736

States	Start date	End date	Pred Window	Predicted Cases
Maryland	04/12/20	05/04/20	50	33,804
Iowa	04/12/20	05/04/20	50	10,297
Texas	04/12/20	05/04/20	50	47,083

Prediction Results

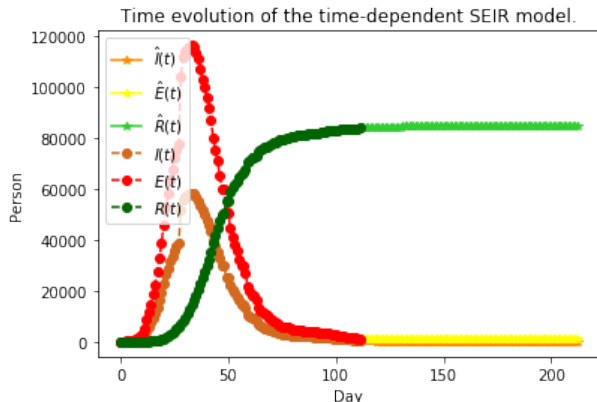


Figure: China. The circle-marked solid curve with dark orange (resp. red, green) color is the real number of infected persons $I(t)$ (resp. exposed person $E(t)$, recovered $R(t)$), the star-marked dashed curve with light orange (resp. yellow, green) color is the predicted number of infected persons $\hat{I}(t)$ (resp. exposed $\hat{E}(t)$, recovered $\hat{R}(t)$).

Prediction Results

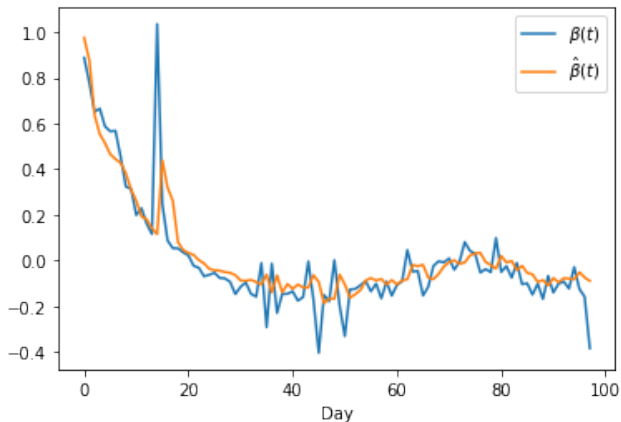


Figure: Trajectory of the transmission rate $\beta(t)$ and predicted transmission rate $\hat{\beta}(t)$ for China.

Prediction Results

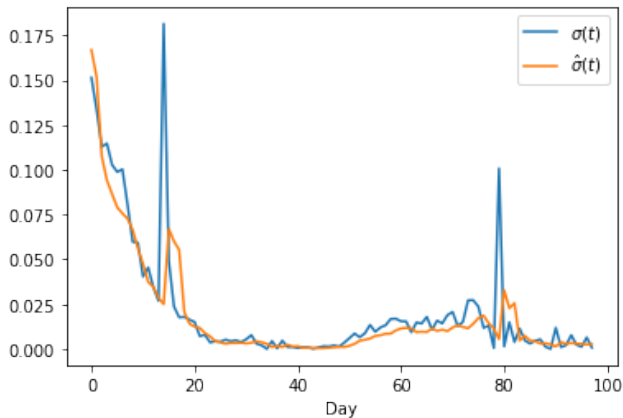


Figure: China: Trajectory of the incubation rate $\sigma(t)$ and predicted incubation rate $\hat{\sigma}(t)$.

Prediction Results

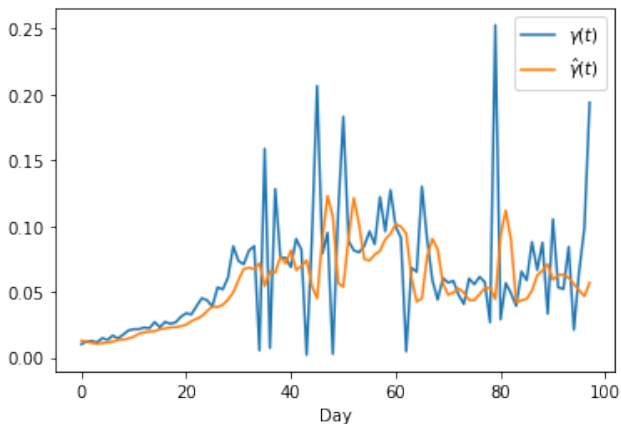


Figure: China: Trajectory of the recovery rate $\gamma(t)$ and predicted recovery rate $\hat{\gamma}(t)$.

Prediction Results

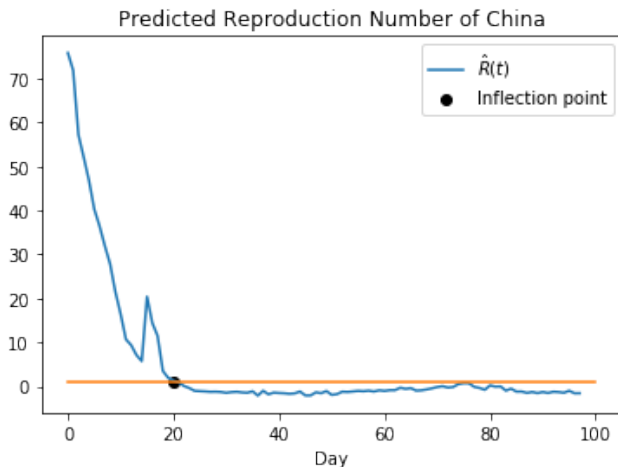


Figure: Trajectory of the basic reproduction number $R_0(t)$ in China.

Summary & Conclusion

- Our model was used to assess the community-wide impact of early lockdown in China, Italy and the US, as well as various levels of lockdown lifting in the US states of Maryland, Iowa, and Texas.

Thanks.

Q-&-A