The effect of behavioral changes on the spread of COVID-19.

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1 Project Overview

1.1 Domain

Our model's domain is epidemiology, specifically the study of how disease spreads.

1.2 Problem Statement

How do behavioral changes affect the spread of COVID-19? Are behavioral changes enough to eradicate COVID-19?

1.3 Scope

What will not be simulated:

- An endemic model
- Population inflows and outflows
- Disease seasonality
- Usage of medical facilities
- Vaccination
- Age based components

What will be simulated:

- An epidemic model
- Pre-symptomatic infectious compartment
- Asymptomatic and symptomatic infectious compartments
- Removed compartment

2 System Description

2.1 System Components

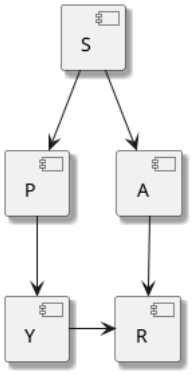

Figure 1: Flowchart for the proposed model.

Variable	Description
S	Susceptible, can be infected
P	Pre-symptomatic, infectious without symptoms currently
A	Asymptomatic, infectious without symptoms forever
Y	Symptomatic, infectious with symptoms
R	Removed, recovered or dead

The above model is derived from the standard SIR model. The Infectious component is divided into three compartments as each is likely to have a different effect on behavioral patterns, though pre-symptomatic and asymptomatic are likely to have the same effect but asymptomatic does not transition into symptomatic.

2.2 System Dynamics

$$S' = -\frac{s(p+a+y)}{T}\beta S(\kappa_1 P + \kappa_2 A + \kappa_3 Y)$$

$$P' = \theta_1 \frac{s(p+a+y)}{T}\beta S(\kappa_1 P + \kappa_2 A + \kappa_3 Y) - \phi P$$

$$A' = \theta_2 \frac{s(p+a+y)}{T}\beta S(\kappa_1 P + \kappa_2 A + \kappa_3 Y) - \gamma A$$

$$Y' = \phi P - \gamma Y$$

$$R' = \gamma Y + \gamma A$$

Symbol	Description
s, p, a, y	rate of contact from component
S, P, A, Y, R	rate of population of component
T	$sS + pP + aA + yY + R$ total rate of contact of components
β	population rate of contact
k_1, k_2, k_3	infection rate per contact
θ_1, θ_2	rate of susceptible to infectious class
ϕ	rate of pre-symptomatic to symptomatic
γ	rate of recovery

2.3 Core Models and Algorithms

2.3.1 SIR Model

The SIR model is a categorical model that can be used to model an epidemic by dividing a population into three categories, Susceptible, Infectious, and Recovered. Over time the population inside each category can be described with a set of differential equations:

$$\frac{ds}{dt} = -\beta si$$

$$\frac{di}{dt} = \beta si - \gamma i$$

$$\frac{dr}{dt} = \gamma i$$

Symbol	Description
s, i, r	rate of population of component
t	time
β	rate of contact
γ	rate of recovery

[2]

2.3.2 Behavioral change in populations

A population demonstrates behavioral change during a pandemic by reducing their rate of contact. This effect can be dependent on which compartment an individual is in. It can be modeled by modifying the SIR differential equations into:

$$\frac{ds}{dt} = -\beta \frac{pq}{T} si$$

$$\frac{di}{dt} = \beta \frac{pq}{T} si - \gamma I$$

Symbol	Description
s, i	rate of population of component
t	time
β	rate of contact
γ	rate of recovery
p, q	change in rate of contact
T	$ps + qi + r$ total rate of contact of components

[1]

2.4 Assumptions

- The population will stay constant.
- The virus will not be affected by seasonal changes.
- The population will mix homogeneously.
- The population will not lose immunity.
- The virus will not mutate significantly.
- Different infectious compartments will recover at the same rate.

3 Implementation Approach

3.1 Programming Language

The programming language to be used for this model will be Python for the following reasons:

- I have experience with Python.
- All my references use Python.
- Python is a popular language for modeling.

3.2 Development Environment

The python libraries used to develop this project will be:

- Pandas
- Matplotlib

Finally, the IDE used will be Emacs since I already have a python development environment setup.

3.3 Simulation Type

The behavioral change model will be a continuous model where the state of the population is dependent on time.

3.4 Data Collection Plan

The following metrics will be tracked:

- Total number of infections
- Time until peak of the outbreak
- Peak number of infections

4 Literature Review

4.1 *Modeling and Simulation in Python*

4.1.1 Summary

This source describes a model to simulate a "Freshman Plague" where 89 students arrive at a campus healthy while 1 student comes carrying some infectious disease. The model is called the *Kermack-McKendrick Model* which is a SIR model where the population is divided into three categories, (S)upsceptible, (I)nfectious, and (R)ecoverd. The number of susceptible becoming infected is

$$\beta siN$$

per day, where β is the contact rate, s is the fraction of the population susceptible, i is the fraction of the population infectious, and N the population number. The number of infectious becoming recovered is

$$\gamma iN$$

, where y is the rate of recovery, i is the number of infectious, and N is the population number. [2]

4.1.2 Adaption and Application

An application for this paper with regards to our project is the component model it describes for epidemics. Specifically, the Kermack-McKendrick model which can be used to model the COVID-19 pandemic within a college campus. The SIR model and the two related equations will become the core part of our project.

4.2 *A simple model for behavior changes in epidemics*

4.2.1 Summary

The above paper models the change in behavior that a population demonstrates during a pandemic. Specifically, it assumes that susceptible members during an pandemic decrease their rate of contact by a fraction p, $0 \leq p \leq 1$, and that infectious members decrease their rate of contact by a fraction q, $0 \leq q \leq 1$. This model then gives a pair of difference equations to represent this change. The first equation is

$$S' = -\beta N \frac{pq}{T} SI$$

where S' is the change in Susceptible with respect to time, β the rate of contact, N the population, p the fraction in change of contact for Susceptible, p the fraction in change of contact for Infectious, q the fraction in change of contact for Infectious, T is $pS + qI + R$, S the fraction of the population that is Susceptible, and I the fraction of the population that is Infectious. The second equation is

$$I' = \beta N \frac{pq}{T} SI - \alpha I$$

where I' is the change in Infectious with respect to time, α the rate of recovery, and I the fraction of the population that is Infectious. [1]

4.2.2 Application and Adaption

This paper introduces a model that can be used to model self-isolation and social distancing for the COVID-19 pandemic. Our model will adapt the rate of contact by fractions and their difference equations for both Susceptible and Infectious.

4.3 *SEIR modeling of the COVID-19 and its dynamics*

4.3.1 Summary

This paper describes a SEIR epidemic model which inputs parameters based on a particle swarm optimization algorithm of the Hubei, China province. The model separates the infectious compartment into two without intervention and with intervention parts. It is further described in Figure 1 and with the following set of difference equations:

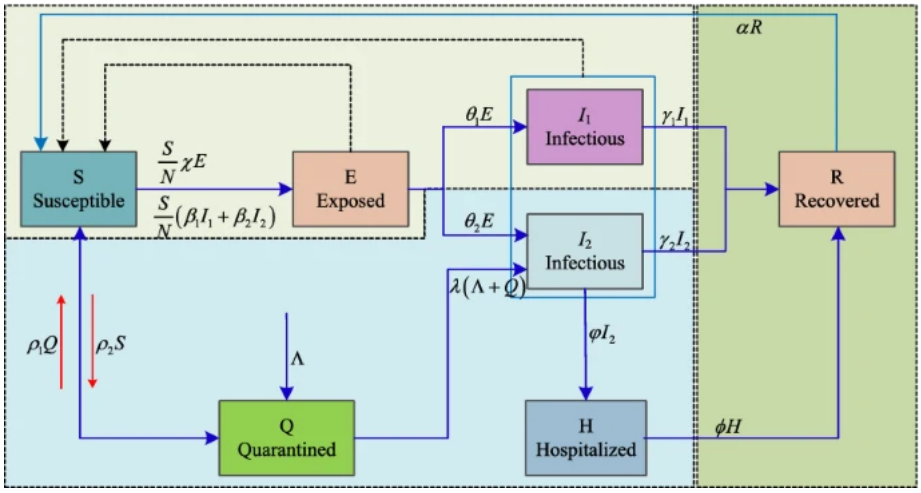

Figure 2: Flowchart model for the *SEIR modeling of the COVID-19 and its dynamics*

$$\dot{S} = -\frac{S}{N}(\beta_1 I_1 + \beta_2 I_2 + \chi E) + \rho_1 Q - \rho_2 S + \alpha R$$

$$\dot{E} = \frac{S}{N}(\beta_1 I_1 + \beta_2 I_2 + \chi E) - \theta_1 E - \theta_2 E$$

$$\dot{I}_1 = \theta_1 E - \gamma_1 I_1$$

$$\dot{I}_2 = \theta_2 E - \gamma_2 I_2 - \phi_2 I_2 - \phi I_2 + \lambda(\Lambda + Q)$$

$$\dot{R} = \gamma_1 I_1 + \gamma_2 I_2 + \Phi H - \alpha R$$

$$\dot{H} = \phi I_2 - \Phi I_2 H$$

$$\dot{Q} = \Lambda + \rho_2 S - \lambda(\Lambda + Q) - \rho_1 Q$$

Variable	Description
α	Temporary immunity rate
β_1, β_2	The contact and infection rate of transmission per contact from infected class
χ	Probability of transmission per contact from exposed individuals
θ_1, θ_2	Transition rate of exposed individuals to the infected class
γ_1, γ_2	Recovery rate of symptomatic infected individuals to recovered
ϕ	Rate of infectious with symptoms to hospitalized
Φ	Recovered rate of quarantined infected individuals
λ	Rate of the quarantined class to the recovered class
ρ_1, ρ_2	Transition rate of quarantined exposed to quarantined infected to wider community
Λ	External input from the foreign countries

[5]

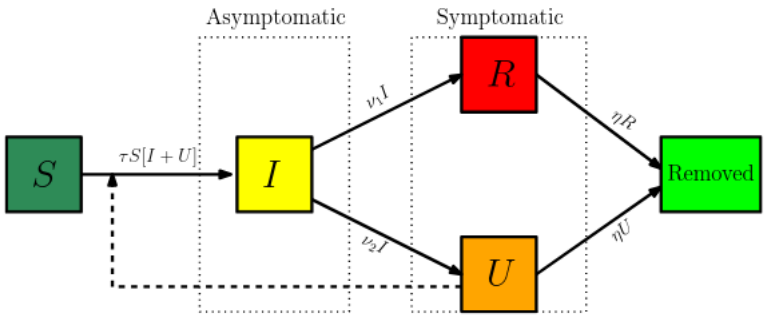

Figure 3: Flowchart model for the *Predicting the cumulative number of cases for the COVID-19 epidemic in China from early data* model

4.3.2 Application and Adaption

This paper describes a set of differential equations to reflect the different rate of infection of multiple infectious compartments. From it we will take $(\beta_1 I_1 + \beta_2 I_2 + \chi E)$ but replace it with three infectious components instead of two and one exposed component. This leads to $(\kappa_1 P + \kappa_2 A + \kappa_3 Y)$ where P is pre-symptomatic, A is asymptomatic, and Y is symptomatic.

4.4 Predicting the cumulative number of cases for the COVID-19 epidemic in China from early data

4.4.1 Summary

This paper describes a SEIRU model in order to analyze the effects of the Chinese governments' imposed public policies in Wuhan from January 23, 2020 to January 29, 2020. The model consists of the following system of ordinary differential equations and is described in Figure 2.:

$$S^{'}(t) = -\tau(t)S(t)[I(t) + U(t)],$$

$$I^{'}(t) = \tau(t)S(t)[I(t) + U(t)] - \nu I(t),$$

$$R^{'}(t) = \nu_1 I(t) - \eta R(t),$$

$$U^{'}(t) = \nu_2 I(t) - \eta U(t)$$

Variable	Description
S	Susceptible
I	Asymptomatic
R	Symptomatic reported
U	Symptomatic unreported
$\tau(t)$	Transmission rate at time t
$\nu_1 = f\nu$	Rate of asymptomatic infectious becoming reported symptomatic
ν	Rate of asymptomatic to symptomatic
$\nu_2 = (1-f)\nu$	Rate of asymptomatic infectious becoming unreported symptomatic
η	Rate of recovery

[3]

4.4.2 Application and Adaption

The above paper describes a model that divides the infectious compartment to accurately model the COVID-19 epidemic. From it we will take the infectious compartments I (Asymptomatic) , R (Symptomatic Reported) , U (Symptomatic Unreported) and remove the division of reported and unreported. Furthermore, we will add a separate asymptomatic compartment, since I in the model is pre-symptomatic rather than true asymptomatic infection, which is important for our analysis.

4.5 The role of asymptomatic and pre-symptomatic infection in SARS-CoV-2 transmission—a living systematic review

4.5.1 Summary

The above study extracts data from multiple sources to determine the role of asymptomatic, pre-symptomatic, symptomatic infection in the transmission of SARS-CoV-2. Specifically, it estimates that asymptomatic viruses have a 1% (95% CI 0%-2%) infection rate, pre-symptomatic 7% (95% CI 3% - 11%), and symptomatic 6% (95% CI 5% - 8%).

[4]

4.5.2 Application and Adaption

The above paper describes the important states of the COVID-19 epidemic and gives us an understanding of how to separate the infectious components of our project. Specifically, it tells us that asymptomatic, pre-symptomatic, and symptomatic states all have an important impact on the spread of COVID-19, which will be adapted into our model.

5 Diagrams

Figure 4: Class Diagram

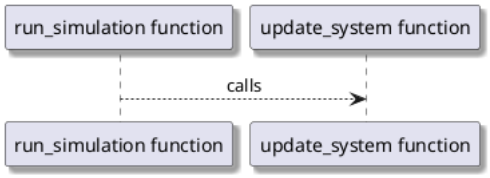

Figure 5: Activity Diagram

References

[1] Fred Brauer. "A simple model for behaviour change in epidemics". In: *BMC Public Health* 11.S1 (Feb. 2011). DOI: 10.1186/1471-2458-11-s1-s3.

[2] Allen Downey. "Epidemiology". In: *Modeling and Simulation in Python*. No Starch Press. URL: https://allendowney.github.io/ModSimPy/index.html.

[3] Zhi Hua Lia. "Predicting the cumulative number of cases for the COVID-19 epidemic in China from early data". In: *Math Biosci Eng* (Apr. 2020). DOI: 10.3934/mbe.2020172.

[4] Xueting Qui. "The role of asymptomatic and pre-symptomatic infection in SARS-CoV-2 transmission—a living systematic review". In: *Clin Microbial Infect* (Jan. 2021). DOI: 10.1016/j.cmi.2021.01.011.

[5] Kehui Sun Shaobo He Yuexi Peng. "SEIR modeling of the COVID-19 and its dynamics". In: *Nonlinear Dynamics* 101 (June 2020). DOI: 10.1007/s11071-020-05743-y.