Mathematical Modeling, Analysis, and Simulation of the COVID-19 Pandemic with Behavioral Patterns and Group Mixing

Comfort Ohajunwa (The Governor's School at Innovation Park), Dr. Padmanabhan Seshaiyer (George Mason University)

Abstract

As COVID-19 cases continue to rise globally, many researchers have developed mathematical models to help capture the dynamics of the spread of COVID-19. Specifically, the compartmental SEIR model and its variations have been widely employed. These models differ in the type of compartments included, nature of the transmission rates, seasonality, and several other factors. Yet, while the spread of COVID-19 is largely attributed to a wide range of social behaviors in the population, several of these SEIR models do not account for such behaviors. In this project, we introduce a new implicit COVID-19 model where contact rates depend on behavioral patterns adopted across the population. Specifically, we consider two sub-populations, one exhibiting normal behavior who do not reduce their contacts and another exhibiting altered behavior who reduce their contacts by practicing non-pharmaceutical interventions such as social distancing and self-isolation. The basic reproduction number for the model will be derived. The dynamics of these populations are modelled through a coupled system of ordinary differential equations that incorporate mixing patterns of individuals differing by activity levels, which could be proportionate mixing, preferred mixing, or like-with-like mixing. We will also expand our model to include risk perception and irrational behavior, with appropriate pay-off functions.

Introduction

Since the start of the COVID-19 pandemic, many researchers have considered variations of the epidemiological SEIR model to model the disease dynamics of COVID-19. The traditional SEIR model is a compartmental model that divides a population of people into Susceptible, Exposed, Infectious, and Recovered. The dynamics of a disease, like COVID-19, can be represented as a system of ordinary differential equations.


https://www.idmod.org/docs/emod/hiv/model-seir.html
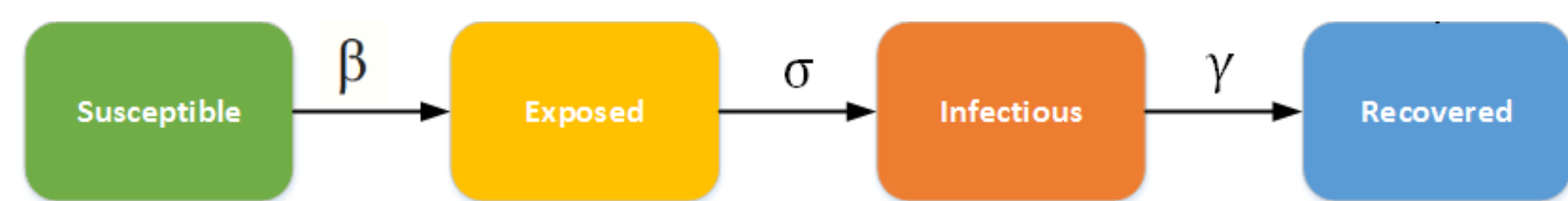
$$\frac{dS}{dt} = -\frac{\beta SI}{N}$$
$$\frac{dE}{dt} = \frac{\beta SI}{N} - \sigma E$$
$$\frac{dI}{dt} = \sigma E - \gamma I$$
$$\frac{dR}{dt} = \gamma I$$

Yet, most models do not account for social behavioral changes such as reducing or maintaining the number of social contacts. In addition, several models do not consider mixing patterns between individuals who possess different behaviors. However, these measures significantly influences the spread of COVID-19 and worth investigating in mathematical models. Therefore, in this project, we explore an extension of the SEIR model that incorporates both behavioral changes and mixing patterns between individuals two groups with different behaviors.

Daily Trends in Number of COVID-19 Cases in the United States Reported to CDC

https://covid.cdc.gov/covid-data-tracker/#trends_dailytrendscases
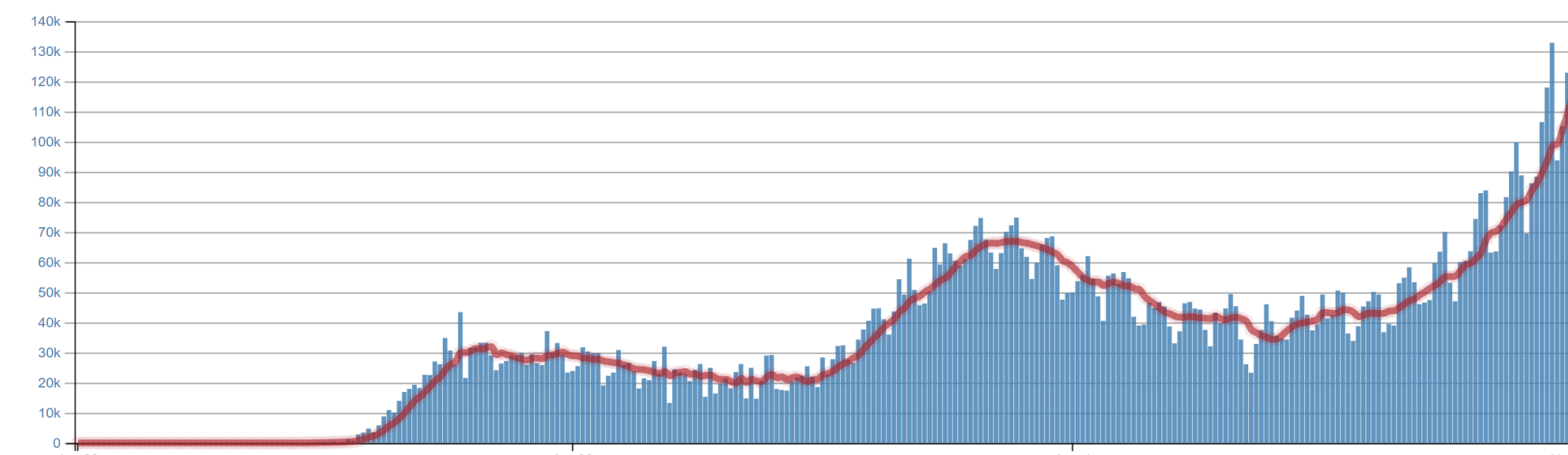
The Mathematical Model and R_0

An COVID-19 Social Behavior Mixing Model

We describe two groups: in a population: individuals with normal behavior (N_n) and individuals with altered behavior (N_a). Normal behavior indicates that the individual does not reduce their contacts, while altered behavior indicates that the individual does reduce their contacts through interventions such as social distancing and confinement.
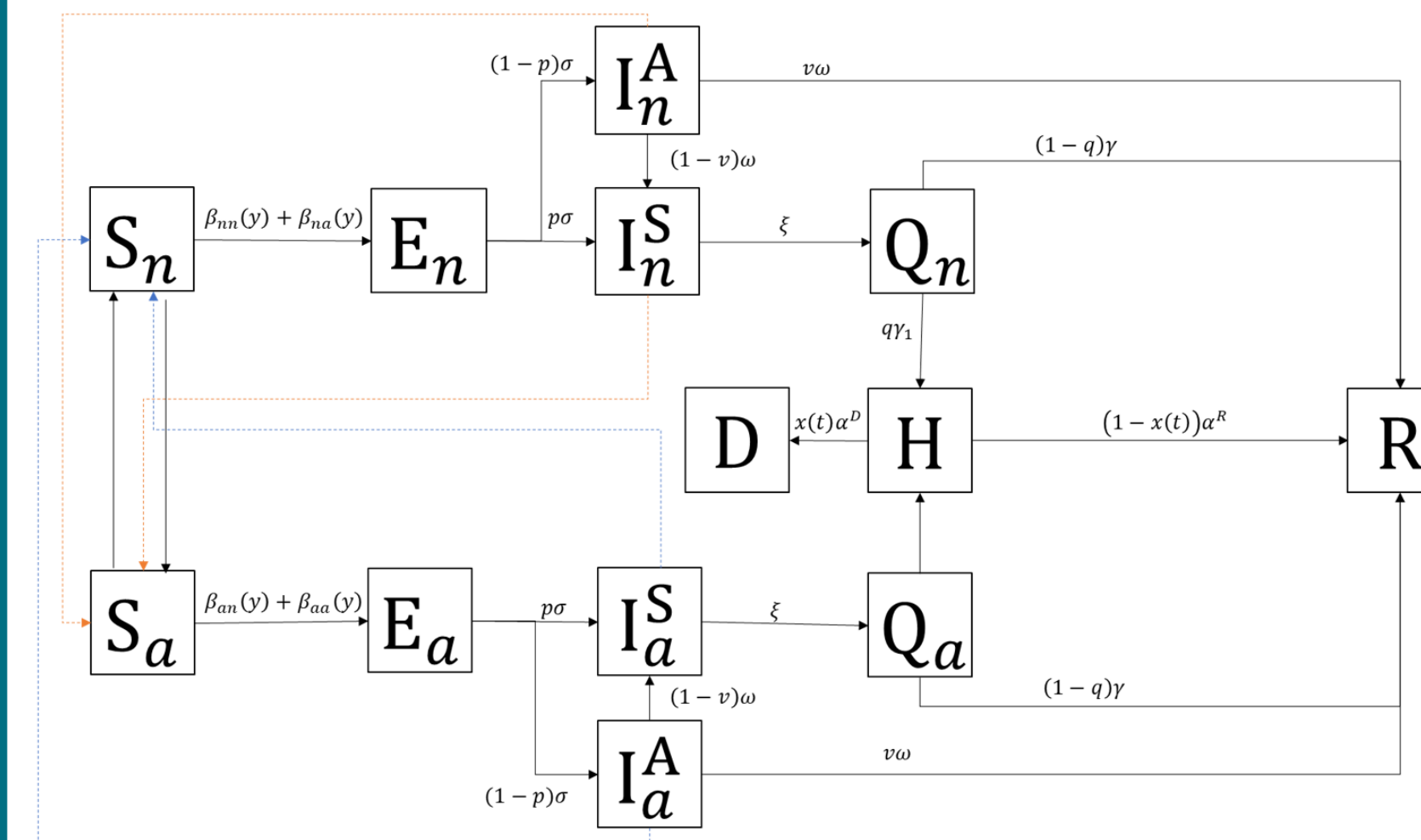
Subpopulations:
- Susceptible (**S**)
- Exposed (**E**)
- Asymptomatic (**I^A**)
- Symptomatic (**I^S**)
- Quarantine (**Q**)
- Hospitalized (**H**)
- Recovered (**R**)
- Dead (**D**)

The Susceptibles of each group may switch behaviors and mix with Infected individuals from both groups.
The impact of such behaviors are captured in four transmission rates corresponding to the interactions between the two groups. Here $b_{nn}(y) = f_{nn} c_n y$, $b_{na}(y) = f_{na} c_n y$, $b_{aa}(y) = f_{aa} c_a (1-y)$, $b_{an}(y) = f_{an} c_a (1-y)$. Here,

f_{ij} - the fraction of contacts made by group i with group j
c_i - the total number of contacts
y - the proportion of Susceptibles that are in the normal behavior group

$$\frac{dS_n}{dt} = -b_{nn}(y)\frac{S(I_n^A + I_n^S)}{N_n} - b_{na}(y)\frac{S(I_a^A + I_a^S)}{N_a}$$
$$\frac{dE_n}{dt} = b_{nn}(y)\frac{S(I_n^A + I_n^S)}{N_n} + b_{na}(y)\frac{S(I_a^A + I_a^S)}{N_a} - \sigma E_n$$
$$\frac{dI_n^A}{dt} = (1-p)\sigma E_n - \omega I_n^A$$
$$\frac{dI_n^S}{dt} = p\sigma E_n + (1-\nu)\omega I_n^A - \xi I_n^S$$
$$\frac{dQ_n}{dt} = \xi I_n^S - \gamma Q_n$$
$$\frac{dS_a}{dt} = -b_{an}(y)\frac{S(I_n^A + I_n^S)}{N_n} - b_{aa}(y)\frac{S(I_a^A + I_a^S)}{N_a}$$
$$\frac{dE_a}{dt} = b_{an}(y)\frac{S(I_n^A + I_n^S)}{N_n} + b_{aa}(y)\frac{S(I_a^A + I_a^S)}{N_a} - \sigma E_a$$
$$\frac{dI_a^A}{dt} = (1-p)\sigma E_a - \omega I_a^A$$
$$\frac{dI_a^S}{dt} = p\sigma E_a + (1-\nu)\omega I_a^A - \xi I_a^S$$
$$\frac{dQ_a}{dt} = \xi I_a^S - \gamma Q_a$$
$$\frac{dH}{dt} = q\gamma(Q_n + Q_a) - ((1-x)\alpha^R + x\alpha^D)H$$
$$\frac{dR}{dt} = \nu\omega I^A + (1-q)\gamma(Q_n + Q_a) + (1-x)\alpha^R H$$
$$\frac{dD}{dt} = x\alpha^D H$$
$$\frac{dy}{dt} = y(1-y)(b_{nn} - b_{an})\left(\frac{I_n^A + I_n^S}{N_n}\right) + y(1-y)(b_{aa} - b_{na})\left(\frac{I_a^A + I_a^S}{N_a}\right)$$

Mixing Models

$$f_i = \frac{(1-\pi_i)c_i N_i}{(1-\pi_n)c_n N_n + (1-\pi_a)c_a N_a}$$

| Proportionate Mixing	Preferred Mixing		Like-with-Like Mixing
$f_{nn} = f_{an} = f_n$	$f_{nn} = \pi_n + (1-\pi_n)f_n$	$f_{aa} = \pi_a + (1-\pi_a)f_a$	$f_{nn} = f_{aa} = 1$
$f_{na} = f_{aa} = f_a$	$f_{an} = (1-\pi_a)f_n$	$f_{na} = (1-\pi_n)f_a$	$f_{na} = f_{an} = 0$

The Basic Reproduction Number

Using the Next Generation Method, we derived the Basic Reproduction Number (R_0), which indicates the number of secondary cases by a single infectious individual. Our theorem is as follows for $i = n, a$:
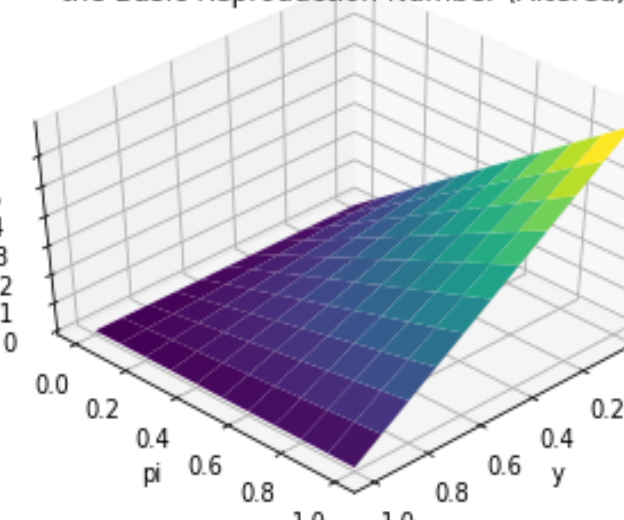
$$\mathcal{R}_0^i = R_0^{1,i} + R_0^{2,i} + R_0^{3,i}$$

$$R_0^{1,i} = \beta_{ii} \cdot \frac{p}{\xi}$$
$$R_0^{2,i} = \beta_{ii} \cdot \frac{(1-p)}{\omega}$$
$$R_0^{3,i} = \beta_{ii} \cdot \frac{(1-\nu)(1-p)}{\xi}$$

$$\beta_{nn} = b_{nn}(y)\frac{N}{N_n}$$
$$\beta_{na} = b_{na}(y)\frac{N}{N_a}$$
$$\beta_{an} = b_{an}(y)\frac{N}{N_n}$$
$$\beta_{aa} = b_{aa}(y)\frac{N}{N_a}$$
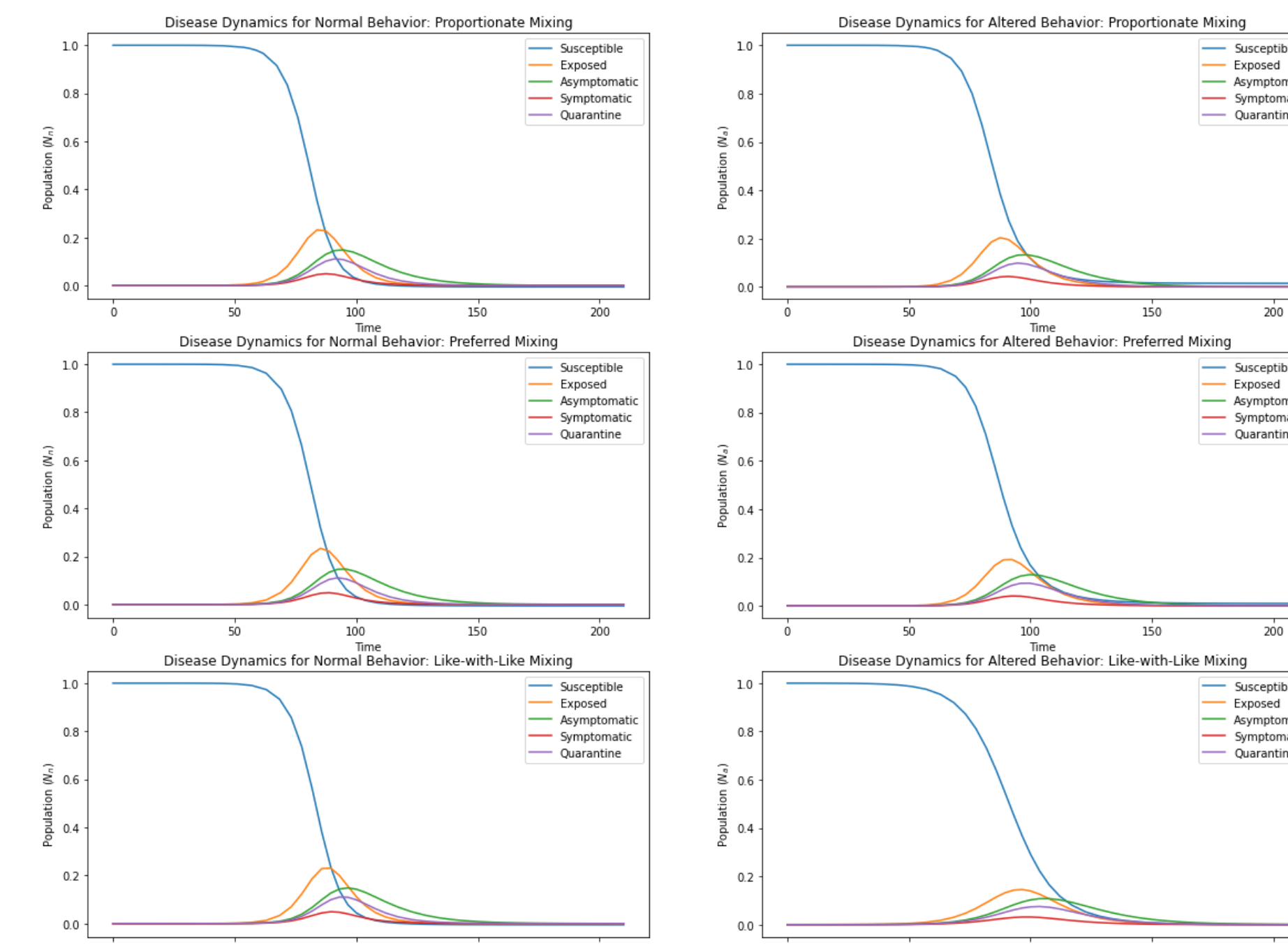
Influence of y and pi on the Basic Reproduction Number (Normal)
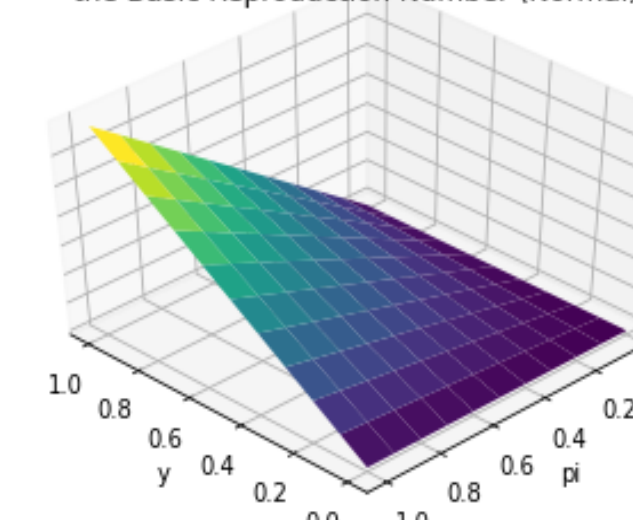
Influence of y and pi on the Basic Reproduction Number (Altered)

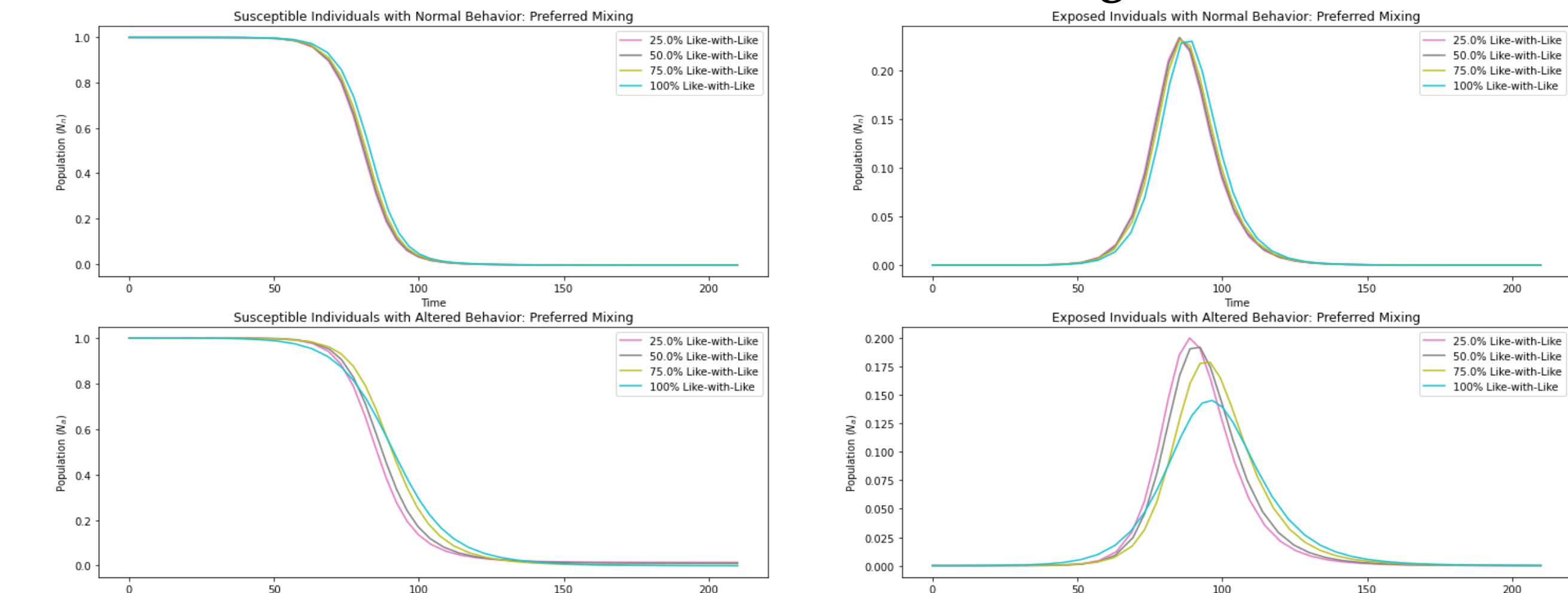## Computational Results

Influence of Mixing Patterns

Disease Dynamics for Normal Behavior: Proportionate Mixing

Disease Dynamics for Altered Behavior: Proportionate Mixing

Disease Dynamics for Normal Behavior: Preferred Mixing

Disease Dynamics for Altered Behavior: Preferred Mixing

Disease Dynamics for Normal Behavior: Like-with-Like Mixing

Disease Dynamics for Altered Behavior: Like-with-Like Mixing

Types of Mixing:
- *Proportionate*: All members of each group mixes at rates that are proportional to the number of contacts
- *Preferred*: A portion of each group mixes only within the group; the rest mix proportionately
- *Like-with-like*: All members of each group only mix within the group

Influence of Preferred Mixing

Susceptible Individuals with Normal Behavior: Preferred Mixing

Exposed Individuals with Normal Behavior: Preferred Mixing

Susceptible Individuals with Altered Behavior: Preferred Mixing

Exposed Individuals with Altered Behavior: Preferred Mixing

Conclusion and Future Work

In this project, we considered a novel epidemiological model that incorporates human behavior and mixing patterns. Specifically, we explore an implicit model for COVID-19 along with three types of mixing: proportionate, preferred, and like-with-like. We also derived a basic reproduction number that corresponds to each of the two groups. We demonstrate how a higher fraction like-with-like mixing increases the basic reproduction number for both groups. In addition, we show how a higher proportion of Susceptibles with normal behavior results in a greater basic reproduction number for the normal behavior group, and thus a higher overall basic reproduction number. We found that mixing did not appear to impact the dynamics for the normal behavior group, but it did influence the altered behavior group. If a larger portion of Susceptible with altered behavior mix only within their group, the disease dynamics improve. This work is still ongoing and will be published in a forthcoming paper. Currently, we plan on investigating the influence of risk perception and irrational behavior.

Acknowledgements