RELATIONSHIPS BETWEEN COVID-19 INFECTION RATES, HEALTHCARE ACCESS, SOCIOECONOMIC STATUS, AND CULTURAL DIVERSITY

by

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The following individuals read and discussed the thesis submitted by student MarGhece P.J. Barnes, and they evaluated her presentation and response to questions during the final oral e xamination. They found that the student passed the final oral examination.

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Tupac Shakur's second album title.

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To my family, I know me being thousands of miles away out of state since 2015 for my undergraduate and graduate education has been rough but thank you for sticking beside me. These last seven years have been hard and I honestly would not have been able to do it without you. My friends, y'all already know how deep my love runs for you. Our laughs over FaceTime, deep intellectual conversations and the links we've had have gotten me though some tough times when this degree TRIED to defeat me. Alexa– play Outstanding by The Gap Band

ABSTRACT

The COVID-19 pandemic has had a disproportionate impact on racial and ethnic minority groups, with high infection rates throughout those communities. There are a complex set of factors that account for COVID-19 disparities. Focusing on infection and death rates alone without also examining health equity, underestimates the true impact of the pandemic. To gain a more clear understanding of COVID-19's impact in these communities, we analyzed the relationship between state COVID-19 infection rates with social determinants of health: cultural diversity, health care access, and socioeconomic status. Our approach to identifying this relationship was to estimate infection rates by fitting John Hopkins COVID-19 data to an SIR compartmental model commonly used in epidemiology to model infectious disease. These infection rates were then analyzed as a function of state indices with regard to healthcare access, and socioeconomic status, as well as measures of each states cultural diversity.

Nationally we do not see a relationship between COVID-19 infection and removal rates to cultural diversity, healthcare access, and socioeconomic status during the time period. However an analysis of states with the highest and lowest infection rates show that more culturally diverse states had higher infection rates during this time period. In addition, states that ranked low in healthcare access had infections an order of magnitude larger than states with good healthcare access. Alternatively, states grouped by low and high socioeconomic status had similar infection rates.

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CHAPTER 1

INTRODUCTION

A global pandemic is an epidemic of an infectious disease that is spread across multiple regions. There have been many comparisons made between the COVID-19 pandemic and previous pandemics, such as the 1916 Polio epidemic, 1918 Spanish Flu, and the 1981 AIDS pandemic and epidemic.[1] Researchers dedicated themselves to identifying the origins of these viruses. However, it took decades for progress to be made and vaccinations or cures to be developed. Unlike COVID-19, the government banned government leaders and the press from reporting on the Spanish Flu epidemic.

Additionally, public outcry of the Polio and AIDS pandemics were different to that of COVID-19.[2] Many blame the government and scientists for causing the disease, while others initially thought and many continue to believe it to be a hoax.[3] This is particularly due to some individuals questioning the science behind COVID-19 vaccines and how quickly vaccine trials were conducted and authorized for public use over the course of several months that would normally take years.[4,5] COVID-19 was also highly publicized compared to previous pandemics and epidemics.[6,7] This is due in part to incentives for receiving a COVID-19 vaccine, media reporting, social media interactions and censorship, and individual ideals surrounding constitutional freedom.[5,8–10]

In this thesis we examine the correlation between COVID-19 infection rates to

healthcare access, socioeconomic status, and cultural diversity. When analyzing a pandemic, we must also examine pre-existing social structures and how it influences these social structures. The impact of individual and community exposure to COVID-19 is the results of multiple structures of inequality. It is important to examine these social determinants of health because research has shown that health disparities are created by social inequities.[11–13]

CHAPTER 2

COVID-19

2.1 Origin of COVID-19

The novel coronavirus disease 2019 (COVID-19) was first declared a Public Health Emergency of International Concern on January 30, 2020. It was then declared a global pandemic by the World Health Organization (WHO) on March 11, 2020. The first known case of COVID-19 was identified in Wuhan, Hubei, China in December 2019.[14] As shown in Figure 2.1, the strain of coronavirus disease that causes COVID-19 is the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2). The origin of COVID-19 is continuously debated amongst scientists and researchers. Most commonly the origin has been speculated to be the product of a laboratory manipulation. However, through a comparative analysis of genomic data, SARS-CoV-2 did not derive from a previously identified virus.[15]

A receptor-binary domain (RBD) is an immunogenic fragment of a virus located on its "spike" domain that allows it to quay to the body to gain entry to cells and lead to infection.[17] It is the most variable part of the coronavirus genome. SARS-CoV-2 is similarly related to other Bat SARS-like coronaviruses. Specifically, Bat coronavirus RaTG13 is the closest known coronavirus to SARS-CoV-2, sharing a 96.1% similarity.[18,19] Further serological studies need to be conducted to determine the ambit of human exposure to SARS-CoV-2 to actuate an origin.

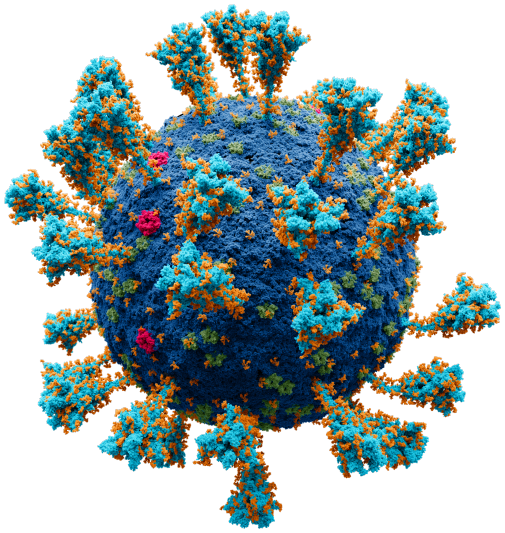

Figure 2.1: Scientifically accurate atomic model of the external structure of the Severe Acute Respiratory Syndrome CoronaVirus 2 (SARS-CoV-2), a strain (genetic variant) of the coronavirus that caused Coronavirus disease (COVID-19), first identified in Wuhan, China, during December 2019
[16]

2.2 Nomenclature

In the early stages of COVID-19, the virus name differentiated from "the coronavirus", "Wuhan coronavirus", or "Wuhan pneumonia", and "the rona". To prevent social stigmas and xenophobia, the WHO tentatively named the virus "2019-nCoV", which is short for "2019 Novel Corona Virus". This was based upon the WHO's 2015 guidelines for naming infectious diseases, which included avoiding the use of geographic locations, cultural references or species and classes of animals.[20] On February 11, 2020 the WHO announced "COVID-19" as the official name of the disease, wherein the Director General Tedros Adhanom Ghebreyesus clarified that CO stands for coronavirus, VI-virus, D-disease, and 19 for the year the outbreak was first discovered.[21]

2.3 Epidemiology

Coronaviruses are pathogens that can affect the lower respiratory tract in humans.[22] Some patients with COVID may experience mild symptoms, while others with pre-existing conditions or other underlying diseases could experience respiratory failure, cardiovascular damage, kidney failure, or liver failure.[23] Some common clinical symptoms of COVID-19 may include fever or chills, cough, fatigue, new loss of taste or smell, headache, or congestion.[24] The most commonly reported symptoms in patients are fever, cough, fatigue, shortness of breath, and phlegm.[25] Amongst patients that show symptoms, only 81% develop mild to moderate symptoms, 14% develop severe symptoms, and 5% suffer critical symptoms.[26] Asymptomatic patients forgo testing which contributes to the spread of the disease. Akin to other contagious infections, there may be a delay between an individual being exposed to COVID-19 and the appearance of symptoms. According to the U.S. Center of Disease Control (CDC), a person is considered infectious two days before developing symptoms, or two days before a positive test if no symptoms are present.[27]

Initially, COVID-19 was thought to be spreading from animal to human, but growing reports indicated that human to human spread is happening.[29] The transmission of COVID-19 will be examined as the passing of the disease from person to person. Shown in Figure 2.2, similar to the transmission of airborne respiratory viruses, COVID-19 is mainly transmitted through respiratory particles released when an infected person coughs, breathes, or sneezes.[30,31] SARS-CoV-2 has also been detected on surfaces such as counter tops, door handles and electronics of people with confirmed COVID-19 cases. Therefore, an individual that may have come into contact with an infected surface could also become infected if they touch their eyes,

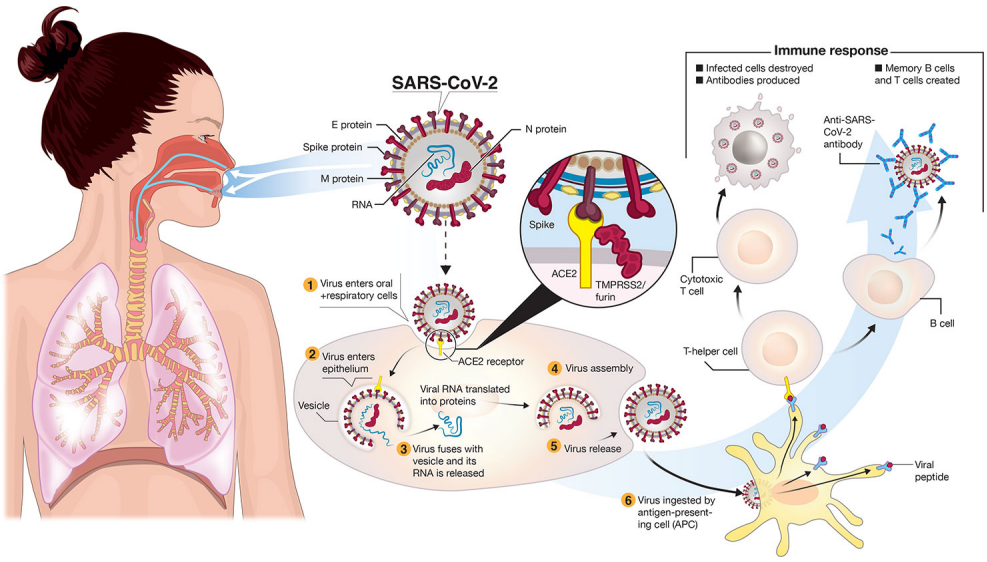

Figure 2.2: Transmission and life-cycle of SARS-CoV-2 causing COVID-19. SARS-CoV-2 is transmitted via respiratory droplets of infected cases to oral and respiratory mucosal cells. The virus, possessing a single-stranded RNA genome wrapped in nucleocapsid (N) protein and three major surface proteins: membrane (M), envelope (E) and Spike, replicates and passes to the lower airways potentially leading to severe pneumonia. The gateway to host cell entry (magnified view) is via Spike-converting enzyme 2 (ACE2) interaction with cleavage of Spike in the prefusion state by proteases TMPRSS-2/furin.

mouth, or nose.

The CDC issued a recommendation of 6ft social distancing from individuals inside your home who are sick and in public if possible.[32] Since aerosols and droplets are concentrated within a few feet, transmission decreases with social distancing and increased ventilation.[30] Long distance transmission can also occur in poorly ventilated areas like concert halls or festivals due to others shouting and singing. It was also recommended that people wear masks in public spaces and in spaces where transmission is high and social distancing is not possible.[33]

Face masks can assist with the mitigation of SARS-CoV-2 and have been classified into three categories: homemade masks, government certified respirators, and surgical masks.[34] Homemade masks are made out of a variation of fabrics with various thread counts. Against surgical masks and respirators, homemade masks are more loosely fit. The protective effects of respirators and surgical masks in blocking out aerosols and droplets can block >99.6% and less than 70% of the infectious viruses respectively.[34] This also leads to higher spreading possibilities due to the lack of filtration efficacy of the material.

2.4 Quarantine

The first U.S. laboratory confirmed case of COVID-19 by the CDC was on January 20, 2020 in Washington; based on a sample collected from a man who recently returned from Wuhan, China.[29] A second travel related case was confirmed January 24, 2020.[35] In a press briefing Dr. Nancy Messonnier, the Director of the National Center for Immunization and Respiratory Diseases, told reporters that the then named 2019-nCoV virus posed no immediate risk the the U.S. at the time.[36] Travelers were

advised to avoid all non essential travel to Wuhan, China and practice certain health precautions when traveling to other parts of China. On January 30, 2020 the CDC confirmed the first instance of person to person spread of the disease.[37] The WHO and CDC released separate guidelines separate guideline relating to quarantine.

Quarantine or self-isolation was a practice used to reduce the transmission of COVID-19. Its key features include staying home, isolating from others, and using no contact delivery services for food, medicine, or other shopping needs.[27] Day zero is considered to be the date of exposure, day one is 24-hours after last interaction with a person confirmed with COVID-19. When exposed to COVID-19, it was recommended that persons stay home and quarantine for 14-days.[27] In situations where individuals may test negative for COVID-19 or may not be experiencing any symptoms, it was still recommended to quarantine because symptoms may appear 2 to 14 days after exposure.[38]

2.5 Testing

COVID-19 cases are confirmed by the detection of SARS-CoV-2 using a reverse transcription polymerase chain reaction (RT-PCR) test. RT-PCR can detect SARS-CoV-2, only containing RNA in a few hours.[39] The method of sample collection varies but may include saliva,[40] throat swab,[41] nasopharyngeal swab,[42] or mucus.[43] SARS-CoV-2 RNA can be detected 2-3 days before symptoms occur and can remain detectable up to 60 days after.[44] The method of collection determines the probability of detecting the virus. Samples that are collected from the upper and lower respiratory tract carry a high detection rate.[45] Sensitivity of various clinical samples by RT-PCR test is 32% for pharyngeal swab, 63% for nasal swab, 72-75% for sputum, 48% for feces,

93-95% for bronchoalveolar lavage, and 1-3% for blood.[46] Some studies show that saliva collection may not be as effective as nasopharyngeal swabs,[40] notwithstanding certainty. Nasal swabs are more sensitive than throat swabs and should be collected when symptoms first arise. Sputum, feces and bronchoalveolar collections contain more virus and increase certainty in testing.[47]

2.6 Vaccinations

On March 17, 2020 a COVID-19 vaccine development began in the U.S. at a Kaiser Permanente Research Facility in Seattle, WA in conjunction with Moderna.[48] Due to prior knowledge of SARS and the coronaviruses that cause SARS variants, the development of COVID-19 vaccines was accelerated.[49] Vaccines against SARS had only been tested in non-human species such as turtles, pangolins, cats, and monkeys; however, a vaccine for preventing coronavirus infections in humans had not been developed yet.[50] The urgency to create such a vaccine led to a reduction in time spent conducting clinical trials to test for safety, immunogenicity, efficacy, effectiveness, and vaccine injury.[51,52] Typically this process would occur over several years.[53] On December 11, 2020 the Food and Drug Administration (FDA) issued an Emergency Use Authorization (EUA) for the Pfizer-BioNTech COVID-19 Vaccine for ages 16 and up.[54] Three days later New York nurse Sandra Lindsay received the first U.S. vaccine dose.[55] Approximately seven days after the first EUA for this COVID-19 vaccine, the FDA issued another for the Moderna COVID-19 Vaccine for ages 18 and up.[56]

The Pfizer-BioNTech and Moderna vaccines both require two doses of the primary series, given 3-8 weeks apart; while the Johnson and Johnson's Janssen COVID-19

vaccine for ages 18 and up only requires one dose.[57] Individuals are considered fully vaccinated two weeks after their final dose.[57] Common side effects include pain, redness, swelling in the arm at site of shot, fatigue, headache, muscle aches, and nausea affecting around 60% of recipients after second dose.[58,59] The initial release of the COVID-19 vaccine was administered in three phases: I for health care workers and long term care facility residents, II for individuals aged 75 or older and essential front-line workers, and III for individuals 65-74 years of age and ages 16-64 with high risk medical conditions.[60] During its phase 3 COVID-19 vaccine clinical trials, the Pfizer-BioNTech and Moderna vaccines showed 95% efficacy and the Janssen vaccine showed 67% efficacy fourteen days post vaccination and 66% 28 days post vaccination.[58,61]

On April 13, 2021, approximately 1 month after the Janssen COVID-19 vaccine EUA, the CDC and FDA released a joint statement recommending the suspension of the vaccine due to a rare and severe blood clot occurring in six patients 6-13 days post vaccination.[62–64] Approximately 10 days later, the advised suspension was recommended to be lifted by the FDA and the CDC.[65,66] Both agencies also issued warnings of a plausible causal relationship the Janssen COVID-19 vaccine and thrombosis with thrombocytopenia syndrome.[57,65,67]

2.7 Variants

The WHO has classified SARS-CoV-2 variants into two categories: variants of concern (VOC), and variants of interest (VOI). A SARS-CoV-2 VOI suggest an emerging risk to global health and a VOC is more infectious, likely due to cause breakthrough or reinfections in previously infected and vaccinated individuals and

cause more severe disease.[68,69] As of December 2021, there were 5 dominant VOCs of SARS-CoV-2 spreading globally: Alpha, Beta, Gamma, Delta, and Omicron.[70] All have been reported in the U.S. with Alpha in November 2020,[71] Beta and Gamma in January 2021,[72,73] Delta in February 2021,[74] and Omicron in November 2021.[75]

The Delta and Omicron variants became the dominant variant and dominant sub-variant in the U.S. by July 2021 and January 2022 respectively.[76,77] The Delta variant is considered to be 2.25 times more transmissible than the original SARS-CoV-2 strain, while the Omicron variant is 4.2 times more likely transmissible than Delta.[78–80] The CDC released updated guidance for everyone in high transmission areas to combat the spread of the variants.[81] On October 21, 2021 the CDC endorsed the Advisory Committee on Immunization Practices (ACIP) recommendation for individuals to receive COVID-19 booster shots six months after full vaccination.[82,83] Vaccinations are still considered to be the best protection against COVID-19 hospitalizations and severe illnesses. With the rise of breakthrough COVID-19 infections and reinfections, as of March 2022, scientists are still researching the effectiveness in vaccines against the Omicron variant.

The time period we chose to model is July 4, 2021 through October 1, 2021. It allows us to consider the assumption that that reinfection with the same variant does not occur within a 90 day time period.[84] It is after the first introduction to the COVID-19 vaccines being widely available for all persons age 16 and over, the emergence of the dominant Delta variant, and all persons residing in the United States have been privy to protective measures surrounding COVID-19. This time period also indicates a goal set by the Biden administration to have the United States population reach a 70% vaccination rate by July 4, 2021. Approximately 67% of eligible persons in the U.S. had received at least one dose of the COVID-19 vaccine and about 157

million people were fully vaccinated by July 4, 2021.[85]

CHAPTER 3

ANALYZING THE IMPACT OF COVID-19 IN CULTURALLY DIVERSE COMMUNITIES AND HEALTHCARE ACCESS

3.1 Health Care Access

As noted by Robert Pearl, M.D.:

> the U.S. lags behind other industrialized nations in many important health measures–partly because citizens of certain races, ethnicities, and incomes experience poorer versions of U.S. healthcare than others[86]

According to the Annual Social and Economic Supplement (ASEC) of the Current Population Survey (CPS), in 2020 28 million (8.6%) of people did not have health insurance at any point during the year.[87] Before the Affordable Care Act (ACA) was enacted in 2010, 48.6 million (16%) of American people did not have health insurance.[88] Health insurance increases health care access by reducing the high and unexpected costs of medical care to individuals and families. Having reasonable access to health care depends on many factors including the availability of services in a given community, healthcare affordability, and care-seeking behavior. Uninsured individuals are far more likely than the insured to abstain from seeking essential medical visits, exams, and medications due to cost. The consequences of inadequate

access to health care can result in poorer health and further jeopardize the ability to find an affordable health insurance plan.

The opportunity to stop the spread of COVID-19 in its early stages was missed on numerous occasions. As the virus swept through the U.S., testing kits were distributed roughly equally amongst labs and testing centers.[89] Population density and testing demands in these areas were not taken into consideration. Differences in health status and population characteristics within communities affect the variability of testing time. Thus, assuming all sites will have an equal demand could impact overall access to testing. The CDC reported the risk of COVID-19 infection, hospitalization, and death by race/ethnicity through March 10, 2022 (Table 3.1). This table, while also showing a disquieting death rate for all races, manifests how minority groups are impacted more and onus the pandemic's health impact. The overrepresentation of minorities among confirmed COVID-19 cases hospitalized, and dead is burgeoning extant inequalities regarding culture, socioeconomic status, and access to healthcare.

Rate ratios compared to White, Non-Hispanic persons	American Indian or Alaska Native	Asian	Black or African American	Hispanic or Latino
Cases	1.5x	0.7x	1.1x	1.5x
Hospitialization	3.1x	0.8x	2.5x	2.3x
Death	2.7x	0.8x	1.7x	1.1x

Source: National Center for Immunization and Respiratory Diseases (NCIRD), Division of Viral Diseases

Table 3.1: Risk for COVID-19 Infection, Hospitalization, and Death By Race/Ethnicity

3.2 Cultural Diversity and Socioeconomic Status

Culture is defined as customary deposits of life in a particular group of people passed down generationally.[90] Cultural diversity is the existence of ethnic and racial diversity in individuals from different cultural groups within a society. Socioeconomic status (SES) is the social class of an individual or group measured in combination with education, income, and occupation.[91] In the context of the COVID-19 pandemic, the factors that affect health equity and put culturally diverse areas at increased risk of becoming infected and dying from the disease include discrimination, inequities in treatment, historical medical events, occupation, SES, and housing.[92,93]

Fear of transmitting COVID-19 can lead to discrimination in medical care. Due to the public accessibility of racial/ethnic COVID-19 data, each aspect of diagnosis and treatment are affected. This begins with whose symptoms are actually taken seriously, who's tested first, who receives better service, and whether or not a medical professional appears to be afraid of you, etc. All instances contribute to an increased risk of minorities contracting COVID-19.

3.3 Occupation and Housing

The U.S. Bureau of Labor Statistics, categorized the characteristics of the labor force by race and ethnicity from the 2020 CPS (Figure 3.1). Occupations where people in some racial and ethnic groups are the majority can contribute to their risk of COVID-19 infection. People in minority groups are often more employed in essential worker jobs such as service, factories, grocery stores, and public transit.[94] Some people who work in these settings may come in close contact with the public, other workers, or must continue to work when sick if no paid sick leave is available.[95]

Comprehensively, the SES of people from some minority groups have less access to high quality education. Without high quality education, limited job options have reduced flexibility in getting jobs that may provide health insurance or offer a work from home option. Studies found that African-American or Black people and Hispanic or Latino people had lower levels of COVID-19 related knowledge about prevention practices, symptoms, and when to seek care.[96–98]

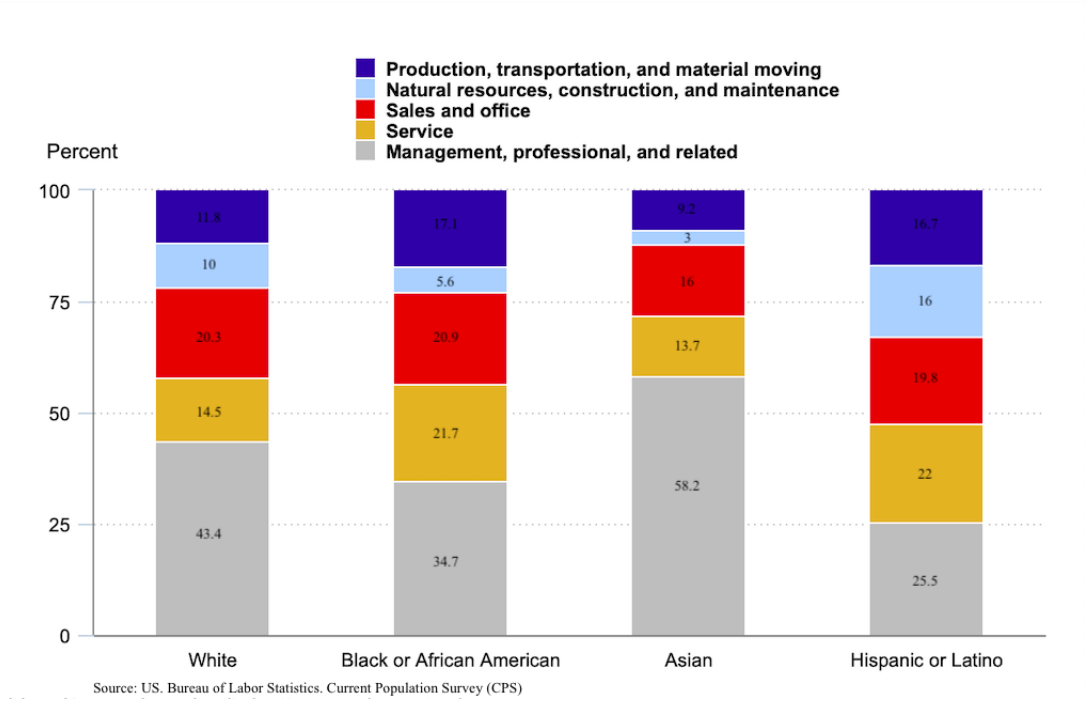

Figure 3.1: Employed People by Occupation 2020 Annual Averages

Although African-Americans or Black people and Hispanic or Latino people only make up 12% and 18% of all employed workers respectively; they are substantially overrepresented in service (43.7%), production and transportation (33.8%), and sales industries (40.7%).[94] In addition to this African-Americans or Black people account for 37%, 35%, and 33% of home health aides, nursing assistants, and correctional officers respectively. Continuous work in these fields could be contributing to COVID-19

health disparities due to an increase in exposure.

Crowded living conditions and unstable housing can hinder COVID-19 prevention strategies like self-isolation. In some cultures, it is common for multiple people to share one room. Due to this, COVID-19 transmission rates are higher amongst said cultures. COVID-19 outbreaks are also reported in correctional facilities, nursing homes, and homeless shelters. According to the 2020 Annual Homeless Assessment Report (AHAR), despite minorities only making up 33.9% of the U.S. population, minorities account for 68% of the nations homeless population.[99] Crowded and shared enviornments such as these cause an increase in interaction amongst staff and residents, as well as correctional officers, and inmates which makes them exceptionally vulnerable to COVID-19.

Disparate COVID-19 mortality rates amongst minority groups reflect longstanding inequalities in the United States. Deeper awareness of these inequalities and the role of healthcare access, socioeconomic status, and cultural diversity ; demonstrates the importance of revitalizing inequitable paradigms in response to COVID-19. These three interrelated elements help us understand how COVID-19 infection and removal rates differ by state.

CHAPTER 4

METHODS

4.1 SIR Model

The SIR model is a compartmental model commonly used in epidemiology to model infectious diseases. It is a system of three coupled ODEs that was used to model COVID-19 to gain a better understanding of how it spreads. SIR, along with its variants, have been used to model the spread of COVID-19 in numerous publications. For example, it was adapted to simulate the effect of wearing masks,[100] to understand how vaccination rates affect spread of the disease,[101] and quarantine and testing were incorporated into the SIR model.[102] The SIR model, however, is based on many assumptions that limit its ability to model observed data. We observe and explore this in this chapter.

4.1.1 Construction of SIR Model

The SIR model divides the population into three groups, called "S","I", "R".

- Group "S" consists of individuals in the U.S. who are susceptible to COVID-19.
- Group "I" consists of individuals that have been exposed and capable of infecting others with COVID-19.

– Group "R" consists of removed individuals from the susceptible population whom either have recovered from COVID-19 or died. Additionally, some individuals may reenter the susceptible population due to the risk of reinfection of COVID-19 by different variants, but this is not represented in the SIR model.

Figure 4.1: SIR Model Population Flow

Using Figure 4.1, assume that individuals move from S to I at the infection rate β and from I to R at the removed rate γ. With this in mind the SIR system is modeled as:

$$\begin{aligned}\frac{dS}{dt} &= -\beta SI \\ \frac{dI}{dt} &= \beta SI - \gamma I \\ \frac{dR}{dt} &= -\gamma I\end{aligned}$$

Thus the critical parameters in the model are β and γ. Their ratio $R_0 = \frac{\beta}{\gamma}$ is the reproduction number that reflects the expected number of cases produced by a single infection. In this thesis we focus on β and γ. For example, since β reflects the rate of spread per infected person per day, we investigate if minority groups' who are

constantly exposed to COVID-19 due to continuously working when sick or living in a household with multiple people, result in a higher rate of secondary COVID-19 cases and hence higher R_0 reproduction numbers.

4.1.2 Initial Value Problem

One of the limiting factors of the SIR model is that it is based on a closed population of N individuals. We denote the fraction of individuals that are susceptible, infected, and removed as $s = \frac{S}{N}$, $i = \frac{I}{N}$, and $r = \frac{R}{N}$. The equivalent ODEs to be solved for $s(t)$, $i(t)$, and $r(t)$ becomes:

$$\begin{aligned}\frac{ds}{dt} &= -\beta si \\ \frac{di}{dt} &= \beta si - \gamma i \\ \frac{dr}{dt} &= -\gamma i\end{aligned}$$

For example if,

$$s(0) = 0.95, i(0) = 0.03, r(0) = 0.02, \tag{4.1}$$

these initial conditions support the scenario that 3% of the population is infected with COVID-19, 2% have been removed, and 95% are still at risk of contracting COVID-19. We used Python's scipy.integrate module equipped with *solve_ivp* function to solve the IVPs. This function uses an explicit runge-kutta method by default, and takes as input a function F satisfying (4.2) given an initial value (4.3):

$$\frac{dy}{dt} = F(t, y) \tag{4.2}$$

$$y(t_0) = y_0, \tag{4.3}$$

where, $y = \begin{bmatrix} s \\ i \\ r \end{bmatrix}$ and $F(t,y) = \mathrm{F(y)} = \begin{bmatrix} -\beta si \\ \beta si - \gamma i \\ \gamma i \end{bmatrix}$. The variable F is coded as function of the β and γ parameters and was used with curve fitting to fit COVID-19 data.

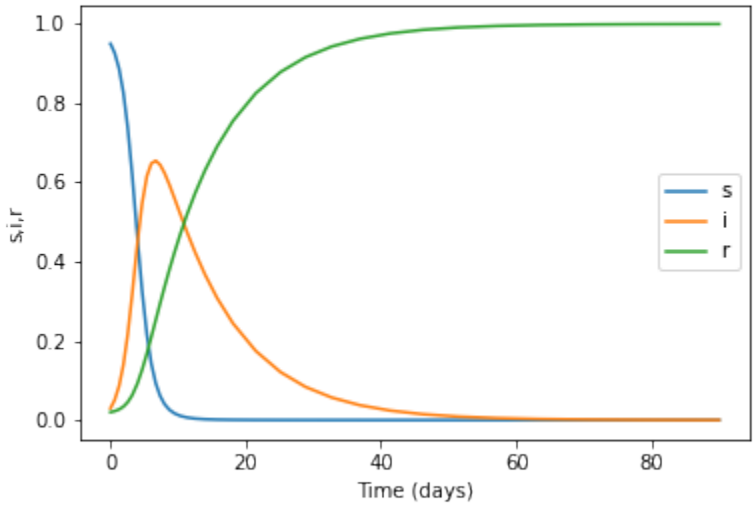

Figure 4.2: SIR Model

For given values of β and γ we can use them to predict the number of infections and deaths that occur in the future. Figure 4.2 shows all three curves with $\beta = 1$ and $\gamma = 0.1$ and the initial conditions in (4.1). We see that the entire susceptible population moved to infected and then were removed with a peak number of infections around 10 days. The bell-shaped I curve, just like in many other disease modelings, is the curve we want to flatten.

4.2 Curve Fitting

The goal of this thesis is to estimate parameters β and γ to better understand the relationship between COVID-19 infection rates and healthcare access, socioeconomic status, and cultural diversity. We will use curve fitting and data to estimate the SIR parameters and construct a curve that is best fit to our data set. Curve fitting with systems of ODEs can be challenging. We begin by describing how to fit a set of data consisting of album sales as a function of years to a one dimensional function.

Consider the data in Figure 4.3 and observe that a simple line fit to this data would not be suitable.

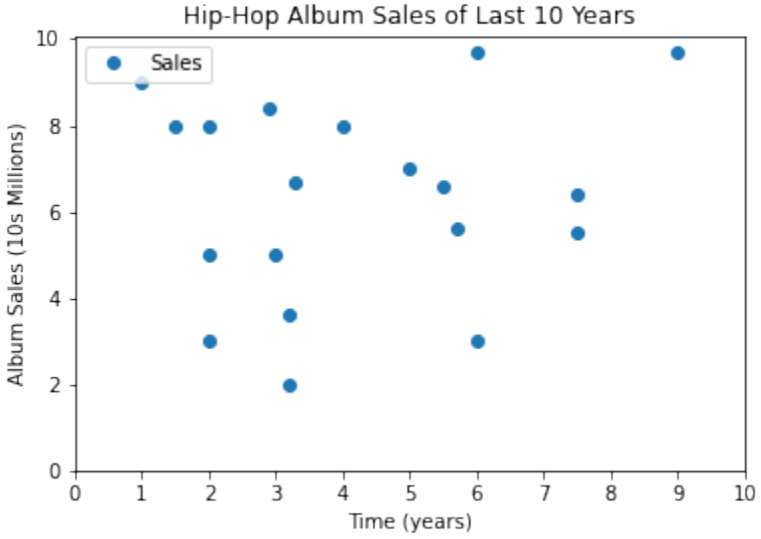

Figure 4.3: Hip-Hop Album Sales

We can however perform a polynomial curve fit for a polynomial order j:

$$s(t) = a_0 + a_1 t + a_2 t^2 + a_3 t^3 + ... + a_j t^j = a_0 + \sum_{k=1}^{j} a_k t^k \tag{4.4}$$

Values for a_k that give the minimal amount of error between the data set and the fit $f(x)$ is the best fit curve. Most methods minimize the square of the error and use

the least squares approach. The general expression for the least squares approach is

$$error = \sum_{i=1}^{n} (\epsilon_i)^2 = (y_1 - s(t_1))^2 + (y_2 - s(t_2))^2 + (y_3 - s(t_3))^2 + ... + (y_n - s(t_n))^2 \quad (4.5)$$

and we want to minimize this error. We substitute (4.4) into (4.5) and get

$$error = \sum_{i=1}^{n} (y_i - (a_0 + a_1 t_i + a_2 t_i^2 + a_3 t_i^3 + ... + a_j t_i^j))^2 \quad (4.6)$$

where i is the current data point being summed, j is the polynomial order, and n is the number of total data points. We can simplify equation (4.6) to

$$error = \sum_{i=1}^{n} (y_i - (a_0 + \sum_{k=1}^{j} a_k t_i^k))^2. \quad (4.7)$$

To find the best fit we must minimize the error (4.7) with respect to a_k. This requires taking the derivative with respect to each coefficient a_0, a_k, $k = 1$,..., j and setting each of them equal to zero.

$$\frac{\partial error}{\partial a_0} = -2 \sum_{i=1}^{n} (y_i - (a_0 + \sum_{k=1}^{j} a_k t_i^k)) = 0 \quad (4.8)$$

$$\frac{\partial error}{\partial a_1} = -2 \sum_{i=1}^{n} (y_i - (a_0 + \sum_{k=1}^{j} a_k t_i^k)) t_i = 0 \quad (4.9)$$

$$\frac{\partial error}{\partial a_2} = -2 \sum_{i=1}^{n} (y_i - (a_0 + \sum_{k=1}^{j} a_k t_i^k)) t_i^2 = 0 \quad (4.10)$$

$$\vdots$$

$$\frac{\partial error}{\partial a_j} = -2\sum_{i=1}^{n}(y_i - (a_0 + \sum_{k=1}^{j} a_k t_i^k))t_i^j = 0 \tag{4.11}$$

We can then rewrite these $j+1$ equations, and place into matrix form $Ax = B$:

$$\begin{bmatrix} n & \sum t_i & \sum t_i^2 & \cdots & \sum t_i^j \\ \sum t_i & \sum t_i^2 & \sum t_i^3 & \cdots & \sum t_i^{j+1} \\ \sum t_i^2 & \sum t_i^3 & \sum t_i^4 & \cdots & \sum t_i^{j+2} \\ \vdots & \vdots & \vdots & & \vdots \\ \sum t_i^j & \sum t_i^{j+1} & \sum t_i^{j+2} & \cdots & \sum t_i^{j+j} \end{bmatrix} \begin{bmatrix} a_0 \\ a_1 \\ a_2 \\ \vdots \\ a_j \end{bmatrix} = \begin{bmatrix} \sum y_i \\ \sum t_i y_i \\ \sum t_i^2 y_i \\ \vdots \\ \sum t_i^j y_i \end{bmatrix}$$

If A is not ill-conditioned or rank deficient, we can solve for the coefficients a_k by $x = A^{-1}B$. For example, consider the following data in Figure 4.4,

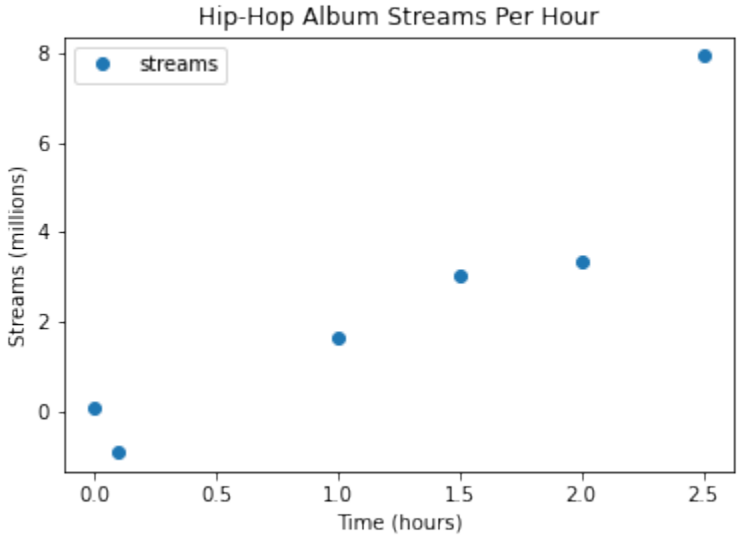

Figure 4.4: Hip-Hop Album Streams

Time (hours) and Streams (millions) represent x and y given by [0, 0.10, 1, 1.5, 2,

2.5] and [0.0674, -0.9156, 1.6253, 3.0377, 3.3535, 7.9409] respectively. Least squares with $j = 2$ applied to this problem results in

$$\begin{bmatrix} a_0 \\ a_1 \\ a_2 \end{bmatrix} = \begin{bmatrix} 6 & 7.5 & 13.75 \\ 7.5 & 13.75 & 28.125 \\ 13.75 & 28.125 & 61.1875 \end{bmatrix}^{-1} \begin{bmatrix} 15.1093 \\ 32.2834 \\ 71.276 \end{bmatrix} = \begin{bmatrix} -0.1812 \\ -0.3221 \\ 1.3537 \end{bmatrix}$$

so our fitted curve is $f(x) = 1.3537x^2 - 0.3221x - 0.1812$ as shown in Figure 4.5.

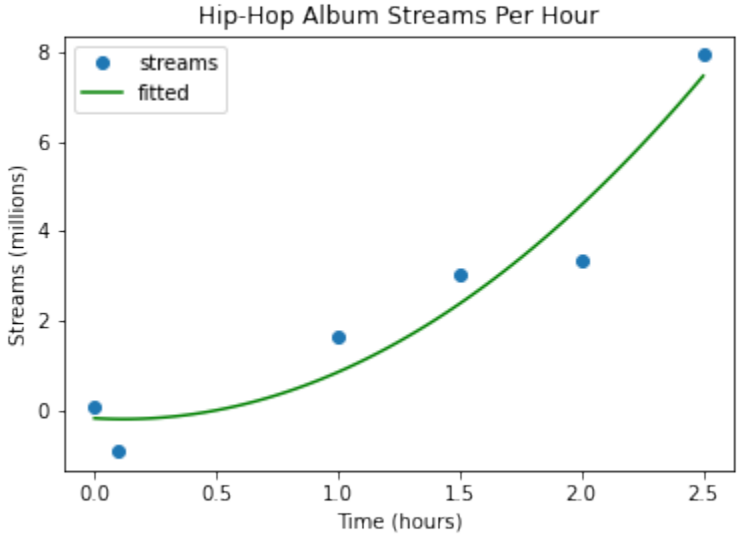

Figure 4.5: Hip-Hop Album Streams with Fitted Curve

The SIR model was fit to data in a similar manner. In this case f is multidimensional, i.e $f = \begin{bmatrix} s(t) \\ i(t) \\ r(t) \end{bmatrix}$ and is output from the solve.ivp function in Python. As noted previously, the ODE is written as a function of β and γ and the function curvefit in Python was used to find optimal β and γ using nonlinear least squares. The optimization problem is solved using the Levenberg–Marquardt algorithm by default in curvefit.

4.3 State Rankings

America's Health Rankings is a unique rankings platform designed to highlight issues regarding public health and garner a clearer understanding of the health of various populations. Their annual reports rank the healthiness of each state's population based on 16 measures of health grouped into four categories including socioeconomic factors and clinical care. The rankings are derived from 74 measures from over 20 data sources which include the U.S. Census Bureau, U.S. Department of Education, and U.S. Department of Health and Human Services.[103] The healthcare access rankings for each state are given in Table 4.1 and bounded between -1.3 and 1.5, with values closer to -1.3 indicating poor healthcare access and those closer to 1.5 indicate greater access to healthcare. The socioeconomic status rankings for each state are given in Table 4.2 and bounded between -1.1 and 1, where a value close to 1 indicates that the state has a high SES and a value of -1.1 indicates indigency. Using state composite scores categorically, we will plot COVID-19 infection rates as a function of healthcare access and SES.

Tracking the cultural diversity of states is crucial to understanding the shifting demographics of race and ethnicity to COVID-19 infection rates. The Census Bureau uses a diversity index (DI) to measure the probability of two people, selected randomly from a given area, belong to different race and ethnic groups.[104] The DI for each state are given in Table 4.3 and are bounded between 0 and 1, where a value close to 1 indicates everyone in that population is from a different racial and ethnic group and a value of 0 indicates indistinguishably. We will also use the DI to plot COVID-19 infection rates as a function of cultural diversity.

STATE	Healthcare Access	STATE	Healthcare Access	STATE	Healthcare Access
Texas	-1.293	West Virginia	-0.260	Delaware	0.427
Mississippi	-1.100	Montana	-0.122	Michigan	0.520
Nevada	-0.854	Kentucky	-0.121	Washington	0.544
Georgia	-0.837	New Mexico	-0.086	Nebraska	0.560
Oklahoma	-0.715	Ohio	-0.086	Minnesota	0.608
Wyoming	-0.672	Kansas	-0.082	Wisconsin	0.647
Tennessee	-0.655	North Carolina	-0.076	Maryland	0.702
Alabama	-0.612	New Jersey	-0.062	Iowa	0.746
Arkansas	-0.583	Utah	0.012	Pennsylvania	0.765
Florida	-0.555	Illinois	0.015	Maine	0.769
Louisiana	-0.551	California	0.103	New Hampshire	0.962
Arizona	-0.531	Oregon	0.160	Connecticut	1.025
Indiana	-0.462	South Dakota	0.186	Hawaii	1.078
Idaho	-0.455	Virginia	0.278	Vermont	1.140
South Carolina	-0.371	New York	0.317	Rhode Island	1.225
Missouri	-0.348	North Dakota	0.385	Massachusetts	1.443
Alaska	-0.339	Colorado	0.388	D.C.	-

Source: America's Health Rankings analysis of America's Health Rankings 2020 Annual Report

Table 4.1: 2020 State Indices for Healthcare Access

STATE	SES	STATE	SES	STATE	SES
Louisiana	-1.036	Texas	-0.121	Delaware	0.322
New Mexico	-0.989	Indiana	-0.119	Connecticut	0.361
Arkansas	-0.792	Nevada	-0.08	Wisconsin	0.393
Mississippi	-0.674	Georgia	-0.054	Colorado	0.397
West Virginia	-0.463	Florida	-0.03	Maine	0.451
Oklahoma	-0.446	California	0.003	Hawaii	0.486
Michigan	-0.347	Pennsylvania	0.003	North Dakota	0.493
Alabama	-0.3	Missouri	0.013	Vermont	0.495
Ohio	-0.261	Montana	0.016	Virginia	0.539
South Carolina	-0.228	Illinois	0.043	Massachusetts	0.542
Tennessee	-0.217	Idaho	0.160	Minnesota	0.546
South Dakota	-0.215	North Carolina	0.167	Iowa	0.551
Wyoming	-0.214	Kansas	0.168	Washington	0.629
New York	-0.213	Oregon	0.206	New Jersey	0.670
Alaska	-0.171	Maryland	0.265	Utah	0.737
Arizona	-0.163	Rhode Island	0.265	New Hampshire	0.965
Kentucky	-0.151	Nebraska	0.300	D.C.	-

Source: America's Health Rankings analysis of America's Health Rankings 2020 Annual Report

Table 4.2: 2020 State Indices for Socioeconomic Status

STATE	Diversity Index	STATE	Diversity Index	STATE	Diversity Index
Maine	0.185	Indiana	0.413	Oklahoma	0.595
Vermont	0.202	Pennsylvania	0.440	Delaware	0.596
West Virginia	0.202	Michigan	0.452	Illinois	0.603
New Hampshire	0.238	Kansas	0.454	Virginia	0.605
Montana	0.301	Oregon	0.461	Arizona	0.615
Iowa	0.308	Tennessee	0.466	Alaska	0.628
Wyoming	0.324	Rhode Island	0.494	New Mexico	0.630
North Dakota	0.326	Arkansas	0.498	Florida	0.641
Kentucky	0.328	Massachusetts	0.516	Georgia	0.641
South Dakota	0.356	Colorado	0.523	New Jersey	0.658
Idaho	0.359	Alabama	0.531	New York	0.658
Wisconsin	0.370	South Carolina	0.546	Texas	0.670
Ohio	0.404	Connecticut	0.557	D.C.	0.672
Minnesota	0.405	Mississippi	0.559	Maryland	0.673
Utah	0.407	Washington	0.559	Nevada	0.688
Missouri	0.408	North Carolina	0.579	California	0.697
Nebraska	0.408	Louisiana	0.586	Hawaii	0.760

Source: 2010 Census Redistricting Data (Public Law 94-171) Summary File; 2020 Census Redistricting Data (Public Law 94-171) Summary File

Table 4.3: 2020 Diversity Index by State

4.4 COVID-19 Case Selection

We used COVID-19 datasets from John Hopkins University's COVID-19 Data Repository by the Center for Systems Science and Engineering (CSSE)[105] in the form of time series spanning 90 days. The time series are composed of columns that represent the population, total cases, and total deaths. This data was used to update SIR model parameters to understand the effects and monitor the infection rates of COVID-19 in the U.S.. By obtaining estimates for the number of deaths, susceptible, and infected populations we are able to model the infection rates against the variables of interest and assess the effectiveness of modeling COVID-19.

All COVID-19 cases reported in the U.S. from July 3, 2021 to October 1, 2021 are being used for comparison with the following exclusions:

- Cases that reside in unincorporated U.S. territories. Although these cases represent a large number of the overall cases and deaths, their exclusion assures appropriate comparisons since these locations are not included in the DI and health rankings systems.
- Cases reported without an assigned location are excluded because location is required in order to assign cases to a state or district.
- Cruise ship case data except those that have been re-categorized by a reporting state.

CHAPTER 5

RESULTS

In appendix A, you will find curve fits of all S, I, and R plots against their reported data of each state modeled separately. We modeled the time period July 4, 2021 through October 1, 2021 and in each graph time in days represents the number of days from the beginning of the time period. Data for I in these models are the reported number of infections from the John Hopkins data set, the R are the reported number of deaths, and the S is calculated from those: $S = N - I - R$. N is not necessarily the total population in the state, rather we found a value for it that results in a best fit of SIR curves to data, while optimizing values for β and γ.

N is a representation of the population in a state that falls into the categories of S, I, or R. The manual adjustment of N is necessary due to the simplicity of the SIR Model to model a closed population. This allowed for majority of S and I curves to be fitted with the data. However with some of the I curves, we are only able to fit some states until a certain point because we can't get Infections (I) to decrease as the data does. We are also unable to produce good fits at this time for majority of R curves because the SIR Model is too simple and it does not include information about vaccines, and quarantine, which would also remove people. Since we cannot reliably fit R, we only interpret the data to make conclusions about β, γ, and R_0 with respect to cultural diversity, healthcare access, and socioeconomic status with data

sets we can fit.

A table with values of N for each state are given in the Appendix C. These values were used to normalize the COVID-19 data and SIR output for Susceptible, Infected, and Removed populations to make meaningful comparisons between states.

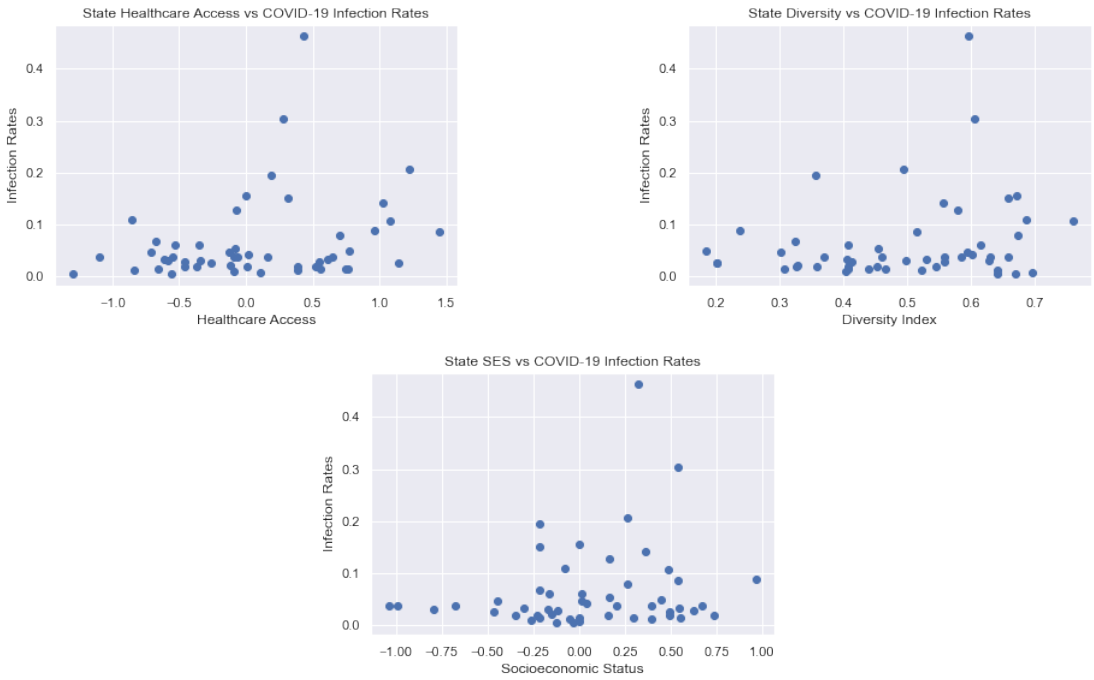

Figure 5.1: Social Health Determinants v COVID-19 Infection Rates

Over the course of our 90-day time period, in Figure 5.1 we see that there appears to be little to no relationship between the number of COVID-19 infection rates and the cultural diversity index in Table 4.3. This result is consistent across all social determinants of health examined. Figure 5.1 also shows the relationship between COVID-19 infection rates and healthcare access, and socioeconomic status indices in Tables 4.1 and 4.2.

Our curve fitting model is capable of producing an S,I,R Model for each state individually, and calculates corresponding β, γ, and R_0 values. Figure 5.2 shows that

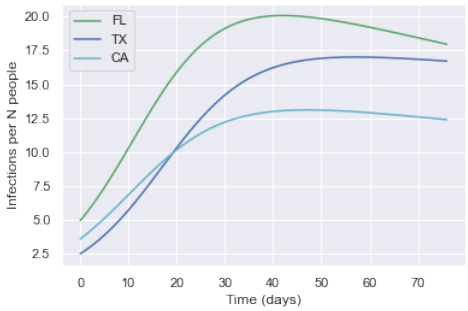

Figure 5.2: Fitted COVID-19 Infection Curves in FL, TX, and CA

states with similarly adjusted population values N, have similar behavior in COVID-19 infection rates over the span of 90 days. Florida, Texas, and California similarly rank the lowest in socioeconomic status and the highest in cultural diversity with values being $-0.03, -0.121, 0.003$ and $0.641, 0.670, 0.697$ respectively. Lastly, these states also rank amongst the lowest in healthcare access with values of -0.555, -1.293, and 0.103 respectively.

Let us comparatively examine the most and least culturally diverse states, Hawaii (0.760) and Maine (0.185). Figure 5.3 contains data that was used to fit SIR Models for Hawaii and Maine.

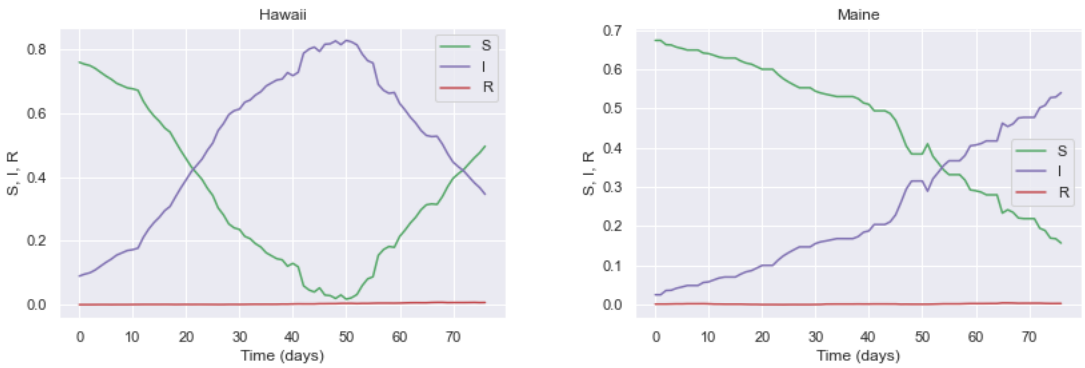

Figure 5.3: Hawaii and Maine SIR Data Adjusted For Population

Hawaii and Maine initially had similar populations susceptible to infection. Over

the 90 day span Maine has had a steady increase in COVID-19 infections with no indication of a decline. Hawaii however, initially had a steady increase in COVID-19 infections until reaching a peak around 50 days from July 4 and declining afterwards. Hawaii and Maine have a calculated β rate of 0.122 and 0.086, respectively. Hawaii's susceptible population reached a low point at the 50 day mark and inversely of its infected population, began to steadily increase. The amount of people susceptible to infection and infected were the same on two occasions, at 22 and 74 days which are July 26 and September 16. Maine only had one occurrence around the 53 day which was August 26.

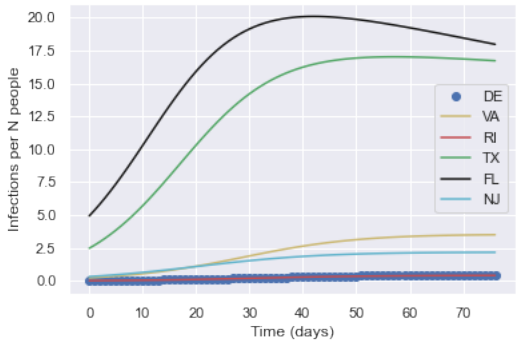

Figure 5.4: Fitted Infection Curves For Three Highest and Lowest Infected States

Similarly if we analyze the top three and bottom three states for number of COVID-19 infections adjusted for population (Figure 5.4); Delaware, Virginia, and Rhode Island rank amongst the top 30 in cultural diversity while Texas, Florida, and New Jersey rank amongst the top 10. We can see even more clearly a relationship between COVID-19 infection rates and culturally diversity. With the exception of NJ, states that are more culturally diverse experience higher COVID-19 infection rates than those that are not.

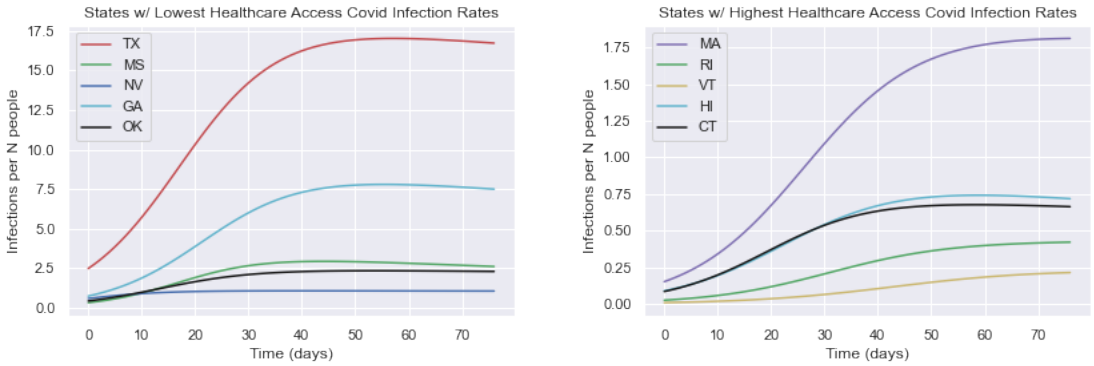

Figure 5.5: Fitted Infection Curves in States Grouped By Healthcare Access

Texas, Mississippi, Nevada, Georgia, and Oklahoma rank amongst the lowest states in healthcare access with indices ranging -1.293 to -0.715. Massachusetts, Rhode Island, Vermont, Hawaii, and Connecticut are amongst the highest ranked with values ranging 1.443 to 1.025. In Figure 5.5, both groups show a relationship between COVID-19 infections and healthcare access. We can see here that states with lower healthcare access are experiencing COVID-19 infections an order of magnitude larger than those with higher healthcare access during the modeled time period.

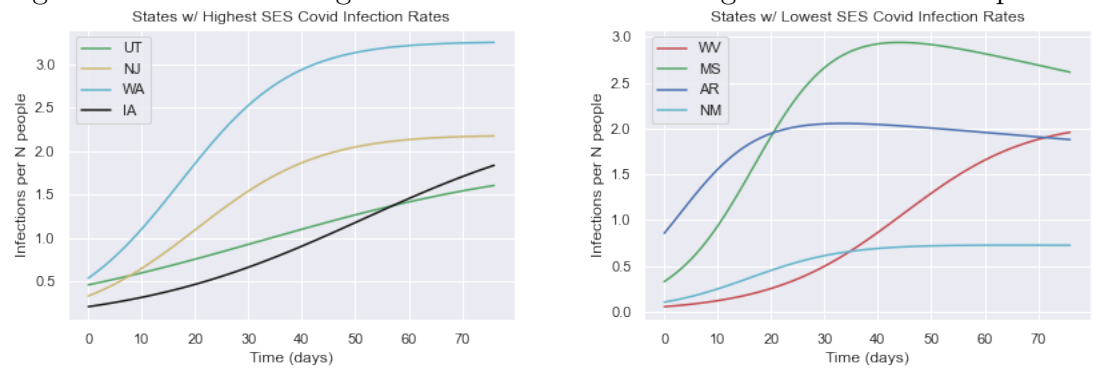

Figure 5.6: Fitted Infection Curves in States Grouped By Socioeconomic Status

Dissimilar to our previous comparisons, a relationship between COVID-19 infections is not clear when we compare our highest and lowest ranked states socioeconomic

statuses. Both groups have similar β values of 0.038 and 0.035, with similar numbers of infections as illustrated in Figure 5.6.

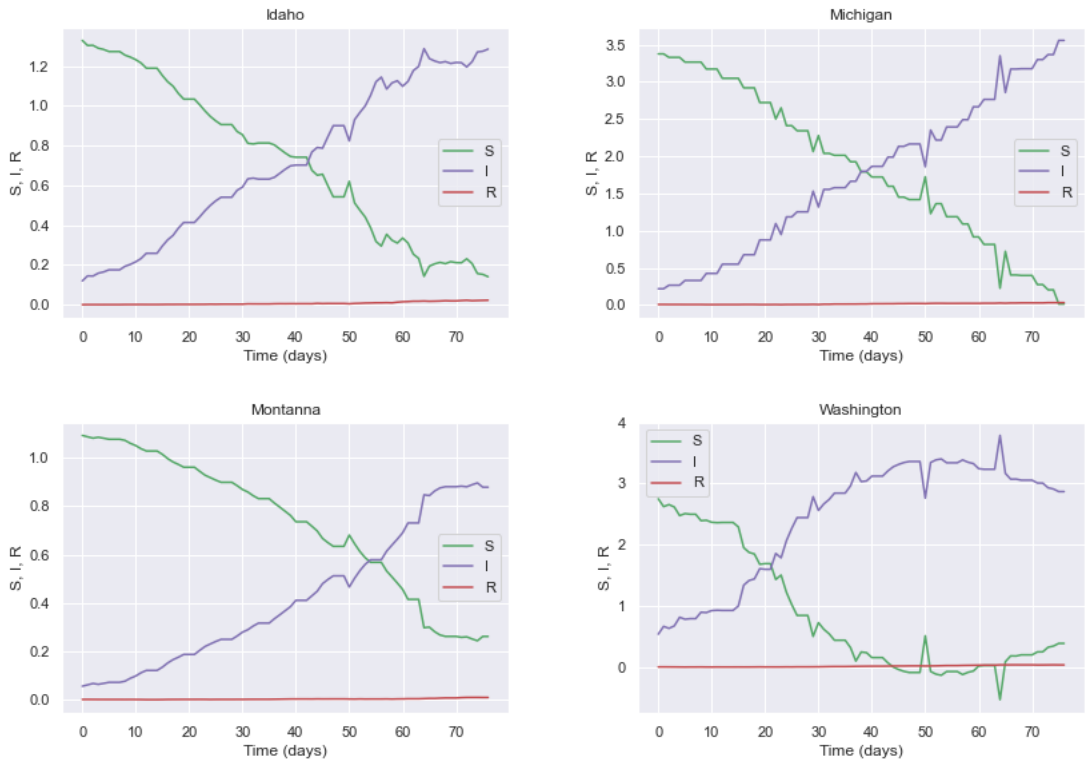

Figure 5.7: ID, MI, MT, WA SIR Data Adjusted For Population

Idaho, Michigan, Montana, and Washington have scattered rankings amongst one another in cultural diversity, healthcare access, and socioeconomic status. We were able to fit S,I,R curves for each of these states, as shown in Appendix A. The data used to fit SIR models for these states are in Figure 5.7, and their fitted SIR curves are in Figure 5.8. The initial population of these four states differed from one another moderately with Michigan and Washington having closely related populations and Montana and Idaho having closely related populations. Idaho and Michigan have the greatest difference in population, yet their S and I curves seem to follow the same behavior with the amount of individuals at risk of infection and those who are infected

occurring between the 35 to 45 day marks starting July 4, 2021. Idaho and Michigan have a calculated β rate of 0.018 and 0.019, respectively.

The Washington and Montana S and I curves almost mirror one another in overall shape similarity. Both states experience equilibrium between S and I around the 21 and 54 days respectively. After this point, I continues to surge and we begin to see a turning point in both curves for another inverse equilibrium. Washington and Montana have a calculated β rate of 0.029 and 0.047, respectively.

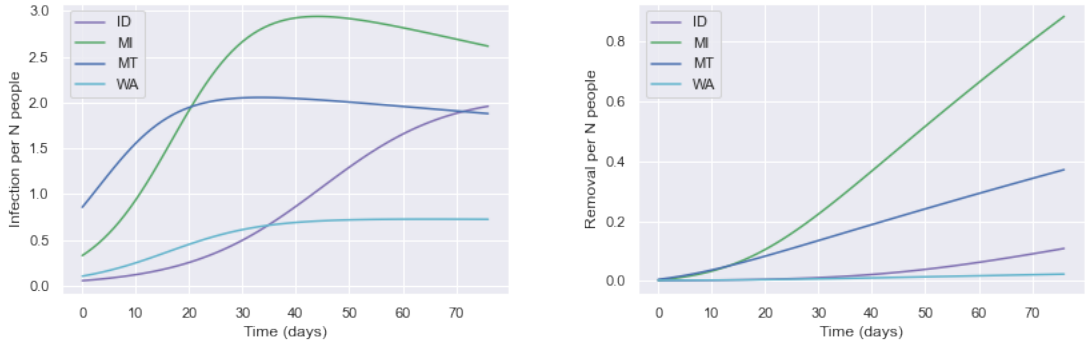

Figure 5.8: Fitted Infection and Removal Curves for ID, MI, MT, WA

The average cultural diversity value amongst these states is 0.418, and average β and γ values of 0.029 and 0.001, produce an $R_0 = 123.812$. Separately, Idaho, Michigan, Montana, and Washington each have an R_0 of 42.222, 82.476, 178.607, and 191.942 respectively. According to these $R_0 s$, Washington should have reported daily COVID-19 infections at a rate 4.55 times more than Idaho, 1.07 times more than Montana, and 2.33 times more than Michigan. This however does not occur although Washington is the most culturally diverse state of the four we are modeling here. Montana appears to have the the highest infection rate even though it is the least culturally diverse state. However, with an R_0 of 178.61, MT should have reported daily COVID-19 infections at a rate 2.17 times more than Michigan as well

as 4.23 times higher than Idaho. Here a relationship between COVID-19 infection and removal rates to cultural diversity is not clear.

The previously mentioned states rank amongst the top 40 states with best access to healthcare, with Idaho and Montana both placing below 30 and Michigan and Washington above 20. Uniformly, with an average healthcare access score of -0.014, a relationship between COVID-19 infection and removal rates to healthcare access is not clear. This sentiment does not transpire amongst socioeconomic status.

The socioeconomic status values of these particular states are Idaho (0.160), Michigan (-0.347), Montana (0.016), and Washington (0.629) with an average value of 0.115. Washington has the highest socioeconomic status value, second highest β, and the largest γ rates. Michigan has the lowest socioeconomic status value, and places third in overall β and γ rates. Here, a negative relationship between a high socioeconomic status and high β and γ rates is clear. Thus amongst these four states we are able to draw a conclusion that states with a higher socioeconomic status may have higher COVID-19 infection and removal rates than those with a lower socioeconomic status.

CHAPTER 6

CONCLUSION

In this thesis we analyzed the relationship between COVID-19 infection rates with the social determinants of health: healthcare access, cultural diversity, and socioeconomic status. Nationally, there appears to be no relationship between infection rates and either of our social determinants of health. We do however see mostly negative relationships amongst COVID-19 infections and healthcare access, cultural diversity, and socioeconomic status. Furthermore we seen a negative relationship between socioeconomic status and COVID-19 infection and removal rates. In order to further address why COVID-19 infections are occurring at higher rates in certain parts of the U.S. than others we will need to analyze the effectiveness of lockdown measures in each state, improve removal rates by incorporating vaccines, quarantine, and masks wearing, and further project benefits of quarantine. Improvements in these areas can assist transforming our system to be better equipped with COVID-19 prevention, testing accessibility, and treatment for minority communities.

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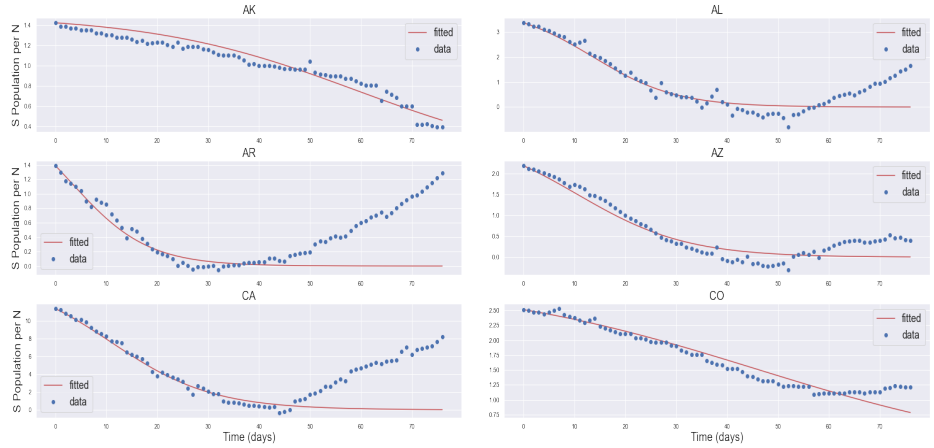
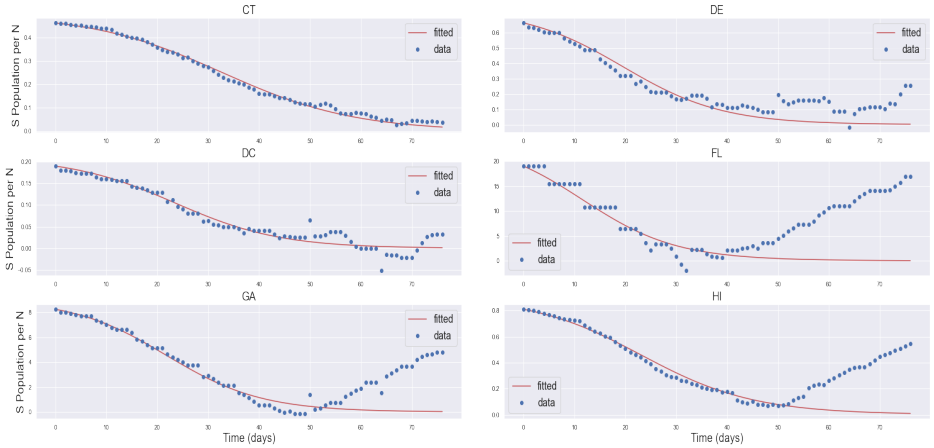
APPENDIX A

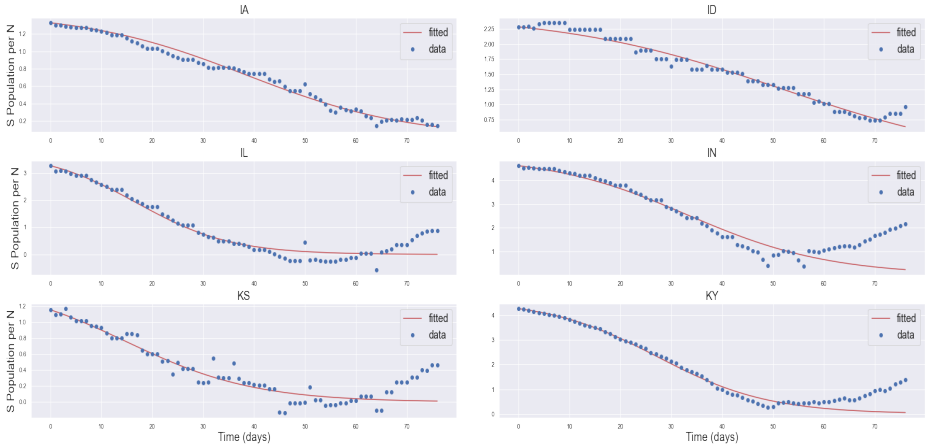
POPULATION GRAPHS BY STATE

Here we show curve fits of John Hopkins data to the SIR model for all 50 states and Washington D.C.. The curves for Susceptible, Infectious, and Removal are plotted separately.

A.0.1 Susceptible Population



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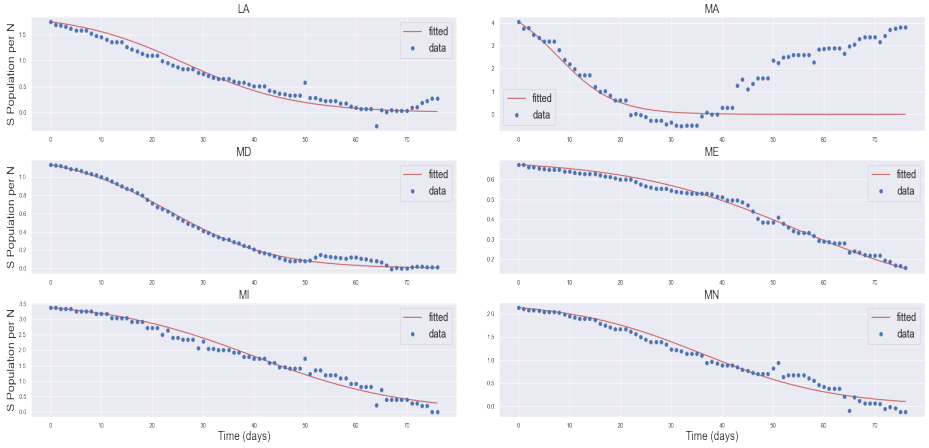
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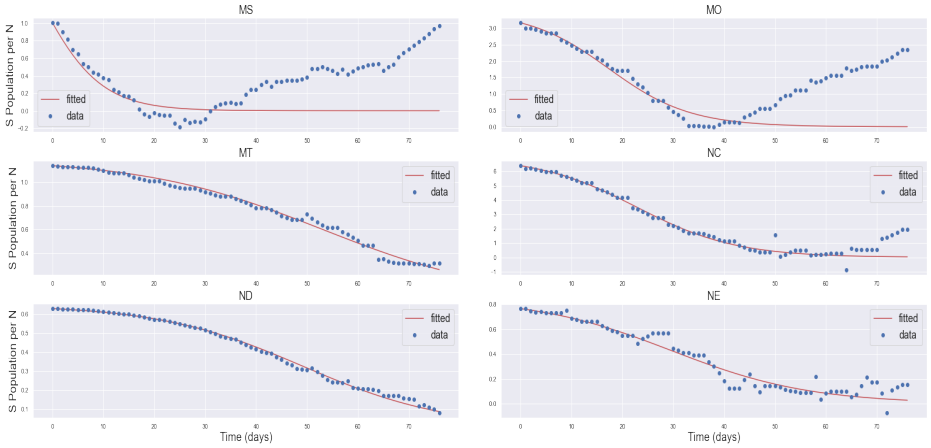
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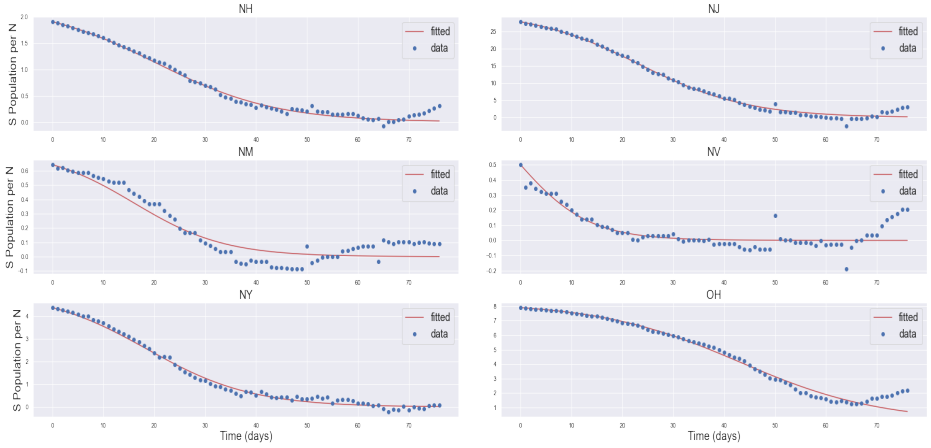
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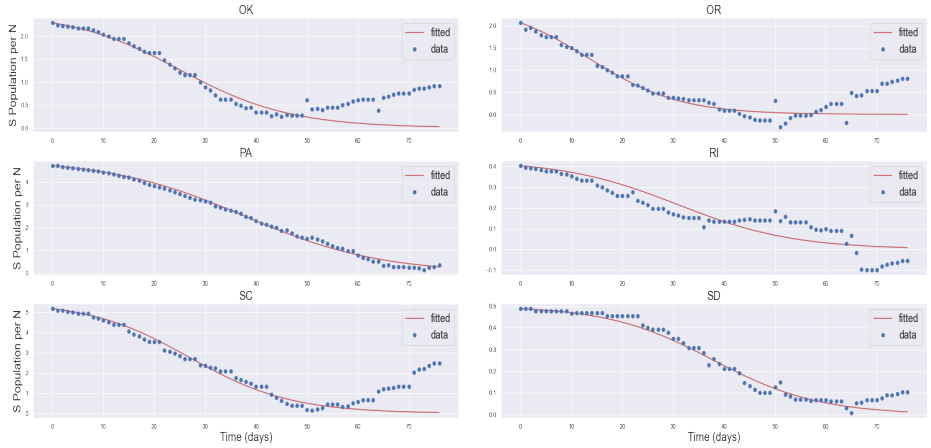
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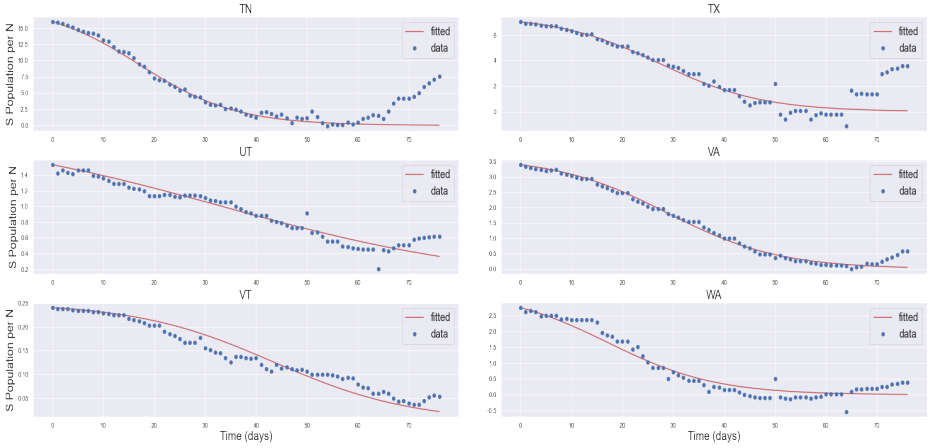
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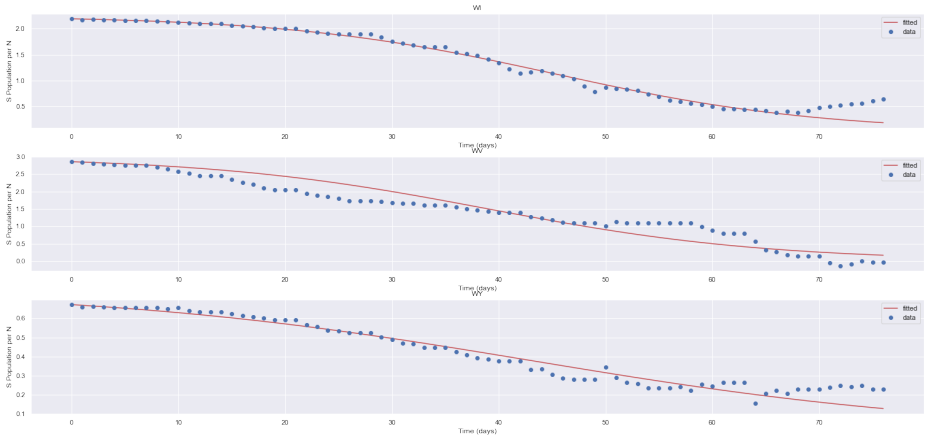
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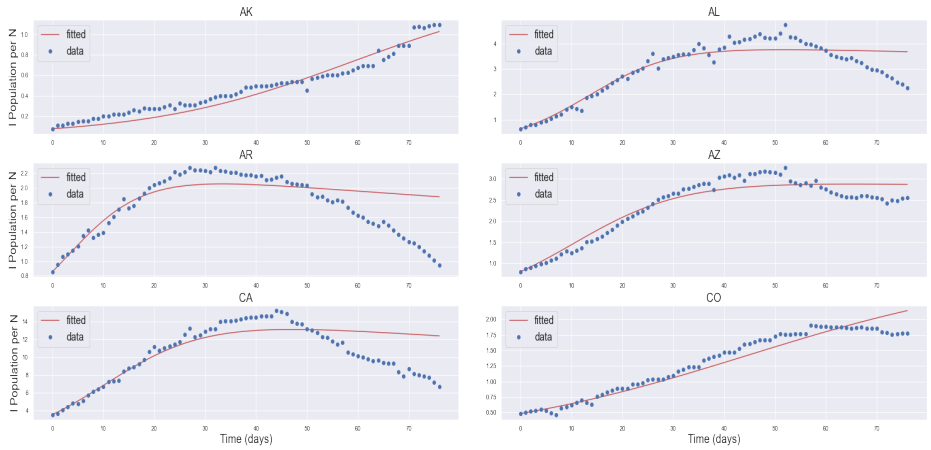
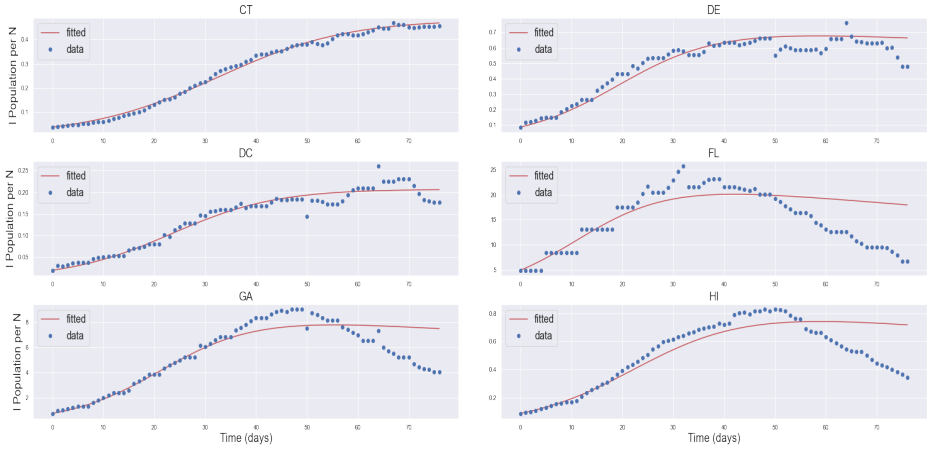
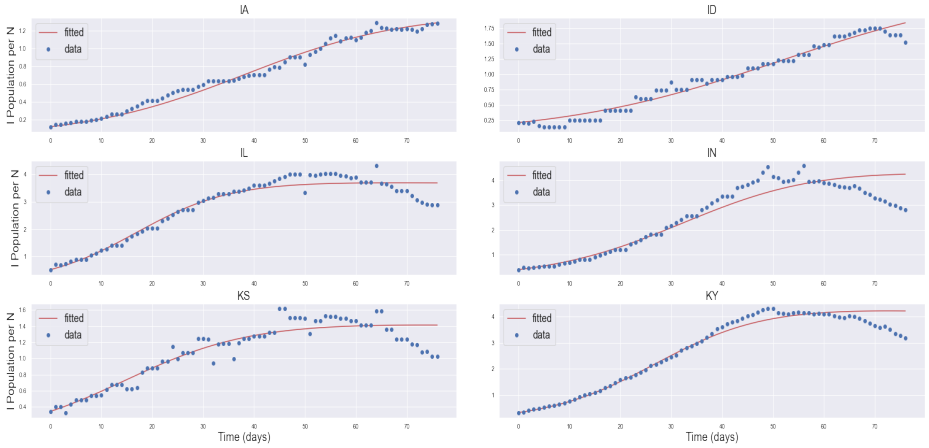
A.0.2 Infected Population



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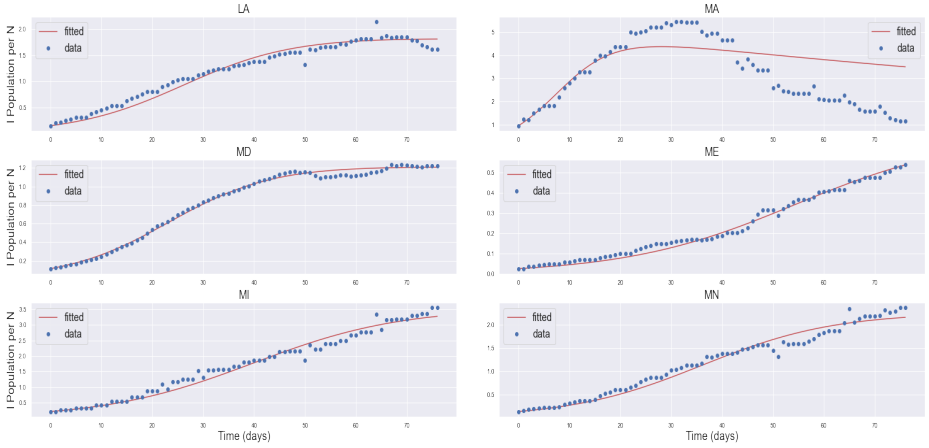
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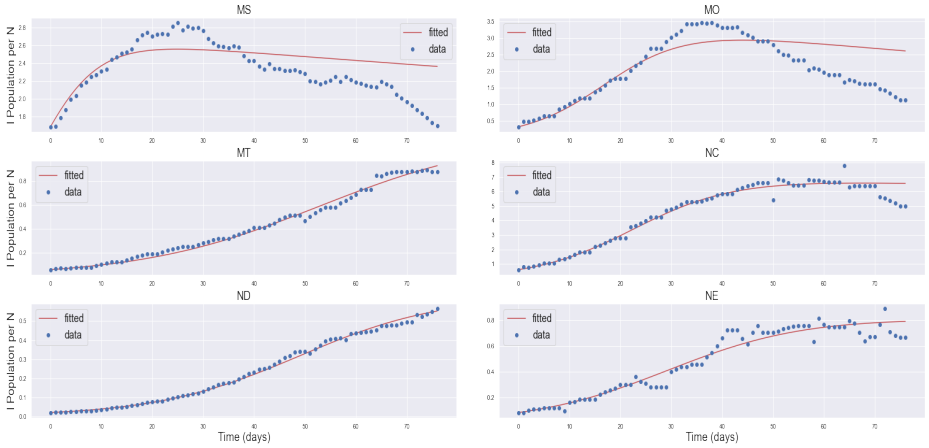
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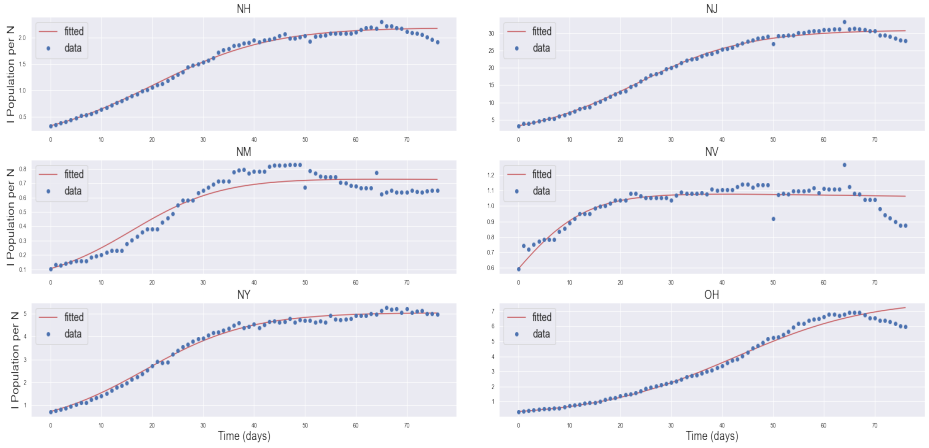
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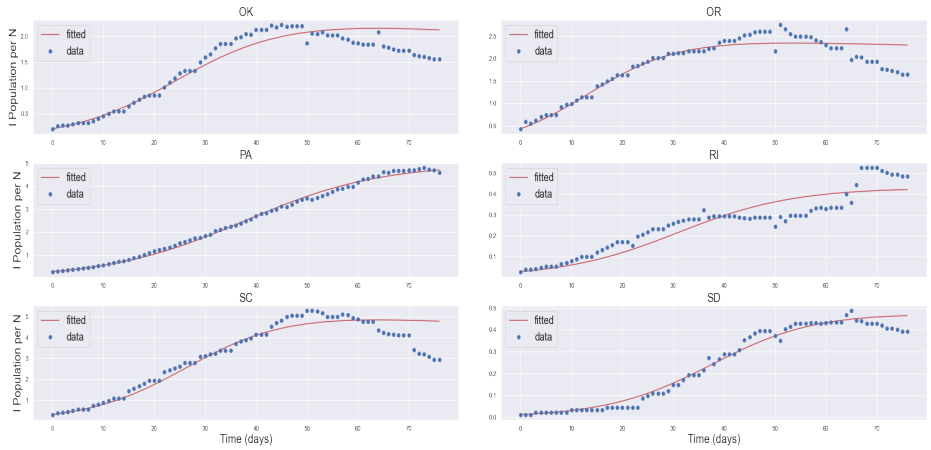
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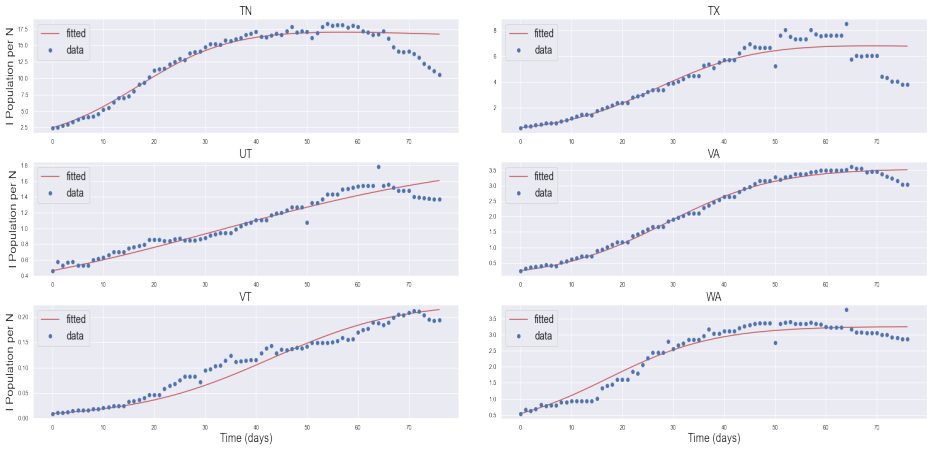
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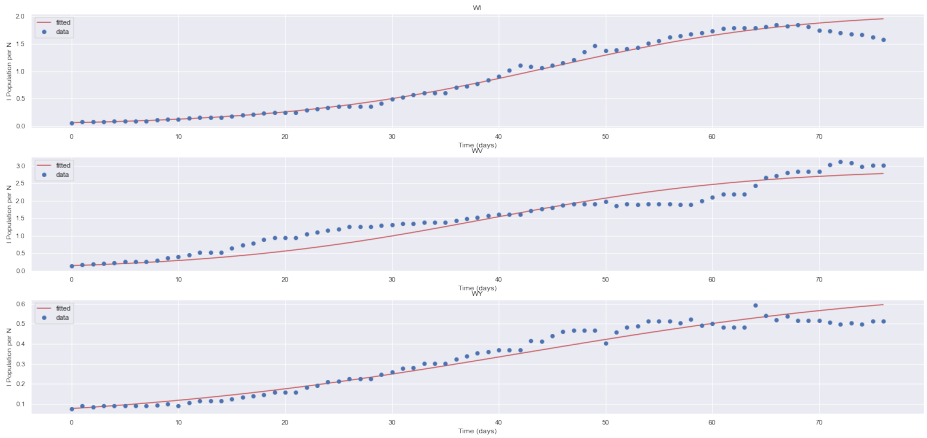
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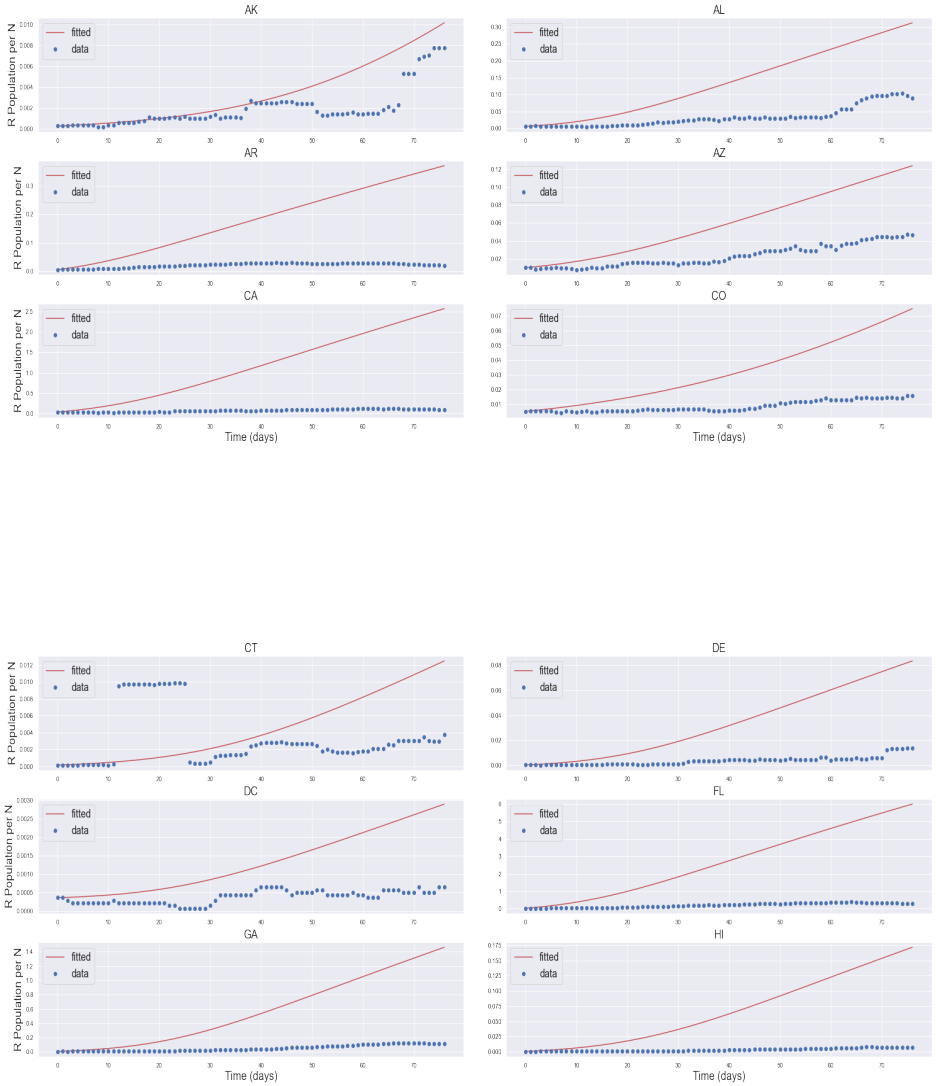
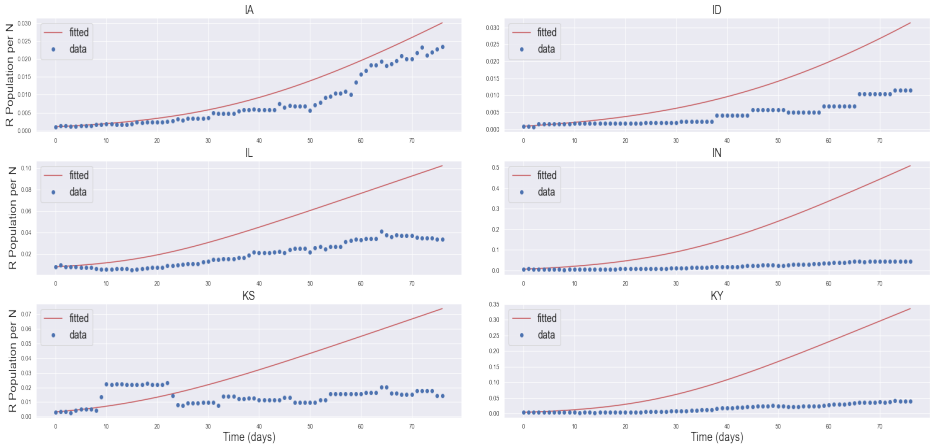
A.0.3 Removed Population

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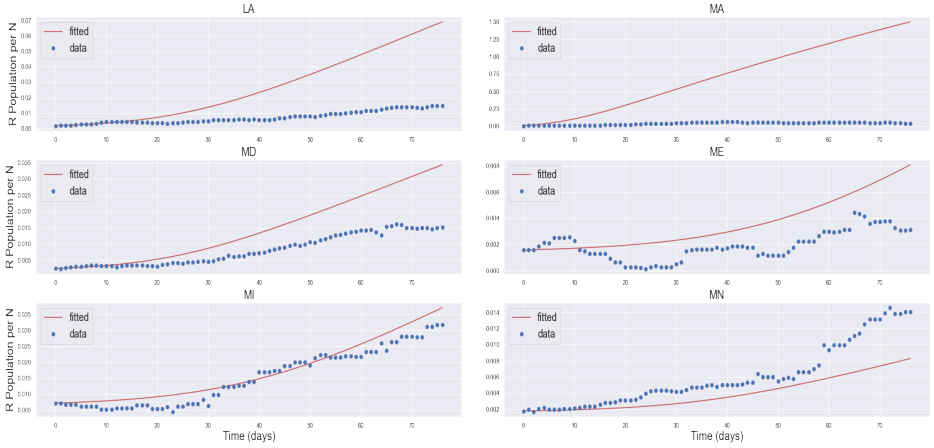
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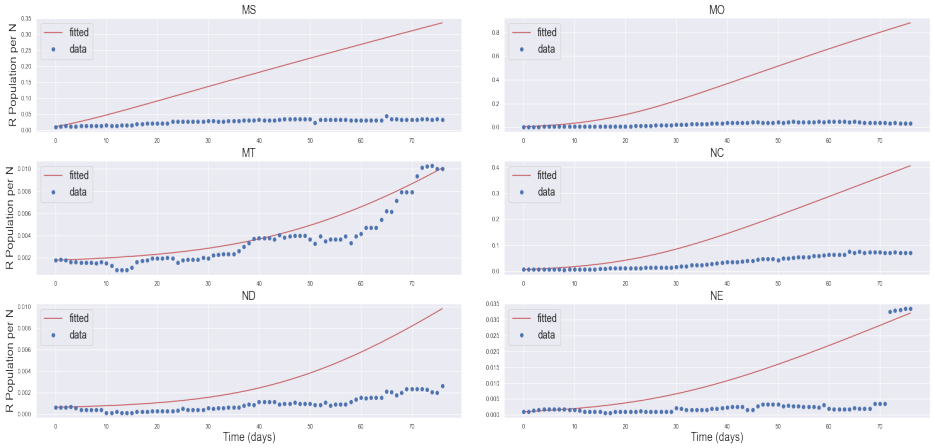
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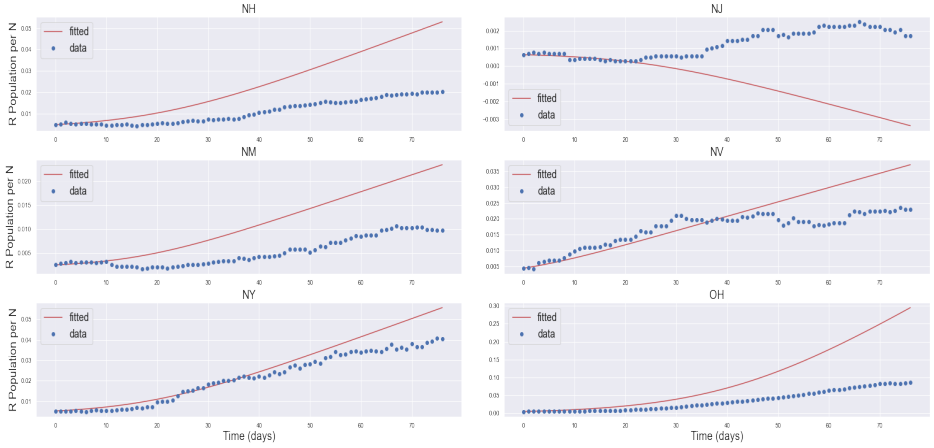
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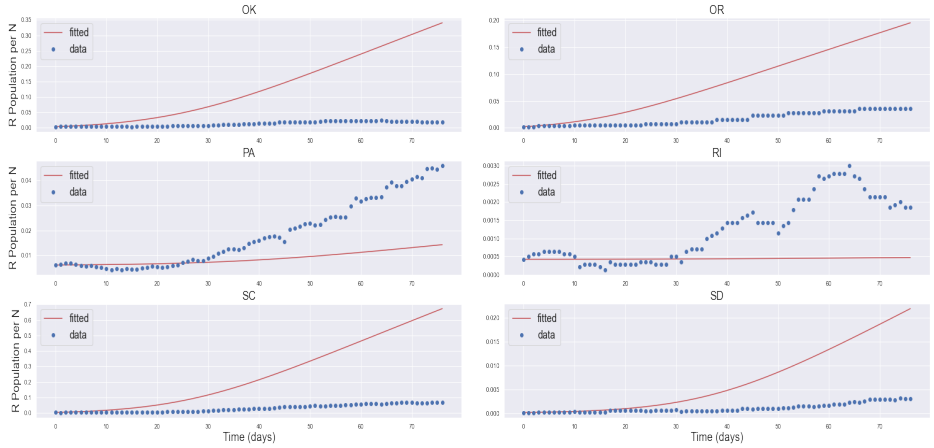
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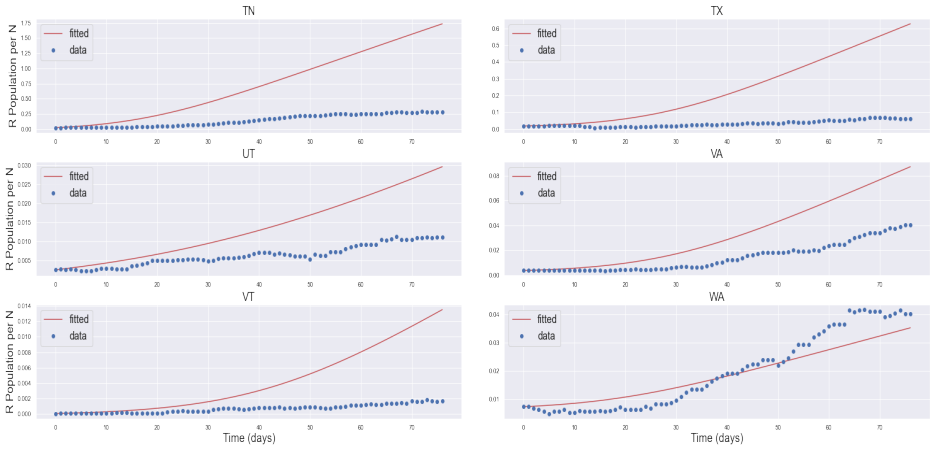
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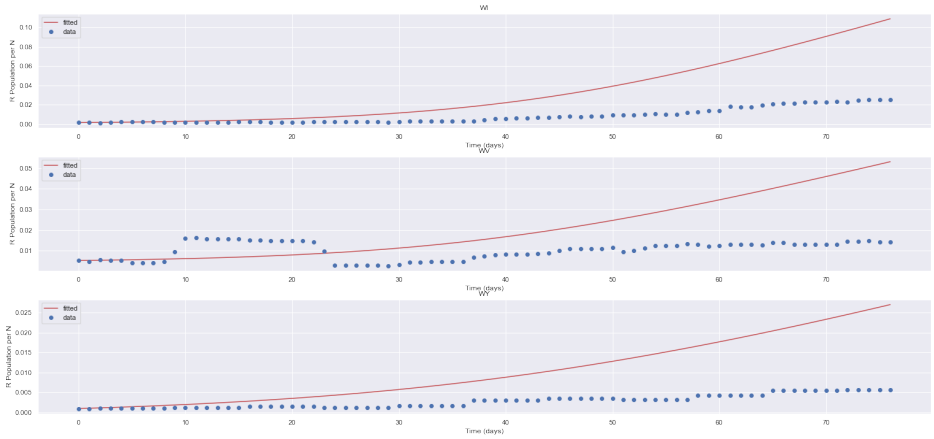
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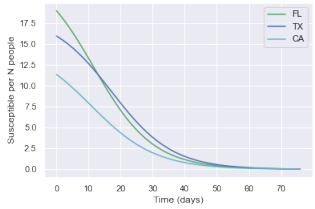
Time (days)

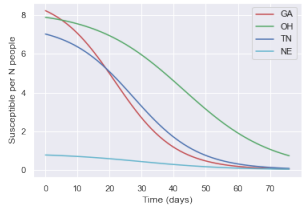
APPENDIX B

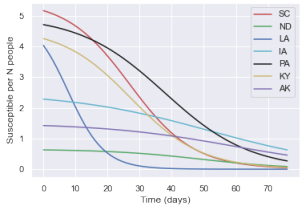
SIR POPULATION GRAPHS OVER TIME

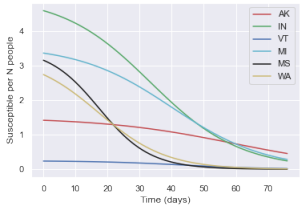
B.0.1

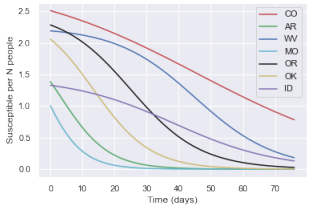
Here we give plots of number of people susceptible to infection overtime, using the SIR model fitted to John Hopkins data. The plots are grouped according to similar populations across states.

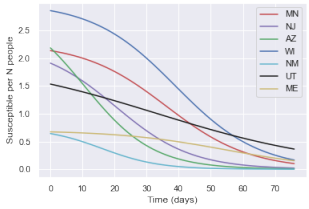


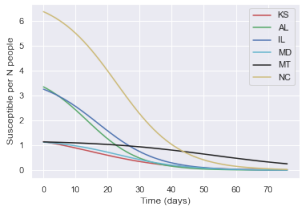


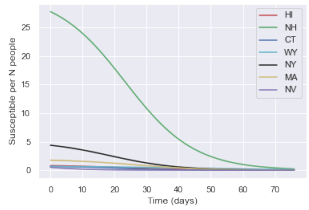


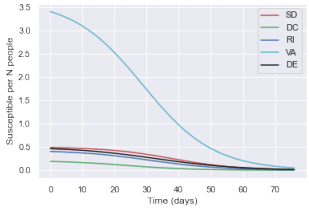






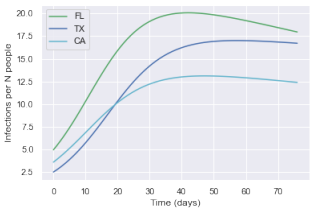


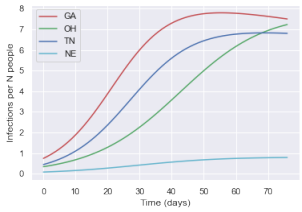


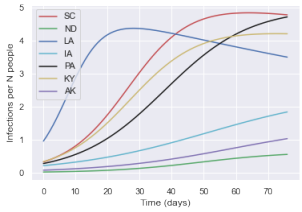


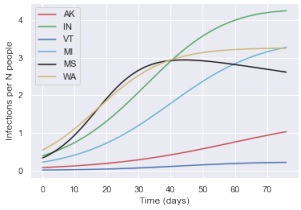
B.0.2

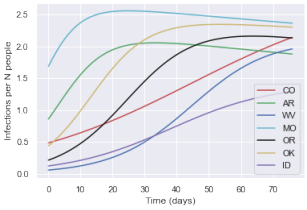
Here we give plots of number of infections overtime, using the SIR model fitted to John Hopkins data. The plots are grouped according to similar populations across states.

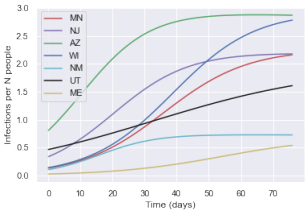


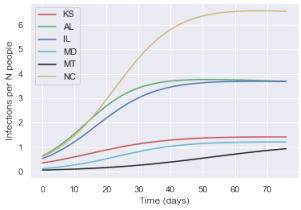


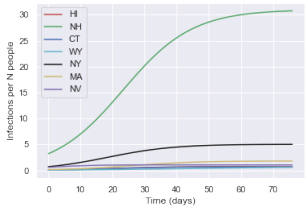


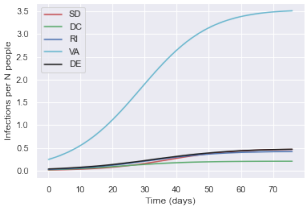












APPENDIX C

STATE N VALUES

Here we give values for N that were used to normalize COVID-19 data and SIR Curves for each state.

STATE	N	STATE	N	STATE	N
Delaware	0.21 x 1e+3	Kansas	1.5 x 1e+3	Michigan	3.6 x 1e+3
Virginia	0.25 x 1e+3	Maine	1.9 x 1e+3	Vermont	3.65 x 1e+3
Rhode Island	0.43 x 1e+3	Utah	2 x 1e+3	Indiana	3.8 x 1e+3
South Dakota	0.5 x 1e+3	Arizona	2.25 x 1e+3	Alaska	4 x 1e+3
D.C.	0.5 x 1e+3	New Mexico	2.25 x 1e+3	Kentucky	4.6 x 1e+3
Nevada	0.65 x 1e+3	New Jersey	2.25 x 1e+3	Louisiana	5 x 1e+3
Massachusetts	0.7 x 1e+3	Wisconsin	2.25 x 1e+3	Iowa	5 x 1e+3
Wyoming	0.75 x 1e+3	Minnesota	2.27 x 1e+3	Pennsylvania	5 x 1e+3
New York	0.75 x 1e+3	Oklahoma	2.5 x 1e+3	North Dakota	5.1 x 1e+3
Connecticut	0.75 x 1e+3	Idaho	2.5 x 1e+3	South Carolina	5.5 x 1e+3
New Hampshire	0.85 x 1e+3	Oregon	2.5 x 1e+3	Nebraska	7 x 1e+3
Hawaii	0.9 x 1e+3	Missouri	2.7 x 1e+3	Tennessee	7.5 x 1e+3
North Carolina	1.1 x 1e+3	Arkansas	3 x 1e+3	Ohio	8.25 x 1e+3
Montana	1.2 x 1e+3	West Virginia	3 x 1e+3	Georgia	9 x 1e+3
Maryland	1.25 x 1e+3	Colorado	3 x 1e+3	California	15 x 1e+3
Illinois	1.45 x 1e+3	Washington	3.3 x 1e+3	Texas	18.5 x 1e+3
Alabama	1.5 x 1e+3	Mississippi	3.5 x 1e+3	Florida	24 x 1e+3

Table C.1: State N Values