Exploring the Sensitivity of Extended SIR Models Through Randomized Simulations and Multiple Factor Analysis

Abstract

COVID-19 has been modeled since its emergence in several ways, most prominently using SIR (Susceptible-Infected-Removed) models. This paper aims to evaluate the robustness of extended SIR models by using multivariate factorial analysis on 13 parametric values commonly used in current published COVID-19 models. These parameters can be used to indicate which Centers for Disease Control (CDC) recommendations are most influential in overcoming the COVID-19 pandemic. Overall, we show that the COVID-19 epidemic projections are very sensitive to minor changes in assumptions, even when using parametric assumptions within ranges provided by the CDC. We found that the estimated spread and disease burden varied dramatically based upon the primary response that was measured (deaths, hospitalizations, or infections), and key parameters impacted different facets of the disease burden. For example, we find that testing, as well as isolation and quarantine measures, are most effective in containing the spread and alleviating disease burden. Similarly, the accuracy of diagnostic tests carries great importance in the total number of individuals infected over the course of the pandemic. Since each of the parameters used in all COVID-19 model projections are estimated values, better care should be used to understand the variability of these parameter estimates when models are shared with the public.

1) Introduction

In December of 2019, a novel coronavirus disease, COVID-19, was identified and reported. Since then, the disease has spread to more than 200 countries, infecting over 152 million people globally as of April 2021 (Johns Hopkins University, 2021). With loss of lives, crashing businesses, loss of jobs and the mental toll of social distancing, woes of COVID-19 have been felt throughout the world. The U.S. census estimated a 51.5 percent loss in employment with economic activity significantly slowing down since the beginning of the pandemic (Census, 2021). Hospitals were quickly overloaded and short-staffed, ICU beds were full, and healthcare workers were put under an immense mental and physical toll, having to work overtime under psychological distress (Mehta et al., 2021).

Governments across the globe have attempted to slow down the spread of this disease by implementing various measures – masking requirements, tracing contacts of infected individuals, quarantine and self-isolation requirements, even city-wide lockdowns – to prevent loss of human lives, economic crises, and to lift the burden off the healthcare infrastructure.

Many mathematical models have been employed to forecast the transmission of COVID-19 and to implement optimal policies since the first reports of the disease, such as Susceptible-Infected-Removed (SIR) models. SIR models are the most basic, compartmental models used to predict the spread and burden of diseases. SIR models assume a closed population, meaning there is an assumption that no members of the population are being added or removed throughout the time frame provided by the model. In the basic SIR model, members of the population are all initially *Susceptible* (S) to the disease. Point estimates are calculated for the number *Infected* (I) and *Removed* (R), which consists of dead and recovered individuals. In this basic model, each person within the population is placed into exactly one of these three compartments for each time increment (each day). Parametric values (such as the transmission rate, incubation rate, recovery rate) are then used to determine the likelihood of moving to a new compartment.

Though SIR models can be insightful, the use of point estimates can also lead to uncertainty in predicted parameters, preventing reliable projections of the outbreak (Castro et al 2020). This misleads efforts to contain outbreaks, worsening the already devastating burdens on the healthcare system and the economy. To overcome this issue, ***we avoided the commonly used modeling techniques that emphasize the use of differential equations and instead created models based upon discrete compartmental parameters. Through simulations we are then able to create both point and interval estimates for each of our primary response variables***. By allowing each of our 13 parameter values to follow binomial distributions instead of a fixed value, we create a more robust projection of disease spread. In essence, when the CDC can only estimate key COVID-19 parameters, such as the spread rate, incubation time, or the hospitalization rate within our population, we believe the models provided to the public should also reflect a measure of variability when discussing total infected, hospitalizations or deaths.

In the following sections, we describe an extended SIR model, discuss our choice of parametric values, describe our simulation study and analysis, and then discuss the implications of this work on public policy. In particular, we aim to shine light on the key parametric values that are most

influential in modeling the burden of COVID-19, as well as highlight the underlying issues associated with models that depend solely on point estimates.

2) Extending the Compartments in the SIR Model

In addition to using a discrete model that can account for variation within each of our parameter values, we also extended the basic three-compartment SIR model to incorporate several additional compartments, based on current literature on COVID-19. The following will briefly describe each of these additional compartments. Additional detailed rationale and references for these compartments can be found in Appendix 1.

Positive-Exposed (E): We add a *Positive-Exposed* (E) compartment between *Susceptible* and *Infected*. This compartment represents the time between when a person is initially exposed to the virus until they become infectious. By adding this compartment, we can model the impact of the delay between exposure and infectiousness. We assume those in the *Positive-Exposed* compartment cannot yet infect others. Moreover, we are assuming everyone in the *Positive-Exposed* compartment will become infected.

Infected asymptomatic (I_a) and Infected symptomatic (I_s): The *Infectious* (I) compartment is divided into two sub-compartments: asymptomatic and symptomatic. Some infected individuals may never show symptoms of disease (i.e. asymptomatic) while others do (i.e. symptomatic). This allows us to address the new level of contagion risk and can help decision makers to implement policies and regulations accordingly.

Quarantine and Hospitalized Compartments (Q_{FP}, Q_s, Q_a, H): An individual testing positive for COVID-19 is immediately moved into a Quarantine (Q) compartment.. We use these groups to model restricted movement of an individual assumed to be infected. By doing so, the delay of spread and therefore the effectiveness of such non-pharmaceutical interventions can be analyzed.

- Individuals who are tested as false positives are moved into *Quarantine False Positive* (Q_{FP}). While people certainly do not know if a test is false, we use this to model the small proportion of the tests that are not accurate. In our model, *Quarantine False Positive* may also include individuals who came into potential contact with an infected person, but never became infectious.
- We also include quarantine groups for people who are asymptomatic (Q_a), symptomatic but do not need hospitalization (Q_s), and people who are hospitalized (H). People who are hospitalized (H) cannot spread the disease further.

***Recovered (R) and Dead (D)*:** We also separate the conventional Removed compartment into *Recovered* (R), including those immune to the disease at the start and those recovered, and *Dead* (D).

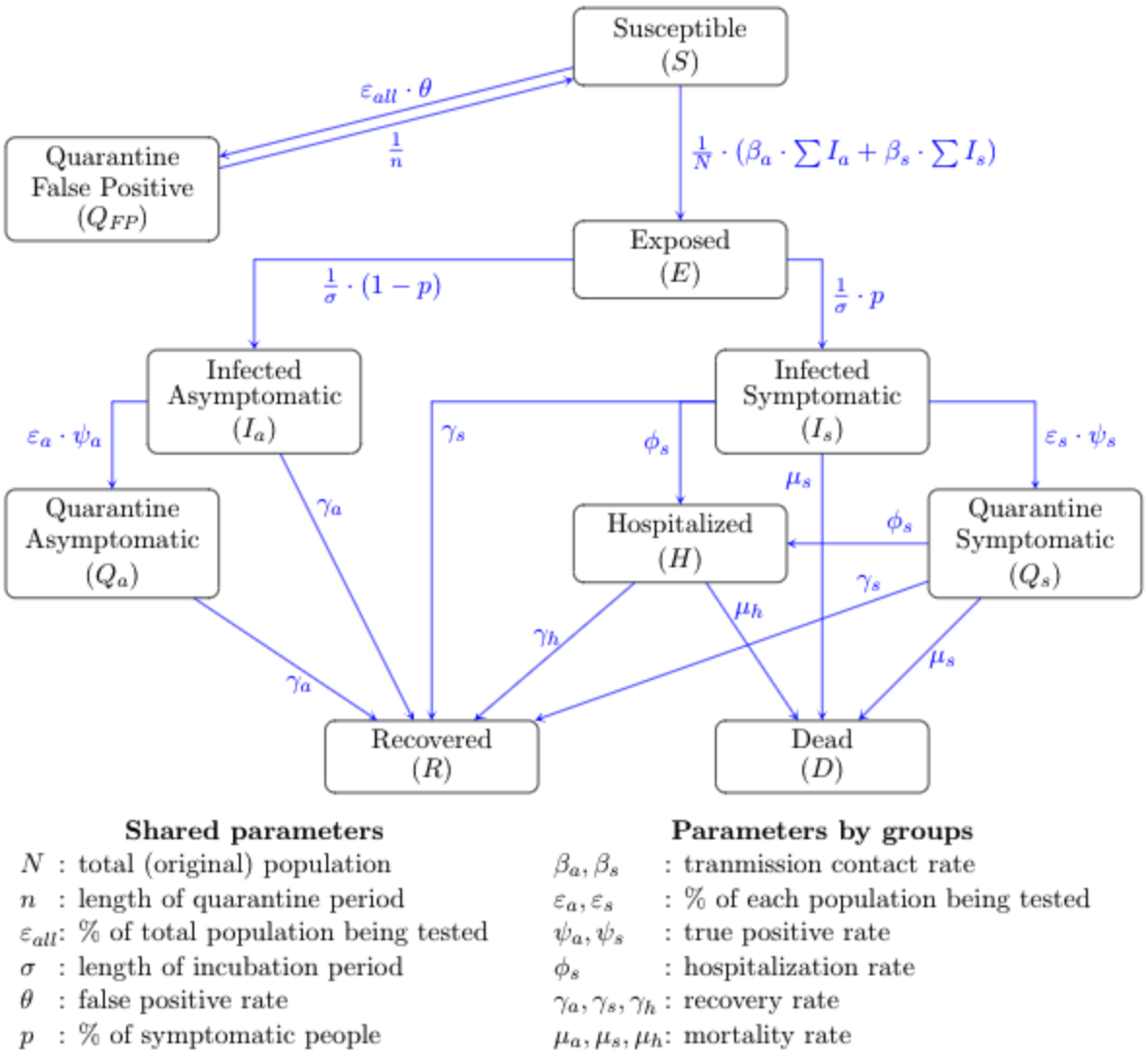

Fig. 1: Schematic flow of compartments

Figure 1. *A schematic flow diagram showing the extended SIR model for the susceptible people within a population. A person is in exactly one compartment at any particular time. The parameter values are used to model the likelihood of moving into a new compartment. In published epidemiology models, sometimes formulas instead of a single parameter are used to model the flow. In our analysis, all disease parameter values are based upon published estimates from the CDC and other health organizations.*

3) Key Model Parameters Within the Extended SIR Models

The parameters and formulas shown in Figure 1 follow published differential equations commonly used for modeling COVID-19 and other diseases. We briefly describe key parameters below and provide more detailed explanations in Appendix B.

Moving from Susceptible to Positive-Exposed to Infected: Upon contact with a person carrying the virus, some portion of the Susceptible (S) compartment is moved to the Positive-Exposed (E) compartment and then to one of the Infected (I) compartments (Asymptomatic or Symptomatic).

- The likelihood of moving to Positive-Exposed depends upon the transmission contact rate, the population size, and the number infected. The **transmission contact rate (β)** is the average number of susceptible people who will be infected when exposed to an infected person.
- Eventually, all people in the Positive-Exposed compartment will move to one of the Infected compartments. The **incubation period (σ)** of the virus determines how long the person will stay in the Positive-Exposed (E) compartment. It ensures that, on average, each person in our model will stay in the Positive-Exposed compartment (i.e. infected but not yet infectious) for a certain amount of time.
- Notice that people in the Susceptible (S) group who might come in contact with an infectious person, but never get the disease, may be tested and put into the Quarantine False Positive (Q_{FP}) compartment and eventually move back to the Susceptible (S) compartment.

Moving out of the Infected asymptomatic (I_a) compartment:
People in the Infected asymptomatic ($\mathbf{I_a}$) compartment may be Quarantined (Q), may Recover (R), or simply stay in the Infected asymptomatic compartment.

- The likelihood of being quarantined depends upon the rate of testing ($\boldsymbol{\mathcal{E}_a}$) and the probability that the test correctly identifies the person as positive for COVID-19 ($\boldsymbol{\psi_a}$).
- Whether someone is quarantined or not, the probability that one moves to the Recovered compartment depends upon the recovery rate **(γ)**. Our model assumes that recovered individuals are no longer infectious and no longer susceptible to the disease.
- We assume people in the Infected asymptomatic ($\mathbf{I_a}$) compartment may expose additional susceptible people to the disease.

Moving out of the Infected symptomatic (I_s) compartment:
People in the Infected symptomatic (I_s) may be Quarantined (Q), Hospitalized (H), may Recover (R), Die (D), or continue to stay in the Infected symptomatic compartment.

- The likelihood of being quarantined depends upon the rate of testing ($\boldsymbol{\mathcal{E}_s}$) and the probability that the test correctly identifies the person as positive for COVID-19 ($\boldsymbol{\psi_s}$). Notice that the subscripts are used to ensure that different values can be used for symptomatic and asymptomatic probabilities.
- The hospitalization rate ($\boldsymbol{\phi_s}$) is used to model the likelihood of being hospitalized.
- As shown in Figure 1, the mortality rate (μ_s) will vary depending upon whether or not a person is hospitalized, quarantined, or in the Infected symptomatic compartment.
- We assume people in the Infected symptomatic (I_s) compartment may expose additional susceptible people to the disease.

4) Additional Model Complexity

While the previous sections discuss the core ideas within our model, there are a few more terms that we considered that are not shown in Figure 1.

***Dividing the Population by Vulnerability to Disease*:** Age and certain comorbidities greatly impact the severity, hospitalization and fatality rates of COVID-19. By accounting for vulnerability, we can assess the impact of implementing semi-targeted policies, such as not allowing visitors in nursing homes. While not shown in Figure 1, our model also divided the population into groups to account for the discrepancies between different risk groups: people who are relatively vulnerable (V) or non-vulnerable (NV) to the disease. Thus our actual model had almost identical compartments for both the (V) and (NV) sub-populations, but the probabilities of moving between compartments varied dramatically between the models for these two groups. We also assumed no hospitalization and no deaths of Infected asymptomatic (I_{asym}) individuals in the non-vulnerable (NV) population.

5) Experimental Design

With these assumptions and initial conditions for the experiment, we focused on evaluating the effect of thirteen parameters on various response variables (number of deaths, number of infected, and measures of disease burden). Parameter values tested correspond to the range of values for COVID-19 provided by the CDC based on recent data (2020).

In our simulation study we decided to test the following parameters, each at 2 levels:

Parameters	**Parameter values**
Hospitalization rate ϕ_s (NV)	.01, .1[1]
Hospitalization rate ϕ_s (V)	.2, .6 [1]
False positive percentage θ (V and NV)	.005, .02
% Tested Symptomatic $\mathcal{E}_s$ (NV)	.2, .6
% Tested Asymptomatic $\mathcal{E}_a$ (NV)	.1, .3
% Tested Symptomatic $\mathcal{E}_s$ (V)	.3, .7
% Tested Asymptomatic $\mathcal{E}_a$ (V)	.2 , .4
Transmission Rate Symptomatic β_s (V and NV)	1, 3 [1]
Transmission Rate Asymptomatic β_a (V and NV)	1, 3 [1]
% Exposed that are Symptomatic, p (NV)	.2, .4
% Exposed that are Symptomatic, p (V)	.2, .4

[1] These values are derived from the real time reports provided by the Centers for Disease Control (2020).

True Positive Symptomatic ψ_s (V and NV)	.9, 1
True Positive Asymptomatic ψ_a (V and NV)	.85, .95

Table I. *Parameter values used in the experimental design.*

Moreover, the following parameters were fixed throughout all simulations.

Fixed Parameters with Notation	
Initial Infected (I_S NV)	5 (All symptomatic)
Initial Infected (I_S V)	5 (All symptomatic)
Incubation Period (**σ)**	7 days
Population (N)	100,000
Percentage Vulnerable	0.2 (20,000 people were vulnerable every simulation)
% Tested Susceptible ε_{all} (NV)	0.05, 0.15[2]
% Tested Susceptible ε_{all} (V)	0.1, 0.2[3]
Quarantine Period for False Positive (n)	14 days
Percentage Non-Susceptible (NV)	0.25
Percentage Non-Susceptible (V)	0
Recovery Rate Sym γ_s (NV)	0.09
Recovery Rate Asym γ_a (NV)	0.1
Recovery Rate Hospitalized γ_h (NV)	0.05333
Death Rate Sym μ_s (NV)	0.01
Death Rate Asym μ_a (NV)	0
Death Rate Hospitalized μ_s (NV)	0.01333
Recovery Rate Sym γ_s (V)	0.09

[2] The two values were dependent on ε_a (NV). It is $\varepsilon_a/2$.

[3] The two values were dependent on ε_a (V). It is $\varepsilon_a/2$.

Recovery Rate Asym γ_a (V)	0.04
Recovery Rate Hospitalized γ_h (V)	0.08
Death Rate Symptomatic μ_s (V)	0.04
Death Rate Asymptomatic μ_a (V)	0.02
Death Rate Hospitalized μ_h (V)	0.1

Table II. *Fixed parameter values used in the experimental design.*

The parameters are used to simulate the progression of the outbreak under different conditions. For example, transmission contact rate can yield insight into the growth of the pandemic when people fail to comply with social distancing guidelines, or occupy densely populated settings, where social distancing is implausible. To acknowledge the corresponding burden of changing parameter levels, total number of deaths, peak deaths, day of peak infections, peak hospitalizations, peak daily infections, and total infections were recorded. In order to address the unpredictability of infectious disease, variability was also incorporated into the model parameters via binomial distribution. Ten simulations of each parameter level against the response variables were run in a multivariate factorial analysis. Main effects and interactions were analyzed for the thirteen parametric assumptions.

The experimental design involves important parametric assumptions about the model. First, those who are tested for COVID-19 are assumed to receive their test results the same day they are tested. This assumption is crucial for the model, as there will be no time lag between when the test was carried out and when the results are received, which prevents additional contacts and therefore infections for individuals positive for COVID-19. There are several shortcomings associated with this assumption. Currently, the most widespread form of diagnostic testing usually takes between 24 to 48 hours (Cleveland Clinic, 2021). Although rapid, at-home testing exists, this diagnostic method is not commonly available in many countries (García-Fiñana & Buchan, 2021). This may be a limitation in the model's application to real-world scenarios, since the time lag between when the test is conducted and the results received may lead to additional cases. Particularly, if the individual does not exhibit symptoms and is carrying the virus, there may be an increased risk of contact with more individuals, inducing a cascade of infections.

- Every person who tests positive, even those who reflect a false positive result, are quarantined in this model. Though infected individuals can stay in the infected compartment for several days before quarantine, those in quarantine should not have a chance to infect another individual, implying full compliance with isolation procedures. This is a bold assumption, since many experts believe at-home quarantines are not enforceable, and government isolation facilities are simply not demandable (Siemaszko 2020). Moreover, various literature sources have demonstrated, for example, that essential workers (e.g. healthcare workers, postal workers, and manufacturing plant workers) are notably vulnerable to quarantine requirements. A lack of staff due to infections may put a further undue strain on the healthcare infrastructure, the production chain and other essential services. Additionally, imprisoned individuals, those seeking

asylum and those in refugee camps lack resources necessary to observe social distancing and quarantine procedures, since individuals seeking asylum or refuge may need to be mobile, further endangering their health and others' (Openshaw & Travassos 2020). Many across the nation live paycheck-to-paycheck, and cannot afford to lose more than a week's worth of wage, specifically in low-paid industries. However, countries that utilized quarantine enforcements while supporting their citizens proved more efficient in control of COVID-19 spread. In South Korea, for example, individuals exposed to the coronavirus were taken to government-run quarantine facilities for 14-days, and those who tested positive for the virus stayed at different facilities until they were cleared of the virus (Janes 2020). This immeasurably helped South Korea's efforts to contain the virus, preventing the collapse of health systems and the country's economy (Scott & Park 2021). Therefore, our assumption of immediate quarantine reflects the potential of the Non-Pharmaceutical Interventions in controlling the spread of COVID-19.

This model does not have time-varying parameters. The transmission rate of a disease is dependent on many factors including the nature of the disease, mask wearing, and social distancing. These parameters change over time and directly affect the Beta term in our model. While this is mitigated by the variability we introduced in our model, it still does not capture the nature of the disease.

In the experimental set up, initial conditions were set such that N=100,000, twenty percent of which are vulnerable. Of the non-vulnerable population (N_{NV}=80,000), 75 percent wereassumed to be susceptible and 25 percent non-susceptible to the disease. Previous research suggests some individuals who have had a coronavirus infection previously will have memory cells sufficient for immunity (Doshi, 2020), and 25 percent falls within the range of suggested non-susceptible population. These individuals are then placed in the Recovered (R) compartment, since an immunity is assumed.

Incubation day for the virus was set to be seven days, consistent with data provided by the CDC (2020). For both non-vulnerable and vulnerable populations, there were five initial infections, both symptomatic. 50% and 75% of non-vulnerable and vulnerable populations were fixed to be symptomatic respectively.

6) Analysis

The analysis conducted shines light on various interactions crucial to determine the progression of the COVID-19 pandemic. For simplicity, we use 'less transmissible' and 'more transmissible' cases, referring to the case when transmission contact rate– for both symptomatic and asymptomatic infections – is 1 and 3 respectively.

In both cases, the percentage of asymptomatic, non-vulnerable individuals tested for COVID-19 is crucial. The burden of infection, hospitalizations and death lessened in response to a higher volume of testing of asymptomatic, non-vulnerable individuals. This can be attributed to decreased 'silent transmissions' among the community, since asymptomatic individuals are quarantined once they test positive. Higher volume of testing on non-vulnerable, asymptomatic

individuals also delays the day of peak infections, meaning the peak infections will occur at a later time.

Interestingly, in the less transmissible case, the pandemic is expected to end later when more asymptomatic, non-vulnerable individuals are tested. This is unexpected, since quarantining individuals who would otherwise silently transmit the disease would be expected to curb the pandemic earlier on. This is the case in the more transmissible case, where the pandemic ends earlier in response to a higher volume of testing asymptomatic, non-vulnerable individuals. Higher percentage testing of symptomatic, non-vulnerable individuals has a similar impact on day of peak infection for both cases, with higher volume of testing corresponding to a delay in peak infections. Higher testing of symptomatic, non-vulnerable individuals is observed to delay the end of the pandemic (Figure 2 & 3). This may reflect a flattening in the curve of peak infections. Though the pandemic seems to end later, daily peak infections are reduced until the end of the pandemic.

In both cases, deaths and hospitalizations increase when a higher percentage of individuals are non-vulnerable and symptomatic. This effect is much greater in the more transmissible case. Finally, the results highlight something interesting about test effectiveness: in the more transmissible case, a higher percentage of false positive tests corresponds to lower infections, as all individuals testing positive are isolated in this model. With more isolation comes less spread of the disease, and therefore the total infection burden of the disease lessens. Interestingly, this does not apply to other response variables to this extent.

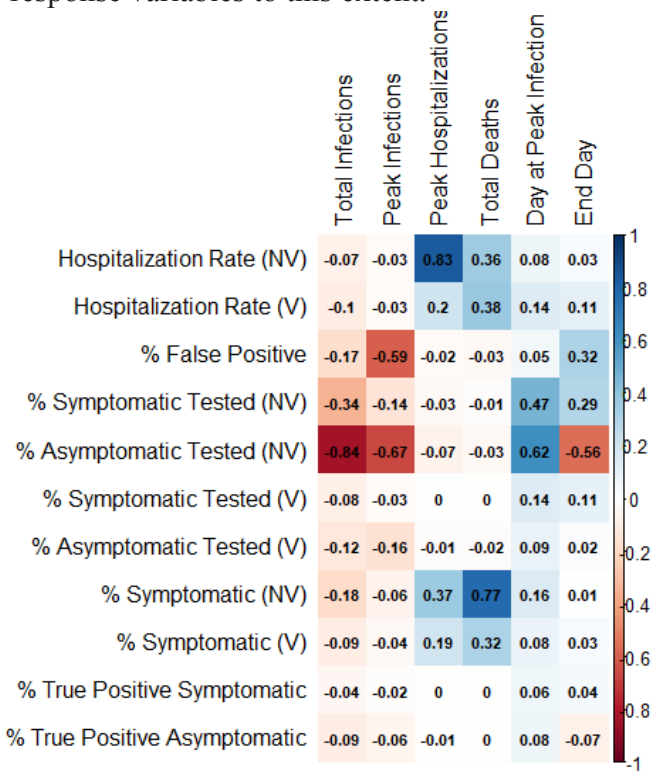

Figure 2. *Correlation plot between the model parameters and response variables at beta=3. This is the more transmissible case of the disease. This plot allows us to visually identify how each explanatory variable influences each response variable within our simulations.*

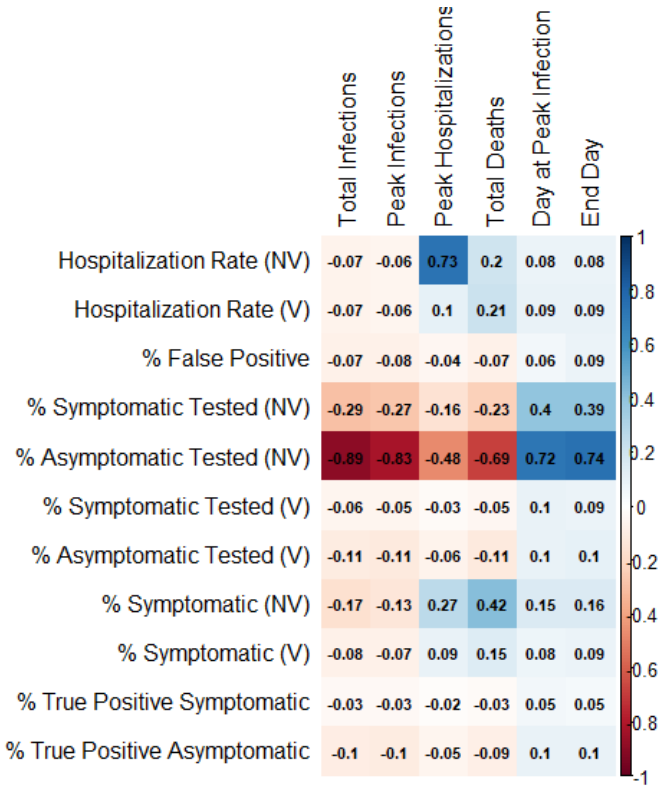

Figure 3. *Correlation plot between the model parameters and response variables at beta=1. This is the less transmissible case of the disease.*

A strange result to note is that a higher percentage symptomatic for the non-vulnerable population seems to strongly correlate with total deaths. The non-vulnerable population is supposed to be less susceptible to the disease's effects. One explanation is that in our simulations, 80% of the population is non-vulnerable. The characteristics of the majority have a more prominent effect on the results. While it is important to make sure vulnerable populations are taken care of, some stress must be given to the non-vulnerable as they are most likely the majority. To view the main effects plots, please see Appendix C.

7) Implications for Public Policy

To repress a pandemic is a difficult task, and policymakers need to race with time to prevent loss of life and alleviate the burden on the healthcare infrastructure and economy. The results from this research have several important implications to public policy. We show that the progression of the pandemic is highly dependent on testing, specifically of groups that are non-vulnerable and do not exhibit symptoms, albeit a significant portion of the population. Literature suggests that silent transmissions by asymptomatic individuals contribute to more than half of forward COVID-19 transmission (Moghadas et al. 2020), and the identification and subsequent isolation of these individuals is crucial in containing the spread of COVID-19. Policymakers then must make enough tests available and accessible to the wider population, and contact tracing is necessary to a great extent in order to identify individuals who may have been exposed to the

virus. In many developed countries, diagnostic tests for COVID-19 are widely available and free of charge, while in other parts of the world, testing is costly and unaffordable, even inaccessible for many. By expanding the scale of testing across regions that lack access, the burdens brought by the pandemic might be alleviated.

This analysis also draws attention to the importance of sensitivity versus specificity of the COVID-19 tests. A test with high sensitivity (a high ability to correctly identify positive individuals) is important since less false negatives means less unidentified transmission. Test specificity, or the ability to correctly identify negatives, is also important. However, we find that even with a relatively lower test specificity where the false positive rate of the test is high, the pandemic can be curbed assuming all those testing positive will be quarantined. This is due to limited contact between quarantined individuals –including false positives– and others. Diagnostic tests need approval before use, and this result implies a possibility for the test specificity criteria to be relaxed, assuming quarantine following a positive test.
The differences in some interactions between the less and more transmissible cases raise important questions future research can address. The analysis suggests that in the less transmissible case, the percentage of asymptomatic, non vulnerable individuals tested *positively* impacts the end day of the pandemic. The opposite is observed for the more transmissible case. Intuitively, it would be expected that in both cases, more testing and subsequent quarantine of infected individuals would shorten the duration of the pandemic.

Another interesting observation is that between the percentage of symptomatic, non-vulnerable individuals and total deaths, specifically in the more transmissible case. With a higher percentage of symptomatic infections being non-vulnerable individuals, higher total deaths are observed. One explanation could be that exhibiting symptoms may translate to a higher load of viruses inside the human body, which in turn may make the disease more possible to be transmitted to others. However, several case reports demonstrated no difference in the viral load of asymptomatic and symptomatic individuals (Lennon et al., 2020; Ra et al., 2021); therefore, this result demands further research.

8) Conclusion

This paper aimed to evaluate the robustness of extended SIR models by using multivariate factorial analysis on 13 parametric assumptions, to explore influential methods to decrease the effects of the COVID-19 pandemic. Our analysis shows that testing of asymptomatic, non-vulnerable individuals is crucial in both less transmissible and more transmissible cases of the pandemic.We find effectiveness of testing, both in speed and accuracy, to be useful in curbing the spread of the disease. Several parametric assumptions, including mandatory quarantine of individuals testing positive for COVID-19, and fast testing, are crucial and can give an idea to policymakers about effective ways to contain the spread of COVID-19.

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Appendix A

Compartments:

I. Adding Positive-Exposed (E) Compartment

In most infectious diseases, the infected organism, upon initial exposure to the pathogen, can only spread the disease after a period of time. This time is known as the incubation period, and basic SIR models do not capture this delay. However, it is crucial to incorporate this time period into the models, as it better demonstrates disease dynamics and facilitates model stability for diseases with a known latent period (Abta et al. 2012). Therefore, an *Exposed* (E) compartment is added to describe the time between when a person is initially exposed to the virus through contact and when they become infectious. This will provide more insight into the impact of isolating exposed individuals on the dynamics of COVID-19 spread.

II. Dividing Compartments into Symptomatic and Asymptomatic

Another complexity of understanding and predicting the spread of COVID-19 stems from the emergence of asymptomatic patients (Pan et al. 2020; Tong et al. 2020; Kimball et al. 2020). Some infected individuals may never show symptoms of disease (i.e. asymptomatic) while others do (i.e. symptomatic). Therefore, there exists a certain number of people who have been infected without knowing. The existence of such asymptomatic carriers and the potential threat of contagion from a silent infection in the local community, violate the assumptions of the family of SIR models, rendering them too idealistic. To overcome these shortcomings, the *Infectious* (I) compartment is divided into two sub-compartments: asymptomatic and symptomatic. This allows us to address the new level of contagion risk and can help decision makers to implement policies and regulations accordingly.

III. Adding Quarantine Compartments (Q_{FP} , Q_s , Q_a) and Hospitalization (H)

To curb the spread of COVID-19, social distancing regulations, such as quarantine, are put in place. It is important to note that much literature differentiate quarantine from isolation; defining quarantine as a measure for those exposed and isolation as a measure for those infected (CDC, 2021). Herein, 'quarantine' is used to describe a measure to restrict the movement of an infected individual. Quarantine of an infected individual restricts exclusively the amount of contact one has with susceptible individuals, therefore reducing subsequent spread of the virus within the community.

This model involves the testing of individuals at the Susceptible (S) and Infected (I_s , I_a) levels, as a public health measure to identify individuals carrying COVID-19. An individual positive for COVID-19 is immediately moved into a *Quarantine* (Q) compartment. By doing so, the delay of spread and therefore the effectiveness of such non-pharmaceutical interventions can be analyzed.

At the Susceptible (S) level, individuals who test positive for COVID-19, who are deemed false positive, are moved into a False Quarantine (Q_{FP}) compartment.Various diagnostic tests exist to determine whether a person has COVID-19, and these range in effectiveness (Fitzpatrick et al. 2021). By including a false positive quarantine compartment, the impact of test accuracy on disease progression can be better understood. Within each subpopulation (non-vulnerable vs vulnerable, symptomatic vs asymptomatic), infected individuals– both isolated and non-isolated – then assume the same rates of recovery, hospitalization, and death as if they hadn't tested positive and were in the infectious compartments. If someone receives a false positive test, they

return back from isolation into the general population on an average of 14 days, according to guidelines from the CDC (2021).

IV. ***Recovered (R) and Dead (D)*****:** We also separate the conventional Removed compartment into Recovered (R), indicating immunity, and Dead (D). For every epidemic, some people are just naturally immune, these people are placed into the recovered group.

V. ***Dividing the Population by Vulnerability to Disease***

Finally, age and certain comorbidities greatly impact the severity, hospitalization and fatality rates of COVID-19. The models developed should account for the discrepancies between different risk groups: people who are relatively vulnerable or non-vulnerable to the disease. Therefore, this paper divides the population into non-vulnerable (NV) and vulnerable (V) subpopulations. By such grouping, different interactions could be assessed and differential analyses on the impact of implementing semi-targeted policies can be conducted, since such policies can significantly outperform optimal uniform policies (Acemoglu et al. 2020). Having this relevant information would help policy-makers tremendously in making wise decisions that could minimize both economic losses and deaths caused by the ongoing COVID-19.

For all of our code and data, click here for our GitHub.

Appendix B

Parameters:

For both non-vulnerable and vulnerable populations:

- **Transmission contact rate, β:** The product of rate of contact between an infectious and susceptible individual (κ) and the probability of disease transmission (c).

$$\beta = \kappa c$$ (Definition adapted from Goswami et al. 2020.)

- **Rate of latent individuals turning infectious, σ:** The rate at which individuals exposed to the virus become infectious. This parameter is dependent on the incubation period (time between exposure and symptom onset) for the novel coronavirus, which CDC reports to be between 2 and 14 days.

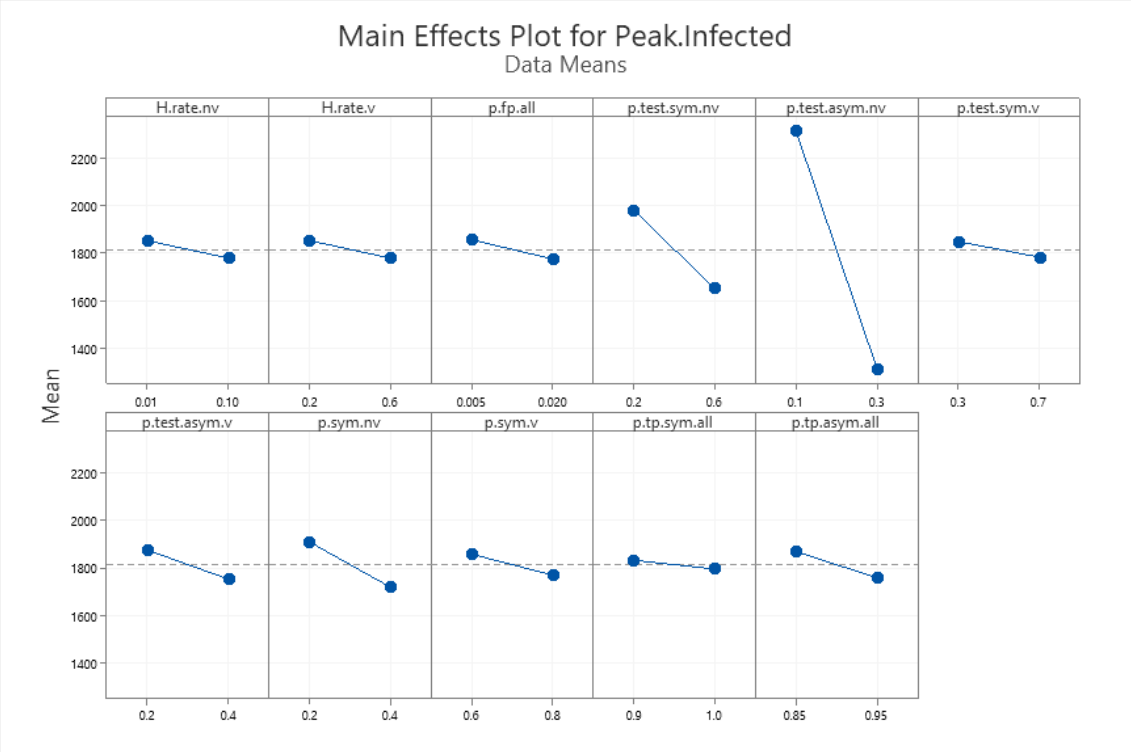
$$\sigma = \frac{1}{incubation\ period}$$

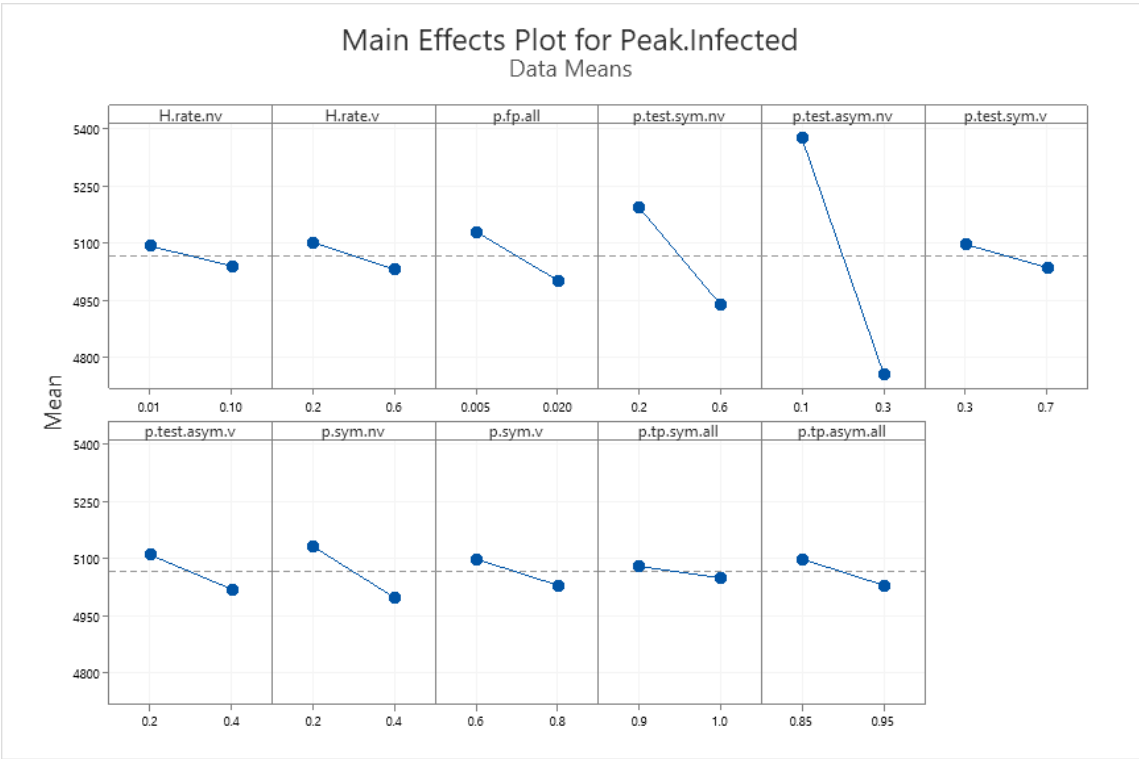
- **Hospitalization rate, φ:** The rate at which infected individuals with symptoms are admitted to the hospital for medical care. We assume asymptomatic individuals do not develop COVID-19 related complications leading to hospitalization.
- **Recovery rate, γ:** The rate at which individuals with COVID-19, including those hospitalized, recover.

- **Death/mortality rate, μ:** The rate at which individuals, hospitalized or not, die from COVID-19 and its associated complications. We assume non-vulnerable asymptomatic individuals do not develop severe enough complications that lead to death.
- **Percentage of false positive, FP:** Describes the amount of times (in %) that a COVID-19 test will show an *inaccurate* positive test result.

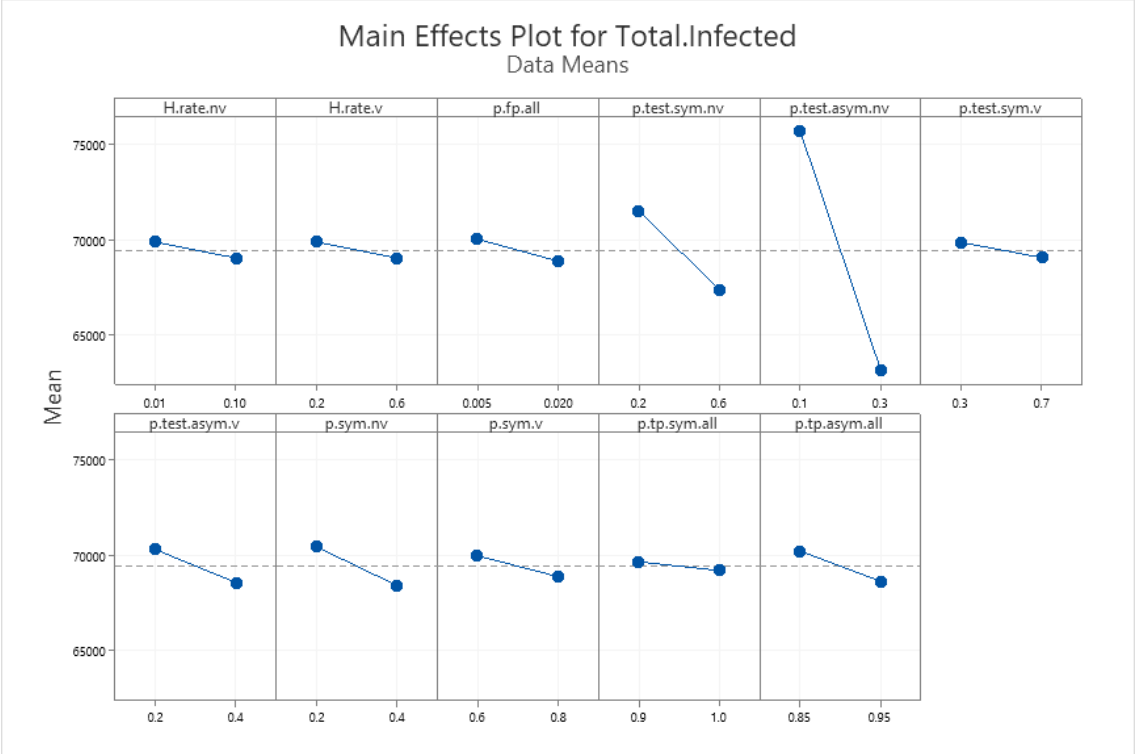
Appendix C:

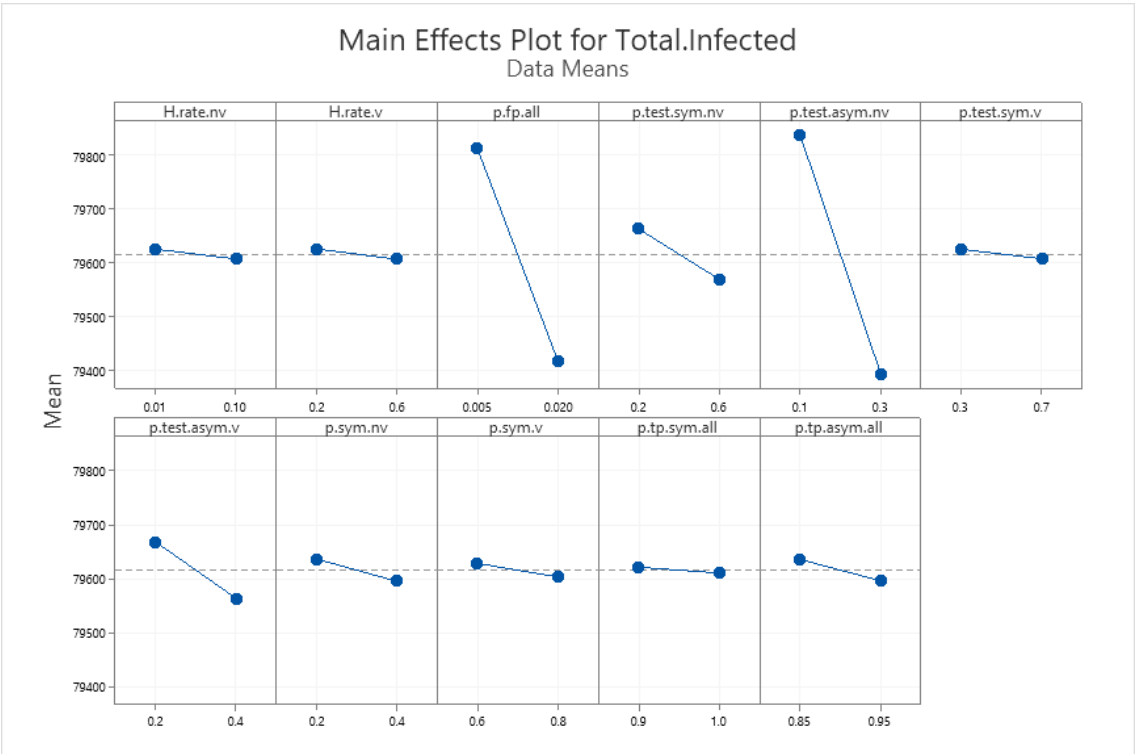
Main Effects Plots for Peak Infected (Transmission Rate of 1 and 3 respectively)



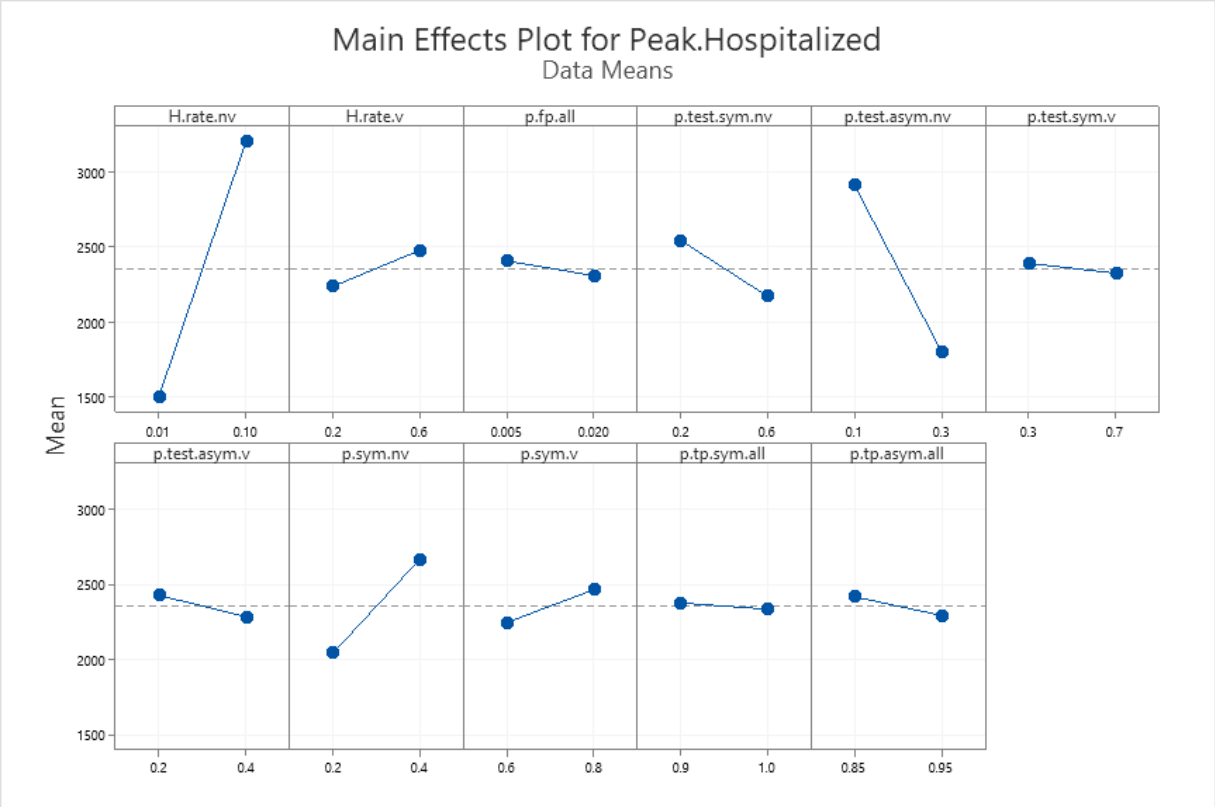


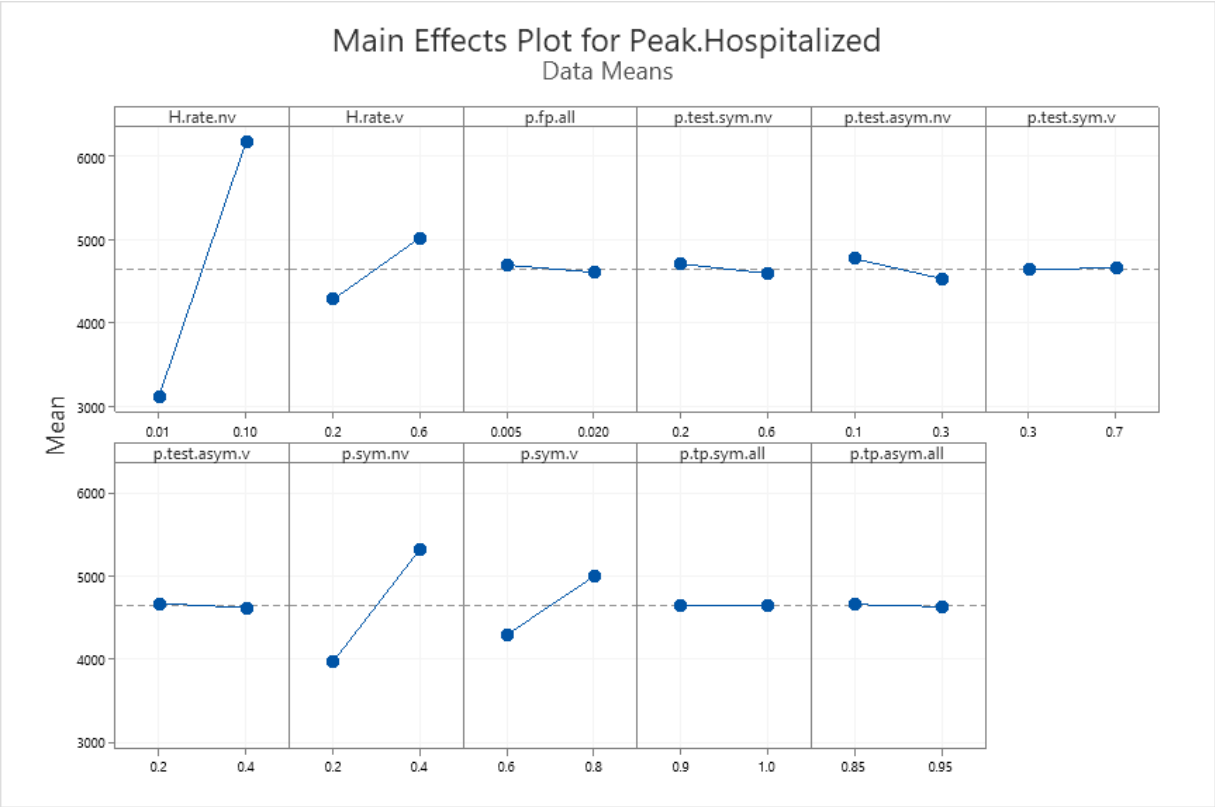
Main Effects Plots for Total Infected (Transmission Rate of 1 and 3 respectively)





Main Effects Plots for Peak Hospitalized (Transmission Rate of 1 and 3 respectively)





Main Effects Plots for Total Dead (Transmission Rate of 1 and 3 respectively)