Modeling the Epidemic Spread of an H1N1 Influenza Outbreak in a Rural University Town With Vaccination

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***Abstract*— In the past few decades, the usage of modeling the viral kinematics within host as well as the progression of the disease across a population have provided fruitful insight into the behavior of a certain infection. By examining a dataset from the 2009 outbreak of H1N1 in Washington State University, we hope to simulate the behavior of the disease if a vaccine was introduced into the population. Here, we compute the optimal vaccination rate v across several modifications made to Naveen et. al's protected, alternate-protected, and quarantine models in order to reach the threshold level of the infection dying.**

I. Introduction

According to the United States Center for Disease Control and Prevention (CDC), the first case of the 2009 H1N1 outbreak occurred in April 2009 in California. In the U.S., the pandemic occurred in two stages and were confined to major cities. The first stage began in a 10-year-old child who was tested for influenza and it was later confirmed that this new strand was unique in its viral encoding as it was a combination of different influenza virus genes "never previously identified in either animals or people" [1]. The second stage occurred when students went back to school in mid-August and early September. However, during the second stage, the virus spread through a rural university town of Pullman, Washington. Since students are in close proximity to one another constantly throughout the day as well as the cross-interaction of students to other students, the virus spread to about 10% of the student population [2]. Due to the CDC's time of planning strategic policies and emergency protocols years before the outbreak, the pandemic lasted only for a year.

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Thus, the use of compartment models has become more frequently used in order for scientists and researchers to understand the underlying mechanisms of certain viruses and how they spread across different kinds of populations. For example, in a closed environment such as a university rural town where students do not leave the town, the incoming rate of people coming into the town would be nearly zero. Thus, we expect that the system would be in constant flux between susceptible and infected populations. Vaidya et. al's work examined several models to predict the infection rate across time with different compartmental assumptions and interactions. [2].

However, not much work has been done in examining the rate of vaccination in order to ensure that the virus will die eventually. This is important as it provides information to public health administrators in developing strategic policies for minimizing the effects and spread of infection. The goal of this paper is to see how the rate of vaccination affects the reproduction number.

II. Model System Description

We introduce several models from Vaidya et. al's paper. However, they are nuanced with a new parameter v which represents the proportion of the population that is to be vaccinated.

A. Legend

- S is the susceptible population of students.
- I is the infected compartment group.
- R is the recovered compartment group.
- Q is the quarantine group. In other words, these are infected individuals who are isolated from the population
- V is the vaccinated group. For the purpose of simplicity, once an individual is vaccinated, then

they are immune to the infection.
- P is the protected group.

The following parameters were also used:

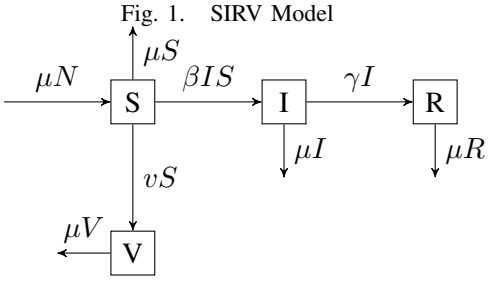
$$\text{Recovery Rate} : \gamma = \frac{1}{6}$$
$$\text{Birth/Death Rate} : \mu = 4.22 \times 10^{-5}$$
$$\text{Disease Transmission Rate} \beta = 5.3306 \times 10^{-5}$$
$$\text{Protection Rate} : b = 0.1354$$
$$\text{Protected Transmission Rate} c = 2.59 \times 10^{-6}$$
$$\text{Quarantine Exit Rate} : g = \frac{1}{6}$$

We note that μ is not part of original model. μ is based on a 65-year life expectancy. The focus of this paper is to analyze v.

Initial values: $S(0) = 18223, I(0) = 11, R(0) = 0, P(0) = 0, V(0) = 0, Q(0) = 0$.

B. Basic SIR Model with Vaccination

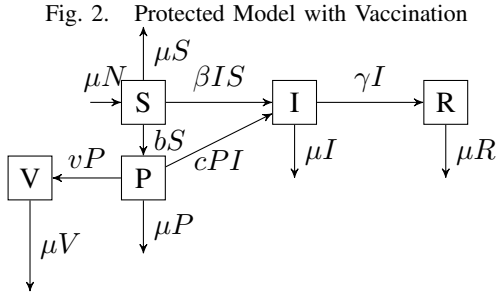
Fig. 1. SIRV Model



The SIRV model represents the traditional SIR model which has been modified to account for people becoming vaccinated. The model assumes that only people who have not already contracted the virus will receive the vaccine. For this reason, the proportion of people who become vaccinated are given by vS, which is a proportion of the susceptible population. This model also assumes that a minuscule proportion of each population will die, while and equally small population is born into the susceptible population.

$$\frac{dS}{dt} = \mu N - vS - \beta IS - \mu S$$
$$\frac{dI}{dt} = \beta IS - \mu I - \gamma I$$
$$\frac{dV}{dt} = v\mu - \mu V$$
$$\frac{dR}{dt} = \gamma I - \mu R$$

Fig. 2. Protected Model with Vaccination



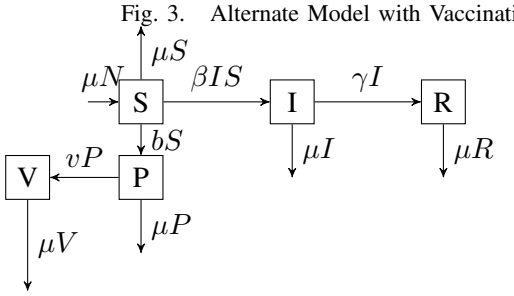
C. Protected Model with Vaccination

The Protected Model with Vaccination represents a population wherein a certain proportion of people are less likely to contract the virus. The protected population are given by bS, which is a proportion of the susceptible population. A proportion of the protected population will still contract the virus, give by cPI. Meanwhile, the remainder will opt to become vaccinated, given by vP. This model also assumes that a minuscule proportion of each population will die.

$$\frac{dS}{dt} = \mu N - \mu S - bS - \beta IS$$
$$\frac{dI}{dt} = \beta IS + cPI - \gamma I - \mu I$$
$$\frac{dP}{dt} = bS - cPI - \mu P - vP$$
$$\frac{dV}{dt} = vP - \mu V$$
$$\frac{dR}{dt} = \gamma I - \mu R$$

D. Alternate Model with Vaccination

Fig. 3. Alternate Model with Vaccination



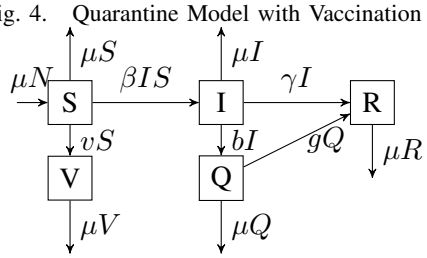
The Alternate Model with Vaccination is a special case of the Protected Model with Vaccination wherein no one from the protected population becomes infected. The proportion of the susceptible population that becomes protected is given by bS. It is assumed that some of the protected group will become vaccinated and is given by vP. Meanwhile, the proportion of the

susceptible population that becomes infected is given by IS. The proportion of the infected population is given by I. It is assumed that a small proportion of each population will die and an equal proportion will be born into the susceptible population.

$$\begin{aligned}
\frac{dS}{dt} &= \mu N - \mu S - bS - \beta IS \\
\frac{dI}{dt} &= \beta IS - \gamma I - \mu I \\
\frac{dP}{dt} &= bS - \mu P - vP \\
\frac{dV}{dt} &= vP - \mu V \\
\frac{dR}{dt} &= \gamma I - \mu R
\end{aligned}$$

E. Quarantine Model with Vaccination

Fig. 4. Quarantine Model with Vaccination



The Quarantine Model with Vaccination represents a model without a protected group, wherein people are still becoming vaccinated and a portion of the infected individuals self-quarantine, thereby reducing the odds that they contribute to the spread of the infection. The model assumes a small amount of deaths in each group and an equal amount of births into the susceptible population. The proportion of susceptible people who become vaccinated is given by vS. The proportion of the susceptible population who become infected is given by IS. The proportion of the infected population who recover is given by I while the proportion that goes into quarantine is given by bI. The proportion of the quarantined population which recovers is given by gQ.

$$\begin{aligned}
\frac{dS}{dt} &= \mu N - \mu S - vS - \beta IS \\
\frac{dI}{dt} &= \beta IS - bI - \gamma I - \mu I \\
\frac{dQ}{dt} &= bI - \mu Q - gQ \\
\frac{dV}{dt} &= vS - \mu V \\
\frac{dR}{dt} &= \gamma I + gQ - \mu R
\end{aligned}$$

III. Method

A. Basic SIR Model with Vaccination

Suppose that there were no vaccination ($v = 0$). Then, the reproduction number would be

$$R_0 = \frac{\beta}{\gamma + \mu}$$

which is the standard SIR model. Chauhan et. al found that by inducing the vaccination rate, the new reproduction number R_v would be a function of the standard reproduction number R_0 and v which is

$$R_v = R_0(1 - p)$$

They performed stability analysis on this model which served as the foundation for our next several modified models. Their work can be found at the reference below[3].

B. Protected Model with Vaccination

To find the disease-free equilibrium, we set $I = 0$, $dI/dt = 0$, and $dP/dt = 0$ find the equilibrium points. Then, the steady state equilibrium is $(S, I, P, V, R)^* = \left(\frac{\mu N}{\mu+b}, 0, \frac{b\mu N}{(\mu+v)(\mu+b)}, \frac{v}{u}, \frac{vbN}{(\mu+v)(\mu+b)}\right)$. The Jacobian J is as follows:

$$\begin{pmatrix}
-\mu - b & -\beta S^* & 0 & 0 & 0 \\
0 & \beta S^* + cP^* - \mu - \gamma & 0 & 0 & 0 \\
b & -cP^* & -\mu - v & 0 & 0 \\
0 & 0 & v & -\mu & 0 \\
0 & \gamma & 0 & 0 & -\mu
\end{pmatrix}$$

Therefore,

$$\begin{aligned}\det(J) &= (-\mu - b)(\beta S^* + cP^* - \mu - \gamma_)(\mu - v)(\mu^2) \\ &\quad + \beta S^*(0) \leq 0 \\ &\quad \beta S^* + cP^* - \mu - \gamma \leq 0 \\ &\quad \frac{\beta S^* + cP^*}{\mu + \gamma} \leq 1 \\ R_0 &= \frac{\beta S^* + cP^*}{\mu + \gamma} \\ R_0 &= \left(\frac{1}{\mu + \gamma}\right)\left(\beta + \frac{bc}{\mu + v}\right)\left(\frac{\mu N}{\mu + b}\right)\end{aligned}$$

C. Alternate Model with Vaccination

Note that the reproduction number for the alternate model is a special case of the reproduction number of the protected model where $c = 0$ (that is, the protected compartment has no risk of infection). Therefore,

$$R_0 = \frac{b\mu N}{(\mu + \gamma)(\mu + b)}$$

Note that when $c = 0$, the vaccination rate v does not affect the reproduction number.

D. Quarantine Model with Vaccination

Similarly, set $I^* = 0$ and setting each differential equation to 0, the steady state disease free equilibrium is $(S, I, Q, V, R)^* = \left(\frac{\mu N}{\mu+v}, 0, 0, \frac{vN}{\mu+v}, 0\right)$. The Jacobian J is as follows:

$$\begin{pmatrix} -v-\mu & -\beta S^* & 0 & 0 & 0 \\ 0 & \beta S^* - \mu - b - \gamma & 0 & 0 & 0 \\ b & b & -\mu - g & 0 & 0 \\ 0 & 0 & v & -\mu & 0 \\ 0 & \gamma & g & 0 & -\mu \end{pmatrix}$$

Therefore,

$$\begin{aligned}\det(J) &= (-v - \mu)(\beta S^* - \mu - b - \gamma)(-\mu - g)(\mu^2) \\ &\quad + 0 \leq 0 \\ \beta S^* &\leq \mu + b + \gamma \\ R_0 &= \frac{\beta S^*}{\mu + b + \gamma} \\ &= \frac{\beta \mu N}{(\mu + b + \gamma)(v + \mu)}\end{aligned}$$

IV. Results

A. Basic SIR Model with Vaccination

The Kermack-McKendrick Model with Vaccination demonstrates the linear relationship of the basic reproduction number R_0 and the proportion of people vaccinated pS. T**Figure 5** confirms the analytic solution that a vaccination rate of 82.48% is needed to ensure that $R_0 < 1$, which means that the virus will be not spread. We also denote that the infection prevalence will reach its peak at around 18 days since the initial outbreak and then dramatically reduce down in the next couple of weeks.

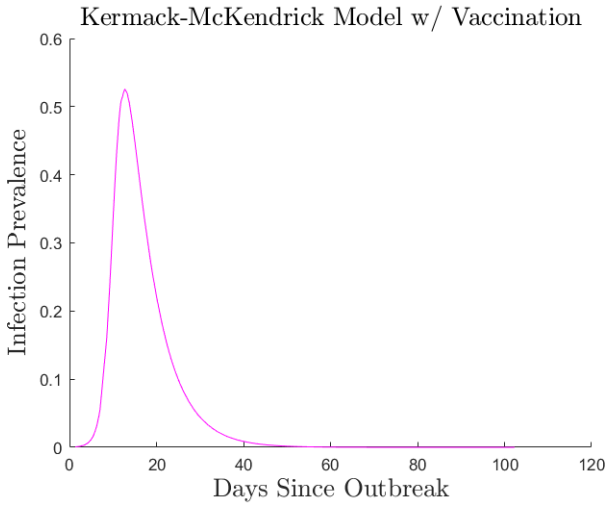


Fig. 5. Model Behavior

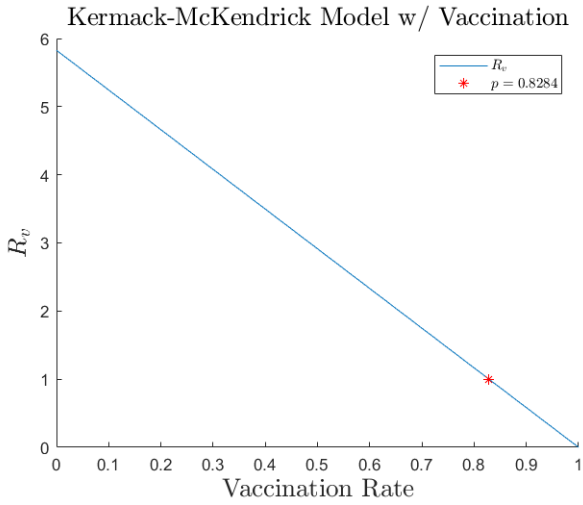


Fig. 6. Reproduction Number for SIRV Model

B. Protected Model with Vaccination

The Protected Model with Vaccination demonstrates that by vaccinating about 10% of the student population, the reproduction number $R_0 < 1$ which means the virus may eventually die. We note that the data fit best with the model. The disease reaches its highest peak at around 17 days. Looking at the original data, the disease gained momentum back about 70 days after

the initial outbreak which is not well-captured to the model. **See Figures 7 and 8**.

Fig. 7. Data Fitting for Protected Model

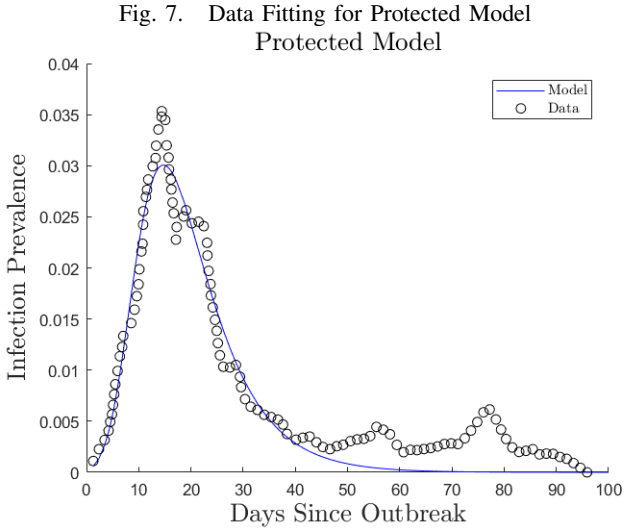
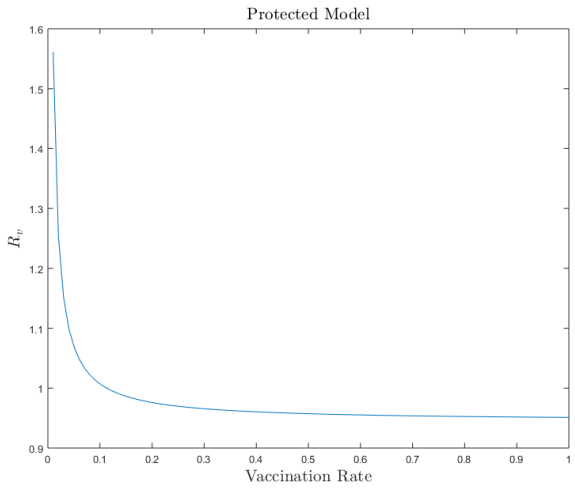


Fig. 8. Reproduction Number for Protected Model



C. Quarantine Model with Vaccination

The Quarantine Model acts very similarly to that of the Protected Model and Kermack-McKendrick Model in that its peak is around 17 days. The parameters used indicate that in the long-run, the prevalence of the disease does approach 0 in the long run. We also denote that a vaccination rate of about 10$ does indicate that the reproduction number can be reduced to below 1. **See Figures 9 and 10**.

V. Conclusion

Considering the models above, it is apparent that the significant factor of controlling a pandemic rests on being able to control the reproduction number. This can be done through inducing a vaccination into the population but it is not required to have everyone vaccinated from the infection. In fact, it is almost logistically impossible to have an entire population vaccinated, even through effective public health policies. If a disease is known to be incredibly infectious in a nearly-closed system such as a university where students are at close proximity with one another, the disease may preserve itself from host to host and thus, a high vaccination rate may be important in curtailing the effects of the infection. We capture a comparison of all the model fitting in **Figure 11**.

In the case of the Protective model, it is significant to note that by inducing a vaccinated compartment, it is necessary to have about 10% of the population to be vaccinated to reduce the reproduction number below 1. Vaidya et. al suggests that it is worth considering "the local population structure, as slowing a rapidly

Fig. 9. Model Behavior for Quarantine Model

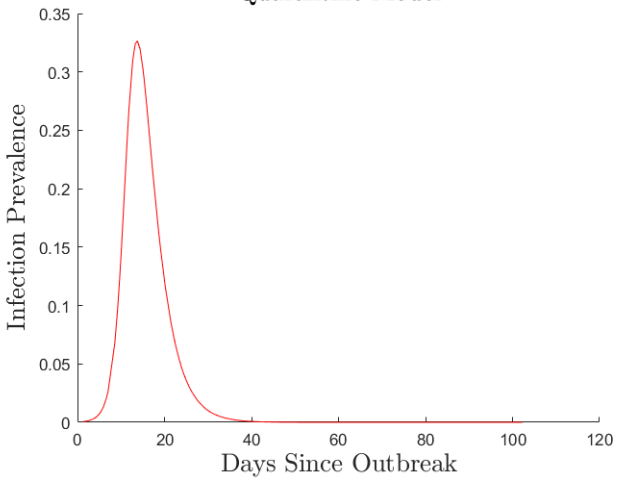
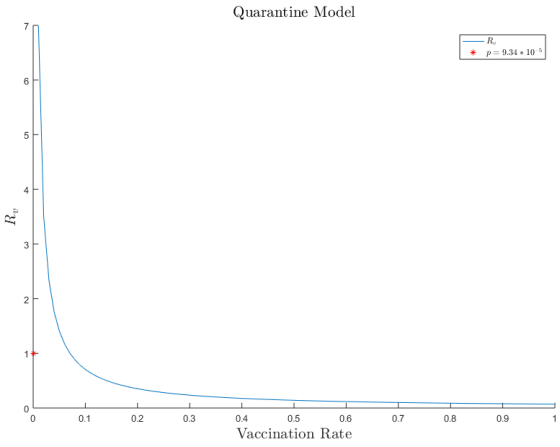


Fig. 10. Reproduction Number for Quarantine Model



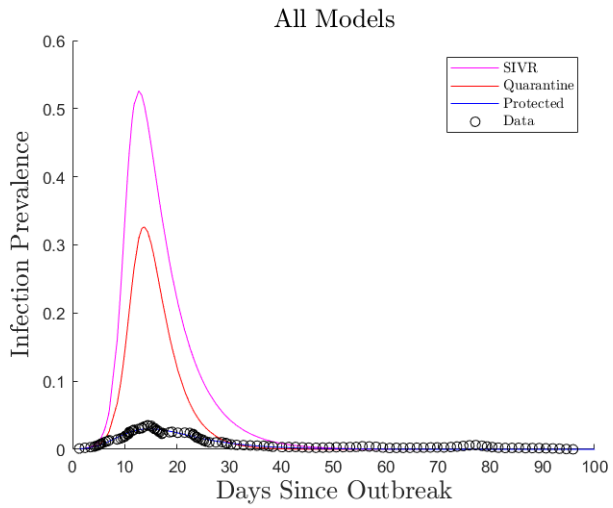


Fig. 11. All model fitting

spreading outbreak may require different interventions than in the case of the general population" [2].

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