Modeling and Analyzing the Transmission of COVID-19 at George Mason University

Clarissa Benitez, Krista Cimbalista, Jolypich Pek, Raina Saha
Mentor: Dr. Padhu Seshaiyer

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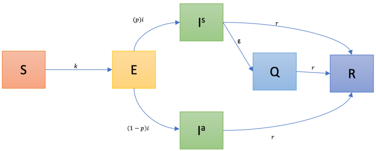
Introduction

- George Mason University has implemented extensive preventative measures to reduce the spread of COVID-19 on their campus including masks, random testing, and surveillance testing.
- A mathematical model is often developed from a basic SEIAQR model to better understand the transmission of disease in a particular environment.
- As the Mason population flows through our model, we must consider parameters specific to GMU such as quarantine disobedience and transmission rate that are relevant to our situation.
- We derive the basic reproduction number for the various models and use computational methods such as Runge Kutta to solve our system of ODEs and study the impact of various parameters.

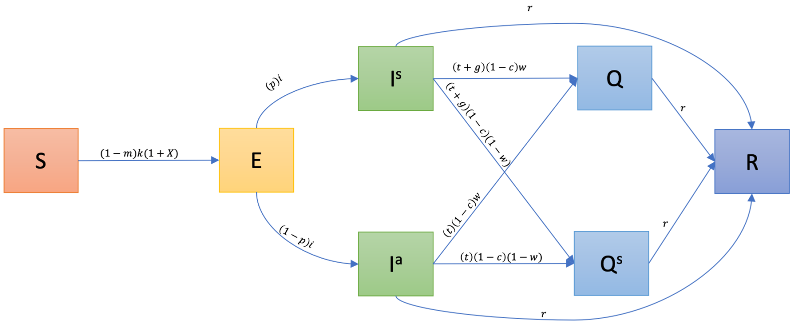
Base Model



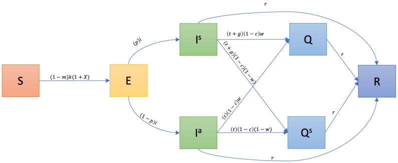
k = transmission rate
N = total population
i = incubation time
p = proportion that will have asymptomatic infection
r = recovery time
g = detection of symptomatic symptoms

- $\dot{S} = \frac{-kS}{N} * (I^s + I^a)$
- $\dot{E} = \frac{kS}{N} * (I^s - I^a) - iE$
- $\dot{I^a} = (1-p)iE - I^a r$
- $\dot{I^s} = piE - I^s g - I^s r$
- $\dot{Q} = I^s g - rQ$
- $\dot{R} = r(I^a + I^s + Q)$

Extension 1: With Semi Quarantine

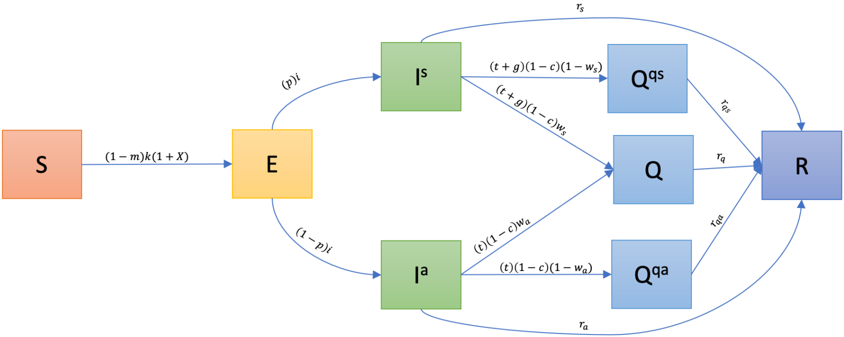


Extension 1: With Semi Quarantine

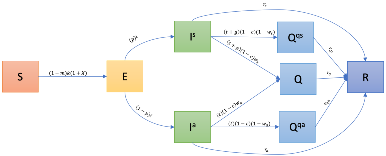


- $\dot{S} = \frac{-k(1-m)S}{N}(I^s + I^a + XQ^s)$
- $\dot{E} = \frac{k(1-m)S}{N}(I^s + I^a + XQ^s) - iE$
- $\dot{I^a} = (1-p)iE - tI^a r(1-c) - rI^a$
- $\dot{I^s} = piE - (t+g)I^s(1-c) - rI^s$
- $\dot{Q} = w(1-c)(I^s(t+g) + I^a t - rQ$
- $\dot{Q^s} = (1-w)(1-c)(I^s(t+g) + I^a t) - rQ^s$
- $\dot{R} = r(I^a + I^s + Q + Q^s)$

Extension 2: With Expanded Quarantine

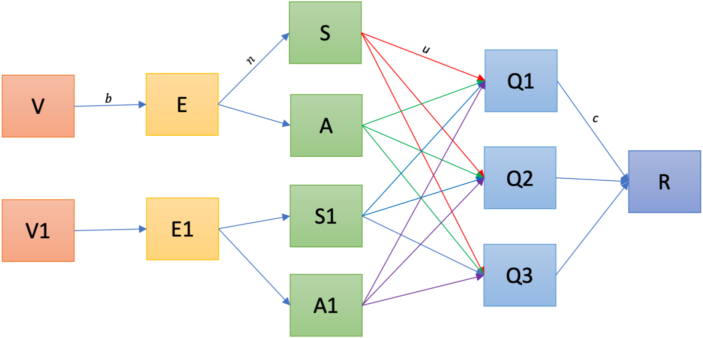


Extension 2: With Expanded Quarantine



- $\dot{S} = \frac{-k(1-m)S}{N}(I^s + I^a + XQ^{qa} + YQ^{qs})$
- $\dot{E} = \frac{k(1-m)S}{N}(I^s + I^a + XQ^s + YQ^{qs}) - iE$
- $\dot{I^a} = (1-p)iE - tI^a r(1-c) - r_a I^a$
- $\dot{I^s} = piE - (t+g)I^s(1-c) - r_s I^s$
- $\dot{Q} = w_a t I^a(1-c) + w_s t I^s(t+g)(1-c) - r_q Q$
- $\dot{Q^{qa}} = tI^a(1-w_a)(1-c) - r_{qa}Q^{qa}$
- $\dot{Q^{qs}} = I^s(1-w_s)(1-c)(t+g) - r_{qs}Q^{qs}$
- $\dot{R} = r_{qs}Q^{qs} + r_{qa}Q^{qa} + r_q Q + r_s I^s + r_a I^a$

Extension 3: With Vaccination Status



Extension 3: With Vaccination Status

- $\dot{V} = \frac{-b_1 VA - b_1 VS}{N_1}$
- $\dot{E} = \frac{b_1 VA + b_1 VS}{N_1} - nE$
- $\dot{S} = npE - u_{s1}S - u_{s2}S - u_{s3}S$
- $\dot{A} = n(1-p)E - u_{a1}A - u_{a2}A - u_{a3}A$
- $\dot{Q}1 = u_{a1}A + u_{s1}S + \tilde{u_{a1}}A1 + \tilde{u_{s1}}S1 - c_1 Q1$
- $\dot{Q}2 = u_{a2}A + u_{s2}S + \tilde{u_{a2}}A1 + \tilde{u_{s2}}S1 - c_1 Q2$
- $\dot{Q}3 = u_{a3}A + u_{s3}S + \tilde{u_{a3}}A1 + \tilde{u_{s3}}S1 - c_1 Q3$
- $\dot{R} = c_1 Q1 + c_1 Q2 + c_1 Q3$
- $\dot{V}1 = \frac{-b_2 V1A1 - b_2 V1S1}{N_2}$
- $\dot{E}1 = \frac{b_2 V1A1 + b_2 V1S1}{N_2} - nE1$
- $\dot{S}1 = nqE1 - \tilde{u_{s1}}S1 - \tilde{u_{s2}}S1 - \tilde{u_{s3}}S1$
- $\dot{A}1 = n(1-q)E1 - \tilde{u_{a1}}A1 - \tilde{u_{a2}}A1 - \tilde{u_{a3}}A1$

Analysis

Definition

R_0 (basic reproduction number) is the number of new cases directly caused by an individual's infectious period.

$F = \frac{kS}{N}(I^s - I^a)$, $V = (iE, -(1-p)iE + I^a r, -piE + I^s g + rI^s)$

$$\Rightarrow F = \begin{bmatrix} 0 & k & k \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{bmatrix}, V = \begin{bmatrix} i & 0 & 0 \\ -(1-p)i & r & 0 \\ -pi & 0 & r+g \end{bmatrix}$$

$$\Rightarrow V^{-1} = \begin{bmatrix} \frac{1}{i} & 0 & 0 \\ \frac{-(p-1)}{r} & \frac{1}{r} & 0 \\ \frac{p}{g+r} & 0 & \frac{1}{g+r} \end{bmatrix}$$

$$\Rightarrow F * V^{-1} = \begin{bmatrix} \frac{kp}{g+r} - \frac{k(p-1)}{r}) & \frac{k}{r} & \frac{k}{g+r} \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{bmatrix}$$

R_0 **for base model:**

$R_0 = R_0^1 + R_0^2$

$R_0^1 = \frac{kp}{g+r}$

$R_0^2 = \frac{k(1-p)}{r}$

$R_0 = \frac{kp}{g+r} + \frac{k(1-p)}{r}$

Analysis

R_0 **for Extension 1:**

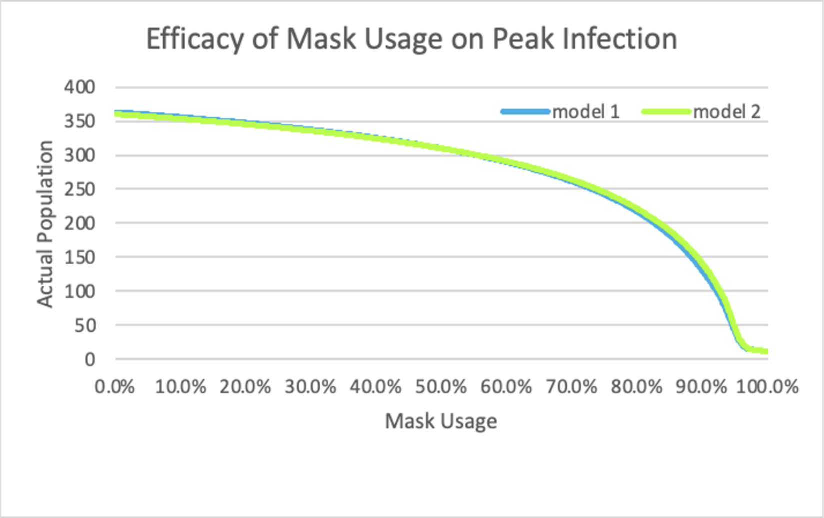
- $R_0 = R_0^1 + R_0^2 + R_0^3$
- $R_0^1 = \frac{(k(1-m)(1-p))}{t(1-c)+r}$
- $R_0^2 = \frac{(kp(1-m))}{(g+t)(1-c)+r}$
- $R_0^3 = \frac{(Xk(1-c)(1-m)(1-w)(t((g+t)(1-c)+r)+gpr)}{(r(1-c)+r)((g+t)(1-c)+r))}$
- $R_0 = \frac{(k(1-m)(1-p))}{t(1-c)+r} + \frac{(kp(1-m))}{(g+t)(1-c)+r} + \frac{(Xk(1-c)(1-m)(1-w)(t((g+t)(1-c)+r)+gpr)}{(r(1-c)+r)((g+t)(1-c)+r))}$

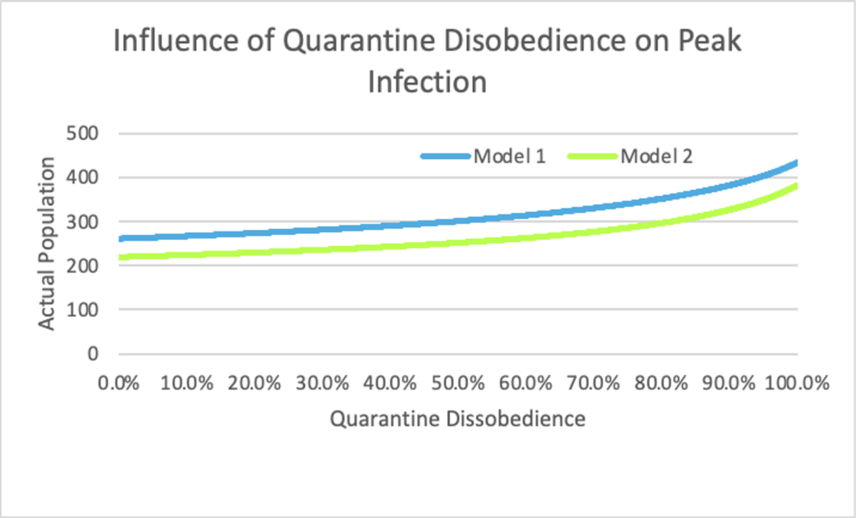
Analysis

R_0 **for Extension 2:**

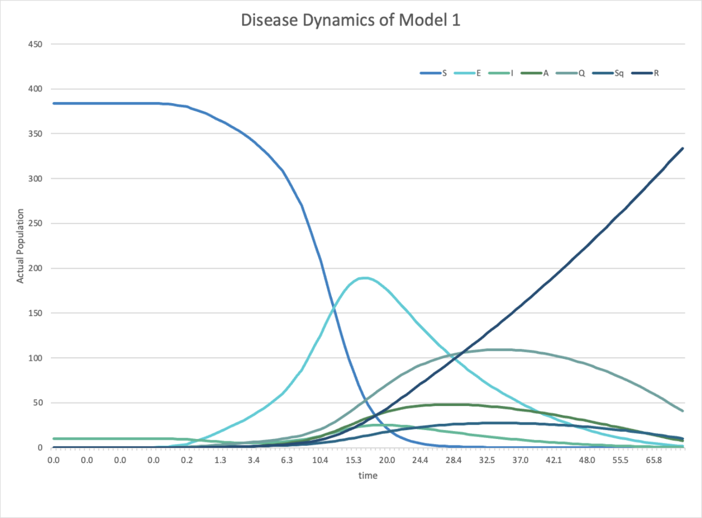
- $R_0 = R_0^1 + R_0^2 + R_0^3 + R_0^4$
- $R_0^1 = \frac{(k(1-m)(1-p))}{t(1-c)+r}$
- $R_0^2 = \frac{(kp(1-m))}{(g+t)(1-c)+r}$
- $R_0^3 = \frac{(Ykp(g+t)(1-c)(1-m)(1-w_s))}{(r_{qs}((g+t)(1-c)+r_s))}$
- $R_0^4 = \frac{(Xkt(1-c)(1-m)(1-p)(1-w_a))}{(r_{qa}(t(1-c)+r_a}$
- $R_0 = \frac{(k(1-m)(1-p))}{(t(1-c)+r_a)} + \frac{(kp(1-m))}{(g+t)(1-c)+r_s} + \frac{(Ykp(g+t)(1-c)(1-m)(1-w_s))}{(r_{qs}((g+t)(1-c)+r_s))} + \frac{(Xkt(1-c)(1-m)(1-p)(1-w_a))}{(r_{qa}(t(1-c)+r_a}$

Computational Results

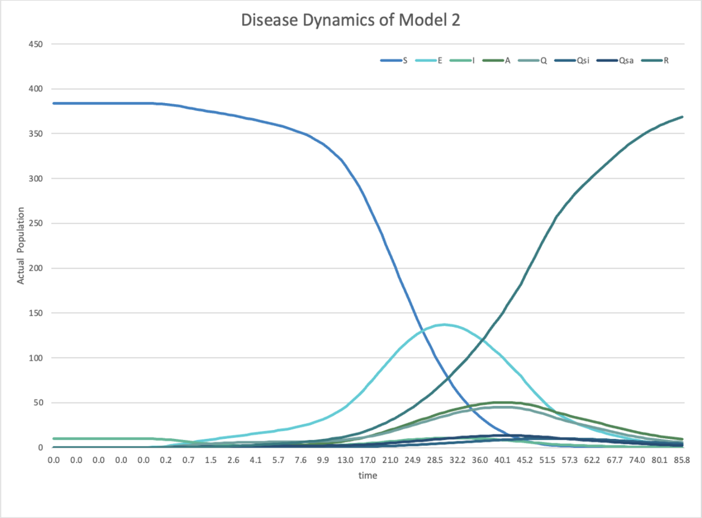



Influence of Quarantine Disobedience on Peak Infection
Model 1
Model 2
Actual Population
500
400
300
200
100
0
0.0%
10.0%
20.0%
30.0%
40.0%
50.0%
60.0%
70.0%
80.0%
90.0%
100.0%
Quarantine Dissobedience

Computational Results



Computational Results



Actual GMU Data Aug 15 - Dec 2

- About 94.5 percent of the Mason population is vaccinated while about 5.5 percent are not vaccinated or did not report their vaccination status
- There were an average of 24.7 new cases each week
- There were 395 total COVID-19 cases this semester at GMU
- Of those cases, 276 were vaccinated individuals, 71 were not vaccinated, and 48 had an unidentified vaccination status
- Roughly approximated, .008 percent of vaccinated people caught COVID while .038 percent of not vaccinated people caught COVID
- Of the cases that reported on symptomatic vs asymptomatic infection, 57 were symptomatic and 7 were asymptomatic

Conclusion

- Parameters unique to GMU must be represented in our models
- From analyzing the extensions of the SEIAQR model, we can predict the impact of various mitigation strategies on transmission to determine the best strategies for George Mason.
- Infection rate and mask usage are inversely proportional while infection rate and quarantine disobedience are directly proportional
- The R_0 value derived from Model 2 is 0.02015, which indicates a very low likelihood of an outbreak.

Future Work

- Improve the accuracy of our models by having them output the actual COVID data
- The vaccination model should be investigated further to better account for multiple types of quarantine and two recovery rates
- For a 3D visualization aspect, research on how to force chaos on a system like this one and a 3D printed solution could be profitable
- A software application could be developed for public use to study the effect of each of the parameters in an accessible way
- There is more to be studied such as social networking and proximity in epidemics to see if there is a better way to incorporate them
- The new variant, Omicron, might need to be accounted for

Acknowledgement

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References

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[3] Kermack, W. O., and McKendrick, A. G. (1927). A contribution to the mathematical theory of epidemics. Proceedings of the Royal Society of London. Series A, 115(772), 700-721.