Modeling and Analyzing the Transmission of COVID-19 at GMU

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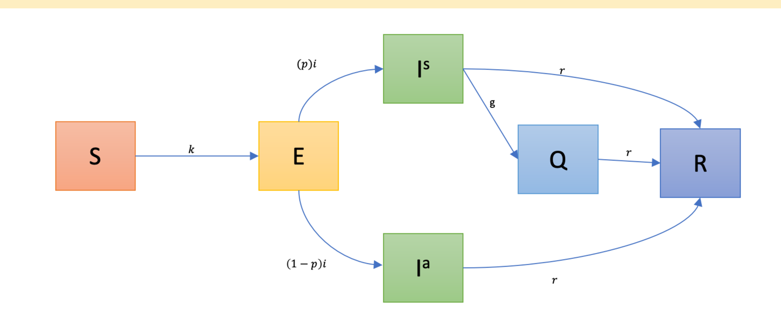
Abstract

This research project is a mathematical model that characterizes the spread of COVID-19 on the GMU campus. It is based on the SEIAQR epidemic model and focuses on the unique situation at George Mason. We take into account the effects of university's preventative measures by analyzing extensions of the SEIAQR model and their reproduction numbers. From this, we can determine how effective the university's guidelines are and better understand the transmission of COVID-19 for this type of environment.

Introduction

An SIR model captures how disease is transmitted by categorizing the disease's tendencies and quantifying the population's reaction. To model the transmission of COVID-19 at GMU, we started our research with a basic SEIAQR epidemic model. Our final model (Extended Model 3), uniquely accounts for vaccination status, a/symptomatic infection, and three different types of quarantine behavior. As the population flows through each of these categories, we consider parameters specific to GMU such as high mask usage, quarantine disobedience, and random testing. Finally, we used MATLAB to graph the affect of these parameters and analyze how they affect the population.



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

Deriving the Basic Reproduction Number R_0 [1, 2]

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

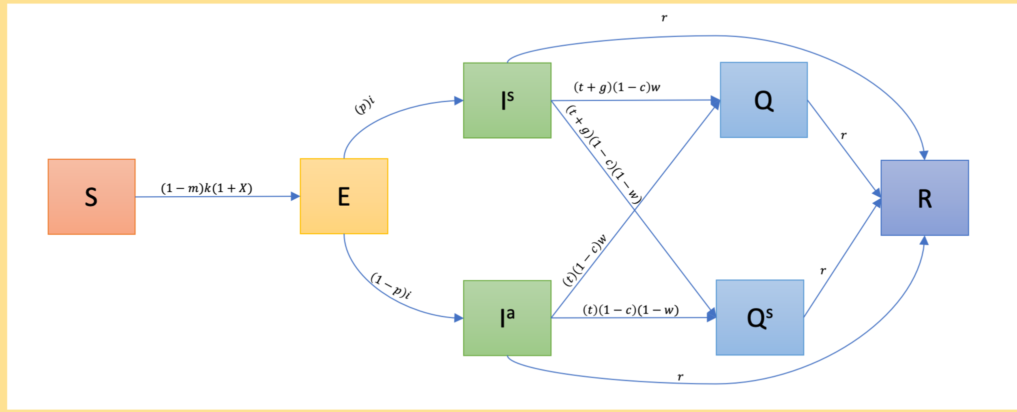
$$\Rightarrow F = \begin{bmatrix} 0 & k & k \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{bmatrix}, V = \begin{bmatrix} i & 0 & 0 \\ -(1-p)i & r & 0 \\ -pi & 0 & r+g \end{bmatrix}$$

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

R_0 for base model:

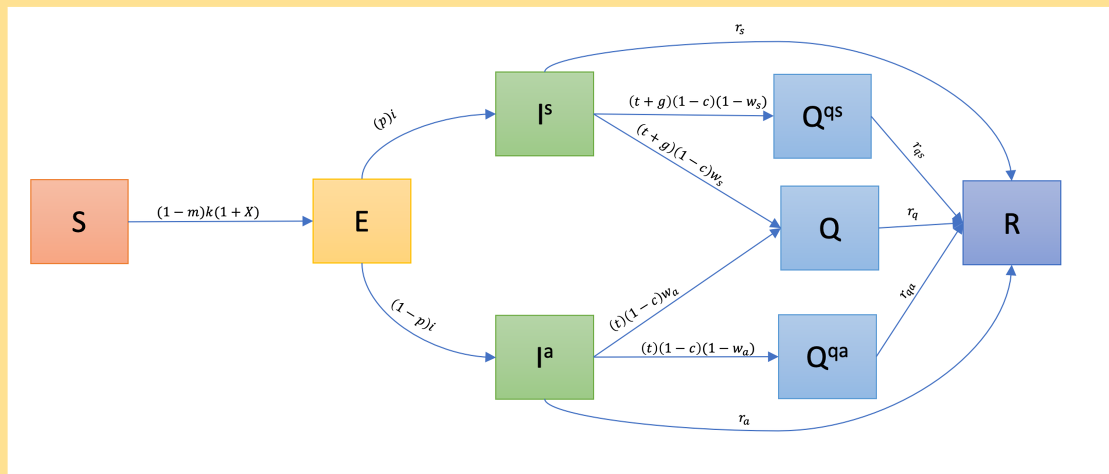
$$R_0 = R_0^1 + R_0^2$$
$$R_0^1 = \frac{kp}{g+r}$$
$$R_0^2 = \frac{k(1-p)}{r}$$
$$R_0 = \frac{kp}{g+r} + \frac{k(1-p)}{r}$$

Extended Model 1: SEIAQR with Semi Quarantine



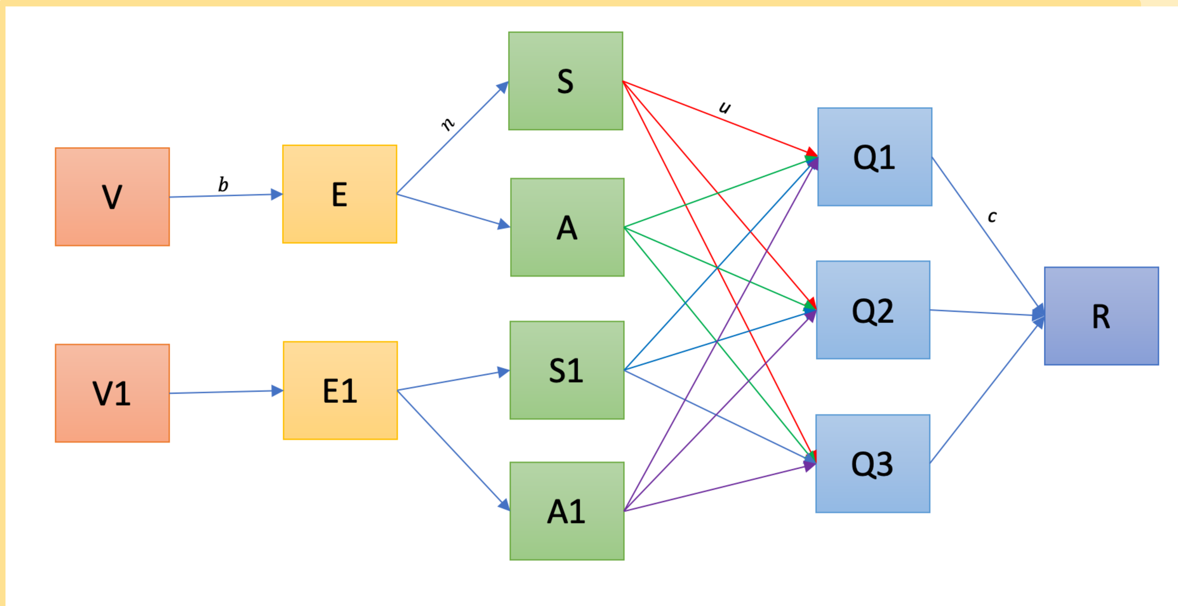
- $\dot{S} = \frac{-k(1-m)S}{N}(I^s + I^a + XQ^s)$
- $\dot{E} = \frac{k(1-m)S}{N}(I^s + I^a + XQ^s) - iE$
- $\dot{I}^a = (1-p)iE - tI^a r(1-c) - rI^a$
- $\dot{I}^s = piE - (t+g)I^s(1-c) - rI^s$
- $\dot{Q} = w(1-c)(I^s(t+g) + I^a t - rQ$
- $\dot{Q}^s = (1-w)(1-c)(I^s(t+g) + I^a t) - rQ^s$
- $\dot{R} =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

Extended Model 2: SEIAQR with Expanded Quarantine



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

Extended Model 3: SEIAQR with Vaccination Status



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

R_0 for the Extended Models

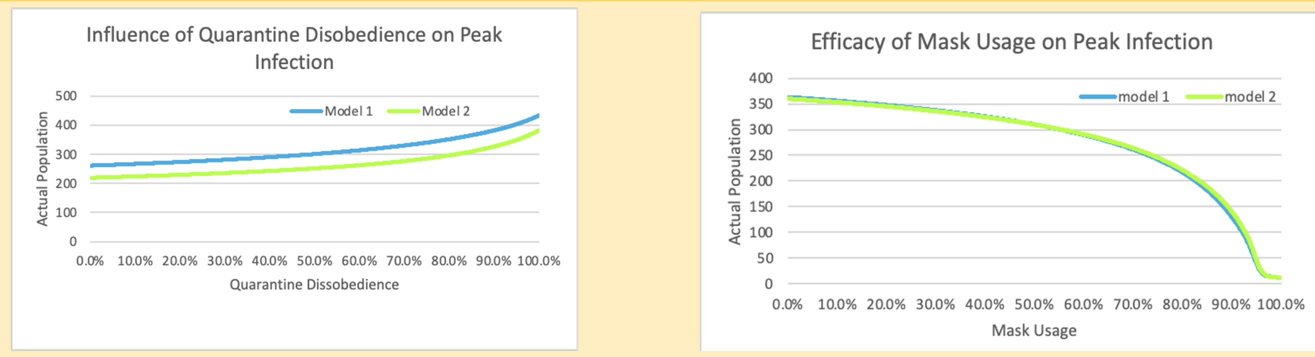
R_0 for Extension 1:

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

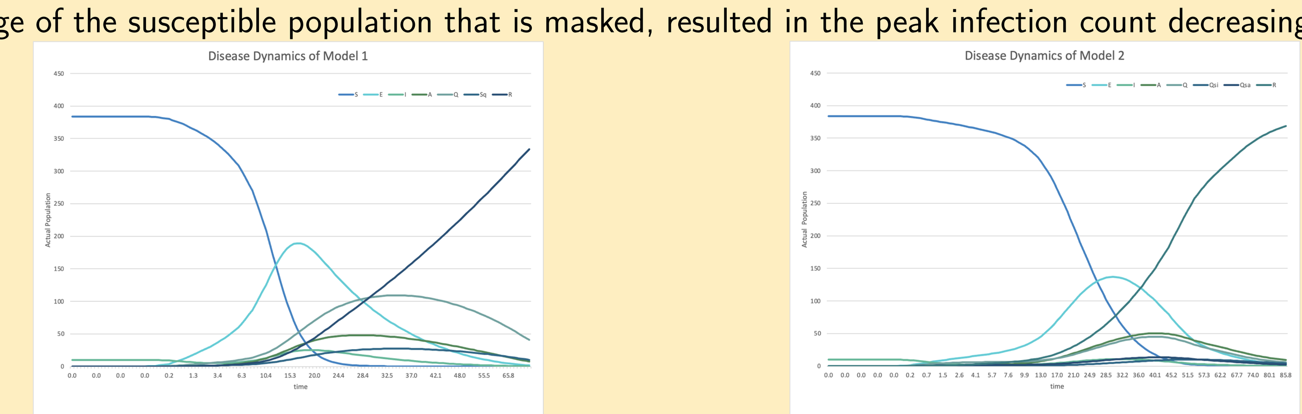
R_0 for Extension 2:

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

Computational Results



(Left) As quarantine disobedience is increased, the peak infection rate increases. (Right) Increasing m, the percentage of the susceptible population that is masked, resulted in the peak infection count decreasing



(Left) SEIAQR with Semi Quarantine. (Right) SEIAQR with Expanded Quarantine.

Conclusion

Here we have introduced three new mathematical models for understanding the transmission of COVID-19 within a university campus environment. The basic reproduction number for each the models have been computed and they each tell us that it is unlikely for an outbreak to occur in this environment. The efficacy of our parameters has been computationally studied and from that we know that the university's preventative measures are working.

- The reproduction number for Model 2 is .02015, which indicates that an outbreak is very unlikely. In order to reduce the likelihood of an outbreak even further, mitigation strategies such as mask use should be increased and quarantine disobedience should be decreased.
- Understanding the effects of each of these strategies will inform other Universities how the guidelines that GMU has implemented would affect the transmission of COVID-19 and allow them to enforce their own preventative measures.

Future Work

- Model 3 will account for quarantine affecting the susceptible population
- We would like to 3D print Model 3's solution
- An application will be developed to study our parameters in more detail
- Networking and proximity will be better accounted for

References

[1]Brauer, F., Castillo-Chavez, C. C. Castillo-Chavez, Mathematical models in population biology and epidemiology, Vol. 2, Springer, 2012.

[2] Diekmann, O., Heesterbeek, J. A. P., Metz, J.A., On the definition and the135 computation of the basic reproduction ratio r 0 in models for infectious diseases in heterogeneous populations, Journal of mathematical biology 28 (4) (1990) 365–382.

[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.