Infectious Disease Modeling

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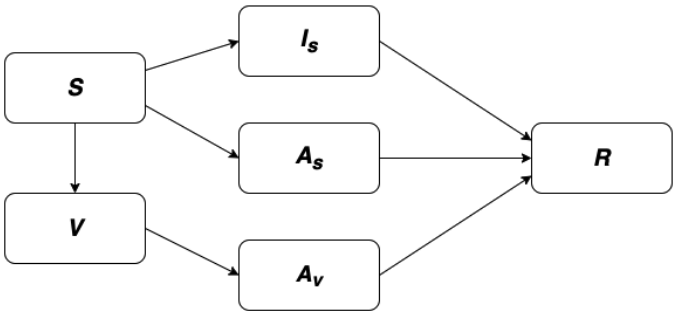
As part of the UW Statistics and Probability Association's Directed Reading Program, I explored how we can use SIR compartmental models to predict future trends for infectious disease with my mentor Anna Neufeld. We were motivated by the current COVID-19 pandemic, especially new upcoming variants we have little knowledge about such as the Delta variant. This pandemic has drastically changed many aspects of our lives, and a return to some sense of normalcy is something many are looking forward to. But how do these new variants affect that? Does the vaccine still work or is it more contagious than past variants? Considering the above, we wanted to see how different scenarios of Delta variant virulency and vaccine efficacy would impact the proportion of people who need to be vaccinated to control the spread, how many contacts people could have per day, and what proportion of people would need to wear masks. While these variables do not represent all that impacts COVID-19 spread, looking at a few variables that do play a role and controlling for others allowed us to see data trends in the face of uncertainty. These trends were then developed in RStudio through ggplot. Through the duration of this modeling project, little was known about the Delta variant, however, recent news suggests that vaccines are slightly less effective against the delta variant than previous variants.

This program has been indispensable for developing my technical skills in a field I aim to pursue in the future. Having only taken a few statistics courses before starting this program, I was worried that I may have bitten off more than I can chew, but my mentor, Anna, was incredibly supportive and accommodating and worked with me where I am at instead of where I thought I should be. Through the duration of this program, I was able to comprehend academic papers on SIR compartmental models, develop differential equations that fit the simulation I was developing, and also practice my applied math and statistical skills through RStudio. With Anna's guidance, we developed the below compartmental model:



Here, we modeled a closed population with differential equations to model movement between each compartment. We added three boxes onto a basic SIR model, V(Vaccinated), A_s

(Asymptomatic non-vaccinated), and A_v (Asymptomatic vaccinated). The differential equations that modeled movement from each box were as the following:

$$\frac{dS}{dt} = -vS - \sum_{i=1}^{4} \beta_{iI} I_i S - \sum_{i=1}^{4} \beta_{iA} A_{Vi} V$$

$$\frac{dI_i}{dt} = p_{iS}(\beta_{iI} I_i S + \beta_{iA} A_{iS} S) + p_{iV}(1-\alpha_i)(\beta_{iI} I_i V + \beta_{iA} A_s V) - \gamma I_i$$

$$\frac{dAs_i}{dt} = (1-\alpha_i)(\beta_{iI} I_i S + \beta_{iA} A_s V) - \gamma A_{si}$$

$$\frac{dV}{dt} = vS - \sum_{i=1}^{4} (1-\alpha_i)\beta_{iA} A_{vi} V$$

Through the above, we were able to run simulations that showcased infection spread for four different scenarios for the Delta variant, and found lower vaccine efficacy to be more closely associated with a need for a higher vaccine threshold for a constant mask compliance and contact rate. I thank my mentor, Anna, for guiding me through SIR modeling and assisting me throughout the duration of this project. I was able to learn a multitude of skills I will utilize in my future endeavors and feel more confident in my ability to apply my newfound knowledge to future infection spread.