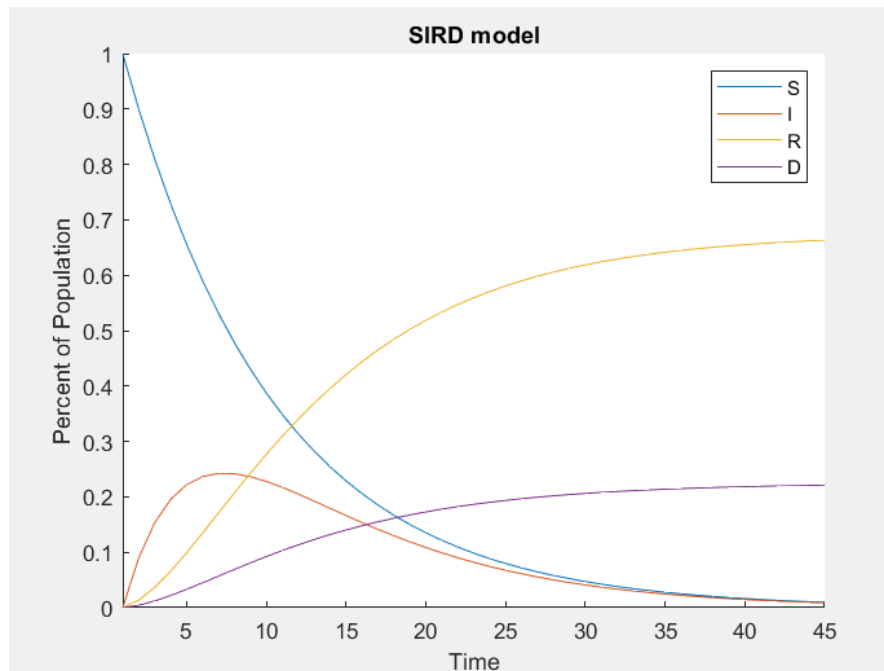
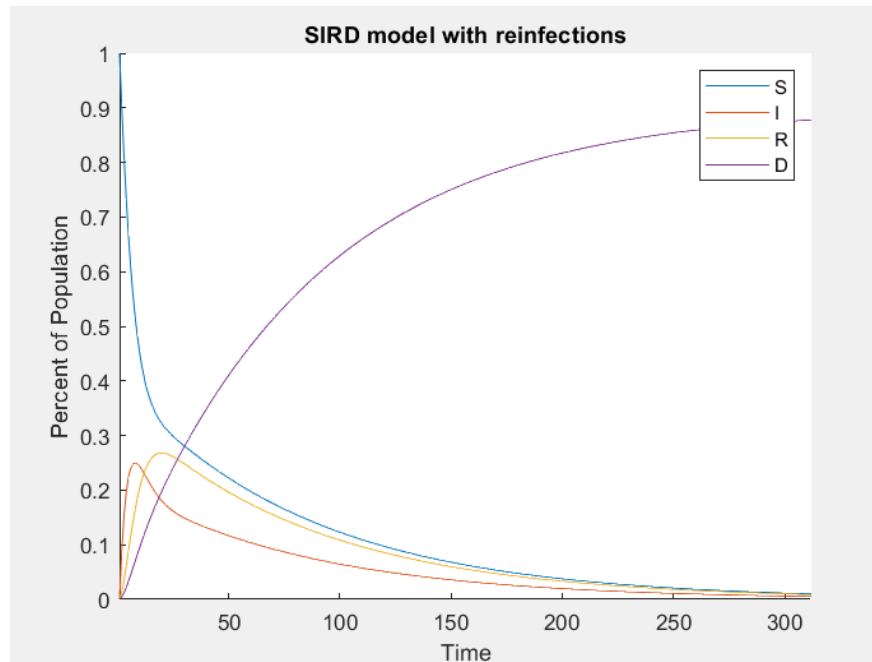


In creating our basic SIRD model for part 1, we managed to create a set of data which shows how a disease spreads through a population.

In the figure below, we can see the plotting of this data. As we can see, the susceptible population declines over time based on how many of the susceptible individuals remain. Our infected population hits its peak early on, and sees a slow decline. The recovered and dead population see a rapid gain in the beginning, but this slows down as the susceptible and infected population declines.

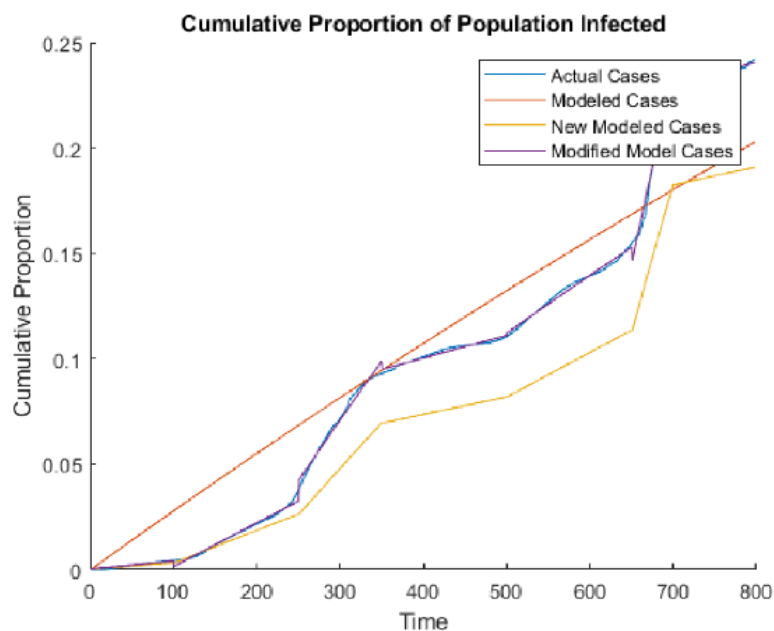


In our next figure, we see the plotting of a modified version of this data. It has been modified to allow for recovered individuals to return to the susceptible population. As we can see this results in the recovered population to follow a similar curve to the infected population, and the dead population eventually overtakes all other populations.

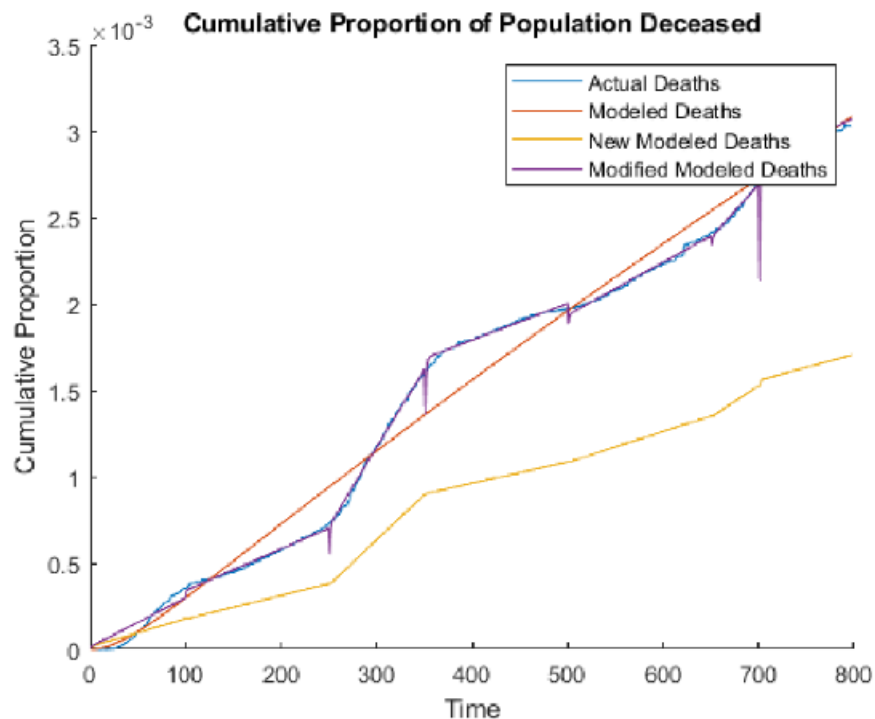


For part 2, we took real data and processed it through an SIRD model.

The figure below shows us our different methods of plotting against the infected population. As we can see our base model encompassing all the data comes out to be a linear dataset, our modified model based on Covid-19 waves is nearly identical to the base data, and our policy data sees a comfortable 25% reduction in infections over time.



The next figure shows the plot of our deceased population. As we can see we have very similar results compared to the infection plot. Actual deaths and segmented model deaths are nearly identical, the model encompassing all the data is still linear, and the policy data still has a 25% reduction. The only problem with this data is a fair few number of errors that plague the segmented data. The connection points between the different segments did not translate well into our SIRD model. It is a limitation of our data. With the results being so small, any little inconsistency can produce significant errors, and in our case, we saw it happen with the connection points of the segments.



For part 3, we were presented with a challenge. Plot the percentage of vaccinated population and the number of breakthrough infections while only knowing the number of infections and total deaths.

From our plot below we can see our predictions for this expected data, as we can see we have very few breakthrough infections, but we hit a limitation. We were unable to determine the percentage of vaccinated individuals because of time constraints

