A Pair Formation Model with Vaccination and Varying Risk for Mpox

BY

Lauren Farrell

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Abstract

Mpox is a disease related to smallpox and cowpox which is endemic in central and west Africa and has been spreading globally since a novel outbreak began in May of 2022. This outbreak is mainly concentrated in men who have sex with men and is transmitted through close prolonged contact. We consider distinct high risk and low risk groups which can interact with one another and extend a pair formation model with recovery designed for mpox in order to incorporate these different risk levels, as well as the possibility of vaccination. We show that most infections in an outbreak are within the high risk group and the maximum infected individuals can be best minimized by focusing on vaccinating the high risk group.

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First I would like to thank Dr. Matt Betti for sharing his knowledge, support, and guidance while supervising this project. Also for his overwhelming encouragement and generosity throughout my degree. His presence at Mount Allison has fundamentally changed my academic trajectory and has allowed me to find a passion for a topic I did not know existed before meeting him.

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1 Introduction

The global outbreak of mpox has resulted in novel transmission patterns when compared to historic behaviour of mpox, as well as other diseases. Mpox is a disease caused by the monkeypox virus, a member of the orthopoxvirus genus, which also includes smallpox and cowpox [1]. Characteristics of a monkeypox infection include a rash, often with lesions on the soles of the feet and palms of the hands [2], as well as fever and headache [3], with infection lasting up to four weeks [2]. The first human mpox case was reported in Democratic Republic of the Congo in 1970 [2]. As a zoonic disease, mpox spreads between animals and humans [2]. The reservoir species of mpox is unknown but contact with infected animals, living or dead, is thought to be the main driver of mpox in endemic regions [2] of west and central Africa [2]. The disease can also spread human-to-human, with this type of transmission occurring through direct contact with skin or lesions, respiratory droplets, or indirect contact from contaminated objects [4]. There are two strains of monkeypox; The Congo Basin Clade which is associated with a higher fatality rate at about 10% and higher human-to-human transmission, and the West African Clade which has a case fatality rate under 1% [1].

As a result of their similarity, the smallpox vaccine provides cross-protection for vaccinated individuals against other orthopoxviruses, including mpox [5], with the effectiveness of the smallpox vaccine in preventing mpox in humans being about 85% [1]. Therefore, the smallpox eradication efforts created widespread protection against mpox. The eradication of smallpox in the 1980s ended this vaccination program, additionally discontinuing the widespread vaccination against mpox. This caused an increase in mpox cases, as well as a buildup of susceptible individuals [2].The inci-

dence of mpox is currently 20 times higher than it was in 1986 [1]. This was considered in the discontinuation of smallpox vaccination, with most models at the time predicting that any outbreaks would be insignificant [1]. This has been true in other outbreaks in non-endemic regions. In 2003 an importation of mpox infected prairie dogs into the United States which were sold as pets caused the first incidence of human mpox outside of Africa and did not lead to a major outbreak [6].

The ongoing global outbreak of mpox has deviated from the pattern of former outbreaks in that it has spread further and more sustained. Additionally, transmission has largely been contained within the community of men who have sex with men (MSM) [7]. As of March 2023, 96.4% of cases with known data were in men, and 84.2% of cases with reported sexual orientation were among men who have sex with men [4]. Further, 68.0% of reported exposure settings are party environments involving sexual contact [4] which suggests that within the MSM community there is varying risk of exposure. However, household exposure has increased as an exposure setting from 10% of reported exposure sites to 22% [4].

In general, mathematical modeling allows us to consider a system in a simplified way and analyze it using mathematical tools. In the case of epidemiological modeling, this can give quick insight into political decision making in newly emerging or quickly changing outbreak situations as it does not require the time, space, or equipment necessary for other avenues to information. One foundational model in mathematical epidemiology is a compartmental model which considers a population as being categorized into different compartments and describes how individuals move from one compartment into another. One of the most basic examples of a categorical model is an SIR model. In this case, the population is broken down into those who are susceptible to the disease, meaning they are able to become

infected, those who have contracted the illness and can pass it on to others who are considered infected, and those who cannot become infected and cannot infect others who are categorized as recovered. In the SIR model the population is assumed to be well mixed and the disease is assumed to transmit through random interactions within the population.

In the case of mpox, the global outbreak is not behaving this way. Instead, it is spreading through close, prolonged contact, and is better modeled through pair formation [8]. In this model, an susceptible individual can only become infected by forming a pair with an infected person and contracting the disease while in that pair [9]. In the case of sexually transmitted infections, most infections are chronic, meaning people who become infected remain infected, or have the possibility of becoming immediately re-infected without any immunity inherited from being ill [10]. However, people who recover from mpox have been shown to have immunity to being re-infected, which necessitates a pair formation model with recovery, as developed by [10]. This model, however, does not take into account the evident distinction between high and low risk members of the MSM community, or the possibility of vaccination.

In situation of novel spread of illness it is important to consider how the spread can be controlled and limited through public health measures. This is especially true in cases like mpox where a vaccine is available. The implementation of these measures can be optimized with the development of a thorough understanding of transmission. Since mpox transmits through pair formation, it is important to understand how the disease is spreading as different risk levels within the MSM community to understand how to best implement vaccination. An understanding for what strategy is best to use can be found through mathematical modeling. One crucial number in developing an understanding of the spread of an illness is the basic

reproduction number, referred to as R_0. The basic reproduction number describes how many new infection will be created by one infected person while they are infectious, and serves as a threshold value where if $R_0 > 1$, disease can always invade the population [11]. In situations such as that occurring with mpox where there is an identifiable high and low risk group within a population, the calculation of a basic reproduction number, and therefore of a vaccination rate, becomes more complex. In idea of optimal vaccination rates can also be found numerically by determining how different vaccination rates within the high and low risk populations affect disease prevalence.

2 The Model

This model extends the pair formation model with recovery developed by [10] by dividing the individual and paired compartments into high and low risk groups, with the possibility of pairs forming within the same risk group, and between the two. Additionally, the model allows for vaccination which results in the transition from the susceptible compartment, directly to the recovered compartment. The set of equations for both low and high risk groups as well as their interactions are:

`Low risk population`

$$\frac{\mathrm{d}S}{\mathrm{d}t} = B - (\mu + \rho + p)S + \sigma(2P_{SS} + P_{SI} + P_{SR} + k_1(P_{S\hat{S}} + P_{S\hat{I}} + P_{S\hat{R}})) + \mu(2P_{SS} + P_{SI} + P_{SR} + P_{S\hat{S}} + P_{S\hat{I}} + P_{S\hat{R}}) - \nu S$$

$$\begin{aligned}
\frac{\mathrm{d}I}{\mathrm{d}t} &= -(\mu+\rho+p+\delta)I + \sigma(2P_{II}+P_{SI}+P_{IR}+k_1(P_{\hat{S}I}+P_{I\hat{R}}+P_{\hat{I}I})) \\
&\quad + \mu(2P_{II}+P_{SI}+P_{IR}+P_{\hat{S}I}+P_{I\hat{R}}+P_{\hat{I}I}) \\
\frac{\mathrm{d}R}{\mathrm{d}t} &= \delta I - (\mu+\rho+p)R + \sigma(2P_{RR}+P_{SR}+P_{IR}+k_1(P_{R\hat{R}}+P_{\hat{S}R}+P_{\hat{I}R})) \\
&\quad + \mu(2P_{RR}+P_{SR}+P_{IR}+P_{R\hat{R}}+P_{\hat{S}R}+P_{\hat{I}R}) + \nu S \\
\frac{\mathrm{d}P_{SS}}{\mathrm{d}t} &= \frac{1}{2}\rho\frac{S^2}{N} - (\sigma+2\mu)P_{SS} - 2\nu P_{SS} \\
\frac{\mathrm{d}P_{SI}}{\mathrm{d}t} &= \rho(1-h)\frac{SI}{N} - (\sigma+\phi h+2\mu+\delta)P_{SI} - \nu P_{SI} \\
\frac{\mathrm{d}P_{II}}{\mathrm{d}t} &= \frac{1}{2}\rho\frac{I^2}{N} + \rho h\frac{SI}{N} + \phi h P_{SI} - (\sigma+2\mu+2\delta)P_{II} \\
\frac{\mathrm{d}P_{SR}}{\mathrm{d}t} &= \delta P_{SI} + \rho\frac{SR}{N} - (\sigma+2\mu)P_{SR} + \nu(2P_{SS}-P_{SR}) \\
\frac{\mathrm{d}P_{IR}}{\mathrm{d}t} &= \rho\frac{IR}{N} + 2\delta P_{II} - (\sigma+2\mu-\delta)P_{IR} + \nu P_{SI} \\
\frac{\mathrm{d}P_{RR}}{\mathrm{d}t} &= \delta P_{IR} + \frac{1}{2}\rho\frac{R^2}{N} + \nu P_{SR} - (\sigma+2\mu)P_{RR}
\end{aligned}$$

`High risk population`

$$\begin{aligned}
\frac{\mathrm{d}\hat{S}}{\mathrm{d}t} &= \hat{B} - (\mu+\hat{\rho}+p)\hat{S} + \sigma(k_1(P_{S\hat{S}}+P_{\hat{S}I}+P_{\hat{S}R}) + k_2(2P_{\hat{S}\hat{S}}+P_{\hat{S}\hat{I}}+P_{\hat{S}\hat{R}})) \\
&\quad + \mu(P_{S\hat{S}}+P_{\hat{S}I}+P_{\hat{S}R}+2P_{\hat{S}\hat{S}}+P_{\hat{S}\hat{I}}+P_{\hat{S}\hat{R}}) - \hat{\nu}\hat{S} \\
\frac{\mathrm{d}\hat{I}}{\mathrm{d}t} &= -(\mu+\hat{\rho}+p+\delta)\hat{I} + \sigma(k_1(P_{\hat{I}I}+P_{S\hat{I}}+P_{\hat{I}R}) + k_2(2P_{\hat{I}\hat{I}}+P_{\hat{S}\hat{I}}+P_{\hat{I}\hat{R}})) \\
&\quad + \mu(P_{\hat{I}I}+P_{S\hat{I}}+P_{\hat{I}R}+2P_{\hat{I}\hat{I}}+P_{\hat{S}\hat{I}}+P_{\hat{I}\hat{R}}) \\
\frac{\mathrm{d}\hat{R}}{\mathrm{d}t} &= \delta\hat{I} - (\mu+\hat{\rho}+p)\hat{R} + \sigma(k_1(P_{R\hat{R}}+P_{S\hat{R}}+P_{I\hat{R}}) + k_2(P_{\hat{S}\hat{R}}+P_{\hat{I}\hat{R}}+2P_{\hat{R}\hat{R}})) \\
&\quad + \mu(P_{R\hat{R}}+P_{S\hat{R}}+P_{I\hat{R}}+P_{\hat{S}\hat{R}}+P_{\hat{I}\hat{R}}+2P_{\hat{R}\hat{R}}) + \hat{\nu}\hat{S} \\
\frac{\mathrm{d}P_{\hat{S}\hat{S}}}{\mathrm{d}t} &= \frac{1}{2}\hat{\rho}\frac{\hat{S}^2}{\hat{N}} - (k_2\sigma+2\mu)P_{\hat{S}\hat{S}} - 2\hat{\nu}P_{\hat{S}\hat{S}} \\
\frac{\mathrm{d}P_{\hat{S}\hat{I}}}{\mathrm{d}t} &= \hat{\rho}(1-h)\frac{\hat{S}\hat{I}}{\hat{N}} - (k_2\sigma+\hat{\phi}h+2\mu+\delta)P_{\hat{S}\hat{I}} - \hat{\nu}P_{\hat{S}\hat{I}} \\
\frac{\mathrm{d}P_{\hat{I}\hat{I}}}{\mathrm{d}t} &= \frac{1}{2}\hat{\rho}\frac{\hat{I}^2}{\hat{N}} + \hat{\rho}h\frac{\hat{S}\hat{I}}{\hat{N}} + \hat{\phi}hP_{\hat{S}\hat{I}} - (k_2\sigma+2\mu+2\delta)P_{\hat{I}\hat{I}}
\end{aligned}$$

$$\frac{\mathrm{d}P_{\hat{S}\hat{R}}}{\mathrm{d}t} = \delta P_{\hat{S}\hat{I}} + \hat{\rho}\frac{\hat{S}\hat{R}}{\hat{N}} - (k_2\sigma + 2\mu)P_{\hat{S}\hat{R}} + \hat{\nu}(2P_{\hat{S}\hat{S}} - P_{\hat{S}\hat{R}})$$
$$\frac{\mathrm{d}P_{\hat{I}\hat{R}}}{\mathrm{d}t} = \hat{\rho}\frac{\hat{I}\hat{R}}{\hat{N}} + 2\delta P_{\hat{I}\hat{I}} - (k_2\sigma + 2\mu + \delta)P_{\hat{I}\hat{R}} + \hat{\nu}P_{\hat{S}\hat{I}}$$
$$\frac{\mathrm{d}P_{\hat{R}\hat{R}}}{\mathrm{d}t} = \delta P_{\hat{I}\hat{R}} + \frac{1}{2}\hat{\rho}\frac{\hat{R}^2}{\hat{N}} + \hat{\nu}P_{\hat{S}\hat{R}} - (k_2\sigma + 2\mu)P_{\hat{R}\hat{R}}$$

Mixing partnerships

$$\frac{\mathrm{d}P_{S\hat{S}}}{\mathrm{d}t} = p\frac{S\hat{S}}{N} - (k_1\sigma + 2\mu)P_{S\hat{S}} - (\hat{\nu} + \nu)P_{S\hat{S}}$$
$$\frac{\mathrm{d}P_{S\hat{I}}}{\mathrm{d}t} = p(1-h)\frac{S\hat{I}}{\hat{N}} - (k_1\sigma + 2\mu + \tilde{\phi}h + \delta)P_{S\hat{I}} - \nu P_{S\hat{I}}$$
$$\frac{\mathrm{d}P_{\hat{S}I}}{\mathrm{d}t} = p(1-h)\frac{\hat{S}I}{N} - (k_1\sigma + 2\mu + \tilde{\phi}h + \delta)P_{\hat{S}I} - \hat{\nu}P_{\hat{S}I}$$
$$\frac{\mathrm{d}P_{I\hat{I}}}{\mathrm{d}t} = p\frac{\hat{I}I}{N} + ph\frac{\hat{S}I}{N} + ph\frac{S\hat{I}}{\hat{N}} + \tilde{\phi}h(P_{\hat{S}I} + P_{S\hat{I}}) - (k_1\sigma + 2\mu + 2\delta)P_{I\hat{I}}$$
$$\frac{\mathrm{d}P_{\hat{S}R}}{\mathrm{d}t} = \delta P_{\hat{S}I} + p\frac{\hat{S}R}{N} - (k_1\sigma + 2\mu)P_{\hat{S}R} + \nu P_{S\hat{S}} - \hat{\nu}P_{\hat{S}R}$$
$$\frac{\mathrm{d}P_{S\hat{R}}}{\mathrm{d}t} = \delta P_{S\hat{I}} + p\frac{S\hat{R}}{\hat{N}} - (k_1\sigma + 2\mu)P_{S\hat{R}} + \hat{\nu}P_{S\hat{S}} - \nu P_{S\hat{R}}$$
$$\frac{\mathrm{d}P_{\hat{I}R}}{\mathrm{d}t} = p\frac{\hat{I}R}{\hat{N}} + \delta P_{I\hat{I}} - (k_1\sigma + 2\mu + \delta)P_{\hat{I}R} + \nu P_{S\hat{I}}$$
$$\frac{\mathrm{d}P_{I\hat{R}}}{\mathrm{d}t} = p\frac{I\hat{R}}{N} + \delta P_{I\hat{I}} - (k_1\sigma + 2\mu + \delta)P_{I\hat{R}} + \hat{\nu}P_{\hat{S}I}$$
$$\frac{\mathrm{d}P_{R\hat{R}}}{\mathrm{d}t} = p\frac{R\hat{R}}{N} + \delta(P_{I\hat{R}} + P_{\hat{I}R}) + \hat{\nu}P_{\hat{S}R} + \nu P_{S\hat{R}} - (k_1\sigma + 2\mu)P_{R\hat{R}}$$

With S, I, and R denoting the low risk susceptible, infectious, and recovered individuals respectively and $\hat{S}$, $\hat{I}$, and $\hat{R}$ denoting the high risk susceptible, infectious, and recovered individuals. The pairs formed are identified by the combination of individuals presented in the subscript. For example, $P_{R\hat{R}}$ represents the pairs comprised of one low risk recovered in-

dividual and one recovered high risk individual. The parameters for this model are given in the following table:

Parameter	Description	Value if Fixed	Reference
B	Recruitment into low risk population	μ	
$\hat{B}$	Recruitment into high risk population	μ	
μ	Removal from the population	0	[10]
ρ	Low risk pair formation rate		
$\hat{\rho}$	High risk pair formation rate		
p	Mixed pair formation rate		
ν	Low risk vaccination rate		
$\hat{\nu}$	High risk vaccination rate		
σ	Low risk pair dissolution rate		
δ	Infection recovery rate	$\frac{1}{30}$	[12]
h	Probability of transmission		
k_1	Mixed pairing shape parameter		
k_2	High risk shape parameter		
ϕ	Contact rate within low risk partnership		
$\hat{\phi}$	Contact rate within high risk partnership		
$\tilde{\phi}$	Contact rate within mixes partnership		

Table 1: Table of model parameters and their interpretations

This model assumes that pairs are monogamous and that if one individual in a pair is removed, the other individual is returned to the single category and may make other pairs.

The equation for the total number of infections is given by:

$$T = I + \hat{I} + 2P_{\hat{I}I} + P_{S\hat{I}} + P_{\hat{I}R} + 2P_{\hat{I}\hat{I}} + P_{\hat{S}\hat{I}} + P_{\hat{I}\hat{R}} + 2P_{II} + P_{SI} + P_{IR}$$

$$\begin{aligned}\frac{\mathrm{d}T}{\mathrm{d}t} = &-\mu(I) - \rho(I) - pI - \delta(I) + \rho\frac{I^2}{N} + \rho(h)\frac{SI}{N} + \phi(h)P_{SI} - 2\mu(P_{II}) - s\delta(P_{II}) + \rho\frac{SI}{N} + \delta(P_{SI}) \\ &- \mu(P_{SI}) + \rho\frac{IR}{N} - \mu(P_{IR}) + \delta(P_{IR}) + p\frac{\hat{S}I}{N} - \mu(P_{\hat{S}I}) - \delta(P_{\hat{S}I)} + p\frac{I\hat{R}}{\hat{N}} - \mu(P_{I\hat{R}}) - \delta(P_{I\hat{R}}) \\ &+ 2p\frac{\hat{I}I}{N} + ph\frac{S\hat{I}}{\hat{N}} + \tilde{\phi}h(P_{S\hat{I}}) - 2\mu(P_{I\hat{I}}) - 2\delta(P_{I\hat{I}}) - \mu(\hat{I}) - \hat{\rho}\hat{I} - p\hat{I} - \delta\hat{I} + \hat{\rho}\frac{(\hat{I})^2}{\hat{N}} + \hat{\rho}h\frac{\hat{S}\hat{I}}{\hat{N}} \\ &+ \tilde{\phi}h(P_{\hat{S}\hat{I}}) - 2\mu(P_{\hat{I}\hat{I}}) - 2\delta(P_{\hat{I}\hat{I}}) + p\hat{h}i\frac{\hat{I}\hat{S}}{\hat{N}} - \mu(P_{\hat{S}\hat{I}}) - \delta(P_{\hat{S}\hat{I}}) + \hat{\rho}\frac{\hat{I}\hat{R}}{\hat{N}} - \mu(P_{\hat{I}\hat{R}}) + \delta(P_{\hat{I}\hat{R}}) \\ &+ p\frac{S\hat{I}}{\hat{N}} - \mu(P_{S\hat{I}}) + \delta(P_{S\hat{I}}) + p\frac{\hat{I}R}{N} - \mu(P_{\hat{I}R}) - \delta(P_{\hat{I}R}) + p(h\frac{I\hat{S}}{N}) + \tilde{\phi}h(P_{\hat{S}I})\end{aligned}$$

3 Methods

The Next Generation Matrix approach considers a disease free equilibrium and states that the basic reproduction number is equal to the eigenvalue with the spectral radius, or highest magnitude eigenvalue, of FV^{-1} where F is a jacobian matrix of the terms from infected classes which represent the creation of new infections and $-V$ is the jacobian matrix of all other terms in infected classes [11]. In this case those classes were determined to be $I, \hat{I}, P_{S\hat{I}}, P_{\hat{S}I}, P_{I\hat{I}}, P_{SI}, P_{\hat{S}\hat{I}}, P_{\hat{I}\hat{I}}, P_{II}$, and T. The calculations were done using Maple 2021.

Numerical analysis of the model was done in Python using scipi's odeint. First, the model was verified by considering the high risk parameters as being equivalent to the low risk parameters modified by a scalar k. A simulation with k set to one and no mixed risk pairs was then compared with a model that only considers one risk level to verify that they gave the same results. The initial conditions given reflected those used in [10] with the initial susceptible population being 902.56, initial infected individuals being 16.97, and initial susceptible-infected pairs being 145.96 for both high and

low risk groups. All parameter values followed those given in Table 1 with the non-constant parameters being sampled from a Latin hypercube. The resulting high and low risk values were summed and compared with a model that only considered one risk group and had doubled initial conditions.

Next, k was set to be some value greater than 1 with the same equal initial conditions for the high and low risk populations in order to clearly compare the differences resulting from the parameters being increased by a factor of k for the high risk population.

Then the model was run using initial conditions reflecting the MSM community in Canada. The susceptible population identified in [10] was taken to be the high risk susceptible population with the low risk population being the remaining 415000 people who identify as gay or bisexual men as reported by Statistics Canada [13]. The results of these values were used to create plots of the high and low risk vaccination rates and the resulting maximum high and low risk infected individuals. It is important to consider the infected individuals specifically as they are the people who can form new pairs and therefore cause new infections.

4 Results and Discussion

The resulting matrices V and F are available in Appendix B. V is too large for its inverse to be calculated in Maple. Therefore, a basic reproduction number could not be calculated for this model using the Next Generation Matrix approach.

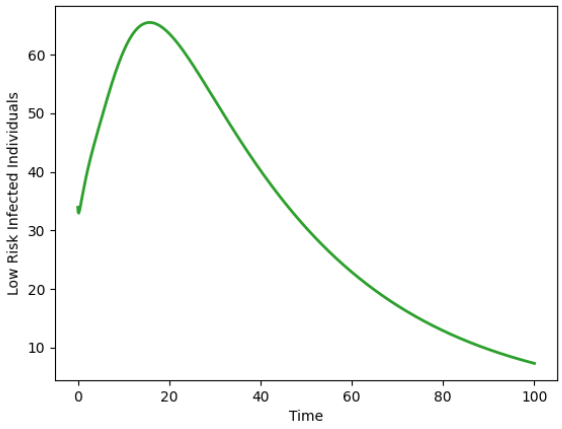

Figure 1: Infected individuals in a homogeneous risk level population.

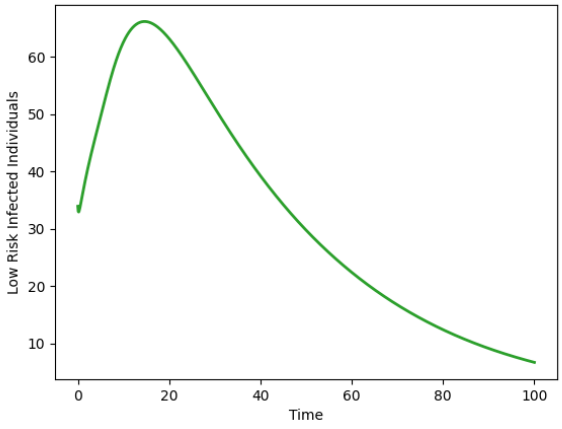

Figure 2: Infected individuals summed high and low risk populations with k=1.

As seen in Figure 1 and Figure 2, having identical parameters between the high and low risk populations creates identical results. This verifies that

the pair-formation dynamics in the high and low risk models are identical, with the distinction between them being the difference in parameter values.

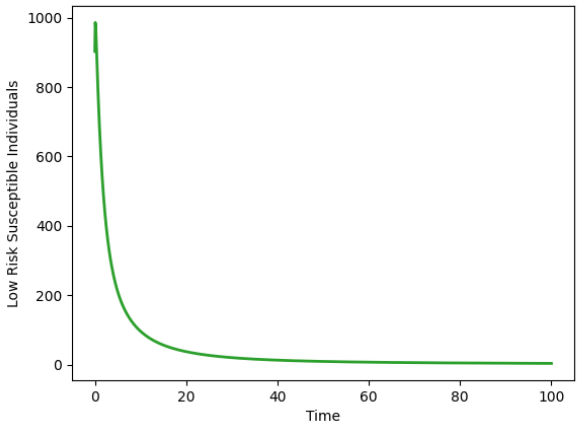

Figure 3: Low Risk Susceptible Individuals with k>1.

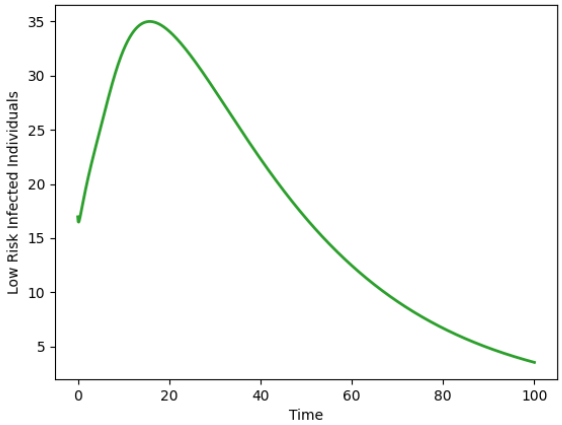

Figure 4: Low Risk Susceptible Recovered Pairs with k>1.

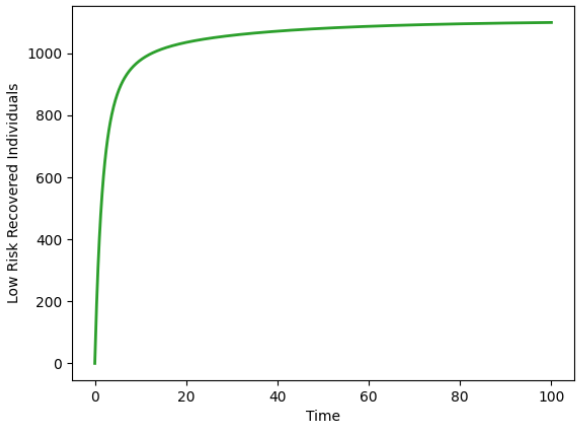

Figure 5: Low Risk Recovered Individuals with k>1.

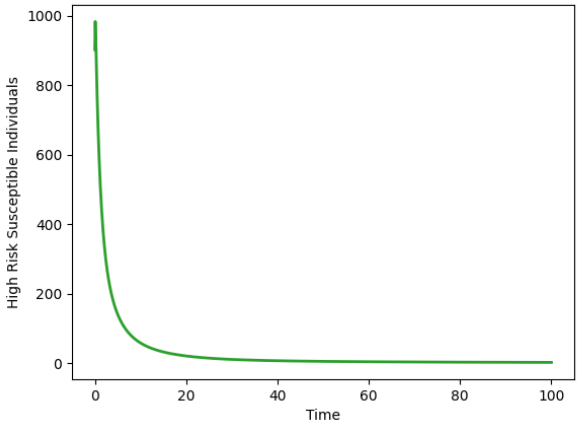

Figure 6: High Risk Susceptible Individuals with k>1.

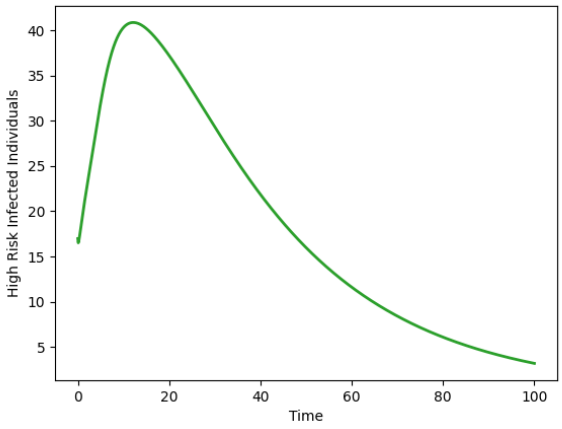

Figure 7: High Risk Infected Individuals with k>1.

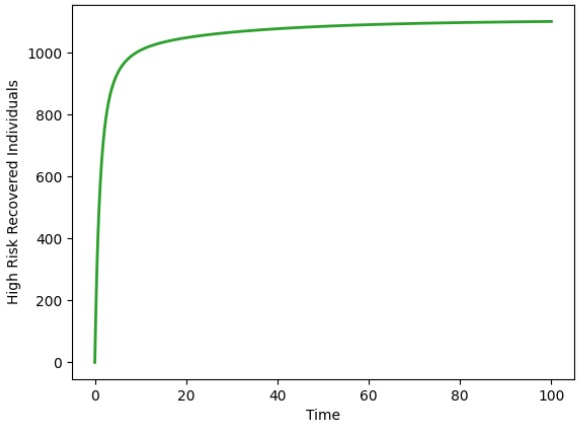

Figure 8: High Risk Recovered Individuals with k>1.

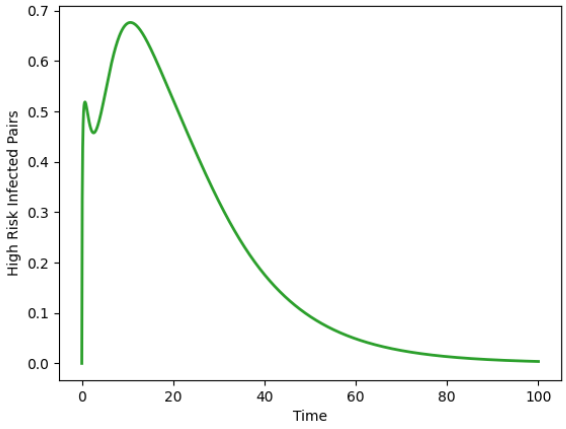

Figure 9: High Risk Infected Pairs with k>1.

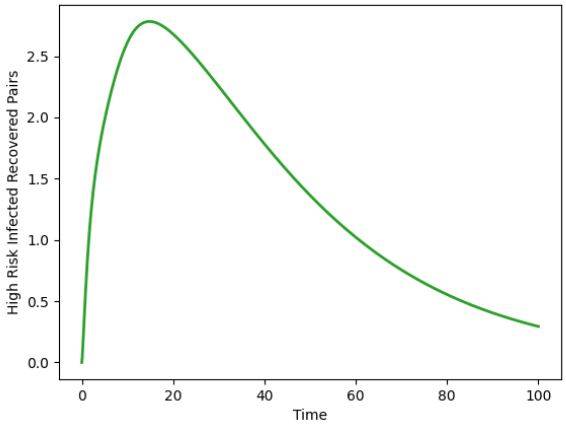

Figure 10: High Risk Infected Recovered Pairs with k>1.

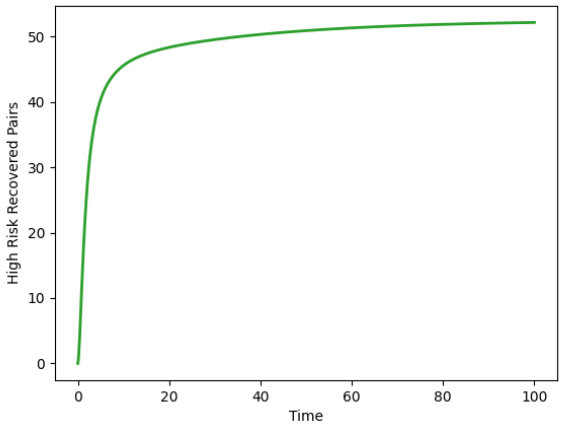

Figure 11: High Risk Recovered Pairs with k>1.

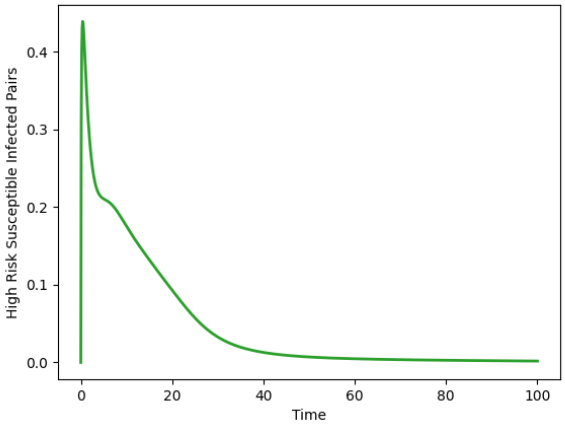

Figure 12: High Risk Susceptible Infected Pairs with k>1.

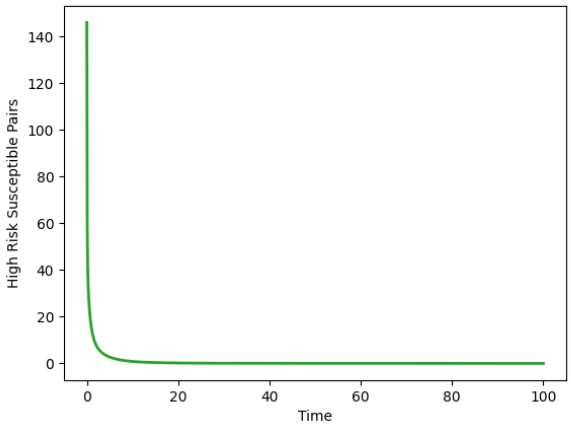

Figure 13: High Risk Susceptible Pairs with k>1.

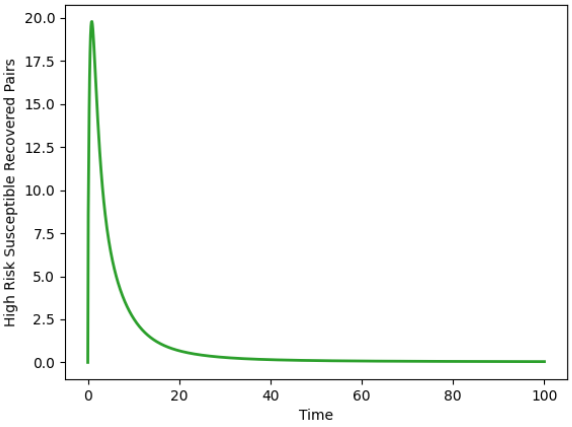

Figure 14: High Risk Susceptible Recovered Pairs with k>1.

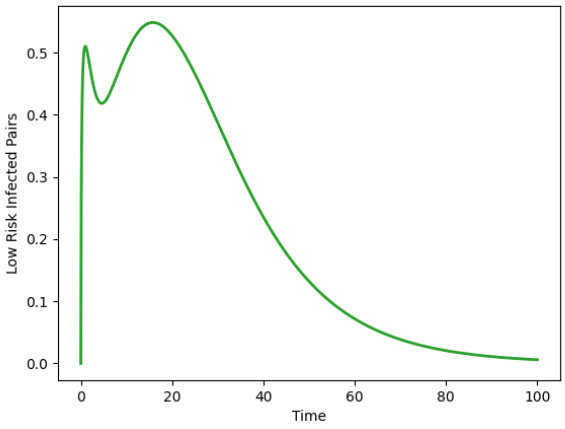

Figure 15: Low Risk Infected Pairs with k>1.

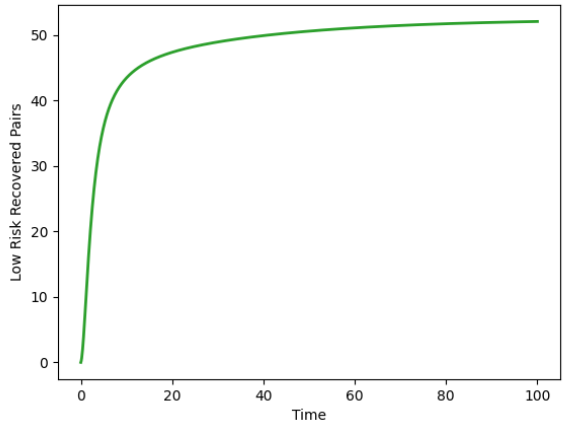

Figure 16: Low Risk Recovered Pairs with k>1.

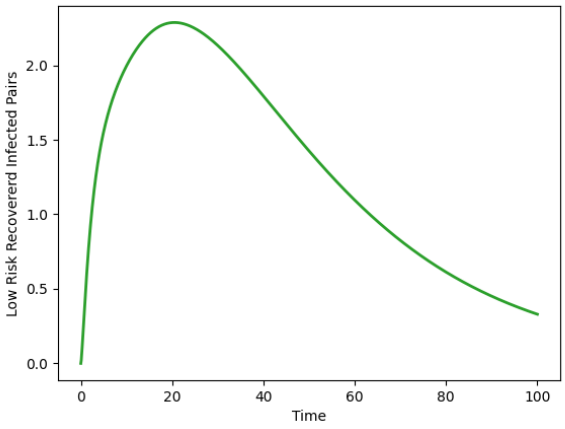

Figure 17: Low Risk Recovered Infected Pairs with k>1.

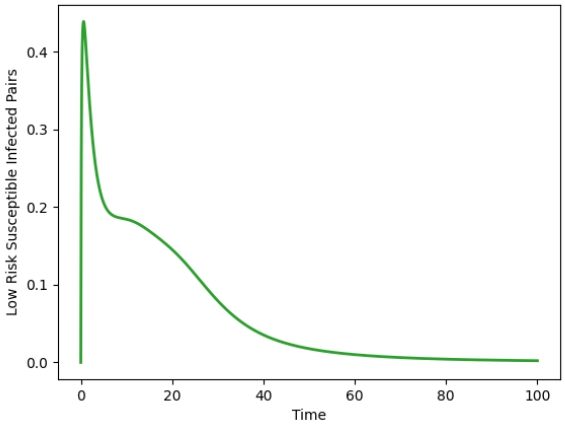

Figure 18: Low Risk Susceptible Infected Pairs with k>1.

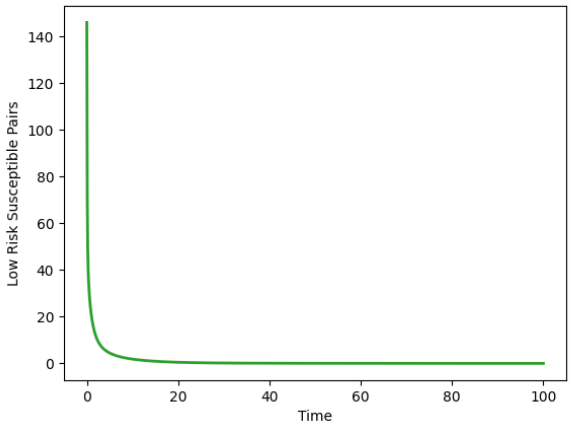

Figure 19: Low Risk Susceptible Pairs with k>1.

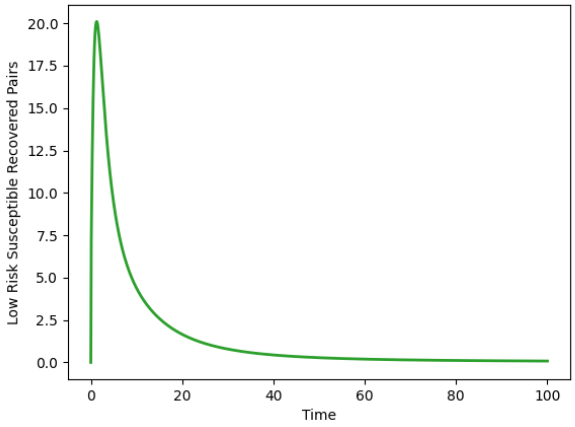

Figure 20: Low Risk Susceptible Recovered Pairs with k>1.

The size of the high and low risk populations in the MSM community are very different, with the high risk population being much smaller than

the low risk population. However, in Figures 3-20, the initial conditions for the high and low risk groups are set as equal to illustrate the differences based solely on the model dynamics. As expected, the susceptible population decreases over time as people are becoming vaccinated. It is noticeable in Figures 3 and 6 that the high risk susceptible individual population decreases slightly faster than the low risk susceptible individual population. This is likely caused by a combination of increased pair formation rates and increased vaccination rates. The peak for the high risk infected individuals is both earlier and higher than that of the low risk infected individuals. Conversely, both the high and low risk recovered populations steadily increase and remain high as recovered individuals do not return to being either susceptible or infected, but can form pairs. For pairs involving infectious people, in the case of their partnership with susceptible, infectious, or recovered individuals it is clear that the high risk populations have peaks which are higher and faster than the equivalent low risk pair. It is also interesting to note the second, peaks visible in both the high and low risk graphs for infected-infected pairs and infected-susceptible pairs, seen in Figures 9, 12, 15, and 18. These peaks are likely more dramatic on this scale which is representative of a smaller initial susceptible population in order to highlight these shapes in the results. These are likely a result of the new pairs forming as pairs dissolve and individuals are returned to the single categories. The peak for recovered and infected pairs is higher and wider than those for other types of pairs, likely because pairs of this type are formed through infected individuals forming pairs withing the increasing recovered population, as well as susceptible people paired with infected people becoming vaccinated, or either infected individual in an infected-infected pairing recovering. The susceptible-susceptible pairings decrease over time which reflects the transition of susceptible individuals to the infected or recov-

ered categories and inability to return. Similarly, the susceptible-recovered pairs have a later and wider peak and recovered-recovered pairs increase and remain high.

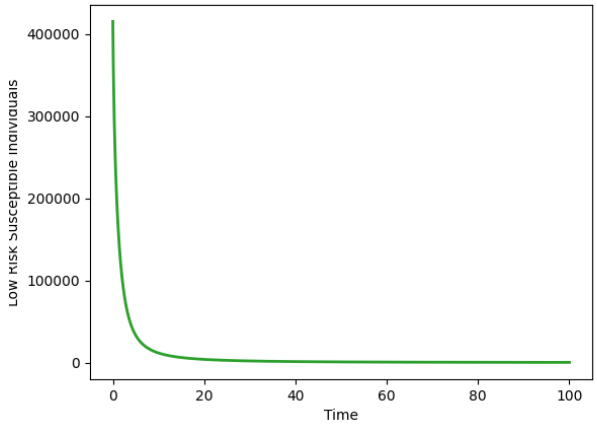

Figure 21: Low Risk Susceptible Individuals

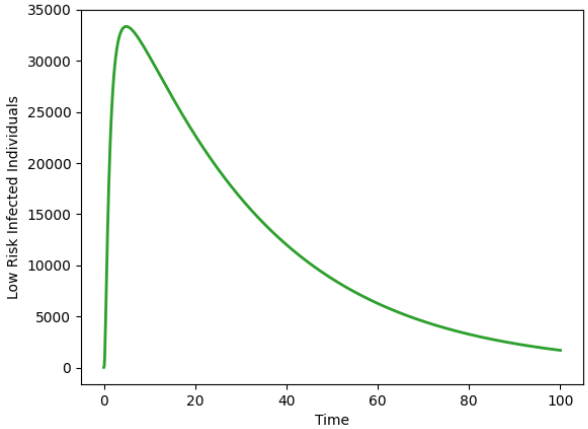

Figure 22: Low Risk Susceptible Recovered Pairs

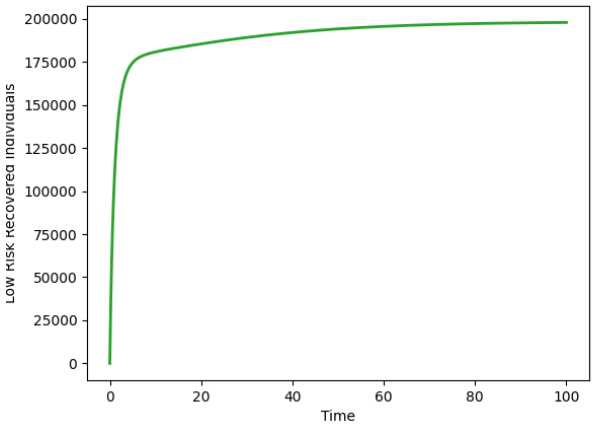

Figure 23: Low Risk Recovered Individuals

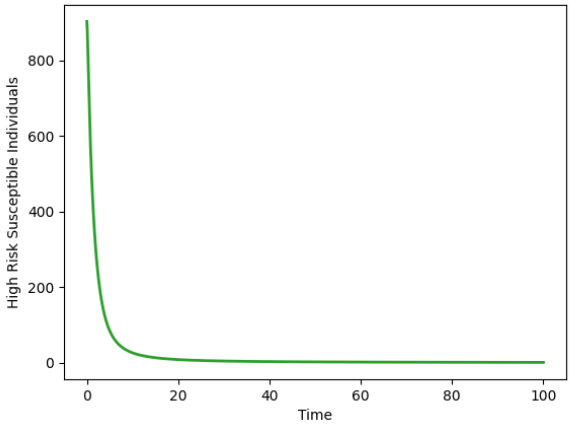

Figure 24: High Risk Susceptible Individuals

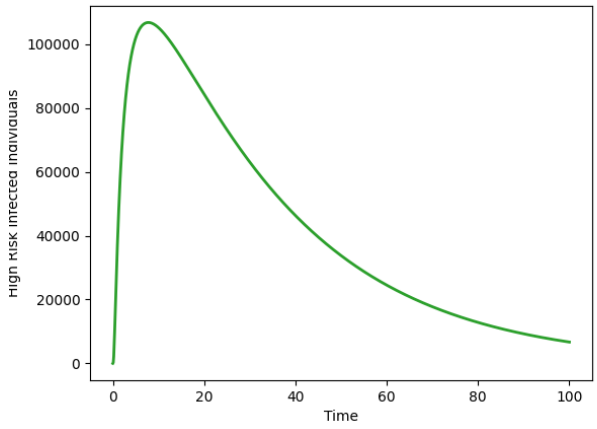

Figure 25: High Risk Infected Individuals

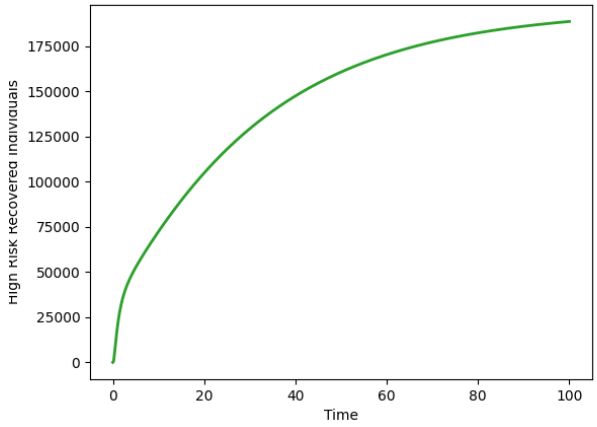

Figure 26: High Risk Recovered Individuals

When including mixed pairing and more accurate initial conditions, both susceptible individual populations behave similarly to the susceptible

single populations in Figures 3 and 6. However, the infected individual population peaks higher wider than the low risk infected individuals, and peaks at a value that is higher than the initial high risk susceptible population. Similarly, the high risk recovered individual population surpasses the initial high risk susceptible population. Also, the high risk recovered individual population increases slower than the low risk recovered individual population, and the low risk recovered individual population slows its growth dramatically at around 200000, which is much lower than the initial susceptible population. This suggests that over time, previously low risk individuals are transitioning to be high risk.

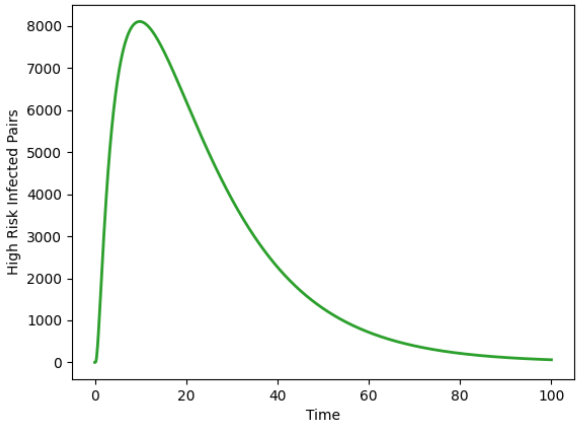

Figure 27: High Risk Infected Pairs

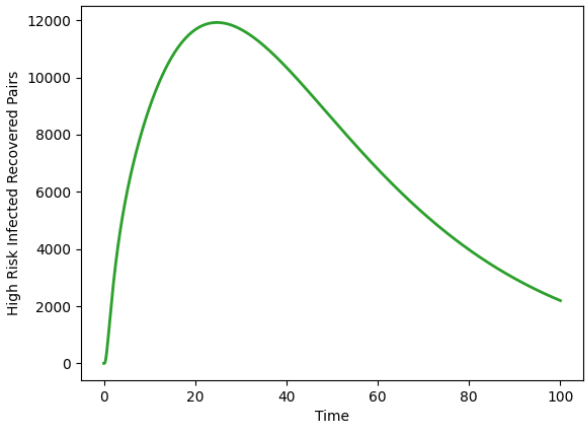

Figure 28: High Risk Infected Recovered Pairs

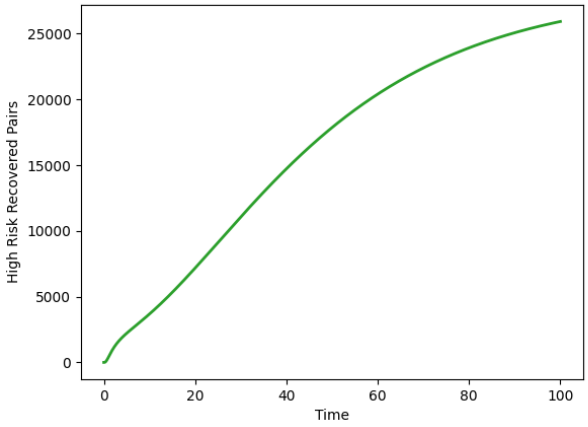

Figure 29: High Risk Recovered Pairs

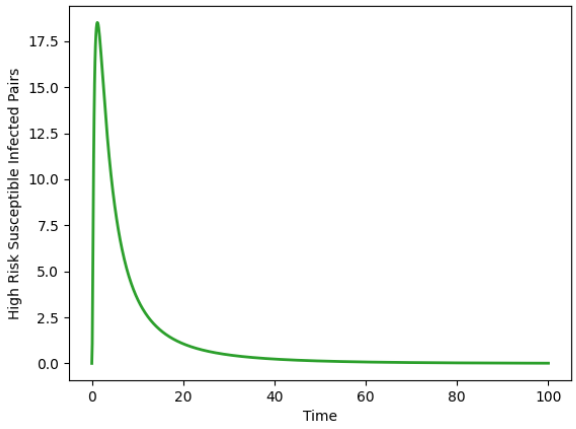

Figure 30: High Risk Susceptible Infected Pairs

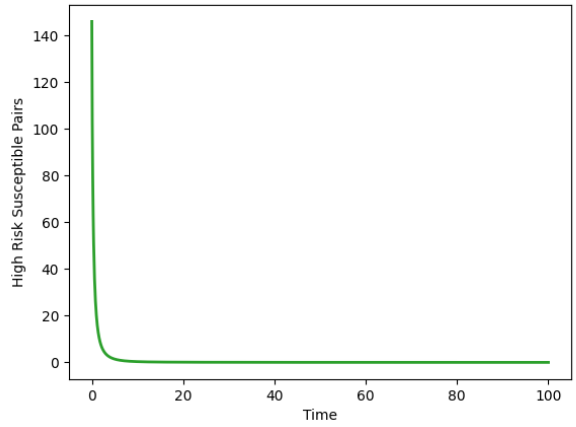

Figure 31: High Risk Susceptible Pairs

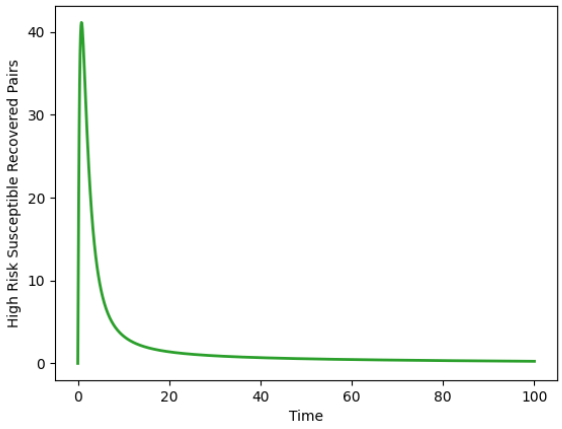

Figure 32: High Risk Susceptible Recovered Pairs

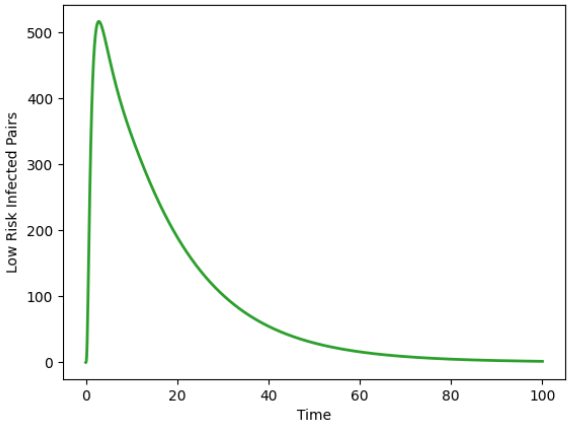

Figure 33: Low Risk Infected Pairs

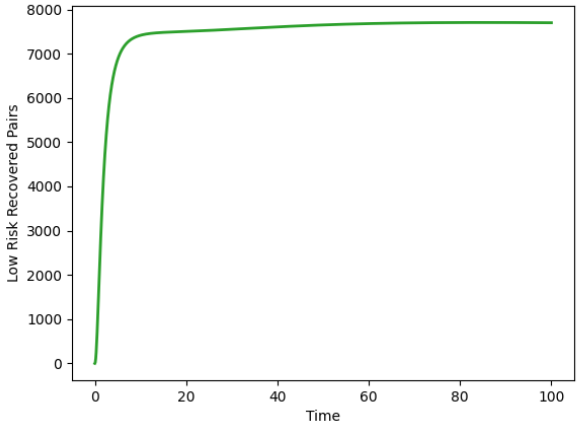

Figure 34: Low Risk Recovered Pairs

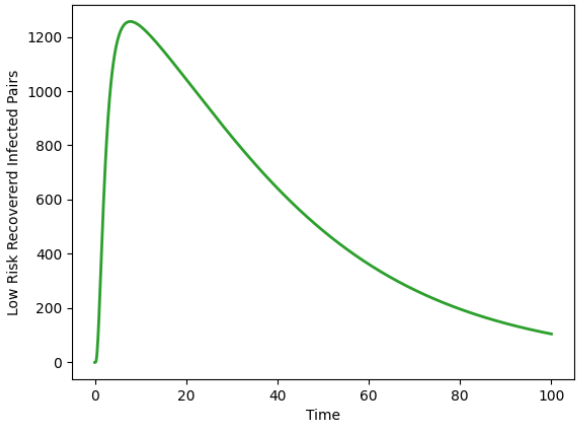

Figure 35: Low Risk Recovered Infected Pairs

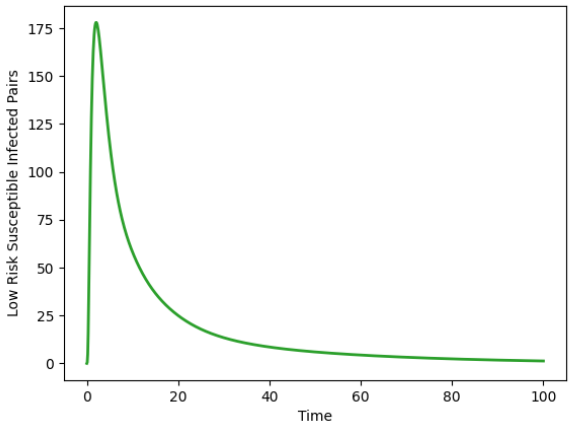

Figure 36: Low Risk Susceptible Infected Pairs

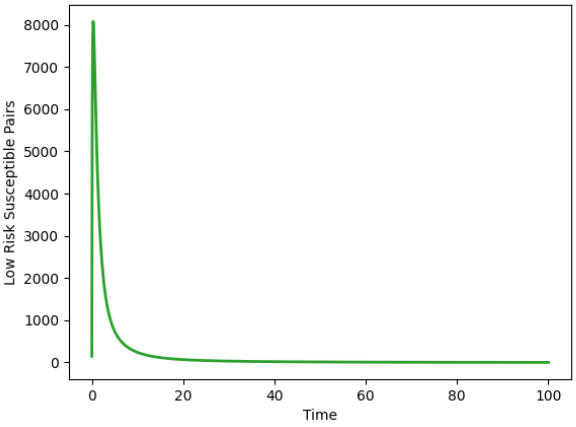

Figure 37: Low Risk Susceptible Pairs

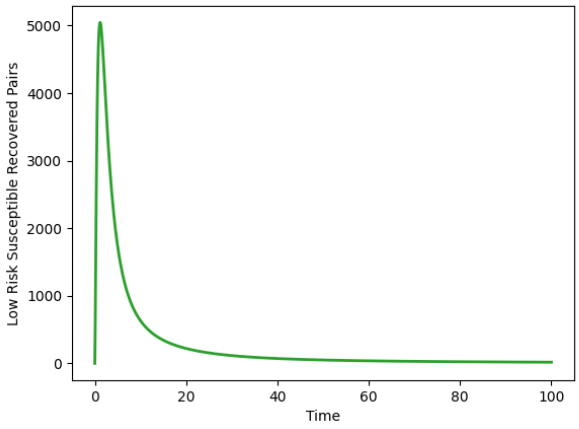

Figure 38: Low Risk Susceptible Recovered Pairs

As seen in Figures 27, 30, 33, and 36, the susceptible-infected and infected-infected pairs at both risk levels do not exhibit the same second-maxima that was evident without mixing. Similar to the individual populations, the low risk recovered-recovered pairs increase much faster than the high risk recovered-recovered pairs. The low risk susceptible-recovered pairs have a much higher and wider peak, likely as a result of the much higher initial susceptible population. Conversely, the high risk infected-infected pairs have a much higher and wider peak than the low risk infected-infected pairs. This could be reflective of the higher risk of infection in the former population, this is also true of the infected-recovered pairs, but not the susceptible-infected pairs.

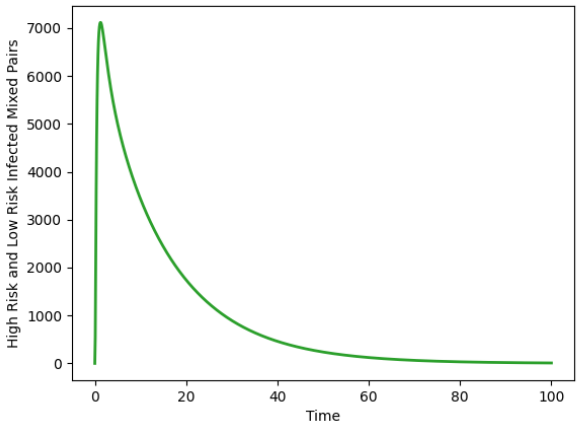

Figure 39: High Risk and Low Risk Infected Mixed Pairs

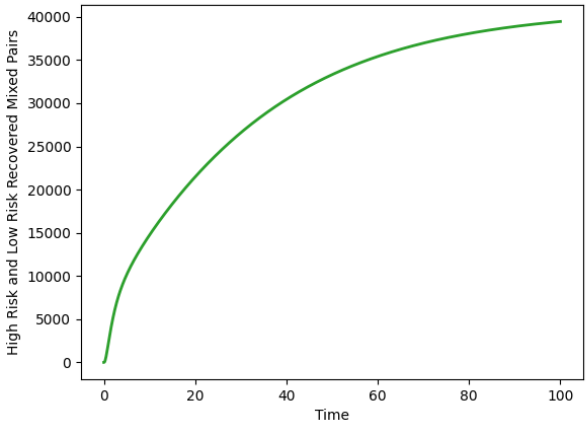

Figure 40: High Risk and Low Risk Recovered Mixed Pairs

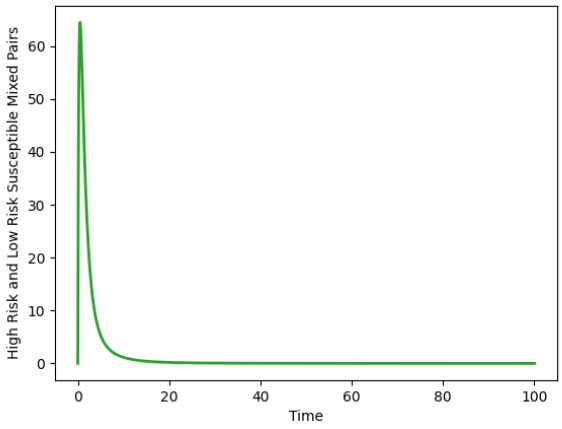

Figure 41: High Risk and Low Risk Susceptible Mixed Pairs

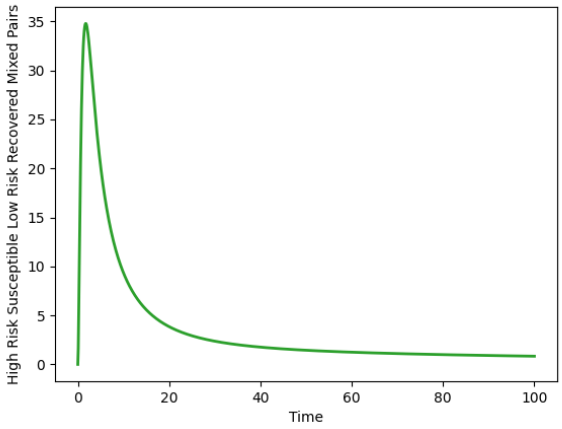

Figure 42: High Risk Susceptible Low Risk Recovered Mixed Pairs

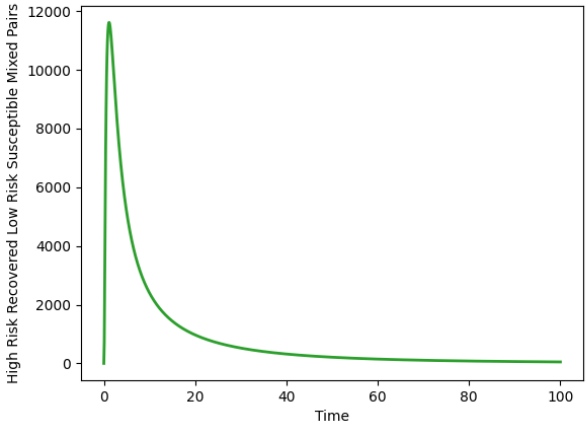

Figure 43: High Risk Recovered Low Risk Susceptible Mixed Pairs

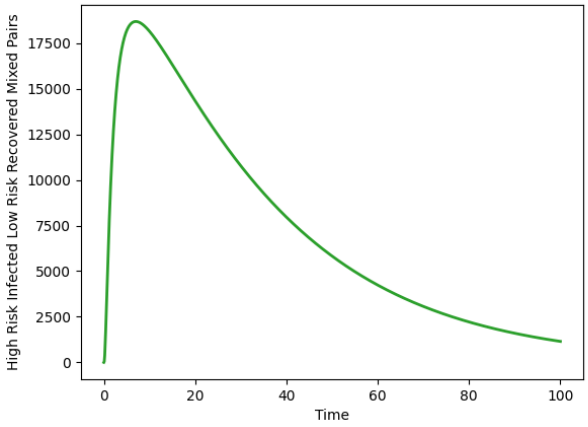

Figure 44: High Risk Infected Low Risk Recovered Mixed Pairs

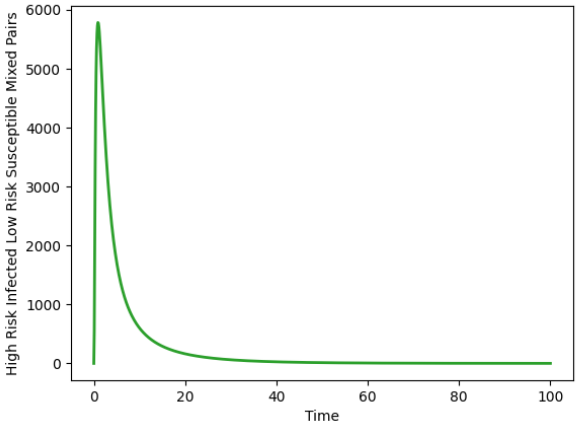

Figure 45: High Risk Infected Low Risk Susceptible Mixed Pairs

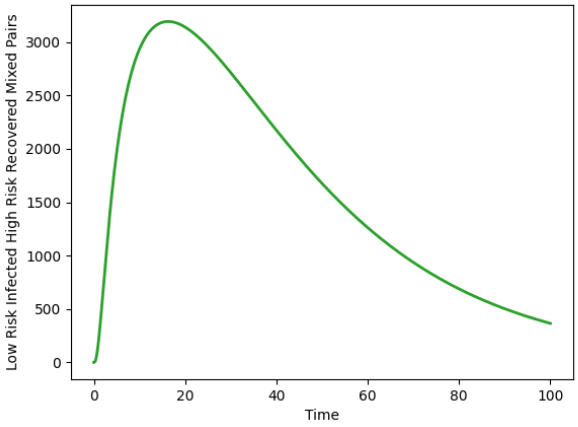

Figure 46: Low Risk Infected High Risk Recovered Mixed Pairs

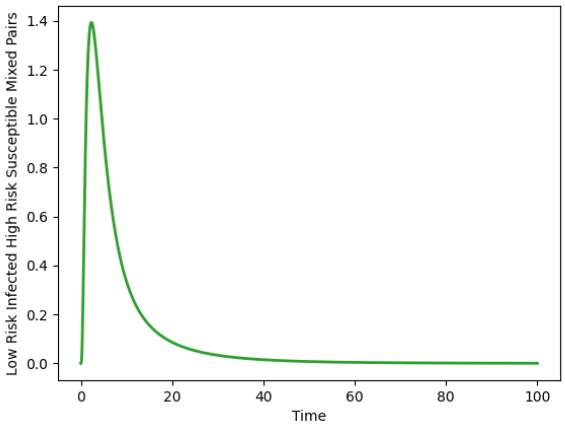

Figure 47: Low Risk Infected High Risk Susceptible Mixed Pairs

One notable aspect of the mixed pairings is the difference in magnitude of the peaks of both types of susceptible-infected pairs. The lower peak of pairs between low risk infected and high risk susceptible individuals likely reflects the much lower proportion of infected individuals there are in the low risk population when compared to the high risk population. It is also important to note that the high risk infected, low risk susceptible pair has the highest peak of any partnership where infection can spread from an infected individual to a susceptible individual.

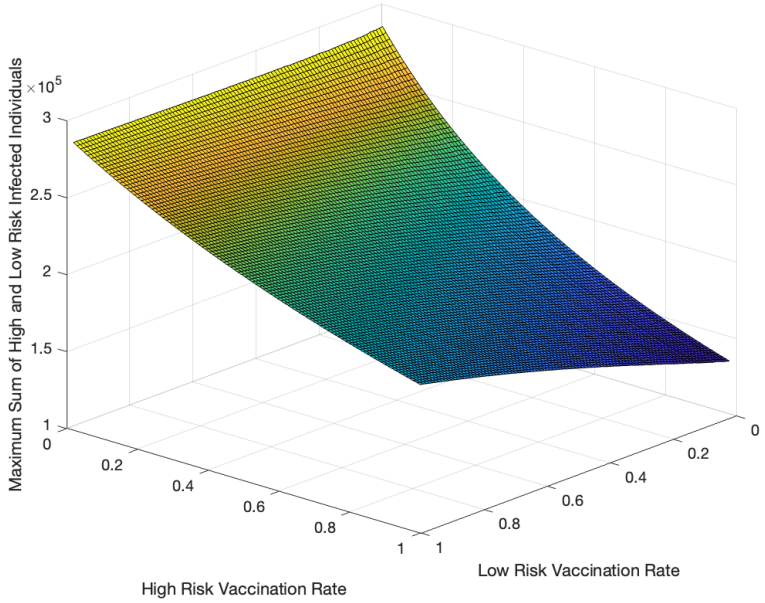

Figure 48: Maximum combined high and low risk infected individuals with changing high and low risk vaccination rates.

It is clear in Figure 48 that vaccination of the high risk population is most effective in reducing infectious individuals. This is evident by the more dramatic drop in the maximum infected single population as high risk vaccination increases. This is contrasted by what is seen in an increase of low risk population vaccination where vaccination has less of an effect in reducing infectious individuals, and, in come cases, an increase in low risk vaccination lead to an increase in infectious individuals.

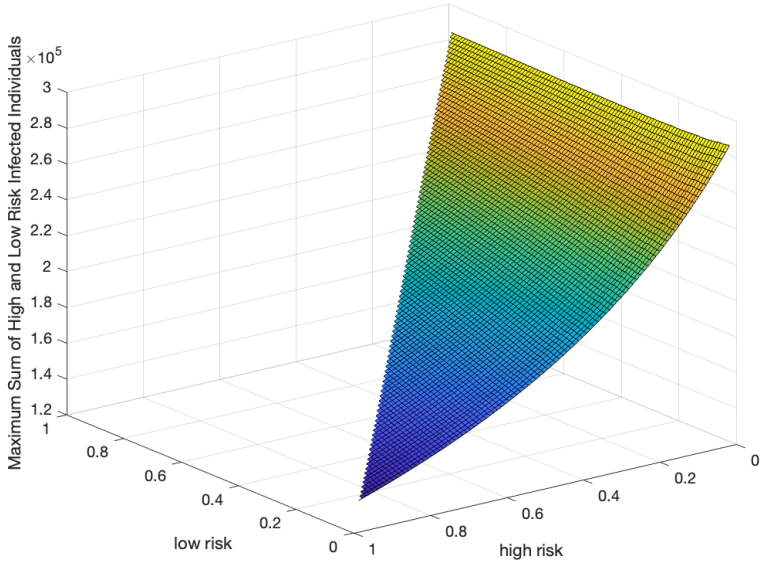

Figure 49: Maximum combined high and low risk infected individuals with changing high and low risk vaccination rates and limited vaccine availability.

Figure 49 shows the case where available vaccination is limited by the sum of the high and low risk vaccination rates remaining equal to or below 1. In this case it is clear that an increase in vaccination of the high risk population results in a decrease in the maximum infected individuals. This is also true for an increased vaccination of the low risk population, however the change is much smaller.

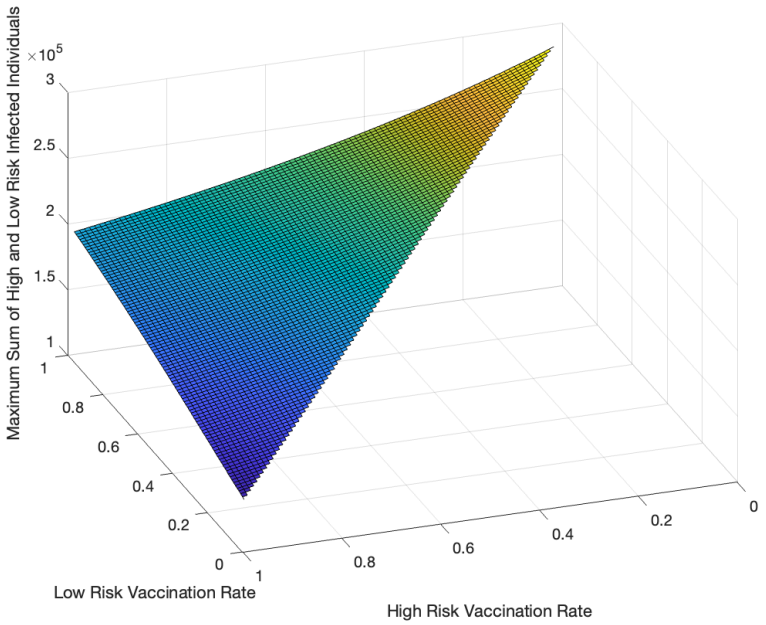

Figure 50: Maximum combined high and low risk infected individuals with changing high and low risk vaccination rates and high vaccine availability.

Figure 50 shows the case where available vaccines are plentiful and is therefore limited by the sum of the high and low risk vaccination rates remaining above 1. In this case an increase in vaccination of the high risk population still results in a decrease in the maximum number of infectious individuals over an outbreak, while in increase in vaccination of the low risk population results in an increased maximum number of infectious individuals. This could be cause by vaccination prompting low risk individuals to make more partnerships than they would have otherwise, leading to an increase in infections.

5 Conclusion

An understanding of the implications of differing levels of risk of mpox and their effect on vaccination is crucial in planning a response. While the model was too large to find a basic reproduction number using the Next Generation Matrix approach, conclusions on vaccination strategies under different levels of vaccine availability and the implications of multiple risk levels were able to be found numerically. It was concluded that there are more infections in the high risk population than the low risk population during an outbreak. Additionally, it is more beneficial to focus on vaccination within the high risk population as a strategy for limiting single infected individuals who can form pairs and create newly infected people. This conclusion is strengthened by the result showing an increase in infected individuals as a result of increased low risk vaccination in the case of an abundance of available vaccines.

A Python Code

Python code where high risk parameters are low risk multiplied by k

```
import numpy as np
import matplotlib.pyplot as plt
from scipy.integrate import odeint
from scipy.stats import qmc
import pandas as pd
import random


def m_eq(y,t,paras):



    #initial conditions
    S = y[0]
    I = y[1]
    R = y[2]
    PSS = y[3]
    PSI = y[4]
    PII = y[5]
    PSR = y[6]
    PIR = y[7]
    PRR = y[8]
    S1 = y[9]
    I1 = y[10]
    R1 = y[11]
    PS1S1 = y[12]
```

```
PS1I1 = y[13]
PI1I1 = y[14]
PS1R1 = y[15]
PI1R1 = y[16]
PR1R1 = y[17]

#parameters
B = 0
mu = 0
rho = paras[0]
p = paras[1]
sigma = 20*paras[2]
nu = paras[3]
delta = (1/30)
phi = paras[4]
h = paras[5]
B1 = 0
rho1 = paras[6]
k_2 = 1
nu1 = paras[8]
phi1 = paras[9]
nu2 = paras[10]
phi2 = paras[11]
k = paras[12] + 1

N = S + I + R
N1 = S1 + I1 + R1
```

```
T = I + PSI + 2*PII + PIR + I1 + PS1I1 + 2*PI1I1 + PI1R1


#equations


dS = B -(mu+rho)*S + sigma*(2*PSS + PSI + PSR) +
mu*(2*PSS + PSI + PSR) - nu*S
dI = -(mu + rho + delta)*I + sigma*((2*PII) + PSI + PIR )
+ mu*(2*PII + PSI + PIR)
dR = delta*I - (mu+rho)*R + sigma*(2*PRR + PSR + PIR)
+ mu*(2*PRR + PSR + PIR) + nu*S
dPSS = (1/2)*rho*((S**2)/N) - (sigma+2*mu)*PSS - 2*nu*PSS
dPSI = rho*(1-h)*((S*I)/(N)) - (sigma + phi*h + 2*mu + delta)*PSI - nu*PSI
dPII = (1/2)*rho*((I**2)/N) + rho*h*((S*I)/N) + phi*h*PSI - (sigma + 2*mu + 2*delta)*P
dPSR = delta*PSI + rho*((S*R)/N) - (sigma+2*mu)*PSR + nu*(2*PSS -  PSR)
dPIR = rho*((I*R)/N) + 2*delta*PII - (sigma + 2*mu + delta)*PIR + nu*PSI
dPRR = delta*PIR + (1/2)*rho*((R**2)/N) + nu*PSR - (sigma + 2*mu)*PRR

#normal
,,,
dS1 = B1-(mu+ rho1)*S1 + sigma*(k_2*(2*PS1S1 + PS1I1 + PS1R1)) +
mu*(2*PS1S1 + PS1I1 + PS1R1) - nu1*S1
dI1 = -(mu+rho1+delta)*I1 + sigma*(k_2*(2*PI1I1+PS1I1+PI1R1)) +
mu*( 2*PI1I1 + PS1I1 + PI1R1)
dR1 = delta*I1 - (mu+rho1)*R1 + sigma*(k_2*(PS1R1 + PI1R1 + 2*PR1R1)) +
mu*( PS1R1 + PI1R1 + 2*PR1R1)+ nu1*S1
dPS1S1 = (1/2)*rho1*((S1)**2/N1) - (k_2*sigma + 2*mu)*PS1S1 - 2*nu1*PS1S1
```

```
dPS1I1 = rho1*(1-h)*((S1*I1)/N1) - (k_2*sigma + phi1*h + 2*mu + delta)*PS1I1 - nu1*PS1
dPI1I1 = (1/2)*rho1*(I1**2/N1) + rho1*h*((S1*I1)/N1) + phi1*h*PS1I1 - (k_2*sigma + 2*m
dPS1R1 = delta*PS1I1 + rho1*((S1*R1)/N1) - (k_2*sigma+2*mu)*PS1R1 + nu1*(2*PS1S1 - PS1
dPI1R1 = rho1*((I1*R1)/N1) + 2*delta*PI1I1 - (k_2*sigma + 2*mu + delta)*PI1R1 + nu1*PS
dPR1R1 = delta*PI1R1 + (1/2)*rho1*((R1**2)/N1) + nu1*PS1R1 - (k_2*sigma + 2*mu)*PR1R1
,,,

#with k

dS1 = B1-(mu+ k*rho)*S1 + sigma*k*(2*PS1S1 + PS1I1 + PS1R1) +
mu*(2*PS1S1 + PS1I1 + PS1R1) - k*nu*S1
dI1 = -(mu + k*rho + delta)*I1 + sigma*(k*(2*PI1I1+PS1I1+PI1R1)) +
mu*(2*PI1I1 + PS1I1 + PI1R1)
dR1 = delta*I1 - (mu + k*rho)*R1 + sigma*(k*(PS1R1 + PI1R1 + 2*PR1R1)) +
mu*(PS1R1 + PI1R1 + 2*PR1R1)+ k*nu*S1
dPS1S1 = (1/2)*k*rho*((S1)**2/N1) - (k*sigma + 2*mu)*PS1S1 - 2*k*nu*PS1S1
dPS1I1 = k*rho*(1-h)*((S1*I1)/N1) - (k*sigma + k*phi*h + 2*mu + delta)*PS1I1 - k*nu*PS
dPI1I1 = (1/2)*k*rho*(I1**2/N1) + k*rho*h*((S1*I1)/N1) + k*phi*h*PS1I1 - (k*sigma + 2*
dPS1R1 = delta*PS1I1 + k*rho*((S1*R1)/N1) - (k*sigma+2*mu)*PS1R1 + k*nu*(2*PS1S1 - PS1
dPI1R1 = k*rho*((I1*R1)/N1) + 2*delta*PI1I1 - (k*sigma + 2*mu + delta)*PI1R1 + k*nu*PS
dPR1R1 = delta*PI1R1 + (1/2)*k*rho*((R1**2)/N1) + k*nu*PS1R1 - (k*sigma + 2*mu)*PR1R1

#with interaction


#dPSS1 = k_1*rho*((S*S1)/N) - (k_1*sigma + 2*mu)*PSS1 - (nu+nu1)*PSS1
#dPSI1 = k_1*rho*(1-h)*((S*I1)/N1) - (k_1*sigma + 2*mu + k_1*phi*h + delta)*PSI1
- nu*PSI1
```

```
    #dPS1I = k_1*rho*(1-h)*((S1*I)/N) - (k_1*sigma + 2*mu + k_1*phi*h + delta)*PS1I - k*nu
    #dPII1 = k_1*rho*((I1*I)/N) + k_1*rho*h*((S*I1)/N1)+k_1*rho*h*((S1*I)/N)
    + k_1*phi*h*(PS1I + PSI1) - (k_1*sigma + 2*mu +2*delta)*PII1
    #dPS1R = delta*PS1I + k_1*rho*((S1*R)/N) - (k_1*sigma + 2*mu)*PS1R + nu*PSS1 - k*nu*PS
    #dPSR1 = delta*PSI1 + k_1*rho*((S*R1)/N1) - (k_1*sigma + 2*mu)*PSR1 + k*nu*PSS1 - nu*P
    #dPI1R = k_1*rho*((I1*R)/N1) + delta*PII1 - (k_1*sigma + 2*mu + delta)*PI1R + nu*PSI1
    #dPIR1 = k_1*rho*((I*R1)/N) + delta*PII1 - (k_1*sigma + 2*mu + delta)*PIR1 + k*nu*PS1I
    #dPRR1 = k_1*rho*((R*R1)/N) + delta*(PIR1 + PI1R) + k*nu*PS1R + nu*PSR1 - (k_1*sigma +

    return [dS, dI, dR, dPSS, dPSI, dPII, dPSR, dPIR, dPRR, dS1, dI1, dR1, dPS1S1, dPS1I1,



cube = qmc.LatinHypercube(d=13)
samples = 1000
initial = [902.56, 16.97, 0, 145.96, 0, 0, 0, 0, 0,902.56, 16.97, 0, 145.96, 0, 0, 0, 0, 0
timeline = 1000
t = np.linspace(0,100, timeline)
S = np.zeros((samples,len(t)))
I = np.zeros((samples,len(t)))
R = np.zeros((samples,len(t)))
PSS = np.zeros((samples,len(t)))
PSI = np.zeros((samples,len(t)))
PII = np.zeros((samples,len(t)))
PSR = np.zeros((samples,len(t)))
PIR = np.zeros((samples,len(t)))
PRR = np.zeros((samples,len(t)))
S1 = np.zeros((samples,len(t)))
```

```
I1 = np.zeros((samples,len(t)))
R1 = np.zeros((samples,len(t)))
PS1S1 = np.zeros((samples,len(t)))
PS1I1 = np.zeros((samples,len(t)))
PI1I1 = np.zeros((samples,len(t)))
PS1R1 = np.zeros((samples,len(t)))
PI1R1 = np.zeros((samples,len(t)))
PR1R1 = np.zeros((samples,len(t)))
#mixing
'''
PSS1 = np.zeros((samples,len(t)))
PSI1 = np.zeros((samples,len(t)))
PS1I = np.zeros((samples,len(t)))
PII1 = np.zeros((samples,len(t)))
PS1R = np.zeros((samples,len(t)))
PSR1 = np.zeros((samples,len(t)))
PI1R = np.zeros((samples,len(t)))
PIR1 = np.zeros((samples,len(t)))
PRR1 = np.zeros((samples,len(t)))
'''



parameters = cube.random(n=samples)

for i in range(samples):
    params = parameters[i]
    stuff = odeint(m_eq, initial, t, args = (params,))
```

```
S[i,:] = stuff[:,0]
I[i,:] = stuff[:,1]
R[i,:] = stuff[:,2]
PSS[i,:] = stuff[:,3]
PSI[i,:] = stuff[:,4]
PII[i,:] = stuff[:,5]
PSR[i,:] = stuff[:,6]
PIR[i,:] = stuff[:,7]
PRR[i,:] = stuff[:,8]
S1[i,:] = stuff[:,9]
I1[i,:] = stuff[:,10]
R1[i,:] = stuff[:,11]
PS1S1[i,:] = stuff[:,12]
PS1I1[i,:] = stuff[:,13]
PI1I1[i,:] = stuff[:,14]
PS1R1[i,:] = stuff[:,15]
PI1R1[i,:] = stuff[:,16]
PR1R1[i,:] = stuff[:,17]
#mixing
'''
PSS1[i,:] = stuff[:,18]
PSI1[i,:] = stuff[:,19]
PS1I[i,:] = stuff[:,20]
PII1[i,:] = stuff[:,21]
PS1R[i,:] = stuff[:,22]
PSR1[i,:] = stuff[:,23]
PI1R[i,:] = stuff[:,24]
PIR1[i,:] = stuff[:,25]
```

```
    PRR1[i,:] = stuff[:,26]
    ,,,


mean_S = np.mean(S,axis=0)
mean_I = np.mean(I,axis=0)
mean_R = np.mean(R,axis=0)
mean_PSS = np.mean(PSS,axis=0)
mean_PSI = np.mean(PSI,axis=0)
mean_PII = np.mean(PII,axis=0)
mean_PSR = np.mean(PSR,axis=0)
mean_PIR = np.mean(PIR,axis=0)
mean_PRR = np.mean(PRR,axis=0)
mean_S1 = np.mean(S1,axis=0)
mean_I1 = np.mean(I1,axis=0)
mean_R1 = np.mean(R1,axis=0)
mean_PS1S1 = np.mean(PS1S1,axis=0)
mean_PS1I1 = np.mean(PS1I1,axis=0)
mean_PI1I1 = np.mean(PI1I1,axis=0)
mean_PS1R1 = np.mean(PS1R1,axis=0)
mean_PI1R1 = np.mean(PI1R1,axis=0)
mean_PR1R1 = np.mean(PR1R1,axis=0)

#mixing
,,,
mean_PSS1 = np.mean(PSS1,axis=0)
mean_PSI1 = np.mean(PSI1,axis=0)
mean_PS1I = np.mean(PS1I,axis=0)
```

```
mean_PII1 = np.mean(PII1,axis=0)
mean_PS1R = np.mean(PS1R,axis=0)
mean_PSR1 = np.mean(PSR1,axis=0)
mean_PI1R = np.mean(PI1R,axis=0)
mean_PIR1 = np.mean(PIR1,axis=0)
mean_PRR1 = np.mean(PRR1,axis=0)
'''



'''
addedS = np.add(mean_S,mean_S1)
addedI = np.add(mean_I,mean_I1)
addedR = np.add(mean_R,mean_R1)
addedPSS = np.add(mean_PSS,mean_PS1S1)
addedPSI = np.add(mean_PSI,mean_PS1I1)
addedPII = np.add(mean_PII,mean_PI1I1)
addedPSR = np.add(mean_PSR,mean_PS1R1)
addedPIR = np.add(mean_PIR,mean_PI1R1)
addedPRR = np.add(mean_PRR,mean_PR1R1)
'''

added = "k>1 S1=S"



plt.plot(t, mean_S, '-', linewidth=2, color='tab:green')
#plt.plot(t, addedS, '-', linewidth=2, color='tab:blue',linestyle='dashed')
plt.xlabel("Time")
plt.ylabel("Low Risk Susceptible Individuals")
```

```
plt.savefig("low risk susceptible " + added)
plt.show()
plt.plot(t, mean_I, '-', linewidth=2, color='tab:green')
#plt.plot(t, addedI, '-', linewidth=2, color='tab:blue',linestyle='dashed')
plt.xlabel("Time")
plt.ylabel("Low Risk Infected Individuals")
plt.savefig("Low Risk Infected Individuals " + added)
plt.show()
plt.plot(t, mean_R, '-', linewidth=2, color='tab:green')
#plt.plot(t, addedR, '-', linewidth=2, color='tab:blue',linestyle='dashed')
plt.xlabel("Time")
plt.ylabel("Low Risk Recovered Individuals")
plt.savefig("Low Risk Recovered Individuals " + added)
plt.show()
plt.plot(t, mean_PSS, '-', linewidth=2, color='tab:green')
#plt.plot(t, addedPSS, '-', linewidth=2, color='tab:blue',linestyle='dashed')
plt.xlabel("Time")
plt.ylabel("Low Risk Susceptible Pairs")
plt.savefig("Low Risk Susceptible Pairs " + added)
plt.show()
plt.plot(t, mean_PSI, '-', linewidth=2, color='tab:green')
#plt.plot(t, addedPSI, '-', linewidth=2, color='tab:blue',linestyle='dashed')
plt.xlabel("Time")
plt.ylabel("Low Risk Susceptible Infected Pairs")
plt.savefig("Low Risk Susceptible Infected Pairs " + added)
plt.show()
plt.plot(t, mean_PII, '-', linewidth=2, color='tab:green')
#plt.plot(t, addedPII, '-', linewidth=2, color='tab:blue',linestyle='dashed')
```

```
plt.xlabel("Time")
plt.ylabel("Low Risk Infected Pairs")
plt.savefig("Low Risk Infected Pairs " + added)
plt.show()
plt.plot(t, mean_PSR, '-', linewidth=2, color='tab:green')
#plt.plot(t, addedPSR, '-', linewidth=2, color='tab:blue',linestyle='dashed')
plt.xlabel("Time")
plt.ylabel("Low Risk Susceptible Recovered Pairs")
plt.savefig("Low Risk Susceptible Recovered Pairs " + added)
plt.show()
plt.plot(t, mean_PIR, '-', linewidth=2, color='tab:green')
#plt.plot(t, addedPIR, '-', linewidth=2, color='tab:blue',linestyle='dashed')
plt.xlabel("Time")
plt.ylabel("Low Risk Recovererd Infected Pairs")
plt.savefig("Low Risk Recovererd Infected Pairs " + added)
plt.show()
plt.plot(t, mean_PRR, '-', linewidth=2, color='tab:green')
#plt.plot(t, addedPRR, '-', linewidth=2, color='tab:blue',linestyle='dashed')
plt.xlabel("Time")
plt.ylabel("Low Risk Recovered Pairs")
plt.savefig("Low Risk Recovered Pairs " + added)
plt.show()

plt.plot(t, mean_S1, '-', linewidth=2, color='tab:green')
plt.xlabel("Time")
plt.ylabel("High Risk Susceptible Individuals")
plt.savefig("High Risk Susceptible Individuals " + added)
plt.show()
```

```
plt.plot(t, mean_I1, '-', linewidth=2, color='tab:green')
plt.xlabel("Time")
plt.ylabel("High Risk Infected Individuals")
plt.savefig("High Risk Infected Individuals " + added)
plt.show()
plt.plot(t, mean_R1, '-', linewidth=2, color='tab:green' )
plt.xlabel("Time")
plt.ylabel("High Risk Recovered Individuals")
plt.savefig("High Risk Recovered Individuals " + added)
plt.show()
plt.plot(t, mean_PS1S1, '-', linewidth=2, color='tab:green')
plt.xlabel("Time")
plt.ylabel("High Risk Susceptible Pairs")
plt.savefig("High Risk Susceptible Pairs " + added)
plt.show()
plt.plot(t, mean_PS1I1, '-', linewidth=2, color='tab:green')
plt.xlabel("Time")
plt.ylabel("High Risk Susceptible Infected Pairs")
plt.savefig("High Risk Susceptible Infected Pairs " + added)
plt.show()
plt.plot(t, mean_PI1I1, '-', linewidth=2, color='tab:green')
plt.xlabel("Time")
plt.ylabel("High Risk Infected Pairs")
plt.savefig("High Risk Infected Pairs " + added)
plt.show()
plt.plot(t, mean_PS1R1, '-', linewidth=2, color='tab:green')
plt.xlabel("Time")
plt.ylabel("High Risk Susceptible Recovered Pairs")
```

```
plt.savefig("High Risk Susceptible Recovered Pairs " + added)
plt.show()
plt.plot(t, mean_PI1R1, '-', linewidth=2, color='tab:green')
plt.xlabel("Time")
plt.ylabel("High Risk Infected Recovered Pairs")
plt.savefig("High Risk Infected Recovered Pairs " + added)
plt.show()
plt.plot(t, mean_PR1R1, '-', linewidth=2, color='tab:green')
plt.xlabel("Time")
plt.ylabel("High Risk Recovered Pairs")
plt.savefig("High Risk Recovered Pairs " + added)
plt.show()


#mixing
'''
plt.plot(t, mean_PSS1, '-', linewidth=2, color='tab:green')
plt.xlabel("Time")
plt.ylabel("High Risk and Low Risk Susceptible Mixed Pairs")
plt.savefig("High Risk and Low Risk Susceptible Mixed Pairs,  final" + added)
plt.show()
plt.plot(t, mean_PSI1, '-', linewidth=2, color='tab:green')
plt.xlabel("Time")
plt.ylabel("High Risk Infected Low Risk Susceptible Mixed Pairs")
plt.savefig("High Risk Infected Low Risk Susceptible Mixed Pairs,  final" + added)
plt.show()
plt.plot(t, mean_PS1I, '-', linewidth=2, color='tab:green')
plt.xlabel("Time")
```

```
plt.ylabel("Low Risk Infected High Risk Susceptible Mixed Pairs")
plt.savefig("Low Risk Infected High Risk Susceptible Mixed Pairs,  final" + added)
plt.show()
plt.plot(t, mean_PII1, '-', linewidth=2, color='tab:green')
plt.xlabel("Time")
plt.ylabel("High Risk and Low Risk Infected Mixed Pairs")
plt.savefig("High Risk and Low Risk Infected Mixed Pairs,  final" + added)
plt.show()
plt.plot(t, mean_PS1R, '-', linewidth=2, color='tab:green')
plt.xlabel("Time")
plt.ylabel("High Risk Susceptible Low Risk Recovered Mixed Pairs")
plt.savefig("High Risk Susceptible Low Risk Recovered Mixed Pairs,  final" + added)
plt.show()
plt.plot(t, mean_PSR1, '-', linewidth=2, color='tab:green')
plt.xlabel("Time")
plt.ylabel("High Risk Recovered Low Risk Susceptible Mixed Pairs")
plt.savefig("High Risk Recovered Low Risk Susceptible Mixed Pairs,  final" + added)
plt.show()
plt.plot(t, mean_PI1R, '-', linewidth=2, color='tab:green')
plt.xlabel("Time")
plt.ylabel("High Risk Infected Low Risk Recovered Mixed Pairs")
plt.savefig("High Risk Infected Low Risk Recovered Mixed Pairs,  final" + added)
plt.show()
plt.plot(t, mean_PIR1, '-', linewidth=2, color='tab:green')
plt.xlabel("Time")
plt.ylabel("Low Risk Infected High Risk Recovered Mixed Pairs")
plt.savefig("Low Risk Infected High Risk Recovered Mixed Pairs,  final" + added)
plt.show()
```

```
plt.plot(t, mean_PRR1, '-', linewidth=2, color='tab:green')
plt.xlabel("Time")
plt.ylabel("High Risk and Low Risk Recovered Mixed Pairs")
plt.savefig("High Risk and Low Risk Recovered Mixed Pairs,  final" + added)
plt.show()
'''



#added
'''

plt.plot(t, addedS, '-', linewidth=2, color='tab:green',linestyle='dashed')
plt.xlabel("Time")
plt.ylabel("Low Risk Susceptible Individuals")
plt.savefig("low risk susceptible ADD" + added)
plt.show()
plt.plot(t, addedI, '-', linewidth=2, color='tab:green',linestyle='dashed')
plt.xlabel("Time")
plt.ylabel("Low Risk Infected Individuals")
plt.savefig("Low Risk Infected Individuals ADD" + added)
plt.show()
plt.plot(t, addedR, '-', linewidth=2, color='tab:green',linestyle='dashed')
plt.xlabel("Time")
plt.ylabel("Low Risk Recovered Individuals")
plt.savefig("Low Risk Recovered Individuals ADD" + added)
plt.show()
plt.plot(t, addedPSS, '-', linewidth=2, color='tab:green',linestyle='dashed')
plt.xlabel("Time")
```

```
plt.ylabel("Low Risk Susceptible Pairs")
plt.savefig("Low Risk Susceptible Pairs ADD" + added)
plt.show()
plt.plot(t, addedPSI, '-', linewidth=2, color='tab:green',linestyle='dashed')
plt.xlabel("Time")
plt.ylabel("Low Risk Susceptible Infected Pairs")
plt.savefig("Low Risk Susceptible Infected Pairs ADD" + added)
plt.show()
plt.plot(t, addedPII, '-', linewidth=2, color='tab:green',linestyle='dashed')
plt.xlabel("Time")
plt.ylabel("Low Risk Infected Pairs")
plt.savefig("Low Risk Infected Pairs ADD" + added)
plt.show()
plt.plot(t, addedPSR, '-', linewidth=2, color='tab:green',linestyle='dashed')
plt.xlabel("Time")
plt.ylabel("Low Risk Susceptible Recovered Pairs")
plt.savefig("Low Risk Susceptible Recovered Pairs ADD " + added)
plt.show()
plt.plot(t, addedPIR, '-', linewidth=2, color='tab:green',linestyle='dashed')
plt.xlabel("Time")
plt.ylabel("Low Risk Recovererd Infected Pairs")
plt.savefig("Low Risk Recovererd Infected Pairs ADD " + added)
plt.show()
plt.plot(t, addedPRR, '-', linewidth=2, color='tab:green',linestyle='dashed')
plt.xlabel("Time")
plt.ylabel("Low Risk Recovered Pairs")
plt.savefig("Low Risk Recovered Pairs ADD" + added)
plt.show()
```

```
,,,
```

Python code for explicitly different high risk parameters

```
import numpy as np
import matplotlib.pyplot as plt
from scipy.integrate import odeint
from scipy.stats import qmc
import pandas as pd
import random

def m_eq(y,t,paras):


    #initial conditions
    S = y[0]
    I = y[1]
    R = y[2]
    PSS = y[3]
    PSI = y[4]
    PII = y[5]
    PSR = y[6]
    PIR = y[7]
    PRR = y[8]
    S1 = y[9]
    I1 = y[10]
    R1 = y[11]
    PS1S1 = y[12]
    PS1I1 = y[13]
```

```
PI1I1 = y[14]
PS1R1 = y[15]
PI1R1 = y[16]
PR1R1 = y[17]
PSS1 = y[18]
PSI1 = y[19]
PS1I = y[20]
PII1 = y[21]
PS1R = y[22]
PSR1 = y[23]
PI1R = y[24]
PIR1 = y[25]
PRR1 = y[26]

#parameters
B = 0  #equal to mu
mu = 0  #equal to B but on paper was fixed at 0
rho = paras[0]
p = paras[1]
sigma = 20*paras[2] #value from other was 11.17
k_1 = paras[3]
nu = paras[4]
delta = (1/30)  #fixed at 1/30
phi = paras[5]
h = paras[6]
B1 = 0 #paras[7]
rho1 = paras[8]
k_2 = paras[9]
```

```
nu1 = paras[10]
phi1 = paras[11]
nu2 = paras[12]
phi2 = paras[13]

N = S + I + R
N1 = S1 + I1 + R1

T = I + I1 + PSI + 2*PII + PIR + PS1I1 + 2*PI1I1 + PI1R1 + PSI1 + PS1I + PII1 + PI1R +



#equations :)
dS = B -(mu+rho+p)*S + sigma*(2*PSS + PSI + PSR + k_1*(PSS1 + PSI1 + PSR1)) +
mu*(2*PSS + PSI + PSR + PSS1 + PSI1 + PSR1) - nu*S
dI = -(mu + rho + p + delta)*I + sigma*((2*PII) + PSI + PIR + k_1*(PS1I + PIR1 + PII1)
+ mu*(2*PII + PSI + PIR + PS1I + PIR1 + PII1)
dR = delta*I - (mu+rho+ p)*R + sigma*(2*PRR + PSR + PIR + k_1*(PRR1 + PS1R + PI1R))
+ mu*(2*PRR + PSR + PIR + PRR1 + PS1R + PI1R) + nu*S
dPSS = (1/2)*rho*((S**2)/N) - (sigma+2*mu)*PSS - 2*nu*PSS
dPSI = rho*(1-h)*((S*I)/(N)) - (sigma + phi*h + 2*mu + delta)*PSI - nu*PSI
dPII = (1/2)*rho*((I**2)/N) + rho*h*((S*I)/N) + phi*h*PSI - (sigma + 2*mu + 2*delta)*P
dPSR = delta*PSI + rho*((S*R)/N) - (sigma+2*mu)*PSR + nu*(2*PSS -  PSR)
dPIR = rho*((I*R)/N) + 2*delta*PII - (sigma + 2*mu + delta)*PIR + nu*PSI
dPRR = delta*PIR + (1/2)*rho*((R**2)/N) + nu*PSR - (sigma + 2*mu)*PRR

dS1 = B1-(mu+ rho1 +p)*S1 + sigma*(k_1*(PSS1 + PS1I + PS1R)+k_2*(2*PS1S1 + PS1I1 + PS1
+ mu*(PSS1 + PS1I + PS1R +2*PS1S1 + PS1I1 + PS1R1) - nu1*S1
dI1 = -(mu+rho1+p+delta)*I1 + sigma*(k_1*(PII1+PSI1+PI1R)+k_2*(2*PI1I1+PS1I1+PI1R1))
```

```
    + mu*(PII1 + PSI1 + PI1R + 2*PI1I1 + PS1I1 + PI1R1)
    dR1 = delta*I1 - (mu+rho1+p)*R1 + sigma*(k_1*(PRR1  + PSR1 + PIR1)+ k_2*(PS1R1 + PI1R1
    + mu*(PRR1  + PSR1 + PIR1 + PS1R1 + PI1R1 + 2*PR1R1)+ nu1*S1
    dPS1S1 = (1/2)*rho1*((S1)**2/N1) - (k_2*sigma + 2*mu)*PS1S1 - 2*nu1*PS1S1
    dPS1I1 = rho1*(1-h)*((S1*I1)/N1) - (k_2*sigma + phi1*h + 2*mu + delta)*PS1I1 - nu1*PS1
    dPI1I1 = (1/2)*rho1*(I1**2/N1) + rho1*h*((S1*I1)/N) + phi1*h*PS1I1
    - (k_2*sigma + 2*mu + 2*delta)*PI1I1
    dPS1R1 = delta*PS1I1 + rho1*((S1*R1)/N1) - (k_2*sigma+2*mu)*PS1R1 + nu1*(2*PS1S1 - PS1
    dPI1R1 = rho1*((I1*R1)/N1) + 2*delta*PI1I1 - (k_2*sigma + 2*mu + delta)*PI1R1 + nu1*PS
    dPR1R1 = delta*PI1R1 + (1/2)*rho1*((R1**2)/N1) + nu1*PS1R1 - (k_2*sigma + 2*mu)*PR1R1

    dPSS1 = p*((S*S1)/N) - (k_1*sigma + 2*mu)*PSS1 - (nu+nu1)*PSS1
    dPSI1 = p*(1-h)*((S*I1)/N1) - (k_1*sigma + 2*mu + phi2*h + delta)*PSI1 - nu*PSI1
    dPS1I = p*(1-h)*((S1*I)/N) - (k_1*sigma + 2*mu + phi2*h + delta)*PS1I - nu1*PS1I
    dPII1 = p*((I1*I)/N) + p*h*((S*I1)/N1) + p*h*((S1*I)/N) + phi2*h*(PS1I + PSI1)
    - (k_1*sigma + 2*mu +2*delta)*PII1
    dPS1R = delta*PS1I + p*((S1*R)/N) - (k_1*sigma + 2*mu)*PS1R + nu*PSS1 - nu1*PS1R
    dPSR1 = delta*PSI1 + p*((S*R1)/N1) - (k_1*sigma + 2*mu)*PSR1 + nu1*PSS1 - nu*PSR1
    dPI1R = p*((I1*R)/N1) + delta*PII1 - (k_1*sigma + 2*mu + delta)*PI1R + nu*PSI1
    dPIR1 = p*((I*R1)/N) + delta*PII1 - (k_1*sigma + 2*mu + delta)*PIR1 + nu1*PS1I
    dPRR1 = p*((R*R1)/N) + delta*(PIR1 + PI1R) + nu1*PS1R + nu*PSR1 - (k_1*sigma + 2*mu)*P

    return [dS, dI, dR, dPSS, dPSI, dPII, dPSR, dPIR, dPRR, dS1, dI1, dR1, dPS1S1, dPS1I1,



cube = qmc.LatinHypercube(d=14)
samples = 1000
```

```
initial = [415000, 16.97, 0, 145.96, 0, 0, 0, 0, 0, 902.56, 16.97, 0, 145.96, 0, 0, 0, 0,
timeline = 1000
t = np.linspace(0,100, timeline)
S = np.zeros((samples,len(t)))
I = np.zeros((samples,len(t)))
R = np.zeros((samples,len(t)))
PSS = np.zeros((samples,len(t)))
PSI = np.zeros((samples,len(t)))
PII = np.zeros((samples,len(t)))
PSR = np.zeros((samples,len(t)))
PIR = np.zeros((samples,len(t)))
PRR = np.zeros((samples,len(t)))
S1 = np.zeros((samples,len(t)))
I1 = np.zeros((samples,len(t)))
R1 = np.zeros((samples,len(t)))
PS1S1 = np.zeros((samples,len(t)))
PS1I1 = np.zeros((samples,len(t)))
PI1I1 = np.zeros((samples,len(t)))
PS1R1 = np.zeros((samples,len(t)))
PI1R1 = np.zeros((samples,len(t)))
PR1R1 = np.zeros((samples,len(t)))
PSS1 = np.zeros((samples,len(t)))
PSI1 = np.zeros((samples,len(t)))
PS1I = np.zeros((samples,len(t)))
PII1 = np.zeros((samples,len(t)))
PS1R = np.zeros((samples,len(t)))
PSR1 = np.zeros((samples,len(t)))
PI1R = np.zeros((samples,len(t)))
```

```
PIR1 = np.zeros((samples,len(t)))
PRR1 = np.zeros((samples,len(t)))
#nu = np.zeros(length)
#nu1 = np.zeros(length)
#maxs = np.zeros(length)

parameters = cube.random(n=samples)

#going = 0
for i in range(samples):
    #normal
    params = parameters[i]
    stuff = odeint(m_eq, initial, t, args = (params,))
    S[i,:] = stuff[:,0]
    I[i,:] = stuff[:,1]
    R[i,:] = stuff[:,2]
    PSS[i,:] = stuff[:,3]
    PSI[i,:] = stuff[:,4]
    PII[i,:] = stuff[:,5]
    PSR[i,:] = stuff[:,6]
    PIR[i,:] = stuff[:,7]
    PRR[i,:] = stuff[:,8]
    S1[i,:] = stuff[:,9]
    I1[i,:] = stuff[:,10]
    R1[i,:] = stuff[:,11]
    PS1S1[i,:] = stuff[:,12]
    PS1I1[i,:] = stuff[:,13]
    PI1I1[i,:] = stuff[:,14]
```

```
PS1R1[i,:] = stuff[:,15]
PI1R1[i,:] = stuff[:,16]
PR1R1[i,:] = stuff[:,17]
PSS1[i,:] = stuff[:,18]
PSI1[i,:] = stuff[:,19]
PS1I[i,:] = stuff[:,20]
PII1[i,:] = stuff[:,21]
PS1R[i,:] = stuff[:,22]
PSR1[i,:] = stuff[:,23]
PI1R[i,:] = stuff[:,24]
PIR1[i,:] = stuff[:,25]
PRR1[i,:] = stuff[:,26]
print(i)

#for vaccination plot
'''
for j in range(samples):
    params = np.append(np.append(np.append(np.append(parameters[0][:4],parameters[i][4
    stuff = odeint(m_eq, initial, t, args = (params,))
    S[going,:] = stuff[:,0]
    I[going,:] = stuff[:,1]
    R[going,:] = stuff[:,2]
    PSS[going,:] = stuff[:,3]
    PSI[going,:] = stuff[:,4]
    PII[going,:] = stuff[:,5]
    PSR[going,:] = stuff[:,6]
    PIR[going,:] = stuff[:,7]
    PRR[going,:] = stuff[:,8]
```

```
            S1[going,:] = stuff[:,9]
            I1[going,:] = stuff[:,10]
            R1[going,:] = stuff[:,11]
            PS1S1[going,:] = stuff[:,12]
            PS1I1[going,:] = stuff[:,13]
            PI1I1[going,:] = stuff[:,14]
            PS1R1[going,:] = stuff[:,15]
            PI1R1[going,:] = stuff[:,16]
            PR1R1[going,:] = stuff[:,17]
            PSS1[going,:] = stuff[:,18]
            PSI1[going,:] = stuff[:,19]
            PS1I[going,:] = stuff[:,20]
            PII1[going,:] = stuff[:,21]
            PS1R[going,:] = stuff[:,22]
            PSR1[going,:] = stuff[:,23]
            PI1R[going,:] = stuff[:,24]
            PIR1[going,:] = stuff[:,25]
            PRR1[going,:] = stuff[:,26]
            nu[going] = params[4]
            nu1[going] = params[10]
            maxs[going] = np.max(np.add(stuff[:,1],stuff[:,10]))
            going += 1
        print(i)
        '''
'''
for_the_plot = pd.DataFrame({"nu": nu, "nu1": nu1, "Max Infected": maxs})
for_the_plot.to_csv("Mixed Pairing inf vax trial100 Results No Header.csv", header = False
'''
```

```
mean_S = np.mean(S,axis=0)
mean_I = np.mean(I,axis=0)
mean_R = np.mean(R,axis=0)
mean_PSS = np.mean(PSS,axis=0)
mean_PSI = np.mean(PSI,axis=0)
mean_PII = np.mean(PII,axis=0)
mean_PSR = np.mean(PSR,axis=0)
mean_PIR = np.mean(PIR,axis=0)
mean_PRR = np.mean(PRR,axis=0)
mean_S1 = np.mean(S1,axis=0)
mean_I1 = np.mean(I1,axis=0)
mean_R1 = np.mean(R1,axis=0)
mean_PS1S1 = np.mean(PS1S1,axis=0)
mean_PS1I1 = np.mean(PS1I1,axis=0)
mean_PI1I1 = np.mean(PI1I1,axis=0)
mean_PS1R1 = np.mean(PS1R1,axis=0)
mean_PI1R1 = np.mean(PI1R1,axis=0)
mean_PR1R1 = np.mean(PR1R1,axis=0)
mean_PSS1 = np.mean(PSS1,axis=0)
mean_PSI1 = np.mean(PSI1,axis=0)
mean_PS1I = np.mean(PS1I,axis=0)
mean_PII1 = np.mean(PII1,axis=0)
mean_PS1R = np.mean(PS1R,axis=0)
mean_PSR1 = np.mean(PSR1,axis=0)
mean_PI1R = np.mean(PI1R,axis=0)
mean_PIR1 = np.mean(PIR1,axis=0)
mean_PRR1 = np.mean(PRR1,axis=0)
```

```
#mean_nu = np.mean(nu,axis=0)
#mean_nu1 = np.mean(nu1,axis=0)
#max_inf = np.max(np.add(I,I1), axis = 0)

'''
for_vax_plot = pd.DataFrame({"nu": mean_nu, "nu1": mean_nu1, "Max Infected": max_inf})
for_vax_plot.to_csv("Mixed Pairing Results No Header.csv", header = False)

results = pd.DataFrame({"Time": t, "S": mean_S, "I": mean_I, "R": mean_R, "PSS": mean_PSS,
results.to_csv("Mixed Pairing Results No Header.csv", header = False)
'''


plt.plot(t, mean_S, '-', linewidth=2, color='tab:green')
plt.xlabel("Time")
plt.ylabel("Low Risk Susceptible Individuals")
plt.savefig("low risk susceptible, final")
plt.show()
plt.plot(t, mean_I, '-', linewidth=2, color='tab:green')
plt.xlabel("Time")
plt.ylabel("Low Risk Infected Individuals")
plt.savefig("Low Risk Infected Individuals , final")
plt.show()
plt.plot(t, mean_R, '-', linewidth=2, color='tab:green')
plt.xlabel("Time")
plt.ylabel("Low Risk Recovered Individuals")
plt.savefig("Low Risk Recovered Individuals, final")
plt.show()
```

```
plt.plot(t, mean_PSS, '-', linewidth=2, color='tab:green')
plt.xlabel("Time")
plt.ylabel("Low Risk Susceptible Pairs")
plt.savefig("Low Risk Susceptible Pairs, final")
plt.show()
plt.plot(t, mean_PSI, '-', linewidth=2, color='tab:green')
plt.xlabel("Time")
plt.ylabel("Low Risk Susceptible Infected Pairs")
plt.savefig("Low Risk Susceptible Infected Pairs final")
plt.show()
plt.plot(t, mean_PII, '-', linewidth=2, color='tab:green')
plt.xlabel("Time")
plt.ylabel("Low Risk Infected Pairs")
plt.savefig("Low Risk Infected Pairs,  final")
plt.show()
plt.plot(t, mean_PSR, '-', linewidth=2, color='tab:green')
plt.xlabel("Time")
plt.ylabel("Low Risk Susceptible Recovered Pairs")
plt.savefig("Low Risk Susceptible Recovered Pairs,  final")
plt.show()
plt.plot(t, mean_PIR, '-', linewidth=2, color='tab:green')
plt.xlabel("Time")
plt.ylabel("Low Risk Recovererd Infected Pairs")
plt.savefig("Low Risk Recovererd Infected Pairs, final")
plt.show()
plt.plot(t, mean_PRR, '-', linewidth=2, color='tab:green')
plt.xlabel("Time")
plt.ylabel("Low Risk Recovered Pairs")
```

```
plt.savefig("Low Risk Recovered Pairs,  final")
plt.show()
plt.plot(t, mean_S1, '-', linewidth=2, color='tab:green')
plt.xlabel("Time")
plt.ylabel("High Risk Susceptible Individuals")
plt.savefig("High Risk Susceptible Individuals,  final")
plt.show()
plt.plot(t, mean_I1, '-', linewidth=2, color='tab:green')
plt.xlabel("Time")
plt.ylabel("High Risk Infected Individuals")
plt.savefig("High Risk Infected Individuals,  final")
plt.show()
plt.plot(t, mean_R1, '-', linewidth=2, color='tab:green' )
plt.xlabel("Time")
plt.ylabel("High Risk Recovered Individuals")
plt.savefig("High Risk Recovered Individuals, final")
plt.show()
plt.plot(t, mean_PS1S1, '-', linewidth=2, color='tab:green')
plt.xlabel("Time")
plt.ylabel("High Risk Susceptible Pairs")
plt.savefig("High Risk Susceptible Pairs, long term")
plt.show()
plt.plot(t, mean_PS1I1, '-', linewidth=2, color='tab:green')
plt.xlabel("Time")
plt.ylabel("High Risk Susceptible Infected Pairs")
plt.savefig("High Risk Susceptible Infected Pairs, final")
plt.show()
plt.plot(t, mean_PI1I1, '-', linewidth=2, color='tab:green')
```

```
plt.xlabel("Time")
plt.ylabel("High Risk Infected Pairs")
plt.savefig("High Risk Infected Pairs, final")
plt.show()
plt.plot(t, mean_PS1R1, '-', linewidth=2, color='tab:green')
plt.xlabel("Time")
plt.ylabel("High Risk Susceptible Recovered Pairs")
plt.savefig("High Risk Susceptible Recovered Pairs,  final")
plt.show()
plt.plot(t, mean_PI1R1, '-', linewidth=2, color='tab:green')
plt.xlabel("Time")
plt.ylabel("High Risk Infected Recovered Pairs")
plt.savefig("High Risk Infected Recovered Pairs,  final")
plt.show()
plt.plot(t, mean_PR1R1, '-', linewidth=2, color='tab:green')
plt.xlabel("Time")
plt.ylabel("High Risk Recovered Pairs")
plt.savefig("High Risk Recovered Pairs,  final")
plt.show()
plt.plot(t, mean_PSS1, '-', linewidth=2, color='tab:green')
plt.xlabel("Time")
plt.ylabel("High Risk and Low Risk Susceptible Mixed Pairs")
plt.savefig("High Risk and Low Risk Susceptible Mixed Pairs,  final")
plt.show()
plt.plot(t, mean_PSI1, '-', linewidth=2, color='tab:green')
plt.xlabel("Time")
plt.ylabel("High Risk Infected Low Risk Susceptible Mixed Pairs")
plt.savefig("High Risk Infected Low Risk Susceptible Mixed Pairs,  final")
```

```
plt.show()
plt.plot(t, mean_PS1I, '-', linewidth=2, color='tab:green')
plt.xlabel("Time")
plt.ylabel("Low Risk Infected High Risk Susceptible Mixed Pairs")
plt.savefig("Low Risk Infected High Risk Susceptible Mixed Pairs,  final")
plt.show()
plt.plot(t, mean_PII1, '-', linewidth=2, color='tab:green')
plt.xlabel("Time")
plt.ylabel("High Risk and Low Risk Infected Mixed Pairs")
plt.savefig("High Risk and Low Risk Infected Mixed Pairs,  final")
plt.show()
plt.plot(t, mean_PS1R, '-', linewidth=2, color='tab:green')
plt.xlabel("Time")
plt.ylabel("High Risk Susceptible Low Risk Recovered Mixed Pairs")
plt.savefig("High Risk Susceptible Low Risk Recovered Mixed Pairs,  final")
plt.show()
plt.plot(t, mean_PSR1, '-', linewidth=2, color='tab:green')
plt.xlabel("Time")
plt.ylabel("High Risk Recovered Low Risk Susceptible Mixed Pairs")
plt.savefig("High Risk Recovered Low Risk Susceptible Mixed Pairs,  final")
plt.show()
plt.plot(t, mean_PI1R, '-', linewidth=2, color='tab:green')
plt.xlabel("Time")
plt.ylabel("High Risk Infected Low Risk Recovered Mixed Pairs")
plt.savefig("High Risk Infected Low Risk Recovered Mixed Pairs,  final")
plt.show()
plt.plot(t, mean_PIR1, '-', linewidth=2, color='tab:green')
plt.xlabel("Time")
```

```
plt.ylabel("Low Risk Infected High Risk Recovered Mixed Pairs")
plt.savefig("Low Risk Infected High Risk Recovered Mixed Pairs,  final")
plt.show()
plt.plot(t, mean_PRR1, '-', linewidth=2, color='tab:green')
plt.xlabel("Time")
plt.ylabel("High Risk and Low Risk Recovered Mixed Pairs")
plt.savefig("High Risk and Low Risk Recovered Mixed Pairs,  final")
plt.show()
```

B Matrices

$$F = \begin{bmatrix}
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
\rho h & 0 & \phi h & 0 & \tilde{\phi} h & 0 & 0 & \varrho h & 0 & \Phi h & 0 & \tilde{\phi} h & 0 & 0
\end{bmatrix}$$

$$
V = \begin{bmatrix}
\mu+\rho+p+\delta & -2\sigma-2\mu & -\sigma-\mu & -\sigma-\mu & -k_1\sigma-\mu & -k_1\sigma-\mu & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
-\rho h & \sigma+2\mu+2\delta & -\phi h & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
-\rho(1-h) & 0 & \phi h+\delta+2\mu+\nu+\sigma & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & -2\delta & -\nu & \sigma+2\mu-\delta & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
-p(1-h) & 0 & 0 & 0 & phih+k_1\sigma+\delta+2\mu+\tilde{\nu} & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & -\tilde{\nu} & k_1\sigma+\delta+2\mu & -\delta & 0 & 0 & 0 & -\tilde{\phi}h & 0 & 0 \\
-ph & 0 & 0 & 0 & -\tilde{\phi}h & 0 & k_1\sigma+2\delta+2\mu & -ph & -2k_2\sigma-2\mu & -k_2\sigma-\mu & -k_2\sigma-\mu & -k_1\sigma-\mu & -k_1\sigma-\mu \\
0 & 0 & 0 & 0 & 0 & 0 & -k_1\sigma-\mu & \mu+\hat{\rho}+p+\delta & -\hat{\rho}h & -\tilde{\phi}h & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & -\hat{\rho}h & k_2\sigma+2\delta+2\mu & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & -\hat{\rho}(1-h) & 0 & \hat{\phi}h+k_2\sigma+\delta+2\mu+\hat{\nu} & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & -2\delta & -\hat{\nu} & k_2\sigma+\delta+2\mu & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & p(1-h) & 0 & 0 & 0 & \hat{\phi}h+k_1\sigma+\delta+2\mu+\nu & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & -\delta & 0 & 0 & 0 & -\nu & k_1\sigma+\delta+2\mu & 0 \\
\mu+p+\delta-p\left(\frac{\hat{N}}{N}\right) & 2\mu+2\delta & \delta+\mu & \delta+\mu & \delta+\mu & 2\mu+2\delta & \mu+\hat{\rho}+p+\delta-p\left(\frac{N}{N}\right) & 2\mu+2\delta & \delta+\mu & \delta+\mu & \delta+\mu & \delta+\mu & \delta+\mu
\end{bmatrix}
$$

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