2 Populations with Migration

Distribution of Resources in an Epidemic Using Two Patch SEIR Model

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1 Introduction

In this paper, we explore how coupling two SEIR models with crossover migrations might affect disease spread and how restrictions on this migration could have an impact on peak infected. We also address how the distribution of resources, namely vaccines, could influence the peak infections of the the disease in question.

1.1 Motivation

During the COVID-19 pandemic, many countries restricted migration in order to reduce the spread of COVID-19. We ask how much these restrictions help in the reduction of infections spread. We also like to study how the distribution of vaccines to other countries may affect a host country and how "sharing" vaccines may benefit all parties involved. By "sharing", we mean that one country has control over the administration of vaccines. Do they keep the vaccines for themselves or do they allocate some of those vaccines to the other countries to help reduce how many people get infected? We will be studying this effect by using real numbers from COVID-19 on two countries, Germany and France.

1.2 Overview of the Project

The overarching objective of our research paper is to explore disease transmission in two countries coupled by migration. In section 2, we construct two-patch SEIR models and formulate equations, clearly stating our assumptions. In addition to this, we discuss the parameters of these models, as well as our methods pertaining to parameter values and the altering of specific parameters that we find compelling.

In section 3.1, we explore how migration rates may impacts the peak number of infected individuals. We look at several cases to solve what the best migration rates between the two countries are. In section 3.2, we discuss the differing outcomes that occur when introducing a fixed and finite amount of vaccine. Thus, we must decide how to distribute our limited supply of vaccines between the two countries. This leads us to experiment with different scenarios pertaining to assisting one's home patch versus giving some help to the neighboring patch.

1.3 Previous work

Multi-patch SEIR models have been studied extensively before. We found lots of good papers that closely relate to what we are studying in our research.

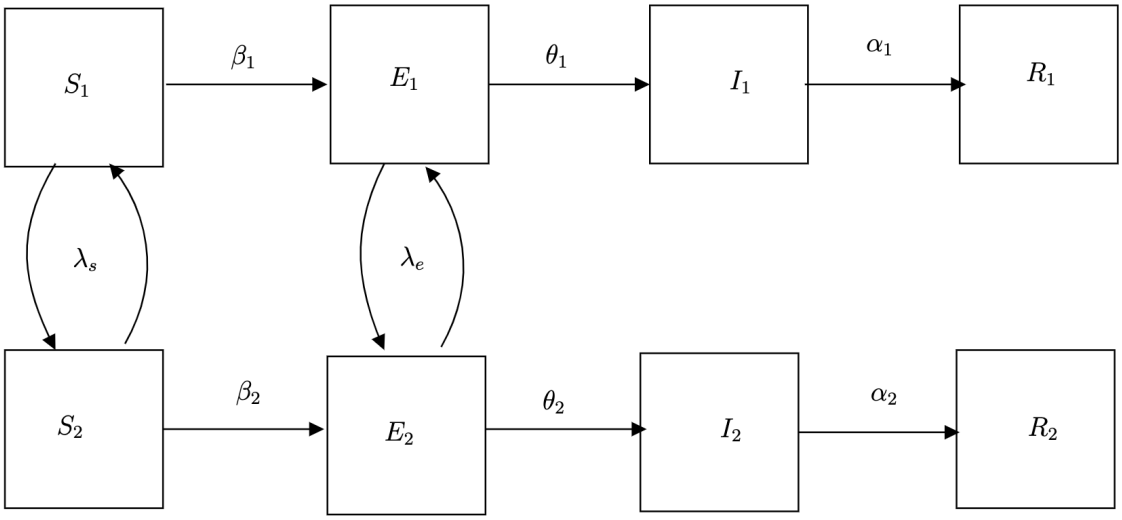
In [5], the effect of human travel on the transmission of dengue disease was studied. Intriguingly, the model included susceptible and infective classes for mosquitoes in addition to the susceptible, infective, and recovered classes for humans. There was a heavy emphasis on basic reproduction number, and it was ultimately concluded that restricting the travel of hosts from a high disease dominant patch can effectively control the disease in a low disease dominant patch.

In [6], research was performed on the transmission rate between 3 different countries with an "A" class that is the unascertained class. The unascertained cases included asymptomatic cases and those with mild symptoms who could recover without seeking medical care and thus were not reported to authorities. This paper gave us clarity as it provided us with a good parameter to change and presented a framework showing how this variable could affect other classes in our model. We also used this paper to get parameters and data for Germany and France.

2 Methods

For this section, we will cover 2 different 2-patch models (one without vaccination and the other with) along with the parameters that connect them together. We will be deriving the differential equations that support the models along with identifying assumptions that justify it. Subsequently, we hypothesize how altering these rates will reduce the spread of infections.

2.1 2 Patch SEIR Model



This model is a two-coupled SEIR model where "S" is the susceptible class, "E" is the exposed class, "I" is the infected class, and "R" is the recovered class. β is the rate at which the susceptible class becomes exposed, θ is the rate at which the exposed class becomes infected, and α is the rate at which infected becomes recovered. The interesting part of this model is λ, the rate at which individuals migrate from one country to another. We will assume that lambda for the susceptible class and the lambda for the exposed class is the same.

2.1.1 Equations

$$\frac{dS_1}{dt} = \lambda_s S_2 - \lambda_s S_1 - \beta_1 S_1 E_1 \tag{1}$$
$$\frac{dE_1}{dt} = \beta_1 S_1 E_1 - \theta_1 E_1 + \lambda_e E_2 - \lambda_e E_1 \tag{2}$$
$$\frac{dI_1}{dt} = \theta_1 E_1 - \alpha_1 I_1 \tag{3}$$
$$\frac{dR_1}{dt} = \alpha_1 I_1 \tag{4}$$

$$\frac{dS_2}{dt} = \lambda_s S_1 - \lambda_s S_2 - \beta_2 S_2 E_2 \tag{5}$$
$$\frac{dE_2}{dt} = \beta_2 S_2 E_2 - \theta_2 E_2 + \lambda_e E_1 - \lambda_e E_2 \tag{6}$$
$$\frac{dI_2}{dt} = \theta_2 E_2 - \alpha_2 I_2 \tag{7}$$
$$\frac{dR_2}{dt} = \alpha_2 I_2 \tag{8}$$

2.1.2 Assumptions of the model

1. The migration will only occur between 2 countries.
2. λ_s and λ_e are the same for simplicity.
3. Individuals do not get the disease during travel. The population is either exposed and travel exposed or are susceptible and travel susceptible.
4. Once individuals get infected by the disease, they become permanently immune to it.
5. Infected individuals do not travel.
6. There is no birth or death within the system.
7. Recovered individuals can migrate but their migration is irrelevant to our model and as such is not modeled.

2.1.3 Model parameters

The parameters we will be implementing into our model can be found in Table 1. These values are associated with the surge of the Coronavirus in 2020 between several European countries, Germany and France. Researchers sought to estimate realistic parameters to predict trends of the epidemic and to ultimately prevent the severity of the infectious outbreak. The research in [6] and our project

share some substantial similarities. The mathematical model in [6] is also an SEIR model, except theirs has an addition of an unascertained and hospitalized class.

2.1.4 Examining 3 Cases

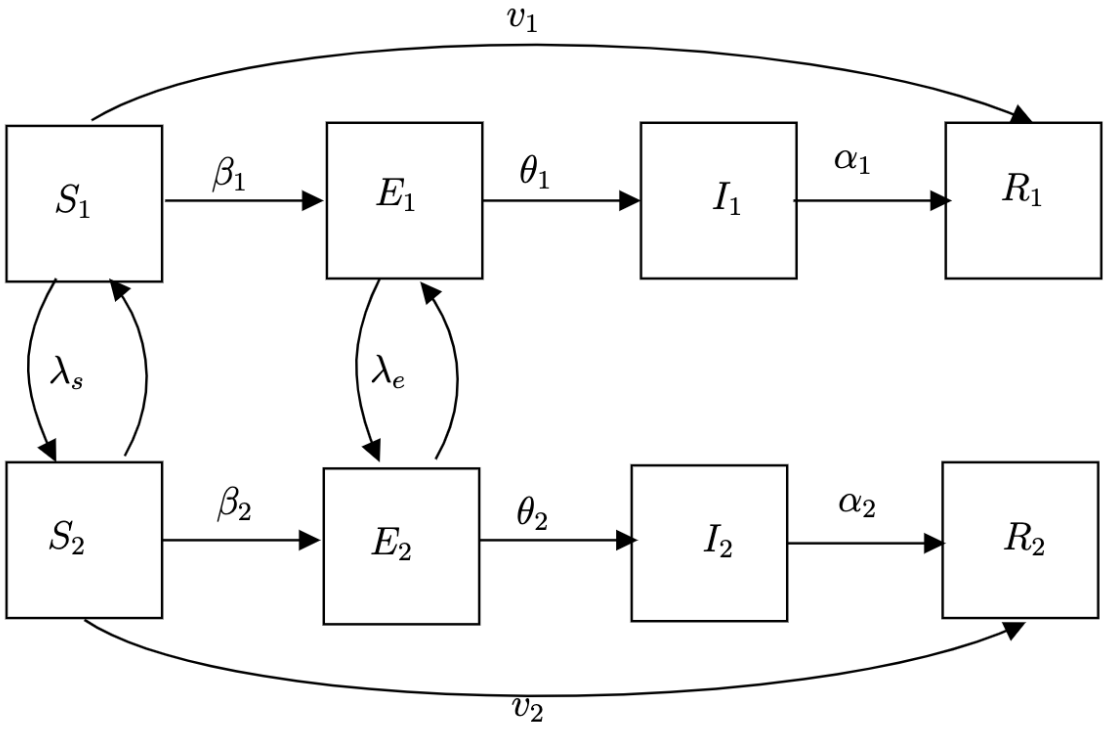
For our model, we will be considering 3 different types of problems:

In case 1, we created a hypothetical scenario and assume that both countries would have the same transmission, exposed, and infection rates with the infection beginning in country 1. The purpose of this is to analyse the impact and effectiveness of shifting the rate of travelling (λ) between the 2 countries, whether it would reduce the peak number of infected or simply have no effect.

In case 2, we chose the parameters of 2 well-developed and greatly populated countries to formulate a more realistic scenario. We are using the rates from [6] to find the optimal strategy to mitigate the outbreak. The initial population of each state/class is shown in Table 1. We assumed that country 1 started infected and country 2 does not.

In case 3, we created an extreme scenario where country 1 is performing much "better" than country 2. By "better", we mean that country 1 has a considerably lower β in comparison to country 2 which has a higher β and starts infected. We then would like to observe the effects λ has on the peak infected in each country.

2.2 2 Patch SEIR Model with Vaccination



We added a v parameter to our 2 Patch SEIR model to create a model with vaccines. v_1 and v_2 are rates of vaccine where $v_1 + v_2$ equals the total number of vaccine (V). In this case, v is a fixed number where once individuals are vaccinated, they cannot get the disease. In this model, λ is the transfer between two countries where $\lambda_s = \lambda_e$.

2.2.1 Equations

$$\frac{dS_1}{dt} = \lambda_s S_2 - \lambda_s S_1 - \beta_1 S_1 E_1 - v_1 \tag{9}$$
$$\frac{dE_1}{dt} = \beta_1 S_1 E_1 - \theta_1 E_1 + \lambda_e E_2 - \lambda_e E_1 \tag{10}$$
$$\frac{dI_1}{dt} = \theta_1 E_1 - \alpha_1 I_1 \tag{11}$$
$$\frac{dR_1}{dt} = \alpha_1 I_1 + v_1 \tag{12}$$

$$\frac{dS_2}{dt} = \lambda_s S_1 - \lambda_s S_2 - \beta_2 S_2 E_2 - v_2 \tag{13}$$
$$\frac{dE_2}{dt} = \beta_2 S_2 E_2 - \theta_2 E_2 + \lambda_e E_1 - \lambda_e E_2 \tag{14}$$
$$\frac{dI_2}{dt} = \theta_2 E_2 - \alpha_2 I_2 \tag{15}$$
$$\frac{dR_2}{dt} = \alpha_2 I_2 + v_2 \tag{16}$$

$$V = v_1 + v_2 \tag{17}$$

2.2.2 Assumptions of model

1. Assumptions earlier apply.
2. Vaccine is 100% effective.
3. There is a limit amount of vaccines each time period V.
4. Country 1 has control over the distribution of the vaccines.

2.2.3 Model parameters

In section 2.1.3 where we discussed the estimation of parameters for the 2-patch SEIR model, the research article we sourced was published in November 9, 2020 [3]. During that period, the Covid-19 vaccination has yet to be released as it was first developed by Pfizer-BioNTech in December 11, 2020. Therefore, we will observe the vaccination rates of both these countries 6-12 months after after the vaccine was invented, between June 2021 and December 2021.

We will be employing vaccination doses produced per time for the vaccination parameter. Using the selected time frame, we will approximate realistic parameters by calculating the averages between

the peak and least number of vaccines administered per day. Refer to Figure 1 from [3] below to observe how the number of doses issued change throughout the period.

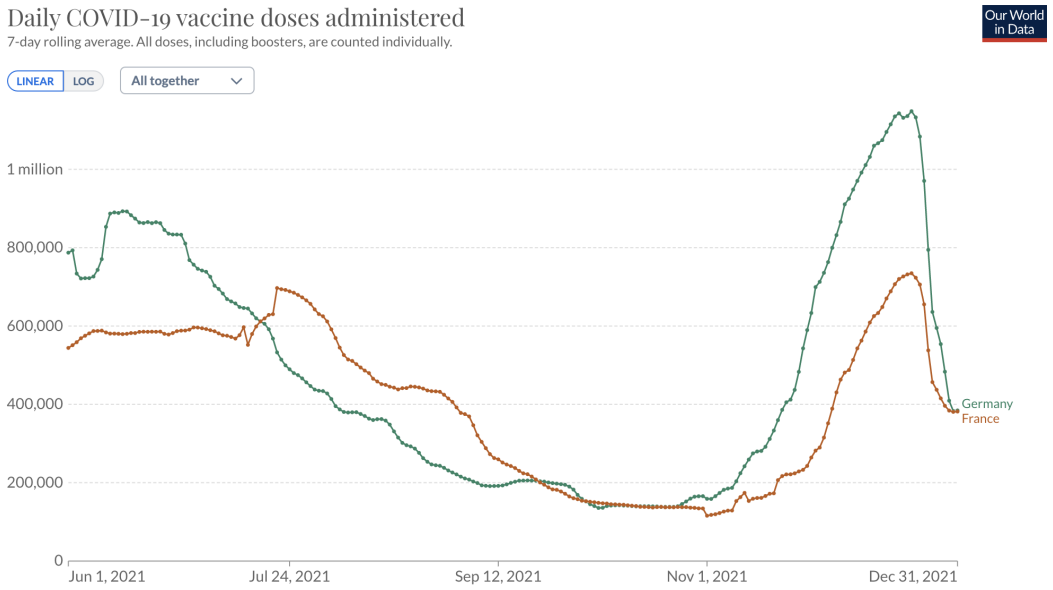


Figure 1: Number of Vaccinations Administered between June 2021 and December 2021

2.2.4 Examining 2 Vaccinated Cases

Given that the administering of a vaccine was an aspect which impacted the spread of COVID-19, we wanted to account for such a factor in our model. Therefore, we will be using the combined average number of vaccinations administered per day (V) from Table 3 in Section 2.3, 1.068mil. For simplicity, we will round this number to 1,000,000 and study how to distribute these vaccines between the two countries. For this model, we will be investigating 2 additional different types of problems:

In case 4, similarly to earlier we are going to look at Germany and France numbers to find an "optimal" distribution of vaccines between them. By "optimal", we mean the best case to lower both curves. We assume that the total number V is a fixed number of vaccines that could be distributed to either country. In this case we are using our real parameters from table 1 and $\lambda = 0.004319$ from [6].

$$v_1 = \text{Number of vaccines administered in Country 1 per day}$$
$$v_2 = \text{Number of vaccines administered in Country 2 per day}$$

In case 5, we created an extreme scenario where there is a large disparity in βs. We assume that country 1 has a significantly lower β than country 2. Only Country 2 started with the disease. We

examined the peak infected number to determine an "optimal" distribution of vaccines. In this case, we are using numbers from table 2 and $\lambda = 0.004319$.

2.3 Data

Using the methods from the estimation of parameters, we have compiled some data to input into our mathematical model in Matlab and Python.

Country	Country 1	Country 2
Population Size	82,927,922	65,228,495
R_0	4.03	4.00
Infectious Period	2.3	2.3
β	$2.1 * 10^{-8}$	$2.666 * 10^{-8}$
θ	$\frac{1}{5.2}$	$\frac{1}{5.2}$
α	1/2.3	1/2.3

Table 1 [1]

Country	Country 1	Country 2
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α	1/2.3	1/2.3

Table 2 [2]

	v_1	v_2	V
Maximum	1.15mil	734,593	1.885mil
Minimum	135,469	115,812	251,281
Average	642,734.5	425,202.5	1.068mil

Table 3 [3]

[1] Data from [6]. We used Germany's data as country 1 and France as country 2

[2] Data from [6]. The only change from table 1 to table 2 is β

[3] Data from [3]. We used Germany's data as country 1 and France's as country 2

3 Results

3.1 Changes in Lambda's Effects

We started by looking at how changes in λ may affect the rate of infection within the population of multiple countries. We looked into 2 different cases as outlined earlier and our results are as follows.

3.1.1 Hypothetical Parameters

For the first case, we took the two countries, used the same parameters and altered the λ to scope for a "best value" for λ that would help reduce the peak number of infected individuals. After running through the experiment, we discovered that the change in λ did not have an influence on the the peak for either of the two countries, but instead it affected the time in which the infected population peaked.

In the figure 2, we can see a horizontal line, indicating that an increase in λ did not change the peak number of infected individuals. This is a conclusion we expected because when two countries have the same parameters, they can be treated as one population and therefore a change in λ will have no effect of the peak infections.

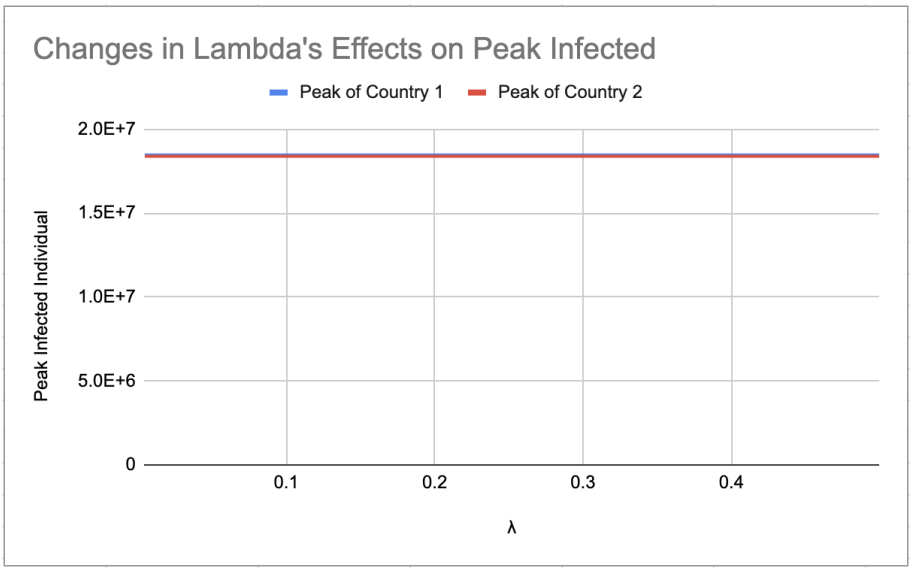


Figure 2: Peak infected individuals vs lambda

From the first results, we decided to graph a chart that shows the difference in time when the two countries peaked for each λ, shown in figure 3. Since, Country 1 starts with the disease, Country

2 will get the disease from Country 1 this causes a delay in when Country 2 will start get the disease. From the graph we see that, around 10% the two countries' peak at the same time. Again, this result is not too surprising. Since Country 1 there is this delay to when Country 2 gets the disease, this causes the peak infection to occur later. Beyond 10%, both lines have stabilized hence increasing the λ after that point will have no impact on number of days taken for both countries to peak their infection.

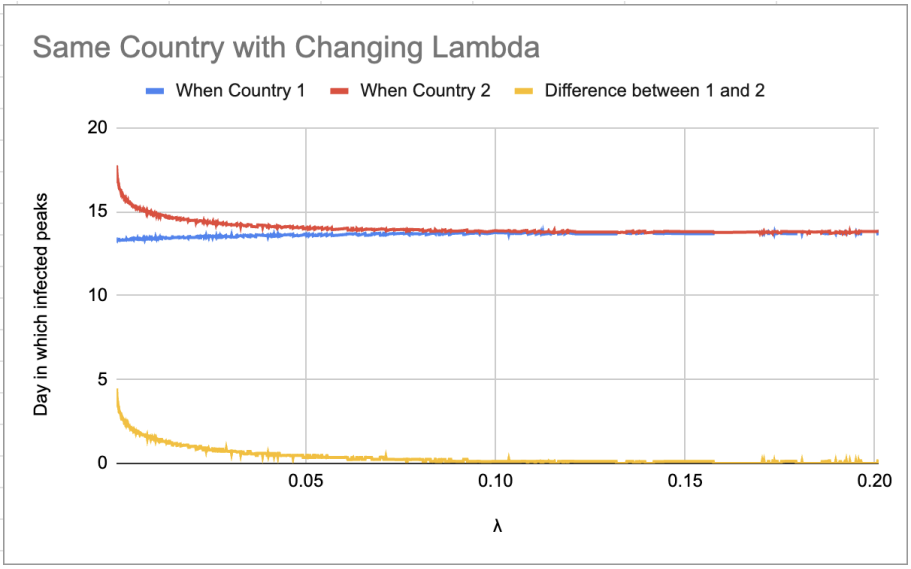
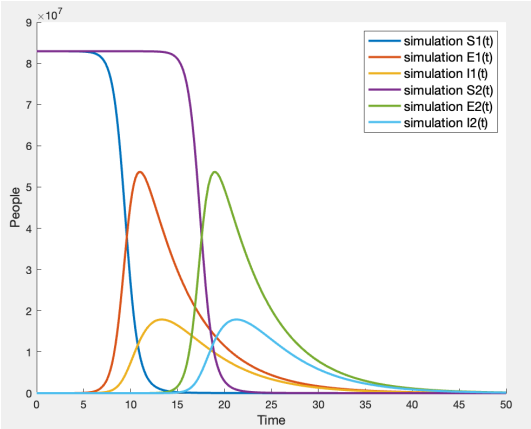
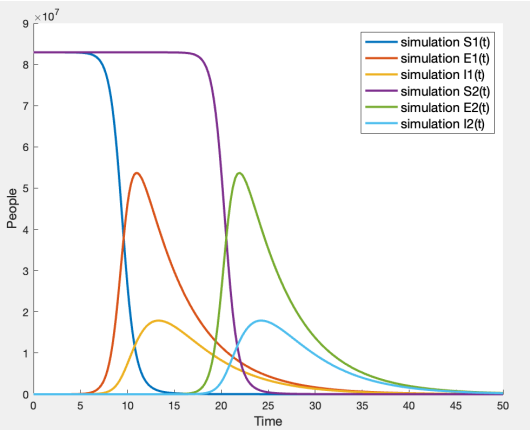


Figure 3: Days until peak vs lambda

Table 4 shows what we mean when we are talking about the difference in peaks between the two countries. We can see that with different λ values, the peaks and the slope of the curves do not change but the distance between when both countries peak does change. When looking at the two graphs in Table 4, we see that the graph on the left has a smaller distance from each peak than the graph on the right. This shows us that a change in λ does not change the peak of infections or the rate at which the infections occur. A change in λ only changes the time in which Country 2 will peak because there is a longer delay in when the Country will be exposed to the disease.



Lambda = 0.00000043



Lambda = 0.0000000043

Table 4

3.1.2 Germany and France

For this section, we wanted to see if the conclusions from section 3.1.1 would hold if we changed our parameters to more accurate depiction of two countries. We decided to use numbers from [6] which is based on COVID-19 in Germany and France.

In Figure 4, we see how the change in λ affects the peak infection from both countries. Employing realistic numbers from Table 1 so that the β for both countries now differs. Germany has a lower exposure rate and starts with the disease, where France has a higher exposure rate and gets the disease from Germany. In this figure as we can see slight curves in the peak infected as λ increases. We can conclude that λ only mildly affects the peak of the curves in both of the countries. It is important to note that in the "best-case" scenario, if France started with no disease, the disease will never transmit to their population if $\lambda = 0$, but this is not realistic so we will not consider this to be the "best" case. It is interesting that Germany is performing better as λ increases. We believe this is because more exposed individuals are leaving Germany and this leads to a drop in their peak as less people are around to affect susceptible individuals. From France's perspective, it is worse for them because Germany's exposed individuals are migrating to France, hence their lower β does not matter when migration numbers are involved. In a holistic standpoint, the λ, does not really affect how many people get infected or not. It seams that Germany's numbers go down as France's numbers so up, so the same total amount of people will get infected. We were not able to find a "best" λ for this case because no matter what the λ is in a global standpoint the same number of people will get infected.

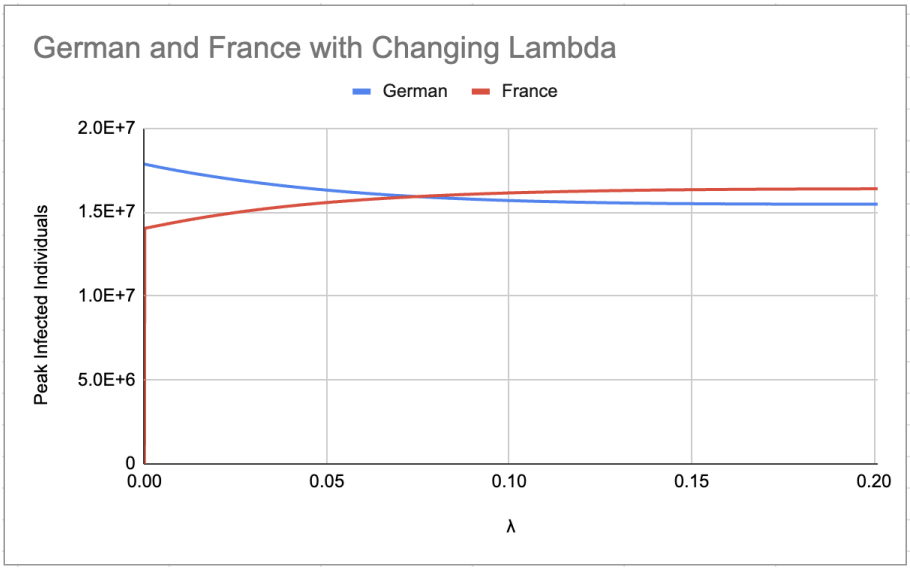


Figure 4: Germany & France's Peak Infection with Changing Lambda

3.1.3 Extreme Values

For Case 3, we took extreme values where Country 1 is handling the pandemic significantly better than Country 2. In Figure 5, we can see that Country 1's peak number of infected individuals increases significantly as λ increases. This is increasing because more exposed individuals from Country 2 where the disease is more severe are migrating over to Country 1. Thus, we notice that Country 1 possessing a low β does not matter as much since they are receiving a lot of exposed individuals. Looking at Country 2, we see that they are doing slightly worse when λ increases but not a significant amount. This is because they are gaining more susceptible individuals. The population vulnerable to getting infected becomes larger in Country 2 but since they lose some of the exposed individuals gaining more susceptible individuals does not affect them very much.
The results in this case, are a little bit different that they were before in case 2. In this case with extreme values, an increasing lambda really hurts Country 1 significantly. This also causes more people to get infected and in a global standpoint more susceptible individuals are getting infected. In the earlier case we said that there was no "best" value for λ, however in this case the "best" value for λ is when $\lambda = 0$ or when λ is as low as possible.

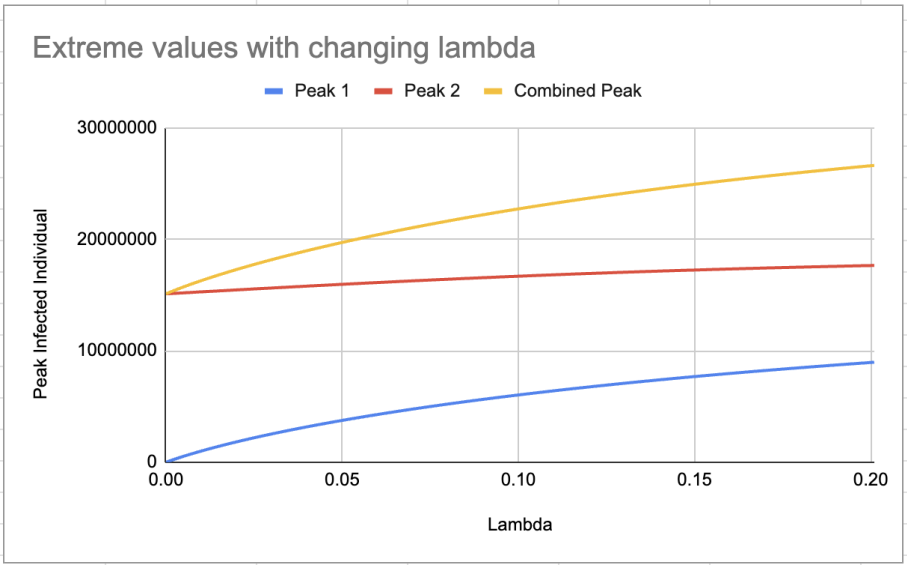


Figure 5: Extreme values with changing lambda

3.2 Vaccines

3.2.1 Germany and France

In Case 4, we investigated how administering vaccines would effect 2 countries, Germany and France. We made the assumption that Country 1 (based off of Germany's data) started with all the vaccines and have the ability to keep 100% of them or allocate a portion of it to Country 2 (based off of France's data). As could reasonably be expected, as Country 1 administered its vaccines to Country 2, the peak infected individual values increased, and vice versa for Country 2 as it was receiving these vaccines from Country 1. While not insignificant, the changes that occurred were far from drastic, implying that the relatively stable nature of these countries somewhat prevented the occurrence of high values for peak infected individuals. Even though Country 1 peaks higher when it giving away vaccines, we see that the combined peak slightly decreases, reflecting a better overall outcome. We can conclude from Figure 6, that there is not an "optimal" distribution of vaccines. If Country 1 is in control of the vaccines, it would make sense for them to keep all the vaccines for themselves. If we look at a global standpoint, it is slightly "better" for Country 1 to give some of the vaccines to the country doing slightly worse than them. This will decrease the total number of peak infected individuals in a global standpoint but would increase the total number of peak infected in Country 1.

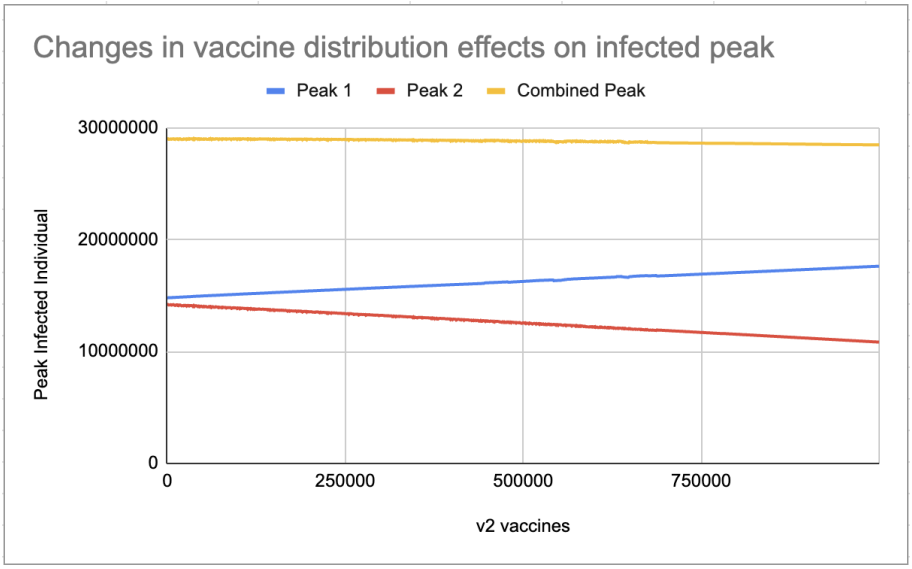


Figure 6: Peak infected vs vaccines given to country 2

3.2.2 Extreme Vaccination Values

For our final case, we took extreme values of β from Table 2 in Section 2.3. We also multiplied V by 8 to discover what the "best" distribution of vaccines would be when Country 1 is performing significantly better than Country 2. From this exaggerated scenario, we drew contrasting outcomes as opposed from the previous case. The results from Figure 7 show that as Country 1 distributes more vaccines, their peak infection seems to escalate steadily. However, as Country 2 receives more vaccines, their peak infected population does not seem to decrease but rather stabilize horizontally at just under 20,000,000 infected individuals. We believe due to the high β, administering any number of vaccines into that population will not benefit the either of the countries. Additionally, the combined peak seems to increase as more vaccines are being distributed to Country 2. Therefore, in extreme cases like this, it is more ideal in both a global and individual standpoint for a country with lower β to keep the vaccines to themselves rather than issuing them to a highly infected country.

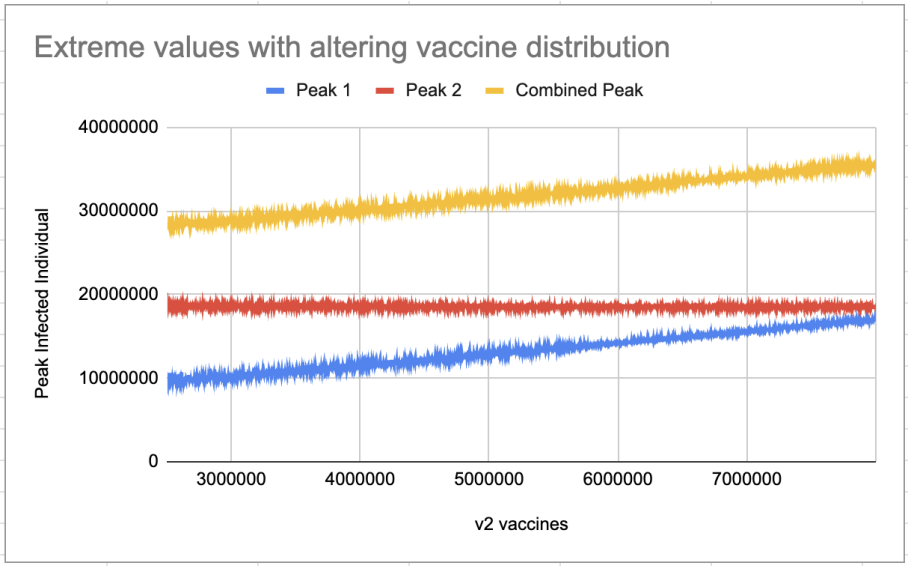


Figure 7: Peak infected individual with extreme data

4 Conclusion

4.1 Conclusion on Migration (λ)

The results from altering λ helped us conclude some interesting notes that may be reflected towards the real-world. Firstly, if two countries hypothetically had the exact same exposure, infection and recovery rate for a particular disease, a change in the rate of migration (λ) will not affect the maximum number of infected individuals but rather the time of occurrence. Now, as λ increases from a realistic standpoint, the country with a higher infection leads to more people getting infected with the disease, but the total patch transmitted population will always stay the same. Therefore, breaking off migration to restrict international contact may not seem as effective as opposed to lowering the rate of exposure from the disease (β).

That being said, assuming a country is doing substantially better in terms of β than the other, increasing λ would only surge the peak infected population of the total patch and healthier country but will have no reduction in the more severe country. Thus, in real-world scenarios like these, we concluded that closing international borders entirely would be an ideal mitigation effort to reduce peak infections between first-world and third-world countries.

4.2 Conclusion on Vaccines (V)

It is obvious that introducing a 100% effective vaccine would mitigate the infection but after the studying its distribution between our patch models, we came up with several notable conclusions. Between two countries with low β, distributing all vaccines to the country performing slightly worse would reduce the total peak infection by a bit. However, this is far from an ideal solution for such a minor reduction as the administration of vaccines should be more even between 2 first-world countries with good healthcare.

In extreme cases where a country is handling the pandemic significantly better than the other, administering all vaccines to country in need would only worsen the situation entirely. They would not receive any benefit even if maximum vaccines due to the absurdly high β and the distributing country's infection would only become more severe, leading to a higher patch peak infection. Hence, a first-country should ideally keep them all instead but wouldn't the condition of the third-world country worsen without the vaccine?

4.3 Limitations & Future Studies

The first limitation is the massive simplification of our parameters. The θs and αs should be different because every country has its own pandemic protocol and healthcare system, hence to assume people from both countries get infected and recover at the same rate is simply unrealistic. Secondly, we should have 4 different λs considering there are 2 directions of migration (towards Country 1 or Country 2) in 2 different medical states (susceptible or exposed). These parameters were all simplified to reduce the complexity of the model as there were too many factors to consider but given the right opportunity in the future, we would use more realistic parameters to gain more reliable results.

The second limitation to our model is the effectiveness of our vaccines. There is no such thing as a 100% effective vaccine as there is always a minor chance of it not working or may potentially even leading to side effects. Again, to avoid complexity, assuming it to be completely effective allows us to add a direct transition process from susceptible to recovered (v_1 & v_2). Depending on the infection chosen in future studies, we will account for its realistic effectiveness and perhaps add another transition process where immunity may be lost or that the vaccination has failed.

The final limitation to our model relates to our conclusions themselves. Although they appear accurate and correspond to our findings, we've only proven most of them to not be a functional solution to the scenarios. For example, in our final case where we declared first-world countries should not administer their vaccines to third-world countries bur rather keep everything for themselves, we solved nothing and so many questions are left unanswered. Wouldn't the infective condition of these suffering countries aggravate more without any vaccines? Should more resourceful and powerful countries not involve themselves in assisting poorer countries entirely? Is there a method to reduce the peak infection of both countries simultaneously?

In retrospect, given more time, we would like to utilize our model and code to extensively look into these questions and to come up with actual solutions that can help our society.

4.4 Acknowledgement

We would like to thank Prof. Rebarber and Austin Eide for constantly reviewing this project and providing constructive feedback in terms of both its content and structure. They also assisted us with our questions regarding the vaccination parameters along with graphing results.

5 References

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