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Problem Chosen

A

2015 Mathematical Contest in Modeling (MCM) Summary Sheet
(Attach a copy of this page to your solution paper.)

Type a summary of your results on this page. Do not include the name of your school, advisor, or team members on this page.

Abstract

A model of the spread of the Ebola in the affected zone has been made. It is based on the evolution of the disease in each of the 54 regions that form the countries Guinea, Liberia and Sierra Leone (which are the most impacted countries) and the interrelationship between them. Working from this model, a distribution of medicines and vaccines - subjected to a certain logistic parameters- has been proposed. This distribution would minimize the time extension of the disease and the number of victims that it takes as well.

It is assumed as a basic foundation of the model that all populations behave in a probabilistic manner over time, following the Law of large numbers. In order to calculate the evolution of this disease in each region, a discrete adaptation of the well-known SIR model for epidemics has been made, taking into account the characteristic effects of the illness that we are dealing with. The consideration of the succeeding states of the patient (with the different characteristics of each of them, i.e., the capacity of spreading the disease, of recovering from it or of contracting it), the repercussion in the rest of the regions and the effect of the vaccines and medicines are the mainstays of our model, which makes it different from other standard epidemic models.

From the data of the last outbreak of Ebola, the parameters that rule the advance of the disease in a patient (such as the incubation period, the disease detection time, the lethality time, etc) are determinated, which means that the model is adjusted as much as possible to this particular disease. Moreover, parameters which determinate the relation between two regions (based on different factors such as the number of people living in each of them) are contemplated, which makes it more probable that a region propagates the disease to another if the connectivity grade between them is high.

On the other hand, a discrete variable for the time (considering a *day* as the temporal unit) allows us to work in a simple and realistic way the distribution of vaccines and medicines. With this variable, our model lies in six recurrence relationships for each city, which can be easily computed. As a result, one can obtain for each day t the number of inhabitants infected in every area and the disease state in order to decide

the best way to distribute the next round of medicines and vaccines.

Since there is no explicit function that can be optimized, it is not possible to calculate the most favorable distribution analytically, so it has been approached using different criteria of decision that are justified by logic arguments until the criterion with the best results is found. It is remarkable the fact that the simplest criterion is the one that has finally triumphed: you should just send the vaccines/medicines to the region with the largest number of infected that day.

Realistic data of the time and the capacity of the vaccine and medicine production, based on actual projects being carried by the United Kingdom (GSK) and the USA (ZMAPP), respectively, has been obtained. With our vaccine distribution proposal the disease extinction time can be reduced by up to 47% and, combined with the distribution of the medicine, over 900 lives could be saved.

How to make biologists work valuable

Team # 41580

February 10, 2015

1 Letter for the world medical association

Since the project of developing a vaccine and a medicine against Ebola seems destined to be a success, a mathematical model for the distribution has been derived in order to ensure its optimal impact on the world, with the aim of eradicating this outbreak as soon as possible.

A deterministic model of spread based on an adaptation of the well-known SIR (epidemiological model par excellence) is considered, and this model takes into consideration all known Ebola characteristics (such as incubation period, detection time, lethally time, etc).
With this model of spread, we can easily make a reasonable prediction of how Ebola will evolve in the affected zones (the model only takes into account the three most involved countries: Guinea, Sierra Leone and Liberia) so that it will be possible to make a decision for the distribution and delivery system well in advance. In fact, the model itself is programmed to estimate what should be the distribution, from the departure time of vaccines, to minimize the effects of the outbreak.

The model predicts that, if we do not take action on the matter, about 3931 people are sentenced to death in the next 6 months. As the data taken is from the beginnings of 2015, this amount of people will be dead in August. If we give both vaccine and medicine treatment, the epidemic will be eradicated in a matter of three months. That is a huge incentive, as living an epidemic in summer in Africa is devastating.

In any case, we must act quickly. The ZMAPP medicine takes a long time to be produced, as its manufacturing process involves a biologic transformation of the tobacco plant. Tobacco needs almost three months to grow fully, so, if we do not start producing it right now, it will not be effective. Moreover, almost 50 kg of tobacco are needed to produce 10 g of drug, and we need a full small greenhouse to get this amount of tobacco.

Following the approach of the model made, the regions that should be given priority are Montserrado County (Liberia) and Conakry (Guinea), as are those who today have a higher rate of infected and therefore are both potentially harmful. According to the model, sending

the first shipments of vaccine to these regions we could dramatically reduce the time of extinction of the disease.

Let us take a brief look at the data: If we provide both medicine and vaccine, we will save 921 people, and we will reduce the 3931 deaths to 3010, shortening it by its 24%. In other terms, 0.028% of the people in the three countries would die if we did not do anything while; if we give both the vaccines and the medicine, we could reduce this rate to 0.021%.

Furthermore, the results are not only remarkable in terms of data, they are socially noteworthy as well. The vaccines are distributed in order to minimize the number of deaths, but they are quite equally distributed in the three countries. Therefore, people from any of them should not complain about discrimination. Moreover, the place where the medicine is delivered does not affect the quantity of deaths. Then, we have either economical (we can bring them where it is cheaper to deliver) or social (we can deliver them uniformly) freedom to operate.

Let us have a little thought about the budget. If, for instance, there is not enough money to both medicine and vaccine, the first priority should be the vaccine. As often said, better safe than sorry. This expression reflects exactly our situation. The delivery of the vaccine is predicted to save about 800 lives, while the delivery of the medicine should save 100. Then, the vaccine is potentially more effective than the medicine.

Finally, we would like to add that we do not only have the capacity of saving 900 people to become terminal patients, but we also have the capacity of facing any epidemic thanks to the biology and models like this one.

2 Introduction

Ebola is a virus that has been around since 1976. However, a quite important outbreak started in 2014, which has even arrived to Europe, although in very few cases. The key problem is then:
Let us assume that we have found a vaccine and a medicine that can prevent and cure Ebola respectively. How should we deliver it if we want to have the minimum amount of deaths?

Our approach is the following one: First of all, we are going to split our countries in many regions, then we are going to study how the disease spreads in these regions and then, considering how the spread evolves, we are going to apply both vaccines and medicines to some given regions in order to minimize the amount of deaths.

3 Assumptions

3.1 Spread of the disease in a region

The following assumptions are the ones that we are going to use to derive the spread of the disease in a region:

- The epidemiological elementary units are going to be people, but as we are dealing with a big amount of people, we are going to consider them to be a continuum. People are going to be in one, and just one, of the following sets:
  - $\mathcal{S}$: People susceptible to get the disease. They neither have the disease but they are still exposed to contract it as they are not immune.
  - $\mathcal{I}$: People who are in the incubation period of the disease. They are all going to have the disease eventually but they cannot infect other people. They are indistinguishable from the people in S, as they do not yet have any symptoms of being sick.
  - $\mathcal{M}$: Infectious patients. They can infect people and they are going to be diagnosed eventually. They have the disease, so they are ill, but they are not aware of having Ebola as the first symptoms are not distinctive from other common diseases.
  - $\mathcal{D}$: Diagnosed patients. They can't infect people, as they have been diagnosed and, therefore, isolated. They can eventually either be cured or become terminal.
  - $\mathcal{T}$: Terminal patients. They can't infect people, as they have been diagnosed and, therefore, isolated. They cannot be cured, neither with a medicine treatment nor for natural causes. This set is specially important, as it is the one we want to minimize to solve our problem. The more terminal patients we have, the less we succeed in eradicating the Ebola with the smallest amount of deaths.
  - $\mathcal{R}$: Recovered patients. They have overcome Ebola and they are immune to it, as they have developed enough antibodies to not be sick again.
- The previous sets are defined in chronological order except for the last one. Therefore, every person in $\mathcal{T}$ has been previously in $\mathcal{D}$, every person in $\mathcal{D}$ has been previously in $\mathcal{M}$, every person in has been previously in $\mathcal{I}$, and every person in $\mathcal{I}$ has been previously in $\mathcal{S}$.
- Geographical effects are not going to be considered. Therefore, we'll assume that a region is punctual, in order to just study the amount of people in every set that has been previously defined.
- We will assume time to be a a discrete variable, which elementary unit is going to be a day.
- As Ebola has not been a long term disease, we are not going to consider demographic effects, just as natal rate or death rate.

- We are going to consider two different types of cure that we will control. We are going to give vaccine to people who are not in the sets $\mathcal{M}$, $\mathcal{D}$, $\mathcal{T}$, or $\mathcal{R}$ as vaccines can just help people who have not got the disease, but we can't distinguish between people in $\mathcal{S}$ or $\mathcal{I}$. We are going to give medicine to people who are in the set $\mathcal{D}$, as they are the only ones who we know that they have Ebola and who are in a period of the disease where we are on time to cure it (in contrast to $\mathcal{T}$ patients).

3.2 Spread in many regions

We are considering a 54 regions problem (regions of Sierra Leone, Uganda and Liberia; the three countries that have been more affected in the current outbreak). As the infection rate in a region depends on the infection rate of that others who are in contact with it, we are going to define a connectivity coefficient to quantify this factor.

Connectivity is a quite abstract concept and actually really difficult to measure. As a first approximation, we consider that the connectivity between two regions is proportional to the people who live in every region, because the more people living in a region, the more people traveling and vice versa.
Indeed, the connectivity between the regions c_i and c_j reflects the probability that a person that has Ebola in the region c_i infects someone in c_j. We will assume that the connectivity between regions is symmetric, because if someone from c_i moves (temporarily, for a business trip, for instance) to c_j he is likely to infect the people in c_j if he has the disease and he is likely to get the disease from someone in c_j he is susceptible.

3.3 Manufacturing and delivering the drug

Since medicines are produced in lots that involve a certain time of production, it is logical to contemplate that deliveries to affected countries are carried out in batches of d medicines that are sent every τ_d time. We are going to give values to these parameters considering the current production of ZMAPP, a drug that is being tested and is likely to become one of the successes against Ebola. Let us comment briefly the meaning of τ_d: It integrates the amount of time needed to manufacture the drug, but it also considers the time that takes to bring the medicine from the US (every ZMAPP producer is in the US) and the time to deliver it from an airport to a region. As an approximation, we will assume that it takes the same for a plane to go from the US to either Monrovia, Conakry or Freetown (that is a good approximation, as our discrete time unit is 1 day and it takes just one more hour to arrive to one of them or another). We will also assume that it takes the same time to go from the airport to a region or to another one, again taking into consideration the fact that our time unit is 1 day, and time is a discrete variable.

3.4 Manufacturing and delivering the vaccine

As we did with medicines, we will assume that every certain amount of time a quantity of vaccine is manufactured, so a quantity v can be delivered every certain amount of time τ_v. We are going to give values to these parameters considering the information given in the bibliography, according to the vaccines that are being produced in the UK. Just as τ_d, τ_v integrates the amount of time needed to make the vaccine, as well as the time spent in the delivery process. The assumptions made in terms of time spent delivering in the previous section are made in this one.

4 Derivation of the model

4.1 Spread in a region

As time is considered to be a discrete variable, we are going to use recurrences to deal with our problem. When these recurrences are solved, we are going to have some information to know when shall we provide the vaccine or medicine to the region.

As we do not consider geographical effects, people get sick uniformly. As the only people that can infect the people in $\mathcal{S}$ are the ones in $\mathcal{M}$, the decrease of[1] $\mathcal{S}$ in a given day t will be proportional to $\mathcal{M}_t$, which denotes the amount of people in $\mathcal{M}$ at the day t. Analogously, the more susceptible people there are in a region, the bigger will be the decrease of them in a day t. Here we derive our first recurrence: $\mathcal{S}_{t+1} - \mathcal{S}_t = -\alpha \mathcal{S}_t \mathcal{M}_t \Rightarrow \mathcal{S}_{t+1} = \mathcal{S}_t - \alpha \mathcal{S}_t \mathcal{M}_t$, for some α, a constant which we will come back later.

People who are not in $\mathcal{S}$ anymore are now in the set $\mathcal{I}$. As, given a day t $\mathcal{I}$ decreases proportionally to $\mathcal{I}_t$ (they become $\mathcal{M}$), our recurrence for $\mathcal{I}$ is the following one: : $\mathcal{I}_{t+1} - \mathcal{I}_t = \alpha \mathcal{S}_t \mathcal{M}_t - \beta \mathcal{I}_t \;\; \Rightarrow \;\; \mathcal{I}_{t+1} = \mathcal{I}_t + \alpha \mathcal{S}_t \mathcal{M}_t - \beta \mathcal{I}_t$, for some β, a constant which we will come back later. Using a similar argument, as people in $\mathcal{I}$ become people in $\mathcal{M}$, who become people in $\mathcal{D}$, the recurrence for $\mathcal{M}$ is $\mathcal{M}_{t+1} = \mathcal{M}_t + \beta \mathcal{I}_t - \mu \mathcal{M}_t$, for some μ, a constant which we will come back later.

As people in $\mathcal{M}$ become people in $\mathcal{D}$, and the decrease of people in $\mathcal{D}$ is proportional to $\mathcal{D}_t$, we have a similar equation again: $\mathcal{D}_{t+1} = \mathcal{D}_t + \mu \mathcal{M}_t - \gamma \mathcal{D}_t$, for some γ, a constant which we will talk about later. However, this case is slightly different. As people in $\mathcal{D}$ can go either to set $\mathcal{T}$ or to set $\mathcal{R}$, we will assume that every person in $\mathcal{D}$ is equally likely to go to $\mathcal{T}$ or $\mathcal{R}$, with a probablity δ of going to $\mathcal{R}$ and a probability $1 - \delta$ of going to $\mathcal{T}$. Therefore, the

[1] From now on when we talk about S we mean the amount of people in $\mathcal{S}$, as it is troublesome to write $|\mathcal{S}|$ every single time (And, of course, that is appliable to every set that we have defined).

equations for $\mathcal{T}$ and $\mathcal{R}$ are the ones given in the following system:

$$\begin{aligned}
\mathcal{S}_{t+1} &= \mathcal{S}_t - \alpha \mathcal{S}_t \mathcal{M}_t \\
\mathcal{I}_{t+1} &= \mathcal{I}_t + \alpha \mathcal{S}_t \mathcal{M}_t - \beta \mathcal{I}_t \\
\mathcal{M}_{t+1} &= \mathcal{M}_t + \beta \mathcal{I}_t - \mu \mathcal{M}_t \\
\mathcal{D}_{t+1} &= \mathcal{D}_t + \mu \mathcal{M}_t - \gamma \mathcal{D}_t \\
\mathcal{T}_{t+1} &= \mathcal{T}_t + \gamma(1-\delta)\mathcal{D}_t \\
\mathcal{R}_{t+1} &= \mathcal{R}_t + \gamma \delta \mathcal{D}_t
\end{aligned}$$

As these equations are nonlinear, we will not be able to solve them analytically, then we need a numerical value for every constant given, and a numerical initial condition for every equation given as well. However, there are some things that we can say about the evolution of these equations without solving the system:
Trivially, we can check $\mathcal{S}_{t+1} + \mathcal{I}_{t+1} + \mathcal{M}_{t+1} + \mathcal{D}_{t+1} + \mathcal{R}_{t+1} = \mathcal{S}_t + \mathcal{I}_t + \mathcal{M}_t + \mathcal{D}_t + \mathcal{R}_t$ which makes sense, as the total amount of population remains constant.

Let us take limits to infinity. When t is big enough, as the limits of these successions exist, $\mathcal{S}_{t+1} = \mathcal{S}_t \Rightarrow \mathcal{S}_t = 0$ or $\mathcal{M}_t = 0$, $\mathcal{I}_{t+1} = \mathcal{I}_t \Rightarrow \mathcal{I}_t = 0$, $\mathcal{M}_{t+1} = \mathcal{M}_t \Rightarrow \mathcal{M}_t = 0$, $\mathcal{D}_{t+1} = \mathcal{D}_t \Rightarrow \mathcal{D}_t = 0$. These results are coherent with the fact that people are going to be eventually in $\mathcal{S}$, $\mathcal{R}$ or $\mathcal{T}$. We will consider the disease to be erradicated when $\mathcal{R} = \mathcal{S} = \mathcal{T} = 0$[2]. Consequently, we will define the extermination time, t_{ext} as the time that takes to erradicate the disease.
In the following section we are going to study how giving a certain amount of vaccine or drug in a certain day can change the previous system and, by doing that, decrease the amount of terminal patients for an arbitarily long time. Of course, that is what we want in the end, as they are the only ones who are going to die from Ebola.

4.2 How our system changes when giving vaccine or medicine

Let us bring an amount of medicine d_t on a given day t. Of course, the medicine is going to be given to people who are in $\mathcal{D}$. Therefore, we shall change equation (4) to

$$\mathcal{D}_{t+1} = \mathcal{D}_t + \mu \mathcal{M}_t - \gamma \mathcal{D}_t - \epsilon_d d_t \tag{1}$$

where ϵ_d is the effectiveness of the drug, so that when giving 1 drug ϵ_d people are going to be cured.
However, if we bring an amount of vaccine v_t on a given day t, we cannot say that the amount of $\mathcal{S}$ will dicrease in $\epsilon_v v_t$, because of the fact that we will give some vaccine to people who are in $\mathcal{I}$, as the people in these two sets are impossible to distinguish. Consequently, we deal with this problem probabilistically: Considering that the amount of people in $\mathcal{S}$ or $\mathcal{I}$ are, on a given day t, $\mathcal{S}_t + \mathcal{I}_t$, the probability of giving a vaccine to a person in $\mathcal{S}$ is $\frac{\mathcal{S}_t}{\mathcal{S}_t + \mathcal{I}_t}$. Otherwise, the probability of giving a vaccine to a person in $\mathcal{I}$ is $\frac{\mathcal{I}_t}{\mathcal{S}_t + \mathcal{I}_t}$. It follows that if, on a given day t, we bring v_t vaccines into a region, equation (1) shall become

[2]As we are dealing with a continuous variable for people, we are going to consider the disease to be erradicated when $\mathcal{R}, \mathcal{S}, \mathcal{T} < 0.5$

$$\mathcal{S}_{t+1} = \mathcal{S}_t - \alpha \mathcal{S}_t \mathcal{M}_t - \epsilon_v \frac{\mathcal{S}_t}{\mathcal{S}_t + \mathcal{I}_t} v_t \tag{2}$$

As equation (4) and (1) change, equation (6) has to change too accordingly to the increase of the people who have been vaccined and cured, and then the system becomes[3]

$$\begin{aligned}
\mathcal{S}_{t+1} &= \mathcal{S}_t - \alpha \mathcal{S}_t \mathcal{M}_t - \epsilon_v \frac{\mathcal{S}_t}{\mathcal{S}_t + \mathcal{I}_t} v_t \\
\mathcal{I}_{t+1} &= \mathcal{I}_t + \alpha \mathcal{S}_t \mathcal{M}_t - \beta \mathcal{I}_t \\
\mathcal{M}_{t+1} &= \mathcal{M}_t + \beta \mathcal{I}_t - \mu \mathcal{M}_t \\
\mathcal{D}_{t+1} &= \mathcal{D}_t + \mu \mathcal{M}_t - \gamma \mathcal{D}_t - \epsilon_d d_t \\
\mathcal{T}_{t+1} &= \mathcal{T}_t + \gamma(1-\delta)\mathcal{D}_t \\
\mathcal{R}_{t+1} &= \mathcal{R}_t + \gamma \delta \mathcal{D}_t + \epsilon_v \frac{\mathcal{S}_t}{\mathcal{S}_t + \mathcal{I}_t} v_t + \epsilon_d d_t
\end{aligned}$$

4.3 Spread in many regions

In this section we will generalize the results derived in the previous sections to a system that considers many regions. Let $c_1, \ldots, c_n$ be the regions that form our system. On a given day t, as the amount of infectious people in c_j, $\mathcal{M}_t^j$ affects the amount of susceptible people in c_i, $\mathcal{S}_t^i$, we will have to add a $-\alpha_{ij}\mathcal{S}_t^i \mathcal{M}_t^j$ term to the equation for $\mathcal{S}_t$. We can apply the same argument for every region different from c_i. If we define α_{ii} as what was previously α, our new equation is

$$\mathcal{S}_{t+1}^i = \mathcal{S}_t^i - \sum_{j=1}^{n} \alpha_{ij} \mathcal{S}_t^i \mathcal{M}_t^j - \epsilon_{v^i} \frac{\mathcal{S}_t^i}{\mathcal{S}_t^i + \mathcal{I}_t^i} v_t^i$$

For a given region c_i, all the other equations remain the same[4], except for

$$\mathcal{I}_{t+1}^i = \mathcal{I}_t^i + \sum_{j=1}^{n} \alpha_{ij} \mathcal{S}_t^i \mathcal{M}_t^j - \beta^i \mathcal{I}_t^i$$

We define the $n \times n$ matrix $\mathcal{A} such that [\mathcal{A}]_{ij} = \alpha_{ij}$. Of course, its entries are proportional to the connectivity between the two regions. $\mathcal{A}$ is a symmetric matrix, because, as we have mentioned before, the connectivity is symmetric. Given the assumptions made, we are going to give approximate values to the entries of the matrix $\mathcal{A}$. Then, we are going to deal with a system of recurrent equations formed by $6n$ equations.

4.4 Manufacturing and delivering the drug

Given some initial conditions of our many-regions problem, and assuming that we do not provide medicine, we can solve the recurrent system numerically by calculating all the terms.

[3]Notice that v_t and d_t are actually numerical sequences, which value is 0 when no products are brought to the region.

[4]Of course, adding the i label to every parameter.

When we give, on a day t, an amount of drug d_t, these does not affect the sets $\mathcal{S}$, $\mathcal{I}$, or $\mathcal{M}$. Therefore, the evolution of the disease will be quite similar, except for one difference, the fact that there are going to be more people recovered finally (for arbitrarily big amounts of time). Therefore, there is no difference in giving the amount of drug to a region c_i or to a region c_j. The only difference may be both social and economical. If we give medicine to just one region or country, this is not socially acceptable. If we spread the medicine all over the regions, this is economically less efficient. As we have huge amounts of money and we are dealing with an epidemic, our priority will be the social aspect, therefore we will distribute the drug uniformly over the regions.

4.5 Manufacturing and delivering the vaccine

In contrast to the last section, we do care about who we shall give the vaccine. Let us consider that vaccine arrives to Africa on a given day t. For instance, if $\frac{\mathcal{S}_t^i}{\mathcal{S}_t^i+\mathcal{I}_t^i} > \frac{\mathcal{S}_t^j}{\mathcal{S}_t^j+\mathcal{I}_t^j}$, we may prefer giving vaccine to the region c_i than to c_j, as we are going to throw away less vaccine. However there are other factors that should be studied as well. For example, if $M_t^i > M_t^j$ then we shall give the vaccine to c_i, as more people are likely to become sick (considering the fact that $\alpha_{ii} \gg \alpha_{ij}$). For every region i, we define a general connectivity coefficient given by $a_i \equiv \sum_{j=1}^n \alpha_{ij}$. Giving the vaccines should also contemplate the fact that some regions are more important to other regions, as they have higher connectivity coefficients and then one person in the region can infect more people abroad. To sum up, if the vaccine arrives on a day t, the region chosen to recieve the vaccine is going to be c_j, the following equation must be satisfied:

$$\frac{\mathcal{S}_t^j \mathcal{M}_t^j}{(\mathcal{S}_t^j+\mathcal{I}_t^j)N^j}p + \frac{a_j}{\sum_{j=1}^n a_j}(1-p) = \max\left(\frac{\mathcal{S}_t^i \mathcal{M}_t^i}{(\mathcal{S}_t^i+\mathcal{I}_t^i)N^i}p + \frac{a_i}{\sum_{i=1}^n a_i}(1-p)\right)$$

where p is a parameter that we can adjust to minimize the amount of deaths (terminal patients) in the end. This should determine the regions where we should give the vaccine. However, for $p \in [0,1)$, the results given by our program could not be more catastrophic. Then, we can consider other variables to maximize. If we take $p = 1$, the results are better, and if we just take $\mathcal{M}_t^i$ the results are even better. Finally, the variable that we have found out to minimize the total amount of deaths (just considering the use of vaccines) is $\mathcal{I}_t^i$. Therefore, for our case, we must choose a city c_j that satisfies

$$\mathcal{I}_t^j = \max\left(\mathcal{I}_t^i\right)$$

4.6 Let us talk about the constants

In the previous sections, we have been defining a certain amount of constants. In this section we are going to discuss about the values of these constants. First of all, we are going to discuss the values α_{ij}:

As we have mentioned before, if $i \neq j$, $\alpha_{ij} \propto N_i N_j$, so we will say $\alpha_{ij} = \frac{N_i N_j}{N^2} k_2$, where N is the total amount of people. Otherwise, we will say $\alpha_{ii} = \frac{1}{N_i} k_1$. This last equation is derived

from the fact that big regions are less likely to infect themselves. This is because, in little towns, family units tend to be bigger, so people are more likely to get the disease. As, for many regions, $\frac{N_i N_j}{N^2} \sim \frac{1}{N_i}$, and $\alpha_{ii} \gg \alpha_{ij}$, because, of course, a city does infect itself much more than others, then k_2 needs to be much smaller than k_1.

About the parameter n, as we split our problem in 54 regions, trivially $n = 54$.

We are going deal with the constants β, μ and γ the same way. As, for dimensional analysis they have dimensions of $\frac{1}{\text{days}}$, then they are indeed frequences. As found in the bibliography, most incubating periods last from 4 to 9 days, so the frequency of becoming $\mathcal{M}$ must take values from $\frac{1}{9}$ to $\frac{1}{4}$. If we do the geometric mean of these values, then our natural frequence must be $\beta \sim \frac{1}{6}$ days^{-1}. Analogously, as the period when the disease does not show really hard symptoms is about three days, then $\mu \sim \frac{1}{3}$ days^{-1}. If we proceed the same way, considering that diagnosed patients tend to be 7 days in $\mathcal{D}$ before they become $\mathcal{T}$ or $\mathcal{R}$, then $\mu \sim \frac{1}{7}$ days^{-1}.

Let us talk about δ. In previous ebola outbreaks, the probability of being dead by the desease was really high. One out of ten diagnosed patients survived the epidemic. This outbreak has been less lethal, with three out of ten diagnosed patients surviving the epidemic naturally, then $\delta \sim 0.3$.

Some of our other constants involve the time of delivery and the amount of medicine or vaccine brought. According to the biblography, $\tau_v \sim 7$ days, $v \sim 250000$, $\tau_d \sim 30$ days, $d \sim 70$, which are the values that are going to be taken.

The efficiencies of our vaccine and drug, considering similar cases, have been taken $\epsilon_v = 0.95$ and $\epsilon_d = 0.8$. Finally, we will discuss the values of k_1 and k_2. Running our program with different values of k_1 and k_2, and taking into consideration that $k_1 \gg k_2$, the most suitable values are $k_1 = 0.1$ and $k_2 = 9 \cdot 10^{-6}$. These values lead to the following results: if no vaccines are brought, Ebola will kill 3931 people in 186 days. This is about 20 deaths every day. Looking at the bibliography[5], which states that this rate is currently 4 deaths every day, this is a bit too much, but the order of magnitude is the same one. Moreover, as this rate is increasing, our approximation is a little better.

After having considered the values of the constants, we shall give values to the initial conditions. The available data can just show us the amount of diagnosed patients.[6]

We have studied the evolution of the spread in many cases (without vaccine) and the values of $\mathcal{D}$ and $\mathcal{M}$ are always close according to our model. Therefore, we consider, as $\mathcal{D} \sim \mathcal{M}$, our initial condicions are going to be given by $\mathcal{M}_0^i = \mathcal{D}_0^i$. The evolution of $\mathcal{I}$ is slightly different, and by studying the means of the values of $\mathcal{I}$ in many cases, we come up to the conclusion that $\mathcal{I} \sim \frac{3}{2}\mathcal{D} \;\Rightarrow\; \mathcal{I}_0^i = \frac{3}{2}\mathcal{D}_0^i$. Analogously, as $\mathcal{R} \sim \delta\mathcal{D}$, our initial conditions will

[5]See [8]
[6]See [11]

be $\mathcal{R}_0^i = \delta\mathcal{D}_0^i$. Our initial conditions for $\mathcal{T}$ are going to be $\mathcal{T}_0^i = 0$, as they do not affect the evolution of the disease and we are going to count them from the moment our model starts running.

5 Results

After all the theoretical derivation and running our program that solves the recurrence numerically, our best result is given by choosing the maximum of $I_t^i, i \in 1, \ldots, 54$ every time we obtain a vaccine, which is once a week. These maximums are the following ones:

Week	Delivery region
1	Montserrado County (Liberia)
2	Montserrado County (Liberia)
3	Conakry (Guinea)
4	Conakry (Guinea)
5	Conakry (Guinea)
6	Montserrado County (Liberia)
7	Western Area Urban (Sierra Leone)
8	Western Area Urban (Sierra Leone)
9	Montserrado County (Liberia)
10	Conakry (Guinea)
11	Kenema (Sierra Leone)
12	Bo (Sierra Leone)

Table 1: Delivery regions on every week

Given these vaccine delivery, t_{ext} goes from 186 (without vaccine delivery) to 88, then it shortens to its 47.31%. It also shortens significantly the quantity of terminal patients, being 3931 in the first case and 3220 in the second one, shortening the amount of T to its 81.91%. If drugs are given as well, (in this case, $70\frac{\text{drugs}}{\text{month}} \cdot 3\text{months} = 210$ drugs), considering that when we give every remittance of 70 there are more than 70 people in D (which of course is always fulfilled), we can save save 210 people more, so the amount of saved people rises to 921, so we can save $\frac{921}{3931} = 23.43\%$ of the initial terminal patients (and by initial we mean that would have become terminal patients if no vaccines or drugs had been applied).
Now we are going to plot the evolution of the 6 sets in Montserrado County, a region where we do apply vaccine treatments, and the following figures show the evolution of the sets in Kailahun, where no vaccine treatments are applied:

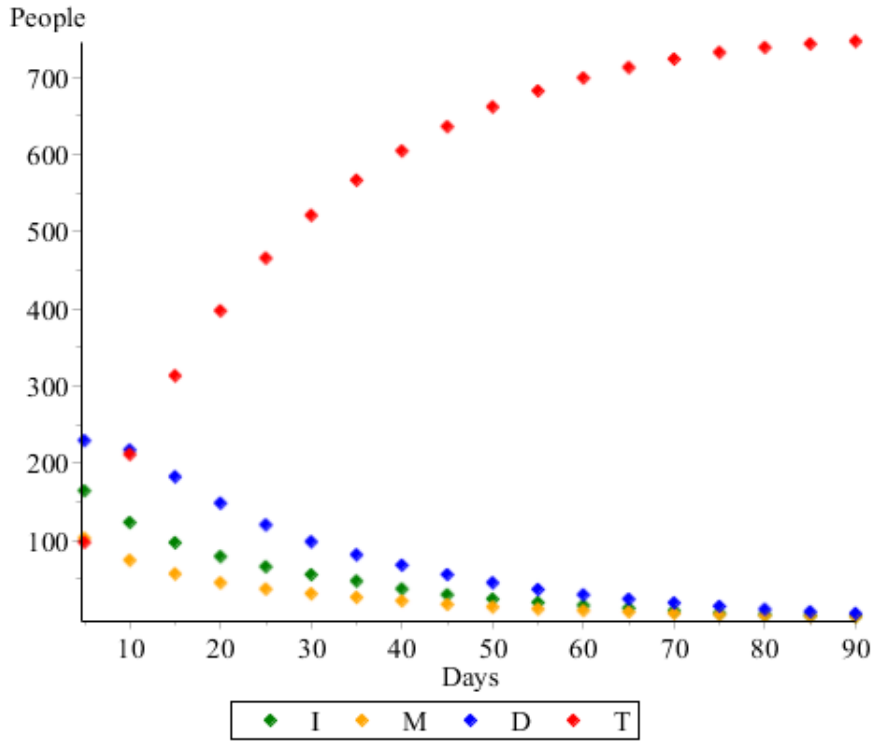

Figure 1: Evolution of the $\mathcal{I}, \mathcal{M}, \mathcal{D}$ and $\mathcal{T}$ sets in Montserrado County.

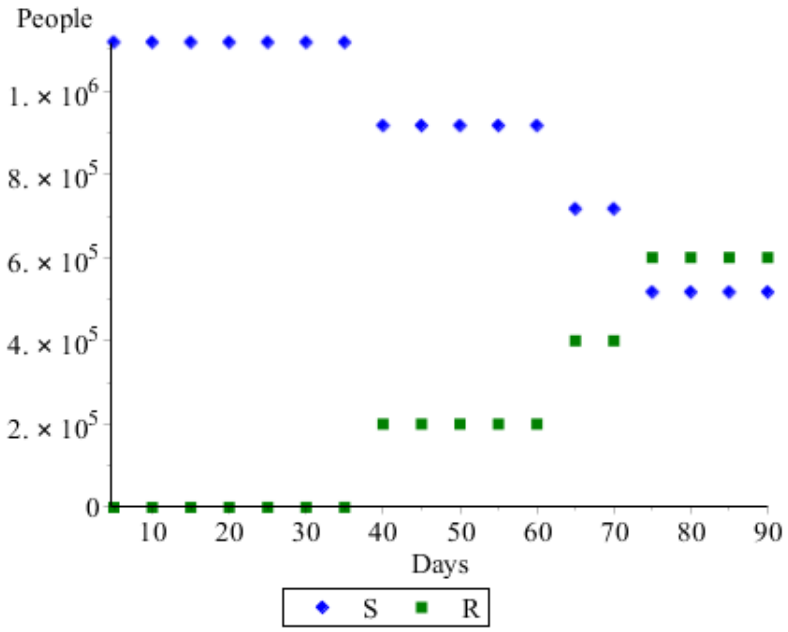

Figure 2: Evolution of the $\mathcal{S}$ and $\mathcal{R}$ sets in Montserrado County.

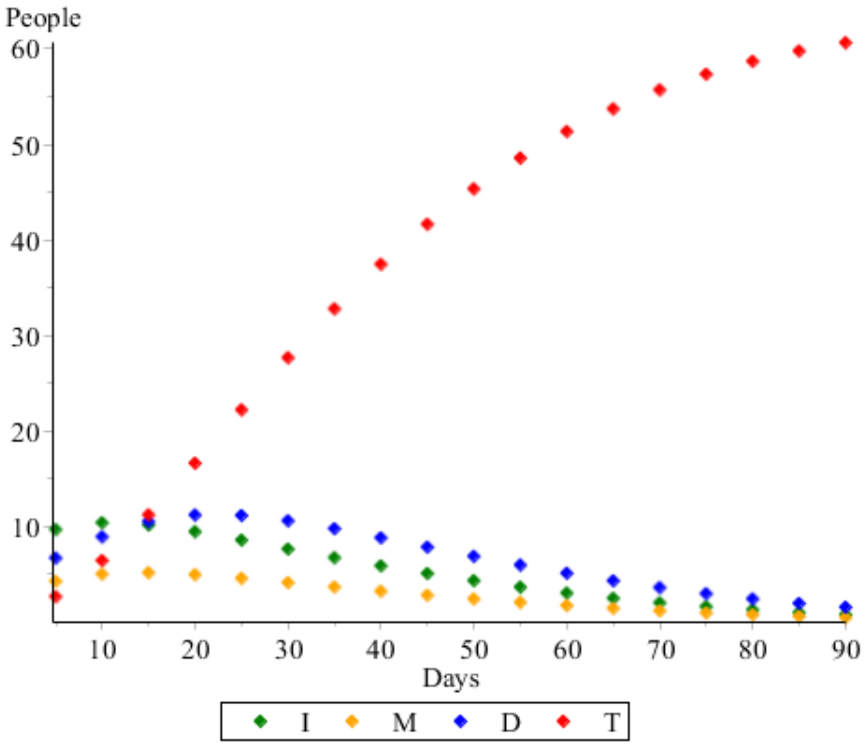

Figure 3: Evolution of the $\mathcal{I}, \mathcal{M}, \mathcal{D}$ and $\mathcal{T}$ sets in Montserrado County.

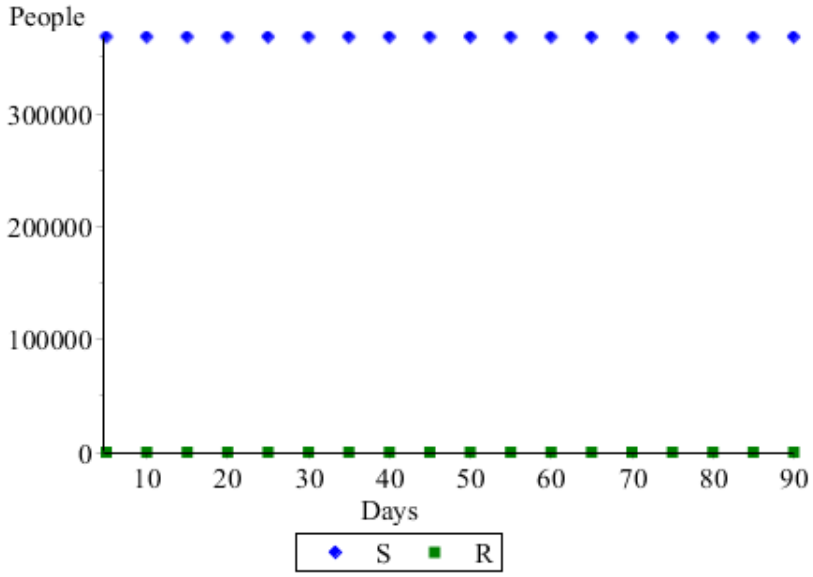

Figure 4: Evolution of the $\mathcal{S}$ and $\mathcal{R}$ sets in Montserrado County.

6 Strengths and weaknesses of the Model

The strengths of our model are the following ones:

- Our model of spread is solid, it considers geographical effects and the relation between the cities. Furthermore, its calculations are really fast. That enables us to try a with lots of parameters and calculating the optimum is achieved in a really short time.
- All our assumptions come from realistic and logical considerations.
- We achieve good results with realistic values and we can check that they cannot be much better.

The weaknesses of our model are the following ones:

- It does not consider the fact that a region is not uniform and that there are people that are more likely to get infected.
- It does not consider demographic effects.
- It works with fixed values of the parameters and not ranges where they could be.
- Some of the parameters have been taken in order to have reasonable data, so they have not been calculated considering its actual meaning.

7 Conclusions

A solid model of spread that considers the most important factors of Ebola has been derived. It makes reasonable predictions with many tests (varying initial conditions) and shows the typical character of the spread of the disease (an exponential growth of cases that eventually falls down and disappears) so it seems reliable and we can work with it.

With the current data that we have, the model predicts that, if we do not take action into the matter, about 3931 people are sentenced to death. It is urgent to act as soon as possible because the more time we waste, the more people will die. With the distribution of medicines and vaccines exposed here, the time of extinction could be reduced from 6 to 3 months and we summer may arrive with Ebola eradicated.

The distribution exposed here has been derived from logical arguments (it is sensible to give vaccines and medicines to the most affected regions) and we have proved that, in fact, these decision criteria are the most effective. Comparing what to give the greater preference, we have seen that giving preference to the regions where the rate of people from $\mathcal{I}$ is higher, we obtain the best results. With this criterion, we could reduce the number of deaths from 3931 to 3010, so we could save about 921 people, which represents a 23% of the people who where estimated to die with neither vaccines nor drugs. Considering that almost 2000 people are assumed to be infected currently, the effectiveness is remarkable.

An important conclusion to be drawn from the model is that 711 of the people that could presumably been saved are due to the effect of vaccines, while the remaining 110 were saved by medicines. This fact makes clear that we should invest as much as possible in the fabrication of vaccines, since they show more effectiveness than drugs. This major effectiveness is not only due to the fact that $\epsilon_v > \epsilon_d$ but also to the speed of manufacturing of each (250000 vaccines are produced in 7 days while only 70 medicines are manufactured per month). Definitely, speed manufacturing of medicines is much lower than the speed of manufacturing of vaccines so it would be interesting to invest in optimizing the manufacturing process of medicines.

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