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Nonlinear modelling of COVID-19 and the significance of testing: the case of Kazakhstan

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THESIS

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Abstract

It has been more than two years since the world faced a global pandemic of COVID-19, which affected the global economy negatively and took many human lives. This paper considers the extended susceptible-exposed-infectious-recovered (SEIR) model and finds out whether it is effective for the government of Kazakhstan to conduct massive free PCR testing of the exposed population. To this end, we constructed a new mathematical model and the government cost function that incorporates the hospital cost for the COVID-19 treatment and the cost of PCR testing. To address the above-mentioned objectives, we constructed nonlinear differential equations for our epidemic model and numerically solved them. Furthermore, the government's cost was modeled as a function that depends on the rate of PCR tests. The findings of the numerical analysis show that the government's cost is minimized if the exposed individuals were tested for the disease as often as possible. Moreover, testing both susceptible and exposed individuals is not beneficial in terms of the economic cost.

Аңдатпа

Жаһандану заманында экономикаға кері әсерін тигізіп, көптеген адамдардың өмірін қиған бүкіләлемдік COVID-19 пандемиясына қарсы күрес екі жылдан астам уақыт бойы әлі де өз жалғаын табуда. Бұл магистрлік жұмыста кеңейтілген сезімтал-инфекцияланған-жұқпалы-аурудан жазылған (SEIR) моделі қарастырылады және Қазақстан Үкіметі осы жаһандық коронавирус ауруына қарсы жаппай тегін ПЦР тестілеуді жүргізу тиімді ме, жоқ па, соны зерттейді. Сондай-ақ, тестілеу барысында инфекцияланған бірақ әлі де жұқпалы топқа жатпайтын қарастырады. Осы мақсатта біз жаңа математикалық модельді және COVID-19 үшін ауруханада емдеу құнын және ПЦР тестілеу құнын қамтитын мемлекеттік шығындвр функциясын жасадық. Жоғарыда келтірілген есептерді шешу үшін біз эпидемиялық модель үшін сызықты емес дифференциалдық теңдеулерді құрдық және оларды сандық түрде шештік. Сонымен қатар, мемлекеттік шығындар ПЦР сынақтарының жиілігінің функциясы ретінде модельденді. Сандық талдау нәтижелері, егер ауруға шалдыққан адамдар мүмкіндігінше жиі ауруға тексерілсе, мемлекеттік шығындар аз болатынын көрсетеді. Сонымен қатар, сезімтал және инфекцияланғау адамдарды тестілеу экономикалық тұрғыдан тиімсіз.

Аннотация

Прошло более двух лет с тех пор, как мир столкнулся с глобальной пандемией COVID-19, которая негативно повлияла на мировую экономику и унесла множество человеческих жизней. В этом документе рассматривается расширенная модель восприимчивых-зараженных-инфекционных-выздоровевших (SEIR) и выясняется, эффективно ли правительство Казахстана проводить массовое бесплатное ПЦР-тестирование подвергшегося воздействию населения. С этой целью мы построили новую математическую модель и функцию государственных расходов, которая включает стоимость лечения COVID-19 в больнице и стоимость ПЦР-тестирования. Для решения вышеупомянутых задач мы построили нелинейные дифференциальные уравнения для нашей модели эпидемии и решили их численно. Кроме того, расходы государства были смоделированы как функция, зависящая от частоты проведения ПЦР-тестов. Результаты числового анализа показывают, что затраты правительства минимальны, если лица, подвергшиеся воздействию, как можно чаще проверялись на наличие заболевания. Кроме того, тестирование как восприимчивых, так и подвергшихся воздействию лиц невыгодно с точки зрения экономических затрат.

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1. Introduction

1.1 General Introduction to the Research Problem

The last two years have been one of the most difficult periods for the world economy due to the contagious coronavirus disease, which has also killed millions of people all over. SARS-CoV-2, a new virus belonging to the Coronaviridae family, causes COVID-19, a Severe Acute Respiratory Syndrome (SARS). The epidemic was initially identified in December 2019 in the Chinese city of Wuhan, and shortly after it lost control turning to the worldwide pandemic. As of May 25 2022,according to the World Health Organization, COVID-19 pandemic has claimed the lives of over 6 million people with more than 500 million confirmed cases, and with 23 million active cases[16]. While some countries were reluctant, most world countries reacted fast and implemented various measures to control the spread of the virus in their countries. In particular, various lockdown measures, social distancing rules, large-scale social event restrictions, social safety net, massive voluntary vaccination, quarantine measures, total lockdown, and PCR testing requirements are put in action. Yet, aside from partial success the pandemic continued to progress with new variants. As a consequence of that, many countries are still attempting to reduce the risks of illness and death while also improving their country's economic situation, which are inextricably linked. Research showed that the virus is capable of mutating depending on the region and population [17]. Furthermore, an alarming retraction rate for the scientific publications on COVID-19, which is about 137 papers a day, implies the disease issue is still relevant and under investigation [17].

1.2 Research Significance and Novelty

In this work we are going to consider the coronavirus disease in terms of the economical view of the government. How many people have already rally vaccinated? How many of them address to the medical centers when they feel sickness such as fever, cough, or other symptoms which potentially belong to COVID-19's as well? How many of them isolate themselves in case of symptoms of COVID-19? And finally, how many of them take PCR testing in case of such symptoms?

The questions mentioned above are open and need to be investigated and tracked properly by authorized individuals. As for our paper, we are going to consider the last question, namely, massive PCR testing and its economical efficiency for the government of Kazakhstan. According to the Central Asian Bureau for Analytical Reporting (CABAR), as of January 2022, it is said that the national economy has slowed dramatically over the previous two years, and as a result, individuals' well-being has decreased significantly [9]. Many people complain about their lives by saying: "“We take loans and micro loans from salary to salary. We do not live, but we simply exist...". Furthermore, COVID-19 had negative affect to population working in the sphere of service, in all other areas of work where people come into contact with each other. As far the lock-down lasted as many people were in troubles losing their jobs and with their daily lives in general. In order to survive, they broke quarantine restriction measures, which led to accelerated the process of infection with the virus and its spread throughout the country.

Since taking the PCR test has been on a paid basis for the population who are not contacted with infected and have no symptoms. Its cost varies between 7200 and 22000 KZT depending on a city and time [1].

In the beginning and during its mutation process, the disease has mainly been accompanied by overt symptoms such as the most common ones: fever, cough, tiredness, loss of taste or smell; less common: sore throat, headache, aches and pains, diarrhea, a rash on skin, or discoloration of fingers or toes, red or irritated eyes; and serious symptoms: difficulty breathing or shortness of breath, loss of speech or mobility, or confusion, chest pain[2].

Nonetheless, since then, COVID-19 has had a problematic characteristic unlike other infectious diseases: it's been found that there are asymptomatic infections,

or people who are infected but have very mild, imperceptible symptoms, or sometimes do not have any symptoms at all. Those people are not aware of their contagious ability and are just carriers of the disease. Hence, there are more susceptible people who can get infected[2].

According to the website Worldometers.info, 99.8% of active cases of COVID-19, in other words more that 23 million people have been experiencing the disease in mild conditions, while only 37608 individuals under serious or critical[4]. Another research states that to prevent the spread of SARS-CoV-2, some countries have instituted social isolation measures. The frequency of asymptomatic carriers is unknown, but it would provide crucial information on viral circulation that is hidden. Despite having no contact with recorded cases, 1.82 percent of 330 asymptomatic restricted people living in the community were infected with SARS-CoV-2 in their cross-sectional study, showing the possibility of undetected transmission [11]. Considering that it was during the quarantine restriction measures in 2020, the data as of 2022 might be even worse.

Thus, it implies that many people who have get infected cannot find out that they are already dangerous to the society. Unaware of their danger, they continue to work infecting others, and increasing the number of active cases[11]. During the peak of COVID-19 in July-August in 2020, Kazakhstan experienced a great loss in terms of died people due to the disease, and in the term of economics. After World War II, there have been a lot of significant economic difficulties, but Covid-19 stands out. As a direct result of the imposed limits, Kazakhstan's entire domestic consumption dropped by forty percent. By September 2020, Kazakhstan's yearly GDP growth rate has dropped to -2.8% compared to the previous year. Between January and September, there was a decline, which caused the dramatic increase of poor population in the country. There are now between 1.1 and 1.5 million Kazakhstan people living in poverty, which is defined as a daily income of less than $5.50 USD, or about 2300 KZT[15].

Despite the fact that people contacted with a lot of people during a day, and some of their acquaintances got infected, they avoided voluntarily PCR testing on a paid basis. As a result, July-August of 2020 is believed as a highest peak of COVID-19 active cases and deaths. These can be explained by several factors, and one of them, of course, the low rate of PCR testing among population. Avoiding paid PCR testing led to more infections to be appeared, and the number of those

who have severe health issues got hospitalized. Medical service was not capable to contain all of them with the treatment and was overwhelmed, and consequently increased the rate of deaths.

1.3 The Main Research Questions

Our work concentrates in this particular issue, and we are trying to answer the following questions:

• What is the basic reproduction number of the following model 1.1?

• To what extent is population-scale testing effective to optimize government costs?

• Should the government consider susceptible individuals in testing along with exposed ones?

Definition 1.1. The basic reproduction number is the average number of secondary infections, produced by one typical primary infected person in a completely uninfected population[12].

The explanation of the basic reproduction number, sometimes also basic reproduction ratio, should be started from very well-known model for epidemic diseases Susceptible-Infected-Recovered, or shortly SIR model.

1.4 Background Information

Daniel Bernoulli developed a mathematical model in the 1760s that demonstrated how effective vaccination is in preventing smallpox[12]. As a direct result of this discovery, there was an approximate three-year rise in the population's average lifespan. This was a positive outcome of the finding. In the 1920s, Kermack and McKendrick developed the compartmental model of the illness, which would go on to become the most widely accepted and widely used model of the disease in the years to come. In order to better understand the condition, the compartmental model was established. He divided the population into three groups, those who were vulnerable, namely "Susceptible", those who were infectious, namely

"Infectious", and those who were recovering, namely "Recovered", and then used a series of ordinary differential equations to demonstrate the connection between the three different subsets of the population that they had previously identified. The model of epidemic propagation that was developed by McKendrick and Kermack is commonly referred to as the classic SIR model. The populations who are susceptible to infection, those that are infectious, and those that are recovering are correspondingly represented in this model by the letters S, I, and R. It is possible to construct other epidemic models by employing this model as a basis for the construction of such models. In the next section 3, the complete process of developing this model is analyzed and broken down into steps. During those times, the SIR epidemic model was able to precisely forecast the peak of the sickness, which only lasted for a short amount of time and then began to decline again.

The SIR epidemic model has both advantages and disadvantages: on the one hand, it is very basic, making it easy to evaluate; on the other hand, it does not account for birth and death rates, rendering it insufficient for characterizing the progression of the disease over time[12]. In addition to the exposure duration and other factors, the model excludes vaccination and disease-related death. The exposed phase happens when a person has the disease but does not transmit it to others. This time frame is crucial for illnesses having a pre-infectious phase. In the years that followed, a multitude of epidemiological models were developed, each of which accounted for at least some of the previously enumerated factors.

There are some of them, which are more commonly used. According to the SIS model, some illnesses, such as the common cold and influenza, may not confer long-term protection [3]. The SIRD model, the Susceptible-Infectious-Recovered-Deceased model, distinguishes between Recovered (meaning individuals who have survived the disease and are now immune) and Deceased; the SIRV model, the Susceptible-Infectious-Recovered-Vaccinated model, is an extended SIR model that accounts for vaccination of the susceptible population; and the MSIR model, the Susceptible-Infectious-Recovered-Vaccinated model, is a model that accounts for (passed across the placenta and additionally through colostrum). This is what passive immunity means. To display this additional knowledge, a M class (for maternally derived immunity) might be inserted at the beginning of the model; some individuals who have had an infectious disease, such as tuberculosis, never

fully recover and continue to carry the infection without experiencing symptoms. They may return to the infectious compartment and acquire symptoms (as is the case with tuberculosis) or continue to infect others without acquiring symptoms. Mary Mallon, who infected 22 people with typhoid, is arguably the most well-known example of this. According to the $SEIR$ model, there is a significant latency period for many important diseases, during which afflicted persons are not contagious. This model needs the latency duration of a random variable with an exponential distribution and some parameters, the average latency period, and the presence of vital dynamics with a birth rate equal to the death rate over this period.

1.5 The Construction of the Model

Since we are considering the latency period of infected individuals, we can going to consider $SEIR$ model, and extend it by adding some more parameters due to the external factors such as the rate of PCR testing, thus adding the group of population D_e, which stands for early diagnosed (at a stage of exposure), then those individuals get infectious with some symptoms. We also divide the group of infectious individuals into two categories: symptomatic, those who have obvious symptoms of COVID-19 and they are usually sent to a hospital, and those who are asymptomatic, who are also carriers of the virus, but have no symptoms specific to COVID-19 - they are often unaware of this fact that they are already infectious to others. Below we can see our flow diagram of COVID-19 we constructed considering above mentioned conditions.

The flow of the disease shown in the Figure 1.1 implies the the extended $SEIR$ model, namely Susceptible-Exposed-Diagnosed early-Diagnosed infectious-Infectious symptomatic-Infectious asymptomatic-Hospitalized-Recovered ($SED_eD_iI_sI_aHR$).

Next what we are going to do is to construct the Ordinary Differential Equations of the model to find out our basic reproduction number R_0.

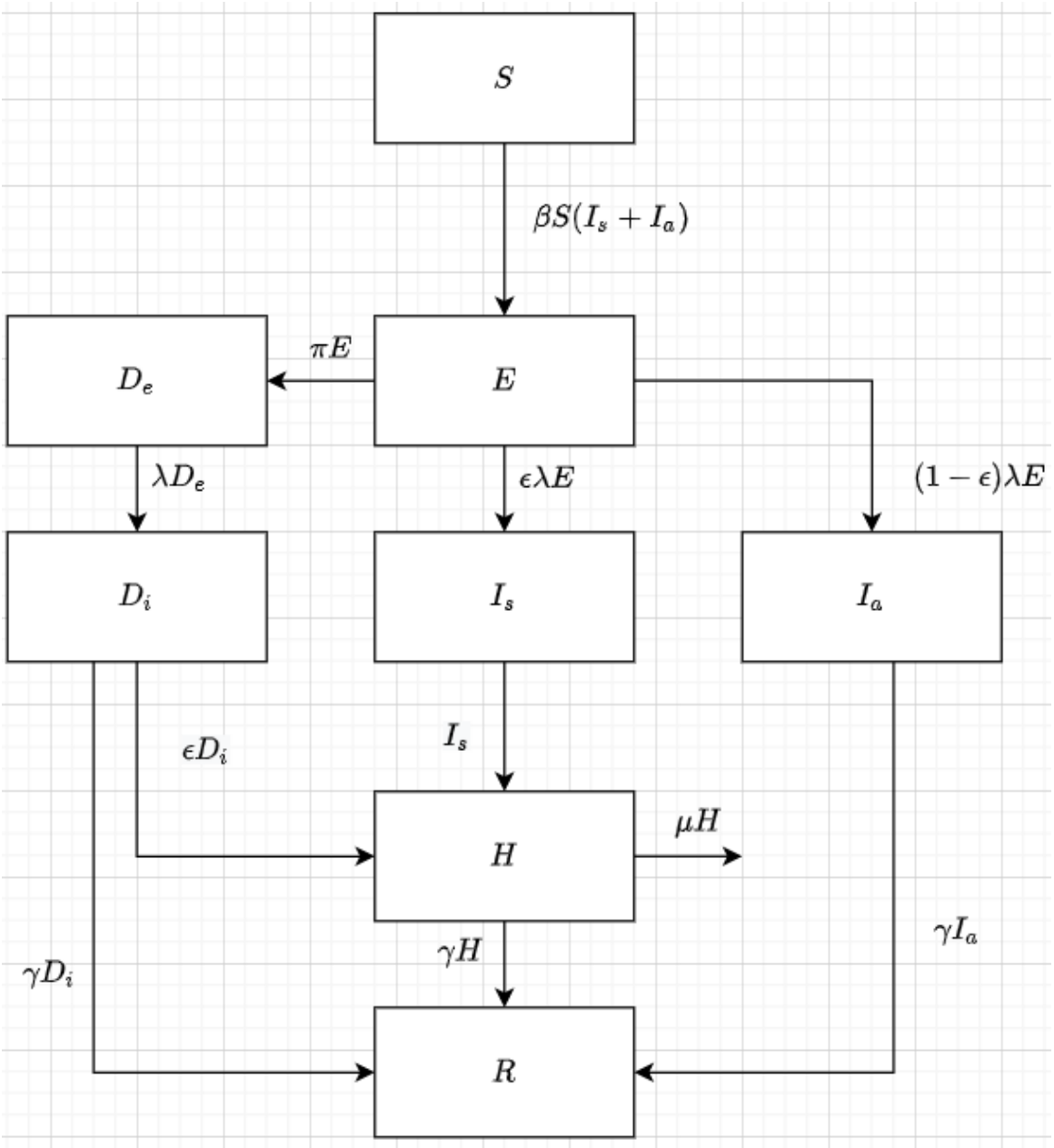

Figure 1.1: $SED_eD_iI_sI_aHR$ model

$$
\begin{aligned}
\frac{dS}{dt} &= \frac{-\beta S(I_s + I_a)}{N} \\
\frac{dE}{dt} &= \frac{\beta S(I_s + I_a)}{N} - (\pi + \lambda)E \\
\frac{dD_e}{dt} &= \pi E - \lambda D_e \\
\frac{dD_i}{dt} &= \lambda D_e - (\epsilon + \gamma)D_i \\
\frac{dI_s}{dt} &= \epsilon\lambda E - \theta I_s \\
\frac{dI_a}{dt} &= (1 - \epsilon)\lambda E - \gamma I_a \\
\frac{dH}{dt} &= \epsilon D_i + I_s - (\gamma + \mu)H
\end{aligned}
$$

where N is the total number of population at a particular time t.

The model above consists of the following six parameters represented in the table:

ODEs parameters		
Name of the parameter	Meaning	Value
β	transmission rate, which is the intensity of spread of the disease during the contact with an infected individual	0.4
π	the rate of PCR testing	varies between 0 and 1
λ	inverse of incubation period	$\frac{1}{5}$ or 0.2
ϵ	the rate of symptomatic cases	0.35
γ	inverse of recovered period	$\frac{1}{14}$
θ	proportion of hospitalized people as they are infectious with symptoms	1
μ	death rate due to the disease	0.01

Table 1.1: The Main Parameters of the $SED_eD_iI_sI_aHR$ model

More detailed explanation of the model and the nonlinear system of Ordinary Differential Equations (ODEs) can be seen in the methodology section 3.

After building the model of ODEs, we are going to find the basic reproduction

number using the Next-Generation Matrix Method.

Using the next-generation matrix, epidemiologists determine the fundamental reproduction number for a compartmental model of how infectious illnesses propagate. It is used in population dynamics to determine the fundamental reproduction number for structured population models. It is also used to compare computations in branching models with more than two kinds. 1990 articles by Diekmann et al. and van den Driessche and Watmough demonstrate how to calculate the fundamental reproduction ratio using the next-generation matrix (2002). To determine the fundamental reproduction number, the entire population is divided into n compartments, each containing mn infected compartments, using a matrix of the next generation. Suppose x_i for $i = 1, 2, 3, ..., m$ infected individuals in the i^{th} infected compartment at time t. The current model for an epidemic looks like this:

$$\frac{dx_i}{dt} = F_i(x) - V_i(x),$$

where $V_i(x) = [V_i^-(x) - V_i^+(x)]$. The detailed solution and explanation of the method is going to be discussed in the methodology section 3.

1.6 The Main Results of the Project

As a result of mathematical analysis of the proposed $SED_eD_iI_sI_aHR$ epidemic model, we obtained two main results of our project:

Theorem 1.1. *The Basic Reproduction Number for the $SED_eD_iI_sI_aHR$ model is:*

$$R_0 = \frac{\beta\lambda(\epsilon\lambda - \epsilon\theta + \theta)}{\gamma\theta(\lambda + \pi)}$$

Having used the Next-Generation Matrix, we got the above expression for our epidemic model. In this expression, it can be clearly seen that the value of the Basic Reproduction Number is also dependent function on the rate of PCR testing.

In this paper, as it was discussed above, the intervention will be based on testing every individual in our country (susceptible and exposed or exposed only); early detection of the disease and isolation of infected people; and sufficient testing and isolation to cause the R_0 of COVID-19 to drop below the index of 1.0, which

means that epidemic can collapse. To construct the government's cost function, first, we have to consider all average daily cost:

$$Dailycost = -Tax + DailyHospitalCost + PCRcost.$$

It implies our next main result:

Theorem 1.2. *The government cost is minimized in case of massive free PCR testing among Exposed individuals, while testing Susceptible and Exposed population would be unfavourable for the Government in terms of economics making the loss positive.*

The proof and explanation of these theorems are in Chapter 3. The following Chapter 2 gives some background information and related works about the disease. Then, in Chapter 3 we are going to prove Theorem 1.1 and 1.2. After that, in Chapter 4, we are going to demonstrate the construction of the government function and its parameters in more detail, and also some Python simulations of our optimized model in term of the government cost. Finally, we are going to sum up our results in Chapter 5.

2. Literature Review

2.1 Epidemiology

The term "epidemiology" refers to two distinct academic disciplines[12]. The first is the study of environmental and behavioral variables that increase an individual's susceptibility to particular illnesses. The second is the research on disease transmission (like smoking in the case of lung cancer or a fat diet in the case of diabetes). The transmission mechanism of infectious illnesses is discussed later. We will consider the second point. One of the most crucial aspects of mathematical epidemiology is having a solid explanation for how illnesses spread. The objective is to utilize models to forecast the duration of an epidemic or to analyze surveillance data. A posteriori epidemic analysis is extremely valuable because it can be used to test models and identify crucial parameters. Another objective is to develop disease-prevention measures. Both methods for preventing disease outbreaks and controlling an epidemic are of interest. Intervention and protection measures include mass immunization, screening, and quarantine, among others. Nobody knows with certainty what will occur when individuals attempt to assist. Even seemingly straightforward actions, such as mass immunizations, might have unanticipated consequences. Mathematical epidemiology is challenging due to the complexity and unpredictability of human behavior, particularly when it comes to diseases that are transmitted from person to person. If there is an infectious sickness in the area, sick individuals will avoid unsafe circumstances and seek medical help immediately. Concerts and other mass gatherings contribute to the spread of infectious illnesses. On commuter trains and foreign flights, infectious diseases can spread. This may occur both inside and between continents. Randomness, which can be caused by a multitude of factors, renders predictions impossible. Because we cannot conduct controlled experiments, determining parameters is

difficult (this is possible and done for animal diseases, in particular with respect to farming). Overall, epidemiology is a complicated topic with both intriguing theoretical and practical challenges.

2.2 Background Information

In any epidemic there is a value named the basic reproduction number, which shows the seriousness of the disease. In simple words, the basic reproduction number R_0 of an infectious disease is the number of people who acquire the disease from an infected person assuming the whole population is susceptible. For disease to spread, the reproduction number needs to be greater than 1. Preliminary reports suggested an R_0 for SARS-CoV-2 of approxiately 2.2, meaning that each infected person is going to infect at least two more people during the course of disease active case. However, estimates of R_0 have a wide range and the true value is not yet known. Making some assumptions, we can just estimate its approximate value and behaviour.

In mathematical biology, to calculate the value of R_0 we can use several approaches such as the Linearization Method, also known as Hartman-Grobman theorem and the Next-Generation Matrix method. The Hartman–Grobman theorem, commonly known as the linearization theorem, describes the behavior of dynamical systems at a point of hyperbolic equilibrium [8]. The hypothesis is named after Philip Hartman and Vadim M. Grobman. A smooth variation in form According to the theory, F is topologically conjugate with DF through a local homeomorphism at a hyperbolic fixed point p. Therefore, this theorem reveals crucial information regarding the behavior of orbits around a fixed point.

Second way of deriving R_0 can be implemented via the Next-Generation Matrix method, which we are going to use to solve our dynamocal system of ODEs. The basic reproduction number, R_0 is given by the spectral radius norm of the product F and the V inverse [5]:

$$R_0 = \rho(FV^{-1})$$

Thus, R_0 is equal to the dominant eigenvalue of FV^{-1} [6]. Here

$F = \mathcal{F}$ is the term which contains only secondary infections;

$V = \mathcal{V}$ contains other things where we do not include secondary infections.

When we have our model constructed, the first thing we have to consider is disease classes. The following steps in the derivation should be done:

Step 1. Regroup the system of ODEs into disease classes and non-disease classes.

Step 2. We use only the disease classes to find $\mathcal{F}$ and $\mathcal{V}$.

N.B. $\mathcal{F}$ contains terms with secondary infection rate.

Step 3. We obtain F, a matrix of partial derivatives of disease classes of $\mathcal{F}$ with respect to original dependent variables. Then we perform similar derivation for V based on $\mathcal{V}$.

Step 4. We find the product of F and the inverse of V, i.e. FV^{-1}.

Step 5. Find the eigenvalue of FV^{-1} and select the dominant one, which yields R_0.

Let us use this concept to derive R_0 for the $SEIR$ Model we discussed so far. Suppose the basic model as following:

$$\begin{aligned}
\frac{dS}{dt} &= \alpha N - \beta SI - \mu S \\
\frac{dE}{dt} &= \beta SI - kE - \mu E \\
\frac{dI}{dt} &= kE - \gamma I - \mu I \\
\frac{dR}{dt} &= \gamma I - \mu R
\end{aligned}$$

Disease classes: $\frac{dE}{dt} = \beta SI - kE - \mu E$ and $\frac{dI}{dt} = kE - \gamma I - \mu I$.

It follows that the matrices $\mathcal{F}$ and $\mathcal{V}$ satisfy

$$\mathcal{F} = \begin{pmatrix} \beta SI \\ 0 \end{pmatrix} \text{ and } \mathcal{V} = \begin{pmatrix} -kE - \mu E \\ kE - \gamma I - \mu I \end{pmatrix}$$

Here our second infection is βSI, so that means the rest of them are not second infection. When it comes to the second component so we do not have any β there, so that is why we have zero. As for the obtaining our $\mathcal{V}$, when we take the second infection away, the rest becomes that since here since we do not have any secondary infection.

So from $\mathcal{F}$ we obtain a matrix of F, and then from $\mathcal{V}$, we obtain a matrix V.

Constructing F matrix: Let $F(E, I) = \beta SI$ and $G(E, I) = 0$

Next, we have to find the partial derivatives of F matrix respect to each element of the matrix. We can see that all partial derivatives of F will be zero, except:

$$\frac{\partial F}{\partial I} = \beta S$$

Then, we get:

$$F = \begin{bmatrix} 0 & \beta S \\ 0 & 0 \end{bmatrix}$$

At disease free equilibrium (DFE), we set: $(S^*, I^*) = (1, 0)$, which means that there no disease exists. Analogically, we calculate the value of V, and find its inverse. By multiplying FV^{-1}, and finding its eigenvalues, we get R_0 as follows:

$$R_0 = \frac{\beta k}{(k + \mu)(\gamma + \mu)}$$

2.3 Related Works

Taipale et al. (2020) offered an additional intervention that would help limit the COVID-19 pandemic, provide better safety for those working in critical occupations, and steer a societal reopening [14]. The solution is centered on routinely testing each person and isolating contaminated people. They demonstrated that if enough people were tested and isolated, the R_0 of SARS-CoV-2 would drop below 1.0, and the epidemic would end. The strategy is based on strong and/or unreasonable assumptions regarding test accuracy, isolation compliance, population structure, and epidemiological characteristics, and its performance may be tracked in real time by tracking the test positive rate over time. The needed rate of testing, in addition to compliance and false negatives, is determined by the testing regime's design, with concurrent testing outperforming random selection of persons. The test frequency necessary to suppress an epidemic is linear in relation to R_0, the infectious duration, and the proportion of susceptible persons if findings are provided quickly. Importantly, the testing regimen would be successful at any level of prevalence, and it would be complementary to existing therapies like contact tracking and social distancing. It would also be resilient to failure,

since even if the testing rate was inadequate to stop the epidemic, the number of sick people in the community would be reduced, improving public health and economic circumstances. Due to the excellent performance of concurrent tests that offer instantaneous findings, a mass-produced, disposable antigen or RNA test that could be utilized at home would be perfect.

Taipale et al. (2021) later in their work stated that disease prevention has resulted in major advancements in public health[13]. The sluggish pace of vaccine and medicine development makes it difficult to prevent a new infectious illness by immunization or drugs. They suggested an additional intervention that would allow for quick control of developing infectious illnesses, as well as the eradication of diseases that are virtually entirely transmitted from person to person. Repeated illness testing and isolation of affected persons are the cornerstones of the strategy. The reproduction number R_0 is dropped to 1.0 at a sufficient pace of testing and isolation, and the epidemic will quickly collapse. The method relies on no strong or unreasonable assumptions regarding test accuracy, isolation compliance, population structure, or epidemiological characteristics, and its performance may be tracked in real time by tracking the test positive rate over time. The needed rate of testing, in addition to compliance and false negatives, is determined by the testing regime's design, with concurrent testing outperforming random selection of persons. The test frequency necessary to suppress an epidemic is monotonic and near-linear in relation to R_0, the infectious period, and the proportion of susceptible persons if findings are received quickly. Importantly, the testing system would be successful against both early and established epidemics, and it would be complementary to existing measures like contact tracking and social distancing. They demonstrate that the strategy is also resilient to failure: any rate of testing decreases the number of affected people in the community, benefiting public health and economic situations. These findings are based on thorough research and simulations of relevant epidemiological models. Due to the optimum performance of concurrent tests that offer instantaneous findings, a mass-produced, disposable antigen or genetic test that could be utilized at home would be perfect.

Another aspect is that LAMP-Seq was developed as a method for population-scale testing for SARS-CoV-2 infection, using the following general steps: A barcoded RT-LAMP reaction using primers specific for the SARS-CoV-2 genome is conducted on an unpurified or lysed swab sample, followed by large-scale sam-

ple pooling, PCR amplification with further barcoding, deep sequencing, and data analysis to identify positive people [10]. Even from unpurified samples, RT-LAMP reactions have been shown to be very sensitive for sequencespecific viral nucleic acid. (Estrela et al., 2019). In order to create a barcoded RT-LAMP reaction, barcode sequences were introduced into the forward inner primer (FIP), allowing for the creation of barcoded palindromic amplification products. When just a small percentage of samples are predicted to be positive during population scale testing, we may use a compressed barcode space to reduce the number of unique barcode primers required for testing a large number of samples.

According to Chen et al. (2020), unlike the Severe Acute Respiratory Syndrome (SARS) and other infectious illnesses, COVID-19 has asymptomatic infections (those with very minor symptoms) [2]. Asymptomatic illnesses are ignorant of their infectious potential, causing more individuals to get sick. In this situation, the transmission rate might substantially rise. Only 87.9% of COVID-19 patients have a fever, and only 67.7% of them have a dry cough, according to a new WHO study. If we utilize body temperature to identify COVID-19 infected patients, we won't be able to detect more than 10% of infected people.

3. Formula for R_0

3.1 SIR model

As for the research methodology, we are going to use well-known the SIR model to build a model of coronavirus disease. Regardless of what kind of disease, if it is of an infectious nature, then such epidemic, in our case, pandemic diseases can be modeled using several methods. One commonly used model is the SIR model for human-to-human transmission, which describes the flow of people through three mutually exclusive stages of infection: susceptible, infected, and recovered. This naked model is taken as a theoretical basis for all epidemic diseases, but in fact there is no such ideal disease in life, or it is very rare. Mostly a more complex modified model is used as in our case $SED_eD_iI_sI_aHR$ model, which considers other external economical, social, and natural factors. However, before discussing our model in more detail, let's have a look at a bare SIR model and derivation of the basic Reproduction Number.

Since the model represents the flow of epidemic disease by time-being, the following three letters of SIR should be represented as the functions of time, so that
$S = S(t)$ – the number of susceptible population;
$I = I(t)$ – the number of infected ones, and
$R = R(t)$ – the number of people recovered from disease.

Then, they are represented as differential equations:

- $\frac{dS}{dt} = -\frac{\beta IS}{N}$
- $\frac{dI}{dt} = \frac{\beta IS}{N} - \gamma I$

- $\frac{dR}{dt} = \gamma I$

The minus sign in the first equation is explained by that many susceptible people by time are getting infected, so their number is decreasing. In the meantime, the number of infected people is increasing due to this, but also decreasing due to those who are recovering. Finally, the change of the number of recovering people is always increasing by time.

The sum of three parameters is $S+I+R = N$, the total number of population of the model that we consider. Hence, $\frac{dS}{dt} + \frac{dI}{dt} + \frac{dR}{dt} = 0$, i.e. number of people is always constant.

There are also two more parameters in the model: β and γ. Basically they are main two parameters assuming that epidemic will die out or spread. β- the infection rate that represents how fast susceptible people get infected, i.e. responsible for the transition from susceptible to infectious group. As for γ- the recovery rate that shows how fast infectious people get recovered, i.e. responsible for the transition from infectious to recovered. If *infection rate* $<$ *recovery rate*, the epidemic will die out. If *recovery rate* $<$ *infection rate*, the epidemic will spread. In the case of COVID-19, the latter case will be considered [8]. The SIR model is used to examine two main questions: What conditions cause an epidemic? In case of epidemic, what portion of population that mixed well gets ill? So as coronavirus is much more beyond of epidemic (recognized as pandemic by World Health Organization), two questions mentioned above will be examined in the paper.

3.2 The Proof of the Theorem 1.1

To derive the formula for the the Basic Reproduction Number, we will apply Next-Generation Matrix method. Furthermore, we have derived the model and the expression for the basic reproductive number of the model, named R_0. In our case, S - susceptible, E - exposed, D_e – diagnosed early, D_i – diagnosed infectious, I_s – infectious symptomatic, I_a – infectious asymptomatic, H – hospitalized. Its model can be seen below:

$$\begin{pmatrix} \dot{E} \\ \dot{D}_e \\ \dot{D}_i \\ \dot{I}_s \\ \dot{I}_a \\ \dot{H} \end{pmatrix} = \begin{pmatrix} \frac{\beta S(I_s+I_a)}{N} - (\pi+\lambda)E \\ \pi E - \lambda D_e \\ \lambda D_e - (\epsilon+\gamma)D_i \\ \epsilon\lambda E - \theta I_s \\ (1-\epsilon)\lambda E - \gamma I_a \\ \epsilon D_i + I_s - (\gamma+\mu)H \end{pmatrix}$$

The epidemic model of these ODEs is splitted into two matrices:

$$\frac{dx_i}{dt} = F_i(x) - V_i(x),$$

as it was already stated in the introduction. $F_i(x)$ signifies the rate at which new infections develop in compartment i in the preceding equations. V_i^+ denotes the number of passengers who enter compartment i by all other ways, whereas V_i^- represents the number of passengers who exit compartment i via all other means. Alternatively, the same idea may be represented as

$$\frac{dx}{dt} = F(x) - V(x)$$

where

$$F(x) = (F_1(x),\ F_2(x), \ldots,\ F_m(x))^T$$

and

$$V(x) = (V_1(x),\ V_2(x), \ldots,\ V_m(x))^T.$$

Suppose x_0 to be the disease-free equilibrium.

Definition 1.2. If the reproduction number is less than one, the disease-free equilibrium point is locally asymptotically stable, but the endemic equilibrium point is locally asymptotically stable if this number exceeds one [8].

The values of the Jacobian matrices $F(x)$ and $V(x)$ are:

$$=> \begin{pmatrix} \frac{\beta S(I_s+I_a)}{N} \\ 0 \\ 0 \\ 0 \\ 0 \\ 0 \end{pmatrix} - \begin{pmatrix} (\pi+\lambda)E \\ -\pi E + \lambda D_e \\ -\lambda D_e + (\epsilon+\gamma)D_i \\ -\epsilon\lambda E + \theta I_s \\ -(1-\epsilon)\lambda E - \gamma I_a \end{pmatrix}$$

Calculating the matrix below using the Gauss-Jordan elimination:

$$\begin{bmatrix} \lambda+\pi & 0 & 0 & 0 & 0 & 0 \\ -\pi & \lambda & 0 & 0 & 0 & 0 \\ 0 & -\lambda & \gamma+\epsilon & 0 & 0 & 0 \\ -\lambda\epsilon & 0 & 0 & \theta & 0 & 0 \\ \lambda(\epsilon-1) & 0 & 0 & 0 & \gamma & 0 \\ 0 & 0 & -\epsilon & -1 & 0 & \gamma+\mu \end{bmatrix}^{-1}$$

In order to find out the inverse matrix, you must first obtain the identity matrix and then transfer it to the left using row operations. On the right, you can see an illustration of the inverse matrix [7].

So, augment the matrix with the identity matrix:

$$\left[\begin{array}{cccccc|cccccc} \lambda+\pi & 0 & 0 & 0 & 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 \\ -\pi & \lambda & 0 & 0 & 0 & 0 & 0 & 1 & 0 & 0 & 0 & 0 \\ 0 & -\lambda & \gamma+\epsilon & 0 & 0 & 0 & 0 & 0 & 1 & 0 & 0 & 0 \\ -\lambda\epsilon & 0 & 0 & \theta & 0 & 0 & 0 & 0 & 0 & 1 & 0 & 0 \\ \lambda(\epsilon-1) & 0 & 0 & 0 & \gamma & 0 & 0 & 0 & 0 & 0 & 1 & 0 \\ 0 & 0 & -\epsilon & -1 & 0 & \gamma+\mu & 0 & 0 & 0 & 0 & 0 & 1 \end{array}\right] \tag{3.1}$$

Divide Row 1 by $\lambda + \pi$: $R_1 = \frac{R_1}{\lambda+\pi}$

$$\left[\begin{array}{cccccc|cccccc} 1 & 0 & 0 & 0 & 0 & 0 & \frac{1}{\lambda+\pi} & 0 & 0 & 0 & 0 & 0 \\ -\pi & \lambda & 0 & 0 & 0 & 0 & 0 & 1 & 0 & 0 & 0 & 0 \\ 0 & -\lambda & \gamma+\epsilon & 0 & 0 & 0 & 0 & 0 & 1 & 0 & 0 & 0 \\ -\lambda\epsilon & 0 & 0 & \theta & 0 & 0 & 0 & 0 & 0 & 1 & 0 & 0 \\ \lambda(\epsilon-1) & 0 & 0 & 0 & \gamma & 0 & 0 & 0 & 0 & 0 & 1 & 0 \\ 0 & 0 & -\epsilon & -1 & 0 & \gamma+\mu & 0 & 0 & 0 & 0 & 0 & 1 \end{array}\right] \tag{3.2}$$

Add Row 1 multiplied by π to Row 2: $R_2 = R_2 + \pi R_1$

$$\left[\begin{array}{cccccc|cccccc} 1 & 0 & 0 & 0 & 0 & 0 & \frac{1}{\lambda+\pi} & 0 & 0 & 0 & 0 & 0 \\ 0 & \lambda & 0 & 0 & 0 & 0 & \frac{\pi}{\lambda+\pi} & 1 & 0 & 0 & 0 & 0 \\ 0 & -\lambda & \gamma+\epsilon & 0 & 0 & 0 & 0 & 0 & 1 & 0 & 0 & 0 \\ -\lambda\epsilon & 0 & 0 & \theta & 0 & 0 & 0 & 0 & 0 & 1 & 0 & 0 \\ \lambda(\epsilon-1) & 0 & 0 & 0 & \gamma & 0 & 0 & 0 & 0 & 0 & 1 & 0 \\ 0 & 0 & -\epsilon & -1 & 0 & \gamma+\mu & 0 & 0 & 0 & 0 & 0 & 1 \end{array}\right] \tag{3.3}$$

Add Row 1 multiplied by $\lambda\epsilon$ to Row 4: $R_4 = R_4 + \lambda\epsilon R_1$

$$\left[\begin{array}{cccccc|cccccc} 1 & 0 & 0 & 0 & 0 & 0 & \frac{1}{\lambda+\pi} & 0 & 0 & 0 & 0 & 0 \\ 0 & \lambda & 0 & 0 & 0 & 0 & \frac{\pi}{\lambda+\pi} & 1 & 0 & 0 & 0 & 0 \\ 0 & -\lambda & \gamma+\epsilon & 0 & 0 & 0 & 0 & 0 & 1 & 0 & 0 & 0 \\ 0 & 0 & 0 & \theta & 0 & 0 & \frac{\lambda\epsilon}{\lambda+\pi} & 0 & 0 & 1 & 0 & 0 \\ \lambda(\epsilon-1) & 0 & 0 & 0 & \gamma & 0 & 0 & 0 & 0 & 0 & 1 & 0 \\ 0 & 0 & -\epsilon & -1 & 0 & \gamma+\mu & 0 & 0 & 0 & 0 & 0 & 1 \end{array}\right] \tag{3.4}$$

Subtract Row 1 multiplied by $\lambda(\epsilon - 1)$ from Row 5: $R_5 = R_5 - \lambda(\epsilon-1)R_1$.

$$\left[\begin{array}{cccccc|cccccc} 1 & 0 & 0 & 0 & 0 & 0 & \frac{1}{\lambda+\pi} & 0 & 0 & 0 & 0 & 0 \\ 0 & \lambda & 0 & 0 & 0 & 0 & \frac{\pi}{\lambda+\pi} & 1 & 0 & 0 & 0 & 0 \\ 0 & -\lambda & \gamma+\epsilon & 0 & 0 & 0 & 0 & 0 & 1 & 0 & 0 & 0 \\ 0 & 0 & 0 & \theta & 0 & 0 & \frac{\lambda\epsilon}{\lambda+\pi} & 0 & 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & 0 & \gamma & 0 & \frac{-\lambda*\epsilon+\lambda}{\lambda+\pi} & 0 & 0 & 0 & 1 & 0 \\ 0 & 0 & -\epsilon & -1 & 0 & \gamma+\mu & 0 & 0 & 0 & 0 & 0 & 1 \end{array}\right] \tag{3.5}$$

Divide Row 2 by λ : $R_2 = \frac{R_2}{\lambda}$

$$\left[\begin{array}{cccccc|cccccc} 1 & 0 & 0 & 0 & 0 & 0 & \frac{1}{\lambda+\pi} & 0 & 0 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 & 0 & 0 & \frac{\pi}{\lambda(\lambda+\pi)} & \frac{1}{\lambda} & 0 & 0 & 0 & 0 \\ 0 & -\lambda & \gamma+\epsilon & 0 & 0 & 0 & 0 & 0 & 1 & 0 & 0 & 0 \\ 0 & 0 & 0 & \theta & 0 & 0 & \frac{\lambda\epsilon}{\lambda+\pi} & 0 & 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & 0 & \gamma & 0 & \frac{-\lambda\epsilon+\lambda}{\lambda+\pi} & 0 & 0 & 0 & 1 & 0 \\ 0 & 0 & -\epsilon & -1 & 0 & \gamma+\mu & 0 & 0 & 0 & 0 & 0 & 1 \end{array}\right] \tag{3.6}$$

Add Row 2 multiplied by λ to Row 3: $R_3 = R_3 + \lambda R_2$

$$\left[\begin{array}{cccccc|cccccc} 1 & 0 & 0 & 0 & 0 & 0 & \frac{1}{\lambda+\pi} & 0 & 0 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 & 0 & 0 & \frac{\pi}{\lambda(\lambda+\pi)} & \frac{1}{\lambda} & 0 & 0 & 0 & 0 \\ 0 & 0 & \gamma+\epsilon & 0 & 0 & 0 & \frac{\pi}{\lambda+\pi} & 1 & 1 & 0 & 0 & 0 \\ 0 & 0 & 0 & \theta & 0 & 0 & \frac{\lambda\epsilon}{\lambda+\pi} & 0 & 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & 0 & \gamma & 0 & \frac{-\lambda\epsilon+\lambda}{\lambda+\pi} & 0 & 0 & 0 & 1 & 0 \\ 0 & 0 & -\epsilon & -1 & 0 & \gamma+\mu & 0 & 0 & 0 & 0 & 0 & 1 \end{array}\right] \tag{3.7}$$

Divide Row 3 by $\gamma + \epsilon$: $R_3 = \frac{R_3}{\gamma+\epsilon}$

$$\left[\begin{array}{cccccc|cccccc} 1 & 0 & 0 & 0 & 0 & 0 & \frac{1}{\lambda+\pi} & 0 & 0 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 & 0 & 0 & \frac{\pi}{\lambda(\lambda+\pi)} & \frac{1}{\lambda} & 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 & 0 & \frac{\pi}{(\gamma+\epsilon)(\lambda+\pi)} & \frac{1}{\gamma+\epsilon} & \frac{1}{\gamma+\epsilon} & 0 & 0 & 0 \\ 0 & 0 & 0 & \theta & 0 & 0 & \frac{\lambda\epsilon}{\lambda+\pi} & 0 & 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & 0 & \gamma & 0 & \frac{-\lambda\epsilon+\lambda}{\lambda+\pi} & 0 & 0 & 0 & 1 & 0 \\ 0 & 0 & -\epsilon & -1 & 0 & \gamma+\mu & 0 & 0 & 0 & 0 & 0 & 1 \end{array}\right] \tag{3.8}$$

Add Row 3 multiplied by ϵ to Row 6: $R_6 = R_6 + \epsilon R_3$.

$$\left[\begin{array}{cccccc|cccccc} 1 & 0 & 0 & 0 & 0 & 0 & \frac{1}{\lambda+\pi} & 0 & 0 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 & 0 & 0 & \frac{\pi}{\lambda(\lambda+\pi)} & \frac{1}{\lambda} & 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 & 0 & \frac{\pi}{(\gamma+\epsilon)(\lambda+\pi)} & \frac{1}{\gamma+\epsilon} & \frac{1}{\gamma+\epsilon} & 0 & 0 & 0 \\ 0 & 0 & 0 & \theta & 0 & 0 & \frac{\lambda\epsilon}{\lambda+\pi} & 0 & 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & 0 & g & 0 & \frac{-\lambda\epsilon+\lambda}{\lambda+\pi} & 0 & 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & -1 & 0 & \gamma+\mu & \frac{\epsilon\pi}{(\gamma+\epsilon)(\lambda+\pi)} & \frac{\epsilon}{\gamma+\epsilon} & \frac{\epsilon}{\gamma+\epsilon} & 0 & 0 & 1 \end{array}\right] \tag{3.9}$$

Divide Row 4 by t : $R_4 = \frac{R_4}{t}$

$$\left[\begin{array}{cccccc|cccccc} 1 & 0 & 0 & 0 & 0 & 0 & \frac{1}{\lambda+\pi} & 0 & 0 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 & 0 & 0 & \frac{\pi}{\lambda(\lambda+\pi)} & \frac{1}{\lambda} & 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 & 0 & \frac{\pi}{\gamma+\epsilon)(\lambda+\pi)} & \frac{1}{\gamma+\epsilon} & \frac{1}{\gamma+\epsilon} & 0 & 0 & 0 \\ 0 & 0 & 0 & 1 & 0 & 0 & \frac{\lambda*\epsilon}{\theta(\lambda+\pi)} & 0 & 0 & \frac{1}{\theta} & 0 & 0 \\ 0 & 0 & 0 & 0 & \gamma & 0 & \frac{-\lambda\epsilon+\lambda}{\lambda+\pi} & 0 & 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & -1 & 0 & \gamma+\mu & \frac{\epsilon\pi}{(\gamma+\epsilon)(\lambda+\pi)} & \frac{\epsilon}{\gamma+\epsilon} & \frac{\epsilon}{\gamma+\epsilon} & 0 & 0 & 1 \end{array}\right] \tag{3.10}$$

Add Row 4 to Row 6: $R_6 = R_6 + R_4$.

$$\left[\begin{array}{cccccc|cccccc} 1 & 0 & 0 & 0 & 0 & 0 & \frac{1}{\lambda+\pi} & 0 & 0 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 & 0 & 0 & \frac{\pi}{\lambda(\lambda+\pi)} & \frac{1}{\lambda} & 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 & 0 & \frac{\pi}{(\gamma+\epsilon)(\lambda+\pi)} & \frac{1}{\gamma+\epsilon} & \frac{1}{\gamma+\epsilon} & 0 & 0 & 0 \\ 0 & 0 & 0 & 1 & 0 & 0 & \frac{\lambda\epsilon}{\theta(\lambda+\pi)} & 0 & 0 & \frac{1}{\theta} & 0 & 0 \\ 0 & 0 & 0 & 0 & \gamma & 0 & \frac{-\lambda\epsilon+\lambda}{\lambda+\pi} & 0 & 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 0 & 0 & \gamma+\mu & \frac{\epsilon(\lambda(\gamma+\epsilon)+\pi\theta)}{\theta(\gamma+\epsilon)(\lambda+\pi)} & \frac{\epsilon}{\gamma+\epsilon} & \frac{\epsilon}{\gamma\epsilon} & \frac{1}{\theta} & 0 & 1 \end{array}\right] \tag{3.11}$$

Divide Row 5 by γ : $R_5 = \frac{R_5}{\gamma}$.

$$\left[\begin{array}{cccccc|cccccc} 1 & 0 & 0 & 0 & 0 & 0 & \frac{1}{\lambda+\pi} & 0 & 0 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 & 0 & 0 & \frac{\pi}{\lambda(\lambda+\pi)} & \frac{1}{\lambda} & 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 & 0 & \frac{\pi}{(\gamma+\epsilon)(\lambda+\pi)} & \frac{1}{\gamma+\epsilon} & \frac{1}{\gamma+\epsilon} & 0 & 0 & 0 \\ 0 & 0 & 0 & 1 & 0 & 0 & \frac{\lambda\epsilon}{\theta(\lambda+\pi)} & 0 & 0 & \frac{1}{\theta} & 0 & 0 \\ 0 & 0 & 0 & 0 & 1 & 0 & \frac{\lambda(1-\epsilon)}{\gamma(\lambda+\pi)} & 0 & 0 & 0 & \frac{1}{\gamma} & 0 \\ 0 & 0 & 0 & 0 & 0 & \gamma+\mu & \frac{\epsilon(\lambda(\gamma+\epsilon)+\pi\theta)}{\theta(\gamma+\epsilon)(\lambda+\pi)} & \frac{\epsilon}{\gamma+\epsilon} & \frac{\epsilon}{\gamma+\epsilon} & \frac{1}{\theta} & 0 & 1 \end{array}\right] \tag{3.12}$$

Divide Row 6 by $\gamma+\mu$: $R_6 = \frac{R_6}{\gamma+\mu}$.

$$\left[\begin{array}{cccccc|cccccc} 1 & 0 & 0 & 0 & 0 & 0 & \frac{1}{\lambda+\pi} & 0 & 0 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 & 0 & 0 & \frac{\pi}{\lambda(\lambda+\pi)} & \frac{1}{\lambda} & 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 & 0 & \frac{\pi}{(\gamma+\epsilon)(\lambda+\pi)} & \frac{1}{\gamma+\epsilon} & \frac{1}{\gamma+\epsilon} & 0 & 0 & 0 \\ 0 & 0 & 0 & 1 & 0 & 0 & \frac{\lambda\epsilon}{\theta(\lambda+\pi)} & 0 & 0 & \frac{1}{\theta} & 0 & 0 \\ 0 & 0 & 0 & 0 & 1 & 0 & \frac{\lambda(1-\epsilon)}{\gamma(\lambda+\pi)} & 0 & 0 & 0 & \frac{1}{\gamma} & 0 \\ 0 & 0 & 0 & 0 & 0 & 1 & \frac{\epsilon(\lambda(\gamma+\epsilon)+\pi\theta)}{\theta(\gamma+\mu)(\gamma+\epsilon)(\lambda+\pi)} & \frac{\epsilon}{(\gamma+\mu)(\gamma+\epsilon)} & \frac{\epsilon}{(\gamma+\mu)(\gamma+\epsilon)} & \frac{1}{\theta(\gamma+\mu)} & 0 & \frac{1}{\gamma+\mu} \end{array}\right] \tag{3.13}$$

We are done. On the left is the identity matrix. On the right is the inverse

matrix. Therefore, the inverse matrix has the following form below:

$$V^{-1} = \begin{bmatrix} \frac{1}{\lambda+\pi} & 0 & 0 & 0 & 0 & 0 \\ \frac{\pi}{\lambda(\lambda+\pi)} & \frac{1}{\lambda} & 0 & 0 & 0 & 0 \\ \frac{\pi}{(\gamma+\epsilon)(\lambda+\pi)} & \frac{1}{\gamma+\epsilon} & \frac{1}{\gamma+\epsilon} & 0 & 0 & 0 \\ \frac{\lambda\epsilon}{\theta(\lambda+\pi)} & 0 & 0 & \frac{1}{\theta} & 0 & 0 \\ \frac{\lambda(1-\epsilon)}{\gamma(\lambda+\pi)} & 0 & 0 & 0 & \frac{1}{\gamma} & 0 \\ \frac{\epsilon(\lambda(\gamma+\epsilon)+\pi\theta)}{\theta(\gamma+\mu)(\gamma+\epsilon)(\lambda+\pi)} & \frac{\epsilon}{(\gamma+\mu)(\gamma+\epsilon)} & \frac{\epsilon}{(\gamma+\mu)(\gamma+\epsilon)} & \frac{1}{\theta(\gamma+\mu)} & 0 & \frac{1}{\gamma+\mu} \end{bmatrix} \tag{3.14}$$

Eventually, we can find the product and the eigenvalue of FV^{-1} and select the dominant one, which yields R_0:

$$R_0 = \frac{\beta\lambda(\epsilon\lambda - \epsilon\theta + \theta)}{\gamma\theta(\lambda + \pi)}$$

3.3 Numerical Solution

Having used the Next-Generation Matrix Method, we got the above expression for our epidemic model. In this expression, it can be clearly seen that the value of the basic reproduction number is also dependent function on the cost of PCR testing. The calculation of its value on python showed:

```
Reproduction=(beta*lamda*(epsilon*gamma - epsilon*theta + theta))/((gamma*theta)*(lamda+pi))
Reproduction
```

```
0.6300000000000002
```

Figure 3.1: Free PCR testing

If $\pi = 1$: the PCR testing is free of charge, then the numerical value of R_0 = 0.63, which means that the disease is locally asymptotically stable, its solution is close to the equilibrium point - the disease free equilibrium, i.e. there is no disease, or it will die out very soon.

```
Reproduction=(beta*lamda*(epsilon*gamma - epsilon*theta + theta))/((gamma*theta)*(lamda+pi))
Reproduction
```

```
3.780000000000001
```

Figure 3.2: Paid-basis PCR testing

If $\pi = 0$: the PCR testing is not free of charge, then the numerical value of $R_0 = 3.78$, which implies the invasion of the disease among population.

Hence, a large-scale PCR testing of exposed individuals is effective to cease the disease invasion.

4. Government Cost Optimisation

4.1 The Government Cost Function

Currently, the pandemic is believed to be the biggest issue for the global economy since the Second World War era [15]. Due to the lockdown measures taken by our government from March 16 to May 11, and in July and August of 2020, domestic consumption decreased by 40% in Kazakhstan. This caused a reduction of the annual GDP growth rate in 2020 compared to the previous year by 2.8%. As a result, the number population who live under the poverty line rapidly grew by 1.1–1.5 million, which is about 2300 tenge a day. Kazakhstan reacted rapidly to the pandemic and designed an anti-crisis package of 10 billion USD (KZT 4.4 trillion, or about 9% of GDP) to augment the social safety net and support businesses. Another solution is the optimization of the government's costs against the disease. According to the media, as of March 2021, the public health department determined tariffs. Over 930 thousand tenge is allocated for the treatment of one patient with a severe form of coronavirus infection. For patients of moderate severity, it costs about 450 thousand tenge. Each case is treated at fixed tariff prices. Today, the financial resources allocated by the Ministry of Health of the Republic of Kazakhstan are sufficient for patients with coronavirus infection. This includes medicine, the salaries of doctors, nurses, and orderlies, and all equipment related to all devices. On average, the cost of treatment is 680 thousand tenge. Meanwhile, the cost of the PCR testing varies between 6000 and 25000 tenge. The average price is 7200 tenge in Almaty.

In this paper, as it was discussed above, the intervention will be based on testing every individual in our country (susceptible and exposed or exposed only);

early detection of the disease and isolation of infected people; and sufficient testing and isolation to cause the R_0 of COVID-19 to drop below the index of 1.0, which means that epidemic can collapse. To construct the government's cost function, first, we have to consider all average daily cost:

$$Daily\,cost = -Tax + Daily\,Hospital\,Cost + PCR\,cost.$$

As of 2021, according to the Ministry of Finance of the Republic of Kazakhstan, the average monthly wage of a Kazakhstani citizen was 256 455 tenge. The tax rate is 10%, and according to the Bureau of National Statistics of the Agency for Strategic Planning and Reforms of the Republic of Kazakhstan, the economically active population in Kazakhstan was more than 9 million people, i.e., half of the population.

Here we can calculate the tax rate income of the government:

$$Tax = \frac{256455}{30} \cdot \frac{N_t}{2}$$

H_t - the number of hospitalized people at particular time t.

$$Daily\,Hospital\,Cost = \frac{680000}{14} \cdot H_t$$

The average daily cost for the PCR testing:

$$PCR\,cost = 7200 \cdot \pi E_t$$

E_t - number of exposed people at particular time t (those who have been infected but are not infectious yet).

Consequently, the government cost function model is:

$$Total\,Cost = \sum_{t=0}^{700} e^{-rt} \cdot (Daily\,Cost) =$$

$$= \sum_{t=0}^{700} e^{-rt} \cdot (-Tax + Daily\,Hospital\,Cost + PCR\,cost)$$

$$= \sum_{t=0}^{700} e^{-rt} \cdot (-\frac{256455}{30} \cdot \frac{N_t}{2} + \frac{680000}{14} \cdot H_t + 7200 \cdot \pi E_t)$$

where e^{-rt} - discount rate.

4.2 Python simulations

Having calculated the value of the basic reproduction number, we got the expression in the theorem 1.1 for our epidemic model. In this expression, it can be clearly seen that the value of the basic reproduction number is also dependent function on the price of PCR testing. We have considered only two cases: when it completely free of charge for exposed population, and on the paid-basis.

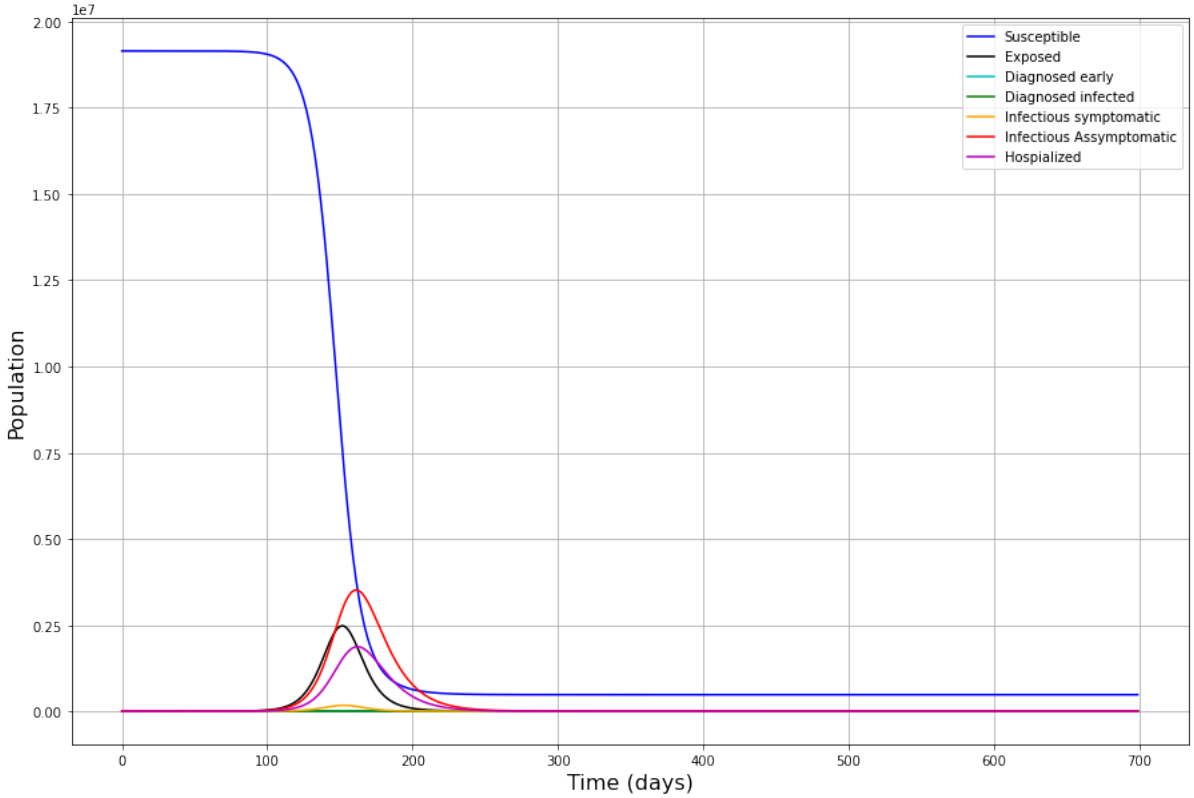

Figure 4.1: $SED_eD_iI_sI_aHR$ model simulation

According to the figure 4.1, we can estimate that the virus would be among the population more than for 200 days before it dies out, reaching its peak within a half of a year. So, the simulation above helps us to see the behavior of our $SED_eD_iI_sI_aHR$ epidemic model and the approximate time when COVID-19 collapses.

Figure 4.2 demonstrates the case without free PCR testing, in other words

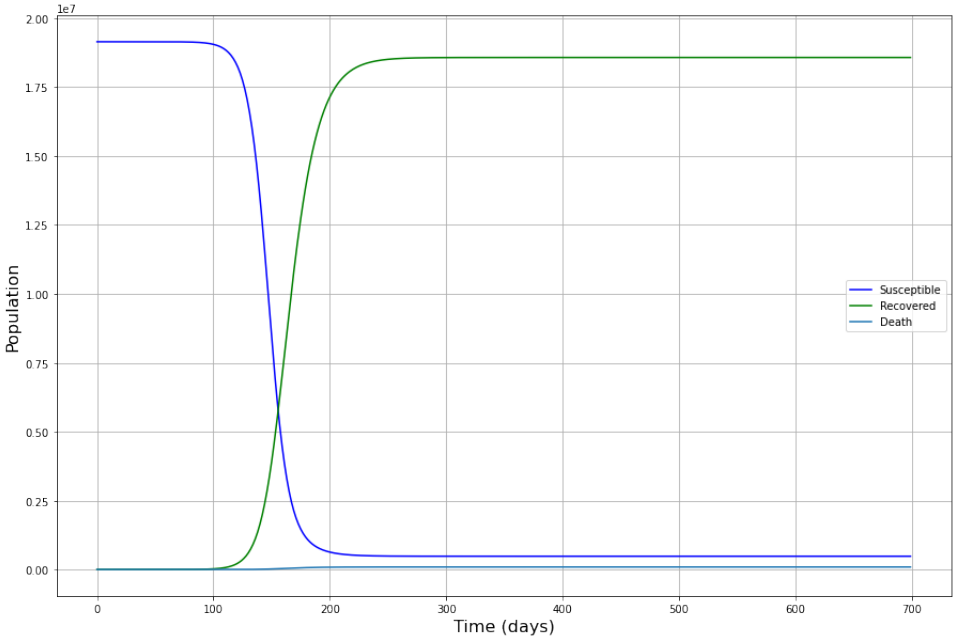

Figure 4.2: Susceptible vs Recovered individuals' simulation in case paid PCR testing

PCR testing is not free for people, thus it will take about 5-7 months until the epidemic dies out.

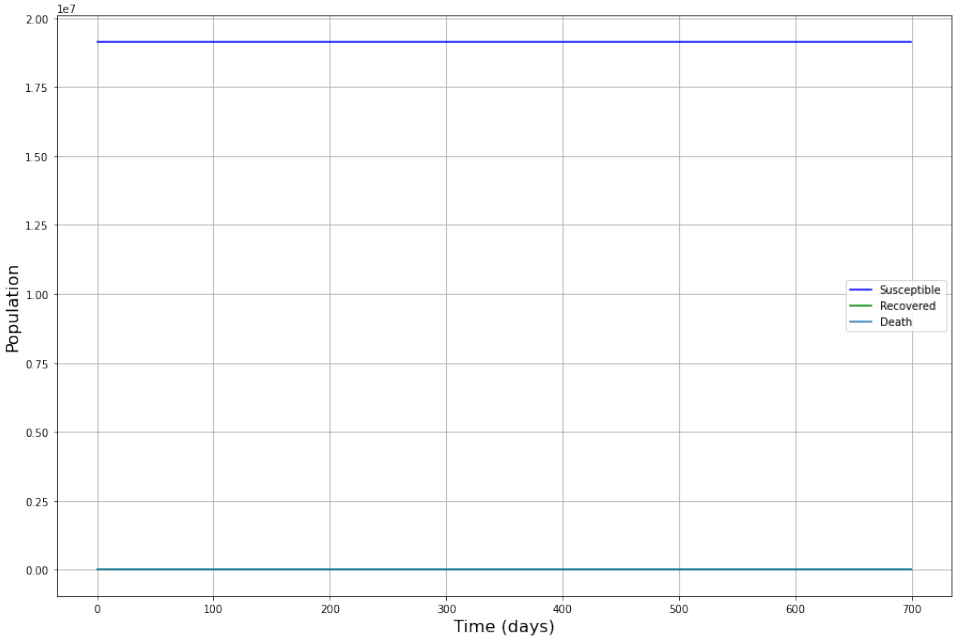

Figure 4.3: Susceptible vs Recovered individuals' simulation in case free PCR testing

As for Figure 4.3, it means that with rapid PCR testing of exposed individuals, the disease can be prevented, and very soon virus dies out.

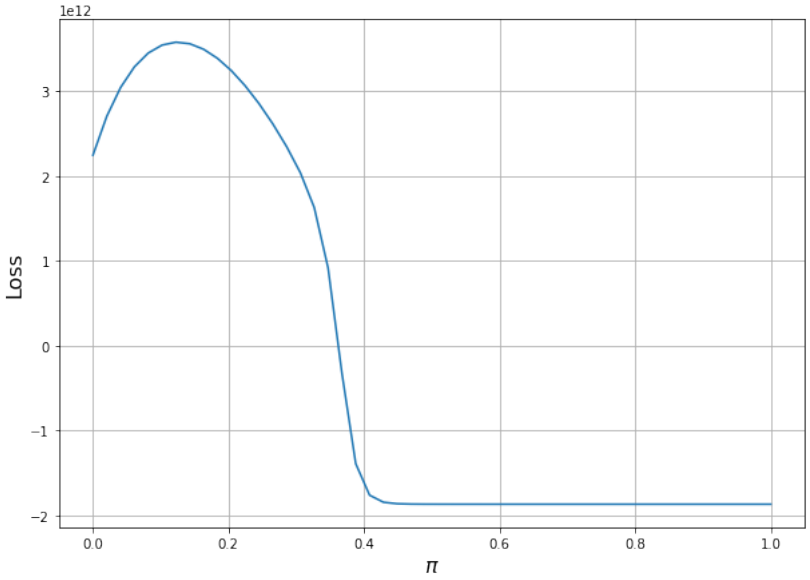

Figure 4.4: The Government Loss function in case of testing exposed people

The Government Cost function illustrated in Figure 4.4 shows that at the rate of free PCR testing of exposed people, very soon the spread of the virus can be stopped. Furthermore, the curve shows that the loss is negative, which means that it is also profitable for the government to do free PCR testing of the exposed population.

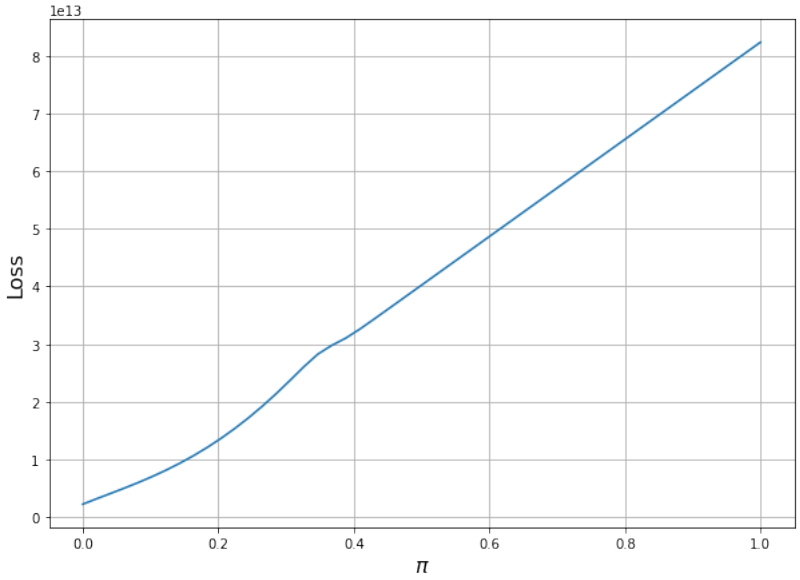

Figure 4.5: The Government Loss function in case of testing exposed and susceptible people

Meanwhile, Figure 4.5 clearly illustrates the positive government loss in the

case when the government does not cover the cost of PCR testing.

5. Conclusion

In this study, we investigated COVID-19 using mathematical and numerical methods. Our PCR-based model is not only more adaptive than previous static SEIR models, but it is also more robust than direct estimation methods. Our numerical results show that if the rate of daily PCR testing were to be > 0.4, then the government would benefit economically in terms of healthcare costs and human lives. Having done the calculations, we can observe that the massive free PCR testing of exposed individuals is effective both in terms of the epidemic model (the value of the Basic Reproduction Number proves it) and in terms of the optimization of the government cost against disease. However, in this case, when we considered the PCR testing of susceptible and exposed individuals, we found that it was not beneficial for the government and increased the loss a lot. In our society, it is hard to find out if an individual is exposed or not at once. That is why it is difficult to differentiate exposed people from susceptible ones. However, in this case, the tracing system Ashyq, which is widely used in our society, could ease the task. Finally, a plethora of arguments and ideas for epidemic prevention have developed in reaction to the experimental findings. In the future, we would like to extend our deterministic SEIR model by constructing an improved model that will depend on the rate of PCR testing, i.e., a model of π as a function of time. Hence, we will be able to find out the approximate number of populations that should be tested daily.

To summarize our paper, we succeeded in meeting our objectives, which included determining the formula for the fundamental reproduction number and its numerical value, as well as reducing government spending. After extending the basic SEIR (Susceptible-Exposed-Infected-Recovered) epidemic model to the SEDeDiIsIaHR model, which incorporates some external factors and is adaptable to Kazakhstan conditions, we used the well-known Linearization Method to

find the ODEs formula for the epidemic model's main value – the basic reproduction number R0. Another goal was to determine whether R0 could be made dependent on government action, i.e., whether extensive PCR testing of exposed people would have an effect on our model. As a result, it was discovered that the Government Loss is negative in the case of free PCR testing of the exposed population, implying that the Government would benefit economically and socially by saving human lives and quickly ending the epidemic ($R_0 = 0.63$), whereas the Government Loss is positive in the case of paid PCR testing, implying that the Government Loss would increase. In this scenario, $R_0 = 3.78$, indicating that the infection is slow to fade away, posing a challenge to the government. As a result of our research, we were able to establish the efficacy of mass PCR testing of exposed individuals. Furthermore, the study discovered that bulk PCR testing of vulnerable and exposed groups is cost-ineffective. Furthermore, determining the precise number of people who have been exposed and diagnosing the obvious symptoms may be difficult. As a result, additional research is required to improve the model. In the future, we hope to improve our deterministic $SEIR$ model by developing a model that is dependent on the rate of PCR testing, i.e., a model as a function of time, allowing us to estimate the number of populations that should be tested daily.

A. Appendix Code

Here we can see our codes to implement some experiments to reach our thesis results written on Python.

```
import numpy as np
import scipy.optimize as optimization
import matplotlib.pyplot as plt
import scipy.integrate
from scipy.integrate import odeint
np.seterr('raise')

def SEIR_ode(y,t,beta,pi, epsilon, theta,lamda,gamma,mu):
    S,E,De,Di,Is,Ia,H,R, Death = y
    dS=-beta*S*(Is+Ia)/N
    dE=beta*S*(Is+Ia)/N-(pi + lamda)*E
    dDe = pi*E - lamda*De
    dDi = lamda*De - (epsilon + gamma)*Di
    dIs= epsilon*lamda*E - theta*Is
    dIa= (1-epsilon)*lamda*E - gamma*Ia
    dH = epsilon*Di + Is - (gamma + mu)*H
    dR = gamma*(H+Di+Ia)
    dDeath = mu*H
    return [dS,dE,dDe, dDi, dIs,dIa,dH,dR, dDeath]
```

Listing A.1: $SED_eD_iI_sI_aHR$ model

```
#Initial Conditions for Kazakhstan
N=19148890 # Total Population 19148890

S0=N      # total population
E0= 1     # number of exposed people by 16 March 2020
De0 = 0
Di0 = 0
Is0= 1    # number of infectious people with clear symptoms by 16 March 2020
Ia0= 0    # number of asymptomatic prople with no symptoms by 16 March 2020
H0 =1
R0=0      # number of recovered people by 16 March 2020
Death0 =0

```

```
beta = 0.4
pi = 0
lamda=1/5  #incubation period 1/5
epsilon = 0.35
gamma=1/14 #recovery rate 1/14
mu=0.001   #death rate 0.0005
theta = 1

#time
numdays = 700
time=np.linspace(0, numdays-1, numdays)
```

Listing A.2: Initial Conditions

```
#Simulation
solution=scipy.integrate.odeint(SEIR_ode,[S0,E0,De0,Di0,Is0,Ia0,H0,R0,Death0
    ],time,args=(beta,pi, epsilon, theta,lamda,gamma,mu))
solution=np.array(solution)

#Plot Results
plt.figure(figsize=(15,10))
plt.plot(time, solution[:,0],color='blue', label='Susceptible')
plt.plot(time, solution[:,1],color='black', label='Exposed')
plt.plot(time, solution[:,2],color='c', label='Diagnosed early')
plt.plot(time, solution[:,3],color='green', label='Diagnosed infected')
plt.plot(time, solution[:,4],color='orange', label='Infectious symptomatic')
plt.plot(time, solution[:,5],color='red', label='Infectious Assymptomatic')
plt.plot(time, solution[:,6],color='m', label='Hospialized')
plt.plot(time, solution[:,7],color='green', label='Recovered')

plt.plot(time, solution[:,8], label='Death')
plt.plot(time, solution[:,4]+solution[:,5],color='darkred', label='Active
    cases')

plt.grid()
plt.legend()
plt.xlabel('Time (days)',fontsize=16)
plt.ylabel('Population',fontsize=16)

plt.show()
```

Listing A.3: Simulation of the model

```
w=1600 #average hourly wage in KZT w.r.t the whole population
tau=0.1 # tax rate

from scipy.optimize import minimize

#Government total Loss due to epidemic
r=0.0004 #discount rate daily
days=700
h=680000/14 # Treatment cost per regular COVID patient in KZT
t=np.linspace(0, days-1, days)

#Governemnt loss function
def Loss(pi):
    sol=scipy.integrate.odeint(SEIR_ode,[S0,E0,De0,Di0,Is0,Ia0,H0,R0,Death0
   ],time,args=(beta,pi, epsilon, theta,lamda,gamma,mu))

    S=sol[:,0]
    H=sol[:,6]
    Death =sol[:,8]
    E=sol[:,1]
    Nt=N-Death-H
    b=0
    for k in range(days):
        b=b-np.exp(-r*k)*(tau*w*Nt[k]-h*(H[k])-7200*pi*(E[k]+S[k]))
        #b=round(b, 10)
    return b
```

Listing A.4: The Government Loss Function Construction

```
#Minimization
from scipy.optimize import minimize_scalar
def optimal_pi():
    res = minimize_scalar(Loss,bounds=(0, 1), method='bounded')
    return res.x
opt_pi=optimal_pi()
print(opt_pi)
print (Loss(opt_pi))
y=[]
for x in np.linspace(0, 1):
    y.append(Loss(x))

plt.figure(figsize=(10,7))
plt.grid()
plt.plot(np.linspace(0, 1),y)
plt.xlabel(r'$\pi$',fontsize=16)
plt.ylabel('Loss',fontsize=16)
plt.show()
```

Listing A.5: The Cost Minimization

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