

Lappeenranta-Lahti University of Technology LUT
School of Engineering Science
Computational Engineering and Analytics
Bachelor's thesis

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SEIQR model-based interactive simulation of COVID-19 restrictive measures

Ohjaaja: Matylda Jablonska-Sabuka

ABSTRACT

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2021

30 pages, 15 figures, 1 table, 1 attachment

Examiner: Matylda Jablonska-Sabuka

Keywords: COVID-19; SARS-CoV2; simulation; SIR model; SEIQR model; Python

The aim of this thesis was to produce an interactive application for simulating the impact of COVID-19 restrictive measures on the spread of the epidemic. The goal was to produce a SIR model-based epidemic model which emulates the dynamics of the epidemic in detail. The program was implemented on Python using open-source libraries.

The mathematical model introduced in this paper is an extended SEIQR system, in which all of the individuals in the simulated population are divided into five compartments. The epidemic model is based on ordinary differential equations, which represent the transmissions between the compartments. The model incorporates COVID-19 specific constants for the incubation time and recovery period of the disease to reproduce the spread of the disease as realistically as possible.

The restrictive measures observed in this paper were Government Stringency Index, face mask usage and the compliance of quarantine. By assessing the results of the simulation, it was discovered that the decrease in the spread of the epidemic is significant when several restrictive measures are included concurrently.

The proposed SEIQR model was estimated to spread infections in a higher rate than SARS-CoV2 in reality. The model could be improved by refining its parameters. The approach in the development could be data-based for a more realistic basis.

TIIVISTELMÄ

Lappeenrannan-Lahden teknillinen yliopisto
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Laskennallisen tekniikan koulutusohjelma

Anette Sarivuo

SEIQR-malliin pohjautuva interaktiivinen simulaatio COVID-19-rajoitustoimenpiteistä

Kandidaatintyö

2021

30 sivua, 15 kuvaa, 1 taulukko, 1 liite

Ohjaaja: Matylda Jablonska-Sabuka

Avainsanat: COVID-19; SARS-CoV2; simulaatio; SIR-malli; SEIQR-malli; Python

Kandidaatintyön päämääränä oli toteuttaa interaktiivinen sovellus, jolla voidaan simuloida rajoitustoimenpiteiden vaikutusta koronavirusepidemian leviämiseen. Simulaation perustaksi oli tavoitteena kehittää SIR-malliin pohjautuva matemaattinen malli, joka havainnollistaa COVID-19-epidemian leviämistä yksityiskohtaisesti.

Työssä esitetty malli on SEIQR-systeemi, jossa simuloidun populaation yksilöt jaetaan viiteen lokeroon. Epidemiologinen malli perustuu differentiaaliyhtälöihin, jotka kuvastavat yksilöiden siirtymiä lokeroitten välillä. Malliin on sisällytetty koronavirusinfektioille ominainen itämisaika ja toipumisaika taudin realistisen mallintamisen mahdollistamiseksi.

Sovelluksen käyttäjä pystyy syöttämään simulaatioon eri parametreja graafisen käyttöliittymän kautta kahden eri skenaarion osalta. Syötetyt parametrit sisällytetään SEIQR-malliin, ja käyttäjä saa tulosteena kummankin skenaarion tuloksia havainnollistavat kuvaajat. Sovellus ohjelmoitiin Pythonilla avoimen lähdekoodin kirjastoja hyödyntäen.

Työssä tutkitaan kasvomaskien käytön, karanteenin noudattamisen sekä hallituksen asettamia poliittisia rajoitteita kuvaavan indeksin vaikutusta epidemian leviämisenopeuteen. Simulaation tulosten perusteella tartuntojen leviäminen hidastuu useiden eri rajoitustoimenpiteiden ollessa voimassa.

Simuloidun SEIQR-mallin arvioitiin levittävän tartuntoja nopeammin kuin virukselle on todellisuudessa tyypillistä. Mallia voitaisiinkin parannella tarkentamalla sen parametreja. Tulevaisuudessa mallin kehitys voisi olla datalähtöistä todenmukaisemman perustan saavuttamiseksi.

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Attachments

Attachment 1: Source code URL

List of symbols and abbreviations

COVID-19	Coronavirus disease 2019
SARS-CoV-2	Severe acute respiratory syndrome coronavirus 2
GSI	Government Stringency Index
t	time
S	susceptible (compartment)
E	exposed (compartment)
I	infectious (compartment)
Q	quarantined (compartment)
R	recovered (compartment)
α	multiplier of restrictive measures based on the GSI
β_1	average rate of contacts by infected individuals wearing a mask
β_2	average rate of contacts by infected individuals not wearing a mask
γ	per-capita recovery rate of infected individuals
η	per-capita quarantine rate of infected individuals
θ	average rate of exposed individuals becoming infectious
σ	proportion of individuals wearing a mask
N	population size

1 INTRODUCTION

1.1 Background

Coronavirus disease 2019 (COVID-19) is a contagious disease caused by severe acute respiratory syndrome coronavirus 2 (SARS-CoV2). The first reported cases of COVID-19 pandemic occurred in Wuhan, China, in December 2019 (Kucharski et al., 2020) and it then has spread worldwide into an ongoing pandemic. Through mathematical modelling of infectious diseases, we are able to estimate the epidemiological situation and to assess whether control measures could be necessary or effective. There are many challenges to producing reliable simulations of the spread of the SARS-CoV-2 due to the incubation period, which delays the symptoms from appearing, the possible lack of symptoms in the infection phase in some individuals and the possibly impermanent immunity for the disease.

1.2 Research objective

A major assumption in the mathematical epidemic modelling is that the population can be divided into a set of compartments, which represent the disease status of an individual. SIR model is a simple mathematical model which calculates the theoretical number of people infected with a contagious disease in a closed population over time. It consists of three states: susceptible (S), infected (I) and removed (R). The model can be specified and applied for estimating the spread of different infectious diseases.

In this paper, the SIR model is extended with two more compartments: exposed (E) and quarantined (Q). This model will be called SEIQR-model. The goal of the work is to produce an interactive application, where the user is allowed to adjust different variables which effect the result graphs of the simulation. These variables include the probability of mask usage or quarantine in the population and the administrative restrictive measures based on the Government Stringency Index.

The purpose of this paper is to introduce and analyze a simulation that allows the user to adjust the model and to test various scenarios. The model incorporates different restriction policies to demonstrate their significance in prevention or deceleration of the spread of COVID-19. The model can also be applied for other highly contagious diseases.

1.3 Methodology and arrangements

The first step in the research was to analyze the specifics of COVID-19 to be able to implement a model simulating its spread. Scientific literature was studied also to define the average constants in the infection dynamics, such as incubation time and recovery period.

In the second step, building the epidemic model started from analyzing the classic SIR model and including relevant dynamics to it. The resulting set of ordinary differential equations was complemented with variables based on scientific research of COVID-19 to specifically simulate the spread of the disease. Some of the parameters in the model were guessed based on personal estimates.

After these steps, the user interface design was drafted. The simulation including the mathematical model and the graphical user interface was then programmed in Python. This was followed by iterations of test runs. When testing the simulation program, the reliability of the resulting graphs was estimated and the mathematical model behind the simulation was adjusted as necessary. The results were compared to the data available on the spread of COVID-19 epidemic in Finland.

The thesis is structured as follows. In Chapter 2, the assessed literature and its relevance to this thesis are described. Chapter 3 presents details on the introduced mathematical model and the assumptions behind it, and Chapter 4 involves the programming environment and the user interface of the simulation. In Chapters 5 and 6, the results of the simulation and the applicability of the epidemic model are observed. Chapter 7 summarizes the background, goals, phases and the results of the work.

2 LITERATURE REVIEW

The research and mathematical modelling of infectious diseases is necessary for estimating the spread of epidemics in different conditions. Erdem et al. (2017) analyzed the impact of quarantine and isolation in the spread of influenza type A disease utilizing a SIQR model. Similar to their research, the approach in this paper is also to indicate the influence of isolation along with other factors in the spread of COVID-19 specifically. In this work, the SIR model-based simulation is extended with another stage for the exposed individuals and several control measures.

Bo et al. (2021) studied the effectiveness of non-pharmaceutical interventions on COVID-19

in 190 countries, and the results indicated that social distancing, traffic restriction, mandatory mask wearing and quarantine measures were significantly associated with a decrease in the spread of the epidemic. In the model introduced in this paper, masks and quarantine are included to be able to simulate their impact.

A SIR model-based epidemiological model with a switching transmission rate was proposed by Chladná et al. (2020). Their model incorporates two thresholds for the number of infected individuals, and temporary prevention measures are implemented or lifted once the corresponding threshold is met. Likewise, in this study the goal is to simulate governmental restriction measures in the observed population, but through a constant multiplier effecting the transmission of the infection α . The constant α is based on Governmental Stringency Index (GSI), which is a measure reflected on nine administrative response metrics. The metrics included are such as school and workplace closures, restrictions on public gatherings and international travel controls. (Data, 2021)

He et al. (2020) studied viral loads in throat swabs of 94 patients with COVID-19 infection and reported that the infectiousness of the patients peaked on or before the beginning of their symptomatic stage. The research was concluded with an estimation of about 44 percent of COVID-19 infections being spread from an individual to another before symptom onset. As the viral transmission of SARS-CoV2 seems to be significant already in the presymptomatic stage, the possible control measures set at the symptom onset might be less effective in slowing down the epidemic spread. This is considered in the proposed mathematical model by representing all exposed individuals as equally infectious as the symptomatic.

The goal of the simulation is to mimic COVID-19 dynamics as realistically as possible. Thus, the incubation period and the recovery period of the disease are based on current literature.

Incubation period means the time between exposure to the virus and the onset of symptoms. Li et al. (2020) researched data on the first 425 confirmed COVID-19 cases in Wuhan and deduced that the mean incubation period is 5.2 days. This is applied in the model as a constant effecting the individuals' transition from exposed to infectious or isolated.

Kampen et al. (2021) researched 129 hospitalized, COVID-19 confirmed individuals to test their respiratory samples for the existence of infectious virus. They defined the median duration of infectious viral shedding to be 8 days after symptom onset, meaning, that on average each individual with COVID-19 infection can spread the virus for 8 days after the beginning of their symptoms. This value is provided in the model as the length of an individual being infectious once symptomatic.

Roy (2020) discussed the possibility of reinfection with SARS-CoV-2 and suggested that it

is unlikely: the assumption was justified with support from a study with COVID-19 infected animals and the current knowledge on viral neutralizing antibody duration from known respiratory diseases among other reasoning. Due to these results, the reinfection with the virus is considered infeasible in this work.

3 MODEL

3.1 Assumptions

The population is presumed to have a constant size of N individuals, which are assumed to mix at random so that each of them have the same probability of contacting others and becoming exposed to the infection. Thus, the population is assumed to be homogeneous as the average rates of transmission (β_1 and β_2) are considered to be constant. Due to the differences in population density, population age structure and social interaction, this assumption may lead to less realistic simulations.

It is assumed that a certain proportion of the exposed and infectious population wears face masks. The transmission rate β_1 of the individuals wearing a mask is assumed to be smaller than β_2 of the individuals not wearing a mask, as the contagiousness of the disease is assumed to be lower once the infected individual wears a mask while in contact with others (Bo et al., 2021). The transmission rates have been formed as the products of transmission probabilities and contact rates. These values have been based on guesswork for the sake of simplicity, which might cause the results be less truthful. The contact rate is considered to be equal in both cases ($\frac{1}{4}$). The transmission probability in the case of a mask being worn is set at $\frac{3}{10}$ and in the case of no mask at $\frac{9}{10}$. Hence, β_1 and β_2 are assumed to be $\frac{3}{10} \cdot \frac{1}{4}$ and $\frac{9}{10} \cdot \frac{1}{4}$, respectively.

The characteristics of the COVID-19 infection are presumed to be stable. Therefore, the simulation does not take different mutations with unlike infection dynamics or diversity in responses to the infection into consideration. These aspects may include the incubation period that it takes for an individual to become symptomatic after being exposed to the virus and the recovery time after symptom onset. These characteristics correlate with the constants θ and γ in the mathematical model introduced in this paper.

In this simulation, both presymptomatic and symptomatic individuals are assumed to spread the SARS-CoV2 equally efficiently to susceptible individuals based on the research by He

et al. (2020). It is presumed that each susceptible individual enters an exposed state immediately after a contact with an exposed or infected individual. The contagiousness of the disease begins 5.2 days before the symptomatic phase (Li et al., 2020).

Only a certain proportion of the infected population is assumed to recognize their infection symptoms and practice quarantine. The rest of the population stays in a socially active state in the frame set by the control measures in the simulation. The proportion of the individuals practicing quarantine can be any value between 0 and 1, and it is based on the user's choice.

An individual with COVID-19 infection is expected to be symptomatic and infectious for 8 days (Kampen et al., 2021). It is assumed that the recovery from the infection leads to a permanent, protective immunity. At this time, it is unclear how long-lasting immunity to SARS-CoV-2 humans are able to generate (Roy, 2020). As the duration of the simulations is kept at a maximum of three months, the assumption of perfect immunity is not considered a disadvantage to the model.

In this model, the dynamics of birth and death are omitted, as the time span t of the simulations is relatively short. The dynamics of the COVID-19 epidemic are assumed to be significantly faster than the vital dynamics.

The restrictive measures based on GSI are applied in the simulation. As a higher GSI score correlates with more strict control measures, the constant multiplier α in the mathematical model is logarithmically proportional to the GSI score. The function for α has been formed by comparing the simulation results with the data from COVID-19 cases by Finnish institute for health and welfare. It is assumed that all the individuals in the simulated population obey the restrictive measures equally. This supposition might lead to slightly inaccurate results, as in reality there is no guarantee of all individuals obeying restrictive measures perfectly.

The compartments S , E , I , Q , and R respectively stand for the number of susceptible, exposed, infectious, quarantined and recovered individuals, so that $S + E + I + Q + R = N$. The first compartment S is composed of the individuals that have not been in contact with the infectious individuals I . Once exposed but not yet symptomatic, they move from S to E . After the incubation period, the virus carried by the exposed individuals enters an infectious state and the individuals move to I or Q depending on whether they recognize the symptoms and choose to isolate for the recovery period. After the recovery, the individuals move to R .

3.2 Extended SEIQR model

The model consists of five variables that change as a function of time, which represent the number of individuals in each compartment at a particular time, as seen below:

- $S(t)$: Number of susceptible individuals at time t
- $E(t)$: Number of exposed individuals at time t
- $I(t)$: Number of infectious individuals at time t
- $Q(t)$: Number of quarantined individuals at time t
- $R(t)$: Number of recovered individuals at time t

In this paper, the SEIQR model is extended with mask usage and restriction policy dynamics. The simulation is based on a system of ordinary differential equations. A complete compartmental diagram for the transition between model states can be seen in Figure 1.

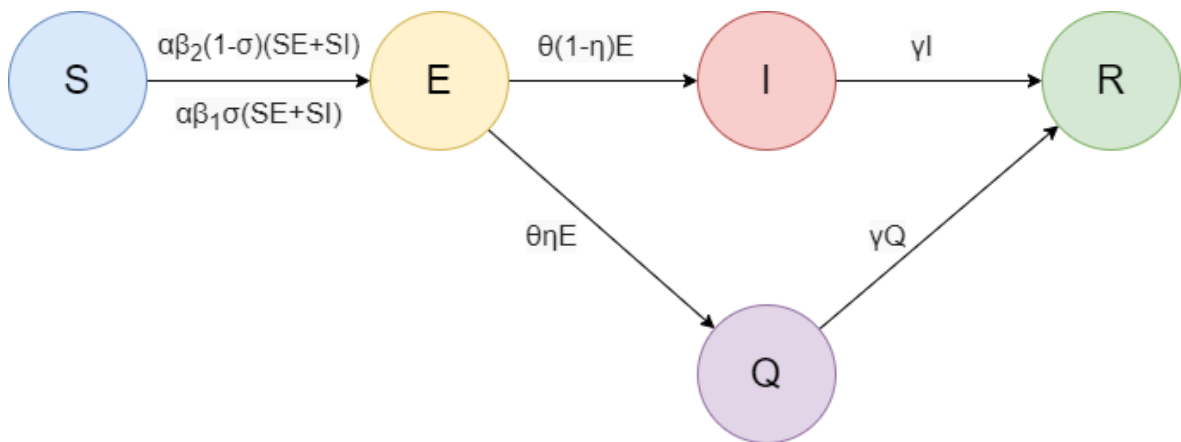


Figure 1. Compartmental diagram for the transition between model states

Once a susceptible individual becomes exposed to the infection by an exposed or a symptomatic infected individual, they are immediately infectious. The exposed and infectious individuals can be divided into two groups: those wearing a face mask and those not wearing one. Because the mask usage effects the probability of spreading the infection, the transition rate from the compartment S to E needs to be formed as a sum. The transition rate is always negative, as the number of susceptible individuals only decreases in the simulation, as defined in Equation (1).

$$\frac{dS}{dt} = -\alpha(\beta_1\sigma(SE + SI) + \beta_2(1 - \sigma)(SE + SI)) \quad (1)$$

In the formula, α is a multiplier representing the restrictive measures, β_1 and β_2 are the average transmission rates by infected individuals wearing and not wearing a mask, respectively, and σ is the proportion of individuals wearing a mask.

The number of exposed individuals increases by each susceptible individual contacting an exposed or infected individual and decreases by each individual becoming symptomatic. A proportion of the individuals becoming symptomatic enters the quarantine, which is taken into account in the transition rate from E to I and E to Q . The transition rate is as follows:

$$\frac{dE}{dt} = \alpha(\beta_1\sigma(SE + SI) + \beta_2(1 - \sigma)(SE + SI)) - \theta\eta E - \theta(1 - \eta)E, \quad (2)$$

where θ is the average rate of exposed individuals becoming symptomatic and η is the per-capita quarantine rate of infected individuals.

The symptomatic and infectious individuals spreading the COVID-19 infection in the population decrease as the individuals recover and move to the compartment of recovered individuals. The recovery dynamics are equal regardless of the individual being quarantined or not. This can be presented as follows:

$$\begin{aligned} \frac{dI}{dt} &= \theta(1 - \eta)E - \gamma I \\ \frac{dQ}{dt} &= \theta\eta E - \gamma Q \end{aligned} \quad (3)$$

In the transition rates, γ is the per-capita recovery rate of infected individuals.

Both infectious and quarantined individuals enter the compartment of recovered with a certain recovery rate, and as the natural, protective immunity is assumed to be permanent, the transition rate of the recovered is as follows:

$$\frac{dR}{dt} = \gamma I + \gamma Q \quad (4)$$

Therefore, the SEIQR system can be expressed by the following set of ordinary differential equations:

$$\begin{aligned} \frac{dS}{dt} &= -\alpha(\beta_1\sigma(SE + SI) + \beta_2(1 - \sigma)(SE + SI)) \\ \frac{dE}{dt} &= \alpha(\beta_1\sigma(SE + SI) + \beta_2(1 - \sigma)(SE + SI)) - \theta\eta E - \theta(1 - \eta)E \\ \frac{dI}{dt} &= \theta(1 - \eta)E - \gamma I \\ \frac{dQ}{dt} &= \theta\eta E - \gamma Q \\ \frac{dR}{dt} &= \gamma I + \gamma Q \end{aligned} \quad (5)$$

The parameters in the system of equations in (5) are described as follows:

- α : A multiplier of restrictive measures based on the GSI
- β_1 : Average rate of transmission by infected individuals wearing a mask
- β_2 : Average rate of transmission by infected individuals not wearing a mask
- γ : Per-capita recovery rate of infected individuals
- η : Per-capita quarantine rate of infected individuals
- θ : Average rate of exposed individuals becoming infectious
- σ : Proportion of individuals wearing a mask

The values of the parameters used in the simulation are listed in the Table 1.

Parameter	Value	Source
α	$\ln(GSI) + 5.6$	estimate
β_1	$\frac{3}{10} \cdot \frac{1}{4}$	estimate
β_2	$\frac{9}{10} \cdot \frac{1}{4}$	estimate
γ	$\frac{1}{8}$	Kampen et al. (2021)
η	0-100 %	user's choice
θ	$\frac{1}{5.2}$	Li et al. (2020)
σ	0-100 %	user's choice

Table 1. The values of the parameters in the simulation

4 SOFTWARE AND APPLICATION

The simulation has been programmed exclusively with Python. In the simulation, the population of N individuals is divided into five compartments, and the transitions between those depends on the user-selected parameters and the COVID-19 characteristics. The transitions in the simulation are based on ordinary differential equations represented in Equation (5). The user gets to test and compare two simulation scenarios per run to visualize how different restrictive measures effect the epidemic spread within the selected time span.

4.1 Programming environment

Python is an open-source, interpreted programming language published in 1990. It supports procedural, functional and object-oriented programming. Its various libraries offer a variety of tools for mathematical calculations and advanced data visualization. (Netguru, 2021) As it is possible to complement several open-source libraries to Python, it can be used in versatile computational tasks which require rapid data processing and analysis.

One goal of the thesis is to produce an application which is simple to understand and to use for anyone not experienced with epidemiology. In this project, `Dear PyGui` library is used for building the graphical user interface. The library offers user-friendly themes, different graphical widgets and adaptable tools for plotting graphs.

`numpy` is a module widely used for mathematical and numerical functionalities. It complements Python with more efficient data structures, arrays and matrices. In this project, `numpy` is used majorly for its array functionalities and mathematical functions.

4.2 Graphical user interface

The priorities in building the graphical user interface of this application are usability, straightforwardness and optimized performance. `Dear PyGui` interface automatically allows all of the windows to be resized and closed as needed, which improves the usability of the application. By keeping the text content of the windows at the minimum, the straightforwardness and clarity is improved. The simulation runs without any noticeable delay as a result of the usage of an efficient programming language and its libraries.

As it can be seen in Figure 2, the user experience begins with a window that requests the user to enter the key information of the simulation by dragging the sliders. The user can modify these slider values freely until they press the "Enter" button.

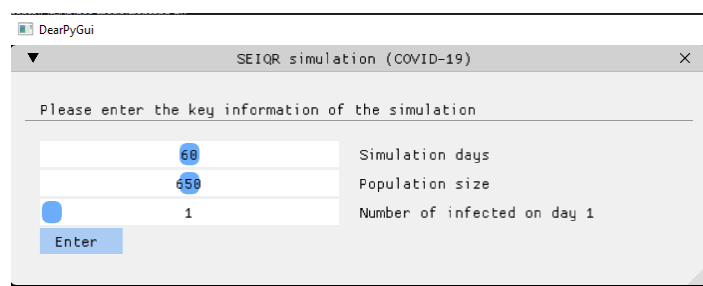


Figure 2. Window for entering the key information of the simulation

Once the "Enter" button has been pressed, the program renders two more windows for the anticipated simulation plots 1 and 2, as seen in Figure 3. The user is requested to enter the parameters regarding the restrictive measures in the simulated population before running the simulation. The simulations in those windows can be started sequentially by pressing the respective "Enter" button.

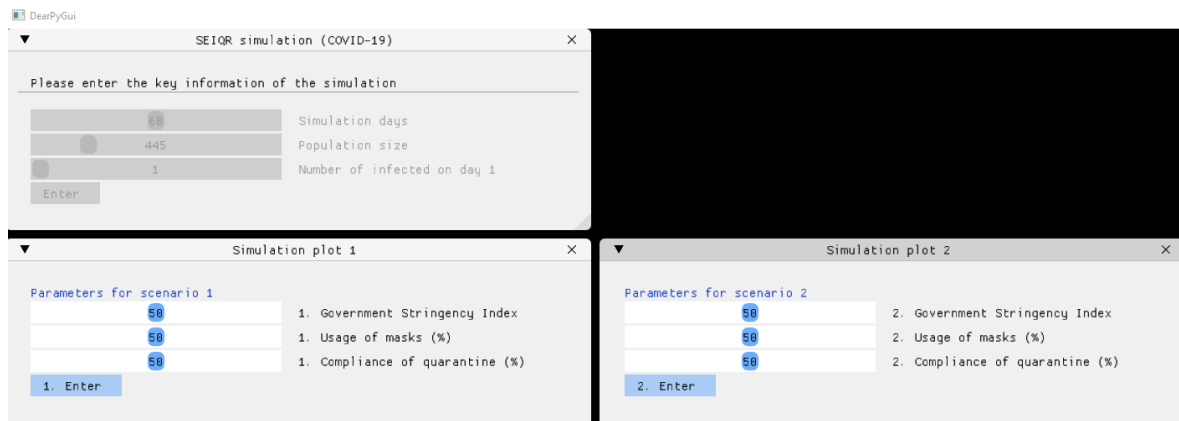


Figure 3. Windows for entering the parameters for the two scenarios

The application incorporates so-called tip windows when hovering the pointer on certain texts. In the Figure 4, the application gives an explanation of "Government Stringency Index" score for making the application more smooth to use.

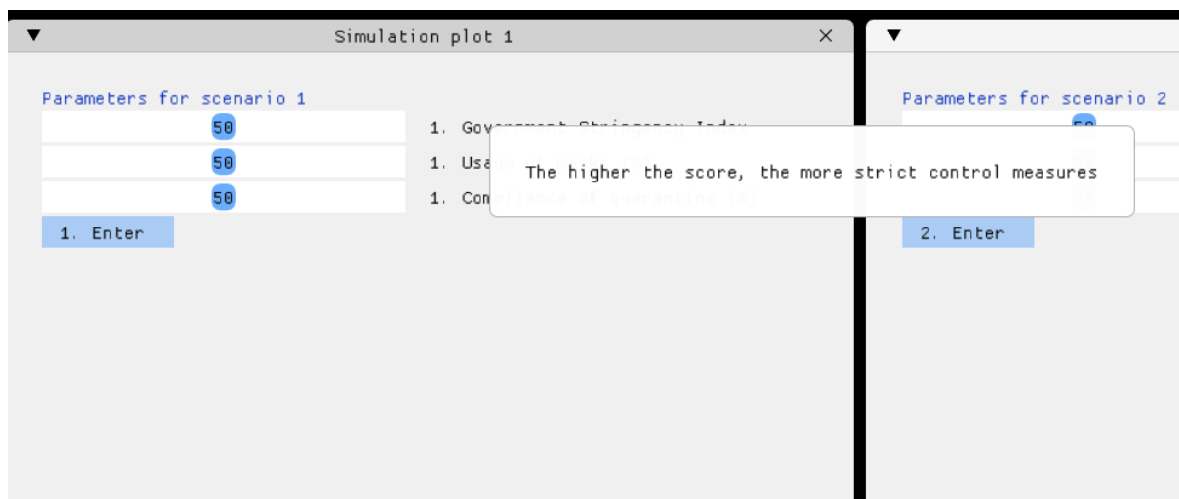


Figure 4. Tip window on "Government Stringency Index"

Once the Enter button of the simulation plot window has been pressed, the program runs the simulation with the user-selected parameters utilizing the extended SEIQR model introduced in this paper. The example views of the plotted graphs can be seen in Figure 5. The colors of the graph lines correspond to the design of the compartmental model.

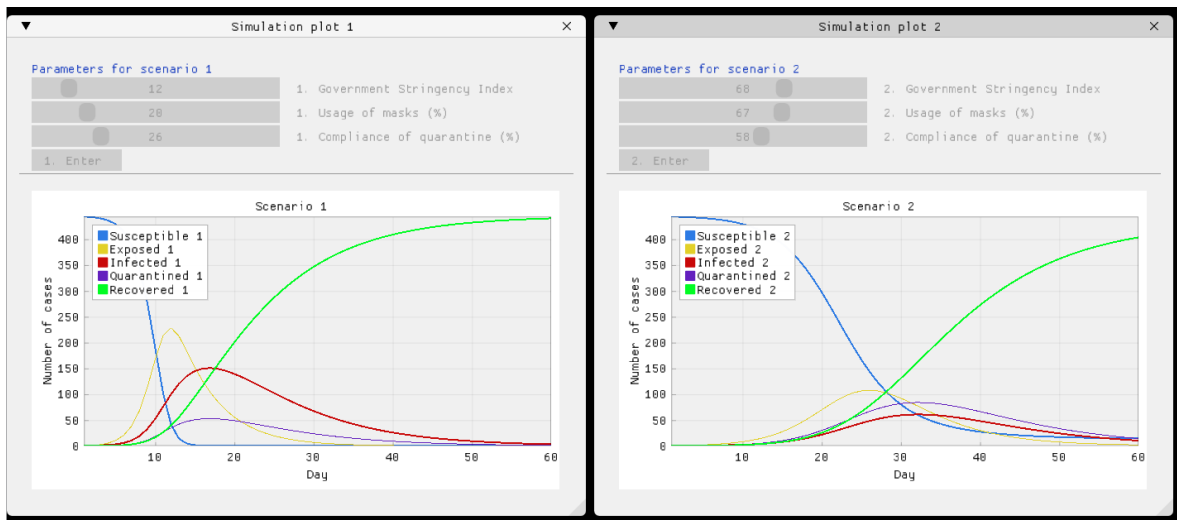


Figure 5. Result view. Plotted graphs.

It is visualized in Figure 6 how the plots can be rescaled effortlessly by scrolling or clicking. In this case, the graph of Infected has also been emphasized by the user hovering their pointer on the "Infected 1" text. The scalability makes comparing the results between the two scenarios uncomplicated.

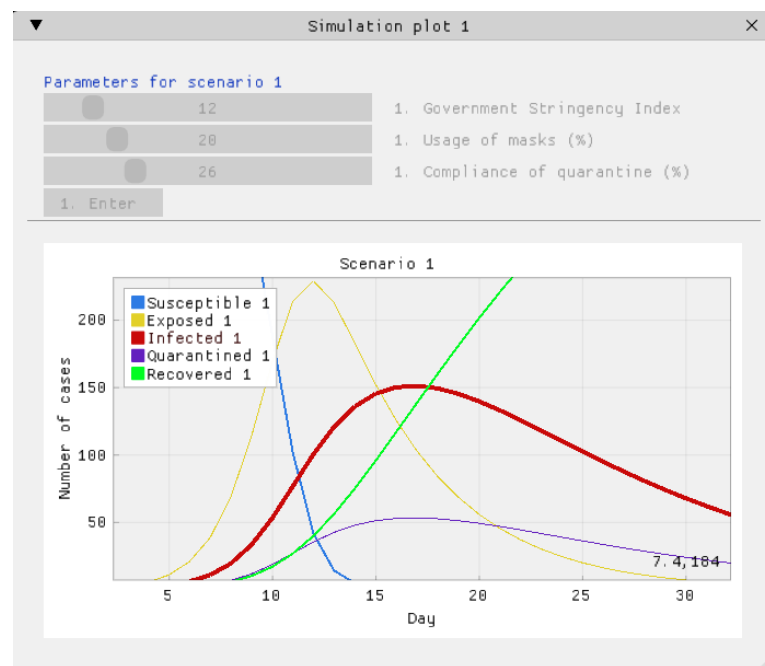


Figure 6. Scalability of the line plots. Infected graph emphasized.

5 RESULTS

In each of the simulations demonstrated in this paper, there is one infected individual in a population of 650 individuals on day 1. The length of each simulation is 60 days. The resulting graphs are visualizing the impact of different restrictive measures on COVID-19 epidemic.

The scenarios that were selected to be analyzed are the impacts of

1. unconstrained spread of the epidemic
2. government stringency
3. face mask usage alone
4. compliance of quarantine alone
5. restrictive measures combined

5.1 Unconstrained spread of the epidemic

When allowed to spread freely without any restrictive measures, the epidemic covers the whole population rapidly, as it can be seen in the graphs in Figure 7. During the first five days of the simulation there is no apparent growth in the number of infected, as the median incubation period of the disease is 5.2 days. The exposed individuals are spreading the virus, however, and it can also be noticed in the extreme peak in the number of exposed individuals on day 10 of the simulation. On that day there are 460 exposed individuals in a 650 individual population.

The peak in the graph of infected individuals covers days from 13 to 16. At its highest, there are 310 infected, symptomatic individuals on day 15. After this peak the transmission of the infection starts slowing down and the majority of the population is recovered by day 20. In this simulation all of the individuals in the population got infected and recovered by day 57.

5.2 Government stringency

To compare the impact of the Government Stringency Index score on the spread of the epidemic, there are two simulation scenarios: one with the GSI of 13 and one of 79.

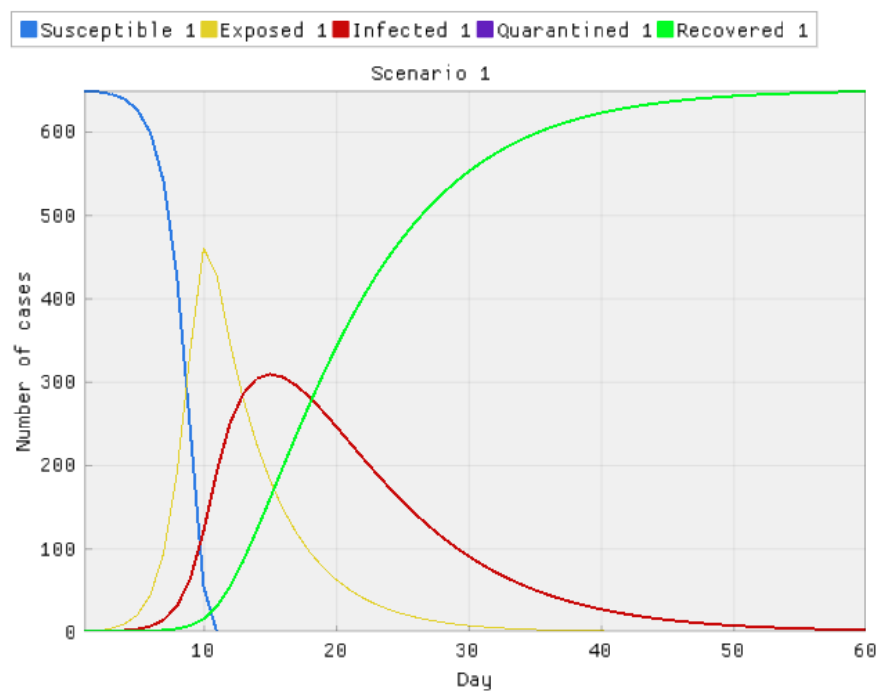


Figure 7. Simulation 1. Unconstrained spread of the epidemic.

A GSI of 13 indicates little restrictive measures in the population, which can be indicated from the plot in Figure 8. The number of exposed individuals climbs to 100 in 11 days after the beginning of the simulation, after which the spread of the SARS-CoV2 is exponential in the simulated population. The number of active carriers of the disease is at its highest on day 18, as the exposed and infected individuals together count down to 524 individuals. Soon after this point, the number of recovered individuals exceeds the number of exposed and symptomatic individuals. There are no susceptible individuals left in the population starting from day 22.

As it can be interpreted from Figure 9, a GSI of 79 suggests extensive restrictive measures. The peak in the number of symptomatic, infectious individuals lasts for 11 days, and its highest point appears on day 41. In the simulation with a GSI of 79 there are still 24 susceptible individuals left on the last day of the simulation. As the number of exposed and symptomatic individuals together is 66 on that day, it can be conjectured that the epidemic would cover the whole population soon in a simulation of slightly more extended time span.

5.3 Face mask usage

To compare the efficiency of mask usage in slowing down the epidemic spread, two scenarios were performed in this simulation: one with face mask usage of 15 % and one of 90 %. The

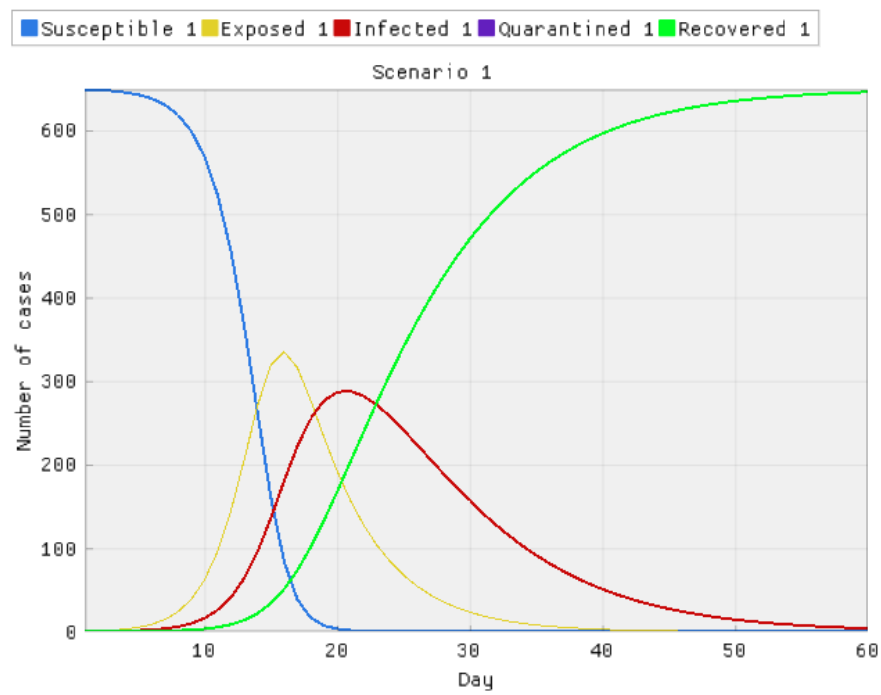


Figure 8. Simulation 2. Governmental Stringency Index = 13.

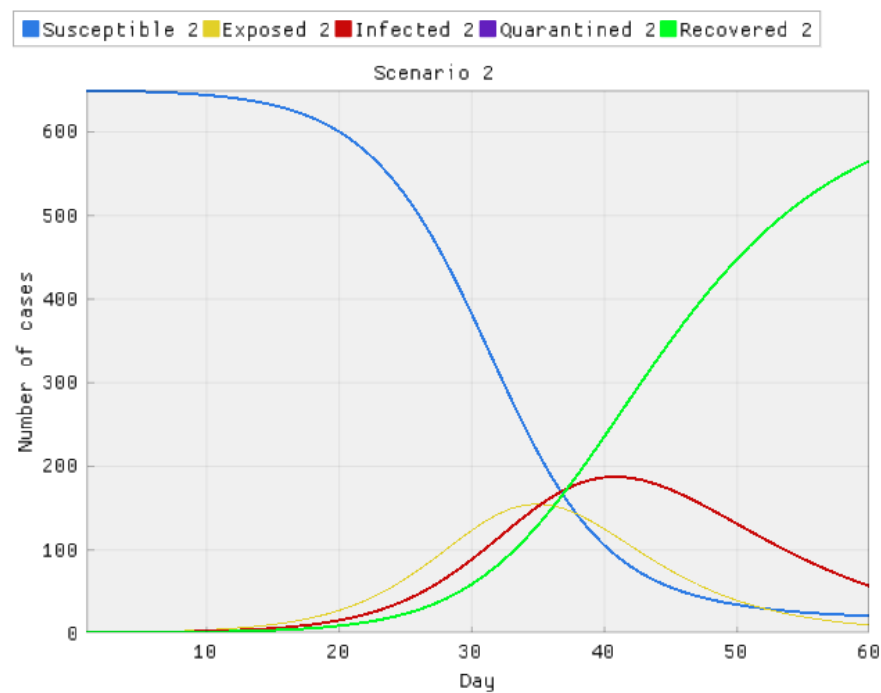


Figure 9. Simulation 2. Governmental Stringency Index = 79.

latter scenario mimics an obligation to wear a face mask in public.

As shown in Figure 10, the number of exposed individuals is already at 445 individuals on day 11 as the number of susceptible is at 3 individuals. Due to the fast spread of the epidemic,

the number of recovered individual reaches 646 individuals in the population of 650 on day 55.

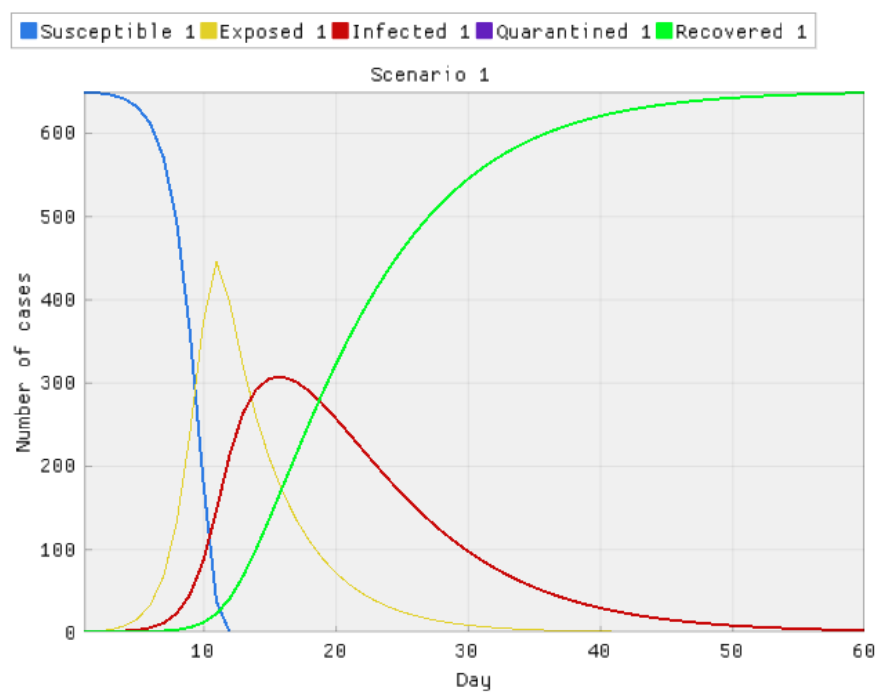


Figure 10. Simulation 3. Usage of masks = 15 %.

Based on the graphs of the second scenario (Figure 11), it can be stated that the number of infections increases slowly between days 0 and 12. After that day, the epidemic spread is rapid, and 644 individuals have recovered from the disease by day 60. The maximum in the number of exposed appears on day 18 with 293 individuals. On the same day, there are still 110 susceptible individuals left in the population. At most, there are 275 symptomatic, infected individuals in the population on day 23 of the simulation. The downward trend in the infected is more steady than the steep rise in the beginning of the simulation. By the end of the simulation, there are still 6 symptomatic individuals left.

5.4 Compliance of quarantine

Two scenarios of different compliance rates of quarantine were executed to visualize the impact of obeying quarantine once infected and symptomatic. The first scenario was based on 38 % of the population practicing quarantine, while in the second one even 65 % did so.

It can be seen in Figure 12, that within the first 5 days of the simulation there are no quarantined individuals. This is because a certain proportion of the individuals only enter the

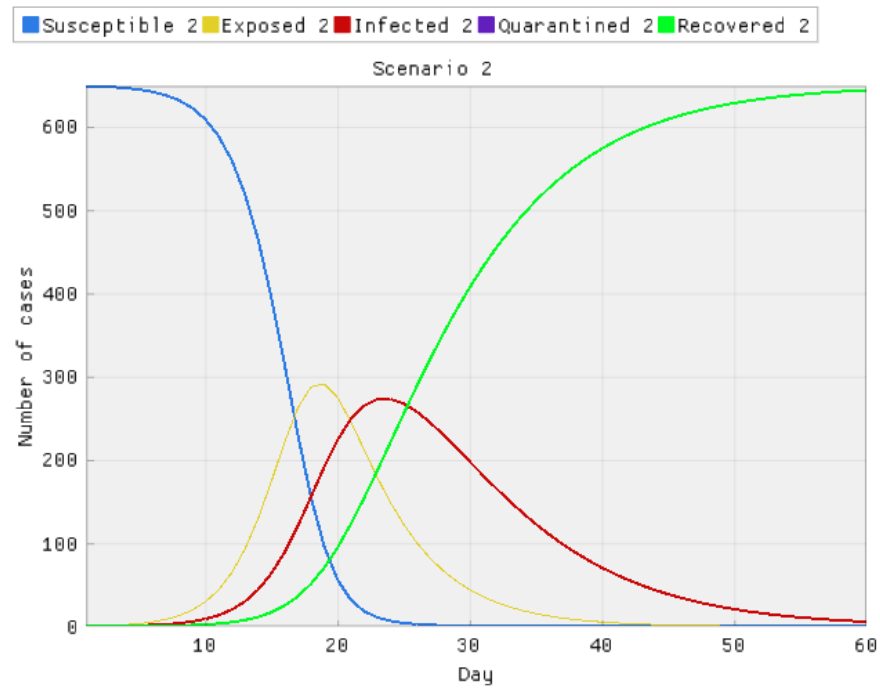


Figure 11. Simulation 3. Usage of masks = 90 %.

quarantine after the symptom onset. At its highest, the number of quarantined individuals is around 118 on day 15. In the scenario of compliance of quarantine being as low as 38 %, there are no susceptible individuals left in the simulated population from day 12.

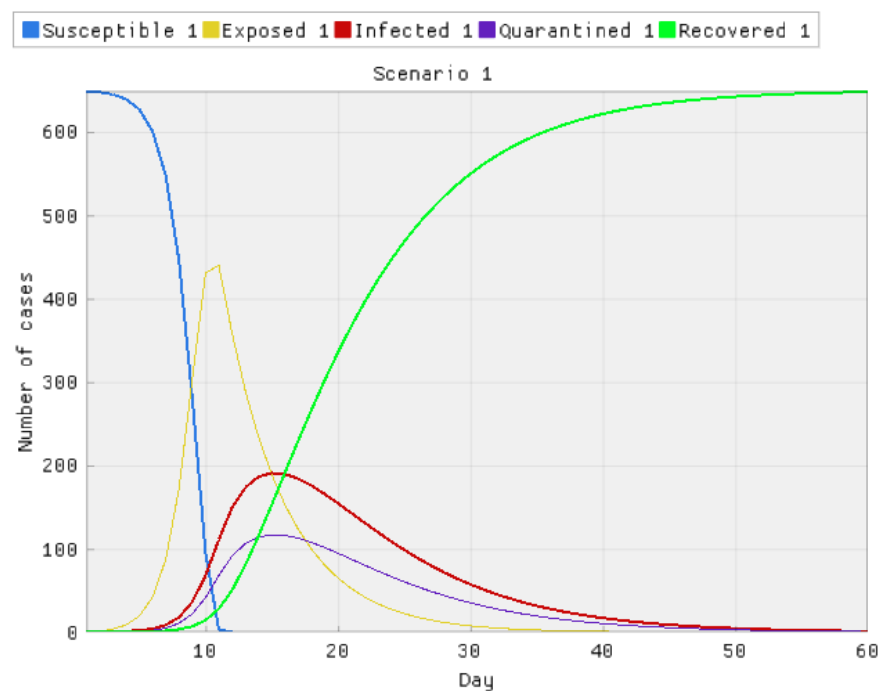


Figure 12. Simulation 4. Compliance of quarantine = 38 %.

As visualized in Figure 13, in the case of the compliance of quarantine being 65 %, there are not any susceptible individuals left starting from day 12 either. Because the quarantine measure only takes place after the 5.2 day incubation period, the infection rates are high already in the beginning of the simulation (from 8 to 16 days). The graph representing the

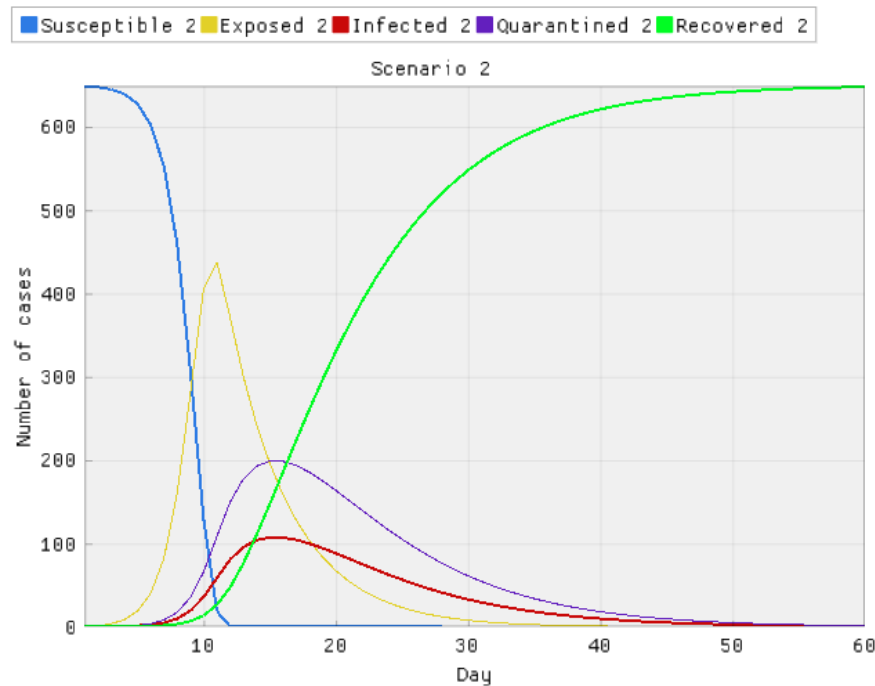


Figure 13. Simulation 4. Compliance of quarantine = 65 %.

number of quarantined peaks on day 15, as 200 individuals are quarantined in the simulation.

5.5 Restrictive measures combined

In order to observe the significance of several non-pharmaceutical interventions in containing the spread of COVID-19, two scenarios with highly different combinations of social constraints were simulated. The first scenario simulated a population in which the Governmental Stringency Index lies at 20, the usage of masks is 27 % and the compliance of quarantine is 38 %. The second scenario concerns a society in which the GSI is 61, mask usage is 61 % and the compliance of quarantine is 65 %.

The first scenario mimics a society with moderate restrictive measures. As Figure 14 shows, the spread of the epidemic is slow within the first 15 days of the simulation. The peak of symptomatic, infectious individuals lasts for about 11 days, and the maximum number of symptomatic individuals at once is about 155.

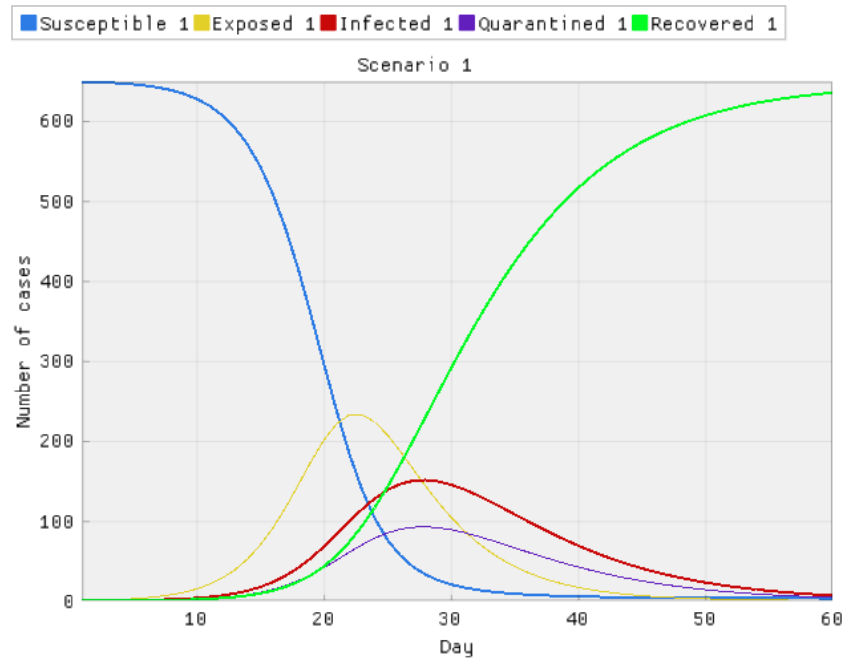


Figure 14. Simulation 5. GSI = 20, usage of masks = 27 %, compliance of quarantine = 38 %.

The second scenario simulates a population with strict social constraints and high compliance of quarantine. The effect of these measures is significant, as it can be seen in Figure 15: the number of the susceptible has decreased by only 120 individuals by the end of the simulation. The increase in the numbers of exposed and infected are steady and mild.

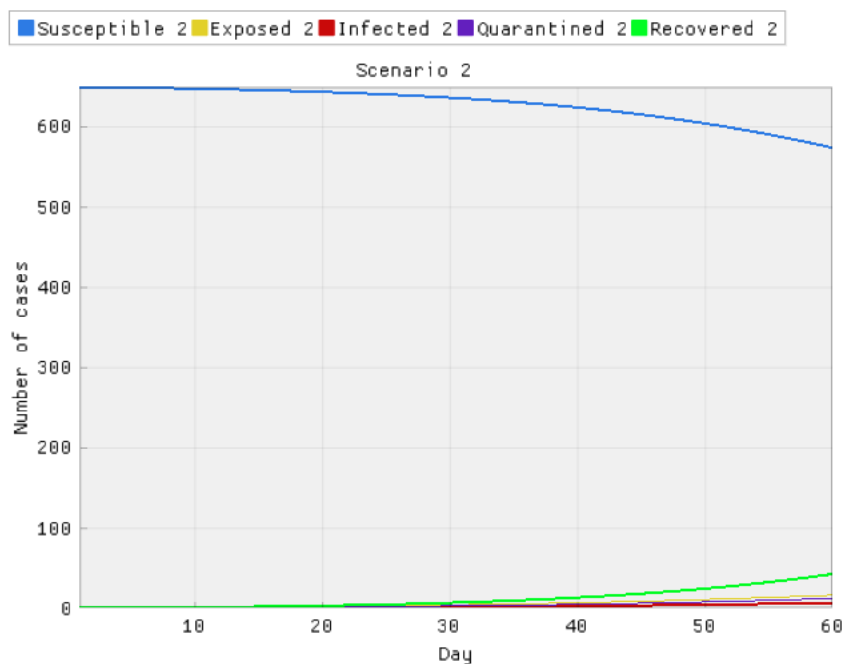


Figure 15. Simulation 5. GSI = 61, usage of masks = 61 %, compliance of quarantine = 65 %.

6 CONCLUSIONS

Based on the results of the assessed scenarios, it can be derived that restrictive measures decrease the spread of COVID-19 epidemic. The strongest impact can be noticed in the case of several measures being in effect at once.

The scenario of unconstrained spread of the epidemic is used for comparing the effects of non-pharmaceutical constraints. It can be reasoned that in this scenario, the spread of the simulated epidemic is fast. The peak reaches almost half of the population already on day 10, which would mean highly strained society due to the burden of healthcare and difficulties of individuals attending to work-life.

This result seems unrealistic, as the spread of the COVID-19 without constraints has not been as fast in reality. This can be concluded from the COVID-19 data from March 2020 by THL (2020). The reason behind the improbable results could lie in the guessed value of transmission rates β_1 and β_2 : they are not proportional to the size of the population, and they are not based on scientific research of COVID-19 transmission probabilities or human-to-human contact rates.

High governmental stringency was noticed to have a strong impact on the spread of the epidemic: as the GSI value covers 9 metrics of political restriction measures, it is the most substantial restrictive measure of the ones compared in this thesis. It was noticed, that through governmental measures the infections spread slower and the final number of infected in the population is moderate. In practice, this would denote less burden on the healthcare system.

The impact of Government Stringency Index seems logical. A GSI of some level should always be included in the model, as there are not any societies without governmentally set guidelines in reality. The mathematical model that derives α is estimated based on guessing and comparing the results to real-world data of COVID-19 spread. For more truthful results, the α could be reassessed through fitting it to data.

The usage of face masks seemed to be advantageous only in the case of 90 % of the infectious individuals wearing them. In that case, the peak in the number of infected was significantly postponed from the spread without constraints and also from the spread in the case of only 15 % wearing the face masks. The graphs of exposed and infected were slightly less steep than in the two compared scenarios.

The impact of the usage of face masks in the model depends solely on the transmission rate β_1 , which could be improved by assessing literature on the change in COVID-19 transmis-

sion rate once the infectious individual is wearing a mask. Because of little literature being yet available, the value is based on a guess, and the present results of face mask usage might be misleading.

The compliance of quarantine did cause a slightly less sharp peak in the number of exposed compared to the unconstrained spread of the epidemic, but the impact of quarantine did not seem to reduce the numbers of infections overall in both of the researched scenarios. The numbers of quarantined and infected individuals in these scenarios summed up to the case of no restrictive measures. Because the exposed individuals are exactly as infectious as symptomatic individuals during the incubation time of 5.2 days, the spread of the disease is intense in the first days of simulation. In a longer time span simulation with a larger population, a decreasing effect of quarantine could be expected. Otherwise simulating the spread of the quarantine seems realistic enough, as the isolated individuals are fully separated from the rest of the compartments.

In the scenarios of restrictive measures being combined, the decreasing impact on the spread of COVID-19 was apparent. Even in the case with relatively low GSI (20), usage of masks (27 %) and compliance of quarantine (38 %), the spread of the epidemic was notably more under control. In the case of more strict GSI (61), wider usage of masks (61 %) and higher compliance of quarantine (65 %), the spread of the epidemic was very well contained. The numbers of exposed and infected were minimal still in the end of the simulation.

Based on these scenarios, quarantine and mask usage alone provide little help in containing the spread of COVID-19. When the restrictions are combined with other measures, the impact is remarkable.

The truthfulness of the results given by the extended SEIQR model can also be less realistic due to the many COVID-19 mutations. The values included in the model are not based on a specific mutation, and it might be possible that different mutations in different societies would produce very different results from the simulation.

The model could be improved by refining the variables by using the available data of confirmed COVID-19 cases. The variables which especially may benefit from more realistic basis would be α , β_1 and β_2 . Also, if the ordinary differential equations were complemented with noise, the results might become more realistic: at the moment the spread of the COVID-19 is pictured as very straight-forward.

The user interface of the simulation is adaptable for educational and recreational use. The application provides the user with a chance to visualize how different measures could effect the spread of COVID-19 epidemic. Based on testing different scenarios and combinations, it

is possible to make conclusions of the epidemic dynamics and to evaluate the use of different restrictive measures.

7 SUMMARY

The aim of the thesis was to introduce a new epidemic model which simulates the spread of COVID-19 epidemic specifically and also emulates the impact of different, non-pharmaceutical restrictions on the spread. A graphical user interface with clear visualization of the results and possibility of comparing different scenarios was intended to support the simulation to become a convenient tool for easier understanding of epidemiology.

The research was started by analyzing the classical SIR model which assumes that any population can be divided into three compartments: susceptible, infected and recovered. The system introduced in the paper is an extended SEIQR model, which expands the SIR model by adding two more compartments for the exposed and quarantined individuals. The extended SEIQR model also involves dynamics of mask usage and governmental stringency to demonstrate the effect of different restrictive measures in the spread of COVID-19.

The extended SEIQR model incorporates constant variables for the dynamics of the infection and the spread of the epidemic. The dynamics of infection include the incubation time and the recovery period, which have been based on scientific literature on COVID-19. The functions behind the average rates of transmission and the restrictive measures have been guessed and refined in several test iterations of the model.

The simulation application was programmed on Python and its open-source libraries. The programming language fit the project well, as the graphical user interface is easily operated and the simulation runs smoothly.

Based on the results of the simulation, it can be concluded that the decrease in the spread of the epidemic is significant when several restrictive measures are included concurrently. The impact of usage of masks or compliance of quarantine alone did not seem effective enough, although the results might be misleading because of the space of improvement in the epidemic model.

The model could be improved by refining the variables by using the available data of confirmed COVID-19 cases. Additionally, if the ordinary differential equations were complemented with noise, the resulting graphs could become more realistic. The user interface of the simulation is adaptable for educational and recreational use, and the simulation enables

the user to visualize how different measures could effect the spread of COVID-19 epidemic.

References

- Bo, Yacong et al. (2021). “Effectiveness of non-pharmaceutical interventions on COVID-19 transmission in 190 countries from 23 January to 13 April 2020”. In: *International Journal of Infectious Diseases* 102, pp. 247–253. ISSN: 1201-9712. DOI: <https://doi.org/10.1016/j.ijid.2020.10.066>.
- Chladná, Zuzana, Kopfová, Jana, Rachinskii, Dmitrii, and Rouf, Samiha C. (2020). “Global dynamics of SIR model with switched transmission rate”. In: *J Math Biol* 80(4), pp. 1209–1233. DOI: [10.1007/s00285-019-01460-2](https://doi.org/10.1007/s00285-019-01460-2).
- Data, Our World in (2021). *COVID-19: Stringency Index*. URL: <https://ourworldindata.org/covid-government-stringency-index>. Referenced 10.4.2021.
- Erdem, Mustafa, Safan, Muntaser, and Castillo-Chavez, Carlos (2017). “Mathematical Analysis of an SIQR Influenza Model with Imperfect Quarantine”. In: *Bull Math Biol* 79(7), pp. 1612–1636. DOI: [10.1007/s11538-017-0301-6](https://doi.org/10.1007/s11538-017-0301-6).
- He, Xi et al. (2020). “Temporal dynamics in viral shedding and transmissibility of COVID-19”. In: *Nature medicine* 26(5), pp. 672–675. DOI: [10.1038/s41591-020-0869-5](https://doi.org/10.1038/s41591-020-0869-5).
- Kampen, Jeroen et al. (2021). “Duration and key determinants of infectious virus shedding in hospitalized patients with coronavirus disease-2019 (COVID-19)”. In: *Nature communications; Nat Commun* 12(1), p. 267. DOI: [10.1038/s41467-020-20568-4](https://doi.org/10.1038/s41467-020-20568-4).
- Kucharski, Adam J. et al. (2020). “Early dynamics of transmission and control of COVID-19: a mathematical modelling study”. In: *Lancet Infect Dis* 20(5), pp. 553–558. DOI: [10.1016/S1473-3099\(20\)30144-4](https://doi.org/10.1016/S1473-3099(20)30144-4).
- Li, Qun et al. (2020). “Early Transmission Dynamics in Wuhan, China, of Novel Coronavirus-Infected Pneumonia”. In: *New England Journal of Medicine* 382(13), pp. 1199–1207. DOI: [10.1056/NEJMoa2001316](https://doi.org/10.1056/NEJMoa2001316).
- Netguru (2021). *What Is Python? A Comprehensive Guide*. URL: <https://www.netguru.com/what-is-python>. Referenced 11.4.2021.
- Roy, Sayak (2020). “COVID-19 Reinfection: Myth or Truth?” In: *SN comprehensive clinical medicine* 2(6), pp. 710–713. DOI: [10.1007/s42399-020-00335-8](https://doi.org/10.1007/s42399-020-00335-8).

THL (2020). *COVID-19 cases in the infectious diseases registry*. URL: https://sampo.thl.fi/pivot/prod/en/epirapo/covid19case/fact_epirapo_covid19case. Referenced 11.4.2021.

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Attachments

Attachment 1: <https://github.com/anettemarjaana/bsc-thesis.git>