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Preface

This volume contains the papers presented at the 18th International Conference for Informatics and Information Technology (CIIT 2021), which was held as an online conference on May 6-7, 2021. The conference was organized by the Faculty of Computer Science and Engineering, Ss. Cyril and Methodius University in Skopje, Republic of North Macedonia. As the COVID-19 pandemic entered 2021, the same restrictions, more or less, were still in effect, unfortunately. It was the reason that the conference was held online for the second year in a row. However, this was also an opportunity for the conference to have increased attendance and for the authors to be able to present their work to a broader audience. The conference was publicly available to everyone interested. Likewise, we have other students and staff of the Faculty of Computer Science and Engineering, as well as attendees from other companies and institutions. Additionally, we had participants at the conference from neighboring countries. In general, we had a lot of excellent submissions from the country and the region. The aim of the 18th edition of the CIIT conference, as in previous editions, was to provide an opportunity for young researchers from the country and abroad to present their work to a broader research community and get valuable feedback on their work. For the 18th edition of the conference, we had 49 paper submissions, of which 22 were accepted as full papers, 5 short papers, and 12 student papers. During the conference, we had 37 presentations organized in 5 paper sessions and 2 student sessions. Additionally, we had three keynote lectures and three workshops as part of the conference.

This year we continued the tradition of this conference and awarded our hard-working students. However, the grading considered several aspects of each paper: technical quality, scientific contribution, and oral presentation. The session chairs and conference chairs graded each paper regarding those qualities, and we also considered the reviewer grades and comments. In the end, we had a difficult job, but we finally reached a consensus and decided to award instead of one, two students, one for the best paper and one for the best presentation.

The online format of the conference allowed the participants to attend all the talks covering a diverse range of topics. We are proud to have participants from almost all academic institutions in Macedonia and several from the state public institutions and business sector as well as neighboring countries. We had the pleasure of hosting three invited speakers. Our first keynote speaker was Jasmina Bogojeska, PhD, a research staff member in the AI Automation group in the Cognitive Computing and Industry Solutions Department at IBM Research – Zurich working in the area of machine learning, deep learning, and natural language processing (NLP). The main focus of her work is application-inspired machine learning, where she is developing and applying machine learning solutions to various challenging real-world problems from the areas of services research and health informatics.

Our second keynote speaker was Milivoj Simeonovski, PhD. Milivoj currently holds the position of the CPO (Chief Product Officer) at AIS Advanced IT-Security Solutions, a company where he is also a founding member. The company was founded as a spin-off of CISPA (Center for Information Security, a German national Big Science Institution within the Helmholtz Association). It touches on different aspects of the security research conducted by Milivoj while working on his PhD.

The third keynote speaker was Gjorgji Strezoski. He started his PhD at the University of Amsterdam as a researcher in the VISTORY project, where he is exploring the multi-task multi-modal nature of artistic data with deep learning methods. As a part of his PhD work he was also a research scientist in the ViSenze computer vision research team in Singapore. His research interests include Computer Vision, Active Learning, and Information Visualization.

Part of the conference success is owed to the support received from our partners and sponsors: Ss. Cyril and Methodius University in Skopje and ICT-ACT Association in Skopje.

September, 2021
Skopje

Hristina Mihajloska Trpcheska
Ivan Kitanovski

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Mathematical modeling of COVID-19 virus

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***Abstract*—The mathematical modelling in epidemiology has high importance. All the infectious diseases can be modeled and represented with mathematical models in order to predict their behavior. In this paper we use the SEIRS-D model for describing the situation with COVID-19 virus. Also, we apply this SEIRS-D model in AnyLogic Simulation Modeling Software. The COVID-19 virus is described depending on various factors as: time for recovery, reproduction number, time for incubation.**

Keywords—SEIRS-D model, COVID-19 virus, AnyLogic, math modeling, simulation.

I. INTRODUCTION

During the human history there were many pandemics and epidemics caused by different viruses and all of them had high influence on the people lives. In the new modern world in 21st century the virus which was named Covid 19 caused pandemic in whole world. The global pandemic, popularly called the coronavirus pandemic (Covid 19) has leave a lasting mark on people's life. It is the biggest global crisis in the world in the last tens of years. The number of infected is growing daily, to date there are about 111 million infected since the beginning of the pandemic in February 2020. This pandemic poses a serious threat to the development of the economy, the further life of people and the survival of institutions, [1].

SARS, EBOLA, MERS and avian influenza, these diseases are responsible for the cause of many deaths in many countries worldwide therefore we can see the strength and power of the word epidemic. The latest pandemic to hit the world, the latest virus that unfortunately humanity has ever heard of, appeared in December 2019 in Wuhan, Hubei Province of China, there are a lot of victims who did not have the strength to fight against it. As a result of the tragic death cases that occurred because of the COVID-19 virus, The World Health Organization (WHO) announced COVID-19 pandemic on 12 March 2020, when 125.600 confirmed cases were reported from 118 countries and regions from all over the world, [2].

Due to the rapid progression of COVID-19, the World Health Organization has decided to recommend to governments around the world to take strict restrictive, drastic measures to slow the spread of this disease known as COVID-19 and flattering the epidemiology curve down to the lowest treatment capacity of the health system in each country. On the other hand, must keep in mind that the health system is only one part of the larger systems in each country and therefore affects the functioning of all other systems.

Sadly, because of the pandemic the economy system is dealing with a lot of consequences, the governments hand no choice but declaring an emergency state "and had issued regulation with drastic measures for education, business, sports, culture and people. As an example, many countries, hotels, restaurants, hypermarkets, schools, universities, theatres, churches, and stadiums were closed. There were created new and special rules such as social distancing for communities and people, avoiding meetings in groups, wearing masks and gloves in public places, and isolation at home Lockdowns and online working from home became almost normal, [3].

The coronavirus was first discovered in the 1930s, when domesticated chickens were infected with an infectious bronchitis virus that caused an acute respiratory infection (IBV). The infection was marked by listlessness and gasping, and the mortality rate ranged from 40 to 90%. Furthermore, the contagious virus that caused the outbreak was cultivated and isolated. During the 1940s, two new animal coronaviruses, the mouse hepatitis virus (MHV) and the transmissible gastroenteritis virus (TGEV), were discovered; however, the relationship between the three fascinating viruses remained unknown.

In 1965, the first human coronavirus was discovered, with the key symptom being a common cold. The connection between human and animal viruses was investigated, and the viruses were given names. Several types of coronaviruses can infect humans. This virus that causes SARS first appeared in China in 2002, and then rapidly spread to 28 other countries, affecting thousands of people until 2003. SARS symptoms ranged from mild to extreme, including headaches, fever, and even respiratory issues such as coughing or shortness of breath. The other virus that emerged was MERS, which first appeared in Saudi Arabia in 2012, with those who live in or have visited the Middle East being the most affected. While the MERS virus has been shown to be less infectious than its ancestor, it has also shown an additional symptom in the enclosed patients: kidney failure. HCoV, NL 63, and other coronaviruses are examples of coronaviruses. [4]

Since 2019, a tissue or blood sample may be used to diagnose the coronavirus. A lab technician performs the test, which entails taking a sample from the nose or throat. The virus can be detected in the blood, or by a PCR test, and the infection is most detectable between the fourth and eighth days of infection. This method can also be used to identify other earlier forms of the coronavirus, such as MERS-CoV and the SARS virus, because the virus can be detected by a PCR test. Isolation of human coronaviruses is another problem that has proved to be difficult, [5].

II. SEIRS-D MODEL

Mathematical and statistical modeling tools are very important for providing epidemiological parameters of infectious diseases such as infection or transmission rate, recovery rate, incubation period, isolation rate, quarantine rate, disease-induced death rate. [6].

Models use mathematical equations to estimate how many cases of a disease may occur in the coming weeks or months. They help researchers simulate real-world possibilities in a virtual environment. Mathematical models of infectious diseases are a helpful tool for analysis of the diseases' spread, for future forecasting of the diseases' course and as a guide of the governments for planning and organizing the health system for infectious disease control.

Stochastic epidemic models are models designed to help us understand the dynamic of infectious diseases. The criticality of a stochastic epidemic model is a threshold in transmission rate such that a subcritical epidemic mostly tends to die out quickly and a supercritical epidemic tends to prevail in the population. Over the past few years as we can see, the behaviors of near-critical epidemics have drawn a lot of attention. [9]

In epidemiology there are many mathematical models which are used for infectious diseases analysis, [10]. In the past year, many researchers who analyze the infection diseases used the mathematical modeling to analyze COVID-19 in different countries and regions through the world, [11-15].

SEIR model which consists of susceptible, exposed, infected, and recovered state is very used model. In the epidemiology, the researchers used it for modeling of many infectious diseases like transmission of tuberculosis [16], modelling of Hepatitis B, [17].

SEIR model can be modified in many ways, so there are SEIRS model, SEIR-D, SEIRS-D etc., depending on the states which are included in it. Scientists use the SEIR-D model for a variety of purposes, most of them nowadays related to the Corona: for modelling the spread of COVID-19 [7,8,18,19].

SEIRS-D model is modified version of SEIR-D where the possibility for transition of the recovered people in the susceptible state. SEIRS-D is the most effective model for explaining how an epidemic is spreading. The SEIRS-D model is consisting on the assumption of a totally susceptible population at time t_0 at the starting point of the pandemic. In the SEIRS-D model, the global population of N individuals are splitted in 5 categories: *susceptible S, exposed E, infected I, recovered R, death D*, but the recovered people can be moved in susceptible state again.

Therefore, $S(t)+E(t)+I(t)+R(t)+D(t)=N$. N is the total population which is considered. It must be accent that this model is not dynamic model i.e., the rate of birth and the death rate from other reasons different than COVID-19 virus are not included in the model. The SEIRS-D model aim is to explain the variation of $S(t), I(t), R(t), E(t), D(t)$. The SEIRS-D model is represented on figure 1.

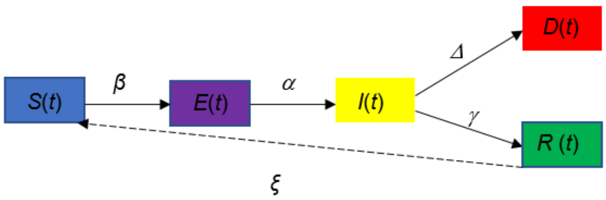


Figure 1. SEIRS-D Model

The difference between SEIR-D model and SEIRS-D model is that in the second one the recovered population can be infected again, with some rate.

The SEIRS-D model is given by the system of the following differential equations:

$$\frac{dS(t)}{dt} = \xi R(t) - \frac{\beta}{N-D} I(t)S(t)$$
$$\frac{dE(t)}{dt} = \frac{\beta}{N-D(t)} I(t)S(t) - \alpha E(t)$$
$$\frac{dI(t)}{dt} = \alpha E(t) - \gamma I(t) - \Delta I(t)$$
$$\frac{dR(t)}{dt} = \gamma I(t) - \xi R(t)$$
$$\frac{dD(t)}{dt} = \Delta I(t)$$

The parameter β is the transmissions rate, the parameter α is an incubation rate i.e., the rate by which the latent patients becoming infectious. Therefore, the incubation time is $\tau_{incubation} = \frac{1}{\alpha}$. While the parameter γ is a recovery rate and the recovery time is $\tau_{recovery} = \frac{1}{\gamma}$. The parameter ξ is the rate by which the recovered people return to the susceptible group due the loss of immunity and $\tau_{immunity} = \frac{1}{\xi}$. The parameter Δ is a rate of death.

$dS/dt, dI/dt, dR/dt, dE/dt, dD/dt$ denote the change in the susceptible, infected, recovered, exposed, died compartments, respectively.

The basic reproduction number $R_0 = \frac{\beta}{\gamma}$ is a very important parameter in the model because it allows us to find out the secondary cases produced by one person in a field. If $R_0 \le 1$ the pandemic will disappear spontaneously, while with $R_0 > 1$ it will continue spreading, [7].

III. SEIRS-D MODEL IN ANYLOGIC SIMULATION MODELLING SOFTWARE FOR COVID-19 MODELLING

In this section is given a simulation of the SEIRS-D model in AnyLogic Simulation Modeling Software.
It is considered sample of 10000 population. At the initial moment the number of infected cases is 1, i.e., $I(0)=1$ and the number of the exposed cases $E(0)=20I(0)=20$. At the beginning as susceptible is taken the total population of 10000.

The simulation of the number of infected, recovered, death and exposed is done depending on the different reproduction number, different incubation period of the virus and different needed time for recovering.

On Figure 2, is given the situation with the number of recovered, deaths, infected, exposed and susceptible people from the 10000 population. At this case, it is assumed that the incubation period $\tau_{incubation} = 5.1$, the recovery time is $\tau_{recovery} = 18.8$ and the reproduction number is $R_0 = 3.3$. The immunity period is assumed to be 90 days. This high reproduction number shows that one person can infect 3 other people. That describes the situation when no control action is taken in order to reduce the transmission of the virus. Because of that there are 540 deaths from the total population of 10000 people. At the x-axis is represented the time period in days and at the y-axis is represented the number of people.

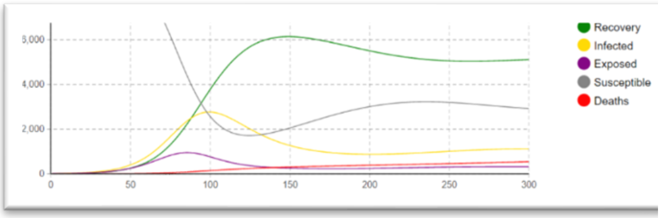


Figure 2. Simulation for $R_0 = 3.3$.

On Figure 3, is given the situation with the number of recovered, deaths, exposed and infected people from the 10000 population. In order to give clear visualization, the number of susceptible which is much larger than the numbers of the other states, is not given in this figure. At this case, it is assumed that the incubation period $\tau_{incubation} = 5.1$, the recovery time is $\tau_{recovery} = 18.8$ and the reproduction number is $R_0 = 0.96$. The immunity period is assumed to be 90 days. In this case, we supposed that there are many control actions like restrictions of people movement at public places and social contacts. Because of that the reproduction number is 0.96, and as consequence of that restrictions the number of deaths from considered population of 10000 is reduced from 540 to only 5 death people.

This simulation shows that the restrictions is needed and necessary if we want to control the virus transmission. The number of deaths and the number of infected will be reduced, if the social contacts and keeping distance will be introduced.

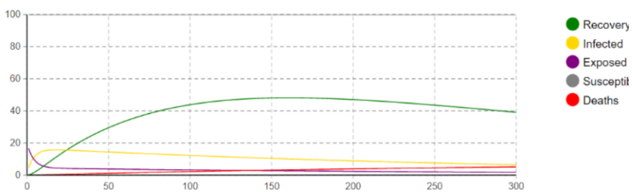
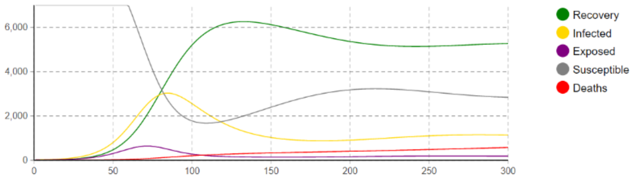
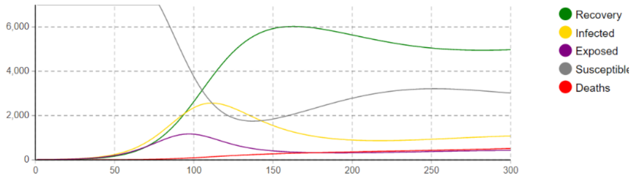


Figure 3. Simulation for $R_0 = 0.96$.

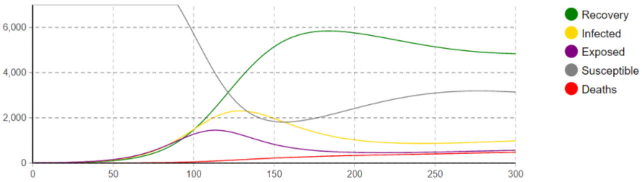
In order to show that the incubation period also influence to the COVID-19 situation, simulations for different incubation period are done at Figure 4.



a) $\tau_{incubation} = 3$ *days*



b) $\tau_{incubation} = 7$ *days*



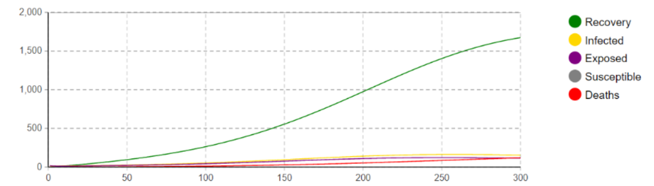
c) $\tau_{incubation} = 10$ *days*

Figure 4. Simulation for different incubation period.

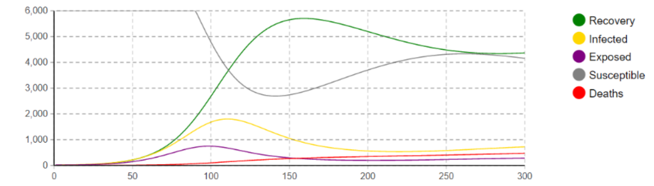
From Figure 4 it can be concluded that the number of infected and number of deaths depends on the time of virus' incubation. Because of that, as consequence of the new more infectious mutations of the COVID-19 virus, which have smaller time of incubation, the number of deaths and infected people is bigger. For population of 10000 people, for which the simulation is done, the number of infected people is 1136, 1076, 982 for incubation period of 3, 7 and 10 days, respectively. For the same population, the number of deaths is 572, 514, 479, for incubation period of 3, 7 and 10 days, respectively. The assumed time for recovery is 18.8 days, and the immunity period is 90 days, according to the most papers which are cited in the introduction. The different assumed incubation periods provide different basic reproduction number. So, the reproduction number is 0.53, 1.24, 1.78.

The situation with infected and death people of COVID-19 virus depends on many other factors. One of that factors is the course of disease, which is connected with time for recovery. That means that if is offered adequate treatment for the COVID-19 infected people with good therapy, the infected people will recover faster, so the time for recovery will be decreased and the number of infected and death people will be decreased also. So, the hospitals and the health system will not be fraughted.

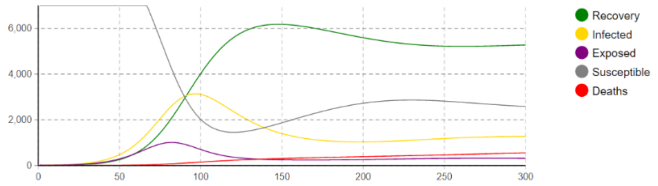
At the next figure, the graphics show the dependence of the number of deaths and infected in relation with time of recovery i.e., the course of the disease.



a) $\tau_{recovery} = 7$ days



b) $\tau_{recovery} = 14$ days



c) $\tau_{recovery} = 21$ days

Figure 5. Simulation for different time of recovery.

From Figure 5 it can be concluded that the number of infected and number of deaths depends on the recovery time. But, as consequence of the new more infected mutations of the COVID-19 virus, which cause more complications at the infected people, the number of deaths and infected people is bigger. For population of 10000 people, for which the simulation is done, the number of infected people is 152, 720, 1270 for recovery time of 7, 14 and 21 days, respectively. For the same population, the number of deaths is 118, 471, 555, for incubation period of 7, 14 and 21 days, respectively. These simulations for different time for recovery are done with assumed immunity period of 90 days and incubation period 5.1 days, according to the most of research papers which are cited in the introduction. The basic reproduction number is 0.96.

IV. Conclusion

In this paper, we considered a simple mathematical SEIRS-D model, in order to investigate the transmission and control of the coronavirus disease (COVID-19) from human to human. We use the ordinary differential equations to obtain the SEIRS-D model. We use the data given in references, like incubation period, average period for recovery, basic reproduction number and immunity period.

It is important for governments and health ministries in the world to understand and predict the number of infected citizens for health concern arrangement of the citizens and for planning a restrictions measures to control virus spread rate.

The implementation of SEIRS-D mathematical model in Anylogic Simulation Modeling Software provide simulations and predictions for the number of infected, recovery people and deaths. These simulations can be applied for every country, considering the basic reproduction number, initial infected people, recovery time and immunity period. In the conditions when the vaccination process is at the beginning, the predictions of the number of infected people with COVID-19 virus is very important for organizations and control measures in order to prevent the strain of the hospitals and all health system in one country.

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