

Time based Meticulous analysis of pandemic spreading ratio using Simpy framework

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ABSTRACT

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Due to the unavoidable spread of COVID-19 and even taking all substantial measures, the ratio of infected people and death rate seems to be out of control. In this increasingly worsening situation, the aim of this article is that it is important to take extraordinary measures to deal with this exceptional pandemic situation, and this is only possible if the actual ratio of the spread of the pandemic is known. Therefore, ingenious pandemic models are being developed to produce real-time infection statistics on an hourly, weekly, and monthly basis. This clever model leverages well-known data sets and when they will be applied to determine the status of three types of infections: the number of infected people, the time the pandemic started, and the time it ended. The time-based results are generated by conduction simulation in the Simpy Python framework, and the resulting results are characteristic of the real-time infection spread ratio. This shows when extraordinary measures for the infection ratio are necessary and when they become reasonable.

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1. Introduction

Infectious diseases in humans and other animals develop when a pathogen is transferred directly between hosts or indirectly through the environment or intermediate hosts (Moudon, 2013). The efficacy of transmission is determined by the Infectiousness of the infected host (or hosts) and the susceptibility of uninfected individuals exposed to infection (Abotsi, 2011). Biological, behavioral, and environmental variables influence Infectiousness (Mello et al., 2021).

Every hour counts in the realm of epidemics, and there is a strong need to foresee the disease's temporal evolution in order to determine the best approach to deal with it and create proper control of its spread (Tenorio, 2018). Recently, the COVID-19 pandemic has been rapidly spreading over the world, and its impact on our lives in general is unavoidable (Zuhair et al., 2023). Thanks to advances in computing, electronic data management, the capacity to share and deposit data through the internet, and rapid diagnostic tests and genetic sequence analysis, precise electronic



surveillance of infectious diseases has become a game-changer in recent years. Biological Infectiousness is determined by infectious pathogen excretion and can refer to viral or bacterial load in specific anatomical areas or the pathogen's life cycle in a more complex fashion (Aslam et al., 2020). The contact patterns of an infected individual, as well as, if relevant, the contact patterns of intermediary hosts or vectors, determine behavioral Infectiousness (Berg et al., 2002). Depending on the disease and the route of transmission, the nature of these encounters varies.

It has been suggested that the rapid proliferation of COVID-19 in humans is linked to a spike protein, which has a location that's triggered by an enzyme called furin. The latter is dangling on the virus's surface, making it easier to infect human cells (Haider et al., 2023). As a result, a suitable mathematical explanation of Covid-19's spread is urgently needed to restrict the disease. This is especially true when it comes to assisting health government agencies worldwide in maximizing the efficiency of medical assistance strategies in the face of such a global disaster (Obaid et al., 2024). In the aftermath of the coronavirus pandemic, however, there were 7818 confirmed cases worldwide, with more than 1370 severe cases and 170 deaths (Rasheed et al., 2022). The majority of it was discovered in China. Over a few weeks, the disease has spread across China's borders, affecting almost every country.

The sickness causes a dry cough, sore throat, and fever. Although the majority of instances are minor, some can result in ARDS (Ashraf et al., 2022), severe pneumonia, pulmonary edema, and organ failure. Following the WHO's declaration of an emergency, various studies have been conducted in modeling and prediction to understand disease spread better, evaluate preventive measures put in place by authorities, and provide early and accurate disease detection, to mention a few. Mathematical modeling has been employed in epidemiological studies for numerous years (Cornellia et al., 2017).

Developing a mathematical model for disease transmission and propagation is of utmost importance, particularly in the COVID-19 pandemic (Zulfa, 2020). This model can significantly aid in the forecast of epidemics' progress, the design of mass vaccination campaigns, and the selection of data for epidemiological research (Prakash & Sathya, 2023). By incorporating real-time statistics, this model can generate output results that are sufficiently proactive to predict the next action, thereby helping to avoid either or limit the unavoidable health hazards (Dash et al., 2023). The model considers various factors, such as the risk of contact transmission, the average number of encounters between persons, and the length of time an infected person can infect others (Woods & Böhme, 2022).

The simulation results are extracted using the Python programming language, specifically the Simpy framework (Harmon, 2022), designed for event simulation. These results provide crucial

statistics on the spreading frequency of the pandemic, measured in terms of Hourly, Weekly, and Monthly rates. The subsequent discussion delves into the causes of pandemic propagation despite strict prevention measures, and a prevention strategy is developed based on the results. Each section of the paper is organized to provide a comprehensive understanding of the research process, from the literature review to the development of the intelligent model, the simulation setup, and the Rigorous analysis of the results.

2. Theoretical Framework

The location and environment of the diseased individual influence environmental infectiousness. Modeling the dynamic of COVID-19 (Ashraf, Saleem, et al., 2020), researching the efficacy of preventative methods such as COVID-19 travel restrictions, and studying the effect of climate on COVID-19 propagation are only a few of the studies being conducted about the present COVID-19 (Wang et al., 2024). In recent studies, the authors have tried to develop similar models to obtain proactive results, but every model has limitations that ultimately affect the results. Some of the related studies are discussed with the shortcomings (Manohara & Kumbinarasaiah, 2024).

The researcher from China, Jiang et al., (2024) created a new model that describes the dynamics of COVID-19 by combining daily intercity movement data with an SEIR model. Using a smartphone application that records human mobility, they acquired daily intercity migration data from 367 cities. According to their findings, the number of infections in most Chinese towns will peak between the middle of February and the beginning of March 2020. Their study is limited to mainland China and focused only on the daily movement. In their research, no prevention measures have been outlined as they just warned the community to avoid traveling these days.

To predict the change in the spread of COVID-19, Fan et al., (2024) devised a combination of SEIR and regression models and utilized the datasets from JH University. This investigation, on the other hand, revealed several hidden factors but could not assign specific liabilities that must be carried out to avoid perplexing circumstances.

Ballesteros-Aguayo et al., (2022) proposed a Masked Face-Net technique to prevent the coronavirus's rapid spread. Their method has revealed the number of face-masked images a machine-learning model generates. It's worth noting that it only checks whether or not someone is wearing a mask. They also explain their research using the Masked Face-Net generation dataset to generate standard images. The lack of use of the Raspberry Pi in this paper is a major flaw compared to the implemented work.

Similarly, Lepeley et al., (2021) pioneered the transmission of COVID-19 and its link to temperature and humidity. The study's findings showed that increasing temperature and humidity

levels helped to control disease transmission, but they couldn't comprehend the situation for people moving in large groups.

Using a system that avoids direct human interaction, Rahmatizadeh et al., (2020) presented a system that intends to thoroughly survey the role of artificial intelligence and machine learning as one critical technique in the field of screening, anticipating, estimating, contact following, and medication advancement for SARS-CoV-2 and its associated pestilence. This technique is conceivable, but no relevant model is offered, and it is difficult to grasp how day-to-day chores may be addressed without direct human involvement.

Chen et al., (2020) developed a time-dependent susceptible-infected-recovered (SIR) model to track the transmission rate and the recovering rate at a specific time and obtained a prediction error of 3% or less for confirmed cases and predicted that the day the recovering rate overtook the transmission rate. This strategy is not feasible for huge gatherings, so no alternative solution is provided.

An edge figuring-based cover recognizable proof structure was proposed by Kong et al., (2021) to support general wellness protections, which can ensure consistent execution on low-power camera gadgets of transportation. Its three main phases are video reclamation, face location, and cover recognizable proof. This system is significantly more perplexing, and the virus recognition ratio is obstructed, lowering the suspected ratio.

Wang et al., (2020) employed CNN with a dataset of 14,800 chest x-ray radiography pictures from 12,725 patients to try to offer doctors a greater understanding of the essential parameters affecting COVID-19 cases. The accuracy, sensitivity, and positive prediction value (PPV) were reported to be 91.6 percent, 88.1 percent, and 94.4 percent, respectively. This method did not elicit statistics on social distance among the patient population, and as a result, it is concerned about the sensitivity issue.

3. Method

Table 1 compares the COVID-19 classification methods generated thus far, with the relevant importance appraised based on accuracy, sensitivity, and positive prediction value.

Table 1. THE COVID-19 CLASSIFICATION METHODS

Methods	Samples	Patients	Source of data corpus	Accuracy	Sensitivity	Positive prediction value
COVID-Net Ashraf et al., (2020)	13,801	13,725	COVIDx data	92.5%	83.1%	96.4%
ResNet50 Abad et al., (2024)	99	49	GitHub	88%	77%	88%
SVM and Random	76	235	DHQ Hospital	82.7%	3.77%	79.8%

Abad et al., (2024)						
MLT and SVM Ashraf, Ahmad, et al., (2020)	40	456	Montgomery County X-ray	97.48%	95.76%	99.7%
SMOTE Ashraf, Gao, et al., (2020)	5840	88	Chest X-Ray Images	96.6%	96.7%	98.3%
Probabilistic Model Wang, (2008)	51	77	Kaggle benchmark dataset	99.4%	67%	77%
NLR&RDW-SD	102	45	Jingzhou Central Hospital	85.7%	90.0%	84.7%
RF based model Allahham et al., (2020)	565	176	Not public	87.5%	56%	93.3%
iSARF Formann et al., (2020)	765	1658	Relevant uni. Hospitals	87.9%	90.7%	84%
Modified U-Net structure Siddiki et al., (2021)	110	60	SIRM	79%	86%	83%
Attention U-Net with an adversarial critic model Khan et al., (2021)	1047	641	JSRT, Montgomery, and Shenzhen	96%	54%	84%
InfNet 28 Khan et al., (2021)	1600	768	CCOVID-19 CT Segmentation	98%	72.5%	89%

Before developing the shrewd COVID-19 model, a significant dataset is essential. Multiple datasets related to COVID-19 have been made available online over the last few months. Most, if not all, of these datasets are open-source, meaning anyone can download and use them. Furthermore, they are constantly being updated with new data from the field (Ashraf et al., 2021). Therefore, different data sources from various corpus have been targeted and applied to the proposed shrewd model. The suggested shrewd model considers the risk of contact transmission, the average frequency of encounters between persons as a function of time, and the amount of time a person remains infected and can infect others. Finally, it will give fruitful results about the people who have been infected. Figure 1 depicts how aggravatedly the COVID-19 pandemic is propagating. The red dots illustrate the effete peoples, and yellow, pink, blue, gray, and green oval shapes represent the various spreading spots such as schools, railway stations, community halls, etc. The link among the red dots shows that the virus is being transmitted from person to person, and every new person inherits it. It is imperative to know how quickly the people are being affected. The proposed intelligent model works exactly for this objective and analyzes the propagation on time-based slots.

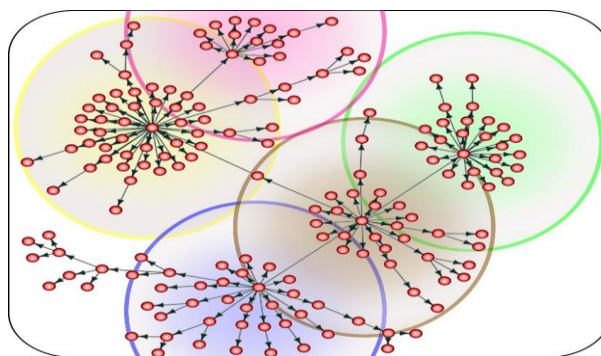


Fig. 1. Pandemic Propagation Phenomenon
Source: Processed by researchers, (2024)

Similarly, it is also crucial to identify the loopholes of various propagation factors, such as depicted in Figure 2. This illustration shows an alarming scenario in that most of the danger zones are the neighboring homes in the society where people live. When they come out, they have entered the danger zone, and mixing with each other increases the chances of infection. Further, how does each person mix, for instance, by handshaking or just by going near each other? The foremost is from the group of normal people if anyone is infected! How are the others going to be infected? The third scenario shows that from every infected person, at least two others have a greater chance of being infected and remain in close contact with the infected person. The fourth scenario is different if people follow the SOPs and know how to maintain social distancing and keep their mouths and noses covered with masks! Such persons can be prevented from transmitting the virus and are subject to short-term contact (Ban, 2017).

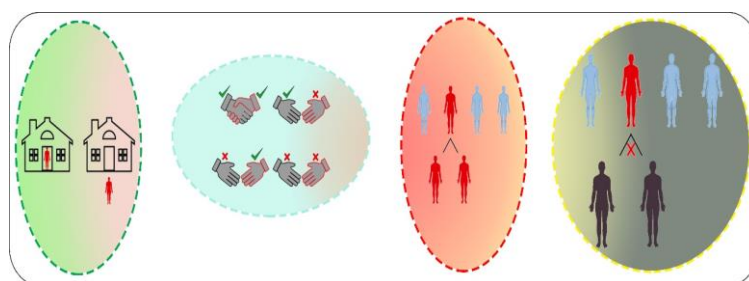


Fig. 2. Pandemic Propagation Phenomenon

Source: Processed by researchers, (2024)

It is essential to understand that when the COVID-19 virus transmits from person to person, it changes its behavior, keeps some attributes in the body of a current person, and sends the newly created behavior to the other person. This situation is harmful and impossible to detect, and Figure 3 illustrates this phenomenon. The two square-shaped boxes having curly red and green lines show the dual behavior of the infection. The first horizontal and vertical red line box shows that when a person gets an infection in the body, the behavior of the infection has a greater impact, and the person does not realize how to behave! The second box of the same vertical and horizontal green lines depicts another infected person nearby near the new virus-infected person, and the lines changing direction, i.e., from completely horizontal to some inclination, shows that virus infection behavior tends to convert into another case. The last yellow line box is the mixture of the first two boxes, which indicates that the person can survive subject to having enough fighting chromosomes, which ultimately can repair the vandalized cells. It is worth mentioning that in this case, no line appears completely, horizontal or vertical, which shows that the tendency to change behavior is much more rapid. The proposed intelligent model establishes the parameters as follows:

- a). The number of infected peoples = P_n
- b). The time when pandemic begins i.e $P_n = 1$
- c). The time when the pandemic disappears for some time i.e $P_n < 1$
- d). The time when pandemic appears more stringently $P_n > 1$

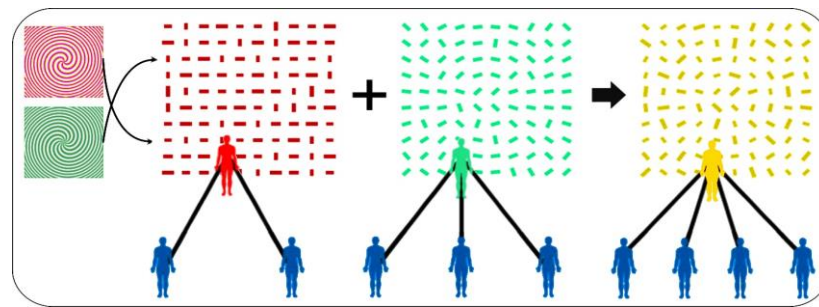


Fig. 3. Changing behavior of Covid-19 during person to person transmission

Source: Processed by researchers, (2024)

When all these three parameters have been applied to the substantial dataset, the resulting output is computed as:

$$\frac{dN_p}{dt} = -\partial Z N_p N_{pi} \quad (1)$$

$$\frac{dN_{pi}}{dt} = \partial Z N_p N_{pi} - \frac{N_{pi}}{T_r} \quad (2)$$

$$\frac{dN_{pa}}{dt} = \frac{N_{pi}}{T_r} \quad (3)$$

The pandemic transmission risk is depicted by ∂ , and Z , represents the average number of transmission contacts among people. Further the T_r , there is a period when people remain infected. Other variables, such as social separation, can modify the P_n components over time.

Numerical analysis is required in many circumstances. Thus, the mathematical answer should be more straightforward. Each differential equation can now be examined separately for completeness. The negative sign in Eq. (1) points that $N_p(t)$ decreases monotonically with time. Similarly, factor $\partial Z N_p N_{pi}$ the factor in equation (2) shows that the number of infected people increases. While looking at equation (3), consider the ratio between infected people and the duration of the infection, i.e., as the number of infected people increases, fewer people are indeed susceptible, being such a ratio proportional to the number of people recovering from the disease. Developing this shrewd model enables us to infer predictions about the spread of the disease.

In addition, when managing a disease outbreak, environmental factors such as the weather can be considered. Such an approach is critical for forecasting epidemiologic outcomes during seasonal shifts in some nations. Environmental conditions, such as temperature fluctuations, can affect the floating time of respiratory droplets in the atmosphere, increasing the risk of infection. The influence of the environment on the spread of the disease can be associated with this ∂ factor.

We can reduce the danger of infection due to several factors. For example, ∂ and Z are reduced when people join the quarantine. The number of persons who come into contact with each other is reduced; on the other hand, when people go to the markets wearing a face mask, ∂ it may be

reduced, but not necessarily Z, because individuals will still be in contact. Such measures are critical for restricting disease propagation and preventing resurgences or minor new outbreaks.

4. Result and Discussion

The available dataset is being applied using equation 3, to the simulation setup in Python using Simpy framework. The relevant parameters have been fixed in table 3, for setting up the Simpy environment.

Table 2. SETTING SIMPY ENVIRONMENT

Import simpy Import random Import statistics
<pre>wait_times = [] class Shrewd_model(object): def __init__(self, env): self.env = env</pre>
<pre>interventions = [SocialDistancingChange('2020-03-12', 0.3), # some restrictions SocialDistancingChange('2020-03-22', 0.9), # stay-at-home order DiagnosisDelayChange('2020-04-13', 7.0), # More testing introduced DiagnosisDelayChange('2020-04-15', 5.0),]</pre>

Further, setting the Random parameters in table 3.

Table 3. SETTING RANDOM PARAMETERS

<pre>params = Parameters ([all_population], SimulationConstants(), interventions=interventions, d0_infections=LogUniformParameter('ny_d0_infections', 10000, 200000), start_date='2020-03-10')</pre>

In the proposed intelligent model, the growth of domains of various groups in a small random field has been tested at a low temperature. The results presented in Figure 4 show the stringent increase in the number of infected persons with COVID-19 hourly. The bar lines indicate that with a huge level of about 91% in the first 5 hours and then follows a non-linear pattern, and at the end of 99 hours, it reached 67%. The ups and downs indicate how rapidly people mix in markets or public places and get infections.

Proceeding to the next result, figure 5 illustrates that the pandemic spreading ratio reaches an aggravated level during the third and fourth week and after the fifth week and becomes weaker and thereby reduces.

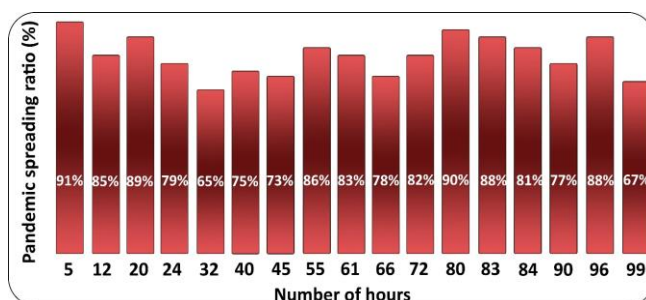


Fig. 4. Hourly basis infection propagation status

Source: Processed by researchers, (2024)

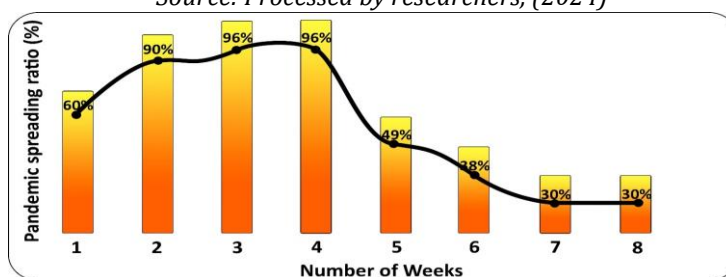


Fig. 5. Weekly number of reported cases

Source: Processed by researchers, (2024)

The final result in Figure 6 indicates that during the first month of the COVID-19 pandemic, the spreading infection speed was at the top and remained the same in the next month. This is because, in the first two months, the people were not aware of the nature of the disease and were taking it as a normal pandemic. However, when the death ratio approached its peak, the aggravated situation turned into precautions, and people started isolation themselves.

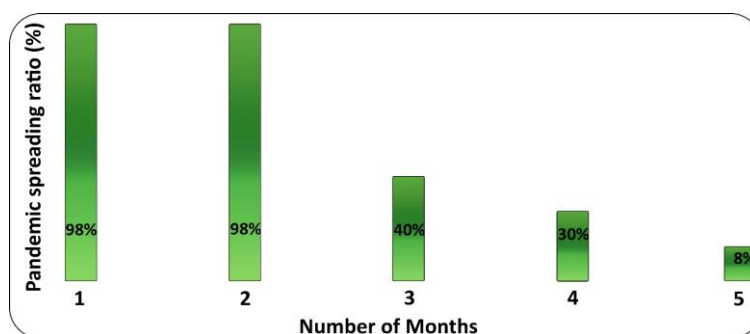


Fig. 6. Monthly pandemic propagation report

Source: Processed by researchers, (2024)

The development of an intelligent model, a crucial tool, aims to predict the propagation of the COVID-19 pandemic and evaluate measures and early and accurate disease identification in patients using time-based samples.

In order to get more authentic results regarding epidemic diseases, some other factors need to be considered, such as some inherent factors of the society that can be developed to minimize the social impact of other epidemics in the future (Ashraf & Ahmed, 2020). These include the pivotal role of health organizations in collecting and disseminating trustworthy data sets in the context of epidemics, a crucial step to prevent or correctly interrupt the outbreak of a disease (Gu, 2005).

Similarly, creating and designing mobile apps can be useful tools for achieving more effective social separation.

5. Conclusion

The shrewd pandemic covid-19 model has revealed that if extraordinary measures are required to handle the infection propagation ratio the hourly, weekly and the monthly basis spreading factor must be considered, and when it seems that situation is aggravated the strict measures become indispensable either lockdown situation must be adopted and when the result shows a declining ratio the measures should be updated accordingly.

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