Analysis and Study of Mathematical Model for Infectious Disease: A Special investigation of Covid-19

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Abstract: This paper explores the infectious disease method along with covid prediction. The research aim is to study and analysis the previous work which is used for infectious disease. The theoretical study of model which could help in prediction of covid. Several infectious illnesses may be transmitted between people. Insects and other animals may spread some. Food or water infected with pathogens, as well as exposure to organisms in the environment might also cause to get illnesses. Fever, exhaustion, and other symptoms may be present, depending on the kind of illness. Rest and home treatments may help treat mild infections, but hospitalisation may be necessary for more serious diseases. Recently we find the covid pandemic which is also the infectious disease. The perfect analysis of expected patients will help in providing the sufficient accommodation and infrastructures. This paper first explores the general model which used to predict and analysis the infectious disease and work out on the covid prediction using Holt-Winters's method.

Keywords: Infectious disease, SIR model, Covid, Holt-Winters's

I. Introduction

Public health treatments may benefit from mathematical models that simulate the progression of infectious illnesses (Basu & Andrews, 2013). Calculations based on the characteristics of various infectious illnesses, such as mass vaccination campaigns, may be made using models that employ fundamental assumptions or gathered data and mathematics. Using the modelling, researchers may determine which interventions should be avoided and which should be tried, as well as forecast future development trends. Vaccines help prevent several infectious illnesses, including measles and chickenpox. Most infectious infections may be prevented if wash hands often and thoroughly. Environmental interactions between pathogens and hosts, which are subjected to the modulatory influence of a variety of factors, including the environment, the biological properties of the pathogens and the host's susceptibility to disease, as well as the influence of behavioural, cultural, and societal factors, are the most important contributors to infectious disease transmission. Disharmonious ecological interactions between pathogens and hosts are the primary cause of infectious disease transmission (Mitchell et al., 2005; Morens et al., 2004). Establishing a relationship between the previously described factors is thus critical if we are to develop effective control mechanisms, health-care interventions, and public policy [2] measures. It is true that antimicrobial drugs and vaccines, along with good hygienic-sanitary practises and prophylactic measures, can effectively treat and even eradicate some infectious diseases, the epidemiological magnitude of these diseases is highly unpredictable due to the constant biological evolution of infectious agents against therapeutic drugs, as well as the constant changes in society and the environment. It is possible that the unpredictable nature of these illnesses may put health systems and services at risk, particularly when dealing with restricted and limited resources in terms of both human and financial resources. In this context, mathematical modelling of infectious illnesses may assist the health-care system by permitting extrapolations of epidemiological behaviour of infectious diseases as well as treatments whose impact can be extrapolated to benefit the public health system. Lockdowns, physical distances, and the use of masks were all investigated using mathematical models to determine how they affected the COVID-19 cumulative incidence and mortality, as well as bed occupancy. The researchers concluded that the preventive measures mentioned would be effective in slowing the epidemic's progression in France, but not enough to prevent the maximum occupancy of ICU beds, while emphasising that the magnitude of the pandemic would be much greater if no such measures were implemented (Ambikapathy & Krishnamurthy, 2020). For almost a century, infectious disease epidemiology has relied heavily on mathematical representation and study of infectious illnesses. Due to advancements in computers, electronic data management, internet sharing, and quick diagnostic testing and genetic sequencing, extensive electronic monitoring of infectious illnesses has become commonplace in recent years. As a result of these continuous breakthroughs, mathematical models are increasingly being used to generate scientific hypotheses and devise practical disease-control measures. Many nations' public health programmes have benefited greatly from mathematical analysis and models, which had previously been unable to explain previously baffling facts.

With an increasing focus on hypothesis testing and parameter estimation, robust statistical approaches have been essential in advancing the field of mathematical epidemiology. It is possible to utilise mathematics to construct hypotheses, guide data collection, and estimate sample sizes to distinguish between conflicting hypotheses in the absence of accurate data. That's why it's said that math is "neither more nor less than a technique of thinking clearly about the issue at hand." As basic as feasible, but not so simple that the conclusions made are influenced by added realistic complexity, should be the goal of model development. Over-simplification and unnecessary complexity may both obfuscate important conclusions. A major aspect of mathematical modelling of infectious illnesses is selecting which model complexity is essential (Adekola et al., 2020).

1.1 Disease transmission

Human and other animal infectious illness epidemics are caused by direct or indirect transmission of a pathogen between hosts, as well as the environment or intermediate hosts. Uninfected people exposed to illness have a higher risk of infection if they are more infectious than the infected host (or hosts). Biological, behavioural, and environmental factors all play a role in infectiousness. Pathogen excretion is a critical component of biological infectiousness, and it may be assessed in terms of the quantity of viral or bacterial load present in certain anatomical locations, or in a more sophisticated way by the pathogen's life cycle, which is described in detail in the next section. The immune system of the host, including both innate and acquired immunity, as well as the dynamics of pathogen replication and spread, as well as virulence factors and drug sensitivity, all play a role in determining the dynamics of the pathogen in the body, according to the World Health Organization. It is also necessary to consider the interplay between the genetic drivers of illness development in both the pathogen and the host. Contact patterns of individuals, as well as those of intermediate hosts or vectors (when appropriate), determine the infectiousness of their behaviour. According on the sickness and manner of transmission, these linkages are made in various ways. Only a small number of individuals have several personal relationships, but the vast majority have only a handful. Because the frequency of contact is so widely separated, it is difficult to disseminate sexually transmitted viruses as a result of this. When it comes to more informal verbal exchanges or handshakes that might result in the transmission of respiratory infections, the frequency of contact and the number of such interactions reported by respondents tend to cluster around the average (Grassly & Fraser, 2008).

1.2 Causes of Disease

- ✓ **Bacteria.** One-celled organisms are responsible for the development of strep throat, urinary tract infections, and tuberculosis.
- ✓ **Viruses.** Infections caused by viruses, which are even more minute in size than bacteria, include anything from the common cold to AIDS.
- ✓ **Fungi.** Ringworm, athlete's foot, and other common skin infections are all caused by fungus. Infections of the lungs or nervous system may be caused by fungus of other kinds.
- ✓ **Parasites.** A mosquito bite is the primary method of transmission for the disease. Other parasites may be spread from animals' excrement to humans.

1.3 Transmission of Disease

Direct contact

The majority of infectious diseases may be acquired simply by coming into contact with an infected person or creature. Direct physical contact, such as when two persons come into direct physical contact, may result in the transmission of infectious diseases.

- **Person to person.** The most common route by which infectious diseases are spread is by direct contact with people who have bacteria, viruses, or other germs from another person's body or environment. An uninfected person may get the virus if an infected person kisses, coughs, or sneezes on the uninfected person.

- **Animal to person.** Even if an animal bite or scrape is infected, it is possible to get unwell or even die as a result of the infection, even if the animal is a pet. The disposal of animal excrement may also be detrimental.
- **Mother to unborn child.** While pregnant, she may be able to transmit bacteria that might cause illness to her unborn child. Certain infections may be transmitted via the placenta or breast milk. The germs from the mother's vaginal discharge may be transferred to the infant after birth.

Indirect contact

Indirect contact with disease-causing bacteria has the ability to disseminate them. An inanimate item, such as a tabletop, a doorknob, or a faucet handle, may be home to a variety of viruses and bacteria. A person might get the flu or a cold if they come into contact with a doorknob that has been touched by a sick person. After touching the eyes, mouth, or nose, wash hands thoroughly to prevent infection.

Insect bites

Mosquitoes, fleas, lice, and ticks are all examples of insects that serve as vectors for the spread of certain pathogens. The term "vectors" refers to these carriers. In addition to the West Nile virus, mosquitoes are vectors for the malaria parasite. The bacteria that cause Lyme disease may be carried by deer ticks.

1.4 Mathematical modelling of infectious diseases

A mathematical model is constructed through the use of equations, it provides a crude general behaviour for an epidemic, allowing predictions about the duration of an epidemic, its magnitude in the population, and evaluations about the influence of determinate factors on disease spread, thereby providing a crude general behaviour for an epidemic proving that mathematical improvements may be made to models in order to make them more similar to real-world data. When it comes to infectious disease epidemics, modelling is a powerful tool that can be used to identify patterns in epidemics as well as extrapolate their behaviour and the effect of interventions such as pharmacological treatment, vaccination, quarantine, and social distance in a dynamic context at a low cost. It can also be used to simulate experiments that would be unethical to conduct on humans. A powerful tool for mimicking studies that would be unethical to execute on individuals, mathematical modelling is a must-have for every scientist. The mathematical models used in infectious disease epidemiology may be split into two types: deterministic and stochastic. 1) Deterministic models that account for non-random rate flows in a population divided into compartments; and 2) stochastic models that account for probabilities in the movements between compartments of the model, such as the likelihood that an infected individual will spread and the likelihood that an infected individual will spread the disease (Li, 2018).

II. Literature Review

Bozzani et al. (2021) had proposed the prioritization of infectious disease management. This approach had become increasingly dependent on the availability of physical input constraints and other real-world limitations affecting implementation and decision-making processes. The viability of treatments and their impact were constrained by the limitations of health-care systems. Meanwhile, mathematical models required additional structure and data availability. The study aimed to provide an overview of methodologies published to introduce limitations into mathematical models of infectious diseases. A total of 36 studies underwent analysis. Stochastic and agent-based simulations were employed to investigate the influence of nonmonetary limits on prioritization in dynamic transmission models. Researchers sought to determine the effect of limits on program roll-out and scaling, as well as estimate the expenditures and resources needed to alleviate these restrictions and achieve desired levels of program coverage.

Prem et al., (2021) the mathematical models used to study directly transmissible viral diseases, including COVID-19, significantly improved the understanding of these diseases and the effectiveness of public health countermeasures. Contact matrices, representing individual interactions, were popular tools. Synthetic contact matrices, developed using survey data on household, school, and classroom demographics, allowed a comprehensive examination. The study expanded its reach to include 177 more locations, comparing synthetic contact matrices for 2017 and 2020 and investigating the consequences of using both empirical and synthetic matrices in modelling the COVID-19 pandemic.

James et al. (2021) highlighted the substantial benefits derived from mathematical modelling during the COVID-19 pandemic. They acknowledged the challenges of model validity due to the proliferation of models with varying forecasts. The study explored fundamental limits of mathematical modelling as a tool for understanding empirical data and guiding decision-making. Various methods for enhancing the validity of conclusions drawn from these studies, especially in the context of infectious diseases, were presented.

Huang et al. (2021) classified social separation into personal choice or government-sponsored initiatives and demonstrated their benefits in preventing contagious disease transmission. The study utilized a mathematical model to investigate the influence of social distance on the outbreak threshold of an infectious disease with asymptomatic infection. Two levels of communication and interaction were proposed to distinguish between spontaneous and public social distancing.

Bekiros & Kouloumpou (2020) introduced a spatiotemporal strategy (SBDiEM) utilizing artificial intelligence for a global monitoring network to combat pandemics. This approach, adaptable to COVID-19 and previous outbreaks, was expected to impact health systems, governments, and policymakers worldwide.

Alahmadi et al. (2020) emphasized the increasing precision in parameterizing disease dynamic models due to enhanced data availability and computing power. Despite improvements, challenges remained, such as parameter identifiability and the difficulty of gathering significant quantities of high-quality data. The study covered the latest developments in these areas.

Husein et al. (2019) focused on epidemiological models, emphasizing the complexity of human social existence. The study proposed the use of an epidemiological random network model to forecast the influence of interaction patterns on the spread of infectious diseases, specifically utilizing the SIRS model.

Jenness et al. (2018) introduced EpiModel, a program for building, simulating, and analyzing infectious disease transmission dynamics in R. The program's distinctive feature was its stochastic framework for simulating epidemic transmission on networks, using real data on contacts potentially transmitting illness.

Dattner & Huppert (2018) delved into the historical impact of infectious diseases on morbidity and mortality, linking them to human development and the demise of civilizations. The study highlighted notable instances and discussed the role of mathematical modelling in infectious disease research. Mathematical modelling played a crucial role in proving that reducing mosquito populations, rather than eliminating them, was sufficient to manage malaria, as demonstrated by Ross's work. The SIR model, established by Kermark and Mckendrick in the early 20th century, became the foundation for contemporary infectious disease models. The model's basic reproduction number (R0) acted as a threshold parameter, influencing epidemic size based on the initial proportion of susceptible individuals.

Blackwood & Childs (2018) emphasized the prevalence of mathematical models in studying infectious disease transmission dynamics, particularly using the susceptible-infectious-recovered (SIR) paradigm. The study provided a brief introduction to illness modelling, addressing inherent problems that needed consideration.

Peter et al. (2018) developed an infectious disease dynamics model using an ordinary differential equation system. The study focused on the three distinct groups in the population susceptible, infected, and recovered and demonstrated the impact of increasing immunization on reducing illness prevalence.

Table 1. Systematic Reviews

Author & Year	Research Area	Methodology	Findings
Bozzani et al. (2021)	Infectious Disease Management	Analysis, simulations	Management techniques are influenced by physical constraints. Viability of treatments constrained by health-care limits. Overview of methodologies for mathematical model limitations.

Prem et al. (2021)	Viral Diseases & Contact Matrices	Synthetic matrices, survey data	Improved understanding of COVID-19 and countermeasures. Use of contact matrices for modelling interactions. Comparison of matrices for 2017 and 2020.
James et al. (2021)	COVID-19 Modeling	Not specified	Benefits of mathematical modelling during the pandemic. Acknowledgment of challenges in model validity. Exploration of fundamental limits. Methods for enhancing modelling validity.
Huang et al. (2021)	Social Separation & Outbreaks	Mathematical model	Classification of social separation. Investigation of social distance influence on outbreak threshold. Proposal of communication levels for social distancing.
Bekiros & Kouloumpou (2020)	Pandemic Monitoring & AI	Spatiotemporal strategy with AI	Development of a global monitoring network with AI. Applicability to COVID-19 and previous outbreaks. Expected impact on health systems and policymakers.
Alahmadi et al. (2020)	Disease Dynamic Models	Not specified	Increased precision in parameterizing models. Challenges in parameter identifiability and data gathering. Coverage of latest developments.
Husein et al. (2019)	Epidemiological Models	Random network model	Emphasis on the complexity of human social existence. Proposal of an epidemiological random network model. Utilization of the SIRS model for forecasting infectious disease spread.
Jenness et al. (2018)	Disease Transmission Dynamics	EpiModel with stochastic framework	Introduction of EpiModel for modeling disease transmission. Utilization of real data on contacts for epidemic modelling.
Dattner & Huppert (2018)	Historical Impact of Diseases	Not specified	Linking diseases to morbidity, mortality, and civilization demise. Discussion of notable instances and the role of mathematical modelling in disease research.
Mathematical Modeling	Mosquito Population & Thresholds	Ordinary differential equations (ODEs)	Proof that reducing mosquito populations manages malaria. Ross's confirmation of threshold dynamics in epidemics. Introduction of the SIR model by Kermark and Mckendrick.
Blackwood & Childs (2018)	Transmission Dynamics	SIR Paradigm	Prevalence of mathematical models in studying disease transmission dynamics. Rise in model usage due to computing tools and data accessibility.
Peter et al. (2018)	Disease Dynamics Model	Ordinary differential	Development of an infectious disease dynamics model using ODEs.

		equations (ODEs)	Impact of increasing immunization on reducing illness prevalence. Influence of basic reproduction number (R0) on equilibrium.

2.1 Research Gaps

Existing research in infectious disease modelling has made significant strides, but notable gaps persist. One gap is the need for more comprehensive studies addressing the practical implementation of management techniques proposed by Bozzani et al. (2021), particularly in diverse healthcare settings. Additionally, the limitations and challenges highlighted by James et al. (2021) underscore the necessity for refined methodologies and standardized approaches to enhance the reliability of mathematical models. Further research is required to bridge the gap between theoretical models and real-world effectiveness. Ongoing efforts should prioritize addressing these gaps to improve the applicability and impact of infectious disease modelling in public health decision-making.

III. Deterministic Mathematical Modelling

Disease epidemics can be roughly predicted using deterministic models of infectious diseases, which divide a population into compartments that correspond to different stages of disease and use differential equations that appear as their derivatives to describe how people move around within these compartments over time (Smith & Moore, 2004). It can be seen from the differential equations below, that the starting location of a pathogen-infected population is in a compartment referred to as susceptible, which eventually migrates to the compartment infected.

$N=S+I, N=S+I,$ ……………………………………………………………… Equ-1

Where,

$dS/st=-\beta+1, dS/st=-\beta+1,$ …………………………………………………... Equ-2

$dI/dt=\beta\ SI.dI/dt=\beta SI.$ ………………………………………………………… Equ-3

The SI model is shown above, where the negative sign preceding the infection rate () indicates that S x I decreases among the people in compartment S, while the number of infected persons grows according to the number of individuals in compartment S.

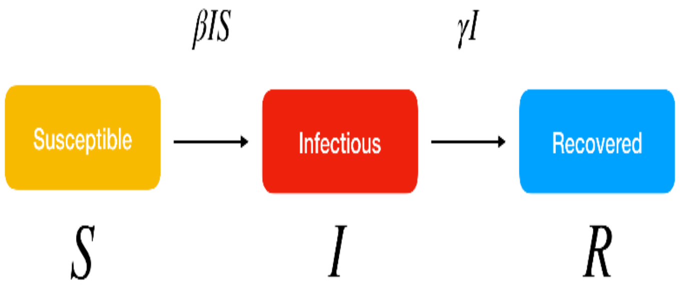

Fig. 1 SIM Model

Ref: Retrieve form COVID-19 dynamics with SIR model (lewuathe.com)

When a system reaches saturation, there are no more susceptible persons to maintain new instances. As a result, this model is unable to effectively reflect the natural decline in the number of cases that happens after infection and the exponential rise in the number of cases that occurs after infection. Thus, the SI model is better suited for infectious diseases that progress to chronic illnesses from which there is no recovery, such as HIV infection. Furthermore, the inclusion of a new compartment capable of capturing the reduction in epidemic curves as a result of acquired immunity or death increases the realism and applicability of the system for diseases that are self-limiting or curable. R equation 7 shows that in order for the new compartment to develop exponentially regardless of the number of persons that are susceptible, the infection rate must be raised by a recovery constant, as illustrated in the graph.

For example, the equations look like this:

$$N=S+I+R, \quad \text{……Equ-4}$$
$$dS/dt=-\beta S/IN, \quad \text{……Equ-5}$$
$$dI/dt=\beta S/IN-\gamma I, \quad \text{……Equ-6}$$
$$dR/dt=\gamma I \quad \text{…… Equ-7}$$

For infectious diseases, this new compartment makes the graphic representation capable of describing their epidemiological behaviour, as shown in Figure 1 (right): the number of susceptible individuals decreases as the number of infections rises, and the number of recovered people rises when there are fewer infected people. The deterministic models are not limited to a single SI or SIR structure, but rather can incorporate a variety of structures and dynamics into the deterministic systems, resulting in more realistic epidemic representations of infectious diseases, such as the incubation period (E), age stratification (A), and spatial structures, to name a few.

3.1 Stochastic mathematical modelling

It is more realistic to use probabilistic models of infectious diseases because they allow for the recognition of epidemic patterns, the analysis of spatial case numbers in a given location, and the estimation of epidemic duration while taking into account differences among individuals in the population, such as age and gender, as well as social and geographical factors that impose non-uniformity in the contingency of the epidemic (Ndii & Supriatna, 2017). These models, which may be classified into three types based on their mathematical formulations, are often characterised by complex and sophisticated mathematical formulations: For example, stochastic differential equations, Markov chains, and Markov chains with discrete time are all examples of stochastic differential equations, as are stochastic differential equations with discrete time. Assumptions in these models include a likelihood of transitioning between systems, as well as an equilibrium condition that does not signal the end of an epidemic, while the deterministic models assume an equilibrium state that indicates the end of an epidemic. As a result, they are well-suited for asymptotic analysis, which is concerned with establishing how a vast population of infected people interacts with one another. It is feasible to generate predictions about the stochastic risk of a big or small epidemic using models of the type Markov chain, which assume that each infection happens independently of the preceding one in a probabilistic form. Stochastic differential equations also address particular probabilities and diffusion coefficients in the vulnerable population. Stochastic models, in order to better represent the dynamics of transmission, take into account the high degree of uncertainty in transmission dynamics, providing a wide range of possible outbreak outcomes. However, because of the complexity involved in formulating a mathematical system and data interpretation through stochastic analysis, stochastic models tend to be limited in their application.

3.2 Deterministic versus stochastic

While the deterministic models may capture the basic features of an epidemic, the models cannot address the issue of how accurate the predictions are for illness peaks, in general, both techniques show the same behaviour. The stochastic model, which takes into account the epidemic's minimal and maximum probable ranges, may thus be utilised to answer this issue. Thus, the deterministic technique offers an overall knowledge of the disease's quick progression, but the stochastic framework provides statistical insights into the transmission events, allowing for the study of a broad range of epidemic scenarios. Statistical models are more sensitive to quantitative changes in populations and subpopulations as well as in modelling parameters in this context, and it is crucial to emphasise that there are other methods of dealing with probability in this context (Allen & Lahodny, 2012).

3.3 SIR models

The Kermack-McKendrik SIR model (Barlow & Baird, 2020), the most prominent and archetypal model in mathematical epidemiology, may be used to demonstrate some of the points raised above. S(t), I(t), and R(t) are functions that represent the proportions of susceptible, infected, and recovered people in the population at time t. (measured, for example, in days). The differential equations explain how these quantities change over time.

$$\frac{ds}{dt} = -\beta SI$$
$$\frac{dI}{dt} = -\beta SI - \gamma I$$
$$\frac{dR}{dt} = -\gamma I$$

With relation to the quantities S (t). When considering that all of an infected person's encounters with susceptible persons result in an infection, the transmission parameter b is defined as the average number of infected individuals that this individual will infect over the course of a certain time period. The consequence is that a disease marked by an increase in the letter b is more infectious. Recovery rate c indicates that an infected individual is infectious for an average of 1/c of the time throughout his or her illness. It is calculated as the product of the total infection rate at time t, which is the proportion of the population that will become infected over time, and the time constant. Despite its simplicity, this fundamental model produces some surprising findings that may be used as a starting point for more complicated investigations. It is possible to construct an epidemic curve based on this model by entering the differential equations listed above into any numerical programme for the numerical solution of differential equations and selecting some values for b and c, as well as the starting values S(0), I(0), and R(0), among other things (0). Analytic tools allow us to draw some general conclusions about the model's responses, which we may then apply to other situations. In this study, the following are the most important findings:

As long as the inequality S(0) R0 > 1 is true, there will be no epidemic: the number of infected persons will quickly drop. There will be an epidemic even if the number of affected persons is quite modest at first.

The extent of an epidemic will not be determined by the initial number of infected people, but rather by the initial percentage of susceptible, denoted by the letters S(0) and R0. The final magnitude of the epidemic (the proportion of the population infected) will always be lower than the proportion of the population that was susceptible at the start of the epidemic, S(0), resulting in the presence of a subpopulation of susceptible people who have not been infected at any point in the epidemic. If these findings are confirmed in the real world, they will have significant ramifications.

The notion of herd immunity, in which a big enough percentage of the population is vaccinated, is based on this finding. If we don't get enough people vaccinated, we won't be able to completely stop the outbreak. There are several approaches to meet the requirement that S(0) = S(c/b) and so terminate an epidemic:

(i) Decreasing the transmissibility parameter b; and
(ii) Raising the recovery rate c. Should this model's forecasts be used as a basis for policymaking?

To begin, there are many reasons to be sceptical. In the SIR models, for example, there are several assumptions that are not practical. In the equations, the term bS(t). I(t) obtained from the assumption that every member of the population has an equal probability of encountering another member of the population, which is supported by the evidence. The notion that encounters are more frequent between individuals who are physically and socially close by is ignored. It is implicitly assumed in this model that the population is large since continuous quantities (fractions of population) are expressed as fractions of the population (strictly speaking, infinite). The threshold property (i.e., the occurrence of an epidemic when S(0) (R0 > 1) predicted by the basic SIR model above remains true for practically all epidemiological models, no matter how complex they are designed to be. It is possible to create an adequate equation incorporating the model's parameters for each of these models, with the result that the pathogen will only survive if the number of such combinations exceeds one. An investigation of this kind provides us with information on how to eradicate the virus in a specific model. In spite of the fact that the SIR model may predict the vaccination coverage necessary to prevent the spread of a virus, we would not trust a quantitative forecast unless it was backed by other models that were more comprehensive in their analysis. This means that even incredibly basic models may be able to make some helpful predictions; however, in this case, the idea of prediction must be restricted to refer to just a few fundamental qualitative characteristics that are regarded as dependable in the first place. They must make their models more realistic and complicated in order to be able to make accurate quantitative forecasts.

IV. Forecasting of Covid

The time series data of covid has been apply over the trend analysis through Adv excel.

Table 2. Forecasting of Covid

Time	Day	Total Case
03-10-2022	1	47
03-11-2022	2	60
03-12-2022	3	74
01-03-2013	4	81
01-03-2014	5	84
01-03-2015	6	110
01-03-2016	7	114
01-03-2017	8	137
01-03-2018	9	150
01-03-2019	10	171
01-03-2020	11	223
01-03-2021	12	283
01-03-2022	13	360
01-03-2023	14	434
01-03-2024	15	519
01-03-2025	16	606

Source: https://covid19.who.int

The data has been continuing from 10 March 2020 to 06 May 2021. Total number of occurrences of covid case has been represented correspondingly. The graph has further forecast from June 2021 to June 2022. The future one-year prediction has been drawn in yellow line. Whereas the current data reflected by blue line. The figure below presented in million in y axis whereas the x axis is time in months. Holt winter's method takes into account average along with trend and seasonality while making the time series prediction.

Forecast equation ^yt+h|t=ℓt+hbt
Level equation ℓt=αyt+(1−α)(ℓt−1+bt−1)
Trend equation bt=β∗(ℓt−ℓt−1)+(1−β∗)bt−1
Where ℓtℓt is an estimate of the level of the series at time t,
bt is an estimate of the trend of the series at time t,
α is the smoothing coefficient

The above model is taken in Python and perform the Holt winter's method to execute the code through standard library. The prediction graph is generated below.

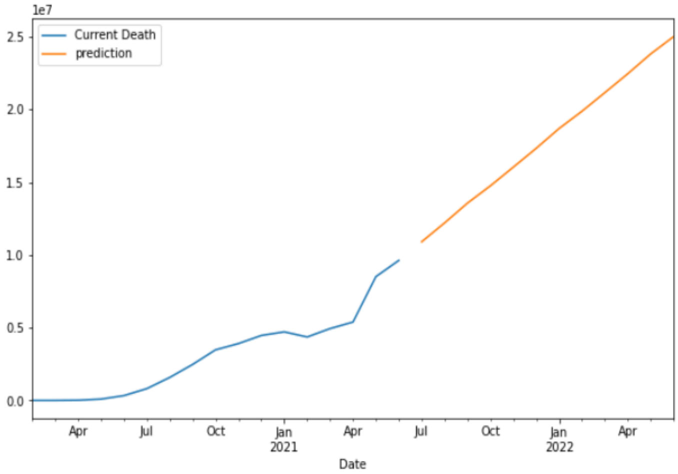

Fig. 2 Covid-19 Prediction Chart
Source: Performed in Python

So, the trend line reflected that the covid case in next year reaches more than 25 lakhs cases. This model used Holt-Winters's method which is **a** highly acceptable time series forecasting method. This method is capable of forecasting the data. As the proposed scenario in this article has apply Data Analysis, Exploration, forecasting whereas the existing research has only exploration based on Data Analysis. The proposed feature profound the prediction and well as the analytical method to this investigation.

V. Conclusion

In this study, both the infectious illness technique and the covid prediction approach are investigated. The purpose of this research is to investigate and conduct an analysis of the prior work that has been employed for infectious illness. The investigation of a theoretical model that has the potential to aid in the prediction of covid. There are a number of infectious diseases that may be passed from person to person. It's possible that insects and other animals may spread some of it. It is possible to get unwell by ingesting pathogen-tainted food or drink, as well as through coming into contact with organisms that are naturally present in the environment. Depending on the sickness that a person has, they may be suffering from a fever, tiredness, and several other symptoms. For the treatment of less severe illnesses, rest and self-care therapies could be sufficient, but for more serious conditions, hospitalisation might be required. Just recently, we have discovered a pandemic of covid illness, which is also an infectious condition. A comprehensive examination of the anticipated patient population will be of great assistance in ensuring that enough housing and other facilities are provided. This article begins by investigating the basic model that is used to forecast and analyse infectious diseases, and then moves on to figure out the specifics of the covid prediction by using Holt-Winters' approach.

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