Mathematical Tools used in Current pandemic crisis

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Introduction

The deadly coronavirus is still propagating over the world, and mathematical models can be used to identify suspected, recovered, and deceased coronavirus sufferers, as well as the population of people who have been tested. Researchers are still unsure whether or not surviving a COVID-19 infection generates long-term immunity, and if so, for how long. We hope that this research will help us better predict the spread of the pandemic in the future. By including isolation class into a mathematical model, we are able to describe the nonlinear properties of COVID-19 infection. The model's formulation is proposed first, followed by an analysis of the model's positivity. The proposed model's local and global stability, which are based on the basic reproduction, are presented.**The proposed model is solved statistically by using nonstandard finite difference (NSFD) scheme and the Runge-Kutta fourth order method.** Finally, certain visualizations of the results can be seen. COVID-19 outbreaks might be caused via interpersonal interactions, as according our findings. As a conclusion, isolating the affected human can reduce the risk of COVID-19 transmitting in the future.

COVID-19 is currently causing immense concern among researchers, governments, and the public in general due to the increasing level of infection spread and the vast

number of deaths that have occurred. Coronavirus, which was first reported in Wuhan, China in December 2019, is an infectious disease caused by a newly discovered coronavirus. COVID-19 is transmitted mostly through droplets that are released when an infected person coughs, sneezes, or exhales. These droplets are too heavy to travel in the air and hit the ground or other surfaces quickly. **Mathematical models are useful for understanding how an infection reacts when it enters a community and assessing whether it will be eradicated or continue under diverse circumstances.**

Objective

Mathematical models are known for supporting the development of possible treatment approaches by providing an approximate description of infectious illness transmission patterns. More accurate disease spread models, as well as ones that are simple to use, are required to develop effective response.

Materials and approaches

We just choose 20 countries with the highest number of COVID-19 cases in the world as of July 1, 2020. We reported the annual number of cases for each country using the **Verhulst–Pearl logistic function formula**. We compared these estimations to the WHO's actual figures from the same span of time. Finally, at t = 18 and t = 40 weeks, the formula was examined for longer-term consistency.

Results

The actual numbers were calculated directly by the Verhulst–Pearl logistic function formula, with only a 0.5 percent error on average for the first month. The predictions for the 40th week were significantly overestimated for all countries in the study and the rest of the world, while the predictions for some countries were still relatively close to the real numbers in the long term forecasting. For the long term, the estimated number for the world itself was nearly 8 times higher than what was actually observed.

Conclusions

The Verhulst–Pearl equation has the advantage of being relatively simple and easy to apply in nursing medicine for assessing hospital demand in the short term of 4–6 weeks, which is usually enough time to reschedule elective therapies and free beds for new waves of patients.

Susceptible–Exposed–Infectious–Recovered Model

Infectious disease spread can also be depicted using a range of models. The "Susceptible–Exposed–Infectious–Recovered" model is a well-defined model in this domain. This is sometimes called **SEIR Model**. The model's central concept is based on clinical progression, epidemiological individuals, and preventive interventions. As a consequence, researchers analyzed further into infectious disease SEIR model, which was coupled with intervention compartments such as treatment, isolation (diagnosis and treatment), and quarantine

Computational results

Only biological approaches can sometimes properly understand the complex models of infectious illness propagation. This is why, in particular, numerical calculations and mathematical analysis are used to aid prevention efforts. Theoretical investigation into these models help biologists in forecasting future model dynamics and defining critical model parameters.

Global initiatives are working on and exploring a wide range of health care solutions to minimize the impact of the pandemic coronavirus on the community. As can be seen, this virus poses a threat to the public and is easily transferred among populations. According to the findings of this research, care services should pay a lot of attention to a set of critical parameters than to less critical criteria. This aims to reduce the number of people who are affected with the disease and to stop the new coronavirus from spreading throughout the population. It could aid community actions aimed at reducing the effects of coronavirus diseases. The computational aspects make some major proposals for healthcare responsibility as the most crucial response method for minimizing illness propagation.

Conclusions

It's challenging to investigate and determine essential model parameters for infectious illness models. Some mathematical techniques are utilized to describe the model dynamics for such systems. Mathematical models and sensitivity analysis, on the other hand, will assist in subsequent research and future predictions concerning model dynamics. The model of coronavirus illness (COVID-19) is extensive, and it involves the use of computational models in order to improve interventions and healthcare strategies. We explored some prior research on this issue in this study and recommended mathematical modelling as a method for further research and

advancement. With the support of some computational simulations, the dynamics of model phases are discussed.

The idea of local sensitivity has been used to calculate the volatility of each model state to model parameters. The model sensitivities are determined employing three different techniques: non-normalizations, half-normalizations, and full-normalizations. These are a significant step forward in terms of understanding model core elements. Computational findings could aid international efforts to reduce the number of people sick with the disease and prevent the spread of new corona viruses across the population. According to our findings, the most effective factors in transmitting coronavirus are the person-to-person transmission rate, quarantined affected rate, and transition rate of affected population to infected individuals. Furthermore, in view of the prospective lack of hospital capacity and its massive impact on national government healthcare efficacy around the world. It appears that a specific strategy, such as putting the vulnerable individuals on quarantine sooner than expected, is required to prevent the hospital beds crisis. As a result, healthcare workers should pay a bit more attention in guarantine zones in order to successfully control the disease. To prevent the virus from being communicated by the touching of shared surfaces, it is strongly recommended that anyone in the quarantine zones be isolated from the others and use only their own equipment, bedroom, and toilet. Unexpectedly, the techniques described here can be further modified and applied to a range of coronavirus models. It can be used to improve future models, treatments, and flu vaccination drives.

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