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Systematic Review of Mathematical Models for Viral Transmission Dynamics: Insights from COVID-19 Studies

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ABSTRACT

The research aims to measure the systematic review related to the mathematical models for viral transmission dynamics. For measuring the research, the study used E views software because the research was based on secondary data analysis. The mathematical models present viral transmission dynamics related to COVID-19 studies. Furthermore, the geographic and social dimensions of viral transmission have been clarified using models that incorporate spatial and network dynamics. The prediction of trends and the assessment of the efficacy of interventions have been made easier by time series analysis. Models evaluating the effect of vaccination on the dynamics of transmission and the development of herd immunity are explored, since vaccination programs have taken center stage in the pandemic response. Behavioral models have investigated how human behavior affects how the epidemic spreads. Sensitivity and uncertainty assessments highlight the importance of recognizing and dealing with model parameter uncertainties. Refinement of the model and continuous research is required due to the dynamic nature of the pandemic and the emergence of new variations. The study summarizes research findings until January 2022. It emphasizes the use of mathematical models in determining crucial factors like the fundamental reproduction number (R_0) and clarifying the effects of treatments like lockdowns and social distance measures. This comprehensive study concludes by highlighting the vital role that mathematical models play in improving our comprehension of the dynamics of COVID-19 transmission. The distribution of resources, policy choices, and public health policies have all benefited from these discoveries. Collaboration between researchers and public health practitioners is crucial to adjusting models and tactics to successfully reduce the effects of the virus as the pandemic progresses.

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1. Introduction

The history of mankind has gained its shape by getting hit by numerous infectious viral outbreaks that have not only affected people in the past but also wiped entire nations from the face of the earth. The list of such lost nations is long and starts from 1715 BC when pharaonic plaques out broke in Egypt. The' cocoliztli' epidemics caused thirteen million deaths and arose in the Mesoamerican region during the 16th century. In 1918, the influenza pandemic erupted and destroyed almost forty million people in Europe, America, and African regions. Between 1957-63, influenza epidemics kept on spreading and erased around two million people globally. The faster rise in advancement in the field of technology and medicine has developed new strategies to work up with these pandemics. It has resulted in enhanced networks of treatment that are growing worldwide. Due to in-depth- knowledge of viral infections, now we can design effective and enhanced drugs, vaccines, and medicine to cope with the effects of these viral infections (Siettos & Russo, 2013).

However, even with such advancements, researchers are still trying to treat and face serious and sudden outbreaks, i.e., Covid-19 viral infection. The reasons for this lie in the fact that viral mutations are never-ending and continuous and the viral disease transmission mechanisms are intricate. Therefore, mathematical models are used to deal with these challenges, which can give insight in solving these problems and making effective decisions. This approach of mathematical modelling was first lectured in 1766 and is defined as the use of multidisciplinary approaches, including field information from biology, mathematics, and epidemiology, to study continuously changing viral dynamics.

This first model was proposed by Daniel Bernoulli who imposed mathematical techniques to make a model dealing with the smallpox outbreak in England (Hernandez-Vargas & Velasco-Hernandez, 2020). He deduced with the help of this model that the age life of a person can be increased up to three years if inoculation methods were used earlier. One of the important needs of such models is the early prediction of viral spread so that the destruction of population masses can be

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hindered. One of the first such type of successful cases was proposed by John Snow, who dealt with London's 1854 epidemic and used spatiotemporal type of data to evaluate the cause of the spread of that pandemic and helped limit the spread and removal of that disease from the susceptible populations (Lin et al., 2020).

The study of viral dynamics of COVID-19 transmission has been done using different mathematical models, including time delay models, SIR models, SARS-CoV-2 models at the microscale level, SIER models, stochastic models, etc. The SIR model divides the infectious populations into three groups: susceptible, infected, and removed populations. This model helps in learning the trend of epidemic disease transmission and its development without considering the period of incubation (Smith et al., 2023). The SIER model used in the COVID-19 outbreak divided the populations into four groups: susceptible, infectious, exposed, and removed. This model takes into account the incubation period and hence is different from the SIR model. In most of the COVID-19 studies, the SIER model is used as it deals with the outbreak by exploring the effect of external factors as well. However, this model is unable to regulate itself.

Therefore, researchers use a combination of different models, like the time series model of prediction with the SIER, to give trends of epidemic spread, prevention, and control. Since COVID-19 symptoms appear afterwards, it has an incubation period and helps study infectious dynamics in a static population (Mizumoto et al., 2020). For the introduction of a time-varying constant into this model, the SIER model is bound to a new version, where the logistic curve is drawn to link the time variation with it. Some models are called agent-based models, as they use different types of data, including the movement, pattern of interactions, and person-to-person changing behaviors, to get more briefed information on spreading COVID-19 viral infections (Meehan et al., 2020).

Moreover, network models are also present that link the mathematical quantifications with the extremely spreading type of infections to deduce results from social connections. The spatial mathematical models have been used to understand the COVID-19 spread in different geographical locations to study the effect in those specific places and determine the impact of geographical interventions on disease spread. Similarly, stochastic models are used to discover the haphazardness and unpredictability of COVID-19 viral dynamics for small regions and limited populations (Kong et al., 2022).

There are certain advantages of using mathematical models for studying viral pandemics. They can help predict a pandemic's results and potential effects so that public health can be preserved. They help assess the intrusions of networking, vaccination strategies, and the effects of quarantine periods. The mathematical models can understand the transmission dynamics with the help of which the never-ending viral mutations can be exposed and incubation rates and recovery rates can be analyzed (Yang et al., 2023).

The strategies used in maintaining public health can be optimized according to the type of pandemic erupted in a region, which, saving time and preventing loss of funds due to implementing less beneficial strategies in the public health sector. The viral groups that are entitled as high-risk groups can be monitored, and they can be altered to minimize the effect as prominently as possible by using mathematical variables in contrast with the biological information (Padmanabhan et al., 2021).

However, there are certain limitations as the use of mathematical models is not that famous right now, but with further advancements and proper research, these models can be found effective in saving masses of people in an epidemic outbreak. The main reason for the limitation is that there is heterogeneity in the world's populations.

Therefore, assessing different parameters in different locations can be challenging, given that the changing results can lead to improper assumptions and cause defects in the literature presented afterward. Also, these models need calibrations and standardization techniques to have completely accurate information with no defects (AlArjani et al., 2022).

2. Literature Review

Researchers claim that the major health crises in the world are caused due to the deadly virus outbreak. The outbreak of covid 19 was one of the deadliest outbreaks that resulted in massive death of humans. also, the role of mathematical models in managing the crisis related to any pandemic condition holds great importance. these models inform the public about the social distancing policies developed to overcome the spread of deadly viruses during the pandemic (Adiga et al., 2020).

Studies reveal that mathematical models aid in assessing the transmission process of any viral diseases. mathematical model uses an advanced computational approach to predict the influence of intervention on viral diseases.in 2020 COVID-19 19was declared a globally spreading virus by the World Health Organization. The increase in public health-related crises due to COVID-19 has raised the mortality rate around the globe (Afzal et al., 2022).studies reveal that the information related to the spread of covid 19 in three phases has been obtained using mathematical models. The transmission dynamics of covid 19 have been predicted using the mathematical models. Knowing about the dynamics behind Covid-19 spreads the possibility of taking effective measures to stop its transmission increases (AlArjani et al., 2022).

Studies highlight that COVID-19 is one of the greatest pandemics faced by people worldwide. During the covid 19 pandemic, all health organizations were united to tackle the spread of this deadly virus. Fractional mathematical models were used during the COVID-19 pandemic onset era to find the cause of the spread of this virus. (Ameen et al., 2021).

Studies claim that mathematical models help to predict the reduction in the transmission rate of covid 19 when a combination of various interventions is used for covid 19 (Biggerstaff et al., 2020).studies suggest that the health sectors have been greatly affected because of covid 19. To overcome the economic problems due to covid 19, various vaccines have been developed to overcome its transmission. Artificial therapies have been developed to tackle the pandemic of Covid 19. To understand the dynamics related to Covid-19, a mechanistic viral dynamics model is used in pharmacological studies (Desikan et al., 2022).

Studies predict that the mathematical modeling techniques help assess the mechanism behind covid 19 fast spread. the modelers dealing with the modelling techniques predict the measure used to control the spread of cov0id 19 shortly (Gnanvi et al., 2021). studies reveal that the onset of covid 19 took place in Wuhan. Since the onset of covid in 2019 it has spread worldwide and attained the position of pandemic virus. Various statistical and theoretical models have been used to understand various parameters related to COVID-19 transmission (Gumel et al., 2021).

Studies show that AI is used in mathematical models to develop various solutions to solve the complexity of COVID-19 19virus. AI-based models predict the complexity of covid 19 in detail and explain the reason behind its sudden spread (Hassan et al., 2022).also, several quantitative approaches have been used to urgently tackle the spread of viral diseases like covid 19. To determine the nature of SARS-COV in every patient, the use of in-host mathematical models is made in clinical procedures (Hernandez-Vargas & Velasco-Hernandez, 2020). studies claim that predictive mathematical models are used for predicting the future of the COVID-19 virus. The predictive model effectively explains the epidemiological features responsible for the spread of the deadliest virus.by predictive mathematical models, the process of controlling the COVID-19 spread becomes easier (Jewell et al., 2020). scholars explain that certain mathematical models suggest that patients recovering from covid 19 develop poor immunity. if the patient of covid 19 gets exposed to the virus after being recovered, the chances of geeing infected are still higher (Kassa et al., 2020).

Studies reveal that the outbreak of Covid-19 in China possessed a great burden on health sectors.to understand this infectious virus, whereas mathematical models are used by pharmacologists working on the SARS-COV virus. these models provide great ID in managing the outbreak of this virus (Lin et al., 2020).studies highlight that the emergence of covid 19 has taken place from the SARS-COV-2. SARS-COV-2 is a syndrome of respiratory track that resulted in the pandemic of covid 19. The use of a mathematical model is common for obtaining the initial data related to covid 19 spread (Meehan et al., 2020). studies suggest that covid 19 has different dynamics that are understandable by using an AI-based mathematical model. The AI-based model provides large databases that help to understand the nature of the virus (Mohamadou et al., 2020).

Studies reveal that after the breakout of COVID-19 19, professional healthcare workers have made full efforts to protect people's lives. health organizations have actively played a part in controlling the spread of deadly viruses.ML and deep learning algorithms are used in the present era to comprehend the data obtained by mathematical models regarding the covid-19 (Saleem et al., 2022).

Scholars predict that the propagation patterns of the COVID-19 virus are predicted using mathematical models. The data obtained through the models suggest that lockdowns and social distancing practices greatly helped reduce the number of coronavirus cases. The reduction in mortality rate is observed due to various preventive practices against COVID-19 (Sameni, 2020).

Scholars predict that quarantining people during the COVID-19 pandemic helped reduce the spread of covid 19.the mathematical models used for developing effective strategies to overcome the spread of covid 19 are used in public health domains. during the covid 19 pandemic, there was a surge in the use of face masks that greatly reduced the spread of the virus from infected patient (Xiang et al., 2021).

Studies claim that it is very difficult to control the spread of covid 19 without an effective vaccine development. Also, human mobility is the major source of transmission of the virus from one human to another. limiting the mobility of humans in an area is one of the strategies to stop the spread of the virus (Zhang et al., 2022). Furthermore, an optimized mathematical model controls the covid 19 epidemic. the SEIR-HC is a technology-based optimized model that predicts that the severity associated with Covid 19 is more as compared to SARS (Zhu et al., 2021).

3. Methodology

The research study determined that systematic review related to the mathematical models also presents COVID-19 studies between them. the research was based on secondary data analysis to determine the research study used E-views software and generated informative results, including descriptive statistics, unit root test analysis, variance analysis, equality test analysis, histogram and state analysis.

3.1 Time Series Analysis

By applying mathematical models to the time series analysis of COVID-19 data, researchers are able to forecast future trends, gauge the success of treatments, and spot possible infection waves.

3.2 Vaccination Modelling

Since the release of COVID-19 vaccinations, mathematical models have been used to evaluate how vaccination campaigns affect herd immunity, transmission dynamics, and the pandemic's overall trajectory.

3.3 Behavioural Models

These models examine how behavioural shifts (such as mask wear or adherence to social separation) impact the progression of the pandemic. They do this by including human behaviour as a dynamic element.

3.4 Sensitivity and Uncertainty Analysis

These studies are essential due to the uncertainties in parameter values. Due to these investigations, researchers can better grasp how resilient model predictions are to changes in important parameters. The world has faced the acute impact of the coronavirus for the past four years. This virus resulted in a pandemic all over the world and caused great and pathetic suffering to all humanity, regardless of origin or habitat. We have got some insights from the studies of the coronavirus. The studies were conducted with the intervention of mathematical models, which can help understand and explain the ways of viral transmission inside the host. It is evident from scientific studies that virus can only get into the host once it finds the proper way to transmit (Biggerstaff et al., 2020). These kinds of Systematic reviews from studies related to mathematical models can have the following applications as follows:

3.4.1 To spread awareness about ways of transmission of the virus

As we know, viruses are considered acellular entities until they find some host so they can use host machinery. Then, it is regarded as a cellular entity because it can reproduce inside the host. To prevent any viral infection, it is quite mandatory to spread awareness about modes of transmission of viruses to the host body. For example, human immunodeficiency virus, which is abbreviated as HIV, is the main cause of AIDS; it spreads through unprotected sexual contact, breastfeeding, saliva transfer, and other ways; if these ways are prevented somehow, the transmission of the virus can be reduced to the host body (Yang et al., 2023). We got such insights from COVID-19 that if these preventive measures are constantly taken, then the spread of the virus will be automatically minimized. The best application of such a Systematic Review study is that it can help people spread accurate information about ways of transmission of the virus (Padmanabhan et al., 2021).

3.4.2 Help to understand the causes of viral infections

A mathematical review is quite helpful for understanding the transmission and causes of viral infections such as COVID-19. Mathematical reviews are far better than other reviews because mathematical reviews can be written in the form of digits, thus rendering quantities data that can be easily processed and analyzed. As we know, the mode of action of every virus is quite different as compared to another virus because each virus has its receptor in the body. For example, the receptor site for HIV is white blood cells (Gnanvi et al., 2021). When we study mathematical reviews of the transmission of viruses, we can get an effective idea about the main causes and receptor sites of these viruses. When there is a better idea about the causes and receptors of viruses, the transmission of viruses can be minimized at a better rate. This application of Mathematical review of the transmission of the virus is the result of insights from COVID-19.

3.4.3 Measurements for improvement of the Healthcare sector

The condition of any Healthcare centre is decisive in providing effective treatment to patients in any particular area. We know that viruses can survive in extreme conditions of temperature, light, and other factors, so there is a dire need to improve our healthcare sectors to provide improved and effective treatment to patients with viral infections (Cao & Liu, 2022). The data obtained from a mathematical review of the transmission of the virus can be easily used to plan what changes are required in the healthcare sector to cope with the increasing challenge of viral diseases across the world. The insights that we got from COVID-19 have also helped us realize that automated technologies should be used in the healthcare sector because there is a higher chance of transmission of viral diseases from patient to physician. This aspect has enabled us to move away from traditional means of diagnosis of viral diseases. All of these factors brought improvement in Healthcare sectors for treating viral infections and can be effectively used in the future as well (Aguiar et al., 2022; Gumel et al., 2021).

3.4.4 Prediction of a virus outbreak in the future

The mathematical review related to the study of the transmission of the virus can not only help combat the presence of any existing virus but also help predict the menace of any virus outbreak shortly. This study can help to understand any possible mutation before the onset of mutation, which can accurately predict the outbreak of a virus before time. This is the insight that we got from the pandemic of COVID-19 because, in the past, we had to face different variants of coronavirus, which made the vaccine null and void to cause any positive effect on the body. From this past experience, scientists have accelerated the efforts to design a way to predict the risk of any kind of virus outbreak before time (Smith et al., 2023). When the basic mutation or causes of mutation are studied under the umbrella of Mathematical review, this study can predict any possible change in mutation before time thus when that particular mutation occurs, the community must have early prediction of it to adopt preventive measures which can minimize the pathetic and drastic effects of virus breakout in any community at any particular area. This is an effective application of Mathematical review related to the study of the transmission of viruses into a host body (Meehan et al., 2020).

3.4.5 Understanding the effectiveness of public measures

We know that some viral diseases cannot be eliminated until and unless the cooperation of society or the community, when there is any viral breakout in any community, some measures are suggested to be followed for the prevention of viral infection and thus reducing the risk of spread of such viral infections for example during COVID-19, it was suggested by medical healthcare sectors to maintain an appropriate distance from fellow people to allay the risk of getting this virus from one another. When we study the mathematical review related to the transmission of the virus into the host body, we can get an idea about the effectiveness of public measures and strategies and whether they worked for analyzing the causes and transmission of viral infections. Suppose there is no suitable response or effectiveness of these preventive measures. In that case, there should be the formulation of new health policies and strategies that can be proven effective for preventing and treating different viral infections such as COVID-19. All of these aspects are possible just because of insights from studies on COVID-19. All of these applications suggest great importance in using the mathematical approach for studying the transmission of the virus into a host body (Lin et al., 2020).

4. Descriptive statistic

Table 1: Result of Descriptive statistic

	VTD1	VTD2	VTD3	COVID19
Mean	1.392656	1.346832	1.261976	1.676502
Median	1.299100	1.321100	1.231100	1.231220
Maximum	2.342100	2.122100	2.121300	9.543300
Minimum	0.342100	1.111000	0.876100	0.321100
Std. Dev.	0.409135	0.226654	0.236154	1.678202
Skewness	0.611808	2.096928	1.670064	4.347315
Kurtosis	4.876219	7.446165	8.495917	20.97972
Jarque-Bera	5.226497	38.91335	43.08496	415.4864
Probability	0.073296	0.000000	0.000000	0.000000
Sum	34.81640	33.67080	31.54940	41.91255
Sum Sq. Dev.	4.017397	1.232926	1.338445	67.59268
Observations	25	25	25	25

The above results describe that descriptive statistical analysis results represent that mean values, median values, maximum values, minimum values, and standard deviation of each variable. the result also represents the probability value, the sum of the square deviation rates of each indicator. The result describes that the mean value of VID1 is 1.3926, the median rate is 1.299, and the standard deviation rate of VTD1 is 40% deviate from mean. According to the result, its probability rate of 0.07 shows a 7% significant level between them. Similarly, the VTD2, VTD3 are all factors of independent variable according to the result its mean values are 1.34, 1.26 average value of mean. The standard deviation rates are 22%, 23% and 1.67 positive deviations from the mean. The probability value is 0.000, showing that there is a 100% significant level between them. the sum of square deviation rate of VTD2, VTd3 is 1.232 and 1.3384 respectively. COVID-19 is the main dependent variable. According to the result, its mean value is 1.67, and the standard deviation rate is 1.67, respectively. The probability value is 0.000, which shows a 100% significant level between the dependent and independent variables. the sum of the square deviation rate of COVID-19 present that 67.59 shows a positive deviation from the mean.

5. Systematic Models

Understanding and forecasting the dynamics of infectious disease transmission depend heavily on mathematical models. Many models have been used in the context of COVID-19 to model and examine the virus's propagation. The following are some salient features and conclusions from research on COVID-19. The SEIR Model for infectious disorders, one popular compartmental model is Susceptible-Exposed-Infectious-Removed (SEIR). Based on the state of infection, it separates the population into several compartments. Key factors like the basic reproduction number (R_0), which indicates the typical number of subsequent infections brought on by one infected person, may be estimated using SEIR models. These models mimic how individual agents, in this example, people interact with their surroundings.

Agent-based models have been applied to assess the effects of different interventions, such as lockdowns and social distance policies, and to incorporate variation in interaction patterns. To implement efficient control measures, it is important to comprehend the geographical distribution of the pathogen. Geographical data is included in spatial models to examine the virus's regional and community distribution. Within particular social networks, network models investigate the transmission dynamics. These models are useful in identifying high-risk nodes, which are places or people critical to the virus's transmission.

6. Unit Root Test Analysis

Table 2: Result of Test Analysis

Null Hypothesis: VTD1 has a unit root			
Exogenous: Constant			
Lag Length: 0 (Automatic - based on SIC, maxlag=5)			
		t-Statistic	Prob.*
Augmented Dickey-Fuller test statistic		-5.868280	0.0001
Test critical values:	1% level	-3.737853	
	5% level	-2.991878	
	10% level	-2.635542	
*MacKinnon (1996) one-sided p-values.			

The above result describes that the unit root test analysis result represents t statistic values and that the probability values of each test statistic included critical values of t statistic. The values of t statistics that 1%, 5% and 10% level its t statistic values are -3.737, -2.991 and -2.6355, showing each factor's negative t statistic rates. Similarly, the overall probability value is 0.0001, showing that there are 100% significant values between them.

Table 3: Result of Augmented Dickey-Fuller Test Equation

Augmented Dickey-Fuller Test Equation				
Dependent Variable: D(VTD1)				
Method: Least Squares				
Sample (adjusted): 2 25				
Included observations: 24 after adjustments				
Variable	Coefficient	Std. Error	t-Statistic	Prob.
VTD1(-1)	-1.217739	0.207512	-5.868280	0.0000
C	1.703142	0.301776	5.643732	0.0000
R-squared	0.610183	Mean dependent var		0.003671
Adjusted R-squared	0.592464	S.D. dependent var		0.651107
S.E. of regression	0.415657	Akaike info criterion		1.161743
Sum squared resid	3.800957	Schwarz criterion		1.259914
Log-likelihood	-11.94091	Hannan-Quinn criteria.		1.187788
F-statistic	34.43671	Durbin-Watson stat		1.985586
Prob(F-statistic)	0.000007			

The above result represents the Dickey-Fuller test equation, which represents each variable's coefficient values, standard error value, t statistic, and probability value. the VTD1's coefficient value is -1.2177, the t-statistic value is -5.868, and the probability value is 0.000, which shows a negative but significant link between them.

The R square value of 0.610 shows that 61% model fit for analysis, the adjusted R square value is 59%, the F statistic value is 34.43, and the probability value is 0.0000, which shows a 100% significant value between them. The mean dependent variable rate is 0.0036. The Schwarz rate shows a 1.25 per cent positive rate between them.

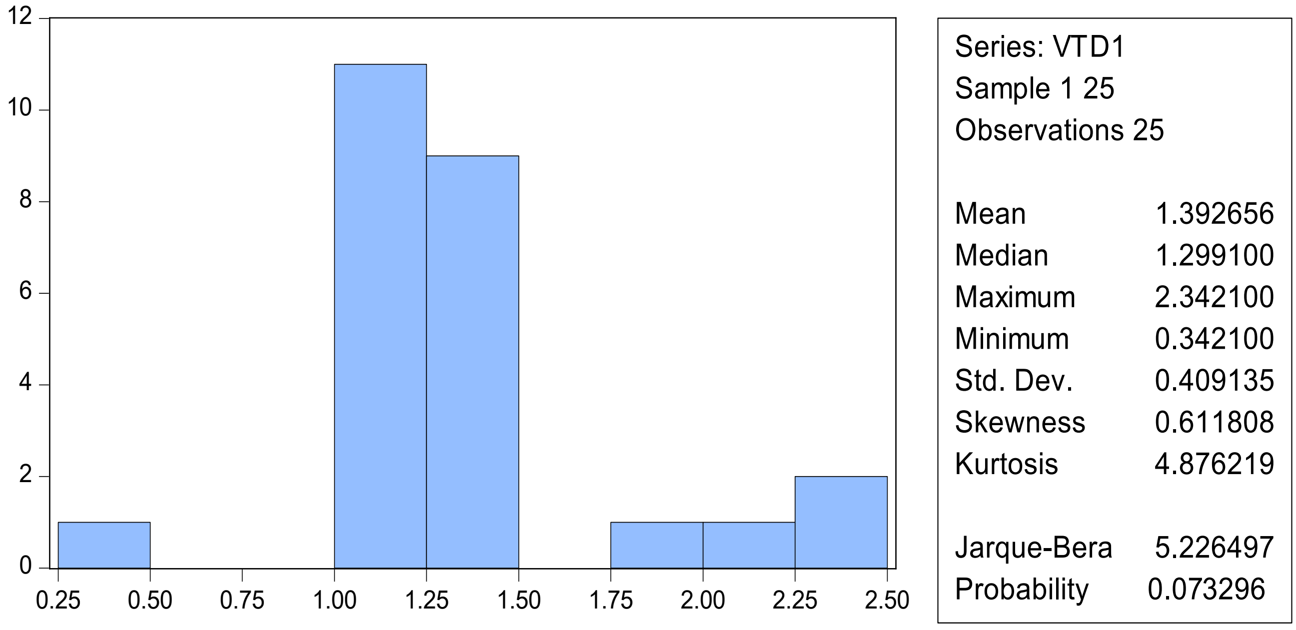
7. Equality test

Table 4: Result of Test for Equality of Means

Test for Equality of Means of VTD1			
Categorized by values of VTD1 and VTD2 and VTD3 and COVID19			
Sample: 1 25			
Included observations: 25			
Method	df	Value	Probability
Anova F-test	(11, 13)	60.21678	0.0000
Analysis of Variance			
Source of Variation	df	Sum of Sq.	Mean Sq.
Between	11	3.940069	0.358188
Within	13	0.077328	0.005948
Total	24	4.017397	0.167392

the above result describes the equality test between the dependent and independent variables. The result shows that the ANOVA F-test rate is 60.21, and the probability value is 0.000, which shows positive and significant rates of the F-test. The result represents that analysis of variance shows that the sum of squares also the mean square rate; the result shows that between and within also the total value of the sum of squares. The values of the sum of squares are 3.94, 0.07, and 4.01, and the mean square values are 0.35, 0.005, and 0.167, showing that 35% and 16% are average mean values.

8. Histogram and state



Series: VTD1
Sample 1 25
Observations 25

Mean	1.392656
Median	1.299100
Maximum	2.342100
Minimum	0.342100
Std. Dev.	0.409135
Skewness	0.611808
Kurtosis	4.876219
Jarque-Bera	5.226497
Probability	0.073296

Figure 1: Result of Histogram and state

The above result describes that histogram and state values also present that graph represents the overall result. The mean value is 1.39, the median rate is 1.299, the maximum value is 2.34, and the minimum value is 0.34. The result represents that the standard deviation rate is 40%, which deviates from the mean. The probability value is 0.07, which shows a 7% significant level between them. The graph shows that the vertical side shows the frequency level starting at 0 and ending at 12 points. The horizontal side shows 0.25 and ends at 2.50, respectively. The above blue line represents the histogram and state between them.

9. Variance analysis

Table 5: Result of Variance analysis

Null Hypothesis: VTD1 is a martingale

Sample: 1 25
Included observations: 24 (after adjustments)
Heteroskedasticity robust standard error estimates
Lags specified as grid: min=2, max=16, step=1

Joint Tests	Value	df	Probability
Max |z| (at period 2)*	1.780934	24	0.6891

Individual Tests

Period	Var. Ratio	Std. Error	z-Statistic	Probability
2	0.408136	0.332333	-1.780934	0.0749
3	0.241019	0.454029	-1.671659	0.0946
4	0.240375	0.522577	-1.453613	0.1461
5	0.218213	0.567731	-1.377038	0.1685
6	0.216944	0.600606	-1.303776	0.1923
7	0.169404	0.627664	-1.323312	0.1857
8	0.119426	0.651935	-1.350708	0.1768
9	0.240686	0.674872	-1.125122	0.2605
10	0.121402	0.698557	-1.257733	0.2085
11	0.183124	0.724030	-1.128235	0.2592
12	0.157934	0.750338	-1.122249	0.2618
13	0.104575	0.776055	-1.153816	0.2486
14	0.088220	0.800392	-1.139167	0.2546
15	0.087547	0.823056	-1.108615	0.2676
16	0.106669	0.844000	-1.058449	0.2899

*Probability approximation using studentized maximum modulus with parameter value 15 and infinite degrees of freedom

the above result demonstrates that variance analysis between the variables describes the values, df rates, and the probability value of the joint test and individual test, including var ratio, standard error, Z statistic, and the probability value of each period. The joint test represents that the value is 1.7809 and the probability value is 68%, respectively. In each period, the variance ratio shows 40%, 24%, 21%, 11%, 8%, and 10%, respectively. The probability values of 7%, 14%, 19%, 17%, 26%, and 28% respectively show a significant level between them.

10. Conclusion

To sum up, mathematical models have been essential in helping us understand the dynamics of COVID-19 transmission. By using different modelling techniques, scientists have been able to learn important things about how the virus spreads, how treatments work, and how the pandemic may develop. Important conclusions include estimating vital factors like the fundamental reproduction number (R_0), identifying high-risk people or regions, and evaluating the efficacy of public health initiatives. A thorough investigation of several facets of the pandemic has been made possible by the adaptability of models, including agent-based models, behavioral models, time series analysis, spatial models, network models, SEIR models, and time series analysis. These models have played a key role in directing choices about public health, formulating policies, and allocating resources as efficiently as possible. Significantly, current research endeavors aim to address the dynamic character of the pandemic and the implementation of vaccination programs by introducing novel models or optimizing preexisting ones. Furthermore, modelling assumptions should take into account changing factors and potential limits, as shown by uncertainty and sensitivity studies. It's crucial to remember that COVID-19 research is a quickly developing subject, and since my previous update, new knowledge and models may have been developed. Research suggest reading current systematic reviews, meta-analyses, or original research publications for the latest information.

By discussing different possible applications of mathematical review models for the transmission of viruses into the host body, we concluded that it can be a bright perspective for reducing viral infections worldwide. The joint efforts of epidemiologists, mathematicians, and specialists in public health to apply mathematical modelling to COVID-19 research have substantially contributed to our capacity to navigate and address the difficulties presented by the epidemic. More research and modelling initiatives will be necessary to ensure effective public health responses and modify tactics as the situation changes. In the study of viral transmission dynamics, mathematical models have shown to be invaluable in providing important insights into the spread of infectious. The main topic of this comprehensive study is the use of several mathematical models to comprehend the dynamics of COVID-19, a worldwide pandemic that has presented hitherto unheard-of difficulties. Important modelling techniques have been used to analyses many aspects of the pandemic, including agent-based models, behavioral models, time series analysis, spatial models, network models, SEIR models, and time series analysis.

11. References

Adiga, A., Dubhashi, D., Lewis, B., Marathe, M., Venkatramanan, S., & Vullikanti, A. (2020). Mathematical models for covid-19 pandemic: a comparative analysis. *Journal of the Indian Institute of Science*, *100*(4), 793-807.

Afzal, A., Saleel, C. A., Bhattacharyya, S., Satish, N., Samuel, O. D., & Badruddin, I. A. (2022). Merits and limitations of mathematical modeling and computational simulations in mitigation of COVID-19 pandemic: A comprehensive review. *Archives of Computational Methods in Engineering*, *29*(2), 1311-1337.

Aguiar, M., Anam, V., Blyuss, K. B., Estadilla, C. D. S., Guerrero, B. V., Knopoff, D., Kooi, B. W., Srivastav, A. K., Steindorf, V., & Stollenwerk, N. (2022). Mathematical models for dengue fever epidemiology: A 10-year systematic review. *Physics of life reviews*, *40*, 65-92.

AlArjani, A., Nasseef, M. T., Kamal, S. M., Rao, B. S., Mahmud, M., & Uddin, M. S. (2022). Application of mathematical modeling in prediction of covid-19 transmission dynamics. *Arabian Journal for Science and Engineering*, *47*(8), 10163-10186.

Ameen, I. G., Ali, H. M., Alharthi, M. R., Abdel-Aty, A.-H., & Elshehabey, H. M. (2021). Investigation of the dynamics of COVID-19 with a fractional mathematical model: A comparative study with actual data. *Results in Physics*, *23*, 103976.

Biggerstaff, M., Cowling, B. J., Cucunubá, Z. M., Dinh, L., Ferguson, N. M., Gao, H., Hill, V., Imai, N., Johansson, M. A., & Kada, S. (2020). Early insights from statistical and mathematical modeling of key epidemiologic parameters of COVID-19. *Emerging infectious diseases*, *26*(11).

Cao, L., & Liu, Q. (2022). COVID-19 modeling: a review. *medRxiv*, 2022.2008. 2022.22279022.

Desikan, R., Padmanabhan, P., Kierzek, A. M., & van der Graaf, P. H. (2022). Mechanistic models of COVID-19: Insights into disease progression, vaccines, and therapeutics. *International journal of antimicrobial agents*, *60*(1), 106606.

Gnanvi, J. E., Salako, K. V., Kotanmi, G. B., & Kakaï, R. G. (2021). On the reliability of predictions on Covid-19 dynamics: A systematic and critical review of modelling techniques. *Infectious Disease Modelling*, *6*, 258-272.

Gumel, A. B., Iboi, E. A., Ngonghala, C. N., & Elbasha, E. H. (2021). A primer on using mathematics to understand COVID-19 dynamics: Modeling, analysis and simulations. *Infectious Disease Modelling*, *6*, 148-168.

Hassan, A., Prasad, D., Rani, S., & Alhassan, M. (2022). Gauging the impact of artificial intelligence and mathematical modeling in response to the COVID-19 pandemic: A systematic review. *BioMed Research International*, *2022*.

Hernandez-Vargas, E. A., & Velasco-Hernandez, J. X. (2020). In-host mathematical modelling of COVID-19 in humans. *Annual reviews in control*, *50*, 448-456.

Jewell, N. P., Lewnard, J. A., & Jewell, B. L. (2020). Predictive mathematical models of the COVID-19 pandemic: underlying principles and value of projections. *Jama*, *323*(19), 1893-1894.

Kassa, S. M., Njagarah, J. B., & Terefe, Y. A. (2020). Analysis of the mitigation strategies for COVID-19: from mathematical modelling perspective. *Chaos, Solitons & Fractals*, *138*, 109968.

Kong, L., Duan, M., Shi, J., Hong, J., Chang, Z., & Zhang, Z. (2022). Compartmental structures used in modeling COVID-19: a scoping review. *Infectious diseases of poverty*, *11*(1), 72.

Lin, Y.-F., Duan, Q., Zhou, Y., Yuan, T., Li, P., Fitzpatrick, T., Fu, L., Feng, A., Luo, G., & Zhan, Y. (2020). Spread and impact of COVID-19 in China: a systematic review and synthesis of predictions from transmission-dynamic models. *Frontiers in Medicine*, *7*, 321.

Meehan, M. T., Rojas, D. P., Adekunle, A. I., Adegboye, O. A., Caldwell, J. M., Turek, E., Williams, B. M., Marais, B. J., Trauer, J. M., & McBryde, E. S. (2020). Modelling insights into the COVID-19 pandemic. *Paediatric respiratory reviews*, *35*, 64-69.

Mizumoto, K., Kagaya, K., & Chowell, G. (2020). Early epidemiological assessment of the transmission potential and virulence of coronavirus disease 2019 (COVID-19) in Wuhan City, China, January–February, 2020. *BMC medicine*, *18*(1), 1-9.

Mohamadou, Y., Halidou, A., & Kapen, P. T. (2020). A review of mathematical modeling, artificial intelligence and datasets used in the study, prediction and management of COVID-19. *Applied Intelligence*, *50*(11), 3913-3925.

Padmanabhan, R., Abed, H. S., Meskin, N., Khattab, T., Shraim, M., & Al-Hitmi, M. A. (2021). A review of mathematical model-based scenario analysis and interventions for COVID-19. *Computer methods and programs in biomedicine*, *209*, 106301.

Saleem, F., Al-Ghamdi, A. S. A.-M., Alassafi, M. O., & AlGhamdi, S. A. (2022). Machine learning, deep learning, and mathematical models to analyze forecasting and epidemiology of COVID-19: A systematic literature review. *International journal of environmental research and public health*, *19*(9), 5099.

Sameni, R. (2020). Mathematical modeling of epidemic diseases; a case study of the COVID-19 coronavirus. *arXiv preprint arXiv:2003.11371*.

Siettos, C. I., & Russo, L. (2013). Mathematical modeling of infectious disease dynamics. *Virulence*, *4*(4), 295-306.

Smith, D. R., Chervet, S., Pinettes, T., Shirreff, G., Jijón, S., Oodally, A., Jean, K., Opatowski, L., Kernéis, S., & Temime, L. (2023). How have mathematical models contributed to understanding the transmission and control of SARS-CoV-2 in healthcare settings? A systematic search and review. *Journal of Hospital Infection*, *141*, 132-141.

Xiang, Y., Jia, Y., Chen, L., Guo, L., Shu, B., & Long, E. (2021). COVID-19 epidemic prediction and the impact of public health interventions: A review of COVID-19 epidemic models. *Infectious Disease Modelling*, *6*, 324-342.

Yang, H., Lin, X., Li, J., Zhai, Y., & Wu, J. (2023). A Review of Mathematical Models of COVID-19 Transmission. *Contemporary Mathematics*, 75-98.

Zhang, M., Wang, S., Hu, T., Fu, X., Wang, X., Hu, Y., Halloran, B., Li, Z., Cui, Y., & Liu, H. (2022). Human mobility and COVID-19 transmission: a systematic review and future directions. *Annals of GIS*, *28*(4), 501-514.

Zhu, H., Li, Y., Jin, X., Huang, J., Liu, X., Qian, Y., & Tan, J. (2021). Transmission dynamics and control methodology of COVID-19: A modeling study. *Applied mathematical modelling*, *89*, 1983-1998.