UDC 005 **DOI: 10.18413/2518-1092-2022-7-4-0-3**

Agha H.R.[1]
Taha A.T.[2]

METHODS OF THE EPIDEMICS SPREAD MATHEMATICAL MODELING

[1] University of Mosul, 41002, Al Majmoaa Street, Mosul, Iraq
[2] Belgorod State National Research University, 85 Pobedy St., Belgorod, 308015, Russia

e-mail: israagha83@gmail.com

Abstract
Modelling the mechanisms of epidemic spread and predicting its evolution can significantly reduce the damage caused by a pandemic. This paper presents a review of SIR mathematical models used for Epidemics modelling over the past years. Mathematical modelling of epidemic spread makes an important contribution to disease control. In this review, we focus on show that mathematical models can be used to predict the future of an epidemic process; however, models may also have a more theoretical use as explanatory tools elucidating fundamental principles of transmission and the factors driving epidemic behaviour. One of the simplest and most fundamental of all epidemiological models is the so-called SIR model which is based upon calculating.

Keywords: mathematical modeling; COVID-19; SIR; epidemic; pandemic
For citation: Agha H.R., Taha A.T. Methods of the epidemics spread mathematical modeling // Research result. Information technologies – T.7, №4, 2022. – P. 25-33. DOI: 10.18413/2518-1092-2022-7-4-0-3

Агха Х.Р[1]
Таха А.Т.[2]

МЕТОДЫ МАТЕМАТИЧЕСКОГО МОДЕЛИРОВАНИЯ РАСПРОСТРАНЕНИЯ ЭПИДЕМИЙ

[1] Университет Мосула, 41002, улица Аль-Маджмуа, Мосул, Ирак
[2] Белгородский государственный национальный исследовательский университет,
ул. Победы д. 85, г. Белгород, 308015, Россия

e-mail: israagha83@gmail.com

Аннотация
Моделирование механизмов распространения эпидемии и прогнозирование ее эволюции может значительно уменьшить ущерб, причиняемый пандемией. В этой статье представлен обзор математических моделей SIR, использовавшихся для моделирования эпидемий за последние годы. Математическое моделирование распространения эпидемии вносит важный вклад в борьбу с болезнями. В этом обзоре мы сосредоточимся на том, чтобы показать, что математические модели могут быть использованы для прогнозирования будущего эпидемического процесса; однако модели могут также иметь более теоретическое применение в качестве объяснительных инструментов, разъясняющих фундаментальные принципы передачи и факторы, определяющие эпидемическое поведение. Одной из самых простых и фундаментальных из всех эпидемиологических моделей является так называемая модель SIR, которая основана на расчете доли населения в каждом из трех классов (Восприимчивые - Больные - Вылеченные) и определении темпов перехода между этими классами. Представлены модели эпидемий SIR, которые являются классической эпидемической моделью, разработанной для инфекционных заболеваний.

Ключевые слова: математическое моделирование; COVID-19; SIR; эпидемия; пандемия
Для цитирования: Агха Х.Р., Таха А.Т. Методы математического моделирования распространения эпидемий // Научный результат. Информационные технологии. – Т.7, №4, 2022. – С. 25-33. DOI: 10.18413/2518-1092-2022-7-4-0-3

INTRODUCTION

COVID-19 is a pandemic respiratory illness. The disease spreads from human to human and is caused by a novel coronavirus SARS-CoV-2. The coronavirus COVID-19 was founded in almost every country in the world. In December 2019, a pneumonia outbreak took place in Wuhan (China), as a result of which a COVID-19 strain was first detected in a nucleic acid analysis in a patient with the pneumonia. By the end of June 2020, the pandemic captured 188 countries, with more than 10 million of detected infection cases, and 505,500 people have died. The 2020th year will be remembered for a long time thanks to the emergence of a new coronavirus – COVID-19. According to the cases detected, the Russian Federation is the third in ranking of infected countries, behind the United States and Brazil, with 484,630 infection cases by June 9, 2020 (see Table 1). At the Russian Federation, the rapid spread of coronavirus infection COVID-19 was also recorded in. Despite the relatively low number of infected, COVID-19 was recorded in all regions of Russia Although a peak of the disease in the world seems to have been passed, no decrease in the number of detected cases has been observed for a sufficiently long period [1, 2].

Table

COVID-19 statistics for five leading countries in the number of cases detected by June 9, 2020 [20]

Таблица

Статистика COVID-19 по пяти странам-лидерам по количеству случаев, выявленных к 9 июня 2020 года [20]

Country	Infected		Deaths	Cured
	Total	New cases		
USA	1961,185	17,250	111,007	524,855
Brazil	707,412	15,654	37,134	396,737
Russia	485,253	8,595	6,141	241,917
Great Britain	288,834	1,213	40,680	1,257

In particular, the first attempt to model and hence predict or explain patterns dates back over 100 years, although it was the work of Kermack and McKendrick that established the basic foundations of the subject [3].

The SIR model developed by Kermack and McKendrick is widely used to describe epidemics, which is based on a scheme of epidemic transition of basic variables from one category to another. The variables used as basic variables are those that denote the number of individuals: those susceptible (S) become infected (I), then recover (R). The SIR model is represented by a system of 1st order coupled differential equations that describe the time dependence of the underlying concepts, where the coupling is given by conditions that stipulate the sum of the variables and their derivatives. Models which implement the concept of epidemic transition have gained wide popularity and development, so the SIR class of models today also contains varieties: SIRS, SEIR, SIS, MSEIR, etc. [4].

MATHEMATICAL MODELING

The COVID-19 hit the world hard. Much research is still ongoing to study the effect and spread of COVID-19 along with producing the vaccine and cure. Over the last years, an intensive worldwide effort is speeding up the developments in the establishment of a global surveillance network for combating pandemics of emergent and re-emergent infectious diseases. Scientists from different fields extending from medicine and molecular biology to computer science and applied mathematics have teamed up for rapid assessment of potentially urgent situations. Toward this aim mathematical modeling plays an important role in efforts that focus on predicting, assessing, and controlling potential outbreaks [5]. Mathematical modeling has become a powerful and important tool to understand infectious disease dynamic behavior and to improve control of the disease in. a population. These models are often described by many forms such as: *SI*, *SIS*, *SIR*, or *SIRS* models, where *S* stands for susceptible subpopulation, *I* is infected subpopulation, and *R* is recovered subpopulation, as shown in figure.

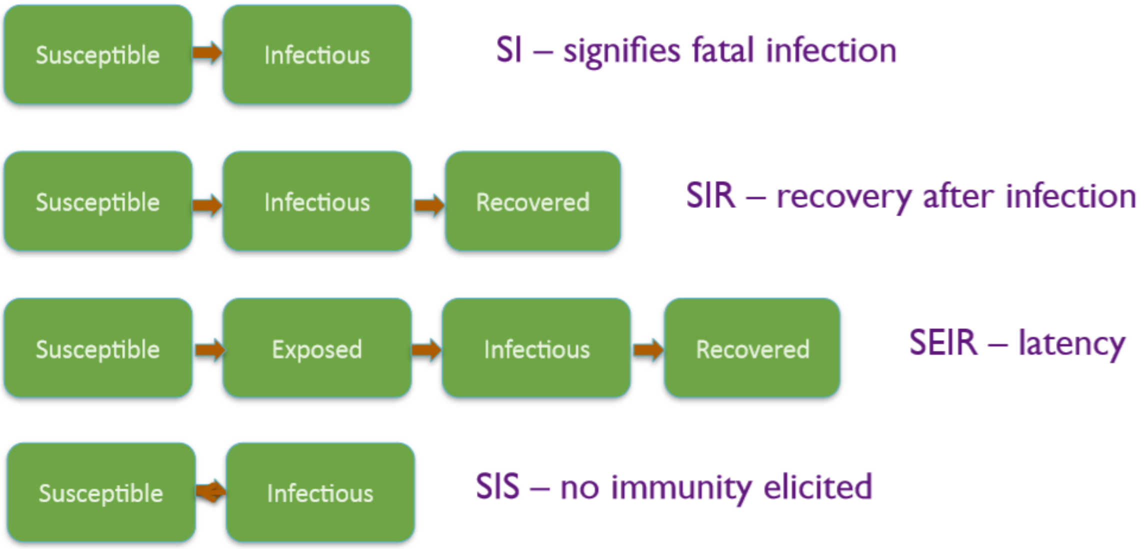

Fig. SIR Models Structure
Рис. Структура моделей SIR

THE SIR MODEL

One of the simplest, yet powerful, disease models is the standard Susceptible-Infected Recovered (SIR) model, which was first introduced by Kermack and McKendrick. For decades, the standard SIR model has been extended to various forms by adding different compartments to suit the biological, spatiotemporal and social aspects of the disease dynamics or to study the impact of intervention strategies on the disease transmission dynamics in different communities. For instance, it has been extended to SIR models with diffusion, contaminated environment, delay terms, several strains of infection, and multiple routes of infection [6].

The SIR model is a classical model of disease transmission within a population. It can be modified to account for several important population dynamics, such as death rate, immigration or birth rate, recovery, and immunity - but even the most basic model has powerful public health applications. Here we examine the most basic model, a good starting point for further study. We assume disease spread depends on population size; infection is instantaneous; no one is resistant to the disease at the start; immunity, once gained, is permanent; and that the disease is not fatal.

The fundamental relation of the SIR model is the following:

$$\mathrm{N} = \mathrm{S(t)} + \mathrm{I(t)} + R(t), \tag{1}$$

where N is the total population size, taken to be constant; S(t) is the size of the susceptible population; I(t) is the size of the infected population; and R(t) is the size of the removed population.

The SIR model works by placing all individuals in the population into one of three classes at any given time: individuals susceptible to disease, infected individuals, and "removed" individuals. The removed class counts those individuals that are not infected and not susceptible; in other words, immune, quarantined, or dead individuals. The SIR model can be modified to account for change in overall population over time; here, however, we look at a model with a constant population. This assumption is reasonable for low mortality epidemics which run their course much faster than a human population can reproduce [7].

In a standard SIR model, the host population is divided into susceptible, infected and recovered individuals, denoted by S(t), I(t) and R(t), respectively. These quantities track the numbers of individuals in each compartment over different time periods. The standard SIR model without birth and death is represented by the set of ordinary differential equations:

$$\frac{dS}{dt} + \frac{dI}{dt} + \frac{dR}{dt} = 0, \tag{2}$$

The SIR model is a classical model of disease transmission within a population. It can be modified to account for several important population dynamics, such as death rate, immigration or birth rate, recovery, and immunity - but even the most basic model has powerful public health applications. Here we examine the most basic model, a good starting point for further study. We assume disease spread depends on population size; infection is instantaneous; no one is resistant to the disease at the start; immunity, once gained, is permanent; and that the disease is not fatal.

The SIR model works by placing all individuals in the population into one of three classes at any given time: individuals susceptible to disease, infected individuals, and "removed" individuals. The removed class counts those individuals that are not infected and not susceptible; in other words, immune, quarantined, or dead individuals. The class is significant; in other SIR model variants, it can account for both permanent or temporary immunity acquired from vaccination or from having the disease. Again, however, we choose to use the simplified model where immunity (or lack of susceptibility) is permanent, and describe the recovery rate as the parameter σ. Our assumption is a reasonable one for diseases like u, for which vaccines have been developed only recently and which generally do not afflict an individual more than once in the course of an epidemic. Individuals may move from one class to another; for example, an individual may move from the infected class to the removed class upon recovery. Thus, the model accounts for the interdependency of the different classes within the population. The SIR model can be modified to account for change in overall population over time; here, however, we look at a model with a constant population. This assumption is reasonable for low mortality epidemics which run their course much faster than a human population can reproduce [7].

In a standard SIR model, the host population is divided into susceptible, infected and recovered individuals, denoted by S(t), I(t) and R(t), respectively. These quantities track the numbers of individuals in each compartment over different time periods. The standard SIR model without birth and death is represented by the set of ordinary differential equations:

$$\begin{aligned} \frac{dS}{dt}(t) &= -\beta S(t)I(t) \\ \frac{dI}{dt}(t) &= \beta S(t)I(t) - \gamma I(t) \\ \frac{dR}{dt}(t) &= \gamma I(t) \end{aligned} \tag{3}$$

Where βis the average number of susceptible individuals infected by one infectious individual per contact per unit of time (the transmission rate), and γ is the average number of infected individuals recovered per unit of time (recovery rate) [8].

A SHORT REVIEW

[2] to create proper scenarios of disease development in Moscow (the largest number of detected cases in Russia) and Novosibirsk region (moderate detection rate) is an important step in taking appropriate measures to curb the epidemic in the regions. inverse problems of finding un known parameters of mathematical models SEIR-HCD and SEIR-D of COVID-19 spread is investigated with additional information about the number of detected cases, mortality, self-isolation coefficient, for the city of Moscow and Novosibirsk region. In SEIR-HCD the population is divided into seven groups, and in

SEIR-D into five groups with similar characteristics and transition probabilities depending on the specific region of interest. An identifiability analysis of SEIR-HCD is made to reveal the least sensitive unknown parameters as related to the additional information and the parameters are corrected by minimizing some objective functional which is made by stochastic methods (simulated annealing, differential evolution, and genetic algorithm).

[4] for mathematical modelling of the spread of the Covid-19 epidemic, the application of specific Covid-19 propagation functions is considered, based on constrained growth functions. The Covid-19 spread functions show high accuracy in approximating statistical data, which demonstrates the good adequacy of these functions in principle. Application of the Covid-19 propagation functions makes it possible to quantitatively describe the basic concepts of the epidemic and conduct a comparative parametric analysis of the epidemic's spread and predict the development of the epidemic. Comparison of parameter values makes it possible to identify differences in indicators and growth rates, based on which the results of epidemic control can be assessed.

[8] the accuracy of such dynamics can be significantly is improved by including global effects of host movements in disease models. The extended SIR model was parameterized using a two-step model-fitting algorithm. The extended SIR model significantly outperformed the standard SIR model and revealed oscillatory behaviors with an increasing trend of infected individuals. The extended SIR model assumes three possibilities for susceptible individuals traveling outside of their community:

- They can return to the community without any exposure to the infection.
- They can be exposed and develop symptoms after returning to the community. as a result of this model, the analytics and predictive accuracy of disease models can be significantly improved by incorporating the global dynamics of the infection.

[9], propose a model of the spread of COVID-coronavirus infection in Moscow and in regional Russia to choose a simplest nonlinear discrete equation describing logistic growth was chosen as the model which contains only two parameters that are chosen based on statistical data at the initial stage of the epidemic. The first parameter is a rate of the increase in the number of cases, the second parameter is a normalization multiplier that only estimates the maximum potential number of residents who may become ill. Four different scenarios of the epidemic development are proposed for Moscow and regional Russia. For each scenario, the growth rates of the population infected with COVID-19 coronavirus were founded, the peak time was calculated, the maximum increase in cases at the peak and the total number of cases during the epidemic were found. Mathematical modeling of the dynamics of the spread of coronavirus infection in the regions of Russia showed that it is delayed by 6 days compared to Moscow, and the growth rates of the number of cases is slightly less than the growth rate in Moscow. The simulation results were compared with the spread of coronavirus in China, in a number of European and Asian countries, and the United States to check the adequacy of the mathematical model.

[10] the local and global dynamics of SIR model has been studied with saturated treatment rate and Beddington-DeAngelis type incidence rate. The analysis of the SIR model shows that there exists only two non-negative equilibrium points (disease free equilibrium (DFE) and endemic equilibrium (EE)). The presence of endemic equilibrium point that is not only globally asymptotically stable but is also independent of the initial values of the susceptible and infected individuals. This refers to the restriction of the disease within endemic zone. The existence of Hopf bifurcation of model is investigated by using Andronov-Hopf bifurcation theorem. Further, numerical simulations are done to exemplify the analytical studies. It has been observed that the number of infected individuals decreases as the treatment rate increases and a decrease in infected individuals with both decline in incidence rate α and an enhancement of inhibition rate (preventive measures) i.e., β. The disadvantage is the limitation on resource increases, this means that for effective treatment the resource limitation should be minimized.

[11] a new mathematical model is proposed that considers the infected individuals using various rate coefficients such as transmission, progression, recovery, and vaccination. By performing stability analysis, the equilibrium with proofs, the local and global behavior of the model is discussed. Since the mathematical model cannot precisely predict the real details of transmission and a better understanding of the variations in trends of different compartments after the outbreak of the disease, so, the simulations

with the available data is running. It is concluded that vaccination is one of the best effective strategies or solutions that is to be adopted so as to have the spread or transmission of epidemic in control.

[12] In order to determine the most efficient strategy that reduce the infection rate to a minimum level while optimizing the cost deploying a therapy and preventive vaccine that is used to control the disease progression. The optimal control in epidemics for a SIR model governed by an ODE system with time delay (representing the incubation period) is developed. Two control strategies in the optimal control model is used namely: the vaccination and treatment strategies. The optimal control is derived to show the effectiveness as well as the applicability of the model for different values of the time delay, the first-order necessary conditions. Also, to show that the model is sensitive to the delays representing the incubation period, a numerical simulation is performed.

[13], a delayed SIR model with generalized incidence function and distributed delay is analyzed as the contact between infected individuals and healthy ones does not result in an immediate infection to reflect the time that it takes to have an infection after the contact. The model also included the two main types of disease control measures: vaccine and treatment. when the disease is endemic, in the absence of the vaccination and treatment, then there are two possible scenarios: (a) if the number of susceptible population is below the threshold, then the disease can be controlled by vaccination and treatment; (b) if the susceptible population is above the threshold, then the disease will persist in the population. This finding reflects the limited capability of the control measure to eradicate the disease if the population is too large.

[14] an SIR model as an extension of the model presented in the work of Ghersheen et al19 is designed and observed the effect of density dependence population regulation on disease dynamics. The complete local and global stability analysis of two boundary equilibrium points revealed that, for small carrying capacity, the disease-free equilibrium point is always stable so a disease cannot persist in a small population, but for relatively large carrying capacity under some conditions, we have one globally stable endemic equilibrium point. The existence of an endemic equilibrium point guarantees the persistence of the disease with a possible future threat of any outbreak in the population. Because the equilibrium point loses its stability and bifurcates to the coexistence equilibrium point, it is worthwhile to show the existence of the coexistence equilibrium in that case to understand the complete dynamics of the disease.

[15], a mathematical model of COVID-19 is formulated and discuss the disease free state and endemic equilibrium of the model. Based on the sensitivity indexes of the parameters, control strategies are designed to reduce the densities of the infected classes but don't satisfy the criteria of threshold condition of the global stability of disease free equilibrium. It is concluded that the disease cannot be eradicated with present resources and the human population needs to learn how to live with corona because the endemic equilibrium of the disease is globally asymptotically stable. For validation of the results, numerical simulations are obtained using fourth order Runge-Kutta method. it is recommended to address the effect of vaccination on the global stability of disease free state.

[16] David and Lang developed a mathematical model (SIR), for the spread of infectious in a given population over a time but some more realistic factors have not been accounted for in their model. Their realistic assumptions will give better understanding of the modelling epidemics if included. The model gives a reasonable and sound results incorporating the assumptions to enhance the analysis of the spread of diseases under different conditions. The results show that the modified model proved to be more efficient than the existing SIR model. However, due to the inclusion of new assumptions to the existing model, the modified model shows faster decrease in infected population and high recovery rate than the existing SIR model.

[17] adopted a new COVID-19 SIR model in the form of differential equations containing three classes; Susceptible S(t), Infected I(t), and Recovered R(t) with the Convex incidence rate and calculate the disease-free and endemic equilibrium. Also, the basic reproduction number R0 is derived for the model. Furthermore, the Global Stability is calculated using the Lyapunov Function construction, while the Local Stability is determined using the Jacobian matrix. The numerical simulation is calculated using the Non-Standard Finite Difference (NFDS) scheme. In the numerical simulation, the data from Pakistan

to simulate how S(t), I(t), and R(t) protection, exposure, and death rates affect people with the elapse of time [15]

[18] a discrete logistic equation describing the increase in the number of cases is used to model the spread of COVID-19 coronavirus in Russian regions and in Moscow, the simulation results were compared with the spread of coronavirus in China, in a number of European and Asian countries, and the United States to check the adequacy of the mathematical model. A comparative analysis of growth rates of COVID-19 infected population for different countries and regions is presented. Various scenarios of the spread of COVID-19 coronavirus in Moscow and in the regions of Russia are considered. For each scenario, curves for the daily new cases and graphs for the increase in the total number of cases were obtained, and the dynamics of infection spread by day was studied. Peak times, epidemic periods. As a result, the number of infected people at the peak and their growth were determined.

[19] propose a mathematical model is STQIR (Susceptible, Traced, Quarantine, Infectious, Recovered) model. The form of the model is a nonlinear differential system with five variables. The step of the method i.e., compute the variables positifity, boundedness of solutions, and the basic reproduction number that computed using next generation matrix. Then the basic reproduction number will be used for testing the local stability of the disease free equilibrium using Routh Hurwitz criteria to examine its epidemiological relevance. This work also investigate the sensitivity of the model with respect to the variation of each one of its parameters and is tested in application to the recent data on Covid-19 outbreak in Central Java Province, Indonesia.

[20] the possibility to predict the spread of COVID-19 in Russia is studied to predict the time instant when the number of infected achieves its maximum (peak). Such a partial prediction allows one to use simple epidemics models: SIR and SEIR. The prediction is carried out according to public WHO datasets from March 10 to April 20, 2020. Comparison of forecast results by SIR and SEIR models are given. In both cases, the peak number of infected persons while maintaining the current level of quarantine measures is forecasted at the end of May 2020 or later. It coincides with the real data obtained in May-June, 2020. The results confirm usefulness of simple nonlinear dynamical models for partial prediction of complex epidemic processes

[21] use a modified system of differential equations constructed according to the SIR compartmental model. The optimal values of the model parameters, that describe the statistical data precisely, were found. The analysis of the current situation of the COVID-19 coronavirus epidemic in China was made, which led to the efficiency mark of the existing measures to struggle against the virus.

CONCLUSION

Epidemic situation analysis with its theoretical back round, decision making, treatment strategies and many other related things can never be complete without the influence of the analysis made with numerical data and probabilistic values of the parameters involved. The models may be designed with the accurate statistics or random data, the associated models determine the measures with analytical and/or numerical results to deal with a unique model either deterministic or stochastic with an appropriate method to derive and solve the mathematical formulation of the problem. The SIR family of models are powerful and flexible tools form understanding the spread of disease and staging public health interventions. Even the most basic of these models, can give us crucial figures. We can find whether the epidemic even occurs, the maximum number of infected individuals at any point in time and hence the severity of the epidemic, and the total number of individuals who get sick over the course of the epidemic. such as the law of mass action (indicating that disease spread is proportional to the population), the complete lack of immunity at the beginning of the epidemic, instantaneous infection (no latency period), and the short duration of the disease relative to lifespan.

References

1. Khrapov P.V., Loginova A.A. Comparative analysis of the mathematical models of the dynamics of the coronavirus COVID-19 epidemic development in the different countries. International Journal of Open Information Technologies ISSN: 2307-8162 vol. 8, no.5, 2020.
2. Krivorot'ko O.I., Kabanikhin S.I., Zyat'kov N.Yu., Prikhod'ko A.Yu., Prokhoshin N.M., Shishlenin M.A. Mathematical Modeling and Forecasting of COVID-19 in Moscow and Novosibirsk Region. ISSN 1995-4239, Numerical Analysis and Applications, 2020, Vol. 13, No. 4, pp. 332–348.
3. Keeling M.J., Danon L. Mathematical modelling of infectious diseases. British Medical Bulletin 2009; 92: 33–42, DOI:10.1093/bmb/ldp038.
4. Molodetskaya K. and Tymonin Yu. Mathematical Modelling of an Epidemic Based on Covid-19 Spread Functions. IDDM-2021: 4th International Conference on Informatics & Data-Driven Medicine, November 19–21, 2021 Valencia, Spain.
5. Siettos C.I., Russo L. Mathematical modeling of infectious disease dynamics. To cite this article: Constantinos I. Siettos & Lucia Russo (2013) Mathematical modeling of infectious disease dynamics, Virulence, 4:4, 295-306, DOI: 10.4161/viru.24041.
6. Azrul Azim Mohd Yunus, Arif Asraf Mohd Yunus and Muhammad Safwan Ibrahim. Future of Mathematical Modelling: A Review of COVID-19 Infected Cases Using S-I-R Model. Baghdad Science Journal. 2021, Vol. 18 No.1 (Suppl. March).
7. Alger C., Todd K. The SIR Model of Disease Spread. December 2015.
8. Hadeel AlQadiID, Majid Bani-Yaghoub. Incorporating global dynamics to improve the accuracy of disease models: Example of a COVID-19 SIR model. Editor: Yury E. Khudyakov, Centers for Disease Control and Prevention, UNITED STATES PLOS ONE | https://doi.org/10.1371/journal.pone.0265815 April 8, 2022.
9. Koltsova E.M., Kurkina E.S., Vasetsky A.M. Mathematical Modeling of the Spread of COVID-19 in Moscow and Russian Regions. https://www.researchgate.net/publication/340826395. April 2020.
10. Dubey B., Dubey P., Dubey U.S. Dynamics of an SIR Model with Nonlinear Incidence and Treatment Rate. Applications and Applied Mathematics: An International Journal (AAM). Available at http://pvamu.edu/aam. Appl. Vol. 10, Issue 2 (December 2015), pp. 718–737.
11. Jonnalagadda J.M. Epidemic Analysis and Mathematical Modelling of H1N1 (A) with Vaccination. Research Article. https://doi.org/10.1515/msds-2020-0143 Received August 28, 2021; accepted January 3, 2022.
12. Moussa Barro, Aboudramane Guiro and Dramane Ouedraogo. Optimal control of a SIR epidemic model with general incidence function and a time delays. CUBO A Mathematical Journal. Vol.20, No 02, (53–66). June 2018.
13. Lamrani Alaoui E.A., Tilioua M., Tridane A. Global stability analysis for a generalized delayed SIR model with vaccination and treatment. https://doi.org/10.1186/s13662-019-2447-z. 2019:532.
14. Ghersheen S., Kozlov V., Tkachev V., Wennergren U. Mathematical analysis of complex SIR model with coinfection and density dependence. https://doi.org/10.1002/cmm4.1042. *Comp and Math Methods*. 2019;1:e1042. Wiley online library.com/journal/cmm4 © 2019 John Wiley & Sons, Ltd.
15. Zamir M., Nadeem F., Alqudah M.A., Abdeljawad T. Future implications of COVID-19 through Mathematical modeling. Journal Pre-proof. DOI: https://doi.org/10.1016/j.rinp.2021.105097 Reference: RINP 105097. 27 November 2021.
16. Adamu H.A., Muhammad M., Jingi A.M., Usman M.A. Mathematical modelling using improved SIR model with more realistic assumptions International Journal of Engineering and Applied Sciences (IJEAS) ISSN: 2394-3661, Volume-6, Issue-1, January 2019.
17. Rahim ud Din, Algehyne E.A. Mathematical analysis of COVID-19 by using SIR model with convex incidence rate. Available online 19 February 2021. 2211-3797/© 2021 The Authors. Published by Elsevier B.V.
18. Koltsova E.M., Kurkina E.S., Vasetsky A.M. Mathematical Modeling of the Spread of COVID-19 in Moscow and Russian Regions.
19. Sutimin W., Sasongko P.S. Mathematical modeling and analysis of COVID-19 transmission dynamics in Central Java Province, Indonesia. ISNPINSA 2020. Journal of Physics: Conference Series 1943 (2021) 012139. IOP Publishing IOP Publishing doi:10.1088/1742-6596/1943/1/012139.
20. Tomchin D., Fradkov A. Partial Prediction of the Virus COVID-19 Spread in Russia Based on SIR and SEIR Models.doi: https://doi.org/10.1101/2020.07.05.20146969. July 7, 2020.
21. Khrapov P.V., Loginova A.A. Mathematical modelling of the dynamics of the Coronavirus COVID-19 epidemic development in China. International Journal of Open Information Technologies ISSN: 2307-8162 vol. 8, no.4, 2020.

Agha Hothayfa Rabea, Assistant, College of Engineering, Department of Computer Engineering, University of Mosul
Taha Asraa Tariq, postgraduate student of the Department of Mathematical and Software Information Systems

Агха Хотайфа Рабеа, ассистент, инженерный колледж, кафедра компьютерной инженерии, университет Мосула
Таха Асраа Тарик, аспирант кафедры математического и программного обеспечения информационных систем