Journal of Namibian Studies, 33 S3 (2023): 5471-5486 ISSN: 2197-5523 (online)

Mathematical Modeling And Analysis Of COVID-19: A Study Of New Variant Omicron

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Abstract

We have devised an innovative mathematical framework to delve deep into the Omicron variant's behavior within the realm of COVID-19. Our model, a meticulous study of the Omicron variant, unfolds its mathematical implications. We've unraveled that this Omicron model maintains local asymptotic stability as long as the basic reproduction number (R0) stays below the critical threshold of 1. Remarkably, if R0 remains less than or equal to 1, our model gracefully attains global asymptotic stability, specifically at the disease-free equilibrium.

To unearth potential patterns of infection waves or stratification, we took a leap into the world of second-order differential equations. This expansion endowed us with a richer comprehension of the disease's dynamics and its inherent periodicity. We didn't stop there; we ventured into the realm of fractional stochastic modeling, conducting an extensive numerical analysis fueled by real-world data from South Africa spanning November 1, 2021, to January 23, 2022. Our model parameters were meticulously calibrated to mirror the actual scenario during that period, with an estimated basic reproduction number (R0) hovering around R0 ≈ 2.1107, mirroring South Africa's ground reality.

But we did not just crunch numbers; we dissected the data further to discern which factors exerted the most influence over R0. Employing the PRCC method in a global sensitivity analysis, we pinpointed the key drivers behind the virus's spread. These insights are invaluable for shaping targeted public health strategies that can either bolster or curtail the virus's transmission.

When it comes to simulating our model, we didn't rely on run-of-the-mill approaches. Instead, we harnessed a novel numerical scheme, meticulously tailored for solving piecewise fractional differential equations. Our simulations manifested as graphical representations that vividly underscore the effectiveness of adhering to recommended measures advocated by esteemed organizations such as the World Health Organization (WHO). These measures, including social distancing, mask-wearing, frequent handwashing, and avoiding gatherings, emerge as crucial tools for mitigating the infection's propagation within the population.

2010 AMS Classification: 93A30

Keywords and phrases: Mathematical model, Omicron, Stability analysis, Estimation of parameters, Numerical results, and discussion.

Article type: Research article

The Omicron variant is a recently identified mutation of the SARS-CoV-2 virus, responsible for the COVID-19 pandemic. South Africa was the first to detect this variant in November 2021, and it swiftly disseminated to various European nations, causing a notable surge in reported cases. Unlike the more severe impact associated with the original COVID-19 virus and other variants like the Delta strain, the Omicron variant seems to induce milder symptoms. However, its defining feature lies in its exceptionally high transmissibility, surpassing both the original virus and the Delta variant. The Center for Disease Control and Prevention (CDC) has expressed concerns that individuals carrying the Omicron virus can transmit it to others, irrespective of their vaccination status or the presence of noticeable symptoms [1].

Symptoms commonly linked to the Omicron variant encompass a range of complaints, including body aches, fatigue, runny nose, cough, congestion, and more. As a response to its emergence in South Africa, many nations worldwide implemented precautionary measures, including the suspension of air travel to and from South Africa, in an attempt to contain the virus's spread.

1. Researchers and epidemiologists have exerted extensive efforts, delving into the intricacies of coronavirus infection dynamics within communities. They've harnessed a plethora of mathematical modeling techniques to gain insight into and take control of the disease's trajectory, particularly in light of emerging variants. Take, for example, a meticulous mathematical model that dissected the early stages of COVID-19's spread in China [2]. Likewise, an optimal control analysis honed in on managing the disease in Pakistan, leveraging real-world COVID-19 case data for precision [3].

In the face of the COVID-19 virus's rapid transmissibility, experts have advocated strategies like isolation and quarantine as potent tools for infection rate reduction. These measures have been subjected to scrutiny through mathematical modeling lenses [4]. Moreover, the profound impact of lockdown measures on disease control has undergone rigorous assessment via mathematical modeling, employing tangible data from regions like Italy and France [5]. Furthermore, researchers have employed SEIR modeling techniques to scrutinize reported COVID-19 cases in Nigeria, dissecting and comparing different scenarios to unveil vital insights [7].

The spotlight has also turned towards the intriguing field of fractional calculus, which has garnered increasing attention due to its unique attributes and relevance across diverse scientific domains [12]. In the realm of COVID-19, scientists have harnessed fractional calculus to tackle various epidemiological facets of the virus [15], [16], [17]. It has also been instrumental in unraveling the intricate wave dynamics shaped by the pandemic [18], [19]. Notably, studies have explored COVID-19 models embellished with time delays and stochastic differential equations [20], along with a diverse array of fractional operators [13], [14]. Fractional models have been tailor-made to fathom COVID-19 infections in distinct geographic regions, spanning from Brazil [29] and Argentina [31] to Spain [34], each offering a unique lens into the virus's behavior and impact.

This research is centered on unraveling the intricacies of the Omicron variant of COVID-19, offering a meticulously formulated mathematical model designed to capture its distinctive dynamics. The model's parameters are fine-tuned using real infection data harvested from South Africa, meticulously covering the timeframe spanning from November 1, 2021, to January 2022. In a bid to comprehend the potential existence of multiple infection waves, the study advances to craft a sophisticated second-order differential epidemic model. Further enriching the analysis, a sensitivity study is carried out to spotlight the pivotal parameters that wield the most influence over the elusive basic reproduction number (R0). The research doesn't stop at deterministic modeling; it delves into the realm of stochastic modeling, unveiling consequential insights.

To enhance clarity and structure, the remainder of this work unfolds as follows: Section 2 unfurls the intricacies of the model formulation, with a dedicated spotlight on the distinct features characterizing the Omicron variant. Transitioning into Section 3, the study pivots to unveil model-driven outcomes, encompassing a comprehensive exploration of local and global stability analyses and the meticulous identification of endemic equilibria.

2. Model framework

With the advent of the Omicron variant of COVID-19, originating in South Africa, stringent safety measures and protocols swiftly returned to the forefront. The populace found itself obligated to strictly adhere to Standard

Operating Procedures (SOPs), which encompassed the obligatory practice of social distancing and donning face masks. Furthermore, recognizing the imminent threat posed by this new variant, numerous nations implemented stringent travel bans on flights to and from South Africa, aiming to contain the rapid proliferation of this formidable foe.

In the quest to unravel the enigmatic nature of the Omicron variant's infection dynamics, we embarked on a pioneering journey. Armed with data gleaned from the South African context, we painstakingly crafted a novel mathematical model, poised to illuminate the intricacies of this viral adversary. Our model casts a comprehensive net over the entire population, denoted as N(t), and methodically partitions it into six distinctive epidemiological classes.

These classes unfold as follows:

1. S(t): An emblem of individuals not yet infectious, signifying those who remain untouched by the virus's reach.
2. E(t): This category comprises the exposed individuals, individuals who've had close encounters with asymptomatic, symptomatic, or Omicron-infected individuals, yet have not manifested symptoms themselves.
3. Ia(t): A separate enclave hosts asymptomatic individuals, carriers of the virus who stealthily evade visible clinical symptoms.
4. Is(t): The symptomatic individuals form a distinctive group, prominently displaying the clinical symptoms of COVID-19 infection.
5. Io(t): A notable segment houses individuals infected with the Omicron variant, presenting evident clinical symptoms. These individuals hold a unique position, capable of transmitting the virus to others, irrespective of vaccination status or symptom manifestation.
6. R(t): Last but not least, a sanctuary is designated for the recovered individuals, those who've emerged victorious from the clutches of infection, whether it was asymptomatic, symptomatic, or Omicron-induced.

Mathematically, this division of the population is expressed as $N(t) = S(t) + E(t) + Ia(t) + Is(t) + Io(t) + R(t)$. To illustrate the flow of transmission between these compartments, please refer to Figure 1. The mathematical representation of these transmission dynamics is provided through a set of differential equations.

This approach allows us to comprehensively model the spread of the Omicron variant and gain insights into its behavior within the population.:

$$dS(t)/dt=\Lambda-\beta(Ia+\kappa Is+\nu Io)/N\ S-\mu S,$$
$$dE(t)/dt=\beta(Ia+\kappa Is+\nu Io)/N\ S-(\tau+\mu)E,$$
$$dIa(t)/dt=\tau\psi E-(\delta1+\mu)Ia,$$
$$dIs(t)/dt=(1-\psi-\phi)\tau E-(\delta2+\mu+d1)Is,$$
$$dIo(t)/dt=\phi\tau E-(\delta3+\mu)Io,$$
$$dR(t)/dt=\delta1Ia+\delta2Is+\delta3Io-\mu R,$$

...(1)

subject to the non-negative initial conditions. In the given system (1), several parameters play essential roles in shaping the dynamics of the model. Let's break down the meaning and significance of these parameters:

- Λ represents the birth rate of the susceptible population, indicating the rate at which new individuals enter the population.
- μ represents the natural death rate, signifying the rate at which individuals pass away due to non-infection-related causes.
- β denotes the rate at which healthy individuals become infected after encountering asymptomatic infected individuals.
- κ and ν represent the probabilities of infectiousness for symptomatic and Omicron variant-infected individuals, respectively.
- τ signifies the incubation period, indicating the duration between exposure to the virus and the appearance of clinical symptoms.
- At a rate of $\tau\psi$, exposed individuals who do not display clinical symptoms transition to the asymptomatic infected class.

- Similarly, individuals who exhibit clinical symptoms of the common COVID-19 infection transition to the symptomatic infected class at a rate of $(1 - \psi - \phi)\tau$. Here, ψ and ϕ denote the proportions that contribute to the asymptomatic and Omicron variant-infected classes, respectively, while the remainder enter the symptomatic class.
- Recovery rates for different categories of individuals are denoted by $\delta 1$ (asymptomatic), $\delta 2$ (symptomatic), and $\delta 3$ (Omicron variant-infected), representing the rates at which individuals recover from their respective infections.
- The parameter d1 represents the rate at which individuals in the symptomatic class succumb to the infection and die.
- It's important to note that all newborn individuals are initially considered susceptible to infection, as they enter the population.

These parameters collectively define the transitions and interactions within the mathematical model, providing insights into the dynamics of infection, recovery, and mortality within the population.

3. Fundamental analysis of the model

Here, we study some of the important results related to the analysis of the model (1). We can get the total dynamics of the system (1) by adding all their equations, given by

$$dN/dt=\Lambda-\mu N-d1Is\leq\Lambda-\mu N. \quad ...(2)$$

After solving the above Eq. (2), we get the following result,

$$N(t)=\Lambda\mu+(N0-\Lambda/\mu)e-\mu t. \quad ...(3)$$

We can see that (3) tends to Λ/μ if $t\to\infty$. Also, it shows that the variables given in the model (1) are nonnegative for each value of $t\geq0$. So, all the started solutions of the model (1) will remain positive for each $t\geq0$. Therefore, the model given in (1) is mathematically well-posed and so its dynamical analysis can be studied in the following feasible region,

$$\Pi=\{(S,E,Ia,Is,Io,R)\in R6+:S+E+Ia+Is+Io+R\leq\Lambda\mu\}.$$

Next, we are trying to show the solution positivity and boundedness of the model (1). The following results are presented:

3.1. Positivity and boundedness

Theorem 1

The variables given in system (1) at $t=0$ ($S(0)>0,E(0)>0,Ia(0)>0,Is(0)>0,Io>0,R(0)>0$) then the solution for $t>0$ of the variables involved in the system will be positive for every $t>0$.

Proof

To show the result, let start from the equation of the model (1),

$dSdt=\Lambda-\lambda(t)S-dS\geq-(\lambda(t)+\mu)S$,

where $\lambda(t)=\beta(Ia+\kappa Is+\nu Io)N$. After taking the integration, we have the following result,

$S(t)\geq S0\exp(-\int t0(\lambda(\tau)+\mu))d\tau>0$.

In the above inequality, $S0$ denotes the initial population which is positive obviously, and thus, $S(t)$ is positive. We can easily follow the above mentioned procedure, to show the positivity of the rest of variables in the model (1), i.e., $E(t)>0$, $Ia(t)>0$, $Is(t)>0$, $Io(t)>0$ and $R(t)>0$.

Further, to show the boundedness of the solution of the system (1), we discussed in the above theorem that the solution is positive and we can use Eq. (3) that for $t\to\infty$ is Λ/μ, the solution is bounded.

3.2. Equilibrium points and its stability analysis

The disease-free equilibrium of the system (1) can be denoted by $E0$ and is given by,

$E0=(S0,0,0,0,0,0)=(\Lambda\mu,0,0,0,0,0)$.

Next, we use the next-generation approach for the computation of the basic reproduction number $R0$ The computation of the basic reproduction number $R0$ can be obtained through the next generation approach . We have the following results.

$$F = \begin{pmatrix} 0 & \beta & \beta\kappa & \beta\nu \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{pmatrix}, \; V = \begin{pmatrix} \mu+\tau & 0 & 0 & 0 \\ -\tau\psi & \mu+\delta_1 & 0 & 0 \\ \tau(\phi+\psi-1) & 0 & \mu+d_1+\delta_2 & 0 \\ -\tau\phi & 0 & 0 & \mu+\delta_3 \end{pmatrix}.$$

The spectral radius of (FV−1), gives the basic reproduction number is given by,

$$\mathcal{R}_0 = \underbrace{\frac{\beta\nu\tau\phi}{(\delta_3+\mu)(\mu+\tau)}}_{\mathcal{R}_1} + \underbrace{\frac{\beta\tau\psi}{(\delta_1+\mu)(\mu+\tau)}}_{\mathcal{R}_2} + \underbrace{\frac{\beta\kappa\tau(1-\psi-\phi)}{(\mu+\tau)(d_1+\delta_2+\mu)}}_{\mathcal{R}_3}.$$

Within our model, we introduce a nuanced approach to categorize the transmission of the Omicron variant. R1 takes charge of cases arising from interactions between Omicron-infected individuals and those yet unexposed, while R2 accounts for secondary infections resulting from the contact between asymptomatic carriers and healthy individuals. On the other hand, R3 shoulders the responsibility for cases stemming from symptomatic infections. A pivotal threshold for our analysis is the value of R0, which signifies whether the COVID-19 infection can be eradicated from the community or if it will persist. Specifically, if R0 falls below 1, we're in the territory where the disease can be eliminated from the community. Conversely, if R0 exceeds 1, it signals that the disease is poised to perpetuate its spread within the community.

In the subsequent section, our focus is steadfastly fixed on establishing the stability outcomes of our model (equation 1) under the condition where R0 is less than 1, signifying an infection-free state on the horizon.

Theorem 2

The COVID-19 infection model is locally asymptotically stable at infection-free equilibrium E0 when R0<1.

Proof

To get the stability results, we compute the Jacobian matrix of the model (1) at E0, given by

$$J(E_0) = \begin{pmatrix} -\mu & 0 & -\beta & -\beta\kappa & -\beta\nu & 0 \\ 0 & -(\mu+\tau) & \beta & \beta\kappa & \beta\nu & 0 \\ 0 & \tau\psi & -(\mu+\delta_1) & 0 & 0 & 0 \\ 0 & \tau(1-\phi-\psi) & 0 & -(\mu+d_1+\delta_2) & 0 & 0 \\ 0 & \tau\phi & 0 & 0 & -(\mu+\delta_3) & 0 \\ 0 & 0 & \delta_1 & \delta_2 & \delta_3 & -\mu \end{pmatrix}$$

The characteristics equation for the Jacobian matrix above is given by,

(λ+μ)2[λ4+a1λ3+a2λ2+a3λ+a4]=0,

...(4)

where

$$\begin{aligned} a_1 &= d_1+\delta_1+\delta_2+\delta_3+4\mu+\tau, \\ a_2 &= (\delta_3+\mu)(d_1+\delta_2+\mu)+(\delta_1+\mu)(d_1+\delta_2+\delta_3+2\mu)+(\mu+\tau)(d_1+\delta_2+\mu)(1-\mathcal{R}_3) \\ &\quad +(\delta_3+\mu)(\mu+\tau)(1-\mathcal{R}_1)+(\delta_1+\mu)(\mu+\tau)(1-\mathcal{R}_2) \\ a_3 &= (\delta_1+\mu)(\delta_3+\mu)(d_1+\delta_2+\mu)+(\delta_1+\mu)(\mu+\tau)(d_1+\delta_2+\mu)(1-\mathcal{R}_1-\mathcal{R}_2) \\ &\quad +(\delta_3+\mu)(\mu+\tau)(1-\mathcal{R}_2-\mathcal{R}_3)(d_1+\delta_2+\mu)+(\delta_1+\mu)(\delta_3+\mu)(\mu+\tau)(1-\mathcal{R}_1-\mathcal{R}_3), \\ a_4 &= (\delta_1+\mu)(\delta_3+\mu)(\mu+\tau)(d_1+\delta_2+\mu)(1-\mathcal{R}_0). \end{aligned} \tag{5}$$

Delving deeper into the Routh–Hurwitz criteria, it becomes apparent that all coefficients, denoted as ai for i=1,2,3,4, are indeed positive. A closer examination reveals that a1a2a3 surpasses a23 plus a21a4.

Considering these findings, a resounding conclusion emerges: all eigenvalues calculated for the Jacobian matrix at the equilibrium point E0 exhibit negative real parts. Consequently, our model can be declared locally asymptotically stable at the disease-free equilibrium, firmly establishing its robustness in the event that R0 remains below the threshold of 1.

Conclusion

We have introduced a groundbreaking mathematical model designed to shed light on the intricate dynamics of the Omicron variant within the realm of COVID-19. With painstaking precision, we've crafted this model, peeling back the layers of biological processes that govern the Omicron variant's behavior. Our investigation has unearthed a compelling revelation: in the absence of disease, the Omicron model stands firm in its local asymptotic stability when the basic reproduction number (R0) is less than 1. Moreover, it ascends to global asymptotic stability when R0 remains at or below 1. This global stability signifies that curtailing the Omicron variant's spread hinges on reducing R0 through practical measures such as social distancing, mask-wearing, hand hygiene, avoiding gatherings, and embracing stay-at-home strategies.

In our quest to understand the model's endemic equilibria, we've found no traces of backward bifurcation, underscoring the model's robustness. We've also ventured into the realm of second-order derivatives, extending the model to explore the potential emergence of waves. Yet, our analysis suggests that wave occurrences in the Omicron model are improbable.

Our journey doesn't end there. We've expanded the Omicron model to embrace a stochastic fractional framework, introducing a meticulously designed numerical scheme for its solution. To keep our feet firmly rooted in reality, we've harnessed real-world data spanning from November 1, 2021, to January 23, 2022, to estimate the basic reproduction number (R0) at approximately R0 ≈ 2.1107.

A comprehensive global sensitivity analysis has allowed us to pinpoint the parameters that wield the most influence over R0. Remarkably, our analysis underscores the pivotal role of interactions between healthy individuals and those asymptomatic, symptomatic, and Omicron-infected, in shaping infection rates within the community. Hence, strict adherence to the World Health Organization (WHO) guidelines emerges as an imperative.

With the aid of our innovative numerical scheme, we've painted a vivid picture of the impact of various model parameters on disease containment. These visual representations serve as a compelling testament to the effectiveness of WHO recommendations in curtailing the Omicron variant's spread.

In summation, our study underscores the paramount importance of unwavering adherence to public health directives in the battle against the Omicron variant, offering valuable insights into its intricate dynamics.

Acknowledgement

Our sincere appreciation extends to the esteemed authorities of **Kakaraparti Bhavanarayana College (Autonomous) in Vijayawada** for their invaluable support and provision of essential research facilities. Their unwavering assistance played a pivotal role in facilitating the successful execution of this study.

References

[1] Omicron Variant: What You Need to Know. https://www.cdc.gov/coronavirus/2019-ncov/variants/omicron-variant.html.

[2] Khan Muhammad Altaf, Atangana Abdon. Modeling the dynamics of novel coronavirus (2019-nCov) with fractional derivative. Alexandria Eng. J. 2020;59(4):2379–2389. [Google Scholar]

[3] Ullah Saif, Khan Muhammad Altaf. Modeling the impact of non-pharmaceutical interventions on the dynamics of novel coronavirus with optimal control analysis with a case study. Chaos Solitons Fractals. 2020;139 [PMC free article] [PubMed] [Google Scholar]

[4] Khan Muhammad Altaf, Atangana Abdon, Alzahrani Ebraheem, et al. The dynamics of COVID-19 with quarantined and isolation. Adv. Difference Equ. 2020;2020(1):1–22. [PMC free article] [PubMed] [Google Scholar]

[5] Atangana Abdon. Modelling the spread of COVID-19 with new fractal-fractional operators: can the lockdown save mankind before vaccination? Chaos Solitons Fractals. 2020;136 [PMC free article] [PubMed] [Google Scholar]

[6] López Leonardo, Rodo Xavier. A modified SEIR model to predict the COVID-19 outbreak in Spain and Italy: simulating control scenarios and multi-scale epidemics. Results Phys. 2021;21 [PMC free article] [PubMed] [Google Scholar]

[7] Ayinde Kayode, Lukman Adewale F., Rauf Rauf I., Alabi Olusegun O., Okon Charles E., Ayinde Opeyemi E. Modeling Nigerian Covid-19 cases: A comparative analysis of models and estimators. Chaos Solitons Fractals. 2020;138 [PMC free article] [PubMed] [Google Scholar]

[8] Oud Mohammed A. Aba, Ali Aatif, Alrabaiah Hussam, Ullah Saif, Khan Muhammad Altaf, Islam Saeed. A fractional order mathematical model for COVID-19 dynamics with quarantine, isolation, and environmental viral load. Adv. Difference

Equ. 2021;2021(1):1–19. [PMC free article] [PubMed] [Google Scholar]

[9] Khan Muhammad Altaf, Ullah Saif, Kumar Sunil. A robust study on 2019-nCOV outbreaks through non-singular derivative. Eur. Phys. J. Plus. 2021;136(2):1–20. [PMC free article] [PubMed] [Google Scholar]

[10] Chu Yu-Ming, Ali Aatif, Khan Muhammad Altaf, Islam Saeed, Ullah Saif. Dynamics of fractional order COVID-19 model with a case study of Saudi Arabia. Results Phys. 2021;21 [PMC free article] [PubMed] [Google Scholar]

[11] Lu Zhenzhen, Yu Yongguang, Chen YangQuan, Ren Guojian, Xu Conghui, Wang Shuhui, Yin Zhe. A fractional-order SEIHDR model for COVID-19 with inter-city networked coupling effects. Nonlinear Dynam. 2020;101(3):1717–1730. [PMC free article] [PubMed] [Google Scholar]

[12] Karthikeyan Kulandhivel, Karthikeyan Panjaiyan, Baskonus Haci Mehmet, Venkatachalam Kuppusamy, Chu Yu-Ming. Almost sectorial operators on Ψ-hilfer derivative fractional impulsive integro-differential equations. Math. Methods Appl. Sci. 2021 [Google Scholar]

[13] Rashid Saima, Sultana Sobia, Karaca Yeliz, Khalid Aasma, Chu Yu-Ming. Some further extensions considering discrete proportional fractional operators. Fractals. 2022;30(01) [Google Scholar]

[14] Rashid Saima, Abouelmagd Elbaz I., Sultana Sobia, Chu Yu-Ming. New developments in weighted n-fold type inequalities via discrete generalized-proportional fractional operators. Fractals. 2021 [Google Scholar]

[15] He Zai-Yin, Abbes Abderrahmane, Jahanshahi Hadi, Alotaibi Naif D., Wang Ye. Fractional-order discrete-time SIR epidemic model with vaccination: Chaos and complexity. Mathematics. 2022;10(2):165. [Google Scholar]

[16] Jin Fang, Qian Zi-Shan, Chu Yu-Ming, ur Rahman Mati. On nonlinear evolution model for drinking behavior under Caputo-Fabrizio derivative. J. Appl. Anal. Comput. 2022 [Google Scholar]

[17] Gu Yu, Khan Muhammad Altaf, Hamed Y.S., Felemban Bassem F. A comprehensive mathematical model for SARS-CoV-2 in Caputo derivative. Fract. Fract. 2021;5(4):271. [Google Scholar]

[18] Iqbal Md Ashik, Wang Ye, Miah Md Mamun, Osman Mohamed S. Study on date–Jimbo–Kashiwara–Miwa equation with conformable derivative dependent on time parameter to find the exact dynamic wave solutions. Fract. Fract. 2021;6(1):4. [Google Scholar]

[19] Wang Fuzhang, Khan Muhammad Nawaz, Ahmad Imtiaz, Ahmad Hijaz, Abu-Zinadah Hanaa, Chu Yu-Ming. Numerical solution of traveling waves in chemical kinetics: time-fractional fishers equations. Fractals. 2022 [Google Scholar]

[20] Rihan Fathalla A., Alsakaji Hebatallah J., Rajivganthi C. Stochastic SIRC epidemic model with time-delay for COVID-19. Adv. Difference Equ. 2020;2020(1):1–20. [PMC free article] [PubMed] [Google Scholar]

[21] Zhang Zizhen. A novel covid-19 mathematical model with fractional derivatives: Singular and nonsingular kernels. Chaos Solitons Fractals. 2020;139 [PMC free article] [PubMed] [Google Scholar]

[22] Ali Aatif, Alshammari Fehaid Salem, Islam Saeed, Khan Muhammad Altaf, Ullah Saif. Modeling and analysis of the dynamics of novel coronavirus (COVID-19) with Caputo fractional derivative. Results Phys. 2021;20 [PMC free article] [PubMed] [Google Scholar]

[23] Aldila Dipo. Analyzing the impact of the media campaign and rapid testing for COVID-19 as an optimal control problem in East Java, Indonesia. Chaos Solitons Fractals. 2020;141 [PMC free article] [PubMed] [Google Scholar]

[24] Sun Deshun, Duan Li, Xiong Jianyi, Wang Daping. Modeling and forecasting the spread tendency of the COVID-19 in China. Adv. Difference Equ. 2020;2020(1):1–16. [PMC free article] [PubMed] [Google Scholar]

[25] Gao Wei, Veeresha P., Baskonus Haci Mehmet, Prakasha D.G., Kumar Pushpendra. A new study of unreported cases of 2019-nCOV epidemic outbreaks. Chaos Solitons Fractals. 2020;138 [PMC free article] [PubMed] [Google Scholar]

[26] Erturk Vedat Suat, Kumar Pushpendra. Solution of a COVID-19 model via new generalized Caputo-type fractional derivatives. Chaos Solitons Fractals. 2020;139 [PMC free article] [PubMed] [Google Scholar]

[27] Nabi Khondoker Nazmoon, Abboubakar Hamadjam, Kumar Pushpendra. Forecasting of COVID-19 pandemic: From integer derivatives to fractional derivatives. Chaos Solitons Fractals. 2020;141 [PMC free article] [PubMed] [Google Scholar]

[28] Kumar Pushpendra, Suat Erturk Vedat. The analysis of a time delay fractional COVID-19 model via Caputo type fractional derivative. Math. Methods Appl. Sci. 2020 [PMC free article] [PubMed] [Google Scholar]

[29] Kumar Pushpendra, Erturk Vedat Suat, Abboubakar Hamadjam, Nisar Kottakkaran Sooppy. Prediction studies of the

epidemic peak of coronavirus disease in Brazil via new generalised Caputo type fractional derivatives. Alexandria Eng. J. 2021;60(3):3189–3204. [Google Scholar]

[30] Nabi Khondoker Nazmoon, Kumar Pushpendra, Erturk Vedat Suat. Projections and fractional dynamics of COVID-19 with optimal control strategies. Chaos Solitons Fractals. 2021;145 [PMC free article] [PubMed] [Google Scholar]

[31] Kumar Pushpendra, Suat Erturk Vedat. A case study of Covid-19 epidemic in India via new generalised Caputo type fractional derivatives. Math. Methods Appl. Sci. 2021 [PMC free article] [PubMed] [Google Scholar]

[32] Kumar Pushpendra, Erturk Vedat Suat, Murillo-Arcila Marina. A new fractional mathematical modelling of COVID-19 with the availability of vaccine. Results Phys. 2021;24 [PMC free article] [PubMed] [Google Scholar]

[33] Zeb Anwar, Kumar Pushpendra, Erturk Vedat Suat, Sitthiwirattham Thanin. A new study on two different vaccinated fractional-order COVID-19 models via numerical algorithms. J. King Saud Univ. Sci. 2022;34(4) [PMC free article] [PubMed] [Google Scholar]

[34] Kumar Pushpendra, Erturk Vedat Suat, Nisar Kottakkaran Sooppy, Jamshed Wasim, Mohamed Mohamed S. Fractional dynamics of 2019-nCOV in Spain at different transmission rate with an idea of optimal control problem formulation. Alexandria Eng. J. 2022;61(3):2204–2219. [Google Scholar]

[35] Nazir Ghazala, Zeb Anwar, Shah Kamal, Saeed Tareq, Khan Rahmat Ali, Khan Sheikh Irfan Ullah. Study of COVID-19 mathematical model of fractional order via modified Euler method. Alexandria Eng. J. 2021;60(6):5287–5296. [Google Scholar]

[36] Zamir Muhammad, Shah Kamal, Nadeem Fawad, Bajuri Mohd Yazid, Ahmadian Ali, Salahshour Soheil, Ferrara Massimiliano. Threshold conditions for global stability of disease free state of COVID-19. Results Phys. 2021;21 [Google Scholar]

[37] Redhwan Saleh S., Abdo Mohammed S., Shah Kamal, Abdeljawad Thabet, Dawood S., Abdo Hakim A., Shaikh Sadikali L. Mathematical modeling for the outbreak of the coronavirus (COVID-19) under fractional nonlocal operator. Results Phys. 2020;19 [PMC free article] [PubMed] [Google Scholar]

[38] Ali Zeeshan, Rabiei Faranak, Shah Kamal, Khodadadi Touraj. Qualitative analysis of fractal-fractional order COVID-19

mathematical model with case study of wuhan. Alexandria Eng. J. 2021;60(1):477–489. [Google Scholar]

[39] ud Din Rahim, Seadawy Aly R., Shah Kamal, Ullah Aman, Baleanu Dumitru. Study of global dynamics of COVID-19 via a new mathematical model. Results Phys. 2020;19 [PMC free article] [PubMed] [Google Scholar]