Differential equation models for infectious diseases: Mathematical modeling, qualitative analysis, numerical methods and applications

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ABSTRACT. Mathematical epidemiology has a long history of origin and development. In particular, mathematical modeling and analysis of infectious diseases has become a fundamental and indispensable approach to discovering the characteristics and mechanisms of the transmission dynamics of epidemics, thereby effectively predicting possible scenarios in reality, as well as controlling and preventing diseases.

In recent decades, differential equations have been widely used to model many important infectious diseases. The study of these differential equation models is very useful in both theory and practice, especially in proposing appropriate strategies for disease control and prevention. This is of great benefit to public health and health care.

In this survey article, we review many recent developments and real-world applications of deterministic ordinary and partial differential equations (ODEs and PDEs) in modeling major infectious diseases, particularly focusing on the following aspects: mathematical modeling, qualitative analysis, numerical methods, and real-world applications. We also present and discuss some open problems and future directions that research in differential equation models for infectious diseases can take.

This article provides a comprehensive introduction to epidemic modeling and insights into nonstandard finite difference (NSFD) methods.

1. Introduction

6 Infectious diseases have always been a major and constant threat to public 7 health. Mankind has always had to face and fight many infectious diseases with 8 varying degrees of danger, such as influenza, hepatitis, Zika, malaria, measles, tu-9 berculosis, hepatitis, vector-borne diseases, Ebola, and most recently the COVID-19 10 pandemic.

The well-known SIR model, proposed by Kermack and McKendrick in 1927 [252], can be considered one of the first epidemic models and is usually used to introduce epidemic modeling. The study of mathematical models of infectious diseases is very useful in both theory and practice, especially in proposing appropriate

²⁰²⁰ Mathematics Subject Classification. Primary 34A34, 35Q92, 37N25, 37N30, 92B05, 65L05, 65L12, 92Dxx .

Key words and phrases. Mathematical modeling, Epidemiology, Epidemics, Infectious diseases, Numerical methods.

15 strategies for disease control and prevention. This is of great benefit to public 16 health and health care.

It is well known that differential equations, including ordinary differential equa-17 tions (ODEs) and partial differential equations (PDEs), have several useful applica-18 tions in real life. They are widely used to describe many important phenomena and 19 processes in science and engineering (see e.g. [30, 55, 78, 79, 80, 81, 82, 83, 258, 20 **323**, **360**, **454**]. One of its prominent applications is the mathematical modeling 21 and analysis of infectious diseases. Over the past few decades, a large number of 22 differential equation models have been extensively developed to explore the trans-23 mission dynamics of major infectious diseases. These models have confirmed the 24 important role of differential equations in epidemic modeling. 25

Nowadays, epidemic models based on differential equations have always been an
important and indispensable approach in modeling infectious diseases, especially in
the context that epidemics are constantly changing and posing new challenges. For
differential equation models of infectious diseases, the following aspects are mainly
focused:

• *Mathematical Modeling:* The use of differential equations and the foundations of mathematical epidemiology to propose mathematical models that describe the transmission of infectious diseases.

• Qualitative study: Investigate mathematical properties of the proposed differential equation models, including existence and uniqueness of solutions, positivity and boundedness of solutions, asymptotic stability properties, conservation laws, physical properties, and basic reproduction number.

- *Numerical Methods:* Construction of efficient numerical methods, especially numerical methods that preserve important mathematical features of the proposed differential equation models.
- Practical Applications: Applying the theoretical results to provide scenarios of disease spread, to suggest anti-epidemic measures and strategies, to evaluate the effectiveness of vaccines and existing anti-epidemic measures, to study the spread of computer viruses, rumors and malware on the Internet, and to model animal diseases. and animal disease modeling with applications in agriculture.

The aim of this review article is to review many recent developments and reallife applications of deterministic differential equation models in modeling major infectious diseases, focusing mainly on the following aspects: mathematical modeling, qualitative analysis, numerical methods, and real-life applications. We also present and discuss some open problems and future directions that research in differential equation models for infectious diseases can take.

The manuscript is expected to cover not only the latest developments in deterministic ODE and PDE models for infectious diseases, but also future research and open problems in this area. Unlike some previous review articles (see, for example, [82, 84, 87, 115, 208, 315, 363, 375, 392, 514]) that focus only on the mathematical modeling of specific diseases, this review provides a comprehensive analysis of all four aspects, where the main differences are outlined as follows:

• In the mathematical modeling aspect: The selected references are systematically reviewed based on common and dangerous diseases. Many common and dangerous diseases (e.g., basic models of virus dynamics,

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63	influenza, severe acute respiratory syndrome (SARS), Ebola, hepatitis B
64	and C, tuberculosis, vector-borne diseases, malaria, measles, Zika virus,
65	dengue fever, COVID-19 pandemic, HIV/AIDS,) have been men-
66	tioned, providing readers with a comprehensive and in-depth insight into
67	infectious disease modeling with applications.
68	• In the qualitative study aspect: We list in detail the essential qualita-
69	tive properties for the proposed models and, in particular, the tools and
70	methods used in qualitative research are rigorously analyzed.
71	• In the numerical methods aspect: We provide a detailed overview of nu-
72	merical methods, including standard and nonstandard methods, for solv-
73	ing differential equations, with an emphasis on those used to solve disease
74	transmission models. This section also provides an introduction to NSFD
75	methods for mathematical models arising in real-world situations and re-
76	cent advances in this area.
77	• In the practical application aspect: We focus on important applications
78	of differential equations for infectious diseases: modeling animal diseases
79	with applications in agriculture, chemostat models to represent micro-
80	bial growth and competition, modeling the spread of computer viruses
81	and rumors on the Internet, modeling addictions (e.g., alcohol, tobacco,
82	heroin, opioids, cocaine, drug use, etc.), understanding disease dynamics
83	and potential scenarios, informing data-driven public health initiatives.
04	In general, this survey provides a systematic overview of infectious disease modeling

In general, this survey provides a systematic overview of infectious disease modeling
for mathematicians, epidemiologists, and all researchers of all experience levels,
whether they are experienced or new to the field, that can help them understand:

• Recent advances in modeling of major diseases.

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- Methods, methodologies, approaches, and tools for modeling infectious diseases.
 - Techniques for extracting insights and shaping public health strategies.
 - Exciting future directions in infectious disease research.

In addition, this manuscript provides an overview of nonstandard finite difference
 (NSFD) methods and their applications in disease modeling.

94 It is important to note that there are many other types of epidemiological models, such as integro-differential models, delayed differential equation models, 95 fractional-order and stochastic differential models (see, for example, [16, 46, 47, 96 59, 90, 97, 159, 184, 352, 388, 413, 426, 460, 497, 516]). However, the 97 98 manuscript focuses only on ODEs and PDEs because the approaches, methodologies, and methods for constructing ODE and PDE models of infectious diseases are 99 very similar. In fact, they share many common features that should be included 100 in a single systematic review. The other types of epidemiological models will be 101 considered in future studies. 102

The outline of this article is as follows: In Section 2, we provide an overview of epidemic models based on differential equations, considering basic models and their variants and extensions. In Section 3 we focus on the qualitative analysis aspect and its practical applications. Numerical methods are presented in Section 4. Future research and open problems are discussed in Section 5. The last section contains concluding remarks and discussions.

2. Mathematical Modeling

In this section, we review results on mathematical modeling based on deterministic ODEs and PDEs for infectious diseases.

2.1. ODE models: Basic Epidemic Models. We start with one of the first
and basic epidemic models introduced by Kermack and McKendrick in 1927 [252].
For this purpose, let us consider general autonomous dynamical systems described
by ODEs of the form

(2.1)
$$\dot{y}(t) = f(y(t)), \quad t > 0, \qquad y(0) = y_0 \in \mathbb{R}^n,$$

where $y = [y_1, y_2, \ldots, y_n]^\top : [0, \infty) \to \mathbb{R}^n$, $f = [f_1, f_2, \ldots, f_n]^\top : \mathbb{R}^n \to \mathbb{R}^n$ and \dot{y} stands for the time derivative of y. Here it is assumed that the right-hand-side function f satisfies all necessary smoothness assumptions so that solutions of (2.1) exist and are unique (see e.g. [55, 258, 454]).

Many mathematical models based on (2.1) have been proposed to study epidemic models. In these models, diseases caused by viruses or bacteria are not modelled directly in the population model, but only indirectly through the number of infected individuals. For example, the classical SI, SIS and SIR epidemic models classify individuals in the population according to their status with respect to the disease: healthy, infected and immune. More clearly, the disease states S, I and Rare defined as follows [**30**, **323**]:

• susceptible S: Individuals who are not infected but are susceptible to acquiring the disease and becoming contagious.

- *infected I*: Individuals who have been infected, are currently contagious, and have the potential to spread the disease to others.
- *removed R*: Individuals who have experienced the disease, recovered, and
 achieved permanent immunity, or are isolated until both recovery and
 permanent immunity are achieved.

Models with these states are called *SIR models*, adapted to the characteristics of the infectious disease, for example:

- SI implies the absence of any possible recovery: $S \to I$;
- SIS indicates the possibility of recovery, but does not guarantee immunity: $S \rightarrow I \rightarrow S;$
 - SIR represents a temporary state of immunity: $S \to I \to R \to S$.
- One of the simplest models involves the dynamics of S-, I-, R- individuals, first introduced by Kermack and McKendrick in 1927 [252] (see also [323]):

(2.2)
$$\dot{S}(t) = -\beta I(t)S(t),$$
$$\dot{I}(t) = \beta I(t)S(t) - \alpha I,$$
$$\dot{R}(t) = \alpha I(t), \quad t > 0,$$

142 where

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- β is the proportionality constant ('transmission rate');
- α is the recovery rate;
 - $\beta I(t)$ is called the force of infection.
 - βSI represents the number of new infections per unit of time (incidence).

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Although the SIR model (2.2) looks analytically simple, finding its exact analytical solution is an interesting problem. Some analytical techniques used to find the solution of (2.2) can be found in [101, 207, 261].

It is not difficult to analyze basic mathematical properties of the Kermack-McKendrick SIR model [252, 323]. More clearly, it can be shown that

$$\lim_{t\to\infty}S(t)=S_\infty>0,\quad \lim_{t\to\infty}R(t)=R_\infty>0,\quad \lim_{t\to\infty}I(t)=I_\infty=0.$$

The quantity S_{∞} is called the *final size of the epidemic*. In particular, the function I(t) of infected individuals can monotonically decrease to zero, or first monotonically increase to some maximum value I_{\max} and then decrease to zero. Here, a necessary and sufficient condition for the initial increase of I(t) is easily determined and is given by

$$S(0) > \frac{\alpha}{\beta}.$$

157 On the other hand, $I_{\rm max}$ can be computed as

$$I_{\max} = -\frac{\alpha}{\beta} + \frac{\alpha}{\beta} \ln \frac{\alpha}{\beta} + S_0 + I_0 - \frac{\alpha}{\beta} \ln S_0.$$

The quantity I_{max} is very useful in estimating the progression of epidemics since it indicates when the number of infections will begin to decline.

Note that the Kermack-McKendrick SIR epidemic model, for example, usessome hypotheses:

- Infected individuals are also infectious;
- the total population remains constant;
 - the population experiences no births or deaths;
- the population is closed, that is, no outside individuals enter or leave the population;
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• all recovered individuals have complete immunity and are impervious to reinfection.

The above assumptions may seem rather restrictive, but they can be satisfied within certain limits. For example, several childhood diseases such as chickenpox, smallpox, rubella, mumps, scarlet fever, hand-foot-and-mouth disease lead to permanent immunity, or many vaccines can create long-lasting or even lifelong immunity [**323**].

Although the Kermack-McKendrick SIR epidemic model is simple and under 173 some strict assumptions, it is still appropriate and effective for modeling many 174 infectious diseases. In fact, once we have given disease-specific time series data, 175 the parameter estimation problem for the SIR model can be solved by compar-176 ing its solution to the given data. Examples of parameter estimation from data 177 can be found in [78, 80, 323]. Recently, the Kermack-McKendrick SIR epidemic 178 model was used to study and predict the transmission dynamics of the COVID-19 179 pandemic [250, 268, 278, 322, 359, 442, 483]. 180

In [253], the limitation of the SIR model (2.2) was improved by considering the effect of the continuous introduction of new susceptible individuals into the population. However, the results presented in [253] had two important limitations. One was that the disease of interest was the only cause of death, and the second was that the age of the individuals did not affect their infectivity, susceptibility, or reproductive capacity. In [254], the first of the above limitations was overcome by the introduction of constant non-specific mortality rates, which, for the sake of generality, are assumed to be different. are assumed to be different for virgins(individuals who have never been infected), sick, and recovered.

In general, the classical SIR model should be adapted to the characteristics ofeach epidemic.

192 2.2. Variants and Extensions of the Basic Models. The classical epi-193 demic models have played an important role in epidemic modeling. Inspired by 194 basic epidemic models and principles of mathematical epidemiology, many math-195 ematical models models have been proposed and developed to study infectious 196 diseases.

There are several types of incidence, depending on the assumption made about 197 the force of infection. One of the simplest forms is the mass action incidence 198 or bilinear incidence function, which is $f(S,I) = \beta SI$. In the model (2.2), the 199 interaction term βIS is a linearly increasing function of the number of infected 200 individuals. As analyzed in [99], while this interaction term may be true for small 201 I, it seems rather unrealistic that it can still hold for large I. For this reason, 202 Capasso and Serio modified (2.2) by replacing the linear interaction term βIS by 203 a non-linear function q(I)S, where q(I) satisfies 204

$$(1) \quad \forall x \in \mathbb{R}_+ \colon g(x) \ge 0;$$

206 (2) g(0) = 0;

207 (3) $\exists c \in \mathbb{R}_+ \setminus \{0\}$ s.t. $\forall x \in \mathbb{R}_+ : g(x) \le c;$

- (4) $g'(x): \mathbb{R}_+ \to \mathbb{R}$, the derivative of g, exists and is bounded on any compact interval of \mathbb{R}_+ , with g'(0) > 0;
- 210 (5) $\forall x \in \mathbb{R}_+ : g(x) \le xg'(0)$, where $\mathbb{R}_+ := [0, \infty)$.

The function q(I) takes into account the "saturation" phenomenon or the other 211 "psychological" effects. Two famous nonlinear incidence functions are the satu-212 rated incidence rate $f(S, I) = \beta SI/(1 + \gamma I)$ and the standard incidence function 213 $f(S, I) = \beta SI/(S+I)$. Epidemic models using generalized nonlinear incidence rate 214 can be found in [165, 166, 179, 211, 231, 285, 294, 296, 329, 415, 440, 468]. 215 In the SIR model, it was assumed (2.2) that the rate of contacts per infective is 216 proportional to the total population size N, which was widely used in all early epi-217 demic models. As mentioned in [78, 82], this assumption is quite unrealistic except 218 in the early stages of an epidemic occurring within a moderately sized population. 219 It is more realistic to consider a contact rate that is a non-increasing function of 220 total population size. The SIR model can then be generalized by assuming that 221 an average member of the population makes C(N) contacts per unit time, with 222 223 $C'(N) \geq 0$, and defining

$$\beta(N) = \frac{C(N)}{N},$$

where $\beta'(N)$ is assumed to be negative to express the idea of saturation in the number of contacts. The following are some special cases of C(N) that have been widely used in epidemic modeling with general contact rates.

• Standard incidence: $C(N) = \lambda$;

- Mass action incidence: $C(N) = \beta N$;
- Interaction of Michaelis-Menten type:

$$C(N) = \frac{aN}{1+bN},$$

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which was used in [147].

• Saturating contact rate based on a mechanistic derivation for pair forma-

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tion [209]

 $C(N) = \frac{aN}{1 + bN + \sqrt{1 + 2bN}}.$

• $C(N) = \lambda N^{\alpha}$ with $\alpha = 0.05$ was used in [332]. It has been shown 233 that this function works quite well for data on contact-borne diseases in 234 medium-sized cities. 235

In recent decades, the basic classical epidemic models and their variants have 236 been extensively developed to describe the transmission dynamics of many major 237 infectious diseases: 238

239	• Basic virus dynamics models and outbreak spread models in epidemiology
240	[36 , 75 , 163 , 215 , 370 , 392 , 471 , 514];
241	• Influenza [8, 10, 102, 198, 434];
242	• Severe acute respiratory syndrome (SARS) [77, 121, 195, 229, 366,
243	518];
244	• Ebola [1, 65, 142, 288, 317, 364];
245	• Hepatitis B and C [168, 216, 221, 319, 324, 351, 369, 393, 452, 458,
246	491, 507, 515];
247	• Tuberculosis [24, 72, 197, 208, 299, 361, 408, 446, 466, 469];
248	• Vector-borne diseases [70 , 85 , 129 , 236 , 287 , 418 , 496];
249	 Malaria [3, 16, 18, 175, 235, 264, 315, 368, 424, 464, 472];
250	• Measles [19]
251	 Zika virus [11, 177, 206, 240, 263, 310, 365, 425, 432, 493, 519];
252	• Dengue fever [14, 107, 155, 239, 365, 395, 401];
253	• COVID-19 pandemic [12, 17, 33, 57, 66, 119, 123, 130, 154, 222,
254	250, 248, 262, 265, 268, 278, 283, 303, 314, 322, 355, 358, 359,
255	$367,\ 375,\ 377,\ 387,\ 403,\ 406,\ 411,\ 442,\ 456,\ 464,\ 483];$
256	• HIV/AIDS [169, 194, 242, 297, 305, 371, 416, 479].
257	Besides, epidemic models are widely used in
258	• Diabetes Mellitus [105 , 361];
259	• cancer: malignant invasion of tumor cells [321];
260	• cervical cancer: human papillomavirus model [89];
261	• animal disease modeling with applications in agriculture [2, 9, 50, 471];
262	• chemostat models to represent microbial growth and competition [20, 21,
263	23, 444];
264	• modeling the spreading of computer viruses and rumors on the Internet
265	[179, 230, 238, 292, 389, 390, 402, 404, 430, 510, 511, 512, 523,
266	524];
267	• modeling addictions, e.g. alcohol drinking [133, 233, 256, 257, 386,
268	419, 420, 436, 495, 503, 504], tobacco [181, 284, 298, 433, 478, 485],
269	heroin [125, 298, 356, 451, 498], opioids [63, 88, 95, 125, 521], cocaine
270	[421, 423], drug consumption $[141, 188, 486]$, obesity $[51, 93, 164, 244,$
271	422], etc.
272	It should be noted that the ODE models of the form (2.1) are also used in the
273	context of:
274	• Delayed systems [7, 104, 127, 163, 173, 174, 214, 381, 407, 445,
275	474 506].

• Time fractional-order systems [7, 38, 115, 313, 455, 471];

for infectious disease modeling. These extended models provide an additional pow-erful approach to disease analysis.

2.3. PDE Models. In addition to ODE models of the form (2.1), PDE models, which extend ODE models, have also been extensively studied for the analysis
of infectious diseases [30, 79, 83, 323, 360, 427].

More specifically, compartmental models in epidemiology can be extended by 283 using spatial reaction-diffusion systems, where each compartment, representing a 284 different species, is allowed to invade a spatial domain $\Omega \subset \mathbb{R}^m$ (or a metric graph 285 network) with a space-dependent density. The densities interact with each other 286 according to the same mathematical laws as for the space-independent case, but are 287 individually subject to a spatial diffusion mechanism, usually associated with the 288 Laplace operator [48]. Then a system of *n* interacting species, each with a spatial 289 density 290

$$\{u_i(x,t): x \in \Omega, \quad t \ge 0\}, \quad i = 1, 2, \dots, n$$

²⁹¹ can be described by a system of semilinear parabolic PDEs of the form

(2.3)
$$\frac{\partial u}{\partial t}(x,t) = D\Delta u(x,t) + f(u(x,t))$$

supplied with suitable boundary conditions, where $D = \text{diag}(d_1, d_2, \dots, d_n), f \colon \mathbb{R}^n \to \mathbb{R}^n$

 $_{293}$ $\,\,\mathbb{R}$ is the interaction law among the species via their densities, and

$$\Delta u(x,t) = \frac{\partial^2 u}{\partial x_1^2}(x,t) + \ldots + \frac{\partial^2 u}{\partial x_n^2}(x,t).$$

Spatial models of the form (2.3) have been used to study the transmission of infection, depending on how a particular disease is transmitted between different populations or subpopulations.

Allen et al. [31] proposed an SIS reaction-diffusion model in a heterogeneous environment to understand the impact of spatial heterogeneity of the environment and movement of individuals on the persistence and extinction of a disease. This model is given in the form:

(2.4)
$$\begin{aligned} &\frac{\partial}{\partial t}S(t,x) = d_S\Delta S(t,x) - \frac{\beta(x)S(t,x)I(t,x)}{S(t,x) + I(t,x)} + \gamma(x)I(t,x), \quad t > 0, \ x \in \Omega, \\ &\frac{\partial}{\partial t}I(t,x) = d_I\Delta I(t,x) + \frac{\beta(x)S(t,x)I(t,x)}{S(t,x) - I(t,x)} - \gamma(x)I(t,x), \quad t > 0, \ x \in \Omega, \end{aligned}$$

301 with the coupling condition

(2.5)
$$\frac{\partial}{\partial \mathbf{n}}S(t,x) = \frac{\partial}{\partial \mathbf{n}}I(t,x) = 0,$$

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•	S(t, x) and $I(t, x)$ denote the density of susceptible and infectious individ-
	uals at location x and time t in a given spatial region Ω , which is assumed
	to be a bounded domain in $\mathbb{R}^n (n \ge 1)$ with a smooth boundary $\partial \Omega$;

• Ω is isolated from the outside for the host, implying the homogeneous Neumann boundary condition; **n** is the outward unit normal vector on $\partial\Omega$, and $\partial/\partial \mathbf{n}$ denotes the normal derivative along **n** on $\partial\Omega$.

- 309 310
- respectively;
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- the positive functions $\beta(x)$ and $\gamma(x)$ are the spatially dependent transmission and recovery rates at position $x \in \Omega$, respectively.

• d_S and d_I are the dispersion for susceptible and infectious individuals,

The existence, uniqueness and asymptotic profile of the equilibria are then analyzed. 313 First, a basic reproduction number is defined for this PDE-SIS model (2.4), which is 314 based on the next generation approach for heterogeneous populations [145, 146]. 315 It is then shown that if the basic reproduction number is less than 1, a unique 316 disease-free equilibrium is globally asymptotically stable and there is no endemic 317 equilibrium, while if the basic reproduction number is greater than 1, the disease-318 free equilibrium is unstable and there is a unique endemic equilibrium. It is also 319 pointed out that the disease-free equilibrium is always unstable for high-risk do-320 mains, and for low-risk domains, the disease-free equilibrium is stable if and only 321 if infected individuals have mobility above a threshold. These results have several 322 useful implications for real-world situations. 323

In [383], Peng provided further understanding of how large and small diffu-324 sion rates of the susceptible and infected populations affect disease persistence and 325 extinction. In another paper [384], Peng and Yi considered a more complicated 326 heterogeneous environment in which the moderate risk area occurs, and dealt with 327 two cases: (i) only the moderate and high risk areas exist; (ii) the low, moderate, 328 and high risk areas coexist. In both works, the asymptotic profile of the positive 329 330 steady state was rigorously investigated, and optimal strategies for eradicating the epidemic disease were proposed. 331

In [232], Huang et al. proposed and studied two modified SIS diffusion models of the form (2.4) but they are associated with the Dirichlet boundary condition S(t,x) = I(t,x) = 0 for $x \in \partial\Omega$ and t > 0, reflecting a hostile environment in the boundary. The analysis of the basic reproduction number and a partial result on the global stability of the endemic equilibrium are also performed.

In [279], a spatially diffusive SIR epidemic model with the mass action infection mechanism and homogeneous Neumann boundary condition was considered in the form

$$\begin{aligned} &(2.6)\\ &\frac{\partial}{\partial t}S(t,x) = k_S \Delta S(t,x) + b(x) - \beta(x)S(t,x)I(t,x) - \mu(x)S(t,x), \quad t > 0, \ x \in \Omega, \\ &\frac{\partial}{\partial t}I(t,x) = k_I \Delta I(t,x) + \beta(x)S(t,x)I(t,x) + (\mu(x) + \gamma(x))I(t,x), \quad t > 0, \ x \in \Omega, \\ &\frac{\partial}{\partial t}R(t,x) = k_R \Delta R(t,x) + \gamma(x)I(t,x) - \mu(x)R(t,x), \quad t > 0, \quad x \in \Omega, \end{aligned}$$

340 with initial data

(2.7)
$$S(0,x) = S_0(x), \quad I(0,x) = I_0(x), \quad R(0,x) = R_0(x), \quad x \in \Omega,$$

341 and boundary conditions

(2.8)
$$\frac{\partial}{\partial \mathbf{n}} S(t,x) = \frac{\partial}{\partial \mathbf{n}} I(t,x) = \frac{\partial}{\partial \mathbf{n}} R(t,x)0,$$

342 where

343 344 • S(t, x), I(t, x) and R(t, x) denote the populations of susceptible, infective and recovered individuals at position x and time t, respectively;

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- k_S , k_I and k_R denote the dissemination rates for susceptible, infectious and recovered individuals, respectively;
- $b(x), \beta(x), \mu(x)$ and $\gamma(x)$ denote the birth rate, the transmission rate, the mortality rate and the recovery rate at position x, respectively.

By discretizing the PDE model (2.6) with respect to the space variable and constructing Lyapunov functions for the corresponding ODE models, the global asymptotic stability of (2.6) has been established [**279**].

In [280], the model (2.6) is extended by a new more realistic model with nonlocal diffusion.

In a recent paper, some extensions of the classical SIR model with non-symmetric spatial dependence are introduced to study the spread of some diseases [461]. The proposed model yields a system of partial integro-differential equations. Also, two methods that handle the integrals of the equations have been provided.

In addition to the above PDE models, a large number of spatial reactiondiffusion models of major infectious diseases such as HBV, malaria, influenza, West Nile virus transmission, Zika, etc. can be found in [56, 100, 118, 134, 255, 266, 267, 290, 300, 301, 354, 405, 437, 447, 457, 482, 488, 489, 490, 502, 505, 507, 522], in which the models proposed in [118, 255, 266, 300, 437, 482, 502, 522] can be directly used to study the COVID-19 epidemic.

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3. Qualitative analysis and applications

Qualitative analysis of differential equations modeling infectious diseases is very important since it can have many useful applications in reality, such as suggesting appropriate strategies for disease control and prevention; evaluating the effects of vaccines; waning immunity; parameter estimation problems; parameter sensitivity analysis and optimal control strategies (usually w.r.t. vaccination strategies, stakeholder decisions (wearing masks, physical isolation, curfews, etc.).

In this section, we emphasize qualitative analytical aspects of differential equation models and their applications, where methods, approaches, and tools used in qualitative analysis are discussed in detail.

3.1. Analysis of ODE models. The first property of interest for ODE models of infectious diseases is well-posedness, including existence, uniqueness of solutions, and continuous dependence on initial data. Well-posedness is easy to establish and is often automatically satisfied due to the smoothness of the right-hand-side functions [**30**, **55**, **258**, **454**]. In general, in addition to well-posedness, qualitative analysis aspects of ODE models of infectious diseases focus mainly on the following issues.

3.1.1. The positivity and boundedness of the solutions. Obviously, positivity 381 should be an obvious property of the solutions of ODE models for infectious diseases, 382 i.e. $y(t) \in \mathbb{R}^n_+ = \{(y_1, y_2, \dots, y_n) \in \mathbb{R}^n | y_1, y_2, \dots, y_n \ge 0\}$ for t > 0 whenever 383 $y(0) \in \mathbb{R}^n_+$. In this case, the set \mathbb{R}^n_+ is called a *positively invariant set*. This 384 property can be easily verified using well-known theorems on the positivity of ODEs 385 [228, Lemma 1], [444]. Meanwhile, boundedness can be established on the basis of 386 comparison theorems for differential equations [330]. Note that positively invariant 387 sets and feasible sets of ODE models follow from their positivity and boundedness. 388

3.1.2. Conservation laws. Many ODE models in population dynamics and also 389 in epidemiology can satisfy some *conservation laws*, such as direct, generalized and 390 subconservation laws [344, 347]. Conservation laws for ODE models of infectious 391 diseases can be established based on the theory of ODEs [20, 30, 258, 444, 454] 392 or comparison theorems for differential equations [330]. 393

3.1.3. Equilibrium points. Equilibrium points of ODE models of the form (2.1) 394 are solutions of the equation f(y) = 0. An equilibrium point is also called a *fixed* 395 point, constant solution, steady state, critical point or a steady-state solution [30, 396 **258**, **454**]. In general, it is not difficult to determine the set of equilibrium points, 397 except when the ODE model under consideration has high dimensions and contains 398 many parameters. Two common types of equilibria are disease-free equilibrium 399 (DFE) and *endemic equilibrium* (EE) points, which correspond to the possibility 400 of the epidemic being suppressed or remaining in the community. 401

3.1.4. Local asymptotic stability (LAS). An equilibrium y^* is said to be locally 402 stable if for every $\epsilon > 0$ there exists a $\delta > 0$ with the property that every solution 403 y(t) starting from the initial condition $y(0) = y_0$ with $||y_0 - y^*|| < \delta$ satisfies 404 $||y(t) - y_0|| < \epsilon$ for all $t \ge 0$. It is said to be *locally asymptotically stable* if it is 405 sable and there exists $\gamma > 0$ such that $||y_0 - y^*|| < \gamma$ implies $\lim_{t \to \infty} y(t) = y^*$ 406 (see, e.g., [30, 258, 454]). The local dynamics of dynamical systems has several 407 important implications in the real world. The LAS of equilibrium points can be 408 studied by the Lyapunov indirect method using the Routh-Hurwitz criteria [30, 409 258, 454]. This approach analyzes the LAS of an equilibrium point by considering 410 the position of the eigenvalues of the Jacobian matrix evaluated at the equilibrium 411 point with respect to the left-half plane. More specifically, an equilibrium point 412 y^* is locally asymptotically stable if all eigenvalues λ of the Jacobian $J(y^*)$ 413 $(\partial f/\partial y)(y^*)$ satisfy $\operatorname{Re}(\lambda) < 0$, and it is unstable if $\operatorname{Re}(\lambda) > 0$ for one or more of 414 the eigenvalues of J. Note that the direct Lyapunov method is only applicable to 415 hyperbolic equilibrium points. Here, an equilibrium point y^* is said to be hyperbolic 416 if none of the eigenvalues of the matrix J lie on the imaginary axis, and non-417 hyperbolic otherwise, cf. [454]. 418

3.1.5. Global asymptotic stability (GAS). An equilibrium point y^* is said to be 419 globally asymptotically stable if it is stable and globally attractive, i.e. $\lim_{t\to\infty} y(t,y_0) =$ 420 y^* for all initial conditions y_0 (see e.g. [30, 258, 454]). The GAS analysis of equilib-421 rium points is a very important problem because it can reveal the future evolution 422 of epidemics. In particular, the GAS of free-disease equilibrium points indicates 423 that epidemics will be extinguished, while the GAS of endemic-equilibrium points 424 indicates that epidemics will exist stably in the population. In general, the GAS 425 problem is not an easy one. One of the most successful approaches to this problem 426 is the Lyapunov stability theory [286, 309]. This approach requires suitable candi-427 date Lyapunov functions that must satisfy some specific conditions. In general, it 428 is not easy to determine a Lyapunov function for a given dynamical system. How-429 ever, several classes of Lyapunov functions have been proposed to analyze the GAS 430 of ODE models in epidemiology [98, 272, 273, 274, 374, 406, 438, 480, 508], 431 where common classes of Lyapunov functions are linear, quadratic and Volterra-432 type Lyapunov functions or combinations of them. In particular, Cangiotti [98] 433 provided an overview of Lyapunov functions for epidemic compartmental models. 434 On the other hand, the geometric method is a remarkable approach to the 435 GAS analysis of ODEs [293, 294, 295]. Also, the Poincaré-Bendixson Theorem

in combination with the Bendixson-Dulac Criterion is very useful in studying the
GAS of two-dimensional dynamical systems governed by ODEs [30, 323].

In [103], Castillo-Chavez et al. discussed some conditions that clarify the connections between the basic reproduction number and its relation to the GAS of disease-free equilibrium points of epidemiological models. Then, global stability conditions for disease-free equilibrium points were given, which are easy to verify.

3.1.6. Basic reproduction number. One of the most important concerns about 443 any infectious disease is its reproductive number \mathcal{R}_0 , which is useful in guiding 444 control strategies [145, 146, 475, 476, 477]. The basic reproduction number 445 can be defined as the expected number of secondary cases produced by a typical 446 infected individual during its entire period of infectiousness in a fully susceptible 447 population [145]. It can also be considered as a threshold parameter for the local 448 asymptotic stability of the disease-free equilibrium [475]. The basic reproduction 449 number of epidemic models is very useful in guiding control strategies with the help 450 451 of sensitivity analysis.

3.1.7. Optimal control problems. Epidemic models based on differential equations are often combined with optimal control strategies to find effective disease
control measures [58, 60, 68, 86, 113, 260, 307, 432, 435, 463]. The proposed optimal control problems can be solved using Pontryagin's maximum principle [391].

3.1.8. Epidemic models with effect of vaccines. It is well known that vaccines
are effective tools to combat infectious diseases and to protect people against disease. For this reason, epidemic models with the effect of vaccines are often considered [8, 25, 156, 157, 163, 167, 180, 193, 196, 234, 277, 414, 439]. The
study of vaccination models [34, 192, 363, 473] can evaluate the efficacy of certain
vaccines and suggest effective vaccination strategies.

3.1.9. Parameter estimation problem. ODE models for infectious diseases can
be combined with real data of diseases to predict possible scenarios in reality. Therefore, the parameter estimation problem is very important to find best-fit parameters [78, 80, 323]. Following this approach, the parameter estimation problem has
been extensively studied for several epidemic models [122, 311, 357, 397, 417],
especially for the COVID-19 pandemic [250, 268, 307, 322, 359].

3.1.10. Bifurcation analysis and chaos. It is well-known that bifurcation theory 469 studies qualitative changes in the state of a system as a parameter is varied [106, 470 **282**]. In general, applications of bifurcation analysis in epidemiology are very 471 diverse, especially in studying the evolution and determining factors that may be 472 associated with the suppression or outbreak of disease. For example, the forward 473 bifurcation phenomenon, first noted by Kermack and McKendrick in [252], can 474 be observed in several disease transmission models [160]. For epidemic models 475 that exhibit forward bifurcation, the condition $\mathcal{R}_0 < 1$ is a necessary and sufficient 476 condition for disease elimination [160, 199]. For many years, bifurcation analysis 477 for epidemic models has been studied extensively with many useful applications, 478 including forward bifurcation, backward bifurcation, Hopf bifurcation, Bogdanov-479 Takens bifurcation, saddle-node bifurcation, flip bifurcation are mainly focused [26, 480 28, 54, 76, 120, 185, 202, 243, 281, 304, 327, 412, 431]. 481

Chaos theory has many useful applications in many fields such as physics, biology, ecology and epidemiology, economics, etc. [73, 217, 328, 428]. In recent decades, chaos theory has been developed and studied with the aim of discovering
chaotic phenomena/dynamics, complicated or even unpredictable dynamical behavior in epidemic models [67, 74, 87, 161, 185, 190, 246, 316, 317, 318, 372, 373].

487 3.2. Analysis of PDE models. In general, the qualitative analysis aspects
 488 for PDE models of infectious diseases are very similar to those for ODE models.

In particular, the qualitative analysis of PDE models also focuses on well-489 posedness of mathematical models, positivity and boundedness of the solution, con-490 servation laws, equilibria and their asymptotic stability, basic reproduction numbers 491 and their implications, optimal control problems, parameter estimation, vaccina-492 tion models, bifurcations and chaos [31, 56, 61, 62, 91, 108, 109, 128, 129, 493 134, 158, 178, 187, 232, 241, 255, 267, 279, 280, 290, 291, 301, 306, 312, 494 353, 354, 385, 405, 437, 447, 448, 450, 457, 461, 482, 487, 488, 489, 490, 495 494, 502, 505, 507, 509, 517, 520, 522, 525]. 496

497 Several methods and tools used in the qualitative analysis of ODE models,
498 such as basic reproduction number, Lyapunov stability theory, optimal control,
499 bifurcation and chaos analysis, can be developed and extended for PDE models.
500 However, the qualitative study for PDE models is more challenging due to the
501 complexity of their structures.

502

4. Numerical methods

4.1. Standard and nonstandard numerical methods. It is well known that both ODEs and PDEs can be solved exactly only in a small number of cases, and that in most real-world situations it is almost inevitable to find approximate solutions. For this reason, numerical methods for differential equations have become one of the most fundamental and practically important research tasks [55, 203, 204, 289, 443, 453, 454, 467].

Numerical solutions for ODE models can be easily obtained using standard 509 numerical methods such as the Runge-Kutta and Taylor (one-step) methods and 510 multistep methods, while finite difference methods are appropriate and efficient for 511 the numerical solution of PDE models [55, 203, 204, 289, 445, 453, 454, 467]. 512 However, mathematical models arising in real-world applications in general, and in 513 infectious disease modeling in particular, often possess several essential qualitative 514 features, such as positivity, boundedness, asymptotic stability properties, conser-515 vation laws, periodicity and physical properties, etc., which must be respected 516 by corresponding numerical schemes. Therefore, an important requirement for 517 numerical methods is that they correctly preserve the essential properties of the 518 corresponding differential equations. However, it has been shown by Mickens in 519 [335, 338, 342, 343, 346, 348] that standard numerical methods cannot preserve 520 the mathematical properties of ODEs for all values of the temporal step size. 521

In the 1980s, Mickens proposed the concept of nonstandard finite difference 522 (NSFD) methods to compensate for drawbacks and shortcomings of standard nu-523 merical methods [335, 338, 342, 343, 346, 348]. One of the main and outstanding 524 advantages of NSFD methods is that they can preserve essential mathematical prop-525 erties of differential equations independently of the values of the step size. Such 526 NSFD methods are said to be *dynamically consistent*. Thus, dynamically consistent 527 NSFD methods are efficient and suitable for simulating the behavior of dynamic 528 differential equation models over long periods of time. 529

In addition to NSFD methods for ODEs, geometric numerical integration [96, 530 191, 205] (or both [93]) and positivity-preserving Runge-Kutta methods [69, 183, 531 228, 462] and modified Patankar-Runge-Kutta schemes [270, 271] have also been 532 developed to construct reliable numerical methods that preserve the positivity as 533 well as other dynamical properties of ODE models. 534

In the next subsection, we provide an overview of NSFD methods for mathe-535 matical models of infectious diseases and their applications. 536

4.2. Nonstandard finite difference methods for epidemiological mo-537 dels of infectious diseases. In numerical analysis, numerical instabilities are 538 solutions of finite difference models that do not correspond to any solution of the 539 counterpart differential equation [346]. Mickens, the creator of the concept of 540 NSFD methods, wrote: "Numerical instabilities are an indication that the discrete 541 models are unable to model the correct mathematical properties of the solutions to 542 the differential equations of interest" [335, 338, 342, 343, 346, 348]. The concept 543 of NSFD schemes was first introduced by Mickens in the 1980s to overcome the usual 544 numerical instabilities associated with standard finite-difference schemes [335, 338, 545 **342**, **343**, **346**, **348**]. A finite difference scheme is said to be *nonstandard* if it is 546 constructed based on a set of basic rules proposed by Mickens [335, 338, 342, 547 **343**, **346**, **348**. In particular, NSFD schemes for the ODE models of the form 548 (2.1) can be defined as follows. 549

Consider a general finite difference scheme for (2.1) of the form 550

...

(4.1)
$$D_{\Delta t}(y_k) = F_{\Delta t}(f; y_k),$$

....

where $D_{\Delta t}(y_k) \approx dy/dt$, $F_{\Delta t}(f; y_k) \approx f(y)$ and $t_k = k\Delta t$, Δt is the step size. 551

DEFINITION 4.1 ([**39**, **44**, **151**]). The finite difference scheme (4.1) is called an 552 NSFD scheme if at least one of the following conditions is satisfied: 553

•
$$D_{\Delta t}(y_k) = \frac{g_{k+1} - g_k}{\phi(\Delta t)}$$
, where $\phi(\Delta t) = \Delta t + \mathcal{O}(\Delta t^2)$ is a non-negative
function and is called a nonstandard denominator function;

•
$$F_{\Delta t}(f; y_k) = g(y_k, y_{k+1}, \Delta t)$$
, where $g(y_k, y_{k+1}, \Delta t)$ is a non-local approx-
imation of the right-hand side of the system (2.1).

NSFD schemes for (parabolic) PDEs [35, 111, 117, 144, 212, 249, 276, 331, 558 **340**, **362**, **379**, **394**], fractional-order differential equations [90], delay differential 559 equations are similarly defined based on the Mickens' methodology. 560

The main advantage of NSFD schemes over standard schemes is expressed in 561 the following definitions. 562

DEFINITION 4.2 ([39, 44]). Assume that the solutions of the equation (2.1)563 satisfy some property \mathcal{P} . The numerical scheme (4.1) is said to be (qualitatively) 564 stable with respect to the property \mathcal{P} (or \mathcal{P} -stable), if for every value of $\Delta t > 0$ the 565 set of solutions of (4.1) satisfies the property \mathcal{P} . 566

DEFINITION 4.3 ([41, 302, 342]). Consider the differential equation dy/dt =567 f(y). Let a finite difference scheme for the equation be $y_{k+1} = F(y_k; \Delta t)$. Let the 568 differential equation and/or its solutions have the property \mathcal{P} . The discrete model 569 equation is dynamically consistent with the differential equation if it and/or its 570 solutions also have the property \mathcal{P} . 571

14

Nowadays, NSFD methods based on the Mickens' methodology have become
an efficient approach for numerically solving ODE models arising in real-world
problems [5, 39, 40, 44, 131, 132, 135, 136, 137, 138, 139, 140, 148, 149,
150, 151, 152, 153, 172, 200, 225, 226, 334, 335, 338, 339, 342, 343, 344,
346, 347, 348, 350, 380, 382, 409, 410, 449, 499, 500, 501]. In particular,
NSFD schemes have been extensively studied for epidemic models, such as

- General epidemiological models [44, 52, 53, 110, 201, 325, 326]
- Influenza disease [**176**, **245**, **259**];
- Ebola [17, 45, 65, 237, 459];
- Hepatitis B [**220**, **221**];
- Visceral Leishmaniasis [4, 441];
- Malaria [**43**, **170**];
- Measles [13, 171];
- Zika [**310**, **465**];

588

- COVID-19 [66, 130, 210, 213, 222, 314, 396, 403, 470];
- Cancer: malignant invasion of tumor cells [49];
 - Computer virus propagation models [139, 218, 402].

Compared to numerical methods for ODE models, numerical methods for PDE 589 models are more challenging. Finite difference methods are one of the most common 590 and efficient approaches for numerical simulation of PDEs [55, 289, 453, 467]. It 591 is important to note that positivity should be an obvious property of the solutions of 592 both ODE and PDE models for infectious diseases. Therefore, positivity preserving 593 numerical methods are essential. To the best of our knowledge, numerical methods 594 that preserve positivity and other dynamical properties for the PDE models are 595 few. However, NSFD methods based on Mickens' methodology have been shown to 596 be suitable and effective for constructing such numerical methods [39, 41, 42, 112, 597 126, 162, 335, 336, 337, 338, 341, 342, 343, 345, 346, 348, 349, 492]. In 598 particular, dynamically consistent NSFD schemes have been applied to solve some 599 PDE models of infectious diseases [182, 319, 320, 378, 393, 457, 458, 513]. 600

Even though NSFD methods have several advantages, most of the existing 601 dynamically consistent NSFD methods are only first-order convergent [116, 124, 602 131, 218, 220, 221, which can be considered as an inherent drawback of NSFD 603 methods. For this reason, the problem of improving the accuracy of NSFD methods 604 has attracted the attention of many researchers [22, 116, 138, 186, 219, 223, 224, 605 226, 227, 269, 325, 326]. However, it is very challenging to construct dynamically 606 consistent NSFD methods, especially high-order methods, for differential equations. 607 In recent years, there has been an increased interest in solving PDEs using 608 *Deep Learning* (see e.g. [64, 71, 210, 398]). More recently, in [275], a deep 609 learning approach has been proposed to improve numerical methods for PDEs. 610 This approach is based on an approximation of the local truncation error of the 611 numerical method used to approximate the spatial derivatives of a given PDE. 612

In general, the construction of numerical methods, especially those that preserve important properties of differential models, is an important problem but not easy to solve. In addition, high-order numerical methods are still an important problem that has not been fully solved, and the reduced spatial accuracy of NSFD methods for PDEs is still an open problem.

NSFD methods for PDEs have lacked guaranteed first-order temporal accuracy
 and consistency for key models such as diffusion and reaction-diffusion systems. In

a recent paper Pasha, Nawaz and Arif [**378**] proposed a novel NSFD scheme that overcomes this limitation and guarantees first-order temporal accuracy and secondorder spatial accuracy while preserving positivity. The question remains as to how one can develop compact higher-order schemes with the NSFD concept.

5. Future research and open problems

Although research on differential equation models for infectious diseases has been extensively developed over the past decades and has achieved many important successes, these models still need to be studied and expanded for the following reasons.

First, mankind is always facing and fighting many infectious diseases, which 629 are not only constantly changing but also difficult to predict, and thus always pose 630 a great and constant threat to public health. In this context, the development of 631 mathematical models of infectious diseases remains a fundamental and effective ap-632 proach to discover the characteristics and mechanisms of transmission of epidemics, 633 and thus effectively predict possible scenarios in reality. On the other hand, as the 634 existing differential equation models are built based on observations, experience, 635 and understanding of the diseases, they often become outdated and therefore need 636 to be updated and modified to keep up with the constant changes in epidemics. 637 Therefore, in addition to building new models, improving existing models is also 638 very important. 639

Second, once mathematical models have been formulated, aspects of qualita-640 tive study and approximate solutions are raised. Addressing these issues is useful 641 for finding appropriate strategies for disease prevention and control, as well as for 642 predicting disease spread scenarios. In addition, infectious diseases often need to 643 be monitored over very long periods of time. This leads to the rapid solution of 644 differential equation models over long time periods. Therefore, efficient numeri-645 cal methods are urgently needed. However, the construction of efficient high-order 646 numerical methods in general, and numerical methods that preserve essential qual-647 itative properties of differential equation models in particular, is still an important 648 problem that has not been fully solved. 649

Lastly, the practical application of mathematical models of infectious diseases is essential, but has not been widely used. In particular, theoretical studies should be combined with observed real-world epidemic data to calibrate the mathematical models and find optimal parameters, thereby building scenarios that better reflect reality and proposing appropriate anti-epidemic strategies.

For the above reasons, differential equation models for infectious diseases need to be studied and developed. To achieve this, it is also necessary to develop and extend research methods to keep pace with the complexity of the proposed models. Another future direction is to use one NSFD scheme not exclusively, but as one element in a *hybrid scheme approach*, e.g. using operator splitting [13, 17], Chebyshev collocation [6], Hermite Polynomials [400] wavelets [399, 481] or a predictor corrector NSFD approach [171].

A special challenge are mimetic / fitted operator schemes for singular perturbed problems, due to the necessary resolution of boundary layers having different scales, e.g. convection-diffusion equations [46, 47, 251], Burgers-Huxley equation [143], differential difference equations [381] or boundary value ODE problems [308, 376].

Finally, most recent research directions for NSFD schemes are integro-differential equations [**333**], the GPU acceleration of the (serial) NSFD code [**247**] and geometric numerical integration, symmetrization of NSFD schemes [**93**].

6. Concluding remarks and discussions

In this work, we have reviewed many but not all recent developments and 670 real-life applications of deterministic ODEs and PDEs of major infectious diseases, 671 mainly focusing on mathematical modeling, qualitative analysis, numerical meth-672 673 ods and real-life applications. We have also presented and discussed some open problems and future directions that research in differential equation models for 674 infectious diseases can take. In the presentation, we focus only on deterministic 675 differential equation models associated with the integer-order derivatives. Delayed 676 models [352], stochastic models [16, 59, 388, 516], and fractional-order models, 677 especially for PDEs [46, 47, 90, 460], will be considered in future work. 678

All the results presented demonstrate the important role of differential equation models in disease modeling. Moreover, they remain an effective and indispensable approach to study the characteristics of infectious diseases and thereby suggest effective measures for disease prevention and public health protection.

683 Declarations

Availability of data and material. Does not apply.

685 **Competing interests.** The authors declare that they have no competing in-686 terests.

Funding. Manh Tuan Hoang was supported by the Vietnam Institute for Ad-vanced Study in Mathematics (VIASM).

689 Authors' contributions.

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Manh Tuan Hoang (M. T.H.). Initiated the concept of the review, defined the scope, conceived the study, designed the methodology, performed critical analysis and comparison of mathematical models and methods.

Matthias Ehrhardt (M.E.). supervised the project and the overall structure and content development, drafted significant portions of the manuscript, focusing on theoretical frameworks and methodological discussions.

All authors: Contributed to manuscript editing, to final revisions and conducted an extensive literature search and approved the final manuscript.

Acknowledgments. The first author, Manh Tuan Hoang, wish to thank Viet nam Institute for Advanced Study in Mathematics (VIASM) for the financial sup port and the excellent working condition. This work was completed while he was
 working at the VIASM.

References

- [1] R. T. Abah, A. B. Zhiri, K. Oshinubi, A. Adeniji, Mathematical analysis and simulation
 of Ebola virus disease spread incorporating mitigation measures. Franklin Open 6 (2024)
 100066.
- [2] M. Abdelheq, O. Belhamiti, L. Bouzid, D. Y. Trejos, J. C. Valverde, A predictive spatiotemporal model for bovine Babesiosis epidemic transmission, Journal of Theoretical Biology 480 (2019) 192-204.

709	[3]	A. I. Abioye, O. J. Peter, E. Addai, F. A. Oguntolu, T. A. Ayoola, Modeling the impact
710		of control strategies on malaria and COVID-19 coinfection: insights and implications for
711		integrated public health interventions, Quality & Quantity (2023).
712	[4]	E. M. Adamu, K. C. Patidar, A. Ramanantoanina, An unconditionally stable nonstandard
713		finite difference method to solve a mathematical model describing Visceral Leishmaniasis,
714		Mathematics and Computers in Simulation 187 (2021) 171-190.
715	[5]	O. Adekanye, T. Washington, Nonstandard finite difference scheme for a Tacoma Narrows
716		Bridge model, Applied Mathematical Modelling 62 (2018) 223-236.
717	[6]	P. Agarwal, A. A. El-Sayed, Non-standard finite difference and Chebyshev collocation meth-
718		ods for solving fractional diffusion equation, Physica A: Statistical Mechanics and Its Ap-
719		plications 500 (2018) 40-49.
720	[7]	P. Agarwal, J. J. Nieto, M. Ruzhansky, D. F. M. Torres, Analysis of Infectious Disease
721		Problems (Covid-19) and Their Global Impact, Springer, Singapore, 2021.
722	[8]	F. B. Agusto, A. B. Gumel, Theoretical Assessment of Avian Influenza Vaccine, Discrete
723		and Continuous Dynamical Systems - B 13 (2010) 1-25.
724	[9]	F. B. Agusto, S. Lenhart, A. B. Gumel, A. Odoi, Mathematical analysis of a model for
725		the transmission dynamics of bovine tuberculosis, Mathematical Methods in the Applied
726		Sciences, 34 (2011) 1873-1887.
727	[10]	F. B. Agusto, A.B. Gumel, Qualitative dyNumerical Partialamics of lowly- aNumerical Par-
728		tiald highly-pathogeNumerical Partialic avian influenza strains, Mathematical Biosciences
729		243 (2013) 147-162.
730	[11]	F. B. Agusto, S. Bewick, W. F. Fagan, Mathematical model of Zika virus with vertical
731		transmission, Infectious Disease Modelling 2 (2017) 244-267.
732	[12]	W. Ahmad, M. Rafiq, A. I. K. Butt, N. Ahmad, T. Ismaeel, S. Malik, H. G. Rabbani, Z.
733		Asif, Analytical and numerical explorations of optimal control techniques for the bi-modal
734		dynamics of Covid-19, Nonlinear Dynamics (2024) 1-30.
735	[13]	N. Ahmed, T. S. Shaikh, M. Rafiq, M. A. Rehman, M. Ali, M. O. Ahmad, Positivity pre-
736		serving operator splitting nonstandard finite difference methods for SEIR reaction diffusion
737		model, Open Mathematics 17(1) (2019) 313-330.
738	[14]	N. Ahmed, M. Rafiq, D. Baleanu, A. S. Alshomrani M. A. Rehman, Positive explicit and
739		implicit computational techniques for reaction-diffusion epidemic model of dengue disease
740		dynamics, Advances in Difference Equations 2020 (2020), 202.
741	[15]	N. Ahmed, M. Rafiq, W. Adel, H. Rezazadeh, I. Khan, K. S. Nisar, Structure preserving nu-
742		merical analysis of HIV and CD4+ T-cells reaction diffusion model in two space dimensions,
743		Chaos Solitons & Fractals 139 (2020) 110307.
744	[16]	N. Ahmed, J. E. Macías-Díaz, A. Raza, D. Baleanu, M. Rafiq, Z. Iqbal, M. O. Ahmad,
745		Design, analysis and comparison of a nonstandard computational method for the solution
746		of a general stochastic fractional epidemic model, Axioms $11(1)$ (2021) 10.
747	[17]	N. Ahmed, T. S. Shaikh, M. Rafiq, S. M. Eldin, A. H. Ganie, M. Ali, A. Raza, I. Khan,
748		M. I. Khan, Structure preserving splitting techniques for Ebola reaction-diffusion epidemic
749		systems, Fractals 31(02) (2023) 2340041.
750	[18]	S. Al-Shanfari, I. M. Elmojtaba, N. Al-Salti, F. Al-Shandari, Mathematical analysis and
751		optimal control of cholera-malaria co-infection model, Results in Control and Optimization,
752		$(2024) \ 100393.$
753	[19]	F. Al-Showaikh, E. Twizell, One-dimensional measles dynamics, Applied Mathematics and
754		Computation 152 (2004), 169-194.
755	[20]	F. K. Alalhareth, Higher-Order Nonstandard Finite Difference Methods for Autonomous
756		Differential Equations with Applications in Mathematical Ecology, PhD dissertation, The
757		University of Texas at Arlington, 2022.
758	[21]	F. K. Alalhareth, H. V. Kojouharov, Analysis and an NSFD method of a model of bacterial
759	[0.2]	competition in the presence of a plasmid, Biomath Communications Supplement (2023).
760	[22]	F. K. Alalhareth, M. Gupta, S. Roy, H. V. Kojouharov, Second-order modified positive and
761		elementary stable nonstandard numerical methods for <i>n</i> -dimensional autonomous differential
762	[0.2]	equations, Mathematical Methods in the Applied Sciences (2023)
763	[23]	F. K. Alainareth, M. Gupta, H. V. Kojouharov, S. Roy, Second-Order Modified Nonstandard
/64		Explicit Euler and Explicit Runge-Kutta Methods for n-Dimensional Autonomous Differen-
/65		that Equations, Computation 12(9) (2024) 183.

- [24] H. T. Alemneh, Z. T. Melese, Modeling, analyzing and simulating the dynamics of
 Tuberculosis- Covid-19 co-infection, Journal of Information & Optimization Sciences 45(1)
 (2024) 73-94.
- [25] M. E. Alexander, C. Bowman, S. M. Moghadas, R. Summers, A. B. Gumel, B. M. Sahai,
 A Vaccination Model for Transmission Dynamics of Influenza, SIAM Journal on Applied
 Dynamical Systems 3 (2004) 503-524.
- [26] M. E. Alexander, S. M. Moghadas, Bifurcation Analysis of an SIRS Epidemic Model with
 Generalized Incidence, SIAM Journal on Applied Mathematics 65 (2005) 1794-1816.
- [27] W. F. Alfwzan, K. Abuasbe, A. Raza, M. Rafiq, M. Awadalla, M. A. Almulla, A non standard computational method for stochastic anthrax epidemic model, AIP Advances 13(7)
 (2023).
- [28] L. J. S. Allen, P. van den Driessche, Stochastic epidemic models with a backward bifurcation,
 Mathematical Biosciences and Engineering 3 (2006) 445-458.
- [29] E. Allen, Modeling with Itô Stochastic Differential Equations, Springer-Verlag, Dordrecht,
 The Netherlands, 2007.
- [30] L. J. S. Allen, An Introduction to Mathematical Biology, Prentice Hall, 2007.
- [31] L. J. S. Allen, B. M. Bolker, Y. Lou, A. L. Nevai, Asymptotic profiles of the steady states
 for an SIS epidemic reaction-diffusion model, Discrete and Continuous Dynamical Systems
 B 21 (2008) 1-20.
- [32] L. J. S. Allen, An Introduction to Stochastic Epidemic Models. In: Brauer, F., van den
 Driessche, P., Wu, J. (eds) Mathematical Epidemiology. Lecture Notes in Mathematics 1945,
 2008, Springer, Berlin, Heidelberg.
- [33] H. Alrabaiah, R. U. Din, K. J. Ansari, B. Ozdemir, Stability and numerical analysis via
 non-standard finite difference scheme of a nonlinear classical and fractional order model,
 Results in Physics 49 (2023) 106536.
- 791 [34] A. Alshareef, Quantitative analysis of a fractional order of the $SEI_cI_{\eta}VR$ epidemic model 792 with vaccination strategy, AIMS Mathematics 9(3) (2024) 6878-6903.
- [35] J. Alvarez-Ramirez, F. J. Valdes-Parada, Non-standard finite-differences schemes for gen eralized reaction-diffusion equations, Journal of Computational and Applied Mathematics
 228(1) (2009) 334-343.
- [36] R. M. Anderson, R. M. May, Infectious Diseases in Humans: Dynamics and Control, Oxford
 University Press, Oxford, 1991.
- [37] H. Andersson, T. Britton, Stochastic Epidemic Models and Their Statistical Analysis,
 Springer, New York, 2000.
- [38] C. N. Angstmann, A. M. Erickson, B. I. Henry, A. V. McGann, J. M. Murray, A. James,
 Fractional Order Compartment Models, SIAM Journal on Applied Mathematics 77 (2017)
 430-446.
- [39] R. Anguelov, J. M.-S. Lubuma, Contributions to the mathematics of the nonstandard finite
 difference method and applications, Numerical Methods for Partial Differential Equations
 17 (2001) 518-543.
- [40] R. Anguelov, J. M.-S. Lubuma, Nonstandard finite difference method by nonlocal approxi mation, Mathematics and Computers in Simulation 61 (2003) 465-475.
- [41] R. Anguelov, J. M.-S. Lubuma, S. K. Mahudu, Qualitatively stable finite difference schemes
 for advection-reaction equations, Journal of Computational and Applied Mathematics 158
 (2003) 19-30.
- [42] R. Anguelov, P. Kama, J. M.-S. Lubuma, On non-standard finite difference models of
 reaction-diffusion equations, Journal of Computational and Applied Mathematics 175 (2005)
 11-29.
- [43] R. Anguelov, Y. Dumont, J. M.-S. Lubum, E. Mureithi, Stability Analysis and Dynam ics Preserving Nonstandard Finite Difference Schemes for a Malaria Model, Mathematical
 Population Studies 20 (2013) 101-122.
- [44] R. Anguelov, Y. Dumont, J. M.-S. Lubuma, M. Shillor, Dynamically consistent nonstandard
 finite difference schemes for epidemiological models, Journal of Computational and Applied
 Mathematics 255 (2014) 161-182.
- [45] R. Anguelov, T. Berge, M. Chapwanya, J. K. Djoko, P. Kama, J. M.-S. Lubuma, Y. Terefe,
 Nonstandard finite difference method revisited and application to the Ebola virus disease
 transmission dynamics, Journal of Difference Equations and Applications 26 (2020) 818-854.

- [46] W. T. Aniley, G. F. Duressa, Uniformly convergent numerical method for time-fractional
 convection-diffusion equation with variable coefficients, Partial Differential Equations in
 Applied Mathematics 8 (2023) 100592.
- [47] W. T. Aniley, G. F. Duressa, Nonstandard finite difference method for time-fractional sin gularly perturbed convection-diffusion problems with a delay in time. Results in Applied
 Mathematics 21 (2024) 100432.
- [48] S. Anita, V. Capasso, Reaction-Diffusion Systems in Epidemiology, An. Stiint. Univ. Al. I.
 Cuza Iasi. Mat. (N.S.) Tomul LXVI, 2020, f. 2.
- [49] A. R. Appadu, G. N. de Waal, Numerical solution of a malignant invasion model using some
 finite difference methods, Demonstratio Mathematica 56(1) (2023) 20220244.
- [50] D. F. Aranda, D. Y. Trejos, J. C. Valverde, R. J. Villanueva, A mathematical model for
 Babesiosis disease in bovine and tick populations, Mathematical Methods in the Applied
 Sciences 35 (2012) 249-256.
- [51] A. J. Arenas, G. González-Parra, L. Jódar, Periodic solutions of nonautonomous differential
 systems modeling obesity population, Chaos, Solitons & Fractals 42 (2009) 1234-1244.
- [52] A. J. Arenas, G. González-Parra, B. M. Chen-Charpentier, A nonstandard numerical scheme
 of predictor-corrector type for epidemic models, Computers & Mathematics with Applica tions 59 (2010) 3740-3749.
- [53] A. J. Arenas, G. González-Parra, B. M. Chen-Charpentier, Construction of nonstandard
 finite difference schemes for the SI and SIR epidemic models of fractional order, Mathematics
 and Computers in Simulation 121 (2016) 48-63.
- [54] J. Arino, C. C. McCluskey, P. van den Driessche, Global Results for an Epidemic Model with
 Vaccination that Exhibits Backward Bifurcation, SIAM Journal on Applied Mathematics
 64 (2003) 260-276.
- [55] U. M. Ascher, L. R. Petzold, Computer Methods for Ordinary Differential Equations and
 Differential-Algebraic Equations, Society for Industrial and Applied Mathematics, Philadel phia, 1998.
- [56] E. Avila-Vales, G. E. García-Almeida, A. G. C. Pérez, Qualitative analysis of a diffusive
 SIR epidemic model with saturated incidence rate in a heterogeneous environment, Journal
 of Mathematical Analysis and Applications 503 (2021) 125295.
- [57] W. S. Avusuglo, N. Bragazzi, A. Asgary, J. Orbinski, J. Wu, J. D. Kong, Leveraging an
 epidemic-economic mathematical model to assess human responses to COVID-19 policies
 and disease progression. Scientific Reports 13 (2024) 12842.
- [58] E. Azhar, S. Batool, M. Jamal, I. Ahmed, H. Ali, Y. Hafeez, Optimizing Vertical Transmission Control: A Hybrid Neural Network Approach with Wolbachia for Zika Virus, International Journal of Computational Materials Science and Engineering (2024).
- [59] M. Z. Baber, A. R. Seadway, M. S. Iqbal, N. Ahmed, M. W. Yasin, M. O. Ahmed, Comparative analysis of numerical and newly constructed soliton solutions of stochastic Fisher-type
 equations in a sufficiently long habitat, International Journal of Modern Physics B 37(16)
 (2023) 2350155.
- [60] S. R. Bandekar, M. Ghosh, A co-infection model on TB-COVID-19 with optimal control
 and sensitivity analysis, Mathematics and Computers in Simulation 200 (2022) 1-31.
- [61] M. Banerjee, S. Ghosh, P. Manfredi, A. d'Onofrio, Spatio-temporal chaos and clustering
 induced by nonlocal information and vaccine hesitancy in the SIR epidemic model, Chaos,
 Solitons & Fractals 170 (2023) 113339.
- [62] M. Barman, N. Mishra, Hopf bifurcation analysis for a delayed nonlinear-SEIR epidemic
 model on networks, Chaos, Solitons & Fractals 178 (2024) 114351.
- [63] N. A. Battista, L. B. Pearcy, W. C. Strickland, Modeling the Prescription Opioid Epidemic,
 Bulletin of Mathematical Biology 81(2019) 2258-2289.
- [64] C. Beck, M. Hutzenthaler, A. Jentzen, B. Kuckuck, An overview on deep learning-based approximation methods for partial differential equations, Discrete and Continuous Dynamical
 Systems-B 28 (2023) 3697-3746.
- [65] T. Berge, J. M.-S. Lubuma, G. M. Moremedi, N. Morrisdan, R. Kondera-Shava, A simple
 mathematical model for Ebola in Africa, Journal of Biological Dynamics 11 (2007) 42-74.
- [66] S. Berkhahn, M. Ehrhardt, A Physics-Informed Neural Network to Model COVID-19 Infec-
- tion and Hospitalization Scenarios, Advances in Continuous and Discrete Models: Theoryand Applications 2022, 61 (2022).

- [67] L. Billings, I. B. Schwartz, Exciting chaos with noise: unexpected dynamics in epidemic outbreaks, Journal of Mathematical Biology 44 (2002) 31-48.
 [68] S. K. Biswas, U. Ghosh, S. Sarkar, Mathematical model of Zika virus dynamics with vector control and sensitivity analysis, Infectious Disease Modelling 5 (2020) 23-41.
- [69] S. Blanes, A. Iserles, S. Macnamara, Positivity-preserving methods for ordinary differential
 equations, ESAIM: M2AN 56 (2022) 1843-1870.
- [70] K. Blayneh, Y. Cao, Hee-Dae Kwon, Optimal control of vector-borne diseases: Treatment
 and prevention, Discrete and Continuous Dynamical Systems B 11 (2009) 587-611.
- [71] J. Blechschmidt, O. G. Ernst, Three ways to solve partial differential equations with neural
 networks A review, GAMM-Mitteilungen 44(2)(2021) e202100006.
- [72] S. M. Blower , P. M. Small, P. C. Hopewell, Control Strategies for Tuberculosis Epidemics:
 New Models for Old Problems, Science 273 (1996) 497-500.
- [73] S. Boccaletti, C. Grebogi, Y.-C. Lai, H. Mancini, D. Maza, The control of chaos: theory
 and applications, Physics Reports 329 (2000) 103-197.
- [74] B. M. Bolker, B. T. Grenfell, Chaos and biological complexity in measles dynamics, Proceedings of the Royal Society B 251 (1993) 75-81.
- [75] S. Bonhoeffer, R. M. May, G. M. Shaw, M. A. Nowak, Virus dynamics and drug therapy,
 The Proceedings of the National Academy of Sciences 94 (1997) 6971-6976.
- [76] F. Brauer, Backward bifurcations in simple vaccination models, Journal of Mathematical
 Analysis and Applications 298 (2004) 418-431.
- 900 [77] F. Brauer, The Kermack-McKendrick epidemic model revisited, Mathematical Biosciences
 901 198 (2005) 119-131.
- [78] F. Brauer, Compartmental Models in Epidemiology, In: Brauer, F., van den Driessche, P.,
 Wu, J. (eds) Mathematical Epidemiology. Lecture Notes in Mathematics, vol. 1945, 2008,
 Springer, Berlin, Heidelberg.
- [79] F. Brauer, P. Driessche, J. Wu, Mathematical Epidemiology, Springer Berlin, Heidelberg,
 2008.
- [80] F. Brauer, C. Castillo-Chavez, Mathematical Models in Population Biology and Epidemiol ogy, Springer, 2012.
- [81] F. Brauer, C. Castillo-Chavez, Mathematical Models for Communicable Diseases, Society
 for Industrial and Applied Mathematics, Philadelphia, 2013.
- [82] F. Brauer, Mathematical epidemiology: Past, present, and future, Infectious Disease Mod elling 2 (2017) 113-127.
- [83] F. Brauer, P. Driessche, Z. Feng, Mathematical Models in Epidemiology, Springer, New
 York, 2019.
- [84] T. Britton, Stochastic epidemic models: A survey, Mathematical Biosciences 225 (2010)
 24-35.
- [85] B. Buonomo, C. Vargas-De-León, Stability and bifurcation analysis of a vector-bias model
 of malaria transmission, Mathematical Biosciences 142 (2013) 59-67.
- [86] B. Buonomo, D. Lacitignola, C. Vargas-De-León, Qualitative analysis and optimal control
 of an epidemic model with vaccination and treatment, Mathematics and Computers in
 Simulation 100 (2014) 88-102.
- [87] B. Buonomo, N. Chitnis, A. d'Onofrio, Seasonality in epidemic models: a literature review,
 Ricerche di Matematica 67 (2018) 7-25.
- [88] C. Butler, P. Stechlinski, Modeling Opioid Abuse: A Case Study of the Opioid Crisis in
 New England, Bulletin of Mathematical Biology 85(6) (2023) 45.
- [89] A. R. Butt, A. A. Saqib, A. S. Alshomrani, A. Bakar, M. Inc, Dynamical analysis of a
 nonlinear fractional cervical cancer epidemic model with the nonstandard finite difference
 method. Ain Shams Engineering Journal, 15(3) (2024) 102479.
- [90] L. Cai, M. Guo, Y. Li, W. Ying, H. Gao, X. Luo, Nonstandard finite difference method
 for nonlinear Riesz space fractional reaction-diffusion equation, International Journal of
 Numerical Analysis & Modeling 16(6) (2019) 925-938.
- [91] Y. Cai, S. Yan, H. Wang, X. Lian, W. Wang, Spatiotemporal Dynamics in a Reaction Diffusion Epidemic Model with a Time-Delay in Transmission, International Journal of
 Bifurcation and Chaos, 25 (2015) 1550099.
- [92] Y. Cai, Y. Kang, W. Wang, A stochastic SIRS epidemic model with nonlinear incidence
 rate, Applied Mathematics and Computation 305 (2017) 221-240.

- [93] J. Calatayud, M. Jornet, Mathematical modeling of adulthood obesity epidemic in Spain
 using deterministic, frequentist and Bayesian approaches, Chaos, Solitons & Fractals 140
 (2020) 110179.
- [94] J. Calatayud, M. Jornet, On the symmetrization and composition of nonstandard finite
 difference schemes as an alternative to Richardson's extrapolation, Journal of Difference
 Equations and Applications 28(5) (2022), 716-724.
- 943 [95] W. K. Caldwell, B. Freedman, L. Settles, M. M. Thomas, E.T. Camacho, S. Wirkus, The Vi944 codin abuse problem: A mathematical approach, Journal of Theoretical Biology 483 (2019)
 945 110003.
- [96] M. Calvo, M. P. Laburta, J. I. Montijano, L. Rández, Projection methods preserving Lya punov functions, BIT Numerical Mathematics 50 (2010) 223-241.
- 948 [97] C. Camacho, R. Desbordes, D. La Torre, A time-space integro-differential economic model
 949 of epidemic control, Economic Theory 77(1) (2024) 307-348.
- [98] N. Cangiotti, M. Capolli, M. Sensi, S. Sottile, A survey on Lyapunov functions for epidemic
 compartmental models, Bollettino dell'Unione Matematica Italiana (2023) 1-17.
- [99] V. Capasso, G. Serio, A generalization of the Kermack-McKendrick deterministic epidemic
 model, Mathematical Biosciences 42 (1978) 43-61.
- [100] V. Capasso, Reaction-Diffusion Models for the Spread of a Class of Infectious Diseases. In:
 H. Neunzert (eds), Proceedings of the Second European Symposium on Mathematics in
- Industry. European Consortium for Mathematics in Industry 3, 1988, Springer, Dordrecht.
 [101] A. M. Carvalho, S. Goncalves, An analytical solution for the Kermack–McKendrick model,
- 958 Physica A 566 (2021) 125659.
- [102] R. Casagrandi, L. Bolzoni, S. A. Levin, V. Andreasen, The SIRC model and influenza A,
 Mathematical Biosciences 200 (2006) 152-169.
- 961 [103] C. Castillo-Chavez, Z. Feng, W. Huang, On the computation of R₀ and its role in global
 962 stability. In: Mathematical Approaches for Emerging and Reemerging Infectious Diseases:
 963 An Introduction, IMA, 125 (2002) 229-250.
- 964 [104] M. A. Castro, C. J. Mayorga, A. Sirvent, F. Rodríguez, Exact numerical solutions and
 965 high order nonstandard difference schemes for a second order delay differential equation,
 966 Mathematical Methods in the Applied Sciences 46(17) (2023) 17962-17979.
- 967 [105] I. T. Cetinkaya, An Application of Nonstandard Finite Difference Method to a Model De 968 scribing Diabetes Mellitus and Its Complications, Journal of New Theory 45 (2023) 105-119.
- [106] A. Champneys, K. Tsaneva-Atanasova, Dynamical Systems Theory, Bifurcation Analysis,
 Encyclopedia of Systems Biology, pp. 632-637.
- [107] K. Chang, Z. Zhang, G. Liang, Dynamics analysis of a nonlocal diffusion dengue model,
 Scientific Reports 13(1) (2023) 15239.
- [108] L. Chang, W. Gong, Z. Jin, G.-Q. Sun, Sparse Optimal Control of Pattern Formations for an
 SIR Reaction-Diffusion Epidemic Model, SIAM Journal on Applied Mathematics 82(2022)
 1764-1790.
- [109] L. Chang, X. Wang, G. Sun, Z. Wang, Z. Jin, A time independent least squares algorithm
 for parameter identification of Turing patterns in reaction-diffusion systems, Journal of
 Mathematical Biology 88(1) (2024) 5.
- [110] M. Chapwanya, J. M.-S. Lubuma, R. E. Mickens, From enzyme kinetics to epidemiological models with Michaelis-Menten contact rate: Design of nonstandard finite difference schemes, Computers & Mathematics with Applications 64 (2012) 201-213.
- 982 equation; nonstandard finite difference metho
- [111] M. Chapwanya, J. M.-S. Lubuma, R. E. Mickens, Nonstandard finite difference schemes for
 Michaelis-Menten type reaction-diffusion equations, Numerical Methods for Partial Differ ential Equations 29(1) (2013) 337-360.
- [112] M. Chapwanya, J. M.-S. Lubuma, R. E. Mickens, Positivity-preserving nonstandard finite
 difference schemes for cross-diffusion equations in biosciences, Computers & Mathematics
 with Applications 68 (2014) 1071-1082.
- [113] L. Chen, J. Sun, Optimal vaccination and treatment of an epidemic network model, Physics
 Letters A 378 (2014) 3028-3036.
- [114] W.-Y. Chen, S. Bokka, Stochastic modeling of nonlinear epidemiology, Journal of Theoretical
 Biology 234(4) (2005) 455-470.
- [115] Y. Chen, F. Liu, Q. Yu, T. Li, Review of fractional epidemic models, Applied Mathematical
 Modelling 97 (2021) 281-307.

- [116] B. M. Chen-Charpentier, D. T. Dimitrov, H. V. Kojouharov, Combined nonstandard nu merical methods for ODEs with polynomial right-hand sides, Mathematics and Computers
 in Simulation 73 (2006) 105-113.
- [117] B. M. Chen-Charpentier, H. V. Kojouharov, An unconditionally positivity preserving scheme
 for advection-diffusion reaction equations, Mathematical and Computer Modelling 57(9-10)
 (2013) 2177-2185.
- [118] C. Cheng, Z. Zheng, Dynamics and spreading speed of a reaction-diffusion system with
 advection modeling West Nile virus, Journal of Mathematical Analysis and Applications
 493 (2021) 124507.
- 1004 [119] M. L. Childs, M. P. Kain, M. J. Harris, D. Kirk, L. Couper, N. Nova, I. Delwel, J. Ritchie,
- A. D. Becker, E. A. Mordecai, The impact of long-term non-pharmaceutical interventions
 on COVID-19 epidemic dynamics and control: the value and limitations of early models,
 Proceedings of the Royal Society B 288 (2021) 20210811.
- [120] N. Chitnis, J. M. Cushing, J. M. Hyman, Bifurcation Analysis of a Mathematical Model for
 Malaria Transmission, SIAM Journal on Applied Mathematics 67 (2006) 24-45.
- [121] G. Chowell, P. W. Fenimore, M. A. Castillo-Garsow, C. Castillo-Chavez, SARS outbreaks
 in Ontario, Hong Kong and Singapore: the role of diagnosis and isolation as a control
 mechanism, Journal of Theoretical Biology 224 (2003) 1-8.
- [122] G. Chowell, Fitting dynamic models to epidemic outbreaks with quantified uncertainty: A
 primer for parameter uncertainty, identifiability, and forecasts, Infectious Disease Modelling
 2 (2017) 379-398.
- [123] A.-S. Ciupeanu, M. Varughese, W. C. Roda, D. Han, Q. Cheng, M. Y. Li, Mathematical
 modeling of the dynamics of COVID-19 variants of concern: Asymptotic and finite-time
 perspectives, Infectious Disease Modelling 7(4) (2022) 581-596.
- [124] D. P. Clemence-Mkhope, Dynamically Consistent NSFD Discretization of Some Productive Destructive Population Models Satisfying Conservations Laws, Open Access Library Journal
 8(4) (2021) 1-12.
- [125] S. Cole, S. Wirkus, Modeling the Dynamics of Heroin and Illicit Opioid Use Disorder,
 Treatment, and Recovery, Bulletin of Mathematical Biology 84 (2022) 48.
- [126] D. Conte, G. Pagano, B. Paternoster, Nonstandard finite differences numerical methods for
 a vegetation reaction-diffusion model, Journal of Computational and Applied Mathematics
 419 (2023) 114790.
- [127] K. L. Cooke, P. van den Driessche, Analysis of an SEIRS epidemic model with two delays,
 Journal of Mathematical Biology 35 (1996) 240-260.
- [128] A. Coronel, F. Huancas, I. Hess, A. Tello, The diffusion identification in a SIS reaction diffusion system, Mathematical Biosciences and Engineering 21 (2024) 562-581.
- [129] C. Cosner, J. C. Beier, R. S. Cantrell, D. Impoinvil, L. Kapitanski, M. D. Potts, A. Troyo, S.
 Ruan, The effects of human movement on the persistence of vector-borne diseases, Journal
 of Theoretical Biology 258 (2009) 550-560.
- [130] G. M. R. Costa, M. Lobosco, M. Ehrhardt, R. F. Reis, Mathematical Analysis and a Nonstandard Scheme for a Model of the Immune Response against COVID-19, in: A. Gumel
 (ed.), Mathematical and Computational Modeling of Phenomena Arising in Population Bi-
- 1037 ology and Nonlinear Oscillations: In honour of the 80th birthday of Ronald E. Mickens,
 1038 AMS Contemporary Mathematics, 2023.
- [131] J. Cresson, F. Pierret, Non standard finite difference scheme preserving dynamical properties, Journal of Computational and Applied Mathematics 303 (2016) 15-30.
- [132] J. Cresson, A. Szafrańska, Discrete and continuous fractional persistence problems the
 positivity property and applications, Communications in Nonlinear Science and Numerical
 Simulation 44 (2017) 424-448.
- [133] N. Crokidakis, L. Sigaud, Modeling the evolution of drinking behavior: A Statistical Physics
 perspective, Physica A 570 (2021) 125814.
- [134] R. Cui, King-Yeung Lam, Y. Lou, Dynamics and asymptotic profiles of steady states of
 an epidemic model in advective environments, Journal of Differential Equations 263 (2017)
 2343-2373.
- [135] Q. A. Dang, M. T. Hoang, Dynamically consistent discrete metapopulation model, Journal
 of Difference Equations and Applications 22 (2016) 1325-1349.

- 1051 [136] Q. A. Dang, M. T. Hoang, Lyapunov direct method for investigating stability of nonstandard
- 1052 finite difference schemes for metapopulation models, Journal of Difference Equations and1053 Applications 24 (2018) 15-47.
- [137] Q. A. Dang, M. T. Hoang, Nonstandard finite difference schemes for a general predator-prey system, Journal of Computational Science 36 (2019) 101015.
- [138] Q. A. Dang, M. T. Hoang, Positive and elementary stable explicit nonstandard Runge-Kutta methods for a class of autonomous dynamical systems, International Journal of Computer Mathematics 97 (2020) 2036-2054.
- [139] Q. A. Dang, M. T. Hoang, Positivity and global stability preserving NSFD schemes for
 a mixing propagation model of computer viruses, Journal of Computational and Applied
 Mathematics 374 (2020) 112753.
- [140] Q. A. Dang, M. T. Hoang, Exact finite difference schemes for three dimensional linear
 systems with constant coefficient, Vietnam Journal of Mathematics 46 (2018) 471–492.
- [141] M. Z. Dauhoo, B. S. N. Korimboccus, S. B. Issack, On the dynamics of illicit drug consumptions
 tion in a given population, IMA Journal of Applied Mathematics 78 (2013) 432-448.
- [142] A. Dénes, A. B. Gumel, Modeling the impact of quarantine during an outbreak of Ebola
 virus disease, Infectious Disease Modelling 4 (2019) 12-27.
- [143] E. B. Derzie, J. B. Munyakazi, T. G. Dinka, A NSFD method for the singularly perturbed
 Burgers-Huxley equation, Frontiers in Applied Mathematics and Statistics 9 (2023) 1068890.
- [144] G. N. de Waal, A. R. Appadu, C. J. Pretorius, Some standard and nonstandard finite
 difference schemes for a reaction-diffusion-chemotaxis model, Open Physics 21(1) (2023)
 20220231.
- 1073 [145] O. Diekmann, J. A. P. Heesterbeek, J. A. J. Metz, On the definition and the computa-1074 tion of the basic reproduction ratio R_0 in models for infectious diseases in heterogeneous 1075 populations, Journal of Mathematical Biology 28 (1990) 365-382.
- [146] O. Diekmann, J. A. P. Heesterbeek, Mathematical Epidemiology of Infectious Diseases:
 Model Building, Analysis and Interpretation, Wiley; 1st edition, New York 2000.
- [147] K. Dietz, Overall patterns in the transmission cycle of infectious disease agents, In: R.M.
 Anderson, R.M. May (eds.) Population Biology of Infectious Diseases. Life Sciences Research
 Report, Vol. 25. Springer, Berlin Heidelberg New York, pp. 87-102 (1982).
- [148] D. T. Dimitrov, H. V. Kojouharov, Complete mathematical analysis of predator-prey models
 with linear prey growth and Beddington-DeAngelis functional response, Applied Mathemat ics and Computation 162 (2005) 523-538.
- [149] D. T. Dimitrov, H. V. Kojouharov, Nonstandard finite-difference schemes for general twodimensional autonomous dynamical systems, Applied Mathematics Letters 18 (2005) 769-774.
- [150] D. T. Dimitrov, H. V. Kojouharov, Positive and elementary stable nonstandard numerical
 methods with applications to predator-prey models Journal of Computational and Applied
 Mathematics 189(1-2) (2006) 98-108.
- [151] D. T. Dimitrov, H. V. Kojouharov, Stability-Preserving Finite-Difference Methods for Gen eral Multi-Dimensional Autonomous Dynamical Systems, International Journal of Numeri cal Analysis and Modeling 4(2) (2007) 282-292.
- [152] D. T. Dimitrov, H. V. Kojouharov, Nonstandard finite-difference methods for predator-prey
 models with general functional response, Mathematics and Computers in Simulation 78(1)
 (2008) 1-11.
- [153] D. T. Dimitrov, H. V. Kojouharov, Dynamically consistent numerical methods for general
 productive-destructive systems, Journal of Difference Equations and Applications 17 (2011)
 1721-1736.
- [154] R. U. Din, K. A. Khan, A. Aloqaily, N. Mlaiki, H. Alrabaiah, Using Non-Standard Finite Difference Scheme to Study Classical and Fractional Order SEIVR Model, Fractal and
 Fractional 7(7) (2023) 552.
- [155] D. Ding, X. Ding, Dynamic consistent non-standard numerical scheme for a dengue disease
 transmission model, Journal of Difference Equations and Applications 20(3) (2014) 492-505.
- 1104 [156] A. d'Onofrio, P. Manfredi, E. Salinelli, Vaccinating behaviour, information, and the dynam-
- ics of SIR vaccine preventable diseases, Theoretical Population Biology 71 (2007) 301-317.
- [157] A. d'Onofrio, On pulse vaccination strategy in the SIR epidemic model with vertical trans mission, Applied Mathematics Letters 18 (2005) 729-732.

- 1108 [158] X. Duana S. Yuan, Z. Qiu, J. Ma, Global stability of an SVEIR epidemic model with ages
- 1109 of vaccination and latency, Computers & Mathematics with Applications 68 (2014) 288-308.
- 1110 [159] T. Duclos, T. Reichert, A Solution to the Kermack and McKendrick Integro-Differential
- 1111 Equations, medRxiv (2022): 2022-04.
- [160] J. Dushoff, W. Huang, C. Castillo-Chavez, Backwards bifurcations and catastrophe in simple
 models of fatal diseases, Journal of Mathematical Biology 36 (1998) 227-248.
- [161] D. J. D. Earn, P. Rohani, B. T. Grenfell, Persistence, chaos and synchrony in ecology and
 epidemiology, Proceedings of the Royal Society of London. Series B 26:57-10.
- [162] M. Ehrhardt, R. E. Mickens, A nonstandard finite difference scheme for convection-diffusion
 equations having constant coefficients, Applied Mathematics and Computation 219 (2013)
 6591-6604.
- [163] M. Ehrhardt, J. Gašper, S. Kilianová, SIR-based Mathematical Modeling of Infectious Dis eases with Vaccination and Waning Immunity, Journal of Computational Science 37 (2019)
 101027.
- [164] K. Ejima, K. Aihara, H. Nishiura, Modeling the obesity epidemic: social contagion and its
 implications for control, Theoretical Biology and Medical Modelling 10 (2013), 1-13.
- 1124 [165] A. M. Elaiw, N. H. AlShamrani, Global stability of humoral immunity virus dynamics models
- with nonlinear infection rate and removal, Nonlinear Analysis: Real World Applications 26 (2015) 161-190.
- [166] A. M. Elaiw, M. Alshaikh, Stability preserving NSFD scheme for a general virus dynamics
 model with antibody and cell-mediated responses, Chaos Solitons & Fractals 138 (2020)
 109862.
- [167] E. H. Elbasha, C. N. Podder, A. B. Gumel, Analyzing the dynamics of an SIRS vaccination
 model with waning natural and vaccine-induced immunity, Nonlinear Analysis: Real World
 Applications 12 (2011) 2692-2705.
- [168] E. H. Elbasha, Model for hepatitis C virus transmissions, Mathematical Biosciences and
 Engineering 10 (2013) 1045-1065.
- [169] S. Elsheikh, R. Ouifki, K. C. Patidar, A non-standard finite difference method to solve a
 model of HIV-malaria co-infection, Journal of Difference Equations and Applications 20(3)
 (2014) 354-378.
- [170] I. Faragó, R. Mosleh, Some qualitative properties of the discrete models for malaria propa gation, Applied Mathematics and Computation 438 (2023) 127628.
- [171] A. Farooqi, R. Ahmad, H. Alotaibi, T. A. Nofal, R. Farooqi, I. Khan, A comparative epidemiological stability analysis of predictor corrector type non-standard finite difference scheme for the transmissibility of measles, Results in Physics 21 (2021) 103756.
- 1143 [172] H. Fatoorehchi, M. Ehrhardt, Numerical and semi-numerical solutions of a modified
 1144 Thévenin model for calculating terminal voltage of battery cells, Journal of Energy Storage
 1145 145 (2022) 103746.
- [173] Z. Feng, H. R. Thieme, Endemic Models with Arbitrarily Distributed Periods of Infection
 I: Fundamental Properties of the Model, SIAM Journal on Applied Mathematics 61 (2000)
 803 833.
- [174] Z. Feng, H. R. Thieme, Endemic Models with Arbitrarily Distributed Periods of Infection II:
 Fast Disease Dynamics and Permanent Recovery, SIAM Journal on Applied Mathematics
 61 (2000) 983-1012.
- [175] F. Forouzanni, A. B. Gumel, Mathematical analysis of an age-structured model for malaria
 transmission dynamics, Mathematical Biosciences 247 (2014) 80-94.
- [176] A. F. Fossi, J. Lubuma, C. Tadmon, B. Tsanou, Mathematical modeling and nonstandard
 finite difference scheme analysis for the environmental and spillover transmissions of Avian
 Influenza A model, Dynamical Systems 36 (2021) 212-255.
- [117] B. M. Fundzama, Design, analysis and simulation of a robust numerical method to solveZika virus models, Master Thesis, University of the Western Cape, 2019.
- [178] C. Gai, D. Iron, T. Kolokolnikov, Localized outbreaks in an S-I-R model with diffusion,
 Journal of Mathematical Biology 80 (2020) 1389-1411.
- [179] C. Gan, X. Yang, W. Liu, Q. Zhu, A propagation model of computer virus with nonlinear
 vaccination probability, Communications in Nonlinear Science and Numerical Simulation 19
 (2014) 92-100.

- [180] S. M. Garba, A. B. Gumel, J.-S. Lubuma, Dynamically-consistent non-standard finite difference method for an epidemic model, Mathematical and Computer Modelling 53(1-2) (2011)
 131-150.
- [181] C. C. Garsow, G. J. Salivia, A. R. Herrera, Mathematical Models for the Dynamics of
 Tobacco use, recovery and relapse, Technical Report Series BU-1505-M, Cornell University,
 UK (2000).
- [182] Y. Geng, J. Xu, Global stability of a delayed and diffusive virus model with nonlinearinfection function, Journal of Biological Dynamics 15 (2021) 287-307.
- [183] A. Gerisch, R. Weiner, The positivity of low-order explicit Runge-Kutta schemes applied in
 splitting methods, Computers & Mathematics with Applications 45 (2003) 53-67.
- 1174 [184] S. Ghosh, V. Volpert, M. Banerjee, An Epidemic Model with Time-Distributed Recovery1175 and Death Rates. Bulletin of Mathematical Biology 84(8) (2022) 78.
- [185] P. Glendinning, L. P. Perry, Melnikov analysis of chaos in a simple epidemiological model,
 Journal of Mathematical Biology 35 (1997) 359-373.
- [186] G. González-Parra, A. J. Arenas, B. M. Chen-Charpentier, Combination of nonstandard
 schemes and Richardson's extrapolation to improve the numerical solution of population
 models, Mathematical and Computer Modelling 52 (2010) 1030-1036.
- [187] E. González, M. J. Villena, On the spatial dynamics of vaccination: A spatial SIRS-V model,
 Computers & Mathematics with Applications 80 (2020) 733-743.
- [188] A. Gragnani, S. Rinaldi, G. Feichtinger, Dynamics of drug consumption: a theoretical model,
 Socio-Economic Planning Sciences 31 (1997) 127-137.
- [189] A. Gray, D. Greenhalgh, L. Hu, X. Mao, J. Pan, A Stochastic Differential Equation SIS
 Epidemic Model, SIAM Journal on Applied Mathematics 71 (2011) 876-902.
- [190] B. T. Grenfell, B. M. Bolker, A. Kleczkowski, Seasonality and extinction in chaotic metapop ulations, Proc. Proceedings of the Royal Society of London. Series B 259:97-103.
- [191] V. Grimm, G. R. W. Quispel, Geometric Integration Methods that Preserve Lyapunov
 Functions, BIT Numerical Mathematics 45 (2005) 709-723.
- [192] F. Guiaş, Equilibrium solutions of a modified SIR model with vaccination and several levels
 of immunity, WSEAS Transactions on Systems and Control 18 (2023) 550-560.
- [193] A. B. Gumel, S. M. Moghadas, A qualitative study of a vaccination model with non-linear
 incidence, Applied Mathematics and Computation 143 (2003) 409-419.
- [194] A. B. Gumel, R. E. Mickens, B. D. Corbett, A non-standard finite-difference scheme for a
 model of HIV transmission and control, Journal of Computational Methods in Sciences and
 Engineering 3(1) (2003) 91-98.
- [195] A. B. Gumel, S. Ruan, T. Day, J. Watmough, F. Brauer, P. van den Driessche, D. Gabrielson,
 Ch. Bowman, M. E. Alexander, S. Ardal, J. Wu, B. M. Sahai, Modelling strategies for
 controlling SARS outbreaks, Proceedings of the Royal Society of London B 271 (2004)
 2223-2232.
- [196] A. B. Gumel, C. C. McCluskey, J. Watmough, An SVEIR Model for Assessing Potential
 Impact of an Imperfect Anti-SARS Vaccine, Mathematical Biosciences 3 (2006) 485-512.
- [197] A. B. Gumel, B. Song, Existence of multiple-stable equilibria for a multi-drug-resistant
 model of mycobacterium tuberculosis, Mathematical Biosciences and Engineering 5 (2008)
 437-455.
- [198] A. B. Gumel, Global dynamics of a two-strain avian influenza model, International Journal
 of Computer Mathematics 86 (2009) 85-108.
- [199] A. B. Gumel, Causes of backward bifurcations in some epidemiological models, Journal of
 Mathematical Analysis and Applications 395 (2012) 355-365.
- [200] A. Gumel (ed.), Mathematical and Computational Modeling of Phenomena Arising in Population Biology and Nonlinear Oscillations: In honour of the 80th birthday of Ronald E.
 Mickens, AMS Contemporary Mathematics, 2024, Volume 793.
- [201] K. F. Gurski, A simple construction of nonstandard finite-difference schemes for small non linear systems applied to SIR models, Computers & Mathematics with Applications 66
 (2013) 2165-2177.
- [202] K. P. Hadeler, P. Van den Driessche, Backward bifurcation in epidemic control, Mathemat ical Biosciences 146 (1997) 15-35.
- [203] E. Hairer, G. Wanner, S. P. Norsett, Solving Ordinary Differential Equations I: Nonstiff
 Problems, Springer Berlin, Heidelberg, 1993.

- [204] E. Hairer, G. Wanner, Solving Ordinary Differential Equations II: Stiff and Differential Algebraic Problems, Springer Berlin, Heidelberg, 1996.
- 1223 [205] E. Hairer, Ch. Lubich, G. Wanner, Geometric Numerical Integration, Springer-Verlag, 2002.
- [206] M. Han, J. Liu, T. Zhang, On the dynamics of a Zika disease model with vector-bias. Int.
 J. Biomath. (2024) 2450009.
- [207] T. Harko, F. S. N. Lobo, M. K. Mak, Exact analytical solutions of the Susceptible-Infected Recovered (SIR) epidemic model and of the SIR model with equal death and birth rates,
 Applied Mathematics and Computation 236 (2014) 184-194.
- [208] R. C. Harris, T. Sumner, G. M. Knight, R. G. White, Systematic review of mathematical models exploring the epidemiological impact of future TB vaccines, Human Vaccines & Immunotherapeutics 12(2016) 2813-2832.
- [209] J. A. P. Heesterbeek, J. A. J. Metz, The saturating contact rate in marriage and epidemic
 models, Journal of Mathematical Biology 31 (1993) 529-539.
- [210] F. Heldmann, S. Berkhahn, M. Ehrhardt, K. Klamroth, PINN Training using Biobjective
 Optimization: The Trade-off between Data Loss and Residual Loss, Journal of Computa tional Physics 488 (2023), 112211.
- [211] S. Henshaw, C. Connell McCluskey, Global stability of a vaccination model with immigra tion, Electronic Journal of Differential Equations 2015 (2015) 1-10.
- [212] E. Hernandez-Martinez, H. Puebla, F. Valdes-Parada, J. Alvarez-Ramirez, Nonstandard
 finite difference schemes based on Green's function formulations for reaction-diffusion convection systems, Chemical Engineering Science 94 (2013) 245-255.
- [213] J. E. Herrera-Serrano, J. E. Macías-Díaz, I. E. Medina-Ramírez, J. A. Guerrero, An efficient nonstandard computer method to solve a compartmental epidemiological model for
 COVID-19 with vaccination and population migration, Computer Methods and Programs
 in Biomedicine 221 (2022) 106920.
- [214] H. W. Hethcote, M. A. Lewis, P. van den Driessche, An epidemiological model with a delay
 and a nonlinear incidence rate, Journal of Mathematical Biology 27 (1989) 49-64
- [215] H. W. Hethcote, The mathematics of Infectious diseases, SIAM Review 42 (2000) 599-653.
- [216] S. Hews, S. Eikenberry, J. D. Nagy, Y. Kuang, Rich dynamics of a hepatitis B viral infection
- model with logistic hepatocyte growth, Journal of Mathematical Biology 60 (2010) 573-590.
- [217] M. W. Hirsch, S. Smale, R. L. Devaney, Differential Equations, Dynamical Systems, and an
 Introduction to Chaos, Third Edition, Elsevier, 2013.
- [218] M. T. Hoang, Dynamically consistent nonstandard finite difference schemes for a virus-patch
 dynamic model, Journal of Applied Mathematics and Computing 68 (2022) 3397-3423.
- [219] M. T. Hoang, A novel second-order nonstandard finite difference method for solving one dimensional autonomous dynamical systems, Communications in Nonlinear Science and
 Numerical Simulation 114 (2022) 106654.
- [220] M. T. Hoang, Reliable approximations for a hepatitis B virus model by nonstandard numer ical schemes, Mathematics and Computers in Simulation 193(2022) 32-56.
- [221] M. T. Hoang, Dynamical analysis of a generalized hepatitis B epidemic model and its dy namically consistent discrete model, Mathematics and Computers in Simulation 205 (2023)
 291-314.
- [222] M. T. Hoang, M. Ehrhardt, A dynamically consistent nonstandard finite difference scheme
 for a generalized SEIR epidemic model, Journal of Difference Equations and Applications
 30(4) (2024) 409-434.
- [223] M. T. Hoang, A class of second-order and dynamically consistent nonstandard finite differ ence schemes for nonlinear Volterra's population growth model, Computational and Applied
 Mathematics 42 (2023) Article number: 85.
- [224] M. T. Hoang, A novel second-order nonstandard finite difference method preserving dy namical properties of a general single-species model, International Journal of Computer
 Mathematics 100 (2023) 2047-2062.
- [225] M. T. Hoang, J. C. Valverde, A generalized model for the population dynamics of a two
 stage species with recruitment and capture using a nonstandard finite difference scheme,
 Computational and Applied Mathematics 43 (2024) article no. 54.
- [226] M. T. Hoang, M. Ehrhardt, A general class of second-order L-stable explicit numerical methods for stiff problems, Applied Mathematics Letters 149 (2024) 108897.

- [227] M. T. Hoang, M. Ehrhardt, A second-order nonstandard finite difference method for a general Rosenzweig-MacArthur predator-prey model, Journal of Computational and Applied
- 1279 Mathematics 444(2024) 115752.
- [228] Z. Horváth, Positivity of Runge-Kutta and diagonally split Runge-Kutta methods, Applied
 Numerical Mathematics 28 (1998) 309-326.
- [229] S.-B. Hsu, Lih-Ing W. Roeger, The final size of a SARS epidemic model without quarantine,
 Journal of Mathematical Analysis and Applications 333 (2007) 557-566.
- [230] Y. Hu, Q. Pan, W. Hou, M. He, Rumor spreading model considering the proportion ofwisemen in the crowd, Physica A 505 (2018) 1084-1094.
- [231] Z. Hu, W. Ma, S. Ruan, Analysis of SIR epidemic models with nonlinear incidence rate and treatment, Mathematical Biosciences 238 (2012) 12-20.
- [232] W. Huang, M. Han, K. Liu, Dynamics of an SIS reaction-diffusion epidemic model for disease
 transmission, Mathematical Biosciences and Engineering 7 (2010) 51-66.
- [233] H.-F. Huo, H. Xue, H. Xiang, Dynamics of an alcoholism model on complex networks with
 community structure and voluntary drinking, Physica A 505 (2018) 880-890.
- [234] M. Iannelli, M. Martcheva, X.-Z. Li, Strain replacement in an epidemic model with super infection and perfect vaccination, Mathematical Biosciences 195 (2005) 23-46.
- [235] M. A. Ibrahim, A. Dénes, Threshold and stability results in a periodic model for malaria
 transmission with partial immunity in humans, Applied Mathematics and Computation 392
 (2021) 125711.
- [236] A. Iggidr, G. Sallet, M. O. Souza, On the dynamics of a class of multi-group models for
 vector-borne diseases, Journal of Mathematical Analysis and Applications 441 (2016) 723 743.
- [237] Z. Iqbal, J. E. Macías-Díaz, N. Ahmed, M. A.-U. Rehman, A. Raza, M. Rafiq, A SEIR
 model with memory effects for the propagation of Ebola-like infections and its dynamically
 consistent approximation, Computer Methods and Programs in Biomedicine 209 (2021)
 106322.
- [238] Z. Iqbal, M. A.-U. Rehman, M. Imran, N. Ahmed, U. Fatima, A. Akgül, M. Rafiq, A. Raza,
 A. A. Djuraev, F. Jarad, A finite difference scheme to solve a fractional order epidemic model of computer virus, AIMS Mathematics 8 (2023) 2337-2359.
- [239] N. Islam, J. R. M. Borhan, R. Prodhan, Application of Mathematical Modeling: A Mathematical Model for Dengue Disease in Bangladesh, International Journal of Mathematical
 Sciences and Computing 10(1) (2024) 19-30.
- [240] M. Jamal, S. Batool, I. Ahmed, E. Azhar, T. Nawaz, Mathematical modeling of Zika virus
 with vertical transmission in the presence of Wolbachia-infected mosquitoes, Journal of
 Applied Mathematics and Computing 71(1) (2025) 605-625.
- [241] J. Jang, H.-D. Kwon, J. Lee, Optimal control problem of an SIR reaction-diffusion model
 with inequality constraints, Mathematics and Computers in Simulation 171 (2020) 136-151.
- [242] M. Jawaz, N. Ahmed, D. Baleanu, M. Rafiq, M. A. Rehman, Positivity preserving technique
 for the solution of HIV/AIDS reaction diffusion model with time delay, Frontiers in Physics
 7 (2020) 229.
- [243] Y. Jin, W. Wang, S. Xiao, An SIRS model with a nonlinear incidence rate, Chaos, Solitons
 & Fractals 34 (2007) 1482-1497.
- [244] L. Jódar, F.-J. Santonja, G. Gonzalez-Párra, Modelling dynamics of infant obesity in the
 region of Valencia, Spain, Computers & Mathematics with Applications 56 (2008) 679-689.
- [245] L. Joáar, R. J. Villanueva, A. J. Arenas, Gilberto C. González, Nonstandard numerical methods for a mathematical model for influenza disease, Mathematics and Computers in Simulation 79 (2008) 622-633.
- [246] A. Jones, N. Strigu, Is spread of COVID-19 a chaotic epidemic, Chaos, Solitons & Fractals
 142 (2021) 110376.
- [247] Y. Kanai, T. Hoshino, T. Ohtani, N. V. Kantartzis, GPU Acceleration of the Nonstandard
 FDTD Method, In: 2023 International Applied Computational Electromagnetics Society
 Symposium (ACES), pp. IEEE, 2023, pp. 1-2.
- [248] K. N. Kavya, P. Veeresha, H. M. Baskonus, M. Alsulami, Mathematical modeling to inves tigate the influence of vaccination and booster doses on the spread of Omicron, Communi cations in Nonlinear Science and Numerical Simulation 130 (2024) 107755.
- [249] S. Kayenat, A. K. Verma, NSFD schemes for a class of nonlinear generalised advection diffusion-reaction equation, Pramana 96(1) (2022) 14.

- [250] L. Kalachev, E. L. Landguth, J. Graham, Revisiting classical SIR modelling in light of the
 COVID-19 pandemic, Infectious Disease Modelling 8 (2023) 72-83.
- [251] O. O. Kehinde, J. B. Munyakazi A. R. Appadu, A NSFD Discretization of Two-Dimensional
 Singularly Perturbed Semilinear Convection-Diffusion Problems, Frontiers in Applied Math-
- ematics and Statistics 8 (2022) 861276.
- [252] W. O. Kermack, A. G. McKendrick, A contribution to the mathematical theory of epidemics,
 Proceedings of the Royal Society of London Series A 115 (1927) 700-721.
- [253] W. O. Kermack, A. G. McKendrick, Contributions to the mathematical theory of epidemics.
 II. The problem of endemicity, Proceedings of the Royal Society of London Series A 138 (1932) 55-83.
- [254] W. O. Kermack, A. G. McKendrick, Contributions to the mathematical theory of epidemics.
- 1346 III. -Further studies of the problem of endemicity, Proceedings of the Royal Society of London
 1347 Series A 141 (1933) 94-122.
- [255] P. G. Kevrekidis, J. Cuevas-Maraver, Y. Drossinos, Z. Rapti, G. A. Kevrekidis, Reactiondiffusion spatial modeling of COVID-19: Greece and Andalusia as case examples, Physical
 Review E 104 (2021) 024412.
- [256] B. Khajji, A. Labzai, A. Kouidere, O. Balatif, M. Rachik, A Discrete Mathematical Modeling
 of the Influence of Alcohol Treatment Centers on the Drinking Dynamics Using Optimal
 Control, Journal of Applied Mathematics 2020 (2020), Article ID 9284698.
- [257] B. Khajji, A. Kouidere, O. Balatif, M. Rachik, Mathematical modeling, analysis and optimal
 control of an alcohol drinking model with liver complication, Communications in Mathemat ical Biology and Neuroscience 2020 (2020) 1–29,
- 1357 [258] H. K. Khalil, Nonlinear systems, Prentice Hall, 2002.
- [259] M. M. Khalsaraei, A positive and elementary stable nonstandard explicit scheme for a
 mathematical model of the influenza disease, Mathematics and Computers in Simulation
 182 (2021) 397-410.
- [260] M. A. Khan, S. Islam, J. C Valverde, S. A. Khan, Control strategies of hepatitis B with
 three control variables, Journal of Biological Systems26(2018) 1-21.
- [261] H. Khan, R. N. Mohapatra, K. Vajravelu, S.J. Liao, The explicit series solution of SIR and
 SIS epidemic models, Applied Mathematics and Computation 215 (2009) 653-669.
- [262] I. U. Khan, A. Hussain, S. Li, A. Shokri, Modeling the Transmission Dynamics of Coronavirus Using Nonstandard Finite Difference Scheme, Fractal and Fractional 7(6) (2023)
 451.
- [263] M. A. Khan, S. W. Shah, S. Ullah, J. F. Gomez-Aguilar, A dynamical model of asymptomatic carrier zika virus with optimal control strategies, Nonlinear Analysis: Real World Applications 50 (2019) 144-170.
- [264] M. I. Khan, K. Al-Khaled, A. Raza, S. U. Khan, J. Omar, A. M. Galal, Mathematical and numerical model for the malaria transmission: Euler method scheme for a malarial model, International Journal of Modern Physics B 37(16) (2023) 2350158.
- [265] O. Khyar, K. Allali, Global dynamics of a multi-strain SEIR epidemic model with general incidence rates: application to COVID-19 pandemic, Nonlinear Dynamics 102 (2020) 489-509.
- [266] K. I. Kim, Z. Lin, L. Zhang, Avian-human influenza epidemic model with diffusion, Nonlin ear Analysis: Real World Applications 11 (2010) 313-322.
- [267] K. Kitagawa , S. Nakaok, Y. Asai, K. Watashi, S. Iwami, A PDE multiscale model of
 hepatitis C virus infection can be transformed to a system of ODEs, Journal of Theoretical
 Biology 448 (2018) 80-85.
- [268] F. Köhler-Rieper, C. H. F. Röhl, E. De Micheli, A novel deterministic forecast model for the
 Covid-19 epidemic based on a single ordinary integro-differential equation, The European
 Physical Journal Plus 135(7) (2020) 599.
- [269] H. V. Kojouharov, S. Roy, M. Gupta, F. Alalhareth, J. M. Slezak, A second-order modified nonstandard theta method for one-dimensional autonomous differential equations, Applied Mathematics Letters 112 (2021) 106775.
- [270] S. Kopecz, A. Meister, On order conditions for modified Patankar-Runge-Kutta schemes,
 Applied Numerical Mathematics 123 (2018) 159-179.
- 1390 [271] S. Kopecz, A. Meister, On the existence of three-stage third-order modified Patankar-Runge-
- 1391 Kutta schemes, Numerical Algorithms 81 (2019) 1473-1484.

- [272] A. Korobeinikov, Lyapunov functions and global properties for SEIR and SEIS epidemic
 models, Mathematical Medicine and Biology 21 (2004) 75-83.
- [273] A. Korobeinikov, P. K. Maini, A Lyapunov function and global properties for SIR and SEIR
 epidemiological models with nonlinear incidence, Mathematical Biosciences & Engineering
 1 (2004) 57-60.
- [274] A. Korobeinikov, Lyapunov Functions and Global Stability for SIR and SIRS Epidemio logical Models with Non-Linear Transmission, Bulletin of Mathematical Biology 68 (2006)
 615-626.
- [275] T. Kossaczka, M. Ehrhardt, M. Günther, Deep FDM: Enhanced finite difference methods
 by deep learning, Franklin Open 4 (2023) 100039.
- [276] E. Kovács, J. Majár, M. Saleh, Unconditionally Positive, Explicit, Fourth Order Method for
 the Diffusion-and Nagumo-Type Diffusion-Reaction Equations, Journal of Scientific Computing, 98(2) (2024) 39.
- [277] C. M. Kribs-Zaleta, J. X. Velasco-Hernández, A simple vaccination model with multiple
 endemic states, Mathematical Biosciences 164 (2000) 183-201.
- [278] N. A. Kudryashov, M. A. Chmykhov, M. Vigdorowitsch, Analytical features of the SIR
 model and their applications to COVID-19, Applied Mathematical Modelling 90 (2021)
 466-473.
- [279] T. Kuniya, J. Wang, Lyapunov functions and global stability for a spatially diffusive SIR
 epidemic model, Applicable Analysis 96 (2017) 1935-1960.
- [280] T. Kuniya, J. Wang, Global dynamics of an SIR epidemic model with nonlocal diffusion,
 Nonlinear Analysis: Real World Applications 43 (2018) 262-282.
- [281] Y. A. Kuznetsov, C. Piccardi, Bifurcation analysis of periodic SEIR and SIR epidemic
 models, Journal of Mathematical Biology 32 (1994) 109-121.
- 1416 [282] Y. A. Kuznetsov, Elements of Applied Bifurcation Theory, Springer New York, 2004.
- [283] W. Lacarbonara, J. Ma, C. Nataraj, Preface to the special issue "Complex dynamics of COVID-19: modeling, prediction and control (part II)", Nonlinear Dynamics 109 (2022)
 [1419] 1-3.
- [284] A. Lahrouz, L. Omari, D. Kiouach, A. Belmaâti, Deterministic and stochastic stability of a
 mathematical model of smoking, Statistics and Probability Letters 81 (2011) 1276-1284.
- [285] A. Lahrouz, L. Omari, D. Kiouach, A. Belmaâti, Complete global stability for an SIRS
 epidemic model with generalized non-linear incidence and vaccination, Applied Mathematics
 and Computation 218 (2012) 6519-6525.
- [286] J. La Salle, S. Lefschetz, Stability by Liapunov's Direct Method. Academic Press, New York,
 1961.
- [287] A. A. Lashari, G. Zaman, Global dynamics of vector-borne diseases with horizontal transmission in host population, Computers & Mathematics with Applications 61 (2011) 745-754.
- [288] J. Legrand, R. F. Grais, P. Y. Boelle, A. J. Valleron, A. Flahault, Understanding the
 dynamics of Ebola epidemics, Epidemiology & Infection 135 (2007) 610-621.
- [289] R. J. LeVeque, Finite Difference Methods for Ordinary and Partial Differential Equations,
 Society for Industrial and Applied Mathematics, Philadelphia, 2007.
- [290] B. Li, Q. Bie, Long-time dynamics of an SIRS reaction-diffusion epidemic model, Journal
 of Mathematical Analysis and Applications 475 (2019) 1910-1926.
- [291] C.-L. Li, C.-H. Li, C.-Y. Cheng, Analysis of an epidemiological model with age of infection,
 vaccination, quarantine and asymptomatic transmission, Journal of the Franklin Institute
 360 (2023) 657-692.
- [292] J. Li, H. Jiang, X. Mei, C. Hu, G. Zhang, Dynamical analysis of rumor spreading model in multi-lingual environment and heterogeneous complex networks, Information Sciences 536 (2020) 391-408.
- [293] M. Y. Li, J. S. Muldowney, On Bendixson's criterion, Journal of Differential Equations 106 (1993) 27-39.
- [294] M. Y. Li, J. S. Muldowney, Global stability for the SEIR model in epidemiology, Mathe matical Biosciences 125 (1995) 155-164.
- [295] M. Y. Li, J. S. Muldowney, A geometric approach to global-stability problems, SIAM Journal
 on Mathematical Analysis 27 (1996) 1070-1083.
- 1447 [296] M. Y. Li, J. S. Muldowney, P. van den Driessche, Global stability of SEIRS models in 1448 epidemiology, Canadian Applied Mathematics Quarterly 7(4) (1999).

- [297] S. Li, I. Bukhsh, I. U. Khan, M. I. Asjad, S. M. Eldin, M. A. El-Rahman, D. Baleanu The
 impact of standard and nonstandard finite difference schemes on HIV nonlinear dynamical
 model, Chaos, Solitons & Fractals 173 (2023) 113755.
- [298] X. Li, R. P. Agarwal, J. F. Gomez-Aguilar, Q. Badshah, G. ur Rahman, Threshold dynamics:
 Formulation, stability & sensitivity analysis of co-abuse model of heroin and smoking, Chaos,
 Solitons & Fractals 161 (2022) 112373.
- [299] Y. Li, X. Liu, Y. Yuan, J. Li, L. Wang, Global analysis of tuberculosis dynamical model and
 optimal control strategies based on case data in the United States, Applied Mathematics
 and Computation 422 (2022) 126983.
- [300] H.-l. Lin, F.-B. Wang, Global dynamics of a nonlocal reaction-diffusion system modeling
 the West Nile virus transmission, Nonlinear Analysis: Real World Applications 46 (2019)
 352-373.
- [301] C. Liu, R. Cui, Qualitative analysis on an SIRS reaction-diffusion epidemic model with
 saturation infection mechanism, Nonlinear Analysis: Real World Applications 62 (2021)
 103364.
- [302] P. Liu, S. N. Elaydi, Discrete Competitive and Cooperative Models of Lotka-Volterra Type,
 Journal of Computational Analysis and Applications 3 (2001) 53-73.
- [303] T. Liu, X. Yin, Q. Liu, A. H. Hounye, Modeling SARS coronavirus-2 omicron variant dynamic via novel fractional derivatives with immunization and memory trace effects, Alexandria Engineering Journal 86 (2024) 174-193.
- [304] X. Liu, B. Dai, Flip bifurcations of an SIR epidemic model with birth pulse and pulse vaccination, Applied Mathematical Modelling 43 (2017) 579-591.
- [305] X.-L. Liu, C.-C. Zhu, A non-standard finite difference scheme for a diffusive HIV-1 infection
 model with immune response and intracellular delay, Axioms 11(3) (2022) 129.
- [306] Y. Lou, R. B. Salako, Mathematical analysis of the dynamics of some reaction-diffusion
 models for infectious diseases, Journal of Differential Equations 370 (2023) 424-469.
- [307] X. Lu, H. Hui, F. Liu, Y. Bai, Stability and optimal control strategies for a novel epidemic
 model of COVID-19, Nonlinear Dynamics 106 (2021) 1491-150.
- [308] J. M.-S. Lubuma, K. C. Patidar, Uniformly convergent non-standard finite difference methods for self-adjoint singular perturbation problems, Journal of Computational and Applied
 Mathematics 191(2) (2006) 228–238.
- [309] A. M. Lyapunov, The General Problem of the Stability of Motion. Taylor & Francis, London,
 1992.
- [310] M. H. Maamar, M. Ehrhardt, L. Tabharit, A nonstandard finite difference scheme for a timefractional model of Zika virus transmission, Mathematical Biosciences and Engineering 21(1)
 (2024) 924-962.
- [311] P. Magal, G. Webb, The parameter identification problem for SIR epidemic models: identi fying unreported cases, Journal of Mathematical Biology 77 (2018) 1629-1648.
- [312] P. Magal, G. F. Webb, Y. Wu, On the Basic Reproduction Number of Reaction-Diffusion
 Epidemic Models, SIAM Journal on Applied Mathematics 79 (2019) 284-304.
- [313] S. Majee, S. Jana, T. K. Kar, S. Barman, D. K. Das, Modeling and analysis of Caputo-type fractional-order SEIQR epidemic model, International Journal of Dynamics and Control 12 (2024) 148-166.
- [314] Y. Mammeri, A reaction-diffusion system to better comprehend the unlockdown: Application of SEIR-type model with diffusion to the spatial spread of COVID-19 in France,
 Computational and Mathematical Biophysics 8(1) (2020) 102-113.
- [315] S. Mandal, R. R. Sarkar, S. Sinha, Mathematical models of malaria a review, Malaria
 Journal 2011, 10:202.
- [316] S. Mangiarotti, Low dimensional chaotic models for the plague epidemic in Bombay (1896-1991), Chaos, Solitons & Fractals 81 (2015) 184-196.
- [317] S. Mangiarotti, M. Peyre, M. Huc, A chaotic model for the epidemic of Ebola virus disease
 in West Africa (2013-2016), Chaos 26 (2016) 113112.
- [318] S. Mangiarotti, M. Peyre, Y. Zhang, M. Huc, F. Roger, Y. Kerr, Chaos theory applied to
 the outbreak of COVID-19: an ancillary approach to decision making in pandemic context,
 Epidemiology and Infection 148 (2020), e95, 1-9.
- Epidemiology and Infection 148 (2020), e95, 1-9.
 [319] K. Manna, S. P. Chakrabarty, Global stability and a non-standard finite difference scheme for
- a diffusion driven HBV model with capsids, Journal of Difference Equations and Applications
 21 (2015) 918-933.

- [320] K. Manna, A non-standard finite difference scheme for a diffusive HBV infection model
 with capsids and time delay, Journal of Difference Equations and Applications 23 (2017)
 1901-1911.
- [321] B. P. Marchant, J. Norbury, A. J. Perumpanani, Traveling shock waves arising in a model
 of malignant invasion, SIAM Journal on Applied Mathematics 60(2) (2000) 463-476.
- [322] T. T. Marinov, R. S. Marinova, Inverse problem for adaptive SIR model: Application to
 COVID-19 in Latin America, Infectious Disease Modelling 7 (2022) 134-148.
- [323] M. Martcheva, An Introduction to Mathematical Epidemiology, Springer New York, NY,2015.
- [324] N. K. Martin, P. Vickerman, M. Hickman, Mathematical modelling of hepatitis C treatment
 for injecting drug users, Journal of Theoretical Biology 274 (2011) 58-66.
- [325] J. Martin-Vaquero, A. Martin del Rey, A. H. Encinas, J. D. Hernandez Guillen, A. QueirugaDios, G. Rodriguez Sanchez, Higher-order nonstandard finite difference schemes for a MSEIR
 model for a malware propagation, Journal of Computational and Applied Mathematics 317
 (2017) 146-156.
- [326] J. Martin-Vaquero, A. Queiruga-Dios, A. Martin del Rey, A. H. Encinas, J. D. Hernandez
 Guillen, G. Rodriguez Sanchez, Variable step length algorithms with high-order extrapolated
 non-standard finite difference schemes for a SEIR model, Journal of Computational and
 Applied Mathematics 330 (2018) 848-854.
- [327] J. P. S. Maurício de Carvalho, A. A. Rodrigues, SIR Model with Vaccination: Bifurcation
 Analysis, Qualitative Theory of Dynamical Systems 22 (2023) article number 105.
- [328] R. M. May, Chaos and the dynamics of biological populations, Proceedings of the Royal
 Society A 413(1844) (1987) 27-44.
- [329] C. C. McCluskey, Y. Yang, Global stability of a diffusive virus dynamics model with general
 incidence function and time delay, Nonlinear Analysis: Real World Applications 25 (2015)
 64-78.
- [330] A. McNabb, Comparison theorems for differential equations, Journal of Mathematical Anal-ysis and Applications 119 (1986) 417-428.
- [331] M. Mehdizadeh Khalsaraei, R. Shokri Jahandizi, Positivity-preserving nonstandard finite
 difference schemes for simulation of advection-diffusion reaction equations, Computational
 Methods for Differential Equations 2(4) (2014) 256-267.
- [332] J. Mena-Lorca, H.W. Hethcote, Dynamic models of infectious diseases as regulators of population size, Journal of Mathematical Biology 30 (1992) 693-716.
- [333] E. Messina, M. Pezzella, A. Vecchio, A non-standard numerical scheme for an age-of infection epidemic model, Journal of Computational Dynamics 9(2) (2022) 239-252.
- [334] R. E. Mickens, I. Ramadhani, Finite-difference schemes having the correct linear stability
 properties for all finite step-sizes III, Computers & Mathematics with Applications 27 (1994)
 1544 77-84.
- [335] R. E. Mickens, Nonstandard Finite Difference Models of Differential Equations, World Sci entific, Singapore, 1994.
- [336] R. E. Mickens, Nonstandard finite difference schemes for reaction-diffusion equation, Nu merical Methods for Partial Differential Equation 15 (1999) 201-214.
- [337] R. E. Mickens, Nonstandard finite difference schemes for reaction-diffusion equations having
 linear advection, Numerical Methods for Partial Differential Equation 16 (2000) 361-364.
- [338] R. E. Mickens, Applications of Nonstandard Finite Difference Schemes, World Scientific,
 Singapore, 2000.
- [339] R. E. Mickens, A nonstandard finite-difference scheme for the Lotka-Volterra system, Ap plied Numerical Mathematics 45 (2003) 309-314
- [340] R. E. Mickens, A nonstandard finite difference scheme for a Fisher PDE having nonlinear
 diffusion, Computers & Mathematics with Applications 45(1-3) (2003) 429-436.
- [341] R. E. Mickens, A nonstandard finite difference scheme for a PDE modeling combustion with
 nonlinear advection and diffusion, Mathematics and Computers in Simulation 69 (2005)
 439-446.
- [342] R. E. Mickens, Dynamic consistency: a fundamental principle for constructing nonstan dard finite difference schemes for differential equations, Journal of Difference Equations and
 Applications 11 (2005) 645-653.
- [343] R. E. Mickens, Advances in the Applications of Nonstandard Finite Difference Schemes,
 World Scientific, Singapore, 2005.

- [344] R. E. Mickens, Numerical integration of population models satisfying conservation laws:
 NSFD methods, Journal of Biological Dynamics 4 (2007) 427-436.
- [345] R. E. Mickens, Calculation of denominator functions for nonstandard finite difference
 schemes for differential equations satisfying a positivity condition, Numerical Methods for
 Partial Differential Equation 23 (2007) 672-691.
- [346] R. E. Mickens, Nonstandard Finite Difference Schemes for Differential Equations, Journal
 of Difference Equations and Applications 8 (2012) 823-847.
- [347] R. E. Mickens, T. M. Washington, NSFD discretizations of interacting population models
 satisfying conservation laws, Computers & Mathematics with Applications 66 (2013) 2307 2316.
- [348] R. E. Mickens, Nonstandard Finite Difference Schemes: Methodology and Applications,
 World Scientific, 2020.
- [349] R. E. Mickens, T. M. Washington, A note on a positivity preserving nonstandard finite
 difference scheme for a modified parabolic reaction-advection-diffusion PDE, Journal of Difference Equations and Applications 26 (2020) 1423-1427.
- [350] R. E. Mickens, I. H. Herron, Approximate rational solutions to the Thomas-Fermi equation
 based on dynamic consistency, Applied Mathematics Letters 116 (2021) 106994.
- [351] L. Min, Y. Su, Y. Kuang, Mathematical analysis of a basic virus infection model with
 application to HBV infection, Rocky Mountain Journal of Mathematics 38 (2008), 15731584
- [352] J. C. Miranda, A. J. Arenas, G. González-Parra, and Luis M. Villada, Existence of Traveling
 Waves of a Diffusive Susceptible–Infected–Symptomatic–Recovered Epidemic Model with
 Temporal Delay, Mathematics 12(5) (2024) 710.
- [353] T. Y. Miyaoka, S. Lenhart, J. F. C. A. Meyer, Optimal control of vaccination in a vectorborne reaction-diffusion model applied to Zika virus, Journal of Mathematical Biology 79 (2019) 1077-1104.
- [354] N. Mohan, N. Kumari, Positive steady states of a SI epidemic model with cross diffusion,
 Applied Mathematics and Computation 410 (2021) 126423.
- [355] J. Mondal, S. Khajanchi, Mathematical modeling and optimal intervention strategies of the
 COVID-19 outbreak, Nonlinear Dynamics 109 (2022) 177-202.
- [356] G. Mulone, B. Straughan, A note on heroin epidemics, Mathematical Biosciences 218 (2009)
 138-141.
- [357] A. Mummert, O. M. Otunuga, Parameter identification for a stochastic SEIRS epidemic
 model: case study influenza, Journal of Mathematical Biology 79 (2019) 705-729.
- [358] L. H. A. Monteiro, An epidemiological model for SARS-CoV-2, Ecological Complexity 43
 (2020) 100836.
- [359] G. A. Munoz-Fernandez, J. M. Seoane, J. B. Seoane-Sepulveda, A SIR-type model describing
 the successive waves of COVID-19, Chaos, Solitons & Fractals 144 (2021) 110682.
- [360] J. G. Murray, Mathematical Biology, II: Spatial Models and Biomedical Applications, third
 ed., Springer, New York, 2003.
- [361] E. M. Musyoki, W. N. Mutuku, N. M. Imbusi, E. O. Omondi, Mathematical modelling
 of tuberculosis and diabetes co-infection using the non-standard finite difference scheme,
 Pan-American Journal of Mathematics 2 (2023) 16.
- [362] M. C. Nava, J. M. Guevara-Jordan, A New Analysis of an Implicit Mimetic Scheme for the
 Heat Equation, Journal of Applied Mathematics and Physics 11(3) (2023) 841-857.
- [363] R. Naz, A. Omame, M. Torrisi, Cost-Effectiveness Analysis of COVID-19 Vaccination : A
 review of some Vaccination Models, Partial Differential Equations in Applied Mathematics
 11(2024) 100842.
- [364] F. Ndairou, M. Khalighi, L. Lahti, Ebola epidemic model with dynamic population and
 memory, Chaos, Solitons & Fractals 170 (2023) 113361.
- [365] M. Z. Ndii, A. K. Supriatna, An application of nonstandard finite-difference scheme for solving autonomous and non-autonomous mathematical model for Wolbachia-carrying mosquito
- population dynamics, Journal of Mathematical and Computational Science 11(1) (2021)
 1039-1052.
- [366] T. W. Ng, G. Turinici, A. Danchin, A double epidemic model for the SARS propagation,
 BMC Infectious Diseases 3 (2003) 19.

- [367] C. N. Ngonghala, E. Iboi, S. Eikenberry, M. Scotch, C. R. MacIntyre, M. H. Bonds, A.
 B. Gumel, Mathematical assessment of the impact of non-pharmaceutical interventions on curtailing the 2019 novel Coronavirus, Mathematical Biosciences 325 (2020) 108364.
- [368] G. A. Ngwa, On the Population Dynamics of the Malaria Vector, Bulletin of Mathematical
 Biology 68 (2006) 2161-2189.
- [369] M. A. Nowak, S. Bonhoeffer, A. M. Hill, R. Boehme R, H. C. Thomas, H. McDade, Viral dynamics in hepatitis B virus infection, The Proceedings of the National Academy of Sciences 93 (1996) 4398-4402.
- [370] M. A. Nowak, R. M. May, Virus Dynamics: Mathematical Principles of immunology and
 Virology, Oxford University Press, New York, 2000.
- [371] H. A. Obaid, R. Ouifki, K. C. Patidar, A nonstandard finite difference method for solving a mathematical model of HIV-TB co-infection, Journal of Difference Equations and
 Applications 23(6) (2017) 1105-1132.
- [372] L. F. Olsen, G. L. Truty, W. M. Schaffer, Oscillations and chaos in epidemics: A nonlinear
 dynamic study of six childhood diseases in Copenhagen, Denmark, Theoretical Population
 Biology 33 (1988) 344-370.
- [373] L. F. Olsen, W. M. Schaffer, Chaos Versus Noisy Periodicity: Alternative Hypotheses for
 Childhood Epidemics, Science 249 (1990) 499-505.
- [374] S. M. O'Regan, T. C. Kelly, A. Korobeinikov, M. J. A. O'Callaghan, A. V. Pokrovskii,
 Lyapunov functions for SIR and SIRS epidemic models, Applied Mathematics Letters 23
 (2010) 446-448.
- [375] R. Padmanabhan, H. S. Abed, N. Meskin, T. Khattab, M. Shraim, M. A. Al-Hitmi, A review
 of mathematical model-based scenario analysis and interventions for COVID-19, Computer
 Methods and Programs in Biomedicine 209 (2021) 106301.
- [376] P. K. Pandey, A method for an approximate numerical solution of two point boundary value
 problems: nonstandard finite difference method on semi open interval, International Journal
 of Computing Science and Mathematics 17(3) (2023) 220-228.
- [377] B. Pant, S. Safdar, M. Santillana, A. Gumel, Mathematical assessment of the role of human
 behavior changes on SARS-CoV-2 transmission dynamics, medRxiv Preprint (2024): 2024 02.
- [378] S. A. Pasha, Y. Nawaz, M. S. Arif, On the nonstandard finite difference method for reaction diffusion models, Chaos, Solitons & Fractals 166 (2023) 112929.
- [379] M. Pathak, P. Joshi, K. S. Nisar, Numerical investigation of fluid flow and heat transfer in
 micropolar fluids over a stretching domain, Journal of Thermal Analysis and Calorimetry
 147 (2022) 10637-10646.
- [380] K. C. Patidar, On the use of nonstandard finite difference methods, Journal of Difference
 Equations and Applications 11 (2005) 735-758.
- [381] K. C. Patidar, K. K. Sharma, ε-Uniformly convergent non-standard finite difference methods
 for singularly perturbed differential difference equations with small delay, Applied Mathematics and Computation 175(1) (2006) 864–890.
- [382] K. C. Patidar, Nonstandard finite difference methods: Recent trends and further develop ments, Journal of Difference Equations and Applications 22 (2016) 817-849.
- [383] R. Peng, Asymptotic profiles of the positive steady state for an SIS epidemic reac tion-diffusion model. Part I, Journal of Differential Equations 247 (2009) 1096-1119.
- [384] R. Peng, F. Yi, Asymptotic profile of the positive steady state for an SIS epidemic reac tion-diffusion model: Effects of epidemic risk and population movement, Physica D: Non linear Phenomena 259(2013) 8-25.
- [385] A. Perasso, B. Laroche, Y. Chitour, S. Touzeau, Identifiability analysis of an epidemiological
 model in a structured population, Journal of Mathematical Analysis and Applications 374
 (2011) 154-165.
- [386] E. Pérez, Mathematical modeling of the spread of alcoholism among Colombian college
 students, Ingeniería y Ciencia 16(32) (2020), 195-223.
- [387] V. Piccirillo, Nonlinear control of infection spread based on a deterministic SEIR model,
 Chaos, Solitons & Fractals 149 (2021) 111051.
- [388] F. Pierret, A non-standard-Euler-Maruyama scheme, Journal of Difference Equations and
 Applications 22(1) (2016) 75–98.
- [389] J. R. C. Piqueira, O. V. Araujo, A modified epidemiological model for computer viruses,
 Applied Mathematics and Computation 213 (2009) 355-360.

- [390] J. R. C. Piqueira, M. Zilbovicius, C. M. Batistela, Daley-Kendal models in fake-news sce nario, Physica A 548 (2020) 123406.
- [391] L. Pontryagin, V. Boltyanskii, R. Gramkrelidze, E. Mischenko, The Mathematical Theory
 of Optimal Processes, Wiley Interscience, 1962.
- [392] L. Pujante-Otalora, B. Canovas-Segura, M. Campos, J. M. Juarez, The use of networks
 in spatial and temporal computational models for outbreak spread in epidemiology: A
 systematic review, Journal of Biomedical Informatics 143 (2023) 104422.
- [393] W. Qin, L. Wang, X. Ding, A non-standard finite difference method for a hepatitis B virus infection model with spatial diffusion, Journal of Difference Equations and Applications 20 (2014) 1641-1651.
- [394] W. Qin, D. Ding, X. Ding, A non-standard finite difference scheme for an advection-diffusion reaction equation, Mathematical Methods in the Applied Sciences 38(15) (2015) 3308-3321.
- [395] M. Rafiq, M. O. Ahmad, Non-Standard Finite Difference Modeling for Transmission Dynam ics of Dengue Fever, University of Engineering and Technology Taxila. Technical Journal
 21(1) (2016) 116.
- [396] M. Rafiq, J. E. Macías-Díaz, A. Raza, N. Ahmed, Design of a nonlinear model for the prop agation of COVID-19 and its efficient nonstandard computational implementation, Applied
 Mathematical Modelling 89 (2021) 1835-1846.
- [397] M. Rahman, K. Bekele-Maxwell, L. L. Cates, H. T. Banks, N. K. Vaidya, Modeling Zika
 Virus transmission Dynamics: parameter estimates, Disease Characteristics, and prevention,
 Scientific Reports 9 (2019) 10575.
- [398] M. Raissi, P. Perdikaris, G. E. Karniadakis, Physics-informed neural networks: A deep
 learning framework for solving forward and inverse problems involving nonlinear partial
 differential equations, Journal of Computational Physics 378 (2019) 686-707.
- [399] M. K. Rawani, A. K. Verma, C. Cattani, A novel hybrid approach for computing numerical solution of the time-fractional nonlinear one and two-dimensional partial integrodifferential equation, Communications in Nonlinear Science and Numerical Simulation 118 (2023) 106986.
- [400] M. K. Rawani, A. K. Verma, L. Verma, Numerical treatment of Burgers' equation based
 on weakly L-stable generalized time integration formula with the NSFD scheme, Applied
 Mathematics and Computation 467 (2024) 128485.
- [401] A. Raza, M. S. Arif, M. Rafiq, A reliable numerical analysis for stochastic dengue epidemic
 model with incubation period of virus, Advances in Difference Equations 2019(1) (2019)
 1-19.
- [402] A. Raza, U. Fatima, M. Rafiq, N. Ahmed, I. Khan, K. S. Nisar, Z. Iqbal, Mathematical analysis and design of the nonstandard computational method for an epidemic model of computer virus with delay effect: Application of mathematical biology in computer science, Results in Physics 21 (2021) 103750.
- [403] N. Raza, A. Bakar, A. Khan, C. Tunç, Numerical simulations of the fractional-order SIQ
 mathematical model of corona virus disease using the nonstandard finite difference scheme,
 Malaysian Journal of Mathematical Sciences 16(3) (2022) 391-411.
- [404] J. Ren, X. Yang, Q. Zhu, L.-X. Yang, C. Zhang, A novel computer virus model and its dynamics, Nonlinear Analysis: Real World Applications 13 (2012) 376-384.
- [405] X. Ren, K. Wang, X. Liu, Dynamics on a degenerated reaction-diffusion Zika transmission
 model, Applied Mathematics Letters 150 (2024) 108935.
- [406] M. Riaz, K. Shah, A. Ullah, M. A. Alqudah, T. Abdeljawad, The Volterr-Lyapunov matrix
 theory and nonstandard finite difference scheme to study a dynamical system, Results in
 Physics 52 (2023) 106890.
- [407] F. A. Rihan, Delay differential equations and applications to biology, Springer, Singapore, 2021.
- [408] P. Rodrigues, M. Gabriela, M. Gomes, C. Rebelo, Drug resistance in tuberculosis-a reinfec tion model, Theoretical Population Biology 71 (2007) 196-212.
- [409] L.-I. W. Roeger, Dynamically consistent discrete Lotka-Volterra competition models derived
 from nonstandard finite-difference schemes, Discrete and Continuous Dynamical Systems -
- 1733 Series B 9(2) (2008) 415-429.
- 1734 [410] L.-I. W. Roeger, G. Lahodny Jr., Dynamically consistent discrete Lotka-Volterra competi-
- tion systems, Journal of Difference Equations and Applications 19 (2013) 191-200.

- [411] G. Rohith, K. B. Devik, Dynamics and control of COVID-19 pandemic with nonlinear
 incidence rates, Nonlinear Dynamics 101 (2020) 2013-2026.
- [412] S. Ruan, W. Wang, Dynamical behavior of an epidemic model with a nonlinear incidence
 rate, Journal Differential Equations 188 (2003) 135-163.
- [413] D. B. Saakian, A simple statistical physics model for the epidemic with incubation period,
 Chinese Journal of Physics 73 (2021) 546-551.
- [414] M. A. Safi, A. B. Gumel, Mathematical analysis of a disease transmission model with quarantine, isolation and an imperfect vaccine, Computers & Mathematics with Applications 61 (2011) 3044-3070.
- 1745[415] P. Saha, N. Bairagi, G. N'Guerekata, Positivity and dynamics preserving discretization1746schemes for nonlinear evolution equations, Malaya Journal of Matematik 12(01) (2024) 1-174720.
- [416] S. M. Salman, A nonstandard finite difference scheme and optimal control for an HIV model
 with Beddington-DeAngelis incidence and cure rate, The European Physical Journal Plus
 135 (2020) 1-23.
- [417] Md. Samsuzzoha, M. Singh, D. Lucy, Parameter estimation of influenza epidemic model,
 Applied Mathematics and Computation 220 (2013) 616-629.
- [418] F. Sanchez, M. Engman, L. Harrington, and C. Castillo-Chavez, Models for dengue transmission and control. In: Mathematical Studies on Human Disease Dynamics: Emerging
 Paradigms and Challenges. American Mathematical Society Contemporary Mathematics
 Series, A. B. Gumel, C. Castillo-Chavez, R. E. Mickens, D. P. Clemence (Eds.), 2007.
- [419] E. A. B. Sandow, B. Seidu, S. Abagna, A non-standard numerical scheme for an alcohol abuse model with induced-complications, Heliyon 9(11) (2023) e22263.
- [420] F.-J. Santonja, E. Sánchez, M. Rubio J.-M. Morera, Alcohol consumption in Spain and its
 economic cost: A mathematical modelling approach, Mathematical and Computer Modelling
 52 (2010), 999-1003.
- [421] F.-J. Santonja, I.-C. Lombana, M. Rubio, E. Sánchez, J. Villanueva, A network model for
 the short-term prediction of the evolution of cocaine consumption in Spain, Mathematical
 and Computer Modelling 52 (2010) 1023-1029.
- [422] F.-J. Santonja, R.-J. Villanueva, L. Jódar, G. Gonzalez-Parra, Mathematical modelling
 of social obesity epidemic in the region of Valencia, Spain, Mathematical and Computer
 Modelling of Dynamical Systems 16 (2010) 23-34.
- [423] F.-J. Santonja, A. C. Tarazona, R. J. Villanueva, Predicting Cocaine Consumption in Spain.
 A mathematical Modelling Approach, Drugs: Education, Prevention & Policy 18 (2011),
 108-115.
- [424] T. Sarkar, O. Biswas, P. K. Srivastava, Modelling the effects of media information and saturated treatment on malaria disease with NSFD method, International Journal of Biomathematics (2024) 2450001..
- 1774 [425] T. Sarkar, S. Das, S. A. Choudhury, P. Biswas, A Zika Virus Model Incorporating the
 1775 Role of Information: Stability, Numerical Methods, and Control Strategies, Modeling Earth
 1776 Systems and Environment 11(2) (2025) 122.
- 1777 [426] M. Schäfer, K. Niedzielewski, T. Götz, T. Krüger, An integro-differential model for the 1778 spread of diseases, arXiv preprint arXiv:2307.10087 (2023).
- [427] W. E. Schiesser, A Mathematical Modeling Approach to Infectious Diseases: Cross Diffusion
 PDE Models for Epidemiology, World Scientific Publishing, 2018.
- 1781 [428] E. Scholl, H. G. Schuster, Handbook of Chaos Control, Wiley-VCH, 2008.
- [429] N. C. Severo, Generalizations of some stochastic epidemic models, Mathematical Biosciences
 4 (1969) 395-402.
- [430] N. Shahid, M. A. Rehman, A. Khalid, U. Fatima, T. S. Shaikh, N. Ahmed, H. Alotaibi, M.
 Rafiq, I. Khan, K. S. Nisar, Mathematical analysis and numerical investigation of advectionreaction-diffusion computer virus model, Results in Physics 26 (2021) 104294.
- [431] C. Shan, H. Zhu, Bifurcations and complex dynamics of an SIR model with the impact of the number of hospital beds, Journal of Differential Equations 257 (2014) 1662-1688.
- [432] N. Sharma, R. Singh, J. Singh, O. Castillo, Modeling assumptions, optimal control strategies
 and mitigation through vaccination to Zika virus, Chaos, Solitons & Fractals 150 (2021)
- 1791 111137.
- [433] O. Sharomi, A. B. Gumel, Curtailing smoking dynamics: A mathematical modeling approach, Applied Mathematics and Computation 195 (2008) 475-499.

- [434] O. Sharomi, C. N. Podder, A. B. Gumel, S. M. Mahmud, E. Rubinstein, Modelling the
 Transmission Dynamics and Control of the Novel 2009 Swine Influenza (H1N1) Pandemic,
 Bulletin of Mathematical Biology 73 (2011) 515-548.
- [435] O. Sharomi, T. Malik, Optimal control in epidemiology, Annals of Operations Research 251
 (2017) 55-71. (2017)
- [436] M. Sher, K. Shah, M. Sarwar, M. A. Alqudah, T. Abdeljawad, Mathematical analysis of fractional order alcoholism model, Alexandria Engineering Journal 78 (2023) 281-291.
- [437] L. Shi, Z. Chen, P. Wu, Spatial and temporal dynamics of COVID-19 with nonlocal dis persal in heterogeneous environment: Modeling, analysis and simulation, Chaos, Solitons &
 Fractals 174 (2023) 113891.
- [438] Z. Shuai, P. van den Driessche, Global Stability of Infectious Disease Models Using Lyapunov
 Functions, SIAM Journal on Applied Mathematics 73 (2013) 1513 1532.
- [439] B. Shulgin, L. Stone, Z. Agur, Pulse vaccination strategy in the SIR epidemic model, Bulletin
 of Mathematical Biology 60 (1998) 1123-1148.
- [440] R. P. Sigdel, C. C. McCluskey, Global stability for an SEI model of infectious disease with
 immigration, Applied Mathematics and Computation 243 (2014) 684-689.
- [441] M. Sinan, K. J. Ansari, A. Kanwal, K. Shah, T. Abdeljawad, Zakirullah, B. Abdalla, Analysis of the mathematical model of cutaneous Leishmaniasis disease, Alexandria Engineering
 Journal 72 (2023) 117-134.
- 1813 [442] R. A. Singh, R. Lal, R. R. Kotti, Time-discrete SIR model for COVID-19 in Fiji, Epidemi-1814 ology and Infection 150, e75, 1-10.
- [443] G. D. Smith, Numerical Solution of Partial Differential Equations: Finite Difference Meth ods, Third Edition, Oxford University Press, 1985.
- [444] H. Smith, P. Waltman, The Theory of the Chemostat: Dynamics of Microbial Competition,
 Cambridge University Press, 1995.
- [445] H. Smith, An Introduction to Delay Differential Equations with Applications to the Life
 Sciences, Springer, New York, 2011.
- [446] B. Song, C. Castillo-Chavez, J. P. Aparicio, Tuberculosis models with fast and slow dynam ics: the role of close and casual contacts, Mathematical Biosciences 180 (2002) 187-205.
- [447] P. Song, Y. Lou, Y. Xiao, A spatial SEIRS reaction-diffusion model in heterogeneous envi ronment, Journal of Differential Equations 267 (2019) 5084-5114.
- [448] Y. Song, T. Zhang, Y. Peng, Turing-Hopf bifurcation in the reaction-diffusion equations and
 its applications, Communications in Nonlinear Science and Numerical Simulation 33 (2016)
 229-258.
- [449] M. E. Songolo, B. Bidégaray-Fesquet, Extending nonstandard finite difference scheme rules
 to systems of nonlinear ODEs with constant coefficients, Journal of Difference Equations
 and Applications (2024) 1-26.
- [450] S. Soubeyrand, L. Roques, Parameter estimation for reaction-diffusion models of biological
 invasions, Population Ecology 56 (2014) 427-434.
- [451] P. T. Sowndarrajan, L. Shangerganesh, A. Debbouche, D. F. M. Torres, Optimal control
 of a heroin epidemic mathematical model, Optimization: A Journal of Mathematical Pro gramming and Operations Research 71 (2022) 3107-3131.
- [452] T. Stocksa, L. J. Martin, S. Kuhlmann-Berenzon, T. Britto, Dynamic modeling of hepatitis
 C transmission among people who inject drugs, Epidemics 30 (2020) 100378.
- [453] J. C. Strikwerda, Finite Difference Schemes and Partial Differential Equations, Second Edi tion, Society for Industrial and Applied Mathematics, Philadelphia, 2004.
- [454] A. Stuart, A. R. Humphries, Dynamical Systems and Numerical Analysis, Cambridge University Press, 1998.
- [455] H. Sun, Y. Zhang, D. Baleanu, W. Chen, Y. Chen, A new collection of real world applications of fractional calculus in science and engineering, Communications in Nonlinear Science and Numerical Simulation 64 (2018) 213-231.
- [456] B. Tadić, R. Melnik, Microscopic dynamics modeling unravels the role of asymptomatic virus
 carriers in SARS-CoV-2 epidemics at the interplay between biological and social factors,
 Computers in Biology and Medicine 133 (2021) 104422.
- [457] C. Tadmon, S. Foko, Modeling and mathematical analysis of an initial boundary value
 problem for hepatitis B virus infection, Journal of Mathematical Analysis and Applications
 474 (2019) 309-350.

- [458] C. Tadmon, S. Foko, Non-standard finite difference method applied to an initial boundary
 value problem describing hepatitis B virus infection, Journal of Difference Equations and
- 1853 Applications 26 (2020) 122-139.
- [459] C. Tadmon, J. N. Kengne, Mathematical modelling and nonstandard finite scheme analy sis for an Ebola model transmission with information and voluntary isolation, Journal of
 Difference Equations and Applications 28 (2022) 299-334.
- [460] M. Taghipour, H. Aminikhah, An Efficient Non-standard Finite Difference Scheme for Solving Distributed Order Time Fractional Reaction–Diffusion Equation, International Journal of Applied and Computational Mathematics 8(2) (2022) 56.
- [461] B. Takács, R. Horváth, I. Faragó, Space dependent models for studying the spread of some diseases, Computers & Mathematics with Applications 80 (2020) 395-404.
- [462] B. M. Takács, G. S. Sebestyén, I. Faragó, High-order reliable numerical methods for epidemic
 models with non-constant recruitment rate, Appl. Numer. Math. 206 (2024) 75–93.
- [463] A. J. O. Tassé, V. B. Kubalasa, B. Tsanou, M-S. Jean, Nonstandard finite difference schemes
 for some epidemic optimal control problems, Mathematics and Computers in Simulation 228
 (2025), 1-22.
- [464] S. Y. Tchoumi, M. L. Diagne, H. Rwezaura, J. M. Tchuenche, Malaria and COVID-19 codynamics: A mathematical model and optimal control, Applied Mathematical Modelling 99 (2021) 294-327.
- [465] Y. A. Terefe, H. Gaff, M. Kamga, L. van der Mescht, Mathematics of a model for Zika
 transmission dynamics, Theory in Biosciences 137 (2018) 209-218.
- [466] J. J. Tewa, S. Bowong, S. C. O. Noutchie, Mathematical analysis of a two-patch model
 of tuberculosis disease with staged progression, Applied Mathematical Modelling 36 (2012)
 5792-5807.
- [467] J. W. Thomas, Numerical Partial Differential Equations: Finite Difference Methods,
 Springer New York, 1995.
- [468] Y. Tian, X. Liu, Global dynamics of a virus dynamical model with general incidence rate
 and cure rat, Nonlinear Analysis: Real World Applications 16 (2014) 17-26.
- [469] S. Treibert, H. Brunner, M. Ehrhardt, Compartment models for vaccine effectiveness and non-specific effects for Tuberculosis, Mathematical Biosciences and Engineering 16(6) (2019), 7250-7298.
- [470] S. Treibert, H. Brunner, M. Ehrhardt, A nonstandard finite difference scheme for the
 SVICDR model to predict COVID-19 dynamics, Mathematical Biosciences and Engineering
 19 (2022) 1213-1238.
- [471] D. Y. Trejos, J. C. Valverde, E. Venturino, Dynamics of infectious diseases: A review of
 the main biological aspects and their mathematical translation, Applied Mathematics and
 Nonlinear Sciences 7 (2022) 1-26.
- [472] J. Tumwiine, J. Y. T. Mugisha, L. S. Luboobi, On global stability of the intra-host dynamics
 of malaria and the immune system, Journal of Mathematical Analysis and Applications 341
 (2008) 855-869.
- [473] M. ur Rahman, M. Yavuz M. Arfan, A. Sami, Theoretical and numerical investigation of
 a modified ABC fractional operator for the spread of polio under the effect of vaccination,
 AIMS Biophysics 11(1) (2024) 97-120.
- [474] P. van den Driessche, Some epidemiological models with delays, In: Differential Equations
 and Applications to Biology and to Industry (Claremont, CA, 1994), pages 507-520. World
 Scientific Publishing, River Edge, NJ (1996).
- [475] P. van den Driessche, J. Watmough, Reproduction numbers and sub-threshold endemic
 equilibria for compartmental models of disease transmission, Mathematical Biosciences 180
 (2002) 29-48.
- [476] P. van den Driessche, J. Watmough, Further Notes on the Basic Reproduction Number. In:
 Brauer, F., van den Driessche, P., Wu, J. (eds) Mathematical Epidemiology. Lecture Notes
 in Mathematics 1945, Springer, Berlin, Heidelberg, 2008.
- [477] P. van den Driessche, Reproduction numbers of infectious disease models, Infectious Disease
 Modelling 2 (2017) 288-303.
- [478] G. A. K. van Voorn, B. W. Kooi, Smoking epidemic eradication in a eco-epidemiological
 dynamical model, Ecological Complexity 14 (2013) 180-189.
- [479] S. Vaz, Sandra, D. F. M. Torres, A dynamically-consistent nonstandard finite difference
 scheme for the SICA model, arXiv preprint arXiv:2105.10826 (2021).

- [480] C. Vargas-De-León, On the global stability of SIS, SIR and SIRS epidemic models with
 standard incidence, Chaos, Solitons & Fractals 44 (2011) 1106-1110.
- 1911 [481] A. K. Verma, M. K. Rawani, Numerical solutions of generalized Rosenau-KDV-RLW equa-
- tion by using Haar wavelet collocation approach coupled with nonstandard finite difference
 scheme and quasilinearization, Numerical Methods for Partial Differential Equations 39(2)
 (2023) 1085-1107.
- [482] A. Viguerie, A. Veneziani, G. Lorenzo, D. Baroli, N. Aretz-Nellesen, A. Patton, T. E.
 Yankeelov, A. Reali, T. J. R. Hughes, F. Auricchio, Diffusion-reaction compartmental models
 formulated in a continuum mechanics framework: application to COVID-19, mathematical
 analysis, and numerical study, Computational Mechanics 66 (2020) 1131-1152.
- [483] B. Wacker, J. C. Schluter, Time-continuous and time-discrete SIR models revisited: theoryand applications, Advances in Difference Equations 2020 (2020) 556.
- [484] B. Wacker, J. C. Schluter, A non-standard finite-difference-method for a non-autonomous
 epidemiological model: analysis, parameter identification and applications, Mathematical
 Biosciences and Engineering 20(7) (2023) 12923-12954.
- [485] G. D. Walters, Spontaneous remission from alcohol, tobacco, and other drug abuse: seeking
 quantitative answers to qualitative questions, The American Journal of Drug and Alcohol
 Abuse 26 (2000), 443-460.
- [486] C. Wan, T. Li, W. Zhang, J. Dong, Dynamics of epidemic spreading model with drug resistant variation on scale-free networks, Physica A 493 (2018) 17-28.
- [487] J. Wang, R. Zhang, T. Kuniya, A reaction-diffusion Susceptible-Vaccinated-Infected Recovered model in a spatially heterogeneous environment with Dirichlet boundary con dition, Mathematics and Computers in Simulation 190 (2021) 848-865.
- [488] J. Wang, X. Wu, T. Kuniya, Analysis of a diffusive HBV model with logistic proliferation and
 non-cytopathic antiviral mechanisms, Communications in Nonlinear Science and Numerical
 Simulation 106 (2022) 106110.
- [489] J. Wang, Z. Teng, B. Dai, Qualitative analysis of a reaction-diffusion SIRS epidemic model
 with nonlinear incidence rate and partial immunity, Infectious Disease Modelling 8 (2023)
 881-911.
- [490] K. Wang, W. Wang, Propagation of HBV with spatial dependence, Mathematical Bio-sciences 210 (2007) 78-95.
- [491] K. Wang, A. Fan, A. Torres, Global properties of an improved hepatitis B virus model,
 Nonlinear Analysis: Real World Applications 11 (2010) 3131-3138.
- [492] L. Wang, L.-I. W. Roeger, Nonstandard finite difference schemes for a class of generalized
 convection-diffusion-reaction equations, Numerical Methods for Partial Differential Equa tions 31 (2015) 1288-1309.
- [493] L. Wang, H. Zhao, Modeling and dynamics analysis of Zika transmission with contaminated
 aquatic environments, Nonlinear Dynamics 104 (2021) 845-862.
- [494] W. Wang, X.-Q. Zhao, Basic Reproduction Numbers for Reaction-Diffusion Epidemic Mod els, SIAM Journal on Applied Dynamical Systems 11 (2012) 1652-1673.
- [495] X.-Y. Wang, H.-F. Huo, Q.-K. Kong, W.-X. Shi, Optimal control strategies in an alcoholism
 model, Abstract and Applied Analysis 2014 (2014) 1–18.
- [496] H. Wei, X. Li, M. Martcheva, An epidemic model of a vector-borne disease with direct transmission and time delay, Journal of Mathematical Analysis and Applications 342 (2008)
 895-908.
- [497] A. Wendler, L. Plötzke, H. Tritzschak, M. J. Kühn, A nonstandard numerical scheme
 for a novel SECIR integro-differential equation-based model allowing nonexponentially dis tributed stay times, arXiv preprint arXiv:2408.12228 (2024).
- [498] E. White, C. Comiskey, Heroin epidemics, treatment and ODE modeling, Mathematical
 Biosciences 208 (2007), 312-324.
- [499] D. T. Wood, D. T. Dimitrov, H. V. Kojouharov, A nonstandard finite difference method for
 n-dimensional productive-destructive systems, Journal of Difference Equations and Appli cations 21 (2015) 240-254.
- [500] D. T. Wood, H. V. Kojouharov, A class of nonstandard numerical methods for autonomous
 dynamical systems, Applied Mathematics Letters 50 (2015) 78-82.
- [501] D. T. Wood, H. V. Kojouharov, D. T. Dimitrov, Universal approaches to approximate
 biological systems with nonstandard finite difference methods, Mathematics and Computers
 in Simulation 133 (2017) 337-350.

- [502] P. Wu, X. Wang, Z. Feng, Spatial and temporal dynamics of SARS-CoV-2: Modeling,
 analysis and simulation, Applied Mathematical Modelling 113 (2023) 220-240.
- [503] H. Xiang, Y.-P. Liu, H.-F. Huo, Stability of an SAIRS alcoholism model on scale-free net works, Physica A 473 (2017) 276-292.
- [504] H. Xiang, N.-N. Song, H.-F. Huo, Modelling effects of public health educational campaigns
 on drinking dynamics, Journal of Biological Dynamics 10(1) (2016) 164–178.
- [505] M.-Z. Xin, B.-G. Wang, Global dynamics of a reaction-diffusion malaria model, Nonlinear
 Analysis: Real World Applications 61 (2021) 103332.
- [506] J. Xu, Y. Geng, J. Hou, A non-standard finite difference scheme for a delayed and diffusive
 viral infection model with general nonlinear incidence rate, Computers & Mathematics with
 Applications 74(8) (2017) 1782–1798.
- [507] R. Xu, Z. Ma, An HBV model with diffusion and time delay, Journal of Theoretical Biology
 257 (2009) 499-509.
- [508] J. Yang, F. Xu, Global stability of two SIS epidemic mean-field models on complex networks:
 Lyapunov functional approach, Journal of the Franklin Institute 355 (2018) 6763-6779.
- [509] J. Yang, L. Yang, Z. Jin, Optimal strategies of the age-specific vaccination and antiviral
 treatment against influenza, Chaos, Solitons & Fractals 168 (2023) 113199.
- L.-X. Yang, X. Yang, J. Liu, Q. Zhu, C, Gan, Epidemics of computer viruses: A complexnetwork approach, Applied Mathematics and Computation 219 (2013) 8705-8717.
- [511] L.-X. Yang, X. Yang, Q. Zhu, L. Wen, A computer virus model with graded cure rates,
 Nonlinear Analysis: Real World Applications 14 (2013) 414-422.
- [512] L.-X. Yang, X. Yang, The impact of nonlinear infection rate on the spread of computer
 virus, Nonlinear Dynamics 82 (2015) 85-95.
- 1990 [513] Y. Yang, J. Zhou, X. Ma, T. Zhan, Nonstandard finite difference scheme for a diffusive
 within-host virus dynamics model with both virus-to-cell and cell-to-cell transmissions, Computers & Mathematics with Applications 72 (2016) 1013-1020.
- [514] T. K. Yano, E. Afrifa-Yamoah, J. Collins, U. Mueller, S. Richardson, Mathematical modelling and analysis for the co-infection of viral and bacterial diseases: a systematic review protocol, BMJ Open 14(12) (2024) e084027.
- [515] B. Yu, J. Shi, Z. Xue, M. Yang, X. Yang, Y. Su, Stability analysis of HCV dynamic model
 with saturation incidence, cellular immunity and interferon effect in intrahepatic and extrahepatic tissues, Mathematics and Computers in Simulation 216 (2024) 301-317.
- [516] Z. U. A. Zafar, M. Inc, F. Tchier, L. Akinyemi, Stochastic suicide substrate reaction model,
 Physica A: Statistical Mechanics and its Applications 610 (2023) 128384.
- [517] C. Zhang, J. Gao, H. Sun, J. Wang, Dynamics of a reaction-diffusion SVIR model in a
 spatial heterogeneous environment, Physica A 533 (2019) 122049.
- [518] J. Zhang, J. Lou, Z. Ma, J. Wu, A compartmental model for the analysis of SARS trans mission patterns and outbreak control measures in China, Applied Mathematics and Com putation 162 (2005) 909-924.
- [519] H. Zhao, L. Wang, S. M. Oliva, H. Zhu, Modeling and Dynamics Analysis of Zika Trans mission with Limited Medical Resources, Bulletin of Mathematical Biology 82 (2020) 99.
- [520] M. Zhou, H. Xiang, Z. Li, Optimal control strategies for a reaction-diffusion epidemic system,
 Nonlinear Analysis: Real World Applications 46 (2019) 446-464.
- 2010 [521] Q. Zhou, Analysis of opioid transmission crisis model in resilient cities based on numerical
- 2011 solutions of differential equations, Sustainable Energy Technologies and Assessments 52 2012 (2022) 102210.
- [522] C.-C. Zhu, J. Zhu, Dynamic analysis of a delayed COVID-19 epidemic with home quarantine
 in temporal-spatial heterogeneous via global exponential attractor method, Chaos, Solitons
 & Fractals 143 (2021) 110546.
- [523] L. Zhu, M. Liu, Y. Li, The dynamics analysis of a rumor propagation model in online social networks, Physica A 520 (2019) 118-137.
- [524] L. Zhu, B. Wang, Stability analysis of a SAIR rumor spreading model with control strategies
 in online social networks, Information Sciences 526 (2020) 1-19.
- [525] L. Zhu, T. Yuan, Optimal control and parameter identification of a reaction-diffusion net work propagation model, Nonlinear Dynamics 111 (2023) 21707-21733.

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