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Stability of the vector-borne disease model with direct transmission using Boubaker polynomials approach

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In this paper, we delve into the analysis of an epidemic model for a vector-borne disease. Our study focuses on utilizing a baseline version of the ordinary differential equations (ODE) model to capture the dynamics of the disease transmission. Specifically, we aim to study the long-term behavior and properties of the model's solutions using a novel analytical approach known as the Boubaker polynomial Expansion Scheme (BPES). Furthermore, to complement our theoretical analysis, we conduct numerical simulations to provide a more practical perspective on the epidemic.

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1. Introduction

Stability analysis of a vector-borne disease model with direct transmission involves the study of the long-term behavior of the disease dynamics in a population. This type of model takes into consideration the transmission of the disease through both vectors (such as mosquitoes) and direct contact between infected individuals. The stability of the model refers to the behavior of the disease in the long run and whether it will die out or persist in the population. The goal of stability analysis is to determine the conditions under which the disease-free equilibrium (when there are no infected individuals in the population) is stable or unstable, and to identify the conditions that lead to the establishment and persistence of the disease in a population. This information is crucial in informing public health policies and intervention strategies aimed at controlling and preventing the spread of the disease.

Disease-transmitting biological agents (anthropoids), known as vectors, are the main means of transmission for infectious diseases produced by viruses, bacteria, protozoa, or rickettsia. Vectors transport the disease without becoming ill themselves. The most widespread vector-borne diseases in the world is malaria, which is spread by mosquitoes. The mosquitoes are carriers of a variety of infectious illnesses, most notably dengue (the second most important vector-borne disease).

Currently, the disease Leptospirosis has emerged as an infectious disease of great importance. This type of infection is found in urban areas of industrialized countries and in rural areas around the world. Due to delays in two diagnoses, absences of adequate clinical infrastructure and capacity, and due the evil that can include pathogenicity of a number of leptospiral strains or genetically determined host immunopathological responses, mortality remains significant. To depict the dynamics of both compartments susceptible, recovered, and infected human population of vectors, several models have been proposed [1–3]. To explore the behavior of the leptospirosis disease, Pongsuumpun et al. [4] offered a mathematical formulation. They define the rate of change for rats as well as for young and old human populations. By looking at various illnesses and leptospirosis in Thailand, Triampo et al. examined deterministic models for the spread of the disease described in [5]. In order to understand

the dynamic behavior and the function of the optimal control theory of the disease, Zaman et al. [6] looked at the real data taken into account in [5]. Two non-linear models of the human race and the vector population were integrated by Zaman et al. [7] who used the Lyapunov method to examine local and global stability.

An analytical continuous solution is proposed in the current study, based on the BPES, the method has several key advantages over comparable approaches, including its ease of use and the validity and trustworthiness of the results it produces [8–10], especially when it is challenging to construct precise solution expressions.

The BPES is a mathematical method used in the field of computational fluid dynamics. It is a numerical technique that allows for the efficient and accurate solution of complex partial differential equations (PDEs) that describe fluid flow phenomena. BPES is based on the idea of expanding the solution of the PDE into a series of orthogonal polynomials. This expansion allows for the representation of the solution in a compact form and reduces the number of degrees of freedom required to solve the PDE. This, in turn, leads to improved computational efficiency and accuracy compared to other numerical methods. BPES has been applied in various fields including aerodynamics, heat transfer, and combustion, and has shown promising results in the simulation of complex fluid flow phenomena.

In this paper, we expand the model offered by Zaman et al. [6, 7] considering the interaction of man likely infected and vector-related illness mortality in both human and infected vectors. In the second section, we present the model and the biological parameters. The third section analyzes the model using BPES. At the end, we provide numerical example to illustrate results obtained through the paper.

2. Mathematical model

Firstly, we extend the model shown in [6, 7] considering the interaction of man likely infected vector-borne disease and related mortality in both human and infected vectors. To comprehend the model of the epidemic and their properties, at the beginning we set the parameter involved in the model and we elaborate the mathematical formulation.

Therefore, in order to gain a deeper comprehension of malaria transmission as well as the impact and contribution of immigration on our topic, as well as the spreading of the disease into free areas, we will develop a mathematical model similar to that of the disease using ODE where mosquitoes and people encounter one another and subsequently pass on the infection through transmission. Our mathematical model explains how contagious are illnesses spread by mosquitoes. The number of people worldwide is $N_h(t) = x_1(t) + x_2(t) + x_3(t)$ and they are classified into three classes: susceptible, x_1; infectious, x_2 and recovered, x_3.

Individuals enter the susceptible class in two ways: either through birth (with all compartments being filled at the natural birth rate b_h) or through immigration at a steady rate Ω_h. Susceptible individuals can become infected either through direct contact with infected humans at a constant rate β_1, or through exposure to infected mosquitoes at a constant rate β_2. Contaminated individuals recover at the rate γ_h, and all compartments depart the population due to a per capita emigration rate that depends on density and a natural death rate, $f_h(N_h) = \mu_{1h} + \mu_{2h}N_h$. Infected individuals are also reduced by disease related death at the rate δ_h.

However, there exist two categories of mosquitoes: those who are susceptible (x_4) and those who are infected (x_5). The total mosquito population is $N_v(t) = x_4(t) + x_5(t)$.

Hence, when a susceptible mosquito bites an infectious human, the mosquito contracts the disease and enters the x_5 class, individuals join the susceptible compartment at the rate Ω_v, and those who are susceptible become infected at the rate $\beta_3 x_5$ and all compartments reach susceptible compartment at the natural birth rate b_v (due to the fact that only female mosquitoes bite humans and animals to obtain lipids and proteins, which are essential components of blood to enable female mosquitoes to reproduce and lay their eggs as a result, male insects are not included in our model) and are decreased according to the affine function $f_v(N_v) = \mu_{1v} + \mu_{2v}N_v$ (mosquito mortality and emigration rates are

contingent on the per capita density of the population). Infected individuals are also reduced by disease related death at the rate δ_v.

Figure 1 explains how malaria transmission proceeds in our mathematical model (see [8]):

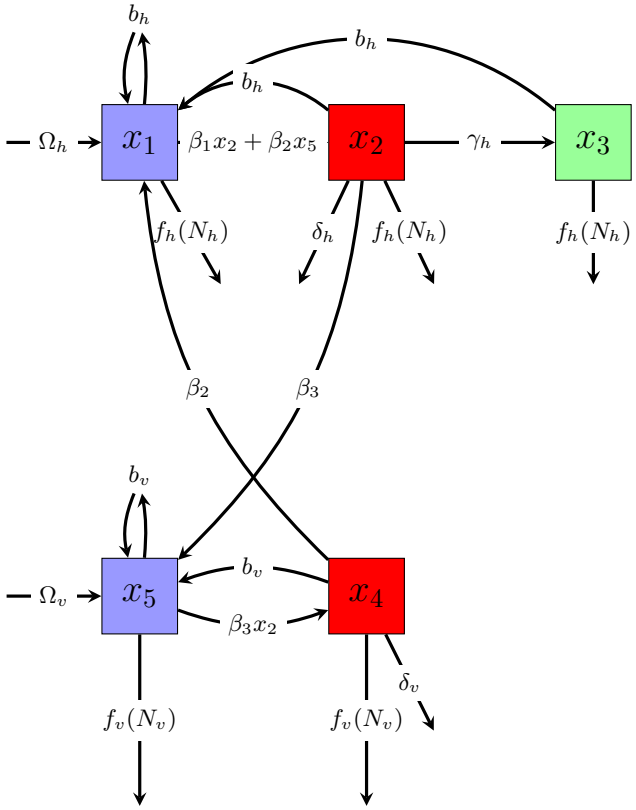

Fig. 1. Schematic diagram of system (1).

$$\begin{cases} \dfrac{dx_1}{dt} = g_h(N_h) - \beta_1 x_1 x_2 - \beta_2 x_1 x_5 - f_h(N_h) x_1, \\ \dfrac{dx_2}{dt} = \beta_1 x_1 x_2 + \beta_2 x_1 x_5 - (\gamma_h + f_h(N_h)) x_2, \\ \dfrac{dx_3}{dt} = \gamma_h x_2 - f_h(N_h) x_3, \\ \dfrac{dx_4}{dt} = g_v(N_v) - \beta_3 x_4 x_2 - f_v(N_v) x_4, \\ \dfrac{dx_5}{dt} = \beta_3 x_4 x_2 - f_v(N_v) x_5, \end{cases} \tag{1}$$

with initial conditions

$$x_1(0) \geqslant 0, \quad x_2(0) \geqslant 0, \quad x_3(0) \geqslant 0, \quad x_4(0) \geqslant 0, \quad \text{and} \quad x_5(0) \geqslant 0, \tag{2}$$

x_1 is number of susceptible human, x_2 is the proportion of the population's people who have the disease, x_3 is the population's number, which is recovered, x_4 is susceptible vector, x_5 is infectious vector, γ_h is disease related death rate of infected individuals, β_1 is direct transmission from infected human, β_2 is direct transmission from infected vector, and β_3 is disease carrying of susceptible vector per host per unit time;

$$\begin{aligned} f_h(N_h) &= \mu_{1,h} + \mu_{2,h} N_h, \\ f_v(N_v) &= \mu_{1,v} + \mu_{2,v} N_v, \\ g_h(N_h) &= \Omega_h + b_h N_h, \\ g_v(N_v) &= \Omega_v + b_v N_v. \end{aligned}$$

The following table provides definitions for parameters and variables:

Table 1. Parameter and variable descriptions for Model (1).

Variables	**Descriptions**
x_1	How susceptible are humans
x_2	How may humans have the disease
x_3	How may humans are recovered
x_4	How susceptibleare mosquitoes
x_5	How may mosquitoes have the disease
N_h	The total population of humans
N_v	The total population of mosquitoes
Parameters	**Descriptions**
Ω_h	Human migration rate
Ω_v	Mosquitoes immigration rate
b_h	Human's birth rate
b_v	Mosquitoes' birth rate
μ_{1h}	Part of the human mortality (and emigration) rate that is not dependent on density
μ_{2h}	Part of the human mortality (and emigration) rate that dependent on density
μ_{1v}	Part of the mosquitoes mortality (and emigration) rate that is not dependent on density
μ_{2v}	Part of the mosquitoes mortality (and emigration) rate that is dependent on density
γ_h	The rate at which humans transition from the infectious state to the recovered state
δ_h	The rate of mortality caused by the disease in humans
δ_v	The rate of mortality caused by the disease in mosquitoes
β_1	Rate of virus transfer from an infected person to a vulnerable person
β_2	Rate of infection from an infected mosquito to a person who is susceptible
β_3	Rate of infection from an infected person to a mosquito that is vulnerable

As a result, it is important to demonstrate that the state variables are not always negative. We demonstrate the solution's boundness and positivity.

The total human population $N_h(t)$ is defined by $N_h(t) = x_1(t) + x_2(t) + x_3(t)$ and it verifies the following equation

$$\begin{aligned}\frac{dN_h}{dt} &= g_h(N_h) - f_h(N_h)N_h - \delta_h x_2\\ &= \Omega_h - (\mu_{1h} - b_h)N_h - \mu_{2h}N_h^2 - \delta_h x_2. \end{aligned} \tag{3}$$

Size of the vectors population $N_v(t)$ can be defined by $N_v(t) = x_4(t) + x_5(t)$ or from the differential equation

$$\begin{aligned}\frac{dN_v}{dt} &= g_v(N_v) - f_v(N_v)N_v - \delta_v x_5\\ &= \Omega_v - (\mu_{1v} - b_v)N_v - \mu_{2v}N_v^2 - \delta_v x_5. \end{aligned} \tag{4}$$

It follows from (3) and (4) that

$$\frac{dN_h}{dt} \leqslant \Omega_h - (\mu_{1h} - b_h)N_h \quad \text{and} \quad \frac{dN_v}{dt} \leqslant \Omega_v - (\mu_{1v} - b_v)N_v.$$

Moreover, we have

$$\begin{cases} \dfrac{dN_h}{dt} \leqslant 0 \quad \text{if} \quad \dfrac{\Omega_h}{\mu_{1h} - b_h} \leqslant N_h \quad \text{and} \quad \mu_{1h} \geqslant b_h, \\ \dfrac{dN_v}{dt} \leqslant 0 \quad \text{if} \quad \dfrac{\Omega_v}{\mu_{1v} - b_v} \leqslant N_v \quad \text{and} \quad \mu_{1v} \geqslant b_v. \end{cases}$$

Let $V_1 = \limsup_{t\to+\infty} N_h$, and $V_2 = \limsup_{t\to+\infty} N_v$. Then,

$$V_1 \leqslant \frac{\Omega_h}{\mu_{1h} - b_h} \quad \text{and} \quad V_2 \leqslant \frac{\Omega_v}{\mu_{1v} - b_v}.$$

Consequently, the system's feasible region (1) is

$$\Omega = \left\{ (x_1, x_2, x_3, x_4, x_5) \in \mathbb{R}_+^5,\ V_1 \leqslant \frac{\Omega_h}{\mu_{1h} - b_h} \text{ and } V_2 \leqslant \frac{\Omega_v}{\mu_{1v} - b_v} \right\}.$$

Lemma 1. *Let $(x_1, x_2, x_3, x_4, x_5)$ represent the system (1)'s solution with initial conditions (2). The closed set $\Omega = \{(x_1, x_2, x_3, x_4, x_5) \in \mathbb{R}^5_+,\ V_1 \leqslant \frac{\Omega_h}{\mu_{1h}-b_h}$ and $V_2 \leqslant \frac{\Omega_v}{\mu_{1v}-b_v}\}$ is attractive and positively invariant.*

Proof. Considering the next Lyapunov function

$$V(t) = (V_1(t), V_2(t)) = (x_1 + x_2 + x_3, x_4 + x_5),$$

its derivative is

$$\frac{dV}{dt} = \big(\Omega_h - (\mu_{1h} - b_h)V_1 - \mu_{2h}V_1^2 - \delta_h x_1, \Lambda_v - (\mu_{1v} - b_v)V_2 - \mu_{2v}V_2^2 - \delta_v x_5\big).$$

It is easy to prove that

$$\begin{cases} \dfrac{dV_1}{dt} \leqslant \Omega_h - (\mu_{1h} - b_h)V_1 \leqslant 0 \quad \text{for} \quad V_1 \geqslant \dfrac{\Omega_h}{\mu_{1h} - b_h}, \\ \dfrac{dV_2}{dt} \leqslant \Omega_v - (\mu_{1v} - b_v)V_2 \leqslant 0 \quad \text{for} \quad V_2 \geqslant \dfrac{\Omega_v}{\mu_{1v} - b_v}. \end{cases} \tag{5}$$

It follows from (5) that $\frac{dV}{dt} \leqslant 0$ that's why the set Ω is positively invariant.

Also,

$$\begin{aligned} &0 \leqslant (V_1, V_2) \\ &\leqslant \left(V_1(0)\, e^{-(\mu_{1h}-b_h)t} + \frac{\Omega_h}{\mu_{1h} - b_h}\big(1 - e^{-(\mu_{1h}-b_h)t}\big), V_2(0)\, e^{-(\mu_{1v}-b_v)t} + \frac{\Omega_v}{\mu_{1v} - b_v}\big(1 - e^{-(\mu_{1v}-b_v)t}\big) \right). \end{aligned}$$

Thus as $t \to \infty$, $0 \leqslant (V_1, V_2) \leqslant \big(\frac{\Omega_h}{\mu_{1h}-b_h}, \frac{\Omega_v}{\mu_{1v}-b_v}\big)$, we conclude that Ω is an attracting set. ∎

The model (1) is correctly stated mathematically and epidemiologically within the domain. Therefore, studying the dynamics of this fundamental model in Ω is adequate.

3. Investigations and analysis

The following lemma, which will be necessary in the sequel.

Lemma 2. *The total population N_h and N_v are in the form:*

$$\begin{aligned} N_h(t) &= N_h^0 + \frac{1}{u(0)e^{2m_{2h}N_h^0 - (b_h - m_{1h})t} + \frac{2m_{2h}}{2m_{2h}N_h^0 - (b_h - m_{1h})}}, \\ N_v(t) &= N_v^0 + \frac{1}{u(0)e^{2m_{2v}N_v^0 - (b_v - m_{1v})t} + \frac{2m_{2v}}{2m_{2v}N_v^0 - (b_v - m_{1v})}}, \end{aligned} \tag{6}$$

where

$$N_v^0 = \frac{(b_v - m_{1v}) + \sqrt{(b_v - m_{1v})^2 + 4m_{2v}D_v}}{2m_{2v}}.$$

Proof. First, the total host population size $N_h(t)$ is calculated by $N_h(t) = x_1(t) + x_2(t) + x_3(t)$ or alternatively, using the differential equation obtained from ((1)),

$$\frac{N_h}{dt} = g_h(N_h) - f_h(N_h)N_h = -m_{2h}N_h^2 + (b_h - m_{1h}N_h) + D_h. \tag{7}$$

The total number of vectors $N_v(t)$ can be found by $N_v(t) = x_4(t) + x_5(t)$ from

$$\frac{N_v}{dt} = g_v(N_v) - f_v(N_v)N_v = -m_{2v}N_v^2 + (b_v - m_{1v}N_v) + D_v.$$

The differential equation (7) is a Ricatti equation. Its solution is written as $N_h = N_h^0 + z$, where a particular solution of equation 7 and z is the solution of the Bernoulli equation as follows:

$$\frac{dz}{dt} = (-m_{2h}N_h^0 + (b_h - m_{1h}))z - 2m_{2h}z^2$$

with the change of variable $u = \frac{1}{z}$, there will be a linear differential equation.

Hence

$$u(t) = u(0)e^{(2m_{2h}N_h^0-(b_h-m_{1h})t} + \frac{2m_{2h}}{2m_{2h}N_h^0-(b_h-m_{1h})}.$$

Therefore

$$z(t) = \frac{1}{u(0)e^{(2m_{2h}N_h^0-(b_h-m_{1h})t} + \frac{2m_{2h}}{2m_{2h}N_h^0-(b_h-m_{1h})}}.$$

So, the expression of the solution is

$$N_h(t) = N_h^0 + \frac{1}{u(0)e^{(2m_{2h}N_h^0-(b_h-m_{1h})t} + \frac{2m_{2h}}{2m_{2h}N_h^0-(b_h-m_{1h})}}.$$

Similarly,

$$N_v(t) = N_v^0 + \frac{1}{u(0)e^{2m_{2v}N_v^0-(b_v-m_{1v})t} + \frac{2m_{2v}}{2m_{2v}N_v^0-(b_v-m_{1v})}},$$

where

$$N_v^0 = \frac{(b_v-m_{1v}) + \sqrt{(b_v-m_{1v})^2+4m_{2v}D_v}}{2m_{2V}}.$$

Expressions of N_h and N_v just allow ourselves to obtain the behavior of variables x_i for $i = 1, \ldots, 5$, which finalize the proof of the Lemma. ■

For given values of the coefficients (2), the solution of Eq. (1) is achieved using the BPES [9–12].

The BPES is a polynomial family with integer coefficients. These polynomials were established as part of an applied physics study. In the following, we recall some basic concepts of $4n$-orde BPES in orthogonal basis that are used throughout the article [9–12].

Theorem 1. *Applying he BPES through adjusting the expressions for solutions the system* (1)*:*

$$x_i(t)|_{i=1,\ldots,5} = \frac{1}{2N_0}\sum_{k=1}^{N_0}\lambda_{k,i} \times B_{4k}(r_k t), \tag{8}$$

where B_{4k} are the $4k$-order BPES, t is the normalized time, r_k are B_{4k} smallest positive roots, N_0 is a prefixed integer, $\lambda_{k,i}|_{(k=1,\ldots,N_0;i=1,\ldots,5)}$ are unknown pondering real coefficients.

Proof. From Eq. (1):

$$\begin{aligned}
\sum_{k=1}^{N_0}\lambda_{k,1}\times r_k\frac{dB_{4k}(r_kt)}{dt} &= \Omega_h + b_hN_h - \frac{\beta_1}{2N_0}\left(\sum_{k=1}^{N_0}\lambda_{k,1}B_{4k}(r_kt)\right)\left(\sum_{k=1}^{N_0}\lambda_{k,2}B_{4k}(r_kt)\right)\\
&\quad - \frac{\beta_2}{2N_0}\left(\sum_{k=1}^{N_0}\lambda_{k,1}B_{4k}(r_kt)\right)\left(\sum_{k=1}^{N_0}\lambda_{k,5}B_{4k}(r_kt)\right)\\
&\quad - (\mu_{1,h}+\mu_{2,h}N_h)\left(\sum_{k=1}^{N_0}\lambda_{k,1}B_{4k}(r_kt)\right),\\
\sum_{k=1}^{N_0}\lambda_{k,2}\times r_k\frac{dB_{4k}(r_kt)}{dt} &= \frac{\beta_1}{2N_0}\left(\sum_{k=1}^{N_0}\lambda_{k,1}B_{4k}(r_kt)\right)\left(\sum_{k=1}^{N_0}\lambda_{k,2}B_{4k}(r_kt)\right)\\
&\quad - \frac{\beta_2}{2N_0}\left(\sum_{k=1}^{N_0}\lambda_{k,1}B_{4k}(r_kt)\right)\left(\sum_{k=1}^{N_0}\lambda_{k,5}B_{4k}(r_kt)\right)\\
&\quad - (\gamma_h+\mu_{1,h}+\mu_{2,h}N_h)\left(\sum_{k=1}^{N_0}\lambda_{k,2}B_{4k}(r_kt)\right),\\
\sum_{k=1}^{N_0}\lambda_{k,3}\times r_k\frac{dB_{4k}(r_kt)}{dt} &= \gamma_h\left(\sum_{k=1}^{N_0}\lambda_{k,2}B_{4k}(r_kt)\right) - (\mu_{1,h}+\mu_{2,h}N_h)\left(\sum_{k=1}^{N_0}\lambda_{k,4}B_{4k}(r_kt)\right),
\end{aligned}$$

$$\sum_{k=1}^{N_0}\lambda_{k,4}\times r_k\frac{dB_{4k}(r_kt)}{dt}=\Omega_v+b_vN_v-\frac{\beta_3}{2N_0}\left(\sum_{k=1}^{N_0}\lambda_{k,4}B_{4k}(r_kt)\right)\left(\sum_{k=1}^{N_0}\lambda_{k,2}B_{4k}(r_kt)\right),$$
$$-(\mu_{1,v}+\mu_{2,v}N_v)\left(\sum_{k=1}^{N_0}\lambda_{k,4}B_{4k}(r_kt)\right)$$
$$\sum_{k=1}^{N_0}\lambda_{k,5}\times r_k\frac{dB_{4k}(r_kt)}{dt}=\frac{\beta_3}{2N_0}\left(\sum_{k=1}^{N_0}\lambda_{k,4}B_{4k}(r_kt)\right)\left(\sum_{k=1}^{N_0}\lambda_{k,2}B_{4k}(r_kt)\right)$$
$$-(\mu_{1,v}+\mu_{2,v}N_v)\left(\sum_{k=1}^{N_0}\lambda_{k,5}B_{4k}(r_kt)\right).$$

Regardless of the main equation features, the BPES confirms the linked boundary conditions expressed by biological conditions. Indeed, using the properties of the first derivatives of BPES (see [9, 10]):

$$\begin{cases}\sum\limits_{k=1}^{N}B_{4k}(x)|_{x=0}=-2N\neq 0,\\ \sum\limits_{k=1}^{N}B_{4k}(x)|_{x=r_k}=0,\end{cases}\quad\text{and}\quad\begin{cases}\sum\limits_{k=1}^{N}\left.\dfrac{dB_{4k}(x)}{dx}\right|_{x=0}=0,\\ \sum\limits_{k=1}^{N}\left.\dfrac{dB_{4k}(x)}{dx}\right|_{x=r_k}=\sum\limits_{k=1}^{N}H_k,\end{cases}\tag{9}$$

with

$$H_n=B'_{4n}(r_n)=\frac{4r_n(2-r_n^2)\times\sum_{k=1}^{N}B_{4k}^2(r_n)}{B_{4(n+1)}(r_n)}+4r_n^3.$$

So, we verify the boundary conditions.

Algorithm. By the next four steps, we find the BPES.

1. Integrating the entire expressions provided by Eq. (4) along the time domain for a certain value of N_0.
2. Establishing the next five systems (for $i=1,\ldots,5$):
$$[\Theta][\lambda]_i=[C],\tag{10}$$
with
$$[\Theta]=(\theta_{i,j})_{i,j=1,\ldots,N_0};\quad[\lambda]_i=(\lambda_{j,i})_{j=1,\ldots,N_0}\quad\text{and}\quad[C]=(c_j)_{j=1,\ldots,N_0}.$$
Utilizing the Householder [13, 14] algorithm, the system (8) is solved.
Householder algorithm consists of establishing a serial of orthogonal square arrays $[H]_\nu|_{\nu=1,\ldots,M_0}$ defined, at a stage ν, by relation (11),
$$[H]_\nu=I_\nu-2[U][U]^T=\begin{pmatrix}1&0&0&0\\0&1&\ldots&0\\0&\ldots&\ldots&0\\0&0&0&1\end{pmatrix}-2\begin{pmatrix}u_1\\u_2\\u_3\\\ldots\end{pmatrix}\begin{pmatrix}u_1&u_2&u_3&\ldots\end{pmatrix},\tag{11}$$
with
$$[\Theta]=[H]_1[H]_2[H]_3\ldots[H]_\nu[R]=[\Omega]_\nu[R],\quad[U]=\frac{[\Theta]-[\Omega]_\nu}{\|[\Theta]-[\Omega]_\nu\|},\quad\sqrt{\sum_{k=1}^{n}u_k^2}=1.$$
As per the Householder algorithm, the array $[H]_\nu$ satisfies the triangulating relation:
$$[H]_\nu=\begin{pmatrix}\sqrt{\sum_{k=1}^{n}a_{k1}^2}&a'_{12}&a'_{13}&\ldots\\0&a'_{22}&a'_{23}&\ldots\\0&a'_{32}&a'_{33}&\ldots\\0&\ldots&\ldots&\ldots\end{pmatrix}.\tag{12}$$
Utilizing the identical method to the remaining array of minor order $[A]'$
$$[A]'=\begin{pmatrix}a'_{22}&a'_{23}&\ldots\\a'_{32}&a'_{33}&\ldots\\\ldots&\ldots&\ldots\end{pmatrix}\tag{13}$$

and to next minors leads to the final equation (14)

$$[A] = [H]_1[H]_2[H]_3 \dots [H]_{M_0}[R] = [\Omega]_{M_0}[R], \tag{14}$$

with $[\Omega]_{M_0}$ orthogonal and $[R]$ upper triangle. Equation (14) can be readily solved using a backward stepping procedure, thanks to the upper triangular nature of the array $[R]$:

$$[\beta]_{sol} = [R]^{-1}[\Omega]^{-1}[B]. \tag{15}$$

To assess convergence, the Minimum Square Method (MSM) is employed. This approach involves halting iterations when the value of the functional quantity (16) becomes smaller than a predetermined threshold value ε_0,

$$\|[A] \times [\beta]_{sol} - [B]\| \leqslant \varepsilon_0. \tag{16}$$

3. Incrementing N_0.
4. Testing the convergence of the coefficients $\lambda_{k,i}^{(Sol.)}|_{k=1,\dots,N_0,i=1,\dots,5}$,

$$x_i^{(Sol.)}|_{i=1,\dots,5} = \frac{1}{2N_0}\sum_{k=1}^{N_0}\lambda_{k,i}^{(Sol.)}B_{4k}(r_k t). \qquad \blacksquare$$

4. Simulations

In this section, we will give a numerical example to illustrate the theoretical approach. Let consider the following initial conditions for our simulation $(x_1(0), x_2(0), x_3(0)) = (3000, 1000, 500)$ for humans and $(x_4(0), x_5(0)) = (5000, 3000)$. The overall boundary conditions and coefficient values are gathered in following Table 2.

Table 2. Model parameter values.

Parameter	Ω_h	Ω_v	β_1	β_2	β_3	$\mu_{1,h}$	$\mu_{1,v}$
Value	0.05	0.02	0.04	0.04	0.04	0.0001	0.001

By applying the algorithm shown in Section 3, we get the following graphs.

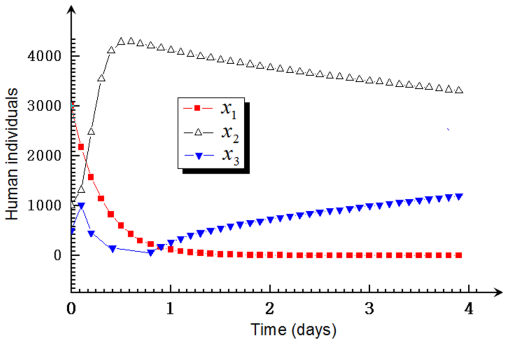

Fig. 2. Plots of the human population.

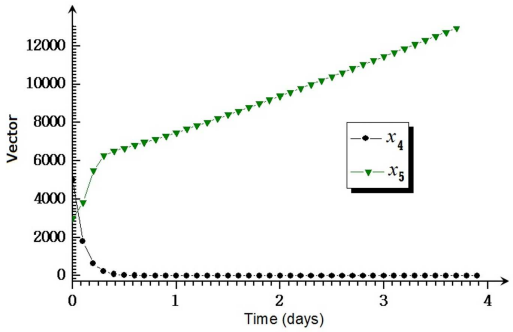

Fig. 3. Plots of the human population.

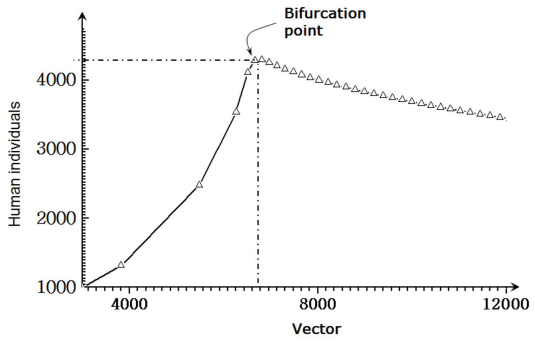

Fig. 4. Dual diagram (Human-vector).

We expanded the model to take into account the interaction of infected humans with susceptibility rates of vector and disease-related death in both infected humans and vectors by using the Boubaker approach to determine the numerical solution and by selecting the parameter appropriate. Because it is challenging to select all the factors for the quantitative estimate, we employ fictitious sets of parameters to confirm the accuracy of our analytical findings. We used the parameter values from Table 2 for the numerical simulation. In fact, we have taken into account various parameter values for the dynamic model of the numerical simulation of biologically relevant scenarios.

The numerical simulation of the human population is shown in Figure 2. The number of susceptible people falls as the number of infected people rises. When humans became infected by growing human declines, they recovered slowly. The population of susceptible and infected vectors is depicted in Figure 3. Population of infected vectors increases due to the interaction of the sensitive men. Figure 3 shows the endemic equilibrium before the bifurcation point.

5. Conclusion

This research introduces an analytical solution and conducts a stability analysis of the novel vector-borne disease model incorporating direct transmission. The utilization of this solution provides a robust framework for implementing the Boubaker Polynomials Expansion Scheme (BPES), especially in cases where exact solution expressions pose challenges. Extensive testing has confirmed the method's convergence, affirming its reliability and effectiveness in modeling vector-borne diseases with direct transmission.

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Стійкість моделі трансмісивних хвороб із прямою передачею з використанням підходу поліномів Бубакера

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У цій статті заглиблюємося в аналіз моделі епідемії трансмісивних хвороб. Наше дослідження зосереджено на використанні базової версії моделі звичайних диференціальних рівнянь (ODE) для опису динаміки передавання захворювання. Зокрема, намагаємося дослідити довгострокову поведінку та властивості розв'язків моделі за допомогою нового аналітичного підходу, відомого як схема розвинення поліномів Бубакера (BPES). Крім того, для доповнення нашого теоретичного аналізу, проведено чисельне моделювання, щоб забезпечити більш практичний погляд на епідемію.

Ключові слова: *малярія; епідемічні моделі; переносні; стійкість, поліном Бубакера.*