Punjab University Journal of Mathematics (2026), 58(02), 218-237
https://doi.org/10.52280/pujm.2026.58(02)04

Modeling the Emergent Dynamics of Conjunctivitis Transmission as a Complex System: A Simulink Based Hybrid Approach

Received
23 September, 2025

Revised
20 April, 2026

Accepted
14 July, 2026

Published Online
29 July, 2026

Shakeel Ahmed, *Saif Ullah
Department of Mathematics,
Government College University, Lahore, Pakistan

Rukhsar Khalid, Iqra Nazir
Department of Mathematics,
University of Sialkot, Sialkot, Pakistan.

Abstract. In this digital world, virtual environments are utilized to understand the dynamics of complex systems. Simulink provides modeling and simulation environment to analyze system's dynamics. In this research paper, a computational model is developed to investigate the emergent dynamics of conjunctivitis transmission. The developed model is novel, and previous literature lacks such framework to explore the transmission mechanism of conjunctivitis in Simulink environment. The model is constructed using population compartments. The disease-free equilibrium as well as local and global stabilities of the possible equilibria of the model are obtained. The threshold quantity R_0 is also computed and analyzed. A Simulink model is also developed to predict the compartments behavior. Furthermore, numerical simulation is performed in MATLAB environment with one step numerical method. The Simulink environment has advantage over traditional numerical methods due to reduced computational complexity. Conjunctivitis spread can be controlled by decreasing the rate of immigrants, enhancing immunity and minimizing contact rate of exposed individuals with infected individuals.

AMS (MOS) Subject Classification Codes: 92D30; 34D20; 37N25; 65L05
Key Words: Mathematical modeling; Conjunctivitis; Sensitivity analysis; Simulink; Stability analysis.

1. Introduction

Conjunctivitis also known as bloodshot as well as pink eyes is inflammation of the conjunctiva, the thin transparent tissues covering the sclera, or white component of the eye,

*Corresponding Author : dr.saifullah@gcu.edu.pk

and the inner surface of the eyelid [19]. Numerous things, including bacterial or viral infections, allergic reactions, and irritants like chemicals or foreign objects in the eye, might result in this syndrome. Conjunctivitis is a widespread disease, involving symptoms as the redness, swelling, and irritation of eyes. It can spread by touching the infected eyes, using the towels, glasses, mascara, contact lens, etc., of the infected person. Most of the time, conjunctivitis is not a dangerous condition and goes away on its own without medical remedies. However, a medical practitioner may prescribe antibiotics or antiviral drugs in situations involving bacteria and serious viral diseases. To stop conjunctivitis from spreading, it is critical to maintain proper hygiene, also including not sharing personal objects like towels and eye makeup, washing hands frequently, and refraining from touching or rubbing eyes. There are several treatments of conjunctivitis depending on its causes, such as drops and antibiotics are prescribed for bacterial as well as corticosteroid eye drops may help for the treatment of allergic conjunctivitis [26].

Mathematical modeling is very useful and effective tool which can help to investigate the disease transmission in living organisms [1, 3, 4, 7, 8, 13, 18, 24, 25]. Mathematical models on disease transmission can help in decision making. The concept of mathematical modeling for the transmission of an infectious disease was initially introduced by Bernoulli in 1760. He studied the effects of variolation, an early kind of vaccination, and the spread of smallpox using mathematical models [11].

The viral or bacterial infections are always harmful for human health. Diseases like Ebola virus, Coronavirus, etc., have always been a threat for human health [9, 16]. In the area of epidemiology and other branches of biology, researchers used various tools to understand the spreading behavior of diseases but mathematical modeling is the most useful tool which helps to investigate the spread of infectious diseases and diseases control strategies [5, 14, 15, 17, 23, 30].

Mathematical models have been employed to investigate the spread and containment of diseases such as influenza, measles, and tuberculosis which have provided valuable insights into the mechanisms driving disease transmission, the impact of interventions such as vaccination and quarantine, and the optimization of control strategies to mitigate disease burden [2, 12, 20]. Neil Ferguson's team has been at the forefront of COVID-19 modeling. Ronald Ross proposed a mathematical model to explain the transmission of malaria parasites between humans and mosquitoes [21].

In 1883, Koch discovered the bacilli of two different forms of infectious conjunctivitis. In 1991 Smith and his companions work remains effective in the field of pink eyes. Their study utilized a compartmental modeling approach to simulate the transmission dynamics of bacterial conjunctivitis in which the model incorporated factors such as contact patterns, duration of infection, and efficacy of antibiotic treatment [27].

In several countries, a sudden increase in conjunctivitis cases recorded, particularly in the densely populated states of the world. A viral eye disease that is very contagious and has become more common throughout the world's various regions is conjunctivitis. According to public health data, in September 2023 more than 86,133 cases were confirmed, surpassing all previous records [22].

The rest of the paper is organized as follows. Section 2 describes mathematical model for the conjunctivitis transmission. Section 3 consists of the model analysis including disease-free equilibrium, basic reproduction number R_0 and the stability of the proposed

model. Section 4 presents the numerical simulation and section 5 consists of Simulink modeling and simulation which support the analysis. Section 6 includes results and discussion while in section 7, the conclusion is presented.

2. Model Formulation

A compartmental model is constructed, based on existing models, to explore the transmission dynamics of conjunctivitis which can help in designing control strategies. The compartmental modeling approach explores the flow of the disease by dividing the complete population in nine compartments. Firstly, the involved variables are identified in the phenomena with necessary assumptions and then the disease dynamics model is presented in the form of differential equations. The flow diagram of the model is presented in Fig. 1.

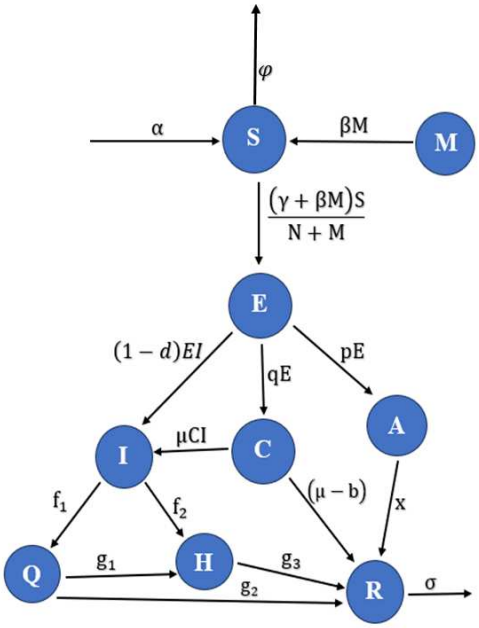


Figure 1: Flow Diagram of the Proposed Model

The model is formulated on the basis of following assumptions.

- People are allowed to migrate in and migrate out from susceptible class.
- Exposed individuals become infectious by the interaction of infected individuals.
- Nobody who has recovered will contract the virus again.
- At the rate of f_2, infected individuals are sent for treatment.
- Infected individuals are sent to isolation at the rate of f_1.
- The asymptomatically infected persons get recover at the rate x.

Table 1: Description of Variables of the Proposed Model

Variables	Description of Variables
$M(t)$	The immigrants become susceptible after coming from disease spreading areas.
$S(t)$	All susceptible individuals come into contact with infected people and become infected.
$E(t)$	Latent individuals, those who are vulnerable to infection but do not yet exhibit symptoms and are unable to spread the infection to other susceptible individuals.
$I(t)$	The group of individuals with conjunctivitis symptoms who are symptomatically infected and have the potential to spread the infection to other vulnerable individuals.
$A(t)$	The group of asymptomatically infected persons who do not have any symptoms of conjunctivitis, but they have the ability to infect susceptible people.
$C(t)$	The group of limited isolated persons not infecting any individuals but become infected after contact with infected individuals.
$Q(t)$	The group of infected people moved to the quarantine class.
$H(t)$	The group of hospitalized individuals came from infected and quarantine classes for treatment.
$R(t)$	The class of recovered persons.

Table 2: Description of Parameters of the Proposed Model

Variables	Description of Parameters
α	Natural birth rate.
φ	Rate of emigration.
β	Rate of immigration.
γ	Rate of disease transmission.
d	Proportion of symptomatic population.
p	Rate of exposed people became asymptomatic.
q	Rate of exposed people got limited quarantine.
x	Rate of asymptomatic people got recovered.
μ	Rate of limited quarantined people got infected.
f_1	Transition rate of infected people that became quarantined.
f_2	Transition rate of infected people got hospitalized.
g_1	Transfer rate of quarantined people got hospitalized.
g_2	Transfer rate of quarantined people got recovered.
g_3	Transfer rate of hospitalized people got recovered.
σ	Removal rate.
b	Rate of limited quarantined people got recovered.

The proposed model in terms of the differential equations is:

$$\begin{cases} \frac{dM}{dt} &= -\beta M, \\ \frac{dS}{dt} &= \alpha + \beta M - \frac{(\gamma+\beta M)S}{N+M} - \varphi S, \\ \frac{dE}{dt} &= \frac{(\gamma+\beta M)S}{N+M} - (1-d)EI - pE - qE, \\ \frac{dA}{dt} &= pE - xA, \\ \frac{dC}{dt} &= qE - \mu CI - (\mu - b)C, \\ \frac{dI}{dt} &= (1-d)EI + \mu CI - f_1 I - f_2 I, \\ \frac{dQ}{dt} &= f_1 I - g_1 Q - g_2 Q, \\ \frac{dH}{dt} &= f_2 I + g_1 Q - g_3 H, \\ \frac{dR}{dt} &= (\mu - b)C + xA + g_3 H + g_2 Q - \sigma R. \end{cases} \tag{2. 1}$$

Subject to the initial conditions:

$$M(0) \geq 0, S(0) \geq 0, E(0) \geq 0, A(0) \geq 0, C(0) \geq 0, I(0) \geq 0, Q(0) \geq 0,$$
$$H(0) \geq 0, R(0) \geq 0.$$

3. Model Analysis

This section presents the analysis of proposed model which includes positivity and boundedness of solutions, and equilibrium in the absence of infection in community known as disease-free equilibrium (DFE) denoted by K_0. It also includes reproduction number and stability at DFE.

3.1. **Positivity of the Model. Theorem 1:** Given that

$$M(0) \geq 0, S(0) \geq 0, E(0) \geq 0, A(0) \geq 0, C(0) \geq 0, I(0) \geq 0, Q(0) \geq 0,$$
$$H(0) \geq 0, R(0) \geq 0.$$

then the system has positive trajectories for all $t \geq 0$.
Proof: Let

$$\hat{t} = \sup\Big\{ t > 0 : M(t) > 0,\ S(t) > 0,\ E(t) > 0,\ A(t) > 0,$$
$$C(t) > 0,\ I(t) > 0,\ Q(t) > 0,\ H(t) > 0,\ R(t) > 0 \Big\} \in (0, t].$$

Solving the differential equations corresponding to the compartments $M(t)$, $S(t)$, $I(t)$, and $R(t)$, we obtain

$$M(t) = M(0) \exp\Big(- \int_0^t \beta \, ds \Big) > 0, \qquad \forall\, t > 0.$$

$$S(t) = \exp\left(-\int_0^t \left(\frac{\gamma + \beta M(s)}{N + M(s)} + \phi\right) ds\right)$$
$$\times \left[S(0) + \int_0^t \big(\alpha + \beta M(s)\big) \exp\left(\int_0^s \left(\frac{\gamma + \beta M(c)}{N + M(c)} + \phi\right) dc\right) ds\right] > 0,$$

for all $t > 0$, since $S(0) > 0$ and $\alpha > 0$.

$$I(t) = \exp\left(-\int_0^t (f_1 + f_2)\, ds\right)$$
$$\times \left[I(0) + \int_0^t \Big[(1-d)E(s)I(s) + \mu C(s)I(s)\Big] \exp\left(\int_0^s (f_1 + f_2)\, dc\right) ds\right] > 0,$$

for all $t > 0$, since $I(0) > 0$, $(1 - d) > 0$.

$$R(t) = \exp\left(-\int_0^t \sigma\, ds\right)$$
$$\times \left[R(0) + \int_0^t \Big[(\mu - b)C(s) + xA(s) + g_3 H(s) + g_2 Q(s)\Big] \exp\left(\int_0^s \sigma\, dc\right) ds\right] > 0,$$

for all $t > 0$, since $R(0) > 0$, $\mu > b$, $x, g_2, g_3 > 0$.
Similarly, for other compartments, $E(t), A(t), C(t), Q(t), H(t) \geq 0$, for all $t > 0$. Hence the system has positive trajectories for all $t > 0$.

3.2. **Invariance and Boundedness of Solutions. Theorem 2:** Let the solution of the proposed model be $(M, S, E, A, C, I, Q, H, R)$ with initial conditions:

$$M(0) \geq 0, S(0) \geq 0, E(0) \geq 0, A(0) \geq 0, C(0) \geq 0, I(0) \geq 0, Q(0) \geq 0,$$
$$H(0) \geq 0, R(0) \geq 0.$$

The set representing the region of epidemiological relevance in the sense of disease transmission is given as:

$$\Omega = \left\{(M, S, E, A, C, I, Q, H, R) \in \mathbb{R}_+^9 : \; T(t) \leq \frac{\alpha}{\sigma}\right\},$$

where $T(t) = M(t) + S(t) + E(t) + A(t) + C(t) + I(t) + Q(t) + H(t) + R(t)$ is the total population.

Proof: The sum of the model's equations gives

$$\frac{dT}{dt} = \alpha - \sigma R \quad \Rightarrow \quad \frac{dT}{dt} \leq \alpha - \sigma R, \qquad R \leq T.$$

Solving above equation gives

$$T(t) \leq \frac{\alpha}{\sigma} + \left(T(0) - \frac{\alpha}{\sigma}\right) e^{-\sigma t}.$$

Now,

$$T(t) \leq \frac{\alpha}{\sigma}, \qquad \text{if} \qquad T(0) \leq \frac{\alpha}{\sigma}, \qquad \text{for all } t > 0.$$

Hence, the total population is bounded above by the factor $\frac{\alpha}{\sigma}$. Also, the right-hand side of the system is locally Lipschitz, indicating that the solutions remain in Ω for all $t > 0$. Thus, the set Ω is positively invariant and hence the model is well posed.

3.3. **Equilibrium Points.** In this section, we determine equilibrium points of system (2.1). To find equilibrium points, consider the equations of system (2.1) equal to zero.

$$\frac{dM}{dt} = \frac{dS}{dt} = \frac{dE}{dt} = \frac{dA}{dt} = \frac{dC}{dt} = \frac{dI}{dt} = \frac{dQ}{dt} = \frac{dH}{dt} = \frac{dR}{dt} = 0. \tag{3. 2}$$

By solving the equations and considering no infection in the system, we get the disease-free equilibrium point denoted by K_0, given as:

$$K_0 = (M, S, E, A, C, I, Q, H, R) \quad \Rightarrow \quad K_0 = \left(\frac{b}{\beta}, \frac{\alpha+\beta}{\gamma}, 0, 0, 0, 0, 0, 0, 0\right).$$

3.4. **Basic Reproduction Number.** We use next generation method [10] to derive the basic reproduction number R_0. The infected compartments of the proposed model consist of E, A, I classes.

$$\mathcal{F} = \begin{pmatrix} p\left(\frac{\alpha+\beta}{\gamma}\right)(I+A) \\ 0 \\ 0 \end{pmatrix} \quad \text{and} \quad \mathcal{V} = \begin{pmatrix} (g_3+p+q)E \\ -qE + (f_1+f_2+g_3)I \\ -pE + (x+g_3)A \end{pmatrix}.$$

The Jacobians of $\mathcal{F}$ and $\mathcal{V}$ matrices are respectively given as:

$$F = \begin{pmatrix} 0 & p\left(\frac{\alpha+\beta}{\gamma}\right) & p\left(\frac{\alpha+\beta}{\gamma}\right) \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{pmatrix}, \quad V = \begin{pmatrix} g_3+p+q & 0 & 0 \\ 0 & f_1+f_2+g_3 & 0 \\ 0 & 0 & x+g_3 \end{pmatrix}.$$

The decomposition of infection process into distinct transmission pathways gives reproduction number. This decomposition is made on the interpretation of next generation matrices $\mathcal{F}$ and $\mathcal{V}$. The infection process is decomposed as R_1 and R_2, contribution from symptomatic class and asymptomatic class, respectively.

$$R_0 = R_1 \cdot R_2 \quad \Rightarrow \quad R_0 = \frac{p(\alpha+\beta)}{\gamma(g_3+p+q)}\left(\frac{q}{f_1+f_2+g_3} + \frac{p}{x+g_3}\right). \tag{3. 3}$$

3.5. **Sensitivity Analysis.** Sensitivity analysis in epidemiological models establishes the influence of parameters, allowing for the derivation of significant conclusions regarding the course of an epidemic. Researchers can better understand how each parameter affects the dynamics of the epidemic by evaluating its separate effect. It also aids in identifying the elements that have the most effects on the containment or transmission of disease. A sensitivity analysis of the biological parameters of the suggested conjunctivitis transmission model is carried out in this section. The partial derivatives of the basic reproduction number R_0 with respect to each parameter are computed for the sensitivity analysis [6]. The calculations are performed using the computing tool MATLAB. The results are presented in Table 3 and Fig. 2. Furthermore, the sensitivity index is computed by

$$S_z^{R_0} = \frac{\partial R_0}{\partial z} \cdot \frac{z}{R_0},$$

where z represents the parameters. The analysis reveals that four of the sensitivity indices are positive and five are negative, as can be seen in Table 3 and Fig. 2. The parameters p, α and β are highly sensitive. The parameters f_1 and f_2 have negative impact on R_0, revealing their limited effect on the spread of disease. It is concluded that enhanced contact and population inflow significantly increase transmission of the disease. Overall, the analysis shows that strengthening isolation strategies and reducing transmission pathways are the most effective strategies for controlling the disease.

Table 3: Sensitivity Index

Parameter	**Value**	**Sensitivity Index**
p	0.006	1.0189
α	0.5	0.71429
β	0.2	0.28571
γ	0.3	-1.000
q	0.8225	0.027171
g_3	0.04	-0.09509
f_1	0.7523	-0.84134
f_2	0.0788	-0.088127
x	0.2	-0.021495

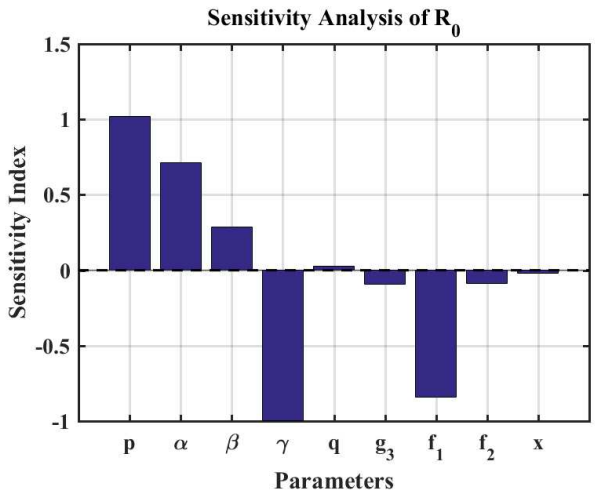


Figure 2: Sensitivity Index

3.6. **Stability Analysis.** After determining the reproduction number, local and global stabilities are discussed in this section.

Theorem 3: The disease-free equilibrium point K_0 of the system (2.1) is locally asymptotically stable if $R_0 < 1$ [28].
Proof: The local stability of K_0 for the proposed model can be determined by taking Jacobian J matrix of the form as given below.

$$J(K_0) = \begin{bmatrix} -b & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & -\gamma & 0 & -p\left(\frac{\alpha+\beta}{\gamma}\right) & -p\left(\frac{\alpha+\beta}{\gamma}\right) & 0 & 0 & 0 & 0 \\ 0 & 0 & -(g_3+p+q) & -p\left(\frac{\alpha+\beta}{\gamma}\right) & -p\left(\frac{\alpha+\beta}{\gamma}\right) & 0 & 0 & 0 & 0 \\ 0 & 0 & q & -(f_1+f_2+g_3) & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & p & 0 & -(x+g_3) & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & \mu & -(b+g_3) & 0 & 0 & 0 \\ 0 & 0 & 0 & f_1 & 0 & 0 & -(g_1+g_2+g_3) & 0 & 0 \\ 0 & 0 & 0 & f_2 & 0 & 0 & g_1 & -g_3 & 0 \\ 0 & 0 & 0 & 0 & x & (\mu-b) & g_2 & g_3 & -\sigma \end{bmatrix}.$$

The Jacobian matrix $J(K_0)$ has a block triangular form:

$$\begin{bmatrix} B_1 & * \\ 0 & B_2 \end{bmatrix}.$$

So, the union of the eigenvalues of B_1 and B_2 gives the eigenvalues of the Jacobian matrix $J(K_0)$. The eigenvalues associated to the removed and demographic compartments are negative, i.e.,

$$-b,\ -\gamma,\ -g_3,\ -(b+g_3),\ -(g_1+g_2+g_3),\ -g_3.$$

Hence, the stability of K_0 is determined by the infected subsystem (E, I, A). The characteristic polynomial of B_2 is

$$\lambda^3 + \lambda^2 w_1 + \lambda w_2 + w_3 = 0, \tag{3. 4}$$

where

$$w_1 = (g_3+p+q) + (f_1+f_2+g_3) + (x+g_3), \qquad w_2 > 0,$$

and

$$w_3 = (g_3+p+q)(f_1+f_2+g_3)(x+g_3)(1-R_0).$$

By the Routh–Hurwitz criterion, all eigenvalues have negative real parts, if and only if

$$w_1 > 0, \qquad w_2 > 0, \qquad w_3 > 0, \qquad w_1 w_2 > w_3.$$

Since $w_1 > 0$ and $w_2 > 0$, it follows that $w_3 > 0$, and hence $R_0 < 1$. Therefore, if $R_0 < 1$, the disease-free equilibrium point is locally asymptotically stable; otherwise, it is unstable whenever $R_0 > 1$.
Theorem 4: The disease-free equilibrium point K_0 is globally asymptotically stable when $R_0 < 1$.
Proof: We construct the following Lyapunov function $V(t)$ to prove stability of the disease-free equilibrium point

$$V(t) = \left(S - S^* - S^* \ln \frac{S}{S^*}\right) + E + I + A,$$

which is non-negative and vanishes at the disease-free equilibrium (DFE). Differentiating $V(t)$ along the solutions of the system yields

$$\frac{dV}{dt} = \left(1 - \frac{S^*}{S}\right)\dot{S} + \dot{E} + \dot{I} + \dot{A}. \tag{3. 5}$$

Substituting the model equations and

$$S^* = \frac{\alpha + \beta}{\gamma},$$

we obtain

$$\frac{dV}{dt} \leq pS^*(I + A) - g_3E - (f_1 + f_2 + g_3)I - (x + g_3)A.$$

Using the definition of R_0, we have

$$pS^*(I + A) \leq R_0 \left[g_3E + (f_1 + f_2 + g_3)I + (x + g_3)A\right].$$

Hence,

$$\frac{dV}{dt} \leq (R_0 - 1) \left[g_3E + (f_1 + f_2 + g_3)I + (x + g_3)A\right]. \tag{3. 6}$$

Equation (3.6) shows that $R_0 < 1$ implies

$$\frac{dV}{dt} \leq 0,$$

with equality if and only if

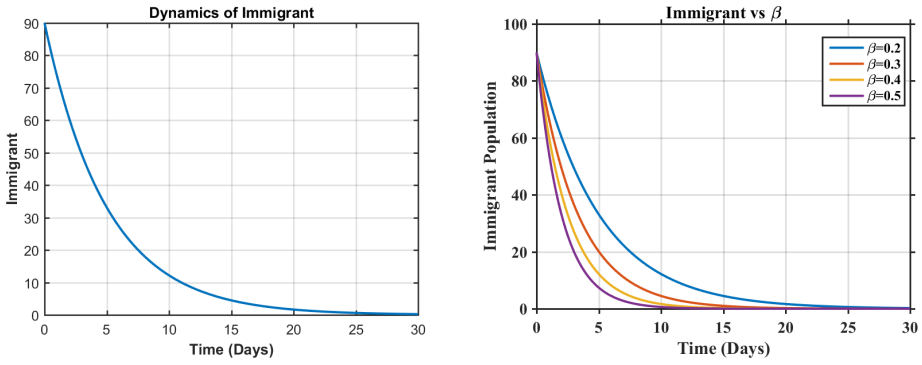
$$E = I = A = 0.$$

Therefore, by LaSalle's Invariance Principle, the disease-free equilibrium is globally asymptotically stable whenever

$$R_0 < 1.$$

4. SIMULATION

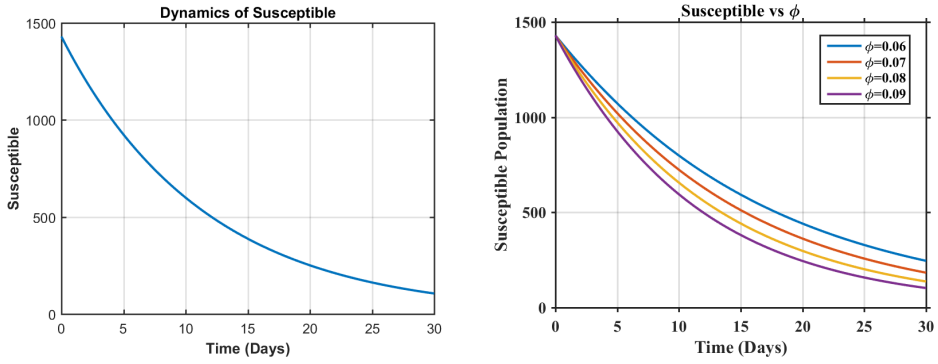
The simulation of the proposed model is performed in MATLAB environment with one step numerical method [29]. The parameter values are taken as $\alpha = 0.5$, $\beta = 0.2$, $\gamma = 0.3$, $d = 0.6$, $p = 0.006$, $q = 0.8225$, $x = 0.2$, $\mu = 0.1$, $f_1 = 0.7523$, $f_2 = 0.0788$, $g_1 = 0.09$, $g_2 = 0.06$, $g_3 = 0.04$, $\sigma = 0.07$, $b = 0.08$, and $\phi = 0.09$. During first thirty days of outbreak in the society, sixteen hundred people were considered as total population in which 90 people were assumed to be immigrants $M(t)$, 1430 were considered susceptible $S(t)$, 25 were taken as exposed $E(t)$, 20 were taken as infected $I(t)$, 15 were assumed to be in limited quarantine $C(t)$, 10 were assumed as asymptomatically infected $A(t)$,10 were declared quarantine $Q(t)$, while hospitalized $H(t)$ and recovered $R(t)$ were chosen 0.



(a) (b)

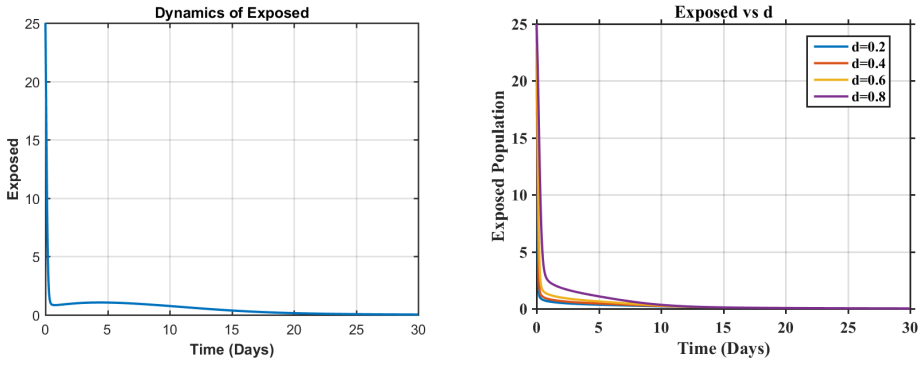
Figure 3: (a) Behavior of $M(t)$ (b) For $M(t)$ taking β = 0.2 to 0.5

Fig. 3(a) shows that the group of immigrants $M(t)$ gradually decreases and Fig. 3(b) shows that $M(t)$ is also decreasing with increasing values of β. Fig. 4(a) shows that population of susceptible $S(t)$ is decreasing after passage of sometime and the infection increases. Fig. 4(b) shows that with the increasing rate of migrants out of the region, $S(t)$ is also decreasing.



(a) (b)

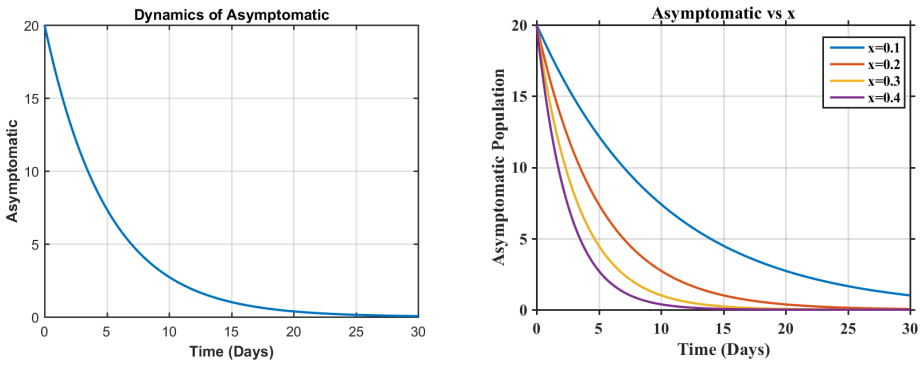
Figure 4: (a) Behavior of $S(t)$ (b) For $S(t)$ taking φ = 0.06 to 0.09



(a) (b)

Figure 5: (a) Behavior of $E(t)$ (b) For $E(t)$ taking d = 0.2 to 0.8

Fig. 5(a) shows that population of exposed $E(t)$ individuals is decreasing by which infected group $I(t)$ is increasing as visible in Fig. 8(a). The decreasing values of d cause decline in $E(t)$ as shown in Fig. 5(b). The asymptomatically infected group $A(t)$ is decreasing as shown in Fig. 6(a) and also $A(t)$ is decreasing with increasing x mentioned in Fig. 6(b).

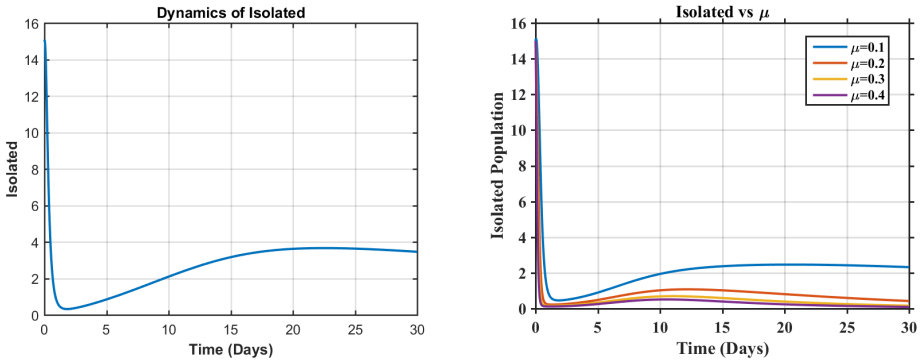


(a) (b)

Figure 6: (a) Behavior of $A(t)$ (b) For $A(t)$ taking x = 0.1 to 0.4

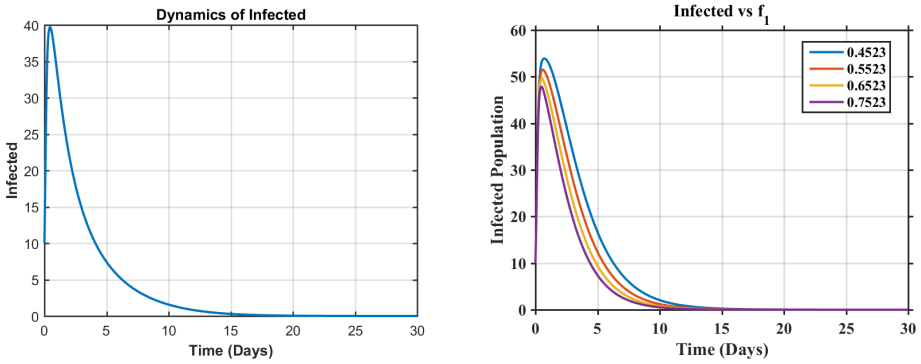
Fig. 7(a) shows that by implementation of initial SOP's the population of limited quarantine $C(t)$ is decreasing rapidly as well as $C(t)$ shows same behavior by increasing the values of μ in Fig. 7(b). Also Fig. 8(a) shows rise in infections to a limit and then decline

which is biologically feasible and ensures the correct estimation of outbreak through the proposed model. Fig. 8(b) shows the impact of parameter f_1 on I(t) which is decreasing with increasing f_1.



(a) (b)

Figure 7: (a) Behavior of $C(t)$ (b) For $C(t)$ taking $\mu = 0.1$ to 0.4

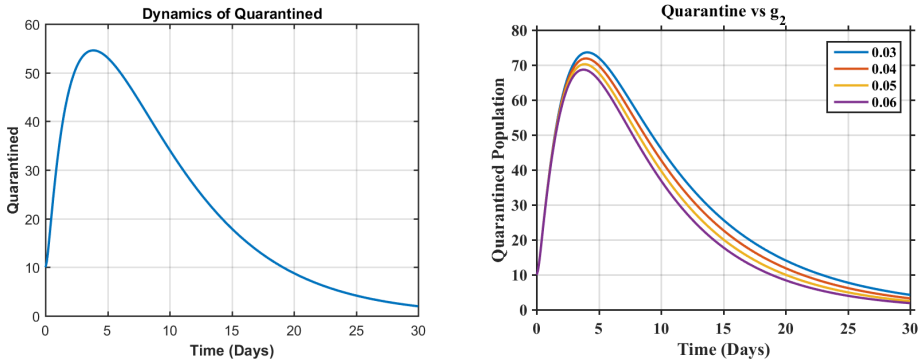


(a) (b)

Figure 8: (a) Behavior of $I(t)$ (b) For $I(t)$ taking $f_1 = 0.4523$ to 0.7523

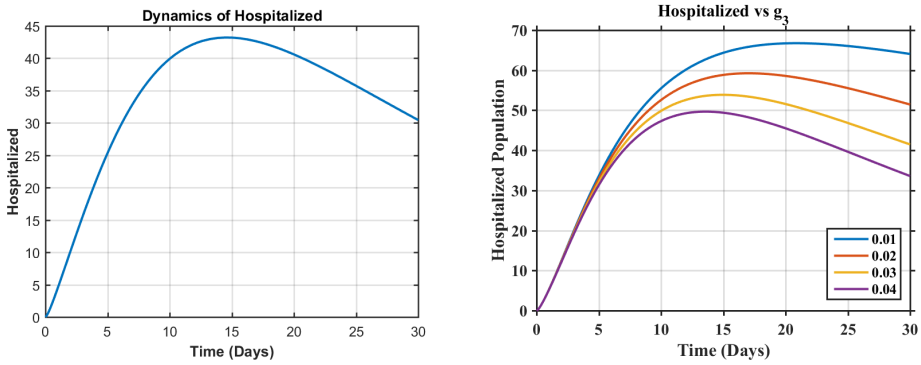
Fig. 9(a) shows the rapid increase in the population of quarantine $Q(t)$ and then gradual decline as a result of increase in the recovered population. Shown in Fig. 9(b) that $Q(t)$ is gradually decreasing with increasing values of g_2. Fig. 10(a) shows that population of $H(t)$ is increasing with passage of time and decreasing with increasing values of g_3 as shown in

Fig. 10(b). Figs. 11(a) and 11(b) show the behavior of recovered class and the impact of parameter σ. The gradual increase in recovered class is consistent with the epidemiological structure of the model.



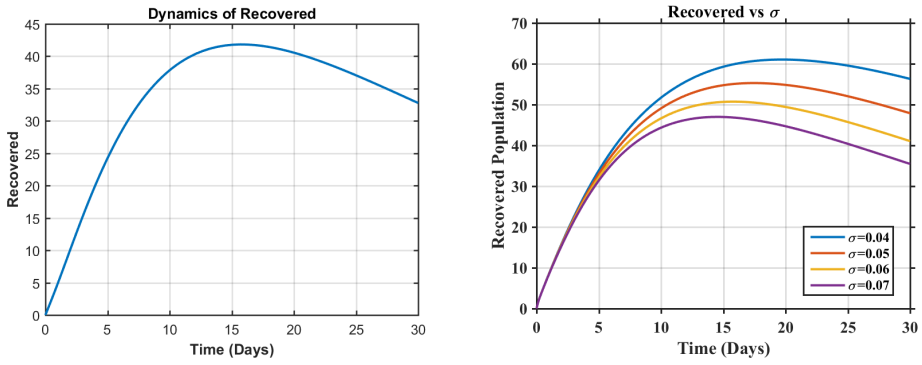
(a) (b)

Figure 9: (a) Behavior of $Q(t)$ (b) For $Q(t)$ taking g_2 = 0.03 to 0.06



(a) (b)

Figure 10: (a) Behavior of $H(t)$ (b) For $H(t)$ taking g_3 = 0.01 to 0.04



(a) (b)

Figure 11: (a) Behavior of $R(t)$ (b) For $R(t)$ taking σ = 0.04 to 0.07

5. Simulation with Simulink

The blocks diagram of the proposed model with Simulink is presented in Fig. 12.

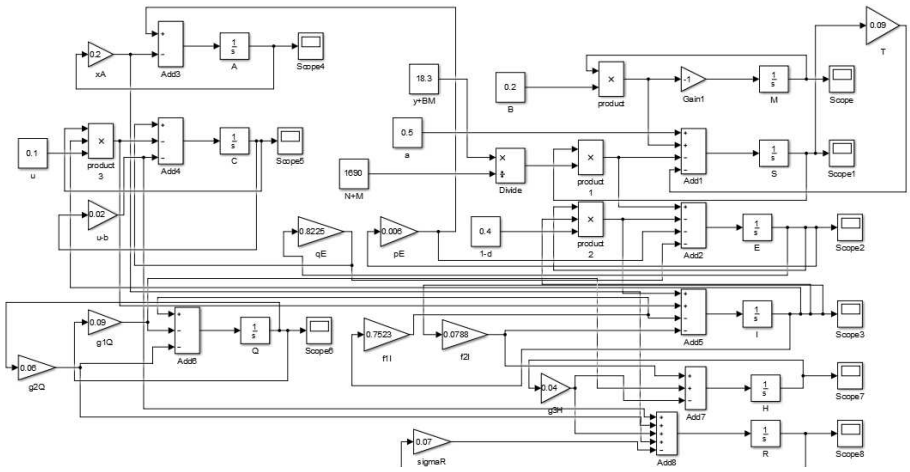


Figure 12: Block Diagram of the Proposed Model with Simulink

Simulink is a graphical programming environment for MATLAB that is used to model, simulate and analyze multidomain dynamic systems. The Simulink plots for compartments of individuals are shown in Figs. 13 to 17. These Simulink plots facilitate in understanding the impact of various parameters as used in simulation, visualizing the dynamics of disease

transmission, and evaluating the efficacy of possible therapies. Simulink plots of $M(t)$, $S(t)$, $E(t)$, $A(t)$ and $C(t)$, as shown in Figs. 13 to 15 respectively, are decreasing with the passage of time. While the Simulink plots of $I(t)$ and $Q(t)$, as shown in Fig. 16 are increasing rapidly and after sometime they are gradually decreasing. The Simulink plots of $H(t)$ and $R(t)$, as shown in Fig. 17 are increasing with time.

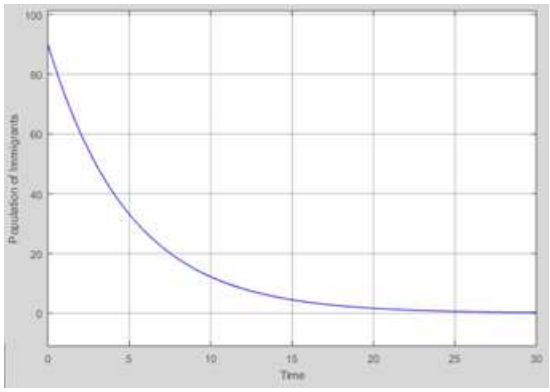
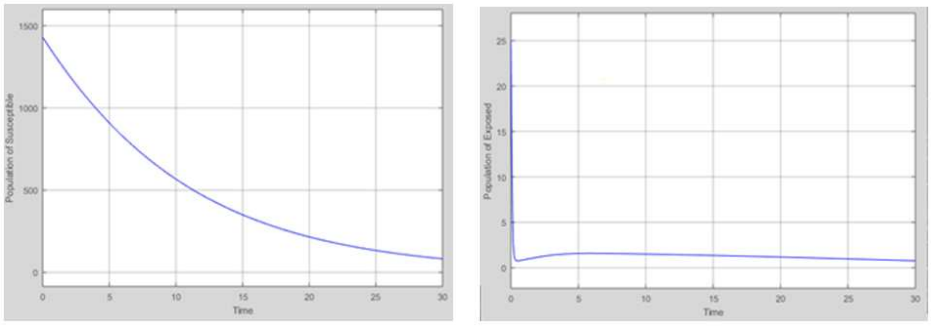


Figure 13: Simulink Plot of $M(t)$

6. Results and Discussion

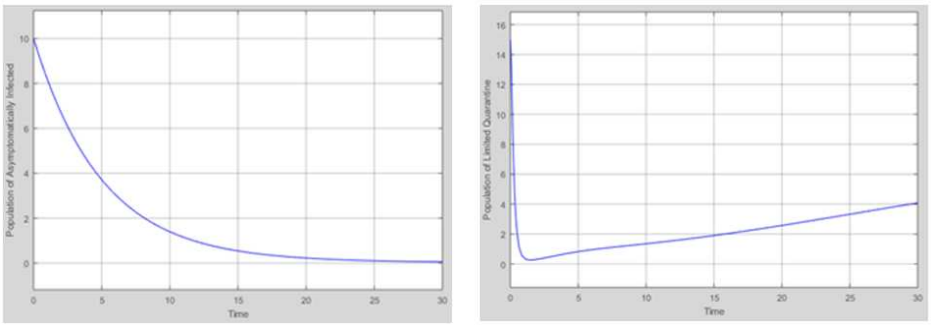
In this paper, we constructed and examined a mathematical model to investigate the transmission dynamics of conjunctivitis. To find the basic reproduction number R_0, we used the next generation matrix approach to first obtain disease-free equilibrium (DFE) points. Then, examined the local stability of DFE points. The global stability of disease-free equilibrium points of the model is computed using the Lyapunov function theory. The positivity and boundedness of the solutions ensured the well posedness of the model. The basic reproduction number is a key factor in assessing the model's stability. If $R_0 < 1$, the disease-free equilibrium point is locally as well as globally asymptomatically stable and if $R_0 > 1$, it is unstable. If R_0 is less than unity the disease will die out and if it is greater than unity, the disease will spread in the population.

The sensitivity analysis indicates that the infection rate and the recruitment rates are highly sensitive parameters in the disease prevalence. The hospitalization and recovery rates play part in controlling the disease, i.e., the minor improvements in recovery rate even decrease the disease transmission. Similarly, the asymptotic recovery rate also indicates the role of effective treatment. These findings highlight the role of reducing transmission pathways, better treatment through improved medical care, i.e., early treatment, quarantine facilities and advanced medical care.



(a) (b)

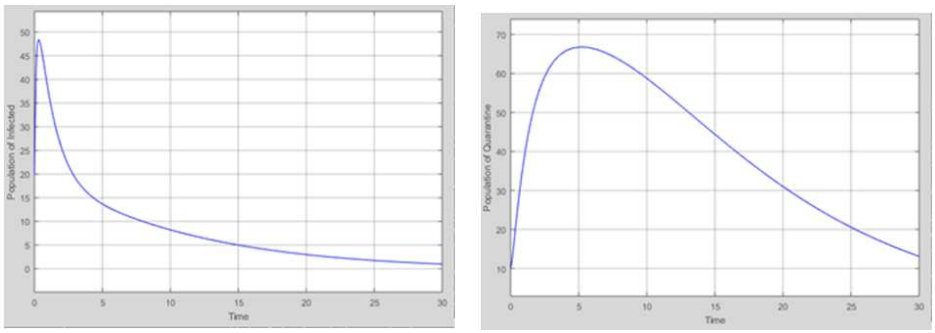
Figure 14: Simulink Plot of (a) $S(t)$ (b) $E(t)$



(a) (b)

Figure 15: Simulink Plot of (a) $A(t)$ (b) $C(t)$

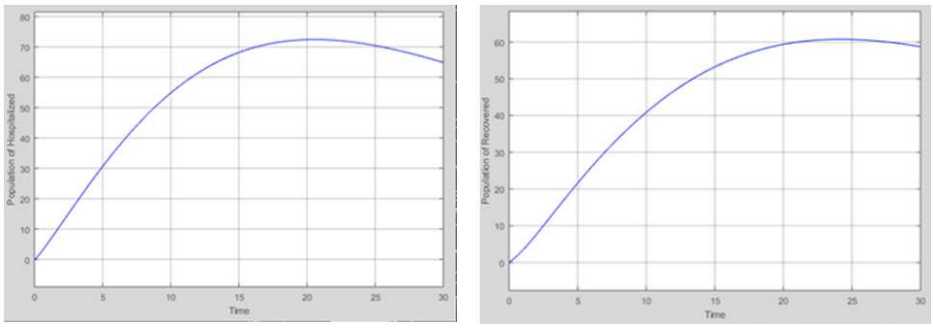
The simulation of the proposed model visualized varying behavior of the system and highlighted the role of both approaches in predicting the system dynamics. The Runge Kutta (RK) method in MATLAB is used for model simulation. Our capacity to comprehend, forecast and optimize the behavior of complex system is improved by useful tool known as Simulink. The Simulink approximations agree well with our numerical approximation and hence give us a deeper understanding of the spreading behavior of the conjunctivitis. The simulation via Simulink has advantage as it does not require manual calculations. Simulation with traditional numerical approaches requires manual calculations and coding. While, Simulink, on the other hand, provides an efficient environment to simulate systems in a small duration of time.



(a) (b)

Figure 16: Simulink Plot of (a) $I(t)$ (b) $Q(t)$

The modeling and simulation of the conjunctivitis transmission throw light on the importance of minimizing transmission pathways and faster treatment interventions which can reduce basic reproduction number and hence the disease transmission can be controlled. This study also highlights the superiority of utilizing Simulink for infectious disease modeling and decision making in epidemic control strategies.



(a) (b)

Figure 17: Simulink Plot of (a) $H(t)$ (b) $R(t)$

7. Conclusion

The major contribution of this work is the computational analysis of the disease transmission in Simulink environment. It has many advantages including fast simulation, efficiency to handle complex systems, accurate solutions and many more. Our approach is novel, effective and easy to understand for scientific community. We conclude, on the basis

of our analysis, that the spread behavior of conjunctivitis can be controlled or minimize by handling transmission pathways, decreasing the rate of immigrants, by decreasing the contact rate of exposed population with infected individuals, by the implementation of very initial SOP's such as to maintain proper hygiene also including not sharing personal objects like towels and eye makeup.

As a future work, it is recommended to extend this modeling and simulation approach to other complex biological systems, i.e., fractional order or stochastic biological systems. The science community can benefit from this approach by utilizing Simulink virtual environment to explore the varying behavior of complex biological systems.

CREDIT AUTHORSHIP CONTRIBUTION'S STATEMENT

Shakeel Ahmed: Conceptualization, Methodology, Investigation, Writing - original draft.
Saif Ullah: Conceptualization, Supervision, Formal analysis, Project administration, Writing - review and editing.
Rukhsar Khalid: Investigation, Mathematical analysis, Writing - review and editing.
Iqra Nazir: Software, Writing - review and editing.

DECLARATIONS

Conflicts of interest: The authors declare no conflict of interest.
Funding: No funding available for this study.
Data availability: Not applicable. No data was generated for this study.

ACKNOWLEDGMENTS

The authors would like to thank the reviewers and editor for their valuable comments and suggestions, which helped to improve the quality of this manuscript.

REFERENCES

[1] H. Abboubakar, P. Kumar, N. A. Rangaig and S. Kumar. *A malaria model with Caputo–Fabrizio and Atangana–Baleanu derivatives*. International Journal of Modeling, Simulation, and Scientific Computing, **12** No. 2, (2021) Article 2150013.

[2] F. B. Agusto. *Optimal chemoprophylaxis and treatment control strategies of a tuberculosis transmission model*. World Journal of Modelling and Simulation, **5** No. 3, (2009) 163–173.

[3] S. Ahmed, S. Ullah and F. T. Rasool. *Modeling the dynamics of Monkeypox epidemic via classical and fractional derivatives*. Discover Public Health, **22** No. 1, (2025) Article 426.

[4] S. Ahmed, S. Ullah, M. Riaz, W. Ahmed and M. Sheikh. *Numerical analysis of fractional logistic growth models using computational methods with MATLAB codes*. International Journal of Applied and Computational Mathematics, **11** No. 5, (2025) Article 198.

[5] U. Ayesha, S. Javeed, M. S. Khan, D. Baleanu, M. Ali and M. Baryam. *A novel deep learning technique for solving dynamical model of infertile women with Polycystic Ovarian Syndrome using the combination of radial basis and log-sigmoid functions*. Punjab Univ. J. Math., **56** No. 11, (2024) 753–769.

[6] E. Borgonovo and E. Plischke. *Sensitivity analysis: A review of recent advances*. European Journal of Operational Research, **248** No. 3, (2016) 869–887.

[7] M. Choisy, J. F. Guégan and P. Rohani. *Mathematical modeling of infectious diseases dynamics*. Encyclopedia of Infectious Diseases: Modern Methodologies, (2007) Article 379.

[8] A. Costa, M. Pires, R. Resque and S. S. M. S. Almeida. *Mathematical modeling of the infectious diseases: Key concepts and applications*. Journal of Infectious Diseases and Epidemiology, **7** No. 5, (2021) Article 209.

[9] K. Dhama, S. Khan, R. Tiwari, S. Sircar, S. Bhat, Y. S. Malik, K. P. Singh, W. Chaicumpa, D. K. Bonilla-Aldana and A. J. Rodriguez-Morales. *Coronavirus disease 2019–COVID-19*, Clinical Microbiology Reviews, **33** No. 4, (2020) Article e00128–20.

[10] O. Diekmann, J. A. P. Heesterbeek and M. G. Roberts. *The construction of next-generation matrices for compartmental epidemic models*. Journal of the Royal Society Interface, **7** No. 47, (2010) 873–885.

[11] S. R. Duncan and C. J. Duncan. *Modelling the dynamics of Smallpox outbreaks in London, 1647 to 1893*. IFAC Proceedings Volumes, **30** No. 2, (1997) 351–355.

[12] W. T. A. Enanoria, F. Liu, J. Zipprich, K. Harriman, S. Ackley, S. Blumberg, L. Worden and T. C. Porco. *The effect of contact investigations and public health interventions in the control and prevention of measles transmission: A simulation study*. PLoS One, **11** No. 12, (2016) Article e0167160.

[13] V. S. Erturk and P. Kumar. *Solution of a COVID-19 model via new generalized Caputo-type fractional derivatives*. Chaos, Solitons & Fractals, **139**, (2020) Article 110280.

[14] M. Farman, E. Hincal, S. Jamil, N. Gokbulut, K. S. Nisar and A. Sambas. *Sensitivity analysis and dynamics of brucellosis infection disease in cattle with control incident rate by using fractional derivative*. Scientific Reports, **15** No. 1, (2025) Article 355.

[15] M. Farman, K. S. Nisar, A. Sambas, M. Bayram and M. Hafez. *Stability and chaos analysis of neurological disorder of complex network with fractional order comparative study*. Scientific Reports, **15** No. 1, (2025) Article 26202.

[16] S. T. Jacob, I. Crozier, W. A. Fischer, A. Hewlett, C. S. Kraft, M. A. D. L. Vega, M. J. Soka, V. Wahl, A. Griffiths, L. Bollinger and J. H. Kuhn. *Ebola virus disease*. Nature Reviews Disease Primers, **6** No. 1, (2020) Article 13.

[17] A. Khan, G. Ali, A. Khaliq, G. Zaman. *Mathematical modeling and dynamical aspects of the co-infection of Buruli Ulcer and Cholera*. Punjab Univ. J. Math., **56** No. 8, (2024) 414–445.

[18] M. A. Khan, S. Ullah, D. C. L. Ching, I. Khan, Saif Ullah, S. Islam, T. Gul. *A mathematical study of an epidemic disease model spread by rumors*. J. Comput. Theor. Nanosci., **13** No. 5, (2016) 2856–2866.

[19] H. M. Leibowitz. *The red eye*. New England Journal of Medicine, **343** No. 5, (2000) 345–351.

[20] L. Mao. *Evaluating the combined effectiveness of influenza control strategies and human preventive behavior*. PLoS One, **6** No. 10, (2011) Article e24706.

[21] S. Mandal, R. R. Sarkar and S. Sinha. *Mathematical models of malaria: A review*. Malaria Journal, **10** No. 1, (2011) Article 202.

[22] S. Nawaz, M. Zeeshan, H. Ayaz, A. Iqbal, F. Ali and A. Ali. *The outbreak of highly contagious conjunctivitis (pink eye) in major cities of Pakistan*. The Open Infectious Diseases Journal, **16** No. 1, (2024) Article e18742793285298.

[23] K. S. Nisar, A. Ahmad, M. Farman, E. Hincal and A. Zehra. *Modeling and mathematical analysis of fractional order eye infection (conjunctivitis) virus model with treatment impact: Prevalence and dynamical transmission*. Alexandria Engineering Journal, **107**, (2024) 33–46.

[24] O. M. Ogunmiloro. *Stability analysis and optimal control strategies of direct and indirect transmission dynamics of conjunctivitis*. Mathematical Methods in the Applied Sciences, **43** No. 18, (2020) 10619–10636.

[25] O. M. Ogunmiloro. *Modeling the dynamics of the consequences of demographic disparities in the transmission of Lassa fever disease in Nigeria*. Modeling Earth Systems and Environment, **9** No. 1, (2023) 865–880.

[26] V. Papa, P. Aragona, A. C. Scuderi, A. R. Blanco, P. Zola, A. Di Bella, M. Santocono and G. Milazzo. *Treatment of acute bacterial conjunctivitis with topical netilmicin*. Cornea, **21** No. 1, (2002) 43–47.

[27] J. Tolles and T. Luong. *Modeling epidemics with compartmental models*. Journal of American Medical Association, **323** No. 24, (2020): 2515–2516.

[28] P. Van den Driessche and J. Watmough. *Reproduction numbers and sub-threshold endemic equilibria for compartmental models of disease transmission*. Mathematical Biosciences, **180** No. 1–2, (2002) 29–48.

[29] I. K. Youssef and M. H. M. Hassan. *A comparative study for some mathematical models of epidemic diseases with application to strategic management*. Applied Sciences, **12** No. 24, (2022) Artical 12639.

[30] S. Zeb, M. Bilal, M. Rafiq, S. A. Mohd Yatim, A. Ahmad, M. Irfan, and M. S. Ehsan. *Mathematical modeling for transmission dynamics of hepatitis B virus*. Punjab Univ .J. Math., **57** No. 9, (2025) 964–991.