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The impact of COVID-19 on a Malaria dominated region: A mathematical analysis and simulations

Mayowa M. Ojo\textsuperscript{a,b,*}, Emile Franc Doungmo Goufo\textsuperscript{b}

\textsuperscript{a} Thermo Fisher Scientific, Microbiology Division, Lenexa, KS, USA
\textsuperscript{b} Department of Mathematical Sciences, University of South Africa, Florida, South Africa

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Abstract One of society’s major concerns that have continued for a long time is infectious diseases. It has been demonstrated that certain disease infections, in particular multiple disease infections, make it more challenging to identify and treat infected individuals, thus deteriorating human health. As a result, a COVID-19-malaria co-infection model is developed and analyzed to study the effects of threshold quantities and co-infection transmission rate on the two diseases’ synergistic relationship. This allowed us to better understand the co-dynamics of the two diseases in the population. The existence and stability of the disease-free equilibrium of each single infection were first investigated by using their respective reproduction number. The COVID-19 and malaria-free equilibrium are locally asymptotically stable when the individual threshold quantities $R_C$ and $R_M$ are below unity. Additionally, the occurrence of the malaria prevalent equilibrium is examined, and the requirements for the backward bifurcation’s existence are provided. Sensitivity analysis reveals that the two main parameters that influence the spread of COVID-19 infection are the disease transmission rate ($b_c$) and the fraction of the exposed individuals becoming symptomatic ($\psi$), while malaria transmission is influenced by the abundance of vector population, which is driven by recruitment rate ($\pi_v$) with an increase in the effective biting rate ($b$), probability of malaria transmission per mosquito bite ($b_m$), and probability of malaria transmission from infected humans to vectors ($b_v$). The findings from the numerical simulation of the model show that COVID-19 will predominate in the populace and drives malaria to extinction when $R_M < 1 < R_C$, whereas malaria will dominate in the population and drives COVID-19 into extinction when $R_C < 1 < R_M$. At the disease’s endemic equilibrium, the two diseases will coexist with the one with the highest reproduction number predominating but not eradicating the other. It was demonstrated in particular that COVID-19 will invade a population where malaria is endemic if the invasion reproduction number exceeds unity. The findings also demonstrate that when the two diseases are at endemic equilibrium,
Malaria is an infectious vector-borne disease caused by parasites of the genus *Plasmodium*. It is a severe, potentially fatal illness that is spread by the bite of an infected adult female Anopheles mosquito which is a serious threat to global health [1]. When a female Anopheles mosquito successfully bites a person, the parasite multiplies in the person’s liver and bloodstream and eventually transforms into an infectious form. After the disease’s incubation period, which lasts between 9 and 14 days, people start to exhibit symptoms [2]. Malaria is characterized by several symptoms, including an increase in body temperature, headache, nausea, and vomiting. Although there isn’t an effective malaria vaccine yet, the disease is still preventable and treatable. The preventive strategies used in reducing malaria spread include the use of insect repellents, mosquito bed-nets, and other mosquito prevention techniques like indoor insecticide spraying and draining stagnant water where mosquitoes breed [3,2]. For decades, malaria has continued to be a significant public health concern, with an estimated two hundred and forty-one million cases reported globally and six hundred and twenty-seven thousand deaths in the year 2020 [4]. In 2008, one hundred and nine countries declared this disease to be endemic, with Sub-Saharan Africa bearing the brunt of the disease’s severe burden [5,2]. The World Health Assembly approved the worldwide procedural strategy for malaria eradication by 2030 in the year 2015 [6]. The sudden emergence of COVID-19 disease is making it more challenging to eradicate malaria, even though numerous organizations, medical professionals, and policymakers are working tirelessly to do so. This is because malaria control mainly depends on the widespread campaign against the disease and the mass distribution of seasonal chemo prevention (SMC), long-lasting insecticide-treated nets (LLINs), and indoor residual spraying (IRS) across communities and households. As an illustration, the lockdown that followed the first outbreak of COVID-19 in 2019 has an impact on the distribution of preventive items from house to house. The prevalence of malaria in the communities has also been influenced by the COVID-19 pandemic’s other unintended consequences, like poverty, malnourishment, and social unrest [7,8]. Due to this, it is therefore questionable whether the World Health Organization (WHO) strategy, which is closely aligned with the Roll Back Malaria Partnership’s Action and Investment to defeat Malaria 2016–2030 (RBM-AIM), will be successful in eliminating malaria in thirty-five nations by 2030 [9,7].

Another infectious disease that is having an impact on the quality of life worldwide is COVID-19, which is caused by Severe Respiratory Syndrome Coronavirus 2 (SARS-Cov-2). The first outbreak was noted near the end of 2019 in Wuhan, China, where it was first discovered. Since then, it has been classified as pandemic disease, affecting over 562 million people with more than six million people worldwide at the time of writing this manuscript (mid-July) [10]. By inhaling infectious respiratory droplets, this highly contagious disease can spread from one person to another. Incubation times for viruses range from 1 to 14 days before a human becomes infected and begins to exhibit symptoms. The signs and symptoms include coughing, fatigue, fever or chills, body aches, taste loss, headaches, and pharyngitis. These conditions can cause mild to severe illness as well as death [11]. To date, several intervention strategies have been put into practice to lessen the impact of COVID-19 all over the world. The government and policy makers first promoted a global lockdown, which was followed by the wearing of facial masks and vaccinations for susceptible people [12]. Despite all control measures that have been implemented, COVID-19 still poses a threat to the humanities due to a number of issues, including insufficient vaccine supplies in some areas, vaccine hesitance, disregard for public health directives, and virus mutation [13]. The potential for COVID-19 to co-infect with other illnesses, such as malaria, presents another challenge for healthcare professionals, as research has shown that multiple infections of a disease have a higher likelihood of deteriorating human health than a single infection [14,15]. Because of the similarity in disease symptoms that makes diagnosis and treatment challenging, co-infection of COVID-19 with vector-borne diseases like malaria is a threat to the public’s health. Multiple confirmed cases of the co-infection of COVID-19 and malaria have been reported in various regions. We direct readers to [16–20] and the references therein for a review of case reports of the co-infection of these diseases. In areas where malaria is an endemic problem, the burden of two disease co-infection is more prevalent, and as a result disease mitigation is more challenging.

Infectious disease modeling has aided in decision-making by offering a framework for comprehending the dynamics of newly emerging and reemerging diseases, especially at the beginning of an epidemic [21]. For many decades, mathematical models have been formulated and examined to study how various epidemic diseases are controlled and spread. For example, see [22–34] and the references therein. To better understand the dynamics of co-infection diseases, some studies have been developed (see [21,35,36,4,37]). However, more work is still needed to understand the co-infection of the recently discovered pandemic disease COVID-19 with other diseases. Understanding the co-dynamics of COVID-19 and malaria in the human populace is particularly understood. To understand more about the interactions between diseases caused by co-infection, we formulated and examined a COVID-19 and malaria co-infection model to study the effects of threshold quantities and co-infection transmission rate on the two diseases’ synergistic relationship. According to our knowledge, this is the first work to study the effects of co-infection on the synergistic relationship between COVID-19 and malaria in the population, as well as the impact of co-endemicity on the dynamics of each disease. This research provides a basis for understanding the conditions that enable the
two diseases to coexist, as well as how to eradicate each disease. It should be noted that while in this work we use classical calculus to develop the proposed model, recent studies have used fractional calculus for real-world problems. See [38–46] and the references therein for some instances.

The remaining manuscript is arranged as follows. The proposed co-infection model is formulated in Section 2. We present the theoretical analysis of each sub-model and the co-infection model in Section 3. The simulation studies and discussion is presented in Section 4. This includes the sensitivity analysis, impact of threshold quantities, and transmission rate of co-infection on disease burden. The concluding remark, limitation of the study, and recommendation for a future study are provided in Section 5.

2. Model Formulation

Numerous research has been performed to better understand the characteristics of the novel SARS-CoV-2. Particularly, many researchers have developed several mathematical models to study the dynamical spread and control of the disease since it first appeared in Wuhan, China [21]. Unfortunately, the altered course of this ongoing pandemic disease continues to pose challenges to the healthcare system and the human population. Even though much has been known because of different research about the disease and its control, there are still several challenges faced by the healthcare system in mitigating the threat it poses to humanity. Among many other challenges are the possibilities of the virus’s mutation, which has led to more complexity in controlling the emergence of disease cases. An example is the newly identified omicron variant, although characterized by mild symptoms but is highly infectious among both vaccinated and unvaccinated individuals [47,48]. Another challenge confronting the healthcare system in mitigating the risk of COVID-19 is the presence of other infectious diseases with similar symptoms of infection, which adds to the difficulty in diagnosing infected people. Examples of these diseases are malaria and influenza [17,19,49]. Following the findings of some study results on a case report of COVID-19 and malaria, co-infection [17,19,20,50], we present in this work seventeen compartmental co-infection deterministic mathematical model to study the co-dynamics of the two disease in a given population. Since the transmission of malaria occurs between two hosts, we group the interacting host population into human and vector populations. The entire human populace at a given time \( t \), represented by \( N(t) \), is grouped into susceptible humans \( S(t) \), vaccinated humans against COVID-19 \( V_c(t) \), exposed humans to COVID-19, malaria, and both disease \( E_c(t), E_m(t) \), respectively, COVID-19 asymptomatic infectious, symptomatic infectious, and hospitalized infectious humans \( A_c(t), I_c(t), H_c(t) \), respectively), malaria infectious human \( I_m(t) \), co-infected infectious humans \( I_{cm}(t) \), people infected with malaria and exposed to COVID-19 \( I_{em}(t) \), people infected with COVID-19 and exposed to malaria \( I_{mc}(t) \), recovered people from COVID-19, malaria, and both disease \( R_c(t), R_m(t), R_{cm}(t) \) respectively). To condense the notations, the time \( t \) in the model variables will be removed, then the entire human population is given as

\[
N = S + V_c + E_c + A_c + I_c + H_c + R_c + E_m + I_m + R_m + E_{cm} + I_{cm} + I_{mc} + I_{em} + R_{cm}.
\]

In the same way, the entire vector population at time \( t \), represented by \( N_v(t) \), are grouped into the population of susceptible \( S_v(t) \), and infected vectors \( I_v(t) \), such that the entire vector population is obtained as

\[
N_v = S_v + I_v.
\]

We note that individuals in the exposed compartment are newly infected with the respective disease but are unable to transmit the disease (i.e., people who are not yet infectious), whereas asymptomatic infectious, symptomatic infectious, and hospitalized infectious individuals are infectious people who can transmit the disease. The subsequent system of equations provides the co-infection model used in studying the co-dynamics of COVID-19 and malaria.

\[
\begin{align*}
\frac{dS}{dt} & = \pi + \kappa_c R_c + \kappa_m R_m + \kappa_{cm} R_{cm} + (\omega V_c - (\nu + \mu + \lambda_e + \lambda_m + \lambda_{cm}) S), \\
\frac{dV}{dt} & = \kappa S - (1 - \rho)(\lambda_e + \lambda_m) V_c - (\sigma + \mu) V_c, \\
\frac{dE_c}{dt} & = (\lambda_e + \lambda_{cm}) S + (1 - \sigma) (\lambda_e + \lambda_m) V_c - (\sigma c + \mu + \lambda_e) E_c, \\
\frac{dE_m}{dt} & = \sigma (1 - \psi) E_c - (\mu + \theta + \delta_e + \phi_h) E_m, \\
\frac{dI_c}{dt} & = \mu E_c - (\gamma_e + \lambda_e) I_c - (\theta + \mu + \delta_i + \phi h) I_c, \\
\frac{dI_m}{dt} & = \gamma_e I_c - (\gamma_m + \mu + \delta_m) I_m, \\
\frac{dA_c}{dt} & = \lambda_m S - (\sigma m + \mu + \lambda e) A_c, \\
\frac{dA_m}{dt} & = \sigma_m A_c - (\gamma_m + \mu + \delta_m + \phi h) A_m, \\
\frac{dI_{cm}}{dt} & = \gamma_m A_c - (\gamma_{cm} + \mu) I_{cm}, \\
\frac{dI_{mc}}{dt} & = \gamma_{cm} I_m - (\gamma_m + \mu) I_{mc}, \\
\frac{dR_c}{dt} & = \mu E_c - (\mu + \sigma) R_c, \\
\frac{dR_m}{dt} & = \mu I_c - (\mu + \sigma + \gamma_c) R_m, \\
\frac{dR_{cm}}{dt} & = \mu I_{cm} - (\mu + \sigma + \gamma_{cm}) R_{cm}, \\
\frac{dS_v}{dt} & = \lambda_{e} S, \\
\frac{dI_v}{dt} & = \lambda_{e} S + \lambda_{m} S + \lambda_{cm} S - \lambda_{e} S, \\
\frac{dR_v}{dt} & = \lambda_{e} S + \lambda_{m} S + \lambda_{cm} S - \lambda_{e} S.
\end{align*}
\]

with the initial conditions

\[
S(0) > 0, V(0) > 0, E(0) > 0, A(0) > 0, I_c(0) > 0, H(0) > 0, R(0) > 0, E_m(0) > 0, L_c(0) > 0, S_v(0) > 0, \lambda(0) > 0, L(0) > 0.
\]

The definitions of the model parameters are provided in Table 1, and the flow diagram is depicted in Fig. 1. In model (3), the respective forces of infection \( \lambda_e, \lambda_m, \lambda_{cm} \), and \( \lambda_{cm} \) are defined below as

\[
\begin{align*}
\lambda_e & = \beta_e (\eta_A A_c + \eta_H H_c + I_c), \\
\lambda_m & = \beta_m I_m, \\
\lambda_{cm} & = \beta_{cm} (I_{cm} + I_{mc}), \\
\lambda_{cm} & = \beta_{cm} (I_{cm} + I_{mc}).
\end{align*}
\]

According to (3), \( \lambda_e \) represents the rate at which susceptible humans become infected with the COVID-19 virus following an effective contact with an individual in the \( A_c, I_c, \) and \( H_c \) classes. The presumed increase in the relative infectiousness of the symptomatic infectious individuals over the asymptomatic and hospitalized infectious individuals is rationalized by the infection modification parameters \( \eta_A \) and \( \eta_H \). Additionally, after having direct contact with a malaria-infectious person \( I_m, I_{mc} \), or an infectious co-infected person \( I_{cm} \), a susceptible individual will become infected with malaria or co-infection of the two diseases at the rates of \( \lambda_m \) and \( \lambda_{cm} \).
respectively. The parameter $\beta_c, \beta_m$, and $\beta_{um}$, represents the effective contact rates that result in the transmission of each disease and their co-infection respectively. Additionally, the parameter $b$ is the vectors’ biting rate, and $\beta_c$ is the likelihood that a mosquito will contract malaria after sucking blood from a person who has the disease. The vaccination rate against COVID-19 is given as $\omega$.

The following list includes the key presumptions that were used to develop the co-infection model (3).

1. According to [19,7], the etiology underlying co-infection of the two diseases is still unclear. It is unknown whether the SARS-CoV-2 infection decreased immunity, causing a flare-up of malaria, or malaria infection increased susceptibility to COVID-19. Thus, we assume that individuals infected with malaria are susceptible to infection with COVID-19 and vice versa.

2. The co-infected individuals can only transmit COVID-19 to a susceptible human and malaria to a susceptible vector because malaria can only be transferred between two different hosts (from vector to human through a bite of a female mosquito).

3. According to the methodology in [53], we assume that the modified parameter $0 \leq \phi \leq 1$ governs the assumed altered susceptibility to COVID-19 in individuals who are already infected with malaria, while $0 \leq \phi_m \leq 1$ represents the presumed altered of susceptibility to malaria individuals who are already infected with COVID-19.

4. We assume that the people who recovered from COVID-19 only develop a transient immunity, in contrast to the assumption of [54]. This indicates that these people revert to the susceptible class at a rate of $\kappa_c$. As a result, $\kappa_{cm}$ is given as the immunity waning rate of recovered individuals with co-infection. The findings of numerous studies, including those by [55,56,52], support the possibility of reinfection.

### Table 1: The parameter’s value and description.

| Parameter | Description | Value | Source |
|-----------|-------------|-------|--------|
| $\pi$     | Recruitment rate of susceptible people | $1.2 \times 10^4$ | [57] |
| $\pi_v$   | Recruitment rate of vectors | $\frac{\mu v}{\mu + v}$ | [21] |
| $\eta_A$  | Asymptomatic infection modification rate | 0.45 | [58] |
| $\eta_H$  | Hospitalized infection modification rate | 0.4509 | [58] |
| $\gamma$  | Vaccination rate against COVID-19 | 0.0203 | [51] |
| $\beta_c$ | Transmission rate of COVID-19 | 0.5249 | [57] |
| $\beta_m$ | Probability of malaria transmission per mosquito bite | $0.125 - 0.5$ | [21,2] |
| $\beta_{um}$ | Transmission rate of co-infection | $\max(\beta_c, \beta_m)$ | Assumed |
| $b$       | Number of effective mosquito bite per day | $4.3 \times 0.33$ | [21,60] |
| $\kappa_c$ | Immunity waning rate of recovered people with COVID-19 | 0.011 | [61] |
| $\kappa_{cm}$ | Immunity waning rate of recovered people with malaria | 0.0005275 | [2,62] |
| $\omega$  | Vaccine waning rate of COVID-19 | 0.000297 | [57] |
| $\zeta$   | COVID-19 vaccine efficacy | 0.70 | [57] |
| $\sigma_c$ | COVID-19 progression rate from exposure to either $A_c$ or $I_c$ | 0.40 | [57] |
| $\sigma_m$ | Malaria progression rate from exposed to infectious | 0.8333 | [21,59] |
| $\sigma_{um}$ | Co-infection progression rate from the exposed to infectious | 0.333 | [21] |
| $\sigma_1$ | Malaria infection rate for COVID-19 infected people | 0.0833 | [21] |
| $\sigma_2$ | COVID-19 infection rate for malaria infected people | 0.40 | [21] |
| $\psi$    | Fraction of COVID-19 exposed people becoming symptomatic | 0.60 | [54] |
| $\mu$     | Humans’ natural mortality rate | 0.0003516 | [57] |
| $\mu_v$   | Vectors’ natural mortality rate | 0.0476 | [21] |
| $\delta_c$ | COVID-19-related mortality rate | 0.008 | [63] |
| $\delta_m$ | Malaria-related mortality rate | 0.0003454 | [2,64] |
| $\delta_{cm}$ | Co-infection-related mortality rate | $\max(\delta_c, \delta_m)$ | Assumed |
| $\tau_c$  | Hospitalization rate of symptomatic COVID-19 infected people | 0.0624 | [65] |
| $\theta_c$ | Recovery rate of asymptomatic COVID-19 people | 0.13978 | [65] |
| $\gamma_c$ | Recovery rate of hospitalized COVID-19 people | 0.125 | [57] |
| $\gamma_m$ | Recovery rate of infectious malaria people | 0.0092 | [64,2] |
| $\gamma_{cm}$ | Recovery rate of infectious co-infected people | 0.025 | [21] |
| $\gamma_1$ | Recovery rate of COVID-19 infectious people | 0.30 | [21,66] |
| $\phi_c$  | Modification of susceptibility to COVID-19 following malaria infection | $0 \leq \phi_c \leq 1$ | [21,67] |
| $\phi_m$  | Modification of susceptibility to malaria following COVID-19 infection | $0 \leq \phi_m \leq 1$ | [21,67] |

3. Model Analysis

To understand more about the dynamics of COVID-19 and malaria transmission in a given population, we conducted a qualitative analysis of each disease in this section. These involve proving the positivity and boundedness of the model and showing the existence and stability of the disease-free steady-state solutions. In addition, we will obtain the threshold quantities to investigate the disease burden in the population.
We first analyze each sub-models in SubSection 3.1 and 3.2, and then present a generalized result of the co-infection model in sub-Section 3.4.

3.1. COVID-19-only model

To obtain the COVID-19 only sub-model, we set \( E_m = I_m = R_m = E_{cm} = I_{cm} = I_{mec} = I_{cem} = S_v = S_e = 0 \).

\[
\begin{align*}
\frac{dS}{dt} &= \pi + \kappa_c R_c + \alpha V_c - (\nu + \lambda_c) S, \\
\frac{dv}{dt} &= \nu S - (1 - \psi) \lambda_c V_c - (\omega + \mu) V_c, \\
\frac{dEc}{dt} &= \lambda_c S + (1 - \psi) \lambda_c V_c - (\sigma_c + \mu) E_c, \\
\frac{dAc}{dt} &= \sigma_c (1 - \psi) E_c - (\mu + \delta_c + \theta_c) A_c, \\
\frac{dIc}{dt} &= \frac{\nu S}{\kappa_m} - (\mu + \delta_c + \gamma_c) I_c, \\
\frac{dHc}{dt} &= \frac{\nu S}{\kappa_m} - (\mu + \delta_c + \gamma_c) H_c, \\
\frac{dRc}{dt} &= \frac{\nu S}{\kappa_m} - (\mu + \delta_c + \gamma_c) R_c.
\end{align*}
\]

We then demonstrate that the state variables of the COVID-19 only sub-model (6) are positive throughout \( t > 0 \) and that the feasible region \( \Omega_c \) is bounded for the model to be epidemiologically meaningful. Thus, the following result can be drawn.

3.1.1. Positivity and boundedness of solutions

Here we demonstrate that the state variables of the COVID-19 only sub-model (6) are positive throughout \( t > 0 \) and that the feasible region \( \Omega_c \) is bounded for the model to be epidemiologically meaningful. Thus, the following result can be drawn.
Theorem 1. The COVID-19 only model satisfy the initial data $S(0) > 0, V_i(0) > 0, E_i(0) > 0, A_i(0) > 0, I_i(0) > 0, H_i(0) > 0$ and $R_i(0) > 0$, so that the model’s solutions with initial positive data remain positive throughout.

Proof. We let $t_f = \sup \{t > 0 : S(t) > 0, V_i(t) > 0, E_i(t) > 0, A_i(t) > 0, I_i(t) > 0, H_i(t) > 0, R_i(t) > 0 \in [0, t_f] \}$, so that $t_f > 0$.

The first compartment of the sub-model (6) is written as
\[
\frac{dS}{dt} = \pi + \kappa_e R_e + \alpha V_e - (\nu + \mu + \lambda_e)S \\
\geq \pi - \lambda S - (\nu + \mu)S.
\]
By using the integrating factor method, Eq. (7) is written as
\[
\frac{d}{dt} \left( S(t) \exp \left[ (\mu + \nu)t + \int_{0}^{t} \lambda_e(\zeta)d\zeta \right] \right) \\
\geq \pi \exp \left[ (\mu + \nu)t + \int_{0}^{t} \lambda_e(\zeta)d\zeta \right].
\]
So that,
\[
S(t_f) \exp \left[ (\mu + \nu)t_f + \int_{0}^{t_f} \lambda_e(\zeta)d\zeta \right] - S(0) \\
\geq \int_{0}^{t_f} \pi \left\{ \exp \left[ (\mu + \nu)y + \int_{0}^{y} \lambda_e(\zeta)d\zeta \right] \right\} dy.
\]
Thus,
\[
S(t_f) \geq S(0) \exp \left[ -(\mu + \nu)t_f - \int_{0}^{t_f} \lambda_e(\zeta)d\zeta \right] \\
+ \exp \left[ -(\mu + \nu)t_f - \int_{0}^{t_f} \lambda_e(\zeta)d\zeta \right] \\
\times \int_{0}^{t_f} \pi \left\{ \exp \left[ (\mu + \nu)y + \int_{0}^{y} \lambda_e(\zeta)d\zeta \right] \right\} dy > 0.
\]
It is clear from the inequality above that $S(t_f) \geq 0$ is positive.

Similarly, we can show that $V_i(t_f) > 0, E_i(t_f) > 0, A_i(t_f) > 0, I_i(t_f) > 0, H_i(t_f) > 0$, and $R_i(t_f) > 0$ are positive for all time $t > 0$. As a result, all solutions of the COVID-19-only model (6) remain positive for all positive initial conditions.

Now, the COVID-19 only model (6) is considered in a biologically feasible region $\Omega_C \subset R^n_+$, so that
\[
\Omega_C = \left\{ (S, V_i, E_i, A_i, I_i, H_i, R_i) \in R^n_+: S + V_i + E_i + A_i + I_i + H_i + R_i \leq \frac{n}{\pi} \right\}.
\]
The feasible region $\Omega_C$ is positively invariant and attracts all of the solutions to the model (6). This suggests that all solutions with a starting point of $\Omega_C$ are eternally present there. Thus, the COVID-19 sub-model is said to be well-posed both mathematically and epidemiologically.

3.1.2. Existence and stability of the COVID-19 free-equilibrium (CFE)

The COVID-19-free equilibrium steady state (CFE) can be derived by equating the infection variables and the right-hand side of all the equations in (6) to zero. Consequently, the CFE denoted by $\mathcal{E}_{CF}$ is calculated as
\[
\mathcal{E}_{CF} = \left\{ (S^*, V_i^*, E_i^*, A_i^*, I_i^*, H_i^*, R_i^*) \right\}
\]
\[
= \left( \frac{\pi (\mu + \omega)}{\mu (\mu + \omega + \nu)} \frac{\pi \nu}{\mu (\mu + \omega + \nu)} 0, 0, 0, 0, 0 \right) \).
\]
Using the next-generation matrix operator as described in [62,68], the threshold quantity known as the reproduction number is obtained to investigate the system’s stability. To achieve this, the new infection and remaining transfer terms Jacobian matrix are respectively given as
\[
F = \begin{bmatrix}
0 & -1 & 0 & 0 & 0 & 0 \\
0 & 0 & -1 & 0 & 0 & 0 \\
0 & 0 & 0 & -1 & 0 & 0 \\
\end{bmatrix},
\]
\[
V = \begin{bmatrix}
k_a & 0 & 0 & 0 \\
-k_a & k_b & 0 & 0 \\
-\psi_s & 0 & k_t & 0 \\
0 & 0 & -\tau_e & k_b \\
\end{bmatrix}.
\]
Consequently, the reproduction number of the COVID-19 sub-model (6), which is determined by the highest eigenvalue of $FV^{-1}$ given by $R_C = \mu (FV^{-1})$ is obtained as
\[
R_C = \frac{\beta \sigma_i (\mu + \omega + k_v y) (\eta c E c + k_h) + \eta k_v k_h k_s \beta}{k_a k_b k_c k_h (\mu + \omega + \nu)}.
\]

The threshold quantity $R_C$ provided in (9) is referred to as the control reproduction number, also known as the effective reproduction number. It estimates the typical amount of new infections that one infected person can generate throughout infectiousness in an entirely susceptible community where control interventions are implemented [69]. As a result, in the presence of vaccination against COVID-19, the threshold quantity $R_C$ in (9) calculates the number of new COVID-19 cases that a single COVID-infected person can replicate in a wholly susceptible community. Now, in the absence of control interventions (i.e., $\nu = \omega = 0$), the threshold quantity known as the basic reproduction number ($R_0$) is obtained as
\[
R_0 = \frac{\beta \sigma_i (\mu + \omega + k_v y) (\eta c E c + k_h) + \eta k_v k_h k_s \beta}{k_a k_b k_c k_h (\mu + \omega + \nu)}.
\]
The $R_0$ calculates the typical size of new cases generated by one infected person in a wholly susceptible community in the absence of disease control interventions (see, for example, [70–73]). By applying Theorem 2 of [74], the effective reproduction number $R_C$ (herein referred to as reproduction number) is used to demonstrate the local stability of the COVID-19-free equilibrium $\mathcal{E}_{CF}$. The Theorem below shows the result.

Theorem 2. The COVID-19-free equilibrium $\mathcal{E}_{CF}$, of the model (6) is locally asymptotically stable (LAS) in the biological region $\Omega_C$ if $R_C < 1$ and unstable otherwise.

Proof. We compute the Jacobian matrix of system (6) at $\mathcal{E}_{CF}$ to prove the aforementioned theorem. Thus, we defined the Jacobian matrix $J(\mathcal{E}_{CF})$ as
Thus, the first eigenvalue of the matrix (11) is obtained as

\[
\lambda_1 = \mu + v + k_2 = 1 - \varepsilon, \quad \lambda_2 = \mu + \omega, \quad \lambda_3 = 1 - \psi, \quad \lambda_4 = \mu + 2\delta + \tau_1, \quad \lambda_5 = \mu + \delta + 2\tau_2, \quad \lambda_6 = \mu + \delta + \tau_3, \quad \lambda_7 = \mu + \delta + 2\tau_4, \quad \lambda_8 = \mu + \delta + \tau_5.
\]

The stability of the COVID-19-free equilibrium is established by showing that the Jacobian matrix \( J(\mathcal{E}_0) \) is negative definite. Thus, the Jacobian matrix (11) is obtained as \(-k_9\) and the reduced sub-matrix \( D_1 \) given below yields the remaining eigenvalues

\[
D_1 = \begin{bmatrix}
-k_4 & 0 & \frac{\beta_m S}{\gamma_m} & 0 & \frac{\beta_m S}{\gamma_m} & 0 & \frac{\beta_m S}{\gamma_m} & 0 \\
0 & -k_2 & \frac{\beta_m S}{\gamma_m} & 0 & \frac{\beta_m S}{\gamma_m} & 0 & \frac{\beta_m S}{\gamma_m} & 0 \\
0 & 0 & -k_4 & \frac{\beta_m S}{\gamma_m} & 0 & \frac{\beta_m S}{\gamma_m} & 0 & \frac{\beta_m S}{\gamma_m} \\
0 & 0 & 0 & -k_4 & \frac{\beta_m S}{\gamma_m} & 0 & \frac{\beta_m S}{\gamma_m} & 0 \\
0 & 0 & 0 & 0 & -k_4 & \frac{\beta_m S}{\gamma_m} & 0 & \frac{\beta_m S}{\gamma_m} \\
0 & 0 & 0 & 0 & 0 & -k_4 & \frac{\beta_m S}{\gamma_m} & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & -k_4 & \frac{\beta_m S}{\gamma_m} \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & -k_4
\end{bmatrix}
\]

In accordance with the Routh-Hurwitz criterion, the submatrix \( D_1 \) would have a real and negative eigenvalues if \( \text{Tr}(D_1) < 0 \) and \( \text{Det}(D_1) > 0 \). By using the sub-matrix (12), we obtain the following

\[
\text{Tr} \ (D_1) = -(k_1 + k_3 + k_4 + k_7 + k_8) < 0 \quad \text{and} \quad \text{Det} \ (D_1) > 0.
\]

The aforementioned findings show that the sub-matrix (11) eigenvalues would be negative if \( R_C < 1 \) and \( k_1, k_3 \geq \text{vola} \). Thus, \( \mathcal{E}_{C0} \) is LAS if \( R_C < 1 \) and unstable otherwise.

**Theorem 2** implies that when \( R_C < 1 \), and the initial sizes of the system’s (6) sub-population are in the \( \mathcal{E}_{C0} \) region of attraction, COVID-19 can be completely eradicated from the populace. This means that when \( R_C < 1 \) a small influx of COVID-19-infected people into the communities cannot cause a large outbreak of the disease, which enables the infection to be eradicated more quickly.

### 3.2. Malaria-only model

To obtain the malaria-only model, we set \( V_r = E_r = A_r = I_r = X_r = R_v = E_v = I_v = R_v = R_m = 0 \) into the co-infection model (3). Thus, the malaria-only model with the human and vector host population is given below as

\[
\frac{dS}{dt} = \pi + \kappa_m R_m - (\mu + \lambda_m) S, \quad \frac{dE}{dt} = \lambda_m S - (\sigma_m + \mu) E_m, \quad \frac{dI}{dt} = \gamma_m E_m - (\gamma_m + \mu + \delta_m) I_m, \quad \frac{dR}{dt} = \delta_m I_m - (\kappa_m + \mu) R_m, \quad \frac{dS_v}{dt} = \pi_v - (\kappa_m + \mu) S_v, \quad \frac{dI_v}{dt} = \lambda_v S_v - \mu I_v,
\]

with the initial conditions \( S(0) > 0, E_v(0) = 0, I_v(0) = 0, R_v(0) = 0, S_v(0) > 0, I_v(0) = 0 \). The forces of infection are given as \( \lambda_m = \frac{b E_m S}{N} \) and \( \lambda_v = \frac{b E_v S_v}{N} \). The total human and vector populations are given as \( N = S + E_m + I_m + R_m \) and \( N_v = S_v + I_v \).

#### 3.2.1. Positivity and boundedness of solutions

By following the approach in sub-Section 3.1.1, the state variables of the malaria-only model (13) can be shown to be non-negative for all time \( t > 0 \). Furthermore, the region \( \Omega_M \) for the malaria-only model, defined as

\[
\Omega_M = \left\{ (S, E_m, I_m, R_m, S_v, I_v) \in \mathbb{R}^6_+ : N(t) \leq \frac{\pi}{\mu}, \frac{\pi_v}{\mu_v} \leq \frac{\pi}{\mu} \right\},
\]

is positively invariant and attracts all the model (13) solutions. Thus, all solutions with a starting point in \( \Omega_M \) remain there for the entire time \( t \geq 0 \). Hence, the dynamics of the malaria-only model can be considered in the region \( \Omega_M \).

#### 3.2.2. Existence and stability of the malaria-free-equilibrium (MFE)

The malaria-free-equilibrium steady state (MFE) is obtained by setting the infection variables \( (E_m, I_m, L) \) and the right-hand side of all the equations in (13) to zero. Thus, the MFE denoted by \( \mathcal{E}_{M0} \) is obtained as

\[
\mathcal{E}_{M0} = (S^*, E_m^*, I_m^*, R_m^*, S_v^*, I_v^*) = \left( \frac{\pi}{\mu}, 0, 0, 0, \frac{\pi_v}{\mu_v}, 0 \right).
\]

By using the same method in sub-Section 3.1.2, the malaria basic reproduction number is obtained through the new infection’s \((F)\) and remaining transfer terms \((V)\) Jacobian matrix given below

\[
F = \begin{bmatrix}
0 & 0 & b \beta_m \\
0 & 0 & 0 \\
0 & 0 & 0
\end{bmatrix}
\quad \text{and} \quad
V = \begin{bmatrix}
\sigma_m + \mu & 0 & 0 \\
-\sigma_m & \gamma_m + \mu + \delta_m & 0 \\
0 & 0 & \mu_v
\end{bmatrix}.
\]

By using the above Jacobian matrices, the basic reproduction number of the malaria-only model is obtained below by computing the highest eigenvalue of \( FV^- \) given by \( R_M = \rho(FV^-) \). Thus, the basic reproduction number is obtained as

\[
R_M = \sqrt{R_m R_v},
\]

where,

\[
R_m = \frac{b \beta_m \sigma_m}{(\sigma_m + \mu)(\gamma_m + \mu + \delta_m)S^*},
\]

and

\[
R_v = \frac{b \beta_v S_v}{\mu_v}.
\]

We note that the threshold quantity \( R_m \) is the average number of infected mosquitoes that one infectious person can replicate during their entire infectious period. Also, \( \frac{1}{(\gamma_m + \mu + \delta_m)} \) is the average duration of the infectiousness. The threshold quantity \( R_v \) is the average number of infected humans that an infectious mosquito can produce during its whole period of infectiousness. By following the same approach in sub-Section 3.1.2, the following result can be established.
**Theorem 3.** The malaria-free equilibrium \( E_{M0} \), of the model (13) is LAS in the region \( \Omega_M \) if \( R_M < 1 \) and unstable otherwise.

**Proof.** We obtain the Jacobian matrix of system (13) at \( E_{M0} \) to prove the aforementioned theorem. Hence, we defined the Jacobian matrix \( J(E_{M0}) \) as

\[
J(E_{M0}) = 
\begin{bmatrix}
-\mu & 0 & 0 & \kappa_m & 0 & 0 \\
0 & -p_1 & 0 & 0 & b\beta_m & \\
0 & \sigma_m - p_2 & 0 & 0 & 0 & 0 \\
0 & 0 & \gamma_m - p_3 & 0 & 0 & 0 \\
0 & 0 & \gamma_m & b\beta_m - S & 0 & -\mu_r & 0 \\
0 & 0 & \beta_m S & 0 & 0 & 0 & -\mu_i \\
\end{bmatrix},
\]

where \( p_1 = \sigma_m + \mu, p_2 = \gamma_m + \mu + \delta_m, \) and \( p_3 = \kappa_m + \mu, \) while \( S^r \) and \( S^r_w \) are given in (14). The stability of the malaria-free equilibrium is established by showing that the Jacobian matrix \( J(E_{M0}) \) eigenvalues are all negative. The first eigenvalue of the matrix (18) is obtained as \(-\mu\) and the reduced sub-matrix \( D_2 \) given below yields the remaining eigenvalues

\[
D_2 = 
\begin{bmatrix}
-p_1 & 0 & 0 & b\beta_m \\
\sigma_m - p_2 & 0 & 0 & 0 \\
0 & \gamma_m - p_3 & 0 & 0 \\
0 & \gamma_m & b\beta_m - S & 0 \\
0 & \beta_m S & 0 & 0 \\
0 & 0 & 0 & 0 \\
\end{bmatrix}.
\]

In accordance with the Routh-Hurwitz criterion, the sub-matrix \( D_2 \) would have a real and negative eigenvalues if \( \text{Tr}(D_2) < 0 \) and \( \text{Det}(D_2) > 0 \). By using the sub-matrix (19), we obtain the following

\[
\text{Tr}(D_2) = -(p_1 + p_2 + p_3 + 2\mu) < 0 \quad \text{and} \quad \text{Det}(D_2) = \mu_1 p_1 p_2 S > 0.
\]

From the above result, the sub-matrix (18) would be negative if \( R_M < 1 \). Thus, \( E_{M0} \) is LAS if \( R_M < 1 \) and unstable otherwise.

### 3.3. Existence of the endemic equilibria

In this section, we show the existence of endemic equilibria of the malaria-only model (13) and the criterion for the likelihood of a backward bifurcation. The endemic equilibria are the steady-state solution of a system in the presence of disease infection. The malaria-endemic equilibrium denoted by \( E_M = (S^r, E^*_m, I^*_m, R^*_m) \) is obtained by first defining the force of infections \( \lambda^*_m \) and \( \lambda^*_m \) as

\[
\lambda^*_r = \frac{b\beta_m E^*_m}{N^r}, \quad \lambda^*_m = \frac{b\beta_m S^r}{N^r},
\]

where the total human population \( N^r = S^r + E^*_m + I^*_m + R^*_m \). The steady states solutions are obtained in the form of the force of infection \( \lambda^*_m \) as

\[
S^r = \frac{z_0 - z_1^*}{r^*_m}, \quad E^*_m = \frac{z_2^*}{r^*_m}, \quad I^*_m = \frac{z_3^*}{r^*_m}, \quad R^*_m = \frac{z_4^*}{r^*_m},
\]

We substitute the above steady state’s solutions (21) into the force of infections (20), to obtain the following polynomial

\[
z_0 = \frac{1}{\pi_0} \pi_0 p_1 (\mu, p_2) z_1^2 (1 - R^*_m),
\]

\[
z_1 = \pi_0 p_1 p_2 p_3 (m_3 + \mu, m_2),
\]

\[
z_2 = m_2 m_3 m_4.
\]

where \( p_1 = \sigma_m + \mu, p_2 = \gamma_m + \mu + \delta_m, p_3 = \mu + \delta_m, m_1 = (\sigma_m + \mu)(\kappa_m + \mu)(\mu + \delta_m) + \mu p_1 p_2 p_3, m_2 = \mu \sigma_m \sigma_m + \mu \sigma_m p_3 + \mu p_3 p_1, m_3 = \mu m_2 + b\beta p_m p_1. \) We use the quadratic Eq. (22) to examine the possibilities of multiple endemic equilibria when the threshold quantity is less than unity. Since all parameter values are said to be positive in the invariant region, the coefficient \( z_2 \) will always be positive, while the constant term \( z_0 \) will be negative if \( R_M < 1 \). Consequently, the result below follows.

**Theorem 4.** The malaria model (13) has

(i) single endemic equilibrium if \( z_0 < 0 \) or \( R_M > 1 \); 
(ii) single endemic equilibrium if \( z_1 < 0 \), and either \( z_0 = 0 \) or \( z_2^* - 4z_1^* z_0 = 0 \); 
(iii) double endemic equilibrium if \( z_0 > 0, z_1 < 0 \), and \( z_2^* - 4z_1^* z_0 > 0 \); 
(iv) no endemic equilibrium otherwise.

The above Theorem 4, case (i) shows that the system (13) has a single endemic equilibrium when \( R_M > 1 \). Also, case (iii) suggests that backward bifurcation may occur (co-occurrence of the disease-free and stable endemic equilibrium) when \( R_M < 1 \) is less than unity [75]. The infers that, while the criteria \( R_M < 1 \) is required for disease removal in the population, it no longer grantee disease elimination. To obtain the backward bifurcation point of system (13) when the threshold quantity \( R_M < 1 \), we set the discriminant \( z_2^* - 4z_1^* z_0 = 0 \) and solve for the critical value of \( R_M \) (represented by \( R^*_m \)) so that

\[
R^*_M = \frac{1}{4z_2^* - 4z_1^* z_0}.
\]

Therefore, it can be demonstrated that backward bifurcation occurs for certain values of \( R_M \) when \( R_M < R^*_M < 1 \). The phenomenon of backward bifurcation in system (13) makes the control or elimination of malaria difficult because the model’s reproduction number must be reduced to a level below unity such that \( R_M < R^*_M < 1 \). This means that in order to eradicate malaria in the population, additional control measures will be highly required.

### 3.4. COVID-19-malaria co-infection model

We present the findings for the co-infection model (3) in this section. The feasible region for the model is given by \( \Omega_{CM} = \Omega_C \times \Omega_M \), where \( \Omega_C \) and \( \Omega_M \) are as described in the preceding sub-sections. It can be demonstrated, using the same method as in sub-Section 3.1 that all solutions of system (3) with positive initial conditions will always be positive. Therefore, the region \( \Omega_{CM} \) is positively invariant and attracts all
the models’ solutions, such that the co-infection model (3) is said to be epidemiologically and mathematically well-posed.

3.4.1. Existence and stability of the COVID-19-malaria co-infection free-equilibrium

The COVID-19-malaria-free equilibrium is obtained as

$$ E_{CM0} = \left( S^*, V^*, E^*, I^*, A^*, L^*, H^*, E_{CM}, I_{CM}, L_{CM}, R_{CM}, S^*, I^* \right). $$

(25)

Following the previous sections’ derivation of the threshold quantities, the COVID-19-malaria reproduction number is given as

$$ R_{CM} = \max \{ R_C, R_M \}, $$

(26)

where $R_C$ and $R_M$ are the associated reproduction number for COVID-19 and malaria respectively. Hence, the following result follows.

**Theorem 5.** The COVID-19-malaria free equilibrium $E_{CM0}$ of the model (3) is LAS in the region $\Omega_{CM}$ if $R_{CM} < 1$ and unstable otherwise.

3.5. Investigating the impact of COVID-19 on malaria dynamics through the invasion reproduction number

It is essential to research how each disease affects the dynamics of the other when modeling co-infection diseases. In other words, it will be important to understand whether the prevalence of one disease affects the other. According to [76], a population that is already suffering from an existing disease may, under certain circumstances, be invaded by a new strain or disease. It is widely known that malaria is endemic in more than one hundred and nine nations, as reported in 2008 [5,2]. While mitigating this deadly disease, the COVID-19 prevalence is becoming more common, increasing the disease’s threat on a global scale. Because of this, we include this section to investigate the invasion criterion of COVID-19 when it is introduced into a malaria-endemic population. In other words, we’re interested in investigating the circumstances under which COVID-19 can spread among people who already have malaria (malaria-endemic). To achieve this, we use the new threshold quantity known as the invasion reproductive number to establish the threshold at which malaria will be invaded by the newly lethal COVID-19 in the general populace. The invasion reproduction number is the average number of new infections that can result from introducing an infected individual with one disease into a population where a different disease is endemic [77,78]. In line with our study, we can define the invasion reproduction number denoted by $R_{CM}^I$, as the average number of secondary infections caused by introducing a COVID-19 infected person into a populace where malaria is endemic. Now, we derive the invasion reproduction number $R_{CM}^I$ around the malaria endemic equilibrium $E^{**}$ defined as

$$ E^{**} = \left( S^{**}, V^{**}, 0, 0, 0, 0, 0, E^{**}, I^{**}, R^{**}, 0, 0, 0, 0, S^*, I^* \right). $$

By using the same methodology in [79,78], the invasion reproduction number is calculated by using the next generation matrix operator method around $E^{**}$, where malaria is endemic (i.e. $R_M > 1$). The malaria-infected compartments considered are $(E, A, L, H, E_{CM}, I_{CM}, I_{CM}, M, S^*, I^*)$. The matrices for the COVID-19 infection terms $F$, and the remaining transfer terms $V$ are defined such that

$$ F - V = \begin{bmatrix} k_sS + k_xV & -k_xE & 0 & 0 & -\sigma_A L & k_sE & k_xE & -\sigma_M M \\ 0 & 0 & 0 & 0 & 0 & -\sigma_L L & 0 & -k_I I \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ \phi_xL & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \end{bmatrix} $$

(27)

It can be shown with the same approach in sub-Section 3.1.2 that the spectral radius of the next generation matrix associated with the system (27), denoted by $FV^{-1}$ is obtained as

$$ R_u = \frac{\beta_s\sigma(A + k_I I + k_hcE_{CM} + k_lL_{CM} + k_mR_{CM} + k_vV_{CM} + k_mk_eE_{CM} + k_mk_hh_lh_mE_{CM} + k_mk_hh_lh_mL_{CM} + k_mk_hh_lh_mR_{CM} + k_mk_hh_lh_mV_{CM})}{k^2} $$

(28)

where $k_2 = 1 - \varepsilon$, $k_4 = \mu + \sigma + k_5 = 1 - \psi$, $k_7 = k_8 + \gamma + k_9 + k_10 = 1 - k_9$, $k_{11} = \mu + \delta_2 + \psi_2$, $k_{12} = \mu + \delta_2 + \gamma + k_9 + k_{10} = 1 - k_{10}$, and $k_{13} = k_{13} + \sigma + k_9$. We note that the force of infection is defined as $\mathcal{R} = \frac{\beta_s\sigma(A + k_I I + k_hcE_{CM} + k_lL_{CM} + k_mR_{CM} + k_vV_{CM})}{k^2}$, with $N^{**} = S^{**} + V^{**} + E^{**} + I^{**}$. Theorem 3.3 of [79] leads to the conclusion that is given below.

**Theorem 6.** The malaria-endemic equilibrium, $E^{**}$, which exists whenever $R_M > 1$, is LAS if $R^C_M < 1$, and unstable if $R^C_M > 1$.

Epidemiologically, Theorem 6 infers that COVID-19 will be effectively controlled in a community where malaria is endemic, if $R^C_M$ can be reduced (and kept at) a value that is below 1.
one. Consequently, the threshold condition $R_C > 1$ can be used as an invasion criterion for COVID-19 in the co-infection model (3). In Fig. 3(d) to Fig. 3(f), we provide examples of the Theorem 6 result. According to the simulation’s findings, the two diseases will coexist in their endemic state, however, COVID-19 will dominate in the population when $R_C$ exceeds unity. Therefore, to hinder COVID-19 from invading a community where malaria is already endemic, an intervention strategy must be implemented to reduce and keep the invasion reproduction number below unity.

4. Numerical simulations

In this section, we perform a numerical simulation on the developed model to investigate the dynamics of COVID-19, malaria, and their co-infection in the human population. Since the general goal of the human population is to attain a disease-free environment, we aim to first simulate the impact of control measures in eradicating each disease. Furthermore, we shall study the co-dynamics and control of COVID-19-malaria co-infection. To achieve this, we first perform a sensitivity analysis on the threshold quantities: reproduction number of COVID-19 and malaria represented by $R_C$ and $R_M$ respectively. Following this, we simulate the co-infection model (3) under different possible scenarios. The model parameter values used in this section, unless otherwise specified, were compiled in Table 1 from various sources of literature. It’s important to note that all parameter values with units are expressed in days. Based on the values for the baseline parameters in Table 1, the estimated reproduction number for COVID-19 and malaria are $R_C = 1.94$ and $R_M = 0.43$, respectively.

4.1. Sensitivity analysis

Again, the reproduction number is most often used in determining the condition for disease elimination (except in the case where the bifurcation phenomenon occurs). Epidemiologically, when it is above one then the disease is said to persist, while the disease can be eliminated when it is below one [74,80]. Thus, it is important and would be informative to investigate the impact of each model parameter on disease transmission dynamics. To achieve this, we performed a sensitivity analysis to evaluate the relationship between the model parameters and the reproduction numbers $(R_C, R_M)$. This will help us understand the effects of each parameter on the threshold levels, which will help public health officials and policymakers prioritize an intervention strategy for stopping the spread of COVID-19 and malaria in the populace. For each of the parameters $s$, the normalized forward sensitivity index $X^s_{R_0}$ on $R_0$ is defined below using the methodology in [81,82].

$$X^s_{R_0} = \frac{\partial R_0}{\partial s} \times \frac{s}{R_0}. \quad (29)$$

By using the parameter values given in Table 1 and the formula given by (29), the respective sensitivity indices values for the COVID-19 and malaria reproduction numbers are tabulated in Table 2 and Table 3 respectively. Additionally, in Fig. 2 we display the bar plot of the sensitivity indices.

| Parameter Description        | Sensitivity Index | Sign |
|------------------------------|------------------|------|
| Recruitment rate of vectors  | 0.5000           | +ve  |
| Probability of malaria       | 0.5000           | +ve  |
| Probability of malaria       | 0.5000           | +ve  |
| Malaria progression rate from exposed to infectious | 0.0002 | +ve |
| Number of effective mosquito bite per day | 1.000 | +ve |
| Humans’ natural mortality rate | 0.4820 | +ve |
| Malaria-related mortality rate | -0.0175 | -ve |
| Recovery rate of infectious malaria people | -0.4648 | -ve |
| Recruitment rate of susceptible people | -0.5000 | -ve |
| Vectors’ natural mortality rate | -1.000 | -ve |

Fig. 2  Sensitivity indices of the model parameters for; (a) COVID-19 reproduction number $R_C$ given in (9); (b) malaria reproduction number $R_M$ given in (15).
Fig. 3  Simulation of the co-infection model (3), showing the impact of threshold quantities on the total infected population at different initial conditions. Parameters are at baseline values except otherwise stated. (a) Baseline parameter values (so that $R_M < 1 < R_C$, for which $R_C = 1.94, R_M = 0.43$); (b) $\beta_c = 0.105, \beta_m = 0.625, b = 2.838$ (so that $R_C < 1 < R_M$, for which $R_C = 0.39, R_M = 1.23$); (c) $\beta_c = 0.105$ (so that $R_C < R_M < 1$, for which $R_C = 0.39, R_M = 0.43$); (d) $\beta_m = 0.625, b = 4.257$ (so that $R_C > R_M > 1$, for which $R_C = 1.94, R_M = 1.84, R_M^* = 5.25$); (e) $\beta_m = 1.250, b = 5.676$ (so that $R_M > R_C > 1$, for which $R_C = 1.94, R_M = 3.47, R_M^* = 1.24$); (f) $\beta_m = 1.563, b = 7.095$ (so that $R_M > R_C > 1$, for which $R_C = 1.94, R_M = 4.85, R_M^* = 0.58$).
The sensitivity indices of the COVID-19 and malaria model parameters presented above have both positive and negative signs. For each of the positive indexes, an increase in the parameter value will directly increase the threshold quantity and vice versa, as a result, there will be an upsurge in the disease burden in the populace. For example, in Table 1, the transmission rate of COVID-19 denoted by $\beta_i$ have the sensitivity index of 1.0000. This means that, if the COVID-19 transmission rate is increased (or decreased) by $y\%$, then the reproduction number of the disease $R_C$ will increase (or decrease) by $y\%$. From Table 1, $\beta_i$ and $\psi$ has the highest sensitivity index with the value 1.0000 and 0.7355 respectively. This implies that an increase in the COVID-19 transmission rate and the fraction of the exposed individuals becoming symptomatic will upsurge the COVID-19 infection burden in the community. Similarly, in Table 2, the parameters $b, \beta_m, \beta_{am}$ and $\mu_i$ are the dominating positive sensitivity index among the model parameters of the malaria reproduction number $R_M$. This means that the abundance of vector population with an increase in the effective biting rate per day will intensify malaria transmission. Additionally, a rise in the probability of malaria transmission per mosquito bite $\beta_m$, and the probability of malaria transmission from infected humans to vectors $\beta_i$ will also influence malaria transmission in the community. It is worth noting that for each negative sensitivity index, an increase in the parameter value will reduce the threshold quantity, and vice versa, causing a decrease in the population’s disease burden. As seen in Table 1, since $\gamma = -0.0653, \tau = -2.1088$ and $\tau = -0.6328$ are negative indexes, it can be inferred that an increase in vaccination rate against COVID-19 with a rise in vaccine efficacy, and the hospitalization rate of symptomatic infectious individuals will reduce COVID-19 transmission in the populace. Similarly, in Table 2, the parameters $\mu_i, \mu_m$ and $\gamma_m$ are the dominating negative sensitivity index among the model parameters of the malaria reproduction number $R_M$. We can deduce that by increasing the recovery rate of malaria infectious people and increasing the elimination of vectors in the population, malaria incidence can be reduced in the community. By using the result from the sensitivity analysis, several control measures can be implemented to attain a COVID-19 and malaria-free population.

From our result, we recommend that to reduce the COVID-19 burden in the community, the public health officials and policymakers should prioritize and implement intervention strategies that can reduce the COVID-19 infection rate $\beta_i$ and the fraction of exposed individuals becoming symptomatic $\psi$. Additionally, the vaccination rate $\gamma$ (with an increase in vaccine efficacy $\psi$) against the disease and hospitalization rate of the symptomatic people $\tau$ should be enhanced to lower COVID-19 transmission in the populace. Similarly, we advise public health officials and policymakers to prioritize and put into practice intervention strategies that can lower the probability of malaria transmission $\beta_i, \beta_m$ and the effective biting rate of mosquitoes per day $b$ in order to lessen the burden of malaria in the community. To decrease malaria transmission in the populace, it is also important to improve the recovery rate of those who are infected with the disease as well as the mortality rate of malaria vectors. These can be accomplished by raising awareness of the use of bed nets and vector repellents. Additionally, the healthcare system’s facilities should be better outfitted to aid in the diagnosis and treatment of infected individuals. 

4.2. Impact of threshold quantities $(R_C, R_M)$ on disease dynamics

Here, we perform a numerical simulation of the co-infection model (3) to investigate the effect of the threshold quantities on the abundance of the COVID-19 and malaria-infected populations under different initial conditions. We should note that throughout the numerical simulations performed in this study, the total number of COVID-19 infected individuals is determined by adding the numbers of infectious individuals who are asymptomatic, symptomatic, hospitalized for COVID-19, and infectious individuals who are exposed to malaria $A_e + I_e + H_e + I_{cov}$. The total infected individual of malaria is defined as the sum of malaria infectious individuals and infectious malaria individuals exposed to COVID-19 $I_m + I_{mco}$. While the total co-infected individuals are chosen as $I_{cov}$. When modeling co-infection diseases, one of the arising questions is the competitive outcome of the co-dynamic behavior of the two diseases at different equilibrium states. For co-infection diseases, coexistence is expected in the population when each strain can invade the other. In other words, it is expected that the two diseases will coexist when they are at endemic equilibrium with reproduction numbers greater than one [83].

Our result in Fig. 3 aligns with the above claim in [83]. As seen in Fig. 3(a), COVID-19 dominates in the population and drives malaria to extinction when $R_M < 1 < R_C$. This is expected since the COVID-19 reproduction number is greater than unity while that of malaria is less than unity. This supports the epidemiological explanation of Theorem 3 which state that malaria disease can be eliminated from the populace when $R_M$ is below one, implying that a small influx of malaria-infected people into the populace cannot result in a large outbreak of the disease. Similarly, Fig. 3(b) shows that malaria will persist in the populace and drives COVID-19 to extinction when $R_C < 1 < R_M$. In accordance with Theorems 2 and 3, it stands to reason that when COVID-19 and malaria reproduction numbers are less than unity, the two diseases should be eradicated from the population. The dynamic of the COVID-19 and malaria-free equilibrium were shown in Fig. 3(c). We see that the total infected population of the two diseases reduces greatly, thus leading to disease eradication in the populace. As a result, to mitigate the burden of COVID-19 and malaria on the human populace, the implementation of intervention strategies must be prioritized to reduce the transmission of each disease by minimizing the reproduction numbers.

In Fig. 3(d), 3(e) and 3(f), we explore the scenario of co-existence equilibria when both threshold quantities are above unity. The result shows that the co-infection model (3) has a co-existence equilibrium (known as the endemic equilibrium) whenever the threshold quantities $R_i > R_j > 1$; for $i, j = C, M; C \neq M$. From this result, we infer that both diseases will co-exist in the population whenever their reproduction number is above unity. It is important to note that even though both diseases co-exist, the disease with the higher reproduction number will dominate the other but not drive it
Fig. 4  Simulation of the co-infection model (3) showing the effect of the transmission rate of co-infection $\beta_{cm}$ on the dynamics and final sizes of the total infected human population when $R_M = R_C = 1.94 > 1$. (a, b) Baseline parameter values with $b = 4.257, \beta_m = 0.694$ and $\beta_{cm} = 0.419$; (c, d) Baseline parameter values with $b = 4.257, \beta_m = 0.694$ and $\beta_{cm} = 2.094$; (e, f) Baseline parameter values with $b = 4.257, \beta_m = 0.694$ and $\beta_{cm} = 0.084$. 
to extinction as shown in Fig. 3(d), 3(e) and 3(f), and Fig. 3(f) respectively. However, for malaria to dominate over COVID-19 its reproduction number must be at least twice of COVID-19 reproduction number (i.e. $R_M > 2R_C$) must be satisfied. As seen in Fig. 3(e), we see that both diseases co-exist in the population but COVID-19 dominates malaria when $R_M > R_C > 1$ at $R_M = 3.47, R_C = 1.94$. These findings suggest that the COVID-19 disease poses a greater threat to humanity. This could be a result of the fact that human-to-human contact is the main method of transmission rather than the need for a vector (another host) to transmit malaria. It should be noted in Fig. 3(d) and 3(e) that COVID-19 will dominate in the population when the reproduction number $R_M^C$ is above unity (i.e. $R_M^C = 5.25$, and $R_M^C = 1.24$) respectively. However, COVID-19 is unable to invade malaria when the reproduction number $R_M^C$ is below unity (i.e. $R_M^C = 0.58$) as shown in Fig. 3(f).

4.3. Impact of the transmission rate of co-infection on disease burden
In this section, we examine the effects of the co-infection transmission rate $\beta_{cm}$ on the burden of both diseases. It should be noted that we set the threshold quantities to be at their endemic equilibria states (i.e. $R_M = R_C = 1.94 > 1$), such that COVID-19 and malaria are expected to persist in the human population. Our goal is to investigate the impact of reducing co-infection transmission on the competitive outcome between the two diseases. In other words, we want to know how the prevalence of co-infection affects each disease’s ability to compete. The simulation of the co-infection model shown in Fig. 4 illustrates how the dynamics and final sizes of the infected human population are impacted by the co-transmission infection rate. As seen in Fig. 4(a), even though the threshold quantities are set to be equal, with the co-infection transmission rate at $\beta_{cm} = 0.419$ COVID-19 dominates in the population but does not drive malaria into extinction. COVID-19 predominates in the population without eradicating malaria.

It is noted that malaria-infected individuals dominate the population in the first eighty-five days before being displaced by the fitness of COVID-19. The final size of the infected populations is shown in Fig. 4(b). We can see that COVID-19 disease has the highest number of infected people, followed by the population with co-infection. In Fig. 4(b) and 4(e), we simulate the impact of higher and lower transmission rate of co-infection at $\beta_{cm} = 2.094$ and $\beta_{cm} = 0.084$ respectively. Overall, the findings indicate that COVID-19 infection is spread more widely by co-infected individuals, which lowers the number of malaria-infected people in the population. This suggests that the presence of COVID-19-malaria co-infection contributes to the worsening of the COVID-19 burden on the human population.

Several confirmed cases of COVID-19 and malaria co-infection have been documented to date in various parts of the globe. Implementing intervention strategies to stop the spread of each disease in the community is crucial. There should be the implementation of medical facilities and equipment that will aid in the diagnosis and treatment of both diseases, especially since the symptoms of the two diseases are similar. The potential threat of co-infection of COVID-19 and malaria on human health should be understood, and this is especially important in areas where malaria is endemic.

5. Concluding remarks
One of the contagious diseases spread by vectors, malaria has long been a problem for public health, especially in areas where it is endemic. Since it was declared endemic in one hundred and nine countries in 2008, it has continued to be a significant public health burden despite decades of ongoing research into its dynamic spread and control [70,5]. While many organizations and healthcare policymakers are working to eradicate malaria among humans, COVID-19’s emergence has overwhelmed the healthcare system, prompting a pandemic declaration as of the end of 2019. Many researchers have recently reported finding cases of COVID-19 and malaria co-infection in various parts of the world. The symptoms of these two illnesses are similar, making it difficult to diagnose and treat patients. This alarming occurrence has led to complications brought on by misdiagnosis or improper treatment, which have worsened human health. Therefore, it’s crucial to comprehend the dynamics of COVID-19-malaria in order to lessen the burden of the disease in the community. To better understand the co-dynamics of the two diseases, we formulated and analyzed a co-infection compartmental model to investigate the impact of co-endemicity on the dynamics of each disease in the populace. The study’s main theoretical conclusions are outlined below.

1. As shown in Theorem 2, the COVID-19-free equilibrium of model (6) is shown to be LAS whenever $R_C$ is below one and unstable otherwise.
2. We show in Theorem 3 that the malaria-free equilibrium of model (13) is LAS whenever $R_M$ is below one and unstable otherwise.
3. The malaria-only model (13) will exhibit the phenomenon of backward bifurcation when the $R_M < R_M^* < 1$, which suggests a case where stable disease-free equilibrium co-exists with a stable endemic equilibrium whenever $R_M$ is less than unity.
4. The COVID-19-malaria free equilibrium of the co-infection model (3) is LAS whenever the associated reproduction number $R_{CM} = \max \{R_C, R_M\}$ is less than unity and unstable otherwise.
5. The malaria-endemic equilibrium is LAS whenever the invasion reproduction number $R_M^* < 1$, and unstable when $R_M^* < 1$. This implies that COVID-19 can invade a population where malaria is endemic if the associated invasion reproduction number $R_M^* < 1$ exceeds unity.

To support the theoretical finding of the study, we first carried out a sensitivity analysis of the sub-models to evaluate the relationship between the model parameters and the reproduction numbers, and then we performed a numerical simulation on the co-infection model to investigate the impact of threshold quantities and the co-infection transmission rate on disease burden. The results are summarized below.

1. The two main parameters that influence the spread of COVID-19 infection are the disease transmission rate $\beta_i$ and the fraction of the exposed individuals becoming symptomatic $\psi$. Therefore, efforts should be made to lessen disease transmission and the percentage of those exposed who progress to the symptomatic stage.
2. Malaria transmission in the community will be influenced by the abundance of vector population, which is driven by recruitment rate $\pi$, with an increase in effective biting rate $b$, probability of malaria transmission per mosquito bite $\beta_m$, and probability of malaria transmission from infected humans to vectors $\beta_s$. As a result, to reduce the malaria burden in the communities, the vector population should be reduced by using some control measures such as eliminating the mosquito larval habitats and spraying insecticides to kill adult mosquitoes.

3. The results of simulating the effect of threshold quantities on disease burden show that COVID-19 will predominate in the populace and drives malaria to extinction when $R_M < 1 < R_C$, whereas malaria will dominate in the population and drives COVID-19 into extinction when $R_C < 1 < R_M$.

4. The two diseases will coexist at the COVID-19 and malaria endemic equilibrium (i.e. $R_C > 1$, $R_M > 1$), with the disease with the highest reproduction number predominating. However, for malaria to dominate in the population, the criterion $R_M > 2R_C$ must be satisfied as shown in Fig. 3(f).

5. When the two diseases are in endemic equilibrium, the prevalence of co-infection raises the burden of COVID-19 on the population and lowers the incidence of malaria.

The burden of malaria on human health has persisted for many years, especially in areas where it is endemic. The burden that malaria has been placing on the community is now being exacerbated by the prevalence of COVID-19. According to several researchers, the similarity of the symptoms experienced by infected people makes it difficult to understand the epidemiology of the co-infection of these two diseases. This work has enabled us to investigate the impact of threshold quantities and co-infection transmission rate on the two diseases’ synergistic relationship. Based on this study’s findings, we advise policymakers and healthcare professionals to promote accurate diagnosis of infected individuals to prevent patients from being mistreated. To lessen the burden of both diseases on the population, it is crucial to ensure that sick people receive accurate diagnoses before receiving treatment, especially in low-income countries where people engage in self-medication. In order to lessen the burden of COVID-19 and malaria on the human population, there is a great need for research on the co-infection of these diseases. The model described here has some limitations that could be addressed in a future study. For instance, we made some assumptions about co-infection parameters, like the co-infection rate of transmission, efforts can be made in partnership with medical centers to validate models with real data to obtain a more precise prediction of the co-infection dynamics. This model can be extended to include the effects of seasonality and climate change on mosquito dynamics and the timing of COVID-19 intervention strategies. Additionally, because both diseases are a burden on human health on a global scale, it is recommended to analyze optimal control and cost-effectiveness to find the best control methods with the lowest possible costs, particularly for low-income communities in developing nations.

Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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