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Mathematical Modeling of the Co-infection of Typhoidfever and Plasmodium Falciparum dynamics

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Abstract
Malaria and Typhoid fever co-infection is the most endemic disease and a major public health problem in many tropical developing countries. Both diseases share similar transmission factor and often have the similar symptom. Because of the high prevalence of malaria and typhoid fever in these developing countries, co-infections are common. In addition to true co-infection of malaria and typhoid fever, the major challenges on managing controlling these diseases are false diagnoses due to similar signs and symptoms and false positive results in testing methods. In this study, we have formulated a mathematical model based on a system of non-linear first order ordinary differential equations to study the dynamics of the co-infection dynamics of plasmodium falciparum and typhoid fever. We have proved the existence of the disease free equilibrium point and endemic equilibrium point of the model and we used a non-linear stability analysis method to prove the local and global stabilities of these equilibrium points. Further, the positivity and boundedness of the solution of the model developed is verified to discover that the model equation is mathematically and epidemiologically well posed. We also computed the basic reproduction number using the next generation matrix approach. The sensitivity analysis is discussed in detail to identify the most influential parameters that enhance the co-infection of plasmodiumfalciparum and typhoid fever disease in a given population.

Key Words: *Typhoid Fever, Malaria, Plasmodium Falciparum, Co-Infection, Reproduction Number, Sensitivity Analysis.*

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I. Introduction

Typhoid fever is an infectious disease. Typhoid fever, also known as enteric fever, is a systemic infection by Salmonella typhi or by the related but less virulent Salmonella paratyphi (S. paratyphi A, S. paratyphi B, S. paratyphi C and S. paratyphi D). Archeologists have found Salmonella typhi in Athenian mass graves from the era of the Peloponnesian Wars, implicating it as the cause of the Great Plague of Athens[19, 22].Based on this idea typhoid fever is an ancient infectious disease basically caused by lack of basic sanitation. Typhoid fever signs and symptoms vary widely and are very much similar to the symptoms of other microbial infections. Some of the common typhoid fever symptoms are Variable degrees of high grade fever in about 75% of cases, Muscle pains and body aches, Chills, Poor appetite, Severe Headaches, vomiting, Nose bleeds, Pain in the abdomen in 20 to 40% of cases, Dizziness, Rose spots (rashes) over the skin, Weakness and fatigue, Constipation or diarrhea, sore throat and a cough [3, 12,16, 19].

Malaria is an infectious disease. The term "Malaria" originated from medieval Italian; "mal" and "aria" meaning "bad air". The disease was formally called "ague" or "marsh fever" due to its association with swamps and marsh land. The term first appeared in the English Literature about 1829. Malaria is an ancient disease – written accounts of similar fevers first appeared around 6000 BC. Missionaries working in Peru in the early 1600s discovered that the powdered bark of the Cinchona tree could be successfully used to treat malaria. However, it wasn't until 1920 that two French chemists isolated the antimalarial compound quinine from the bark [24].

Malaria is a protozoan disease and is one of the febrile illness and the most common fatal disease in the world caused by one or more species of plasmodium. These are plasmodium falciparum, plasmodium Vivax, plasmodium Ovale, plasmodium Malariae, and plasmodium Knowlesi. Most deaths are caused by P. falciparum because others generally cause a milder form of malaria. Recent evidence suggests that P. vivax malaria is also potentially life threatening disease. The biology of the five species of *Plasmodium* is generally similar and consists of two distinct phases: a sexual stage at the mosquito host and an asexual stage at the

human host. The disease is transmitted by the biting of female Anopheles mosquitoes, and the symptoms usually begin ten to fifteen days after being bitten. A single bite by a malaria-carrying mosquito can lead to extreme sickness or death. Malaria starts with an extreme cold, followed by high fever and severe sweating. These symptoms can be accompanied by fever, joint pains, abdominal pains, headaches, vomiting, lassitude, occasional nausea, diarrhea and extreme fatigue. For severe and complicated malaria, symptoms such as yellow skin, seizures, splenomegaly, anemia, cerebral malaria, respiratory distress syndrome, acute renal failure, and in particular, convulsions ,coma or death may arise[1,2, 4,15, 21, 25].

In sub-Saharan Africa, the pattern of malaria transmission varies markedly from region to region, depending on climate and biogeography and broad ecological categories [20]. Plasmodium falciparum, which is the most prevalent, deadliest and predominant in sub-Saharan Africa, is the major cause of malaria infections[1,6,20 , 21,24] and Anopheles gambiae is the primary vector for its transmission [24].

The World Health Organization (WHO) estimated that there were 214 million malaria cases in 2015, resulting in about 438,000 deaths. According to the reference there were over 100 countries where there was a risk of malaria transmission, and these were visited by more than 125 million international travelers every year [1].

An association between malaria and typhoid fever (malaria–typhoid co-infection) was first described in the Medical Literature in the middle of the 19th century and was named typhoid-malarial fever by the United State Army Doctor Joseph J. Woodward (1833 – 1884) in 1862. Typhoid -malaria fever was found among young soldiers during the American Civil War who were suffering from febrile illness that seemed to be typhoid fever rather than a new species of disease . However, in the end of 19th century the developed laboratory test rejects this theory, because they found that it was either one thing or other or in rare instance it is co-infection with both Salmonella typhi and the Plasmodium species . Although, malaria and typhoid fever are caused by two different organisms in which one is protozoan and other is gram negative bacilli, which transmit by two different mechanisms and both diseases share similar symptomology, because both typhoid fever and malaria share social circumstances which are important for their transmission. The People living in the area which are endemic for both typhoid fever and malaria are at risk of getting disease either concurrently or acute infection superimpose the chronic one[13, 15, 17, 23].

The co-infection of malaria parasite and Salmonella species is common, especially in the tropics where malaria is endemic. The common detection of high antibody titre of these Salmonella serotypes in malaria patients has made some people to believe that malaria infection can progress to typhoid fever or that malaria always co-infect with typhoid/paratyphoid fever in all patients. Hence, some people treat malaria and typhoid fever concurrently once they have high antibody titre for Salmonella serotypes, even without adequate laboratory diagnoses for malaria and vice versa [9].

Co-infection of malaria and typhoid can result in serious complications and conditions such as maternal anemia, fever, fetal anemia, abortion, still-birth and even death of the child or mother before birth or soon after delivery. Co-infection of malaria and typhoid fever leads to chronic anemia and placental malaria infection, reducing the birth weight and increasing the risk of neonatal death. Severe maternal anemia has been associated with an increased risk of infant death in the prenatal and post neonatal periods[14].It is known that anemia occurs in malaria infected individuals resulting in excessive deposition of iron in the liver, which supports the growth of salmonella bacteria that causes typhoid fever [11, 18].

Some deterministic mathematical models have been formulated on the co-infection dynamics of malaria and typhoid fever. But, none of them explained the dynamics of plasmodium falciparum co-infected with typhoid fever separately based on appropriate treatments. In this paper, we developed a deterministic mathematical model that accounts for different kinds of treatments which impact on the dynamics of plasmodium falciparum-typhoid fever co-infection. The study aims to investigate that how much the co-infection is stronger in our transmission dynamics of the diseases. In this study we assumed that co-infected individuals displaying clinical symptoms of one disease may be treated either both infections or single infection.

II. The Mathematical Model Formulations and Descriptions

To study the transmission and spread of the co-infection of plasmodium falciparum and typhoid fever, we formulate a model which sub-divides the total human population size at time t, denoted by $N_h(t)$, into compartments, namely: susceptible humans $S_h(t)$, infectious humans singly-infected with typhoid fever $I_t(t)$, recovered humans from typhoid fever only $R(t)$, infectious humans with plasmodium falciparum only I_{hf}, co-infected individuals with plasmodium falciparum and typhoid fever C_{ft} , treated individuals from plasmodium falciparum and typhoid fever T_{ft} and treated individuals from plasmodium falciparum T_f.The susceptible human becomes infected with plasmodium falciparum after bitten by infected mosquitoes with plasmodium falciparum. Hence, the total human population is given by

$N_h = S_h + I_t + R + I_{hf} + C_{ft} + T_{ft} + T_f$.Similarly, the total mosquitoes (vectors) populations size at time t, denoted by$N_m(t)$, is divided into two compartments, namely : susceptible mosquitoes $S_m$and infectious

mosquitoes with plasmodium falciparum only I_{mf}. The mosquitoes remain infectious for life and have no recovered class due to their short life span. The susceptible mosquito becomes infected with plasmodium falciparum after it bites infected humans with plasmodium falciparum. Thus, the total mosquito population is given by$N_m = S_m + I_{mf}$. $\Lambda_h$andΛ_m are the new recruitment rates into the susceptible humansand mosquitoes populations respectively , μ_h and $\mu_m$are natural death rates for humans and mosquitoes populations respectively; $\delta_t$and δ_f are typhoid fever andplasmodium falciparum disease- induced death rates for humans and mosquitoes populations respectively, malaria infected individuals with plasmodium falciparum in I_{hf} class progress to the co-infected class C_{ft}at the rate$\gamma\lambda_t$, where γ is the modification parameter, typhoid fever infected individuals in I_t class progress to the co-infected class C_{ft}at the rate$\alpha_2\lambda_{hf}$, where $\alpha_2$is the modification parameter accounting for increased rate of co- infection due to weakened individuals by typhoid fever; individuals in C_{ft}class suffer disease-induced death at the rate $\theta_2\delta_{ft}$, where $\theta_2$accounts for increased mortality due tothe co-infection impactof the two diseases, $\omega$is the recovery rate of humans from typhoid fever due to treatment,$\phi_2$is the treatment rate of the co-infected classC_{ft}, malaria infected individuals with plasmodium falciparum in I_{hf} class progress to the treatment class T_f at the treatment rate ε. Susceptible humans acquire typhoid fever at the rate of $\lambda_t = \frac{\beta I_t}{N_h}$. The force of infection of susceptible humans withplasmodium falciparum is at the rate of $\lambda_{hf} = \frac{a_2 b I_{mf}}{N_h}$. The force of infection of susceptible mosquito by plasmodium falciparum infected human is given by$\lambda_{mf} = \frac{a_4 b(I_{hf} + \eta_2 C_{ft})}{N_h}$. In the malaria transmission process between human and mosquito, we apply the concept of "conservation of bites"; that is, the total number of bites made by mosquitoes equals the number of bites received by the human hosts.

In our work we assumed the following basic assumptions:The populations are homogenously mixing.There is no simultaneous infection of the diseases.Susceptible individuals get typhoid fever infection through contact with infected individuals of the disease. In other words, we assumed that there is a direct transmission of typhoid fever from infected to susceptible individuals. We assumed that birth rate and natural death rates are constant.We further assume that there is no natural recovery from typhoid fever infection. Individuals in the co-infected class are much weakened due to the impact of the two diseases.All the associated parameters in the system are non-negative for all time$t \geq 0$.The susceptible human becomes infected with malaria after bitten by infected female anopheles mosquitoes. The susceptible mosquito becomes infected with the disease after it bites infected humans with the disease. Even if the recovered class becomes susceptible again, our focus is typhoid fever infectious class that leads to co-infection with plasmodium parasites.Mosquitoes are not infected by typhoid fever and they do not transmit the disease.

The Dynamical Flow Diagram of the Model is given by

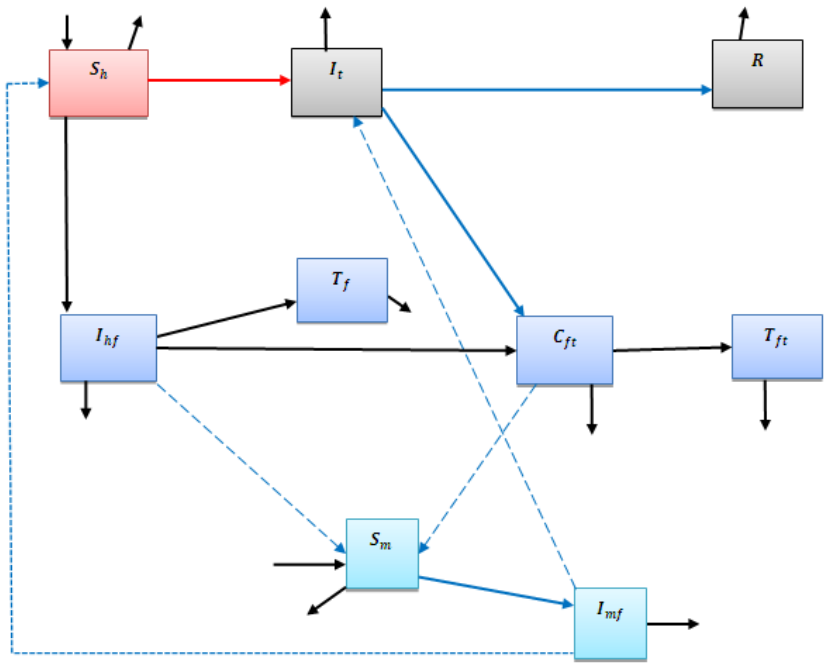

Figure 1: The graph of the co-infection dynamics of malaria and typhoid fever diseases.

Note: The dotted lines with arrows indicate human-mosquito interaction (or the direction of the infection). The solid lines with arrows show progress from one class to another.
The co-infection dynamics of the system is given by

$\frac{dS_h}{dt} = \Lambda_h - (\lambda_{hf} + \lambda_t + \mu_h)S_h$[1]

$\frac{dI_t}{dt} = \lambda_t S_h - (\alpha_2\lambda_{hf} + \omega + \delta_t + \mu_h)I_t$[2]

$\frac{dR}{dt} = \omega I_t - \mu_h R$ [3]

$\frac{dI_{hf}}{dt} = \lambda_{hf} S_h - (\gamma\lambda_t + \varepsilon + \delta_f + \mu_h)I_{hf}$[4]

$\frac{dC_{ft}}{dt} = \alpha_2\lambda_{hf} I_t + \gamma\lambda_t I_{hf} - (\phi_2 + \theta_2\delta_{ft} + \mu_h)C_{ft}$[5]

$\frac{dT_{ft}}{dt} = \phi_2 C_{ft} - \mu_h T_{ft}$[6]

$\frac{dT_f}{dt} = \varepsilon I_{hf} - \mu_h T_f$[7]

$\frac{dS_m}{dt} = \Lambda_m - (+\lambda_{mf} + \mu_m)S_m$[8]

$\frac{dI_{mf}}{dt} = \lambda_{mf} S_m - \mu_m I_{mf}$[9]

with initial conditions$S_h(0) > 0, I_t(0) \geq 0, R(0) \geq 0, , I_{hf}(0) \geq 0,\ C_{ft}(0) \geq 0, T_{ft}(0) \geq 0, T_f(0) \geq 0, S_m(0) > 0, I_{mf}(0) \geq 0.$

Table 1: Malaria and Typhoid Fever Model State Variables, Parameters, Force of Infections and Their Definitions.

State Variables	Definitions
S_h	Number of Susceptible human population size at time t
I_t	Number of Infectious human infected with typhoid fever only at time t
R	Number of individuals that have recovered from typhoid fever disease at time t
I_{hf}	Number ofInfectious human with plasmodium falciparum only at time t
C_{ft}	Number ofCo-infected individuals with plasmodium falciparum and typhoid fever at time t
T_{ft}	Number ofTreated individuals both from plasmodium falciparum and typhoid fever at time t
T_f	Number ofTreated individuals from plasmodium falciparum at time t
S_m	Number of Susceptible mosquito population size at time t
I_{mf}	Number ofInfectious mosquitoes with plasmodium falciparum only at time t
N_h	Number of total human population size at time t
N_m	Number of total mosquito population size at time t
Λ_h	New recruitment rate into the susceptible human population
Λ_m	New recruitment rate into the susceptible mosquito population
μ_h	Natural death rate for human population
μ_m	Natural death rate for mosquito population
δ_t	Typhoid fever disease- induced death rate for human population
δ_f	Plasmodium falciparum disease- induced death rate for human population
α_2	The modification parameter from infected typhoid fever to co- infection class
γ	The modification parameter for typhoid fever to co-infection
θ_2	The modification parameters accounts for increased mortality due tothe co-infection impactof the two diseases
ω	The treatment rate of humans from typhoid fever.
ϕ_2	The treatment rate of the co-infected class C_{ft}.
β	The effective transmission rate of typhoid fever on contact with infected individuals
a_2	The transmission probability of human infection due to per bite of an infected mosquito with plasmodium falciparum
a_4	The transmission probability that a mosquito will become infected by biting an infected human with plasmodium falciparum
b	Per capita biting rate of mosquito.
η_2	The modification parameters for mosquitoes to be infected from the co-infected individuals
ε	The rate of treatment for malaria
λ_t	The force of infection of susceptible humans acquire typhoid fever
λ_{hf}	The force of infection of susceptible humans withplasmodium falciparum
λ_{mf}	The force of infection of susceptible mosquito by plasmodium falciparum infected human

2.1.Invariant region and Boundedness of Solutions

In this section, we will find a region in which the solution of [1-9]is bounded. The total number of human population at any time t is given by $N_h = S_h + I_t + R + I_{hf} + C_{ft} + T_{ft} + T_f$.Then, after differentiating the human population N_h with respect to time t and substituting the corresponding values of the rates, we obtain the following result.

$$\frac{dN_h}{dt} = \frac{dS_h}{dt} + \frac{dI_t}{dt} + \frac{dR}{dt} + \frac{dI_{hf}}{dt} + \frac{dC_{ft}}{dt} + \frac{dT_{ft}}{dt} + \frac{dT_f}{dt} = \Lambda_h - \mu_h N_h - \left[\delta_t I_t + \delta_f I_{hf} + \theta_2 \delta_{ft} C_{ft}\right]$$

If there is no infection and mortality of typhoid fever and malaria diseases, we get $\frac{dN_h}{dt} \leq \Lambda_h - \mu_h N_h$ .Thus, $\frac{dN_h}{dt} + \mu_h N_h \leq \Lambda_h$. After integrating and simplifying both sides of this inequality, we obtain $N_h(t) \leq \frac{\Lambda_h}{\mu_h} + (N_h(0) - \frac{\Lambda_h}{\mu_h})e^{-\mu_h t}$.Therefore, $\lim_{t\to\infty} sup N_h(t) \leq \lim_{t\to\infty} sup\left(\frac{\Lambda_h}{\mu_h} + (N_h(0) - \frac{\Lambda_h}{\mu_h})e^{-\mu_h t}\right) = \frac{\Lambda_h}{\mu_h}$.

Hence, the total human population N_h is bounded in the region:

$\Omega_h = \left\{\left(S_h, I_t, R, I_{hf}, C_{ft}, T_{ft}, T_f\right) \in \mathbb{R}_+^7 : 0 \leq N_h \leq \frac{\Lambda_h}{\mu_h}\right\}$(a)

Similarly, the total number of mosquito population at any time t is given by $N_m = S_m + I_{mf}$.Differentiating, substituting the corresponding values and simplifying both sides of this equation gives $\frac{dN_m}{dt} = \frac{dS_m}{dt} + \frac{dI_{mf}}{dt} = \Lambda_m - \mu_m N_m$.This implies that $\frac{dN_m}{dt} \leq \Lambda_m - \mu_m N_m$.After integrating and simplifying both sides of this inequality, we obtain $N_m(t) \leq \frac{\Lambda_m}{\mu_m} + (N_m(0) - \frac{\Lambda_m}{\mu_m})e^{-\mu_m t}$.Therefore, $\lim_{t\to\infty} sup N_m(t) \leq \lim_{t\to\infty} sup\left(\frac{\Lambda_m}{\mu_m} + (N_m(0) - \Lambda m\mu m)e - \mu ht = \Lambda m\mu m\right.$

Hence, the total mosquito population N_m is bounded in the region:

$\Omega_m = \left\{\left(S_m, I_{mf}\right) \in \mathbb{R}_+^2 : 0 \leq N_m \leq \frac{\Lambda_m}{\mu_m}\right\}$(b)

From (a)and(b)**,** we can see that the model is well posed epidemiologically and mathematically. So, we can study the dynamics of the model in the region:

$\Omega = \Omega_h \text{ X } \Omega_m \subset \mathbb{R}_+^7 \text{X} \mathbb{R}_+^2 = \left\{\left(S_h, I_t, R, I_{hf}, C_{ft}, T_{ft}, T_f, S_m, I_{mf}\right) \in \mathbb{R}_+^9 : 0 \leq N_h \leq \frac{\Lambda_h}{\mu_h}; 0 \leq N_m \leq \frac{\Lambda_m}{\mu_m}\right\}$.

Therefore, the total human population N_h and the total mosquito population N_m are bounded in the region Ω and hence, all solutions of the dynamical system are bounded (i.e. all solutions with initial conditions in Ω remain in Ω for all time $t > 0$).

2.2. Positivity of Solutions

The positivity of the solution of a dynamical system can be shown by considering each differential equation separately and proving its solution is positive.For the model represented by [1-9]to be epidemiologically meaningful, it is important to prove that all its state variables are non-negative for all times.

Theorem-1: If$\left\{\left(S_h, I_t, R, I_{hf}, C_{ft}, T_{ft}, T_f, S_m, I_{mf}\right) \in \mathbb{R}_+^9 : S_h > 0, I_t \geq 0, R \geq 0,\ I_{hf} \geq 0, C_{ft} \geq 0, T_{ft} \geq 0, T_f \geq 0, Sm > 0, Imf \geq 0\right.$, then the set of solutions *Sh,It,R,Ihf,Cft,Tft,Tf, Sm,Imf* are non-negative for $t \geq 0$ in the feasible region Ω.

Proof: All the forces of infections are positives and we apply this concept in the next subsequent proofs.

Let us consider the first equation [1]of the model [1-9]:$\frac{dS_h}{dt} = \Lambda_h - \left(\lambda_{hf} + \lambda_t + \mu_h\right)S_h$

The solution of this first order linear ordinary differential equation is obtained as

$S_h(t) = S_h(0)e^{-p\tau} + \Lambda_h e^{-p\tau}\int_0^t e^{p\tau} d\tau > 0$, since $\Lambda_h > 0, S_h(0) > 0, e^{-p\tau} > 0 \text{ and } e^{p\tau} > 0$.

Hence, $S_h(t)$ is positive for all time $t \geq 0$.

Let us take equation [2]:$\frac{dI_t}{dt} = \lambda_t S_h - \left(\alpha_2\lambda_{hf} + \omega + \delta_t + \mu_h\right)I_t$

The solution of this first order linear ordinary differential equation is obtained as

$I_t(t) = I_t(0)e^{-pt} + e^{-pt}\int_0^t e^{p\tau}\lambda_t S_h(\tau) d\tau > 0$, since $\lambda_t > 0, S_h > 0, I_t(0) > 0, e^{-pt} > 0 \text{ and } e^{p\tau} > 0$. Hence, $I_t(t)$ is positive for all time $t \geq 0$.

Again, let us consider equation [3]:$\frac{dR}{dt} = \omega I_t - \mu_h R$.

The solution of this differential equation is $R(t) = R(0)e^{-\mu_h t} + e^{-\mu_h pt}\int_0^t e^{\mu_h\tau}\omega I_t(\tau) d\tau > 0$, since $I_t > 0, \omega > 0, R(0) > 0, e^{-\mu_h t} > 0 \text{ and } e^{\mu_h\tau} > 0$. Hence, $R(t)$ is positive for all time $t \geq 0$.

From equation [4],we have: $\frac{dI_{hf}}{dt} = \lambda_{hf} S_h - \left(\gamma\lambda_t + \delta_f + \varepsilon + \mu_h\right)I_{hf}$

The solution of this differential equation is $I_{hf}(t) = I_{hf}(0)e^{-pt} + e^{-pt}\int_0^t e^{p\tau}\lambda_{hf} S_h(\tau) d\tau > 0$, since$\lambda_{hf} > 0, Sh > 0, Ihf0 > 0, e - pt > 0 \text{ and } ep\tau > 0.$ Hence, *Ihft* is positive for all time $t \geq 0.$

In equation [5], we have: $\frac{dC_{ft}}{dt} = \alpha_2\lambda_{hf} I_t + \gamma\lambda_t I_{hf} - \left(\phi_2 + \theta_2\delta_{ft} + \mu_h\right)C_{ft}$

The solution of this equation is$C_{ft}(t) = C_{ft}(0)e^{-pt} + e^{-pt}\int_0^t e^{p\tau}(\gamma\lambda_t I_{hf} + \alpha_2\lambda_{hf} I_t)(\tau) d\tau > 0$, since$(\gamma\lambda_t I_{hf} + \alpha_2\lambda_{hf} I_t) > 0, S_h > 0, C_{ft}(0) > 0, e^{-pt} > 0 \text{ and } e^{p\tau} > 0$. Hence, $C_{ft}(t)$ is positive for all time $t \geq 0$.

In equation [6], we have: $\frac{dT_{ft}}{dt} = \phi_2 C_{ft} - \mu_h T_{ft}$

The solution of this differential equation is $T_{ft}(t) = T_{ft}(0)e^{-\mu_h t} + e^{-\mu_h t}\int_0^t e^{\mu_h \tau}\phi_2 C_{ft}(\tau)d\tau > 0$, since $C_{ft} > 0, \phi_2 > 0, T_{ft}(0) > 0, e^{-\mu_h t} > 0 \; and \; e^{\mu_h \tau} > 0$. Hence, $T_{ft}(t)$ is positive for all time $t \geq 0$.

In equation [7], we have: $\frac{dT_f}{dt} = \varepsilon I_{hf} - \mu_h T_f$

The solution of this equation is $T_f(t) = T_f(0)e^{-\mu_h t} + e^{-\mu_h t}\int_0^t e^{\mu_h \tau}\varepsilon I_{hf}(\tau)d\tau > 0$, since $\varepsilon I_{hf} > 0, \phi_2 > 0, T_f(0) > 0, e^{-\mu_h t} > 0 \; and \; e^{\mu_h \tau} > 0$. Hence, $T_f(t)$ is positive for all time $t \geq 0$.

In equation [8], we have: $\frac{dS_m}{dt} = \Lambda_m - (\lambda_{mf} + \mu_m)S_m$

The solution of this equation is $S_m(t) = S_m(0)e^{-pt} + e^{-pt}\int_0^t e^{p\tau}\Lambda_m d\tau > 0$, since $\Lambda_m > 0, S_m(0) > 0, e^{-pt} > 0 \; and \; e^{p\tau} > 0$. Hence, $S_m(t)$ is positive for all time $t \geq 0$.

From equation [9], we have: $\frac{dI_{mf}}{dt} = \lambda_{mf} S_m - \mu_m I_{mf}$

The solution of this equation is $I_{mf}(t) = I_{mf}(0)e^{-\mu_m t} + e^{-\mu_m t}\int_0^t e^{\mu_m \tau}\lambda_{mf} S_m(\tau)d\tau > 0$, since $S_m > 0, \lambda_{mf} > 0, I_{mf}(0) > 0, e^{-\mu_m t} > 0 \; and \; e^{\mu_m \tau} > 0$. Hence, $I_{mf}(t)$ is positive for all time $t \geq 0$.Then, the above proofs complete the proof of the theorem.

Having established a biologically feasible region where the model is biologically and mathematically well-posed, the next step is to consider the dynamics of the two sub-models, namely; Typhoid Fever only and Plasmodium Falciparum only models separately. This helps us to analyze the dynamics of the full model.

III. The Dynamics of Typhoid Fever Sub-Model Only

Using the full model [1-9], the dynamics of the typhoid feversub-model only isobtained by setting$I_{hf} = C_{ft} = T_{ft} = T_f = S_m = I_{mf} = 0$and given by

$\frac{dS_h}{dt} = \Lambda_h - (\lambda_t + \mu_h)S_h$[10]

$\frac{dI_t}{dt} = \lambda_t S_h - (\omega + \delta_t + \mu_h)I_t$[11]

$\frac{dR}{dt} = \omega I_t - \mu_h R$ [12]

with initial conditions$S_h(0) > 0, I_t(0) \geq 0, R(0) \geq 0$, force of infection$\lambda_t = \frac{\beta I_t}{N_h}$and total population$N_h = S_h + I_t + R$

3.1. Invariant Region, Boundedness andPositivityof Solutions for Typhoid Fever Sub-Model Only

The total human population is given by$N_h = S_h + I_t + R$. Then, differentiating both sides of this equation gives $\frac{dN_h}{dt} = \frac{dS_h}{dt} + \frac{dI_t}{dt} + \frac{dR}{dt}$.After substituting the corresponding values of the rates and simplifying the terms we obtain: $\frac{dN_h}{dt} = \Lambda_h - \mu_h N_h - \delta_t I_t$. It gives $\frac{dN_h}{dt} + \mu_h N_h \leq \Lambda_h$. Thus, $N_h(t) \leq \frac{\Lambda_h}{\mu_h} + (N_h(0) - \frac{\Lambda_h}{\mu_h})e^{-\mu_h t}$.Therefore, $\limsup_{t\to\infty} N_h(t) \leq \lim_{t\to\infty} sup\left(\frac{\Lambda_h}{\mu_h} + (N_h(0) - \frac{\Lambda_h}{\mu_h})e^{-\mu_h t}\right) = \frac{\Lambda_h}{\mu_h}$.

Hence, the system of the sub-model is bounded for the total human population $N_h$in the region: $\Omega_h = \left\{(S_h, I_t, R) \in \mathbb{R}_+^3 : 0 \leq N_h \leq \frac{\Lambda_h}{\mu_h}\right\}$ and hence, all solutions of the dynamical system are bounded in Ω_h.

Also, we have already proved in section 2.2above the positivity of the solutions of the population in the compartments $S_h, I_t \; and \; R$ and hence, all solutions of the dynamical system are positively invariant in the region Ω_h.

3.2. Disease-Free Equilibrium (DFE) Point for Typhoid Fever Sub-Model Only

The disease-free equilibrium (DFE) point is obtained when we assume that the susceptible populations do not consist of infected individuals. Hence, we have $I_t = R = 0$.To find this DFE point, we set the right hand side of the non-linear system of differential equations given by the sub-model [10-12]to zero. Thus, the DFE point of the sub-model is $E_0 = (\frac{\Lambda_h}{\mu_h}, 0, 0)$.

3.3. Basic Reproduction Number (R_{0t}) for Typhoid Fever Sub-Model Only

The basic reproduction number, R_{0t}, is defined as the average number of secondary infections caused by a single infectious individual, introduced into the entire susceptible populations, during his or her infectious period. We use the next generation matrix method to calculate R_{0t} for the system [10-12].When $R_{0t} < 1$, the disease will decline and eventually dies out. When $R_{0t} > 1$, the disease will spread in the population[10]. In the dynamical system [10-12]the rate of appearance of new infections $\mathcal{F}$and the transfer rate of individuals V at the disease free equilibrium point$E_0 = \left(\frac{\Lambda_h}{\mu_h}, 0, 0\right)$ are given by the following functions as:

$F = [\beta]$, $V = [\omega + \delta_t + \mu_h]$ and $V^{-1} = \left[\frac{1}{\omega+\delta_t+\mu_h}\right]$.

The basic reproduction number R_{0t} of the typhoid fever sub-model only is the largest eigenvalue of the next generation matrix $\mathcal{F}V^{-1}$ and given by $\rho(\mathcal{F}V^{-1}) = R_{0t} = \frac{\beta}{(\omega+\delta_t+\mu_h)} > 0$.

3.4. Local Stability of the Disease Free Equilibrium Point for Typhoid Fever Sub-Model Only

Theorem-2: The disease free equilibrium point E_0 of the typhoid fever sub-model is locally asymptotically stable (LAS) if $R_{0t} < 1$ and unstable if $R_{0t} > 1$.

Proof: The Jacobian matrix of the dynamical system [10-12]at E_0 is given by:

$$J(E_0) = \begin{bmatrix} -\mu_h & -\beta & 0 \\ 0 & \beta - (\omega + \delta_t + \mu_h) & 0 \\ 0 & \omega & -\mu_h \end{bmatrix}$$

The corresponding characteristic equation of the Jacobian matrix isobtained by:

$$\begin{vmatrix} -\mu_h - \lambda & -\beta & 0 \\ 0 & \beta - (\omega + \delta_t + \mu_h) - \lambda & 0 \\ 0 & \omega & -\mu_h - \lambda \end{vmatrix} = 0$$

Simplifying this determinant, we get:$(-\mu_h - \lambda)^2(\beta - (\omega + \delta_t + \mu_h) - \lambda) = 0$

Thus, the roots of this polynomial are given by:

$$\lambda_1 = -\mu_h < 0 \; or \; \lambda_2 = -\mu_h < 0 \;\; or \; \lambda_3 = \beta - (\omega + \delta_t + \mu_h) = (\omega + \delta_t + \mu_h)(R_{0t} - 1)$$

Hence, the DFE E_0 is locally asymptotically stable (LAS) if $R_{0t} < 1$. Otherwise, it is unstable if $R_{0t} > 1$.

3.5. Global Stability of the Disease Free Equilibrium Point for Typhoid Fever Sub-Model Only

Theorem-3: The disease free equilibrium point E_0 of the typhoid fever sub-model is globally asymptotically stable (GAS) if $R_{0t} < 1$.

Proof: We define a Lyapunov function$L: R_+^3 \longrightarrow R_+$ by$L(S_h, I_t, R) = \frac{1}{\omega+\delta_t+\mu_h} I_t$.

The function L and its partial derivatives with respect to the corresponding state variables are all continues. L has a minimum value at the DFE point $E_0 = (\frac{\Lambda_h}{\mu_h}, 0, 0)$ which is $L(E_0) = 0$.

Also, $\frac{dL}{dt} = \frac{dL}{dS_h}\frac{dS_h}{dt} + \frac{dL}{dI_t}\frac{dI_t}{dt} + \frac{dL}{dR}\frac{dR}{dt} = 0 + \frac{1}{\omega+\delta_t+\mu_h}\frac{dI_t}{dt} + 0 = \frac{1}{\omega+\delta_t+\mu_h}\frac{dI_t}{dt}$. After substituting for$\frac{dI_t}{dt}$and simplifying different expressions we obtain the value of $\frac{dL}{dt}$ at the DFE $E_0 = (\frac{\Lambda_h}{\mu_h}, 0, 0)$ as: $\frac{dL}{dt} = (R_{0t} - 1)I_t$.

Thus, $\frac{dL}{dt} < 0$ if $R_{0t} < 1$. Furthermore, $\frac{dL}{dt} = 0 \; if \; R_{0t} = 1 \; or \; I_t = 0$. Hence, L is a Lyapunov function. From this we conclude that the DFE E_0 is the only singleton in the region. That is, the largest invariant set contained in $\Omega_h = \left\{(S_h, I_t, R) \in \mathbb{R}_+^3 : \frac{dL}{dt} = 0\right\}$ is reduced to the DFE E_0. Therefore, the DFE E_0 is globally asymptotically stable (GAS) on Ω_h if $R_{0t} < 1$.

3.6. Existence of Endemic Equilibrium (EE) Point for Typhoid Fever Sub-Model Only

Endemic equilibrium points are steady state solutions where the disease persists in the population or community. To find this EE point, we set the right hand side of the non-linear system of differential equations given by [10-12] to zero. Therefore, the unique endemic equilibrium point of the typhoid fever sub-model is given by $E^* = (S_h^*, I_t^*, R^*) = \left(\frac{N_h}{R_{0t}}, \frac{R_{0t}\Lambda_h - \mu_h N_h}{\beta}, \frac{\omega(R_{0t}\Lambda_h - \mu_h N_h)}{\mu_h \beta}\right)$.

3.7. Local Stability of the Endemic Equilibrium (EE) Point for Typhoid Fever Sub-Model Only

Theorem-4: The endemic equilibrium point E^* of the typhoid fever sub-model [10-12] is locally asymptotically stable if$R_{0t} > 1$.

Proof: The Jacobian matrix of the dynamical system [10-12] at the EE point E^* is given by:

$$J(E^*) = \begin{bmatrix} \frac{-\Lambda_h R_{0t}}{N_h} & \frac{-\beta}{R_{0t}} & 0 \\ (\frac{\Lambda_h R_{0t}}{N_h} - \mu_h) & \frac{\beta}{R_{0t}} - e_1 & 0 \\ 0 & \omega & -\mu_h \end{bmatrix}, \text{ where } e_1 = (\omega + \delta_t + \mu_h)$$

The characteristic equation of the Jacobian matrix at the EE point E^* is

$$\begin{vmatrix} \frac{-\Lambda_h R_{0t}}{N_h} - \lambda & \frac{-\beta}{R_{0t}} & 0 \\ (\frac{\Lambda_h R_{0t}}{N_h} - \mu_h) & \frac{\beta}{R_{0t}} - e_1 - \lambda & 0 \\ 0 & \omega & -\mu_h - \lambda \end{vmatrix} = 0$$

After simplifying this determinant, we get: $(-\mu_h - \lambda)(\lambda^2 + \left(\frac{\Lambda_h R_{0t}}{N_h} - \frac{\beta}{R_{0t}} + e_1\right)\lambda + \frac{\Lambda_h R_{0t} e_1}{N_h} - \frac{\mu_h \beta}{R_{0t}}) = 0$

The first root (eigenvalue) of this polynomial is $\lambda_1 = -\mu_h < 0$ and the remaining two eigenvalues can be obtained from thequadratic equation part. We have proved that all coefficients of this quadratic equation are

positive and by Routh-Hurwitz criteria all roots of this quadratic equation have negative real parts. Therefore, the EE E^* is locally asymptotically stable (LAS) if $R_{0t} > 1$.

3.8. Global Stability of the Endemic Equilibrium Point for Typhoid Fever Sub-Model Only

Theorem-5: The endemic equilibrium E^* of the typhoid fever sub-model **(10-12)**is globally asymptotically stable if$R_{0t} > 1$.

Proof: We define a Lyapunov function $L: R_+^3 \longrightarrow R_+$ by

$L(S_h, I_t, R) = A\left(S_h - S_h^* + S_h^* ln\frac{S_h^*}{S_h}\right) + B\left(I_t - I_t^* + I_t^* ln\frac{I_t^*}{I_t}\right) + C\left(R - R^* + R^* ln\frac{R^*}{R}\right)$, where $A, B\ and\ C$ are positive constants to be determined later. Then,

The function L and its partial derivatives with respect to the corresponding state variables are all continues. L has a minimum value at the DFE point $E_0 = (\frac{\Lambda_h}{\mu_h}, 0, 0)$ which is $L(E_0) = 0$.

Also, $\frac{dL}{dt} = \frac{\partial L}{\partial S_h}\frac{dS_h}{dt} + \frac{\partial L}{\partial I_t}\frac{dI_t}{dt} + \frac{\partial L}{\partial R}\frac{dR}{dt} = A(1 - \frac{S_h^*}{S_h})\frac{dS_h}{dt} + B(1 - \frac{I_t^*}{I_t})\frac{dI_t}{dt} + C(1 - \frac{R^*}{R})\frac{dR}{dt}$

After substituting the values of$\frac{dS_h}{dt}, \frac{dI_t}{dt}\ and\ \frac{dR}{dt}$and simplifying different expressions we obtain the value of $\frac{dL}{dt}$ at the EE $E^* = (S_h^*, I_t^*, R^*)$as:

$$\frac{dL}{dt} = -[A(\lambda_t + \mu_h)\left(1 - \frac{S_h^*}{S_h}\right)^2 S_h + B(\omega + \delta_t + \mu_h)\left(1 - \frac{I_t^*}{I_t}\right)^2 I_t + C\mu_h\left(1 - \frac{R^*}{R}\right)^2 R] < 0$$

$\Longrightarrow \frac{dL}{dt} \leq 0$, for any positive values of $A, B\ and\ C$. Moreover, $\frac{dL}{dt} = 0$at the EE E^*.Thus, L is a Lyapunov function. From this we conclude that $E^* = (S_h^*, I_t^*, R^*)$ is the largest compact invariant singleton set in the region.Therefore, the endemic equilibrium point E^* is globally asymptotically stable (GAS) in the invariant region if $R_{0t} > 1$.

IV. The Dynamics of Plasmodium Falciparum Sub-Model Only

Using the fullmodel [1-9],the plasmodium falciparum sub-model dynamics is obtained by setting$I_t = R = C_{ft} = T_{ft} = 0$ and is given by

$\frac{dS_h}{dt} = \Lambda_h - (\lambda_{hf} + \mu_h)S_h$ [13]

$\frac{dI_{hf}}{dt} = \lambda_{hf}S_h - (\varepsilon + \delta_f + \mu_h)I_{hf}$ [14]

$\frac{dT_f}{dt} = \varepsilon I_{hf} - \mu_h T_f$ [15]

$\frac{dS_m}{dt} = \Lambda_m - (\lambda_{mf} + \mu_m)S_m$ [16]

$\frac{dI_{mf}}{dt} = \lambda_{mf}S_m - \mu_m I_{mf}$ [17]

, with initial conditions $S_h > 0,\ I_{hf} \geq 0, T_f \geq 0, S_m > 0, I_{mf} \geq 0$, force of infections $\lambda_{hf} = \frac{a_2 b I_{mf}}{N_h}and\lambda_{mf} = \frac{a_4 b I_{hf}}{N_h}$and total human population $N_h = S_h + I_{hf} + T_f$, total mosquito population $N_m = S_m + I_{mf}$.

4.1. Invariant Region,Boundedness and Positivity of solutions

The total human population is $N_h = S_h + I_{hf} + T_f$ .Then, $\frac{dN_h}{dt} = \frac{dS_h}{dt} + \frac{dI_{hf}}{dt} + \frac{dT_f}{dt}$.After substituting and simplifying different terms we get:$\frac{dN_h}{dt} + \mu_h N_h \leq \Lambda_h$ .Thus, $N_h(t) \leq \frac{\Lambda_h}{\mu_h} + (N_h(0) - \frac{\Lambda_h}{\mu_h})e^{-\mu_h t}$.

Therefore, $\lim_{t\to\infty} sup\ N_h(t) \leq \lim_{t\to\infty} sup\left(\frac{\Lambda_h}{\mu_h} + (N_h(0) - \frac{\Lambda_h}{\mu_h})e^{-\mu_h t}\right) = \frac{\Lambda_h}{\mu_h}$.

Hence, the system of the sub-model is bounded for the total human population $N_h$in the region: $\Omega_h = \left\{(S_h, I_{hf}, T_f) \in \mathbb{R}_+^3 : 0 \leq N_h \leq \frac{\Lambda_h}{\mu_h}\right\}$.

Similarly, the total mosquito population is $N_m = S_m + I_{mf}$. Then,$\frac{dN_m}{dt} = \frac{dS_m}{dt} + \frac{dI_{mf}}{dt}$. After substituting and simplifying different terms we get:$\frac{dN_m}{dt} + \mu_m N_m \leq \Lambda_m$.This implies that $N_m(t) \leq \frac{\Lambda_m}{\mu_m} + (N_m(0) - \frac{\Lambda_m}{\mu_m})e^{-\mu_m t}$.

Therefore, $\lim_{t\to\infty} sup N_m(t) \leq \lim_{t\to\infty} sup\left(\frac{\Lambda_m}{\mu_m} + (N_m(0) - \frac{\Lambda_m}{\mu_m})e^{-\mu_h t}\right) = \frac{\Lambda_m}{\mu_m}$

Hence, the system of the sub-model is bounded for the total mosquito population $N_m$in the region: $\Omega_m = \left\{(S_m, I_{mf}) \in \mathbb{R}_+^2 : 0 \leq N_m \leq \frac{\Lambda_m}{\mu_m}\right\}$.

From Ω_h and $\Omega_m$we can see that the sub-model for Plasmodium falciparum malaria is well posed epidemiologically and mathematically. So, we can study the dynamics of the sub-model in the region:$\Omega = \Omega h \text{X}\ \Omega m \subset \mathbb{R}+3\text{X}\mathbb{R}+2 = Sh, Ihf, Tf, Sm, Imf \in \mathbb{R}+5 : 0 \leq Nh \leq \Lambda h \mu h; 0 \leq Nm \leq \Lambda m \mu m.$

Therefore, the total human population N_h and the total mosquito population N_m are bounded in the region Ω and hence, all solutions of the dynamical system are bounded (i.e. all solutions with initial conditions in Ω remain in Ω for all time $t > 0$).Also, we have already proved in section 2.2above the positivity of the solutions of the population in all compartments and hence, all solutions of the dynamical system are positively invariant in the regionΩ.

4.2. Disease-Free Equilibrium (DFE) Point for Plasmodium Falciparum Sub-Model Only

The disease-free equilibrium (DFE) point of the sub-model [13-17]is obtained by setting$I_{hf} = T_f = I_{mf} = 0$ and is given by $E_0 = \left(\frac{\Lambda_h}{\mu_h}, 0, 0, \frac{\Lambda_m}{\mu_m}, 0\right)$.

4.3. Basic Reproduction Number (R_{0f}) for P. Falciparum Sub-Model Only

Using the next generation matrix we will obtain the reproduction numberR_{0f} of the sub-model.In the dynamical system [13-17]the rate of appearance of new infections $\mathcal{F}$and the transfer rate of individuals V at the disease free equilibrium point $E_0 = \left(\frac{\Lambda_h}{\mu_h}, 0, 0, \frac{\Lambda_m}{\mu_m}, 0\right)$ are given by the following functions as:$F = \begin{bmatrix} 0 & a_2 b \\ \frac{a_4 b \mu_h \Lambda_m}{\mu_m \Lambda_h} & 0 \end{bmatrix}$, $V = \begin{bmatrix} (\varepsilon + \delta_f + \mu_h) & 0 \\ 0 & \mu_m \end{bmatrix}andV^{-1} = \begin{bmatrix} \frac{1}{(\varepsilon+\delta_f+\mu_h)} & 0 \\ 0 & \frac{1}{\mu_m} \end{bmatrix}$

The basic reproduction number R_{0f} of the plasmodium falciparum sub-model only is the largest eigenvalue of the next generation matrix $\mathcal{F}V^{-1}$and given by $\rho(\mathcal{F}V^{-1}) = R_{0f} = \sqrt{\frac{a_2 a_4 b^2 \mu_h \Lambda_m}{\mu_m^2 \Lambda_h (\varepsilon+\delta_f+\mu_h)}} > 0$.

4.4. Local Stability of the Disease Free Equilibrium point for Falciparum Sub-Model Only

Theorem-6: The disease free equilibrium point is locally asymptotically stable if $R_{0f} < 1$ and unstable if$R_{0f} > 1$.

Proof: The Jacobian matrix of the dynamical system [13-17]at the DFE pointE_0 is given by:

$$J(E_0) = \begin{bmatrix} -\mu_h & 0 & 0 & 0 & -a_2 b \\ 0 & -(\varepsilon + \delta_f + \mu_h) & 0 & 0 & a_2 b \\ 0 & \varepsilon & -\mu_h & 0 & 0 \\ 0 & -\frac{a_4 b \mu_h \Lambda_m}{\mu_m \Lambda_h} & 0 & -\mu_m & 0 \\ 0 & \frac{a_4 b \mu_h \Lambda_m}{\mu_m \Lambda_h} & 0 & 0 & -\mu_m \end{bmatrix}$$

The corresponding characteristic equation of the Jacobian matrix isobtained by:

$$\begin{vmatrix} -\mu_h - \lambda & 0 & 0 & 0 & -a_2 b \\ 0 & -(\varepsilon + \delta_f + \mu_h) - \lambda & 0 & 0 & a_2 b \\ 0 & \varepsilon & -\mu_h - \lambda & 0 & 0 \\ 0 & -\frac{a_4 b \mu_h \Lambda_m}{\mu_m \Lambda_h} & 0 & -\mu_m - \lambda & 0 \\ 0 & \frac{a_4 b \mu_h \Lambda_m}{\mu_m \Lambda_h} & 0 & 0 & -\mu_m - \lambda \end{vmatrix} = 0$$

Simplifying this determinant gives:

$$(-\mu_h - \lambda)(-\mu_m - \lambda)(-\mu_m - \lambda)[\lambda^2 + (\varepsilon + \delta_f + \mu_h + \mu_m)\lambda + (\varepsilon + \delta_f + \mu_h)\mu_m - \frac{a_2 a_4 b^2 \mu_h \Lambda_m}{\mu_m \Lambda_h}] = 0$$

$$\Longrightarrow \lambda_1 = -\mu_h,\ \lambda_2 = \lambda_3 = -\mu_m \text{ or } \lambda_4 = \frac{-(\varepsilon+\delta_f+\mu_h+\mu_m) - \sqrt{(\varepsilon+\delta_f+\mu_h+\mu_m)^2 - 4((\varepsilon+\delta_f+\mu_h)\mu_m - \frac{a_2 a_4 b^2 \mu_h \Lambda_m}{\mu_m \Lambda_h})}}{2} \text{ or} \lambda_5 = \frac{-(\varepsilon+\delta_f+\mu_h+\mu_m) + \sqrt{(\varepsilon+\delta_f+\mu_h+\mu_m)^2 - 4((\varepsilon+\delta_f+\mu_h)\mu_m - \frac{a_2 a_4 b^2 \mu_h \Lambda_m}{\mu_m \Lambda_h})}}{2}$$

From these eigenvalues we can see that $\lambda_1, \lambda_2, \lambda_3$ *and* λ_4 are all less than zero. So, the DFE will be stable if $\lambda_5 < 0$. Then, $\frac{-(\varepsilon+\delta_f+\mu_h+\mu_m) + \sqrt{(\varepsilon+\delta_f+\mu_h+\mu_m)^2 - 4((\varepsilon+\delta_f+\mu_h)\mu_m - \frac{a_2 a_4 b^2 \mu_h \Lambda_m}{\mu_m \Lambda_h})}}{2} < 0$

Simplifying this inequality gives: $\sqrt{\frac{a_2 a_4 b^2 \mu_h \Lambda_m}{(\varepsilon+\delta_f+\mu_h)\mu_m^2 \Lambda_h}} < 1$. It implies that$R_{0f} < 1$.

Therefore, the DFE E_0 is locally asymptotically stable if $R_{0f} < 1$ and unstable if $R_{0f} > 1$.

4.5. Global Stability of the Disease Free Equilibrium point for P. Falciparum Sub-Model Only

Theorem-7: The disease free equilibrium point is globally asymptotically stable if $R_{0f} < 1$.

Proof: We define a Lyapunov function $L: R_+^5 \longrightarrow R_+$by

$L(S_h, I_{hf}, T_f, S_m, I_{mf}) = C\left(S_h - S_h^* + S_h^* ln\frac{S_h^*}{S_h}\right) + I_{hf} + T_f + D\left(S_m - S_m^* + S_m^* ln\frac{S_m^*}{S_m}\right) + I_{mf}$, where C *and* D are positive constants to be determined later.

The function L and its partial derivatives with respect to the corresponding state variables are all continues. L has a minimum value at the DFE point $E_0 = \left(\frac{\Lambda_h}{\mu_h}, 0, 0, \frac{\Lambda_m}{\mu_m}, 0\right)$which is $L(E_0) = 0$.

Also, $\frac{dL}{dt} = \frac{\partial L}{\partial S_h}\frac{dS_h}{dt} + \frac{\partial L}{\partial I_{hf}}\frac{dI_{hf}}{dt} + \frac{\partial L}{\partial T_f}\frac{dT_f}{dt} + \frac{\partial L}{\partial S_m}\frac{dS_m}{dt} + \frac{\partial L}{\partial I_{mf}}\frac{dI_{mf}}{dt}$

$$\Longrightarrow \frac{dL}{dt} = C\left(1 - \frac{S_h^*}{S_h}\right)\frac{dS_h}{dt} + 1\frac{dI_{hf}}{dt} + 1\frac{dT_f}{dt} + D\left(1 - \frac{S_m^*}{S_m}\right)\frac{dS_m}{dt} + 1\frac{dI_{mf}}{dt}$$

After substituting the values of $\frac{dS_h}{dt}, \frac{dI_{hf}}{dt}, \frac{dT_f}{dt}, \frac{dS_m}{dt}$ *and* $\frac{dI_{mf}}{dt}$and simplifying different expressions we obtain the value of $\frac{dL}{dt}$ at the DFE point $E_0 = \left(\frac{\Lambda_h}{\mu_h}, 0, 0, \frac{\Lambda_m}{\mu_m}, 0\right)$ as:

$$\frac{dL}{dt}(E_0) = -[C\left(1 - \frac{S_h^*}{S_h}\right)^2(\lambda_{hf} + \mu_h)S_h + D\left(1 - \frac{S_m^*}{S_m}\right)^2(\lambda_{mf} + \mu_m)S_m]$$

Thus,$\frac{dL}{dt} \leq 0$, for any positive constants C *and* D. Furthermore, $\frac{dL}{dt} = 0$ at the DFE point E_0. Hence, L is a Lyapunov function. From this we conclude that the DFE E_0 is the only singleton in the region. That is, the largest invariant set contained in the region $\Omega_h = \left\{(S_h, I_{hf}, T_f, S_m, I_{mf}) \in \mathbb{R}_+^5 : \frac{dL}{dt} = 0\right\}$ is reduced to the DFE E_0. Therefore, the DFE E_0 is globally asymptotically stable (GAS) on Ω_h if $R_{0f} < 1$.

4.6. Existence of Endemic Equilibrium (EE) Point for P. Falciparum Sub-Model Only

Endemic equilibrium points are steady state solutions where the disease persists in the population or community. To find this EE point, we set the right hand side of the non-linear system of differential equations given by [13-17] to zero. Then, an arbitrary endemic equilibrium point E^* is given by $E^* = (S_h^*, I_{hf}^*, T_f^*, S_m^*, I_{mf}^*)$, where

$S_h^* = \frac{N_{0h}N_h(a_4 b\Lambda_h + N_h\mu_m e)}{\mu_m e N_{0h}^2 R_{0f}^2 + N_h a_4 b\Lambda_h}, I_{hf}^* = \frac{N_{0h}\mu_h\mu_m(N_{0h}^2R_{0f}^2 - N_h^2)}{\mu_m e N_{0h}^2 R_{0f}^2 + N_h a_4 b\Lambda_h}, T_f^* = \frac{\varepsilon N_{0h}\mu_m(N_{0h}^2R_{0f}^2 - N_h^2)}{\mu_m e N_{0h}^2 R_{0f}^2 + N_h a_4 b\Lambda_h}$

$S_m^* = \frac{\Lambda_m N_h(\mu_m e N_{0h}^2 R_{0f}^2 + N_h a_4 b\Lambda_h)}{a_4 b N_{0h}\mu_h\mu_m(N_{0h}^2R_{0f}^2 - N_h^2) + \mu_m N_h(\mu_m e N_{0h}^2 R_{0f}^2 + N_h a_4 b\Lambda_h)}$ & $I_{mf}^* = \frac{\Lambda_m a_4 b N_{0h}\mu_h(N_{0h}^2R_{0f}^2 - N_h^2)}{a_4 b N_{0h}\mu_h\mu_m(N_{0h}^2R_{0f}^2 - N_h^2) + \mu_m N_h(\mu_m e N_{0h}^2 R_{0f}^2 + N_h a_4 b\Lambda_h)}$

4.7. Local Stability of the Endemic Equilibrium (EE) Point for P. Falciparum Sub-Model Only

Theorem-8: The endemic equilibrium point E^* of the plasmodium falciparum sub-model **(13-17)** is locally asymptotically stable if$R_{0f} > 1$.

Proof: The Jacobian matrix of the dynamical system [13-17]at the EE point $E^*$is given by:

$$J(E^*) = \begin{bmatrix} -(\frac{a_2 b I_{mf}^*}{N_h} + \mu_h) & 0 & 0 & 0 & -\frac{a_2 b S_h^*}{N_h} \\ \frac{a_2 b I_{mf}^*}{N_h} & -e & 0 & 0 & \frac{a_2 b S_h^*}{N_h} \\ 0 & \varepsilon & -\mu_h & 0 & 0 \\ 0 & -\frac{a_4 b S_m^*}{N_h} & 0 & -(\frac{a_4 b I_{hf}^*}{N_h} + \mu_m) & 0 \\ 0 & \frac{a_4 b S_m^*}{N_h} & 0 & \frac{a_4 b I_{hf}^*}{N_h} & -\mu_m \end{bmatrix}$$,where $e = \varepsilon + \delta_f + \mu_h$

The characteristic equation of the Jacobian matrix at the EE point E^* is

$$\begin{vmatrix} -(\frac{a_2 bI^*_{mf}}{N_h} + \mu_h) - \lambda & 0 & 0 & 0 & -\frac{a_2 bS^*_h}{N_h} \\ \frac{a_2 bI^*_{mf}}{N_h} & -e-\lambda & 0 & 0 & \frac{a_2 bS^*_h}{N_h} \\ 0 & \varepsilon & -\mu_h - \lambda & 0 & 0 \\ 0 & -\frac{a_4 bS^*_m}{N_h} & 0 & -(\frac{a_4 bI^*_{hf}}{N_h} + \mu_m) - \lambda & 0 \\ 0 & \frac{a_4 bS^*_m}{N_h} & 0 & \frac{a_4 bI^*_{hf}}{N_h} & -\mu_m - \lambda \end{vmatrix} = 0$$

Simplifying this determinant gives:$(-\mu_h - \lambda)(\mu_m + \lambda)(\lambda^3 + A_2\lambda^2 + A_1\lambda + A_0) = 0$, where

$A_0 = \frac{a_2 bI^*_{mf}}{N_h}(\frac{a_4 bI^*_{hf}}{N_h} + \mu_m)e + \frac{a_4 bI^*_{hf}}{N_h}\mu_h e + \mu_m\mu_h e - \mu_h\frac{a_2 a_4 b^2 S^*_h S^*_m}{N_h^2}$,

$A_1 = (\frac{a_2 bI^*_{mf}}{N_h} + \mu_h)(\frac{a_4 bI^*_{hf}}{N_h} + \mu_m + e) + \frac{a_4 bI^*_{hf}}{N_h}e + \mu_m e - \frac{a_2 a_4 b^2 S^*_h S^*_m}{N_h^2}$and

$A_2 = \frac{a_2 bI^*_{mf}}{N_h} + \mu_h + \frac{a_4 bI^*_{hf}}{N_h} + \mu_m + e$ .As indicated above, $S^*_h, I^*_{hf}, S^*_m, I^*_{mf} > 0$.

The first two roots (eigenvalues) of this polynomial are$\lambda_1 = -\mu_h < 0 \; and \; \lambda_2 = -\mu_m < 0$ and the remaining three eigenvalues can be obtained from the cubic polynomial part. We have proved that all coefficients of this cubic polynomial are positive and by Routh-Hurwitz criteria all roots of this cubic polynomial have negative real parts. Therefore, the EE E^* is locally asymptotically stable (LAS) if $R_{0f} > 1$.

4.8. Global Stability of the Endemic Equilibrium Point for P. Falciparum Sub-Model Only

Theorem-9: The endemic equilibrium E^* of the plasmodium falciparum sub- model [13-17]is globally asymptotically stable if$R_{0f} > 1$.

Proof: We define a Lyapunov function $L: R^5_+ \longrightarrow R_+byL(S_h, I_{hf}, T_f, S_m, I_{mf}) = A\left(S_h - S^*_h + S^*_h ln\frac{S^*_h}{S_h}\right) +$

$B\left(I_{hf} - I^*_{hf} + I^*_{hf} ln\frac{I^*_{hf}}{I_{hf}}\right) + C\left(T_f - T^*_f + T^*_f ln\frac{T^*_f}{T_f}\right) + D\left(S_m - S^*_m + S^*_m ln\frac{S^*_m}{S_m}\right) + E\left(I_{mf} - I^*_{mf} + I^*_{mf} ln\frac{I^*_{mf}}{I_{mf}}\right)$

where $A, B, C, D \; and \; E$are positive constants to be determined later.

The function L and its partial derivatives with respect to the corresponding state variables are all continues. L has a minimum value at the EE point E^*which is $L(E^*) = 0$.

Also, $\frac{dL}{dt} = A\frac{\partial L}{\partial S_h}\frac{dS_h}{dt} + B\frac{\partial L}{\partial I_{hf}}\frac{dI_{hf}}{dt} + C\frac{\partial L}{\partial T_f}\frac{dT_f}{dt} + D\frac{\partial L}{\partial S_m}\frac{dS_m}{dt} + E\frac{\partial L}{\partial I_{mf}}\frac{dI_{mf}}{dt}$

$\Longrightarrow \frac{dL}{dt} = A(1 - \frac{S^*_h}{S_h})\frac{dS_h}{dt} + B(1 - \frac{I^*_{hf}}{I_{hf}})\frac{dI_{hf}}{dt} + C(1 - \frac{T^*_f}{T_f})\frac{dT_f}{dt} + D(1 - \frac{S^*_m}{S_m})\frac{dS_m}{dt} + E(1 - \frac{I^*_{mf}}{I_{mf}})\frac{dI_{mf}}{dt}$After substituting the corresponding values of $\frac{dS_h}{dt}, \frac{dI_{hf}}{dt}, \frac{dT_f}{dt}, \frac{dS_m}{dt} \; and \; \frac{dI_{mf}}{dt}$and simplifying different terms, the value of $\frac{dL}{dt}$ at the EE point E^* will be:

$$\frac{dL}{dt} = -[A\left(1 - \frac{S^*_h}{S_h}\right)^2(\lambda_{hf} + \mu_h)S_h + B\left(1 - \frac{I^*_{hf}}{I_{hf}}\right)^2(\varepsilon + \delta_f + \mu_h)I_{hf} + C\left(1 - \frac{T^*_f}{T_f}\right)^2\mu_h T_f +$$
$$D\left(1 - \frac{S^*_m}{S_m}\right)^2(\lambda_{mf} + \mu_m)S_m + E\left(1 - \frac{I^*_{mf}}{I_{mf}}\right)^2\mu_m I_{mf}]$$

Thus,$\frac{dL}{dt} \leq 0$ for any positive values of $A, B, C, D \; and \; E$. Furthermore, $\frac{dL}{dt} = 0$at the EE point E^*. Hence, L is a Lyapunov function. From this we conclude that $E^*$is the largest compact invariant singleton set in the region. Therefore, the endemic equilibrium point E^* is globally asymptotically stable (GAS) in the invariant region if $R_{0f} > 1$.

V. The Full Dynamics of the Co-Infection of P.Falciparum and Typhoid Fever Model

After we analyzed the dynamics of the two sub-models, that is, Typhoid Fever-only and Plasmodium Falciparum-only models, the full typhoid Fever and malaria co-infection model [1-9]will be considered and analyzed in the positively invariant region Ω.

5.1. Disease-Free Equilibrium Point for Co-Infection of Malaria and Typhoid Fever Model

The disease-free equilibrium (DFE) point of the non-linear system of differential equations given by **(1-9)** is obtained by setting $I_t = R = I_{hf} = C_{ft} = T_{ft} = T_f = I_{mf} = 0$.Thus, we get the disease-free equilibrium (DFE) point as $E_0 = \left(\frac{\Lambda_h}{\mu_h}, 0, 0, 0, 0, 0, \frac{\Lambda_m}{\mu_m}, 0\right)$.

5.2. The Basic Reproduction Number (R_0) for the Co-Infection of P.Falciparum and Typhoid Fever Model

Using the next generation matrix we will obtain the co-infection reproduction numberR_0 of the model [1-9]. In the dynamical system [1-9]the rate of appearance of new infections $\mathcal{F}$and the transfer rate of individuals V at the disease free equilibrium point $E_0 = (\frac{\Lambda_h}{\mu_h}, 0, 0, 0, 0, 0, 0, \frac{\Lambda_m}{\mu_m}, 0)$ are given by the following functions as:F $=$

$$\begin{bmatrix} \beta & 0 & 0 \\ 0 & 0 & a_2 b \\ 0 & \frac{a_4 b \mu_h \Lambda_m}{\mu_m \Lambda_h} & 0 \end{bmatrix}, \text{V} = \begin{bmatrix} e_1 & 0 & 0 \\ 0 & e_3 & 0 \\ 0 & 0 & \mu_m \end{bmatrix} \text{ and } \text{V}^{-1} = \begin{bmatrix} \frac{1}{e_1} & 0 & 0 \\ 0 & \frac{1}{e_3} & 0 \\ 0 & 0 & \frac{1}{\mu_m} \end{bmatrix}$$

Hence, the basic reproduction number R_0 of the full dynamics of theco-infection of Plasmodiumfalciparum and typhoid fever is the largest eigenvalue of the next generation matrix $\mathcal{F}V^{-1}$ or the spectral radius of $\mathcal{F}V^{-1}$ and given by $R_0 = Max\{R_{0t}, R_{0f}\}$,where $R_{0t} = \frac{\beta}{(\omega + \delta_t + \mu_h)}$which is the reproduction number for typhoid fever and $R_{0f} = \sqrt{\frac{a_2 a_4 b^2 \mu_h \Lambda_m}{\mu_m^2 \Lambda_h (\varepsilon + \delta_f + \mu_h)}}$ that is the reproduction number for plasmodium falciparum.

5.3. Local Stability of the Disease Free Equilibrium (DFE) Point for Co-Infection of P.Falciparum and Typhoid Fever Model

Theorem-10: The disease free equilibrium point E_0 of the co-infection of p. falciparum and typhoid fever is locally asymptotically stable (LAS) if $R_0 < 1$ and unstable if $R_0 > 1$.

Proof: The Jacobian Matrix of the model at the disease free equilibrium $E_0$is given by

$$J(E_0) = \begin{bmatrix} -\mu_h & -\beta & 0 & 0 & 0 & 0 & 0 & 0 & -a_2 b \\ 0 & \beta - e_1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & \omega & -\mu_h & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & -e_3 & 0 & 0 & 0 & 0 & a_2 b \\ 0 & 0 & 0 & 0 & -e_5 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & \phi_2 & -\mu_h & 0 & 0 & 0 \\ 0 & 0 & 0 & \varepsilon & 0 & 0 & -\mu_h & 0 & 0 \\ 0 & 0 & 0 & \frac{-a_4 b \mu_h \Lambda_m}{\mu_m \Lambda_h} & \frac{-a_4 b \eta_2 \mu_h \Lambda_m}{\mu_m \Lambda_h} & 0 & 0 & -\mu_m & 0 \\ 0 & 0 & 0 & \frac{a_4 b \mu_h \Lambda_m}{\mu_m \Lambda_h} & \frac{a_4 b \eta_2 \mu_h \Lambda_m}{\mu_m \Lambda_h} & 0 & 0 & 0 & -\mu_m \end{bmatrix}$$

The corresponding characteristic equation of the Jacobian matrix is

$$\begin{vmatrix} -\mu_h - \lambda & -\beta & 0 & 0 & 0 & 0 & 0 & 0 & -a_2 b \\ 0 & \beta - e_1 - \lambda & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & \omega & -\mu_h - \lambda & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & -e_3 - \lambda & 0 & 0 & 0 & 0 & a_2 b \\ 0 & 0 & 0 & 0 & -e_5 - \lambda & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & \phi_2 & -\mu_h - \lambda & 0 & 0 & 0 \\ 0 & 0 & 0 & \varepsilon & 0 & 0 & -\mu_h - \lambda & 0 & 0 \\ 0 & 0 & 0 & \frac{-a_4 b \mu_h \Lambda_m}{\mu_m \Lambda_h} & \frac{-a_4 b \eta_2 \mu_h \Lambda_m}{\mu_m \Lambda_h} & 0 & 0 & -\mu_m - \lambda & 0 \\ 0 & 0 & 0 & \frac{a_4 b \mu_h \Lambda_m}{\mu_m \Lambda_h} & \frac{a_4 b \eta_2 \mu_h \Lambda_m}{\mu_m \Lambda_h} & 0 & 0 & 0 & -\mu_m - \lambda \end{vmatrix} = 0$$

Simplifying this determinant gives

$$(-\mu_h - \lambda)^4 (\beta - e_1 - \lambda)(-e_5 - \lambda)(-\mu_m - \lambda)\left([(e_3 + \lambda)(\mu_m + \lambda) - \frac{a_2 a_4 b^2 \mu_h \Lambda_m}{\mu_m \Lambda_h}] \right) = 0$$

$\Longrightarrow \lambda_1 = \lambda_2 = \lambda_3 = \lambda_4 = -\mu_h < 0, \lambda_5 = \beta - e_1, \lambda_6 = -e_5 < 0, \lambda_7 = -\mu_m < 0,$

$\lambda_8 = \frac{-(e_3 + \mu_m)}{2} - \sqrt{\frac{(e_3 - \mu_m)^2}{4} + \frac{a_2 a_4 b^2 \mu_h \Lambda_m}{\mu_m \Lambda_h}} < 0$ Or $\lambda_9 = \frac{-(e_3 + \mu_m)}{2} + \sqrt{\frac{(e_3 - \mu_m)^2}{4} + \frac{a_2 a_4 b^2 \mu_h \Lambda_m}{\mu_m \Lambda_h}}$, where$e_3 = \varepsilon + \delta_f + \mu_h$.

From these eigenvalues we can see that $\lambda_1, \lambda_2, \lambda_3, \lambda_4, \lambda_6, \lambda_7 \; and \; \lambda_8$are all less than zero. So, the DFE will be stable if $\lambda_5 < 0 \; and \; \lambda_9 < 0$. Then, $\lambda_5 = \beta - e_1 = e_1(\frac{\beta}{e_1} - 1) = e_1(R_{0t} - 1) < 0$ if $R_{0t} < 1$.Next, we

have$\frac{-(e_3+\mu_m)}{2}+\sqrt{\frac{(e_3-\mu_m)^2}{4}+\frac{a_2a_4b^2\mu_h\Lambda_m}{\mu_m\Lambda_h}}<0$.Simplifying this gives$\sqrt{\frac{a_2a_4b^2\mu_h\Lambda_m}{\mu_m^2\Lambda_h(\varepsilon+\delta_f+\mu_h)}}<1$. Hence,$R_{0f}<1$.
Therefore, $R_0<1$ if $R_{0t}<1\ and\ R_{0f}<1$.
Finally, the DFE E_0 of the co-infection of Plasmodiumfalciparum and typhoid fever is locally asymptotically stable (LAS) if $R_0<1$ and unstable if $R_0>1$.

5.4. Global Stability of the Disease Free Equilibrium (DFE) Point for Co-Infection of Malaria and Typhoid Fever Model

Theorem-11: The disease free equilibrium E_0 of theco-infection of malaria and typhoid fever is globally asymptotically stable (GAS) if $R_0<1$.

Proof: We define a Lyapunov function $L: R_+^9\longrightarrow R_+byL(S_h,I_t,R,I_{hf},C_{ft},T_{ft},T_f,S_m,I_{mf})=A\left(S_h-S_h^*+\right.$
$\left.Sh*lnSh*Sh+It+R+Ihf+Cft+Tft+Tf+B(Sm-Sm*+Sm*lnSm*Sm)+Imf\right.$

The function L and its partial derivatives with respect to the corresponding state variables are all continues. L has a minimum value at the DFE point $E_0=\left(\frac{\Lambda_h}{\mu_h},0,0,0,0,0,0,\frac{\Lambda_m}{\mu_m},0\right)$ which is $L(E_0)=0$.Also, $\frac{dL}{dt}=$
$\frac{\partial L}{\partial S_h}\frac{dS_h}{dt}+\frac{\partial L}{\partial I_t}\frac{dI_t}{dt}+\frac{\partial L}{\partial R}\frac{dR}{dt}+\frac{\partial L}{\partial I_{hf}}\frac{dI_{hf}}{dt}+\frac{\partial L}{\partial C_{ft}}\frac{dC_{ft}}{dt}+\frac{\partial L}{\partial T_{ft}}\frac{dT_{ft}}{dt}+\frac{\partial L}{\partial T_f}\frac{dT_f}{dt}+\frac{\partial L}{\partial S_m}\frac{dS_m}{dt}+\frac{\partial L}{\partial I_{mf}}\frac{dI_{mf}}{dt}$
$\Longrightarrow\frac{dL}{dt}=A(1-\frac{S_h^*}{S_h})\frac{dS_h}{dt}+1\frac{dI_t}{dt}+1\frac{dR}{dt}+1\frac{dI_{hf}}{dt}+1\frac{dC_{ft}}{dt}+1\frac{dT_{ft}}{dt}+1\frac{dT_f}{dt}+B(1-\frac{S_m^*}{S_m})\frac{dS_m}{dt}+1\frac{dI_{mf}}{dt}$
Substituting the corresponding values of $\frac{dS_h}{dt},\frac{dI_t}{dt},\frac{dR}{dt},\frac{dI_{hf}}{dt},\frac{dC_{ft}}{dt},\frac{dT_{ft}}{dt},\frac{dT_f}{dt},\frac{dS_m}{dt},and\ \frac{dI_{mf}}{dt}$and
simplifyingdifferent expressionsgives$\frac{dL}{dt}=-\left[A\left(1-\frac{S_h^*}{S_h}\right)^2e_1S_h+B\left(1-\frac{S_m^*}{S_m}\right)^2e_6S_m\right]$.
Thus, $\frac{dL}{dt}\leq 0$, for any positive constants $A\ and\ B$. Furthermore, $\frac{dL}{dt}=0$at the DFE point E_0. Hence, L is a Lyapunov function. From this we conclude that the DFE E_0 is the only singleton in the region. That is, the largest invariant set contained in$\Omega=\left\{(S_h,I_t,R,\dots,I_{mf})\in\mathbb{R}_+^9:\frac{dL}{dt}=0\right\}$ is reduced to the DFE E_0.Therefore, the DFE E_0 is globally asymptotically stable on Ω if$R_0<1$.

5.5. Existence of Endemic Equilibrium (EE) Point for Co-Infection of p.falciparum and Typhoid Fever Model

To determine the endemic equilibrium point of the dynamical system [1-9]we make the right hand side of the dynamical system equal to zero and we solve for the state variables in terms of positive force of infections and other parameters. Then, we obtained the endemic equilibrium point
$E^*=\left(S_h^*,I_t^*,R^*,\ I_{hf}^*,\ C_{ft}^*,T_{ft}^*,\ T_f^*,S_m^*,\ I_{mf}^*\right)$ where,$S_h^*=\frac{\Lambda_h}{\lambda_{hf}^*+\lambda_t^*+\mu_h}$, $I_t^*=\frac{\Lambda_h\lambda_t^*}{(\alpha_2\lambda_{hf}^*+e_1)(\lambda_{hf}^*+\lambda_t^*+\mu_h)}$, $R^*=$
$\frac{\omega\Lambda_h\lambda_t^*}{\mu_h(\alpha_2\lambda_{hf}^*+e_1)(\lambda_{hf}^*+\lambda_t^*+\mu_h)}$, $I_{hf}^*=\frac{\Lambda_h\lambda_{hf}^*}{(\gamma\lambda_t^*+e_3)(\lambda_{hf}^*+\lambda_t^*+\mu_h)}$,$C_{ft}^*=\frac{\Lambda_h\lambda_{hf}^*\lambda_t^*}{e_5(\lambda_{hf}^*+\lambda_t^*+\mu_h)}\left(\frac{\gamma}{(\gamma\lambda_t^*+e_3)}+\frac{\alpha_2}{(\alpha_2\lambda_{hf}^*+e_1)}\right)$
$,T_{ft}^*=\frac{\phi_2\Lambda_h\lambda_{hf}^*\lambda_t^*}{\mu_he_5(\lambda_{hf}^*+\lambda_t^*+\mu_h)}\left(\frac{\gamma}{(\gamma\lambda_t^*+e_3)}+\frac{\alpha_2}{(\alpha_2\lambda_{hf}^*+e_1)}\right)$, $T_f^*=\frac{\varepsilon\Lambda_h\lambda_{hf}^*}{\mu_h(\lambda_{hf}^*+\lambda_t^*+\mu_h)(\gamma\lambda_t^*+e_3)}$, $S_m^*=\frac{\Lambda_m}{\lambda_{mf}^*+\mu_m}$, $I_{mf}^*=$
$\frac{\Lambda_m\lambda_{mf}^*}{\mu_m(\lambda_{mf}^*+\mu_m)}$, with $e_1=\omega+\delta_t+\mu_h$,$e_3=\varepsilon+\delta_f+\mu_h$ and $e_5=\phi_2+\theta_2\delta_{ft}+\mu_h$.
After substituting appropriate values of one into the other and simplifying expressions we get
$\lambda_{hf}^*[A_1(\lambda_{hf}^*)^2+A_2\lambda_{hf}^*+A_3]=0$, where $A_1,A_2\ and\ A_3$are constants. Since $\lambda_{hf}^*=0$ corresponds to the DFE of the system, we consider the second quadratic equation to determine the EE point of the model given by
$A_1(\lambda_{hf}^*)^2+A_2\lambda_{hf}^*+A_3=0$ [18]
Thus, positive endemic equilibrium points $E^*$are obtained by solving for $\lambda_{hv}^*$from the quadratic equation [18]. Then, the number of possible real roots of this quadratic polynomial depends on the signs of $A_1,A_2\ and\ A_3$. Therefore, the co-infection dynamical system will have an endemic equilibrium point E^* when:
Case-1:$A_1>0,\ A_2<0$, and $A_2^2-4A_1A_3=0$
Case-2:$A_1<0,\ A_2>0$, and $A_2^2-4A_1A_3=0$
Case-3:$A_1>0,\ A_2<0$, and $A_3=0$
Case-4:$A_1>0,\ A_2>0, A_2^2-4A_1A_3>0$ and $\sqrt{A_2^2-4A_1A_3}>A_2$
Case-5:$A_1<0,\ A_2>0, A_2^2-4A_1A_3>0$ and $\sqrt{A_2^2-4A_1A_3}>A_2$
Finally, from the above cases we conclude that we can get an endemic equilibrium point E^* in the first quadrant for the full co-infection dynamics of typhoid fever and malaria diseases.

5.6. Local Stability of Endemic Equilibrium (EE) Point for the Co-Infection of Malaria and Typhoid Fever Model

Theorem-12: The endemic equilibrium point E^* of the co-infection of malaria and typhoid fever model [1-9]is locally asymptotically stable (LAS) if$R_0 > 1$.

Proof: The Jacobian matrix of the dynamical system [1-9]at the EE point E^* is given by:

$$J(E^*) = \begin{bmatrix} -D_1 & -D_2 & 0 & 0 & 0 & 0 & 0 & 0 & -D_3 \\ \lambda_t^* & D_4 & 0 & 0 & 0 & 0 & 0 & 0 & -D_5 \\ 0 & \omega & -\mu_h & 0 & 0 & 0 & 0 & 0 & 0 \\ \lambda_{hf}^* & -D_6 & 0 & -D_7 & 0 & 0 & 0 & 0 & D_3 \\ 0 & D_8 & 0 & \gamma\,\lambda_t^* & -e_5 & 0 & 0 & 0 & D_5 \\ 0 & 0 & 0 & 0 & \phi_2 & -\mu_h & 0 & 0 & 0 \\ 0 & 0 & 0 & \varepsilon & 0 & 0 & -\mu_h & 0 & 0 \\ 0 & 0 & 0 & -D_9 & -D_{10} & 0 & 0 & -D_{11} & 0 \\ 0 & 0 & 0 & D_9 & D_{10} & 0 & 0 & \lambda_{mf}^* & -\mu_m \end{bmatrix}$$

where,$D_1 = (\lambda_{hf}^* + \lambda_t^* + \mu_h)$, $D_2 = \frac{\beta}{N_h}S_h^*$, $D_3 = \frac{a_2 b}{N_h}S_h^*$, $D_4 = D_2 - (\alpha_2\,\lambda_{hf}^* + e_1)$, $D_5 = \frac{\alpha_2 a_2 b}{N_h}I_t^*$,$D_6 = \frac{\gamma\beta}{N_h}I_{hf}^*$,$D_7 = \gamma\,\lambda_t^* + e_3$, $D_8 = D_6 + \alpha_2\,\lambda_{hf}^*$, $D_9 = \frac{a_4 b}{N_h}S_m^*$, $D_{10} = \frac{a_4 b\eta_2}{N_h}S_m^*$, $D_{11} = \lambda_{mf}^* + \mu_m$.

The characteristic equation of the Jacobian matrix at the EE point E^* is

$$\begin{vmatrix} -D_1-\lambda & -D_2 & 0 & 0 & 0 & 0 & 0 & 0 & -D_3 \\ \lambda_t^* & D_4-\lambda & 0 & 0 & 0 & 0 & 0 & 0 & -D_5 \\ 0 & \omega & -\mu_h-\lambda & 0 & 0 & 0 & 0 & 0 & 0 \\ \lambda_{hf}^* & -D_6 & 0 & -D_7-\lambda & 0 & 0 & 0 & 0 & D_3 \\ 0 & D_8 & 0 & \gamma\,\lambda_t^* & -e_5-\lambda & 0 & 0 & 0 & D_5 \\ 0 & 0 & 0 & 0 & \phi_2 & -\mu_h-\lambda & 0 & 0 & 0 \\ 0 & 0 & 0 & \varepsilon & 0 & 0 & -\mu_h-\lambda & 0 & 0 \\ 0 & 0 & 0 & -D_9 & -D_{10} & 0 & 0 & -D_{11}-\lambda & 0 \\ 0 & 0 & 0 & D_9 & D_{10} & 0 & 0 & \lambda_{mf}^* & -\mu_m-\lambda \end{vmatrix} = 0$$

After simplifying this determinant, we get:

$(\lambda + \mu_h)^3[\lambda^6 + P_1\lambda^5 + P_2\lambda^4 + P_3\lambda^3 + P_4\lambda^2 + P_5\lambda + P_6] = 0$, where $P_i,\ i = 1, \ldots 6$ are constants. Thus, the roots of this polynomial are given by: $\lambda_1 = \lambda_2 = \lambda_3 = -\mu_h < 0$ or

$\lambda^6 + P_1\lambda^5 + P_2\lambda^4 + P_3\lambda^3 + P_4\lambda^2 + P_5\lambda + P_6 = 0$.[19]

Here in applying Routh-Hurwitz stability criterion for the polynomial [19]of degree six we proved that when $R_0 > 1$ all roots of the polynomial equation has negative real parts.Therefore,the endemic equilibrium point $E^*$is locally asymptotically stable (LAS) if$R_0 > 1$.

5.7. Global Stability of Endemic Equilibrium (EE) Point for the Co-Infection of Malaria and Typhoid Fever Model

Theorem-13: The endemic equilibrium point E^* of the co-infection of malaria and typhoid fever model [1-9]is globally asymptotically stable (GAS) if$R_0 > 1$.

Proof: We define a Lyapunov function $L: R_+^9 \longrightarrow R_+$ by$L\left(S_h^*, I_t^*, R^*,\ I_{hf}^*,\ C_{ft}^*, T_{ft}^*,\ T_f^*, S_m^*,\ I_{mf}^*\right) =$

$J_1\left(S_h - S_h^* + S_h^* ln\frac{S_h^*}{S_h}\right) + J_2\left(I_t - I_t^* + I_t^* ln\frac{I_t^*}{I_t}\right) + J_3\left(R - R^* + R^* ln\frac{R^*}{R}\right) + J_4\left(I_{hf} - I_{hf}^* + I_{hf}^* ln\frac{I_{hf}^*}{I_{hf}}\right) +$

$J_5\left(C_{ft} - C_{ft}^* + C_{ft}^* ln\frac{C_{ft}^*}{C_{ft}}\right) + J_6\left(T_{ft} - T_{ft}^* + T_{ft}^* ln\frac{T_{ft}^*}{T_{ft}}\right) + J_7\left(T_f - T_f^* + T_f^* ln\frac{T_f^*}{T_f}\right) + J_8\left(S_m - S_m^* + S_m^* ln\frac{S_m^*}{S_m}\right) +$

$J_9\left(I_{mf} - I_{mf}^* + I_{mf}^* ln\frac{I_{mf}^*}{I_{mf}}\right)$, where $J_1, J_2, J_3, \ldots, J_9$ are positive constants to be determined later.

The function L and its partial derivatives with respect to the corresponding state variables are all continues.L has a minimum value at the EE point E^* which is $L(E^*) = 0$.

Also, $\frac{dL}{dt} = J_1\frac{\partial L}{\partial S_h}\frac{dS_h}{dt} + J_2\frac{\partial L}{\partial I_t}\frac{dI_t}{dt} + J_3\frac{\partial L}{\partial R}\frac{dR}{dt} + J_4\frac{\partial L}{\partial I_{hf}}\frac{dI_{hf}}{dt} + J_5\frac{\partial L}{\partial C_{ft}}\frac{dC_{ft}}{dt} + J_6\frac{\partial L}{\partial T_{ft}}\frac{dT_{ft}}{dt} + J_7\frac{\partial L}{\partial T_f}\frac{dT_f}{dt} + J_8\frac{\partial L}{\partial S_m}\frac{dS_m}{dt} +$

$J_9\frac{\partial L}{\partial I_{mf}}\frac{dI_{mf}}{dt}$

After substituting and simplifying different expressions we obtain the value of $\frac{dL}{dt}$ at the EE E^* as:$\frac{dL}{dt} =$

$-[J_1\left(1 - \frac{S_h^*}{S_h}\right)^2(\lambda_{hf} + \lambda_t + \mu_h)S_h + J_2\left(1 - \frac{I_t^*}{I_t}\right)^2(\alpha_2\lambda_{hf} + \omega + \delta_t + \mu_h)I_t + J_3\left(1 - \frac{R^*}{R}\right)^2\mu_h R + J_4\Big(1 -$

$\frac{I_{hf}^*}{I_{hf}}\Big)^2(\gamma\lambda_t+\varepsilon+\delta_f+\mu_h)I_{hf}+J_5\left(1-\frac{C_{ft}^*}{C_{ft}}\right)^2(\phi_2+\theta_2\delta_{ft}+\mu_h)C_{ft}+J_6\left(1-\frac{T_{ft}^*}{T_{ft}}\right)^2\mu_hT_{ft}+J_7\Big(1-\frac{T_f^*}{T_f}\Big)^2\mu_hT_f+J_8\left(1-\frac{S_m^*}{S_m}\right)^2(\lambda_{mf}+\mu_m)S_m++J_9\left(1-\frac{I_{mf}^*}{I_{mf}}\right)^2\mu_mI_{mf}]$

Thus, $\frac{dL}{dt}\leq 0$ for any positive values of $J_1, J_2, J_3, \dots, J_8$ and J_9. Furthermore, $\frac{dL}{dt}=0$ at the EE point. Hence, L is a Lyapunov function. From this we conclude that E^* is the largest compact invariant singleton set in the region. Therefore, the endemic equilibrium point E^* is globally asymptotically stable (GAS) in the invariant region if $R_0>1$.

VI. Numerical Analysis

In this section we will present numerical simulations of our model in order to illustrate our theoretical and mathematical results which were previously established. The simulations describe the dynamics of the co-infection of Plasmodiumfalciparum and typhoid fever based on the separate diseases basic reproduction numbers of typhoid fever only and Plasmodium falciparum only with parameter values obtained from different sources.

The numerical values of the modelare given in table **2**below.

Table 2: Typhoid fever and malaria model parameter values and their descriptions.

Parameters Descriptions	Parameters Symbol	Values	Source
New recruitment rate into the susceptible human population	Λ_h	0.05/day	[8]
New recruitment rate into the susceptible mosquito population	Λ_m	1000/day	[9]
Natural death rate for human population	μ_h	0.00004/day	[11]
Natural death rate for mosquito population	μ_m	0.1429/day	[8]
Typhoid fever disease- induced death rate for human population	δ_t	0.002/day	[11]
The treatment rate of humans from typhoid fever.	ω	0.002485/day	[5]
The effective transmission rate of typhoid fever on contact with infected individuals	β	0.01/day	[9]
Plasmodium falciparum disease- induced death rate for human population	δ_f	0.0019/day	[11]
The modification parameter from infected typhoid fever to co-infection class	α_2	varied	
The modification parameter for typhoid fever to co-infection	γ	varied	
The modification parameter for mortality due tothe co-infection	θ_2	varied	
The treatment rate of the co-infected class C_{ft}.	ϕ_2	varied	
The transmission probability of human infection due to per bite of an infected mosquito with plasmodium falciparum	a_2	0.15096/day	[11]
The transmission probability that a mosquito will become infected by biting an infected human with plasmodium falciparum	a_4	0.24/day	[7]
Per capita biting rate of mosquito.	b	0.29/day	[7]
The modification parameter for mosquitoes to be infected from the co-infected individuals	η_2	varied	
The rate of treatment for p. falciparum	ε	0.038 /day	[11]

Next, to get a clear idea about the numerical analysis of the co-infection of p. falciparum and typhoid fever we consider the following cases one by one as follows.

Case-1: If the basic reproduction number $R_0<1$ i.e. $R_{0t}<1$ and $R_{0f}<1$, then the co-infection of p. falciparum and typhoid fever dies out with time and approaches the disease free equilibrium point E_0 when appropriate treatment is considered for the single disease infected or the co-infected population.

Case-2:If the basic reproduction number $R_0>1$ i.e. $R_{0t}>1$ and $R_{0f}>1$, there is always a co-existence of p. falciparum and typhoid fever no matter which of the reproduction numbers is greater. Hereafter, we consider the case when $R_0>1$ for the co-infection of the diseases.

Case-3: If $R_0=Max\{R_{0t},R_{0f}\}=R_{0t}$ and $R_{0t}>1$ and also the other is less than unity (i.e.$R_{0f}<1$), then the typhoid fever disease persists in the population .That means if $R_{0t}>1$and$R_{0f}<1$, the malaria disease dies out with time and the typhoid fever disease continues to be endemic in the community. This implies that the co-infection of p. falciparum and typhoid fever decreases in the community. Thus, the numerical analysis of the typhoid fever disease under this situation will be discussed as follow.

6.1. Estimation of Basic Reproduction Number R_{0t} for typhoid fever

We computedR_{0t} as:$R_{0t}\ \ (\beta,\omega,\delta_t,\mu_h)=\frac{\beta}{\omega+\delta_t+\mu_h}=\frac{0.01}{0.002485+0.002+0.00004}=2.20994475138$

From this value of the basic reproduction number we can conclude that the typhoid fever disease spreads in the community because $R_{0t} = 2.20994475138 > 1$.

6.1.1. Basic Reproduction Number R_{0t} Versus effective transmission rate β

The graph represents the graph of the basic reproduction number R_{0t} versus the effective transmission rate of typhoid fever on contact parameter β with infected individuals and keeping all other parameters constant.

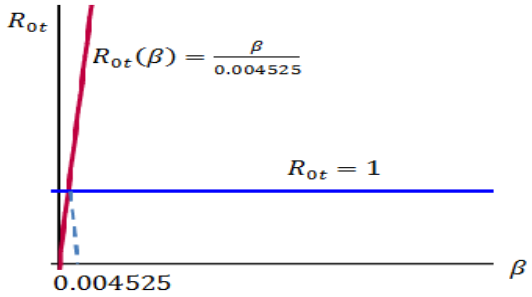

Figure2: The graphof thereproduction number R_{0t} versus the effective transmission rate of typhoid fever on contact parameter β.

From figure2 we observe that if $\beta < 0.004525$, then the reproduction number R_{0t} increases but $R_{0t} < 1$.This implies that the typhoid fever disease does not spread in the community and hence, it dies out through time. If $\beta > 0.004525$, then the reproduction number R_{0t} increases with $R_{0t} > 1$.That means the typhoid fever disease persists in the community.

6.1.2. Basic Reproduction Number R_{0t} Versus the treatment rate from typhoid fever, ω

Here we consider the graph of the basic reproduction number R_{0t} versus the treatment rate from typhoid fever $\omega$and keeping all other parameters constant.

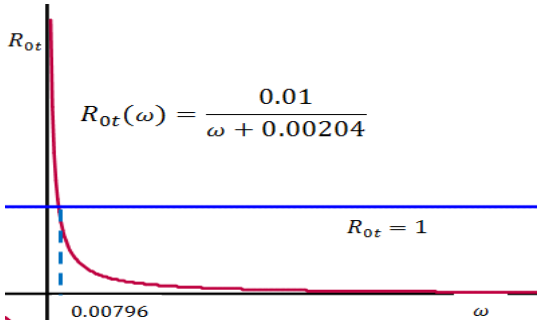

Figure3: The graphof thereproduction number R_{0t} versus the treatment rate from typhoid fever ω.

From figure3we see that if $\omega < 0.00796$, then the reproduction number R_{0t} decreases but $R_{0t} > 1$.This implies that the typhoid fever disease spreads and persists in the community. If $\omega > 0.00796$, then the reproduction number R_{0t} decreases with $R_{0t} < 1$.That means the typhoid fever disease treatment rate from typhoid fever is effective and it dies out through time from the community.

Case-4:If $R_0 = Max\{R_{0t}, R_{0f}\} = R_{0f}$ and $R_{0f} > 1$ and also the otheris less than unity (i.e.$R_{0t} < 1$), then the plasmodium falciparum disease persists in the population. That means if $R_{0f} > 1$, and$R_{0t} < 1$, the typhoid fever diseases die out with time and theplasmodiumfalciparum disease continues to be endemic in the community. This implies that the co-infection of plasmodiumfalciparum and typhoid fever decreases in the community. Thus, the numerical analysis of the p.falciparum disease under this situation will be discussed as follow.

6.2. Estimation of Basic Reproduction Number R_{0f} for p.falciparum

We computed R_{0f}as:$R_{0f} = \sqrt{\frac{a_2 a_4 b^2 \mu_h \Lambda_m}{\mu_m^2 \Lambda_h (\varepsilon + \delta_f + \mu_h)}} = \sqrt{\frac{(0.15096)(0.24)(0.29)^2(0.00004)(1000)}{(0.1429)^2(0.05)(0.038+0.0019+0.00004)}} = 1.7287941991$

From this value we conclude that the p. falciparum disease spreads in the community because$R_{0f} = 1.7287941991 > 1$.

6.2.1. Basic Reproduction Number R_{0f} Versus the transmission probability of human infection due to per bite of an infected mosquito with plasmodium falciparum, a_2

Here the graph represents the graph of the basic reproduction number R_{0f} versus the transmission probability a_2 of human infection due to per bite of an infected mosquito with plasmodium falciparumand keeping all other parameters constant.

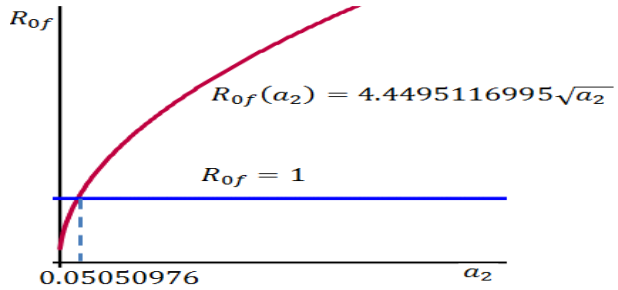

Figure4: The graphof thereproduction number R_{0f} versus the transmission probability a_2 of human infection by infected mosquito with plasmodium falciparum.

From figure4 we see that if $a_2 < 0.05050976$, then the reproduction number R_{0f} increases but $R_{0f} < 1$.This implies that the transmission probability of human infection by infected mosquito with plasmodium falciparum decreases and finally, it dies out from the community. If $a_2 > 0.05050976$, then the reproduction number R_{0f} increases with $R_{0f} > 1$.That means the transmission probability of human infection by infected mosquito with plasmodium falciparum increases and the disease persists in the community.

6.2.2. Basic Reproduction Number R_{0f} Versus the transmission probability that a mosquito will become infected by biting an infected human with plasmodium falciparum, a_4

Here the graph represents the graph of the basic reproduction number R_{0f} versus the transmission probability $a_4$that a mosquito will become infected by biting an infected human with plasmodium falciparumand keeping all other parameters constant.

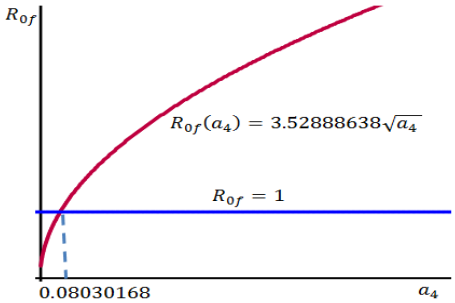

Figure5: The graphof thereproduction number R_{0f} versus the transmission probability $a_4$that a mosquito will become infected by biting an infected human with plasmodium falciparum.

From figure5we see that if $a_4 < 0.08030168$, then the reproduction number R_{0f} increases but $R_{0f} < 1$.This implies that the transmission probability that a mosquito will become infected by biting an infected human with plasmodium falciparum decreases and finally, it dies out from the community. If $a_4 > 0.08030168$, then the reproduction number R_{0f} increases with $R_{0f} > 1$.That means the transmission probability that a mosquito will become infected by biting an infected human with plasmodium falciparum increases and the disease persists in the community.

6.2.3. Basic Reproduction Number R_{0f} Versus Per capita biting rate of mosquito, b

The graph represents the graph of the basic reproduction number R_{0f} versus per capita biting rate of mosquito b and keeping all other parameters constant.

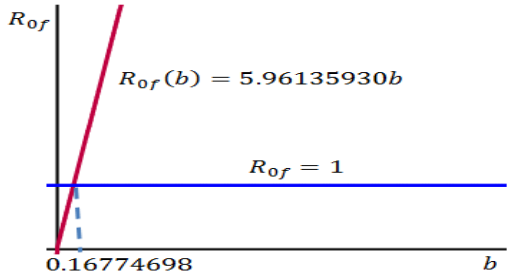

Figure6: The graphof thereproduction number R_{0f} versus per capita biting rate of mosquito b.

From figure6we see that if $b < 0.16774698$, then the reproduction number R_{0f} increases but $R_{0f} < 1$.This implies that the per capita biting rate of mosquito decreases and the disease dies out through time from the community. If $b > 0.16774698$, then the reproduction number R_{0f} increases with $R_{0f} > 1$.That means the per capita biting rate of mosquito increases and the disease persists in the community.

6.2.4. Basic Reproduction Number R_{0f} Versus the rate of Treatment for malaria, ε

The graph represents the graph of the basic reproduction number R_{0f} versus the rate of treatment for malaria ε and keeping all other parameters constant.

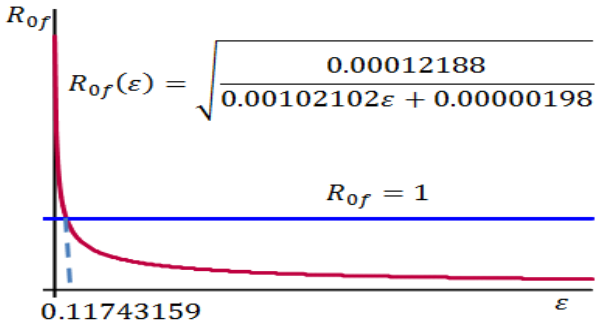

Figure7: The graphof thereproduction number R_{0f} versus the rate of treatment for malaria ε.

From figure7we see that if $\varepsilon < 0.11743159$, then the reproduction number R_{0f} decreases but $R_{0f} > 1$.This implies that the malaria disease caused by p. falciparum spreads and persists in the community. If $\varepsilon > 0.11743159$, then the reproduction number R_{0f} decreases with $R_{0f} < 1$.That means the treatment rate from malaria disease caused by p. falciparum is effective and it dies out through time from the community.

VII. Sensitivity analysis

Next, we perform some sensitivity analysis to determine the parameters that have great influence on the basic reproduction number R_0 of our dynamics of disease transmissions. We use the sensitivity analysis technique given in [10] by the following definition.

Definition: The normalized forward sensitivity index of a variable R_0 that depends differentially on a parameter p is defined as: $SI(p) = \frac{\partial R_0}{\partial p} X \frac{p}{R_0}$.

Thus, the most sensitive parameter is the one with the highest magnitude as compared to the others.The larger the magnitude of the number, the greater impact that parameter has on R_0 and correspondingly, the smaller the magnitude, the weaker the impact onR_0. Since $R_0 = Max\{R_{0t}, R_{0f}\}$, we obtain the sensitivity analysis ofR_{0t} and R_{0f} separately with respect to each parameter to decide the influential parameters on the co-infection of p. falciparum and typhoid fever disease as follow.

First let us consider the basic reproduction number R_{0t} of typhoid fever.

$SI(\beta) = \frac{\partial R_{0t}}{\partial \beta}\frac{\beta}{R_{0t}} = 1 > 0, SI(\omega) = \frac{\partial R_{0t}}{\partial \omega}\frac{\omega}{R_{0t}} = \frac{-\omega}{(\omega+\delta_t+\mu_h)} < 0$

$SI(\delta_t) = \frac{\partial R_{0t}}{\partial \delta_t}\frac{\delta_t}{R_{0t}} = \frac{-\delta_t}{(\omega+\delta_t+\mu_h)} < 0, \qquad SI(\mu_h) = \frac{\partial R_{0t}}{\partial \mu_h}\frac{\mu_h}{R_{0t}} = \frac{-\mu_h}{(\omega+\delta_t+\mu_h)} < 0$

Based on the data given on table 2 for typhoid fever disease the sensitivity indices of R_{0t} with respect to the four parameters are computed and listed in the following table.

Table3: The sensitivity index of R_{0t} with respect to the four parameters.

Parameters	sensitivity index
β	1
ω	-0.54917127
δ_t	-0.38095238
μ_h	-0.00883978

From the sensitivity index table, it is observed that the effective transmission rate of typhoid fever on contact with infected individualsβ is the most sensitive parameter. The second sensitive parameter for typhoid fever transmission is the treatment rate of humans from typhoid fever ω.

Finally, let us consider the basic reproduction number R_{0f} of plasmodium falciparum.

$SI(a_2) = \frac{\partial R_{0f}}{\partial a_2}\frac{a_2}{R_{0f}} = \frac{1}{2} > 0, SI(a_4) = \frac{\partial R_{0f}}{\partial a_4}\frac{a_4}{R_{0f}} = \frac{1}{2} > 0, SI(b) = \frac{\partial R_{0f}}{\partial b}\frac{b}{R_{0f}} = 1 > 0, \quad SI(\mu_h) = \frac{\partial R_{0f}}{\partial \mu_h}\frac{\mu_h}{R_{0f}} = \frac{(\varepsilon+\delta_f)}{2(\varepsilon+\delta_f+\mu_h)} > 0, SI(\mu_m) = \frac{\partial R_{0f}}{\partial \mu_m}\frac{\mu_m}{R_{0f}} = -1 < 0,$

$SI(\varepsilon) = \frac{\partial R_{0f}}{\partial \varepsilon}\frac{\varepsilon}{R_{0f}} = \frac{-\varepsilon}{2(\varepsilon+\delta_f+\mu_h)} < 0 \ , \ SI(\delta_f) = \frac{\partial R_{0f}}{\partial \delta_f}\frac{\delta_f}{R_{0f}} = \frac{-\delta_f}{2(\varepsilon+\delta_f+\mu_h)} < 0$

Based on the data given on table 2 for p. falciparum disease the sensitivity indices of R_{0f} with respect to the seven parameters are computed and listed in the following table.

Table4: The sensitivity index of R_{0f} with respect to the seven parameters

Parameters	sensitivity index
a_2	0.5
a_4	0.5
b	1
μ_h	0.49949925
μ_m	-1
ε	-0.47571357
δ_f	-0.11266900

From the sensitivity index table, it is observed that the per capita biting rate of mosquito$b$ is the most sensitive parameter. The transmission probability of human infection due to per bite of an infected mosquito with plasmodium falciparum a_2 and the transmission probability that a mosquito will become infected by biting an infected human with plasmodium falciparum a_4 are also the influential parameters in malaria transmission dynamics.

VIII. Results and Discussions

In this study, we considered and analyzed a non-linear system of ordinary differential equation to study the transmission dynamics of the co-infection of p.falciparum and typhoid fever disease with treatment in a community.We got different theoretical results that can give important insights about the co-infection disease. To get clear idea about the real transmission dynamics of the co-infection of p.falciparum and typhoid fever disease, we have investigated the basic reproduction numbers of each disease in the numerical and sensitivity analysis of the co-infection of p.falciparum and typhoid fever disease. In our investigation we applied the basic mathematical epidemiology concept which is known as the basic reproduction number R_0 that indicates how much the disease spreads in the community in the form of co-infection. We used the Next Generation Matrix Method to calculate the reproduction number R_0 for the co-infection dynamics of p.falciparum and typhoid fever disease. In doing so, we obtained the basic reproduction number R_0 of the co-infection in terms of the dynamicsof the two basic reproduction numbers of the separate diseases i.e.R_{0t} and R_{0f}that represent basic reproduction numbers for typhoid fever and p. falciparum respectively. From this we conclude that the basic reproduction number for the co-infection of p.falciparum and typhoid fever disease is $R_0 = Max\{R_{0t}, R_{0f}\}$.We know that the reproduction number R_0 of the system helps us to decide the number of secondary infections that one infectious individual generates. After computing the disease free equilibrium and the endemic equilibrium points of the co-infection dynamics of the system, we have checked the local and global stabilities of the co-infection model using the Jacobian matrix method for local stability and the Lyapunov function method for global stability. Also, the full p.falciparum -typhoid fever model has a locally asymptotically stable disease-free equilibrium point when its basic reproduction number is less than unity, and unstable if it exceeds unity. The separate diseases disappear from the community whenever the reproduction number $R_0$is very small and less than unity. On the other hand, the diseases co-exist whenever their reproduction numbers exceed unity

(regardless which of the numbers is larger).That means the disease persists in the community and we need to start treatment for the infected people.

Before we discuss the sensitivity analysis of the co-infected dynamics of the model to determine the most influential parameters of the system, we investigated the sensitivity analysis on each parameters of the separate diseases based on the standard data taken from different journal sources. For this purpose we used the basic reproduction numbers of the separate diseases obtained from the basic reproduction number of the co-infection disease model.

We discussed and presented in detail the numerical simulation results of the separate diseases based on the standard data taken from different journal sources in the form of graphics to support the dynamics of the co-infection disease. Thus, based on these ideas we discussed each basic reproduction numbers versus some of the corresponding influential parameters of the diseases one by one as follows.

We obtained the basic reproduction number R_{0t} of the typhoid fever infection from the co-infection model as $R_{0t} = \frac{\beta}{\omega+\delta_t+\mu_h}$ with four parameters.Also, we got the numerical value of the basic reproduction number based on the standard data taken from different journal sources as $R_{0t} = 2.20994475138 > 1$. This shows us that the disease spreads in the population. From graph 2we see that when $\beta > 0.004525$, the reproduction number R_{0t} increases with $R_{0t} > 1$. That means the basic reproduction number R_{0t} increases when the effective transmission rate of typhoid fever on contact with infected individuals β increases and the disease persists in the community. On the other hand, in figure 3the reproduction number R_{0t} decreases with $R_{0t} < 1$ if $\omega > 0.00796$. That means the typhoid fever disease treatment rate ω is effective and the disease dies out through time from the community.

We also computed the basic reproduction number R_{0f} of the plasmodium falciparum disease sub-model as $R_{0f} = \sqrt{\frac{a_2 a_4 b^2 \mu_h \Lambda_m}{\mu_m^2 \Lambda_h(\varepsilon+\delta_f+\mu_h)}}$ with nine parameters. The graph in figure 4 shows us that if $a_2 > 0.05050976$, then the reproduction number R_{0f} increases with $R_{0f} > 1$. That means if the transmission probability of human infection by infected mosquito with plasmodium falciparum a_2 increases, the basic reproduction number R_{0f} increases and the disease persists in the community. If $a_2 < 0.05050976$, then the reproduction number R_{0f} increases with $R_{0f} < 1$ and the disease dies out from the community through time. Thus, a_2 affects the reproduction number R_{0f}. In figure 5we see thatif $a_4 > 0.08030168$, then the reproduction number R_{0f} increases with $R_{0f} > 1$.That means the transmission probability that a mosquito will become infected by biting an infected human with plasmodium falciparum a_4 increases, the basic reproduction number R_{0f} increases and the disease persists in the community. If$a_4 < 0.08030168$, then the reproduction number R_{0f} increases with $R_{0f} < 1$ and the disease dies out from the community through time. Thus, a_4 affects the reproduction numberR_{0f}. From figure 6we observe that when the per capita biting rate of mosquito b increases, the basic reproduction number R_{0f} also increases and the disease persists in the community.

In figure 7we see that the mosquito treatment rate ε influences the basic reproduction number R_{0f}. If $\varepsilon < 0.11743159$, then the reproduction number R_{0f}decreases with$R_{0f} > 1$. This implies that the malaria disease caused by plasmodium falciparum spreads and persists in the community. If $\varepsilon > 0.11743159$, then the reproduction number R_{0f} decreases with $R_{0f} < 1$.That means the treatment rate ε from malaria disease caused by plasmodium falciparum is effective and it dies out through time from the community.

From table 3ofsensitivity index of typhoid fever disease sub-model we see that the most sensitive parameters are the effective transmission rate of typhoid fever on contact parameter β and the treatment rate of humans from typhoid fever ω. Also,from table 4ofsensitivity indices of plasmodium falciparum disease sub-model we observe that the most sensitive parameter is the per capita biting rate of mosquito b as well as the transmission probabilities of the malaria infection parametersa_2 and a_4. Thus, having analyzed the sensitivity of the parameters for the two separate diseases that are typhoid fever and plasmodium falciparum, we discussed in detail the sensitive parameters for the full p. falciparum and typhoid fever co-infection disease dynamics.

IX. Conclusion

In this study, we presented and analyzed a non-linear system of ordinary differential equation to study the transmission dynamics of the co-infection of p. falciparum and typhoid fever disease with treatment in a community. That means we developed a mathematical model in order to understand the malaria and typhoid fever disease co-infection to improve the treatments and control of the diseases. We found the basic reproduction number of the full co-infection model of p. falciparum and typhoid fever disease. When we analyze the co-infection model, the disease free equilibrium and the endemic equilibrium points are locally asymptotically stable and globally asymptotically stable.

From the sensitivity analysis of the typhoid fever we observed that the effective transmission rate of typhoid fever on contact with infected individual parameter β is the most sensitive (influential) parameter in

changing the reproduction number of the system and the transmission dynamics of typhoid fever. Also, from the sensitivity analysis of the malaria disease we see that the most sensitive parameter is the per capita biting rate of mosquito b as well as the transmission probabilities of the malaria infection parameters.

Thus, the results in this study show us that controlling the transmission means of the diseases and getting appropriate treatment are very important to eradicate the diseases from the community. Therefore, to reduce the reproduction number of the dynamical system we have to focus on the influential parameters.

X. Recommendations

In this study we have observed that the reproduction number of the co-infection of p. falciparum and typhoid fever disease is greater than unity. This implies that typhoid fever and malaria diseases as well as the co-infection of these diseases spread and persist in the community. Thus, to reduce the spread of the diseases we have to give attention for the sensitive parameters like the effective transmission rate of typhoid fever on contact parameter β, the per capita biting rate of mosquito b and the transmission probabilities of the malaria infection parameters a_2 and a_4.In other words, to control these diseases we must get that the effective transmission rate of typhoid fever on contact parameter β should be less than 0.004525, the per capita biting rate of mosquito b must be less than 0.08226229 and also the transmission probabilities of the p. falciparum infection parametersa_2 and a_4 should be less than 0.05050976, and 0.08030168 respectively.

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