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Modelling the Transmission Dynamics of Anthrax Disease with Simultaneous Vaccination for both Human and Animal Population Using the Saturated Incidence Rate

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ABSTRACT

In this study, a mathematical model based on saturated incidence rate that explores the transmission dynamics of anthrax as a zoonotic disease with vaccination compartment introduced into the human and animal population was formulated using ordinary differential equations. The model's flow diagram was presented with qualitative and quantitative analysis carried out on the model. The local and global stability analysis of the equilibrium points were investigated using the Ruth-Hurwitz criterion and Castillo-Chaves method respectively, the results from both analysis showed the model to be locally asymptotically stable when the basic reproduction number is less than one and unstable when the basic reproduction number is greater than one. Test for backward bifurcation was done with the result showing no backward bifurcation in the system. The sensitivity analysis of the model's parameters was performed to determine the contribution of each parameter to the basic reproduction number and a plot of partial ranking correlation (PRCC) obtained. The analysis revealed that, by decreasing human and animal contact rate, it would cause a decrease in the basic reproduction number. Also, numerical simulation further showed that increase in vaccination for both human and animal population reduces the spread of anthrax disease in the population.

1. Introduction

An anthrax disease is a deadly infectious illness that is causes by Bacillus anthracis which is a gram-positive, rod-shaped bacterium (Baloba *et al.*, 2020). The anthrax disease can be described as a zoonosis disease (transmissible from animals to humans) which typically affects ruminants (WHO 2016). The bacteria produce extremely potent toxins which are responsible for the symptoms, causing a high lethality rate and humans can catch the disease from infected animals or through contaminated animal products (WHO, 2016). There are different types of anthrax disease depending on the type of illness a person develops after contracting anthrax disease or on how the anthrax enters the body (CDC, 2020). Cutaneous anthrax is consider the most common form of anthrax infection which occurs when spores get into the skin, usually through a cut or scrape, a person can develop cutaneous anthrax, is most common on the head, neck, forearms, and hands. It affects the skin and tissue around the site of infection. Another form of anthrax is the Inhalation anthrax which is considered to be the most deadly form. It infection usually develops within a week after exposure, when a person breathes in anthrax spores. People who work in places such as wool mills, slaughterhouses, and tanneries may breathe in the spores when working with infected animals or contaminated animal products from infected animals. Inhalation anthrax starts primarily in the lymph nodes in the chest before spreading throughout the rest of the body, ultimately causing severe breathing problems and shock. Gastrointestinal anthrax occurs when a person eats raw or undercooked meat from an animal infected with anthrax, they can develop gastrointestinal anthrax. Once ingested, anthrax spores can affect the upper gastrointestinal tract (throat and esophagus), stomach, and intestines, causing a wide variety of symptoms. Recently, anthrax infection was identified in heroin-injecting drug users in northern Europe which is now called Injection anthrax with symptom similar to those of cutaneous anthrax (CDC, 2020)

The concept of mathematical models in describing the phenomenon and dynamics of infectious diseases in epidemiology has indeed help in the controls and eradication of so many diseases. Many authors have proposed several mathematical models on the transmission dynamics of anthrax disease using different concept. One of such is Osman *et al.*, (2018) who developed and investigated a mathematical model for the transmission dynamics of anthrax disease using ordinary differential equations. The disease-free equilibrium of the anthrax model was analyzed for locally asymptotic stability and the associated epidemic basic reproduction number. The model's disease free equilibrium was showed to be locally asymptotically stable when the basic reproductive number is less than unity. The model also was found to exhibit the existence of multiple endemic equilibria. They carried out

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sensitivity analysis on the model's parameters to investigate the most sensitive parameters in the dynamics of the diseases.

In Baloba *et al.*, (2022), a mathematical model of anthrax epidemic with behavioral change in both animal and human populations taking into accounts, saturation effects within the animal population and behavioral change of the general public towards the outbreak of the disease was proposed. Result from the analysis showed that the model has two unique equilibrium points, namely; the anthrax-free and endemic equilibrium points. The anthrax-free equilibrium point is globally asymptotically stable whenever the reproduction number is less than unity $R_0 < 1$ and the endemic equilibrium point is locally asymptotically stable whenever $R_0 > 1$. Sensitivity analysis was done including numerical simulations which demonstrated the saturation effect and behavioral change of the general public towards the outbreak of the disease. Findings of their research shows that anthrax epidemic can be controlled by reducing the rate of anthrax infection and pathogen shedding rate while increasing the rate of pathogen decay through proper environmental hygiene as well as increasing treatment to ensure higher recovery rate in infected animals.

Saad-Roy *et al.* (2017) proposed a mathematical model of anthrax (caused by Bacillus anthracis) transmission. The model formulated considers only the animal population that include live animals, infected carcasses and spores in the environment. The basic reproduction number was calculated and existence of a unique endemic equilibrium was established. Using data from the literature, elasticity indices for the reproduction numbers were computed to quantify anthrax control measures. For these animals, oscillatory solutions arising from Hopf bifurcations are numerically shown to exist for certain parameter values and to have periodicity as observed from anthrax data. Numerical result showed that oscillations in spore growth may drive oscillations in animal populations. However, the total number of infected animals remains about the same as with constant spore growth.

Rezapour *et al.* (2020) studied a fractional-order model for the anthrax disease between animals based on the Caputo–Fabrizio derivative. They derive an existence criterion of solutions for the proposed fractional CF-system of the anthrax disease model by utilizing the Picard–Lindelof technique. The basic reproduction number, R_0 of the fractional CF-system were computed and two disease-free and endemic equilibrium points were established. Also, the check of asymptotic stability property was done and by applying an iterative approach based on the Sumudu transform the stability of the fractional CF-system was investigated. Finally, after the convergence analysis of the numerical method HATM, they presented a numerical simulation of the CF-fractional anthrax disease model and reviewed the dynamical behavior of the solutions of this CF-system during a time interval.

Though there are research works on mathematical model of anthrax disease, however, to the best our knowledge very few studies have been done considering vaccination and nonlinear force of infection. In this paper, we focus on a mathematical model of anthrax disease transmission using saturated incidence rate and introducing vaccination simultaneously for both human and animal population with regards to possible eradication of the disease.

2. Formulation of Anthrax Model and Description

The model divides human and animal population at any time, (t) into compartments with respect to their disease status. The total animal population $N_a(t)$ is subdivided into susceptible animals S_a, infectious animals I_a, vaccinated animals V_a and recovered animals R_a. Hence, the total animal population is given as:

$$N_a(t) = V_a(t) + S_a(t) + I_a(t) + R_a(t)$$

Similarly, the total human population denoted by $N_h(t)$ is also sub-divided into susceptible humans S_h, vaccinated humans V_h, infectious humans I_h and Recovered humans R_h. Hence, the total human population represented as:

$$N_h(t) = V_h(t) + S_h(t) + I_h(t) + R_h(t).$$

Susceptible humans are recruited at a rate Λ_h, humans leave the susceptible class to the vaccinated class at the rate α_2, and humans return to the susceptible class from the vaccinated class at the rate α_1. Humans acquire anthrax through direct contact, inhalation, and ingestion of contaminated animal products at a rate β_h. Infected humans recover from anthrax disease at a rate γ. Humans infected with anthrax die at a rate δ_1. Recovered humans may lose immunity and return to the susceptible class at a rate ω_1. The entire human population has a natural death rate of μ_h.

Susceptible animals are recruited at a rate Λ_a, the progression rate of animals from the susceptible class to the vaccinated class is ε_2, and animals return to the susceptible class from the vaccinated class at rate ε_1. The disease can be obtained through contact with infectious animals at the rate β_a. Death rate as a result of anthrax infection is δ_2, animals recover at the rate ω_2, then recovered animals may lose immunity and join susceptible class at rate λ. Natural death in animals is at the rate μ_a. The schematic diagram and model equations for the transmission dynamics of the disease are presented in figure 1 and equation (1) respectively.

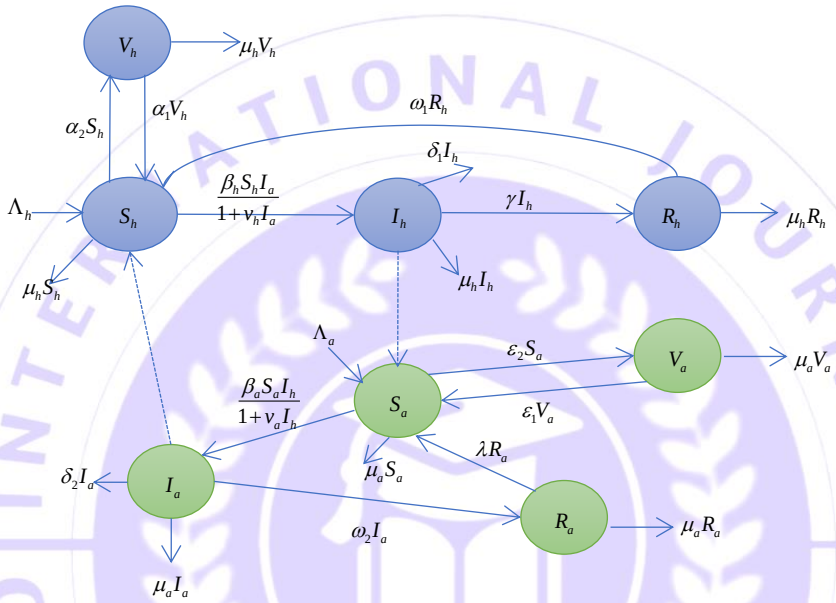

Figure 1: Schematic diagram of the Anthrax model

We therefore present the equations for the Anthrax model

$$\left.\begin{aligned}
\frac{dV_h}{dt} &= \alpha_2 S_h - (\alpha_1 + \mu_h)V_h \\
\frac{dS_h}{dt} &= \Lambda_h - \frac{\beta_h S_h I_a}{1+\nu_h I_a} + \alpha_1 V_h + \omega_1 R_h - (\alpha_2 + \mu_h)S_h \\
\frac{dI_h}{dt} &= \frac{\beta_h S_h I_a}{1+\nu_h I_a} - (\delta_1 + \gamma + \mu_h)I_h \\
\frac{dR_h}{dt} &= \gamma I_h - (\omega_1 + \mu_h)R_h \\
\frac{dV_a}{dt} &= \varepsilon_2 S_a - (\varepsilon_1 + \mu_a)V_a \\
\frac{dS_a}{dt} &= \Lambda_a - \frac{\beta_a S_a I_h}{1+\nu_a I_h} + \varepsilon_1 V_a + \lambda R_a - (\varepsilon_2 + \mu_a)S_a \\
\frac{dI_a}{dt} &= \frac{\beta_a S_a I_h}{1+\nu_a I_h} - (\omega_2 + \delta_2 + \mu_a)I_a \\
\frac{dR_a}{dt} &= \omega_2 I_a - (\lambda + \mu_a)R_a
\end{aligned}\right\} \quad (1)$$

with initial conditions

$$\left.\begin{aligned}
&V_h(0) > 0, S_h(0) > 0, I_h(0) > 0, \\
&R_h(0) > 0, V_a(0) > 0, S_a(0) > 0, \\
&I_a(0) > 0, R_a(0) > 0
\end{aligned}\right\} \quad (2)$$

Table 1: The Model Parameters and Description

Parameters	Description	Value	Ref.
Λ_h	Recruitment rate of human	0.92	Sinkie *et al.*, (2016)
β_h	Infection rate of susceptible human	0.0001	Baloba *et al.*, (2020)
Λ_a	Recruitment rate of animal	0.99	Sinkie *et al.*, (2016)
β_a	Infection rate of susceptible animal	0.02	Baloba *et al.*, (2020)
ω_2	The recovery rate of infected animals	0.0025	Baloba *et al.*, (2022)
γ	The recovery rate of infected humans	0.04	Baloba *et al.*, (2022)
μ_h	Natural death rate in humans	0.0001	Baloba *et al.*, (2022)
μ_a	Natural death rate in animals	0.0001	Baloba *et al.*, (2022)
δ_1	Disease induced death of the animal population	0.6	Baloba *et al.*, (2022)
δ_2	Disease induced death of the human population	0.5	Assumed
ν_h	Rate of behavioural change		Baloba *et al.*, (2022)
ω_1	Rate at which recovered humans become Susceptible	0.55	Assumed

λ	Rate at which recovered animal become Susceptible	0.45	Assumed
α_1	Human vaccination Waning rate	0.004	Assumed
α_2	Human vaccination rate	0.3	Assumed
ε_1	Animal vaccination rate	0.2	Assumed
ε_2	Animal vaccination Waning rate	0.004	Osman *et al.*, (2018)

3. Basic Analysis of the Anthrax Model

3.1 Positivity and boundedness of solutions

In epidemiological models, conditions under which the system should have non negative solutions is paramount. The model would be biologically meaningful if all the solutions with positive initial conditions remain positive at every point in time.

Theorem 1: Let $\Pi = V_h(t), S_h(t), I_h(t), R_h(t), V_a(t), S_a(t), I_a(t), R_a(t) \in \mathbb{R}_+^8$: $V_h(0), S_h(0), I_h(0), R_h(0), V_a(0), S_a(0), I_a(0), R_a(0) > 0$. Then the solutions of $V_h(t), S_h(t), I_h(t), R_h(t), V_a(t), S_a(t), I_a(t), R_a(t)$ are non-negative for all $t \geq 0$.

Proof:

Human total population at any given time:

$$N_h(t) = V_h(t) + S_h(t) + I_h(t) + R_h(t) \tag{3}$$

and by taking the derivatives we have

$$\frac{dN_h}{dt} = \frac{dV_h}{dt} + \frac{dS_h}{dt} + \frac{dI_h}{dt} + \frac{dR_h}{dt}$$

$$\frac{dN_h}{dt} = \Lambda_h - \mu_h V_h - \mu_h S_h - (\delta_1 + \mu_h) I_h - \mu_h R_h$$

In the absence of mortality due to anthrax infections, the above equations become;

$$\frac{dN_h}{dt} \leq \Lambda_h - \mu_h N_h \tag{4}$$

Solving (4) as $t \to \infty$, $N_h \to \frac{\Lambda_h}{\mu_h}$

$$0 \leq N_h \leq \frac{\Lambda_h}{\mu_h} \quad \text{and} \quad N_h(t) \leq \frac{\Lambda_h}{\mu_h}.$$

also, if $N_h(0) \leq \frac{\Lambda_h}{\mu_h}$, then $N_h(t) \leq \frac{\Lambda_h}{\mu_h}$

$$\Pi_h = \left\{ (V_h, S_h, I_h, R_h) \in \mathbb{R}_+^4 : V_h + S_h + I_h + R_h \leq \frac{\Lambda_h}{\mu_h} \right\} \tag{5}$$

Considering the total animal population at any given time also, we have.

$$N_a(t) = V_a(t) + S_a(t) + I_a(t) + R_a(t) \tag{6}$$

$$\frac{dN_a}{dt} = \frac{dV_a}{dt} + \frac{dS_a}{dt} + \frac{dI_a}{dt} + \frac{dR_a}{dt}$$

$$\frac{dN_a}{dt} = \Lambda_a S_a - \mu_a V_a - \mu_a S_a - (\delta_2 + \mu_a) I_a - \mu_a R_a$$

In the absence of mortality due to Anthrax infections, the above equation becomes;

$$\frac{dN_a}{dt} = \Lambda_a - \mu_a N_a$$

Solving the differential equation and as t→∞, the population size, $N_a \to \frac{\Lambda_a}{\mu_a}$

$$0 \le N_a \le \frac{\Lambda_a}{\mu_a} \text{ and } \quad N_a(t) \le \frac{\Lambda_a}{\mu_a}$$

Also, if $N_a(0) \le \frac{\Lambda_a}{\mu_a}$, then $N_a(t) \le \frac{\Lambda_a}{\mu_a}$

$$\Pi_a = \left\{ (V_a, S_a, I_a, R_a) \in \mathbb{R}_+^4 : V_a + S_a + I_a + R_a \le \frac{\Lambda_a}{\mu_a} \right\} \tag{7}$$

Hence, feasible region for the dynamical system in (1) is given by:

$$\Pi = \Pi_h \times \Pi_a \subset \mathbb{R}_+^4 \times \mathbb{R}_+^4 \tag{8}$$

Where Π is positively invariant.

3.2 Anthrax disease-free equilibrium

The anthrax free equilibrium point is steady-state solution where there is no anthrax infection in the population. It implies that

$$I_h = 0,\ R_h = 0,\ I_a = 0,\ R_a = 0 \tag{9}$$

Solving equation (1) with respect to the condition of (9), we therefore have the anthrax-free equilibrium presented as

$$E^0 = \left(V_h^0, S_h^0, I_h^0, R_h^0, V_a^0, S_a^0, I_a^0, R_a^0\right) = \left(\frac{\alpha_2 \Lambda_h}{\mu_h(\alpha_1 + \alpha_2 + \mu_h)}, \frac{\Lambda_h(\alpha_1 + \mu_h)}{\mu_h(\alpha_1 + \alpha_2 + \mu_h)}, 0, 0, \frac{\varepsilon_2 \Lambda_a}{(\mu_a + \varepsilon_1 + \varepsilon_2)\mu_a}, \frac{\Lambda_a(\varepsilon_1 + \mu_a)}{(\mu_a + \varepsilon_1 + \varepsilon_2)\mu_a}, 0, 0\right) \tag{10}$$

3.3 Anthrax endemic equilibrium points

The anthrax endemic equilibrium points are steady-state solution where anthrax persists in the population. At endemic,

$I_h \neq 0,\ R_h \neq 0,\ I_a \neq 0,\ R_a \neq 0$ and so we have the endemic equilibrium as follows

$$\left.\begin{aligned}
V_h^* &= \frac{\alpha_2\left[(\omega_1+\mu_h)(\gamma+\delta_1+\mu_h)(k_1-\Lambda_h)-\gamma\omega_1 k_1\right](\alpha_1+\mu_h)(\alpha_2+\mu_h)}{(\alpha_1+\mu_h)(\alpha_2+\mu_h)(\omega_1+\mu_h)(\gamma+\delta_1+\mu_h)\left[\alpha_1\alpha_2-(\alpha_1+\mu_h)(\alpha_2+\mu_h)\right]}\\
S_h^* &= \frac{\left[(\omega_1+\mu_h)(\gamma+\delta_1+\mu_h)(k_1-\Lambda_h)-\gamma\omega_1 k_1\right](\alpha_1+\mu_h)(\alpha_2+\mu_h)}{(\alpha_2+\mu_h)(\omega_1+\mu_h)(\gamma+\delta_1+\mu_h)\left[\alpha_1\alpha_2-(\alpha_1+\mu_h)(\alpha_2+\mu_h)\right]}\\
I_h^* &= \frac{k_1}{(\gamma+\delta_1+\mu_h)}\\
R_h^* &= \frac{\gamma k_1}{(\omega_1+\mu_h)(\gamma+\delta_1+\mu_h)}\\
V_a^* &= \frac{\varepsilon_2\left[(k_2-\Lambda_a)(\lambda+\mu_a)(\delta_2+\omega_2+\mu_a)-\lambda\omega_2 k_2\right](\varepsilon_1+\mu_a)(\varepsilon_2+\mu_a)}{(\varepsilon_1+\mu_a)(\lambda+\mu_a)(\delta_2+\omega_2+\mu_a)(\varepsilon_2+\mu_a)\left[\varepsilon_1\varepsilon_2-(\varepsilon_1+\mu_a)(\varepsilon_2+\mu_a)\right]}\\
S_a^* &= \frac{\left[(k_2-\Lambda_a)(\lambda+\mu_a)(\delta_2+\omega_2+\mu_a)-\lambda\omega_2 k_2\right](\varepsilon_1+\mu_a)(\varepsilon_2+\mu_a)}{(\lambda+\mu_a)(\delta_2+\omega_2+\mu_a)(\varepsilon_2+\mu_a)\left[\varepsilon_1\varepsilon_2-(\varepsilon_1+\mu_a)(\varepsilon_2+\mu_a)\right]}\\
I_a^* &= \frac{k_2}{(\omega_2+\delta_2+\mu_a)}\\
R_a^* &= \frac{\omega_2 k_2}{(\lambda+\mu_a)(\omega_2+\delta_2+\mu_a)}
\end{aligned}\right\} \tag{11}$$

where $k_1 = \dfrac{\beta_h S_h I_a}{1+\nu_h I_a}$ and $k_2 = \dfrac{\beta_a S_a I_h}{1+\nu_a I_h}$

3.4 Basic reproduction number

The basic reproduction number, R_0 defined as the average number of secondary infections caused by a typical infectious individual in a completely susceptible population was used to determine the overall dynamical behavior of the model (1). One of the methods used in obtaining this threshold parameter is the next generation operator method by (Diekmann, Heesterbeek, and Roberts, 2010) as demonstrated below.

$$F = \begin{bmatrix} \dfrac{\beta_h S_h I_a}{1+\nu_h I_a} \\ \dfrac{\beta_a S_a I_h}{1+\nu_a I_h} \end{bmatrix}, \quad V = \begin{bmatrix} (\delta_1+\gamma+\mu_h) I_h \\ (\omega_2+\delta_2+\mu_a) I_a \end{bmatrix}$$

The Jacobian matrix of *F* and *V* we obtained as follows:

$$F = \begin{bmatrix} 0 & \dfrac{\beta_h S_h}{\left(1+V_h I_a\right)^2} \\ \dfrac{\beta_a S_a}{\left(1+V_a I_h\right)^2} & 0 \end{bmatrix} \tag{12}$$

$$V = \begin{bmatrix} \left(\delta_1+\gamma+\mu_h\right) & 0 \\ 0 & (\omega_2+\delta_2+\mu_a) \end{bmatrix} \tag{13}$$

$$R_0 = \rho(FV^{-1})$$

$$R_0 = \sqrt{\frac{\Lambda_h \beta_h (\alpha_1 + \mu_h)\Lambda_a \beta_a (\varepsilon_1 + \mu_a)}{\mu_h (\delta_1 + \gamma + \mu_h)(\alpha_1 + \alpha_2 + \mu_h)\mu_a (\delta_2 + \omega_2 + \mu_a)(\varepsilon_1 + \varepsilon_2 + \mu_a)}} \tag{14}$$

$$R_0 = \sqrt{R_h R_a}$$

where

$$R_h = \sqrt{\frac{\Lambda_h \beta_h (\alpha_1 + \mu_h)}{\mu_h (\delta_1 + \gamma + \mu_h)(\alpha_1 + \alpha_2 + \mu_h)}}, \quad R_a = \sqrt{\frac{\Lambda_a \beta_a (\varepsilon_1 + \mu_a)}{\mu_a (\delta_2 + \omega_2 + \mu_a)(\varepsilon_1 + \varepsilon_2 + \mu_a)}}$$

with R_h describing the number of humans that one infectious animal infects over the expected infection period in a completely susceptible human population and R_a describing the number of animal infected by one infectious human during the period of infectiousness in a completely susceptible animal population.

3.5 Local stability of the anthrax model

Theorem 2: The anthrax model free equilibrium of the system (1) is locally and asymptomatically stable if $R_0 < 1$ and unstable if otherwise

Proof: The Jacobian matrix of the system (1) at anthrax free equilibrium $J(E^0)$ is given by

$$\begin{bmatrix} -r_1 & \alpha_2 & 0 & 0 & 0 & 0 & 0 & 0 \\ \alpha_1 & -r_2 & 0 & \omega_1 & 0 & 0 & -b_1 & 0 \\ 0 & 0 & -r_3 & 0 & 0 & 0 & b_1 & 0 \\ 0 & 0 & \gamma & -r_4 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & -r_5 & \varepsilon_2 & 0 & 0 \\ 0 & 0 & -c_1 & 0 & \varepsilon_1 & -r_6 & 0 & \lambda \\ 0 & 0 & c_1 & 0 & 0 & 0 & -r_7 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & \omega_2 & -r_8 \end{bmatrix} \tag{15}$$

where

$$\left.\begin{aligned} &r_1 = (\alpha_1 + \mu_h), r_2 = (\alpha_2 + \mu_h), r_3 = (\gamma + \delta_1 + \mu_h), r_4 = (\mu_h + \omega_1), \\ &r_5 = (\varepsilon_1 + \mu_a), r_6 = (\varepsilon_2 + \mu_a), r_7 = (\delta_2 + \omega_2 + \mu_a), \\ &r_8 = (\lambda + \mu_a), b_1 = \frac{\Lambda_h (\alpha_1 + \mu_h)\beta_h}{\mu_h (\alpha_1 + \alpha_2 + \mu_h)}, c_1 = \frac{\Lambda_a (\varepsilon_1 + \mu_a)\beta_a}{\mu_a (\varepsilon_1 + \varepsilon_2 + \mu_a)} \end{aligned}\right\}$$

The Characteristics polynomial for $J(E^0)$ in (15) is hereby defined as follows:

$$A_0\lambda^8 + A_1\lambda^7 + A_2\lambda^6 + A_3\lambda^5 + A_4\lambda^4 + A_5\lambda^3 + A_6\lambda^2 + A_7\lambda^1 + A_8 = 0 \tag{16}$$

where the coefficients of (16) are given in the appendix.

By applying Routh-Hurwitz criteria which asserts that all roots of the polynomial (16) have a negative real component if and only if the coefficient are positive and the determinant of the matrix $H_i > 0$ for $i = 1,...,8,$ it is clear that $A_i > 0$ for $i = 0,...,8$ are positive and when $R_0 < 0.$ Since the necessary condition for Routh-Hurwitz criteria for the characteristics polynomial in (16) is satisfied, we conclude that, the anthrax free equilibrium is locally asymptotically stable (LAS) when $R_0 < 1.$

3.6 Global stability of the anthrax disease-free equilibrium

The method of Castillo-Chavez, Feng and Huang (2002) is used to obtain the global asymptotic stability of the anthrax disease-free equilibrium. By this method two conditions which guarantee the global stability of the disease-free state were considered. Therefore, our system of equations (1) is re-written in the following form:

$$\left.\begin{aligned}\frac{dX}{dt} &= F\left(X,Z\right)\\ \frac{dZ}{dt} &= G\left(X,Z\right), G\left(X,0\right)=0\end{aligned}\right\} \tag{17}$$

where $X=\left(S_h, \mathrm{V}_h, R_h, S_a, V_a, R_a\right)$ denotes the populations that are not infected $X\in\mathbb{R}^6$, while $Z=\left(I_h, I_a\right)$ denotes the populations that are infected $Z\in\Re^2$. We represent the anthrax-free state by $E^0=\left(X^0,0\right)$. The following two conditions H_1 and H_2 must be met to guarantee a global asymptotic stability:

$$H_1: \frac{dX}{dt}=F\left(X^0,0\right), X^0 \text{ is globally asymptotically stable (G.A.S)} \tag{18}$$

$$H_2: \hat{G}\left(X,Z\right)=CZ-G\left(X,Z\right), \text{where } G\left(X,Z\right)\geq 0, \; for\left(X,Z\right)\in\Omega \tag{19}$$

where, $C=D_Z G\left(X^0,0\right)$ is an $M-matrix$ (the off diagonal of C are non-negative) and Ω is the biological feasible region.

Lemma 1: The point $K^0=\left(X^0,0\right)$ is called stable global asymptotic equilibrium point, if in addition $R_{0m}<1$ and the conditions H_1 & H_2 holds. The following theorem is formed:

Theorem 3: The disease free equilibrium point for the anthrax model is globally asymptotically stable when $R_0<1$ and unstable when $R_0>1$.

Proof:

For condition H_1

Let $X=\left(V_h, S_h, R_h, V_a, S_a, R_a\right)$ as the uninfected state variables (compartments) and all the infected variables $Z=\left(I_h, I_a\right)$ are all zero. The Jacobian matrix of $F(X,0)$ is given as

where $X^0=(\frac{\alpha_2\Lambda_h}{\mu_h(\alpha_1+\alpha_2+\mu_h)}, \frac{\Lambda_h(\alpha_1+\mu_h)}{\mu_h(\alpha_1+\alpha_2+\mu_h)}, 0, \frac{\varepsilon_2\Lambda_a}{(\mu_a+\varepsilon_1+\varepsilon_2)\mu_a}, \frac{\Lambda_a(\varepsilon_1+\mu_a)}{(\mu_a+\varepsilon_1+\varepsilon_2)\mu_a}, 0)$

$X\in\mathbb{R}^3 \Rightarrow$

$$\left.\begin{aligned}\frac{dV_h}{dt} &= \alpha_2 S_h-(\alpha_1+\mu_h)V_h\\ \frac{dS_h}{dt} &= \Lambda_h-\frac{\beta_h S_h I_a}{1+\nu_h I_a}+\omega_1 R_h+\alpha_1 V_h-(\alpha_2+\mu_h)S_h\\ \frac{dR_h}{dt} &= \gamma_1 I_h-(\omega_1+\mu_h)R_h\\ \frac{dV_a}{dt} &= \varepsilon_2 S_a-(\varepsilon_1+\mu_a)V_a\\ \frac{dS_a}{dt} &= \Lambda_a-\frac{\beta_a S_a I_a}{1+\nu_a I_a}+\varepsilon_1 V_a+\lambda R_a-(\varepsilon_1+\mu_a)S_a\\ \frac{R_a}{dt} &= \omega_2 I_a-(\lambda+\mu_a)R_a\end{aligned}\right\} \tag{20}$$

Evaluating (20) base on the condition of the matrix $F(X,0)$, we have

$$F(X,0)=\begin{bmatrix} \alpha_2 S_h-(\alpha_1+\mu_h)V_h \\ \Lambda_h+\omega_1 R_h+\alpha_1 V_h-(\alpha_2+\mu_h)S_h \\ -(\omega_1+\mu_h)R_h \\ \varepsilon_2 S_a-(\varepsilon_1+\mu_a)V_a \\ \Lambda_a+\varepsilon_1 V_a+\lambda R_a-(\varepsilon_1+\mu_a)S_a \\ -(\lambda+\mu_a)R_a \end{bmatrix} \tag{21}$$

Evaluating the Jacobean matrix of equation (21) at malaria free equilibrium, we have:

$$J_{F(X,0)}=\begin{bmatrix} -(\alpha_1+\mu_h) & \alpha_2 & 0 & 0 & 0 & 0 \\ \alpha_1 & -(\alpha_2+\mu_h) & \omega_1 & 0 & 0 & 0 \\ 0 & 0 & -(\omega_1+\mu_h) & 0 & 0 & 0 \\ 0 & 0 & 0 & -(\varepsilon_1+\mu_a) & \varepsilon_2 & 0 \\ 0 & 0 & 0 & \varepsilon_1 & -(\varepsilon_1+\mu_a) & \lambda \\ 0 & 0 & 0 & 0 & 0 & -(\lambda+\mu_a) \end{bmatrix} \tag{22}$$

Clearly, we see that equation (22) has negative real roots for all the eigen values and by Hurwitz criteria and these are true. Thus, $H_1: \dfrac{dX}{dt}=F(X^0,0)$ is globally asymptotically stable since the eigenvalues are negative.

For condition H_2:

Taking the infected compartment of the system (1), we have

$$\left.\begin{aligned} \frac{dI_h}{dt} &= \frac{\beta_h S_h I_a}{1+\nu_h I_a}-(\delta_1+\gamma+\mu_h)I_h \\ \frac{dI_a}{dt} &= \frac{\beta_a S_a I_h}{1+\nu_a I_h}-(\omega_2+\delta_2+\mu_a)I_a \end{aligned}\right\} \tag{23}$$

Evaluating the Jacobian matrix of equation (23) at anthrax free equilibrium, we have

$$C=\begin{bmatrix} -(\delta_1+\gamma+\mu_h) & \dfrac{\beta_h \Lambda_h(\alpha_1+\mu_h)}{\mu_h(\alpha_1+\alpha_2+\mu_h)} \\ \dfrac{\beta_a \Lambda_a(\varepsilon_1+\mu_a)}{(\mu_a+\varepsilon_1+\varepsilon_2)\mu_a} & -(\omega_2+\delta_2+\mu_a) \end{bmatrix}\begin{bmatrix} I_h \\ I_a \end{bmatrix} \tag{24}$$

and

$$\hat{G}(X,Z)=CZ-G(X,Z),$$

$$\hat{G}(X,Z)=CZ-\begin{bmatrix} G_1(X,Z) \\ G_2(X,Z) \end{bmatrix}$$

$$=\begin{bmatrix} \beta_h I_a(S_h^*-\dfrac{S_h}{1+\nu_h I_a}) \\ \beta_a I_h(S_a^*-\dfrac{S_a}{1+\nu_a I_h}) \end{bmatrix} \tag{25}$$

From (26), $S_h^* > \frac{S_h}{1+v_h I_a}$ and $S_a^* > \frac{S_a}{1+v_a I_h}$ then it implies $\hat{G}_2(X,Z) \geq 0.$ Therefore the population is bounded and $\hat{G}(X,Z) \geq 0.$ Since, C is an $M-matrix$, hence the two conditions H_1 & H_2 holds by lemma 1. And we conclude that the global stability of disease-free equilibrium $E^0 = \left(\frac{\alpha_2 \Lambda_h}{\mu_h(\alpha_1+\alpha_2+\mu_h)}, \frac{\Lambda_h(\alpha_1+\mu_h)}{\mu_h(\alpha_1+\alpha_2+\mu_h)}, 0, 0, \frac{\varepsilon_2 \Lambda_a}{(\mu_a+\varepsilon_1+\varepsilon_2)\mu_a}, \frac{\Lambda_a(\varepsilon_1+\mu_a)}{(\mu_a+\varepsilon_1+\varepsilon_2)\mu_a}, 0, 0 \right)$ of the system (1) is globally asymptotically stable when $R_0 < 1.$

3.7 Bifurcation analysis of the anthrax model

In this subsection, we apply Castillo-Chavez and Song (2004) method of the centre manifold theory to establish stability near the DEF (E^0) and $R_0 = 1$. Therefore, from equation (10), we let Φ be the bifurcation parameter and $R_b = 1$ be the bifurcation point.

Evaluating for $\Phi = \beta_h$ from equation (10), we have

$$\beta_h = \frac{\mu_h(\gamma+\delta_1+\mu_h)\mu_a(\alpha_1+\alpha_2+\mu_h)(\delta_2+\omega_2+\mu_a)(\varepsilon_1+\varepsilon_2+\mu_a)}{\Lambda_h(\alpha_1+\mu_h)\beta_a\Lambda_a(\varepsilon_1+\mu_a)} \tag{26}$$

Using the centre manifold theory, the following changes of variables are made for convenience sake to the anthrax system of equation (1) by denoting,

$$\left.\begin{aligned} V_h = x_1,\ S_h = x_2,\ I_h = x_3,\ R_h = x_4, \\ V_a = x_5,\ S_a = x_6, I_a = x_7,\ R_a = x_8 \end{aligned}\right\} \tag{27}$$

Substituting (27) into equation (1), we have

$$\left.\begin{aligned} \dot{x}_1 &= f_1 = \alpha_2 x_2 - (\alpha_1+\mu_h)x_1 \\ \dot{x}_2 &= f_2 = \Lambda_h - \frac{\beta_h x_2 x_7}{1+v_h x_7} + \alpha_1 x_1 + \omega_1 x_4 - (\alpha_2+\mu_h)x_2 \\ \dot{x}_3 &= f_3 = \frac{\beta_h x_2 x_7}{1+v_h x_7} - (\delta_1+\gamma+\mu_h)x_3 \\ \dot{x}_4 &= f_4 = \gamma x_3 - (\omega_1+\mu_h)x_4 \\ \dot{x}_5 &= f_5 = \varepsilon_2 x_6 - (\varepsilon_1+\mu_a)x_5 \\ \dot{x}_6 &= f_6 = \Lambda_a - \frac{\beta_a x_6 x_3}{1+v_a x_3} + \varepsilon_1 x_5 + \lambda x_8 - (\varepsilon_2+\mu_a)x_6 \\ \dot{x}_7 &= f_7 = \frac{\beta_a x_6 x_3}{1+v_a x_3} - (\omega_2+\delta_2+\mu_a)x_7 \\ \dot{x}_8 &= f_8 = \omega_2 x_7 - (\lambda+\mu_a)x_8 \end{aligned}\right\} \tag{28}$$

Evaluating the Jacobian of (28) at anthrax free equilibrium we have

$$J(E_0)=\begin{bmatrix} -A_1 & \alpha_2 & 0 & 0 & 0 & 0 & 0 & 0 \\ \alpha_1 & -A_2 & 0 & \omega_1 & 0 & 0 & -B_1 & 0 \\ 0 & 0 & -A_3 & 0 & 0 & 0 & B_2 & 0 \\ 0 & 0 & \gamma & -A_4 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & -A_5 & \varepsilon_2 & 0 & 0 \\ 0 & 0 & -B_3 & 0 & \varepsilon_1 & -A_6 & 0 & \lambda \\ 0 & 0 & B_4 & 0 & 0 & 0 & -A_7 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & \omega_2 & -A_8 \end{bmatrix} \tag{29}$$

where

$$\left.\begin{aligned} &A_1=(\alpha_1+\mu_h), A_2=(\alpha_2+\mu_h), A_3=(\gamma+\delta_1+\mu_h), A_4=(\mu_h+\omega_1),\\ &A_5=(\varepsilon_1+\mu_a), A_6=(\varepsilon_2+\mu_a), A_7=(\delta_2+\omega_2+\mu_a),\\ &A_8=(\lambda+\mu_a), B_1=B_2=\frac{\Lambda_h(\alpha_1+\mu_h)\beta_h}{\mu_h(\alpha_1+\alpha_2+\mu_h)}, B_3=B_4=\frac{\Lambda_a(\varepsilon_1+\mu_a)\beta_a}{\mu_a(\varepsilon_1+\varepsilon_2+\mu_a)} \end{aligned}\right\}$$

$$w_1=\frac{\alpha_2}{A_1}w_2$$

$$w_2=\frac{\alpha_1\alpha_2}{A_1A_2}w_2+\left(\frac{\omega_1\gamma B_2B_4}{A_2A_4A_1A_7}-\frac{B_1B_4}{A_2A_7}\right)w_3$$

$$w_3=\frac{B_2}{A_1}\frac{B_4}{A_7}w_3$$

$$w_4=\frac{\gamma B_2B_4}{A_4A_1A_7}w_3$$

$$w_5=\frac{\varepsilon_2}{A_5}w_6$$

$$w_6=\frac{\varepsilon_1\varepsilon_2}{A_6A_5}w_6+\left(\frac{\lambda\omega_2B_4}{A_6A_7A_8}-\frac{B_3}{A_6}\right)w_3$$

$$w_7=\frac{B_4}{A_7}w_3$$

$$w_8=\frac{\omega_2B_4}{A_7A_8}w_3$$

$$v_1 = \frac{\alpha_1}{A_1} v_2$$

$$v_2 = \frac{\alpha_1 \alpha_2}{A_1 A_2} v_2$$

$$v_3 = \frac{\gamma v_4 \omega_1}{A_3 A_4} v_2 - \frac{B_3 v_6}{A_3} + \frac{B_4}{A_3}\left(\frac{A_3}{(A_3 - B_4)}\left(\left(\frac{B_2}{A_7}\frac{\gamma v_4 \omega_1}{A_3 A_4} - \frac{B_1}{A_7}\right)v_2 + \left(\frac{\lambda \omega_2}{A_7 A_8} - \frac{B_3}{A_3}\right)v_6\right)\right)$$

$$v_4 = \frac{\omega_1}{A_4} v_2$$

$$v_5 = \frac{\varepsilon_1}{A_5} v_6$$

$$v_6 = \frac{\varepsilon_1 \varepsilon_2}{A_5 A_6} v_6$$

$$v_7 = \frac{A_3}{(A_3 - B_4)}\left(\left(\frac{B_2}{A_7}\frac{\gamma v_4 \omega_1}{A_3 A_4} - \frac{B_1}{A_7}\right)v_2 + \left(\frac{\lambda \omega_2}{A_7 A_8} - \frac{B_3}{A_3}\right)v_6\right)$$

$$v_8 = \frac{\lambda}{A_8} v_6$$

Computation of a and b.

$v_1 = v_2, ..., v_8 \neq 0,$ There are no partial derivatives equal to zero.

$$a = \sum_{k,i,j=1}^{n} v_k w_i w_j \frac{\partial^2 f_k}{\partial x_i \partial x_j}(0,0)$$

$$\frac{\partial^2 f}{\partial x_2 \partial x_6} = \Phi, \frac{\partial^2 f}{\partial x_6 \partial x_3} = \beta_a,$$

$$a = \left(\frac{\omega_1 \gamma B_2 B_4}{A_2 A_4 A_1 A_7} - \frac{B_1 B_4}{A_2 A_7}\right) v_2 \Phi w_3 - v_2 \frac{\alpha \alpha_1}{A_1 A_2} \Phi w_2 + \frac{B_2}{A_1}\frac{B_4}{A_7} w_3 v_3 - \frac{\varepsilon_1 \varepsilon_2}{A_6 A_5} w_6 \left(\frac{\lambda \omega_2 B_4}{A_6 A_7 A_8} - \frac{B_3}{A_6}\right) w_3 \beta_a v_2 v_6 + \frac{B_4}{A_7} \beta_a v_2 w_3 v_7 > 0$$

$$\frac{\partial^2 f}{\partial \Phi \partial x_7} = -\frac{\Lambda_h (\alpha_1 + \mu_h)}{\mu_h (\alpha_1 + \alpha_2 + \mu_h)}$$

$$b = -\frac{\Lambda_h (\alpha_1 + \mu_h) \alpha_1 \alpha_2}{\mu_h (\alpha_1 + \alpha_2 + \mu_h) A_1 A_2} v_2 w_2 < 0$$

From the above computation, we have that $a > 0$ and $b < 0$. The local dynamics of system (28) around equilibrium are totally governed by the signs of a and b base on the following conditions:

i. $a > 0,\ b > 0,$ when $\Phi < 0$ with $|\theta| << 1,\ 0$ is locally asymptotically stable, and there exists a positive unstable equilibrium; when $0 < \theta << 1,$ The equilibrium is unstable and there exists a negative and locally asymptotically stable equilibrium.

ii. $a < 0,\ b < 0$ when $\Phi < 0$ with $|\theta| << 1,\ 0$ is unstable; when $0 < \theta << 1,$ the equilibrium is locally asymptotically stable, and there exists a positive unstable equilibrium.

iii. $a > 0, b < 0,$ when $\Phi < 0$ with $|\theta| << 1,$ 0 is unstable, and there exists a locally asymptotically stable negative equilibrium; when $0 < \theta << 1,$ 0 is stable, and a positive unstable equilibrium appears.

iv. $a < 0, \ b > 0,$ when Φ changes from negative to positive, 0 changes its stability from stable to unstable. Correspondingly, a negative unstable equilibrium becomes positive and locally asymptotically stable. Particularly if $a > 0,$ and $b > 0,$ then a backward bifurcation occurs at $\theta = 0:$

Having obtained $a > 0, b < 0,$ therefore as established in (Castillo Chavez and Song, 2004), we conclude that when $\Phi < 0$ with $\Phi << 1,$ E_0 is unstable and there exists a locally asymptotically stable negative equilibrium but for $0 < \Phi << 1,$ E_1 is stable and a positive unstable equilibrium appears.

3.8 Sensitivity analysis of the model parameters

Sensitivity analysis helps to check and identify the parameters that have impact on the basic reproductive number R_0. To carry out the analysis, we followed the technique outlined by (Chitnis *et al*., 2008) and (Blower and Dowlatabadi, 1994). This technique develops a formula to obtain the sensitivity index of all the basic parameters, defined as:

$\Delta_x^{R_0} = \frac{\partial R_0}{\partial x} \times \frac{x}{R_0}$, where χ represents all the basic parameters.

Solving for the parameters of interest, we obtained the results as presented in table 2

Table 2: Sensitivity indices for R_0

Par.	Baseline values	References	Sensitivity Index	Remarks
α_1	0.004	Assumed	-0.05865103	Negative
α_2	0.3	Assumed	-0.43988269	Negative
β_a	0.02	Baloba *et al.*, (2020)	+0.5000000	Positive
Λ_a	0.99	Sinkie *et al.*, (2016)	+0.5000000	Positive
β_h	0.0001	Baloba *et al.*, (2020)	+0.5000000	Positive
Λ_h	0.92	Sinkie *et al.*, (2016)	+0.5000000	Positive
ε_1	0.2	Assumed	-0.48780487	Negative
ε_2	0.004	Osman *et al.*, (2018)	-0.00975609	Negative
μ_h	0.0001	Baloba *et al.*, (2022)	-0.50224631	Positive
μ_a	0.0001	Baloba *et al.*, (2022)	-0.00243909	Negative
ω_2	0.0025	Baloba *et al.*, (2022)	-0.0000000	Negative
δ_1	0.6	Baloba *et al.*,(2022)	-0.46801872	Negative
δ_2	0.5	Assumed	+0.06598000	Positive
γ	0.04	Baloba *et al.*,(2022)	-0.03120125	Negative

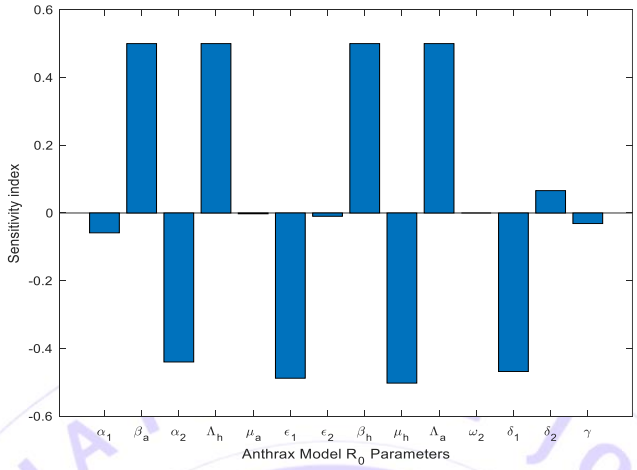

Figure 2: PRCC of the influence of each parameter on the anthrax model R_0 .

4.0 Numerical simulations

In this section we examine the dynamics of the population plotted against time. We use the variables and parameters value in the Table 1 to carry out the simulation. The results are presented in Figures (2) - (8) using the following strategies:

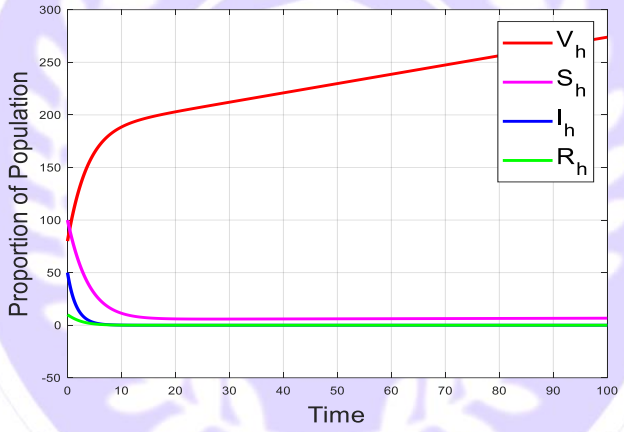

Figure 3: Showing the dynamics of anthrax model for only the human population

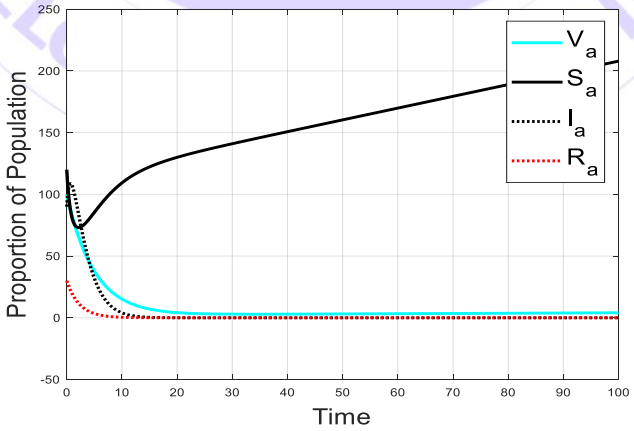

Figure 4: Dynamics of anthrax model for only the animal population

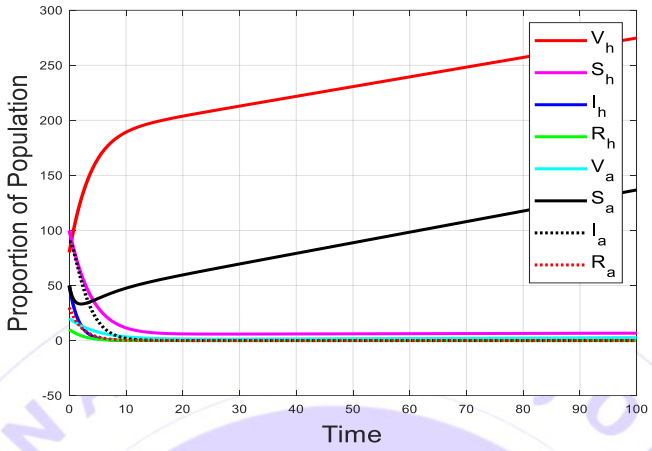

Figure 5: Dynamics of anthrax model for both human and animal population

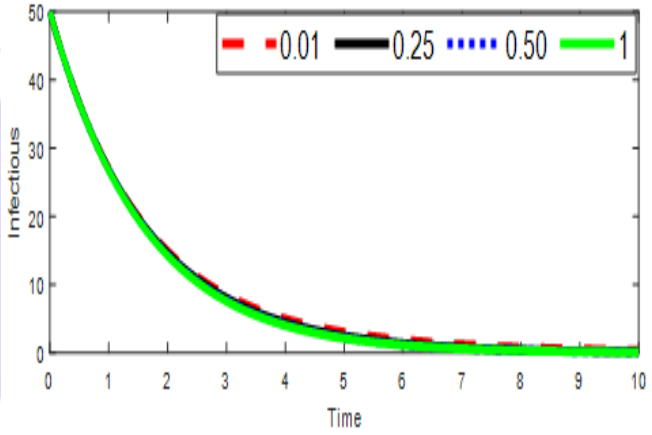

Figure 6: Dynamics of the anthrax model with variations in vaccination rate in the human population

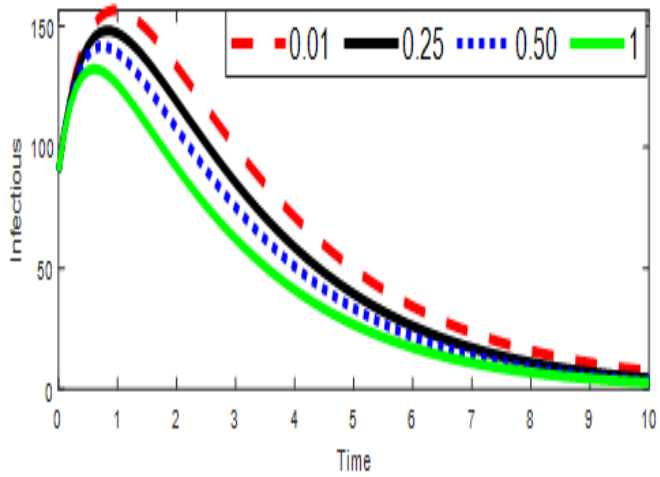

Figure 7: Dynamics of the anthrax model with variations in vaccination rate

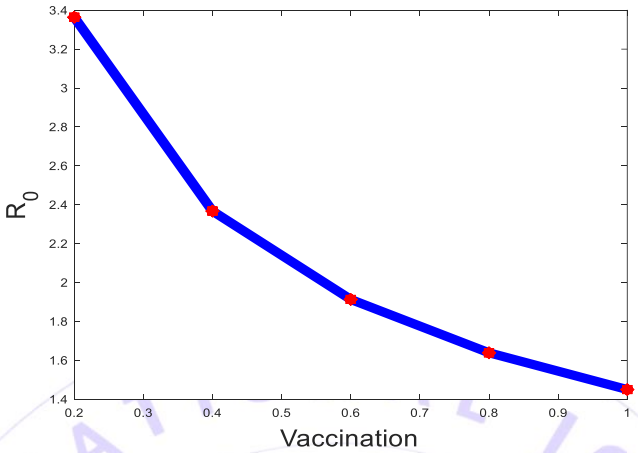

Figure 8: Plot of the basic reproduction number with vaccination varying

5. Discussion of Results

In this section, the focus is to discuss the analytical result and that of the numerical simulation as shown in Figures (2) – (8).

5.1 Analytical results

In this study, result of the analysis carried out in section 3.1 on the formulated model clearly establish the positivity of solutions, showing that all the state variables are non-negative for all time (t) in line with the result of Osman *et al*, (2018). What this implies is that the model is epidemiologically meaningful as there cannot be negative living thing and hence good for study. Also, the boundedness property and the feasible region where the model was found to be positively invariant model were established, meaning that the Anthrax model of system (1) is not just epidemiologically meaningful but also mathematically well posed in a feasible region.

The result of sections 3.2 and 3.2.1 established the steady states of the models in the absence of anthrax, this further gives epidemiological meaning to the model such that even in the absence of disease the system will still exists as shown in equation (10). Similar result was obtained for the endemic equilibrium represented in equation (11). The Next generation matrix method by Van den Driesch and Watmoug, 2002; Namamejj, 2011 was used to established the reproduction number of the model. Equations (14) describe the number of infection generated by either infected human or animal over the expected infection period in a completely susceptible human or animal population. The local stability of the disease free and endemic equilibrium exists when the basic reproduction number is less or greater than unity, respectively. If the value of R_0 is less than one then the disease free equilibrium is locally stable, and if it exceeds, the endemic equilibrium is locally stable. Using the Routh-Hurwitz method our results shows that the anthrax model is locally asymptomatically stable. By saying an equilibrium point is local it means the initial conditions that start near an equilibrium point stay near that equilibrium point. On the other hand, an equilibrium point is (locally) asymptotically stable if it is stable and, in addition, the state of the system converges to the equilibrium point as time increases. Bifurcation analysis was carried out in all the models and the results shows that the anthrax model does not exhibit backward bifurcation. What this means is that there is only one stability point existing in the system and so the epidemiological requirement of reproduction number being less than unity becomes a necessary and sufficient condition for the disease elimination. The result from the sensitivity analysis shows that; Infection rate of susceptible animal, Recruitment rate of animal, Natural death rate in animals, Recruitment rate of human, Infection rate of susceptible human, Disease induced death of the human population are positive parameters and this means that they account for the rise in the reproduction number which will lead to anthrax outbreak in the population. Any increase in any of these parameters when other parameters are place constant will amount to increase in the spread of the disease. Likewise the parameters with negative indices are $(\alpha_1, \alpha_2, \varepsilon_1, \varepsilon_2 \mu_a, \delta_1, \gamma)$ and it implies that an increase in one of these parameters while maintaining the others lowers the effective reproduction number, and hence lowering the disease spread in the population.

5.2 Discussion of numerical simulations

Figure 3 represents the dynamics of the anthrax model with consideration of only the human population. The plot shows the susceptible human population increasing while the infected human and recovery human population

reduces as the vaccinated individuals increases which actually conform to reality. Also the plot of figure 4 shows that as vaccination implementation is placed constant in the animal population, the infected and recovery animal population reduces. Figure 5 shows the dynamics of the entire system of the anthrax model and the impact of increase or decrease in vaccination. Also figure 6 and 7 further shows the plots are the dynamics of the infection classes as vaccination is been varies with different values. Increasing the level of vaccination decreases not just the disease prevalence as shown in Figure 6 and 7 but it also brings down the disease incidence as obviously indicated on the plot of Figure (8) where the basic reproduction number is seen to be declining as vaccination rate is raised up. The general result simply shows that vaccination is a key solution to bring down and probably eradicate anthrax disease in the population.

6. Conclusion

The study successfully identifies the high possibility of the spread of anthrax disease base on the mode of transmission and as such a deterministic model for the anthrax disease is formulated to understand the dynamics of the disease and proffer solutions by incorporating vaccination for both the human population and the animal population as a control measure. The basic properties of the model were analyzed analytically and result shows the model conformed to realities and is epidemiologically well posed. To be able to follow the dynamics of the spread of the diseases, the basic reproduction number which determined the rate of new secondary infection was computed and the disease-free equilibrium point were proven to be locally and globally asymptotically stable. Sensitivity analysis shows that, raising one of the parameters with positive indices will increase the risk of the disease outbreak and raising parameters with negative indices will reduce the disease outbreak. The result from the numerical simulation suggests that the burden of Anthrax disease both in the human and animal populations can be brought down if when vaccination is implemented and the rate is increased in both populations. Based on the finding of the study, it is strongly recommended that the government, stakeholders, NGO and other policy makers with respect to disease intervention programs should make policy which will fully implement vaccination on both the human and animal population to help eradicate anthrax disease. In addition, sensitizing the people on the need for proper sanitation when dealing with animals or any animal products is highly recommended too

Reference:

Blower S.M., Dowlatabadi H. (1994). Sensitivity and uncertainty analysis of complex models of disease transmission: An hiv model, as an example *International Statistical Review/Revue Internationale de Statistique*. pp. 229-243

Baloba, E. B., Seidu, B. and Bornaa, C. S. Mathematical analysis of the effects of controls on the transmission dynamics of anthrax in both animal and human populations. *Computational and Mathematical Methods in Medicine*, 2020 (2020), 1581358. https://doi.org/10.1155/2020/1581358.

Carlos Castillo-Chavez and Baojun Song. (2004). Dynamical Models of Tuberculosis and Their Applications. *Mathematical Bioscience and Engineering*, **1**(2), 361-404

Castillo-Chavez, C., Feng, Z. and Huang, W. (2002). On the Computation of R0 and its Role on Global Stability; *Institute for mathematics and its applications*, 125,229.

Centre for disease Control and Prevention (2020), National Center for Emerging and Zoonotic Infectious Diseases (NCEZID), Division of High-Consequence Pathogens and Pathology (DHCPP). http://www.cdc.gov/*Anthrax*/health-professionals/index.html Retrieved 25 January 2024.

Chitnis N, Hyman J.M and Cushing J.M. (2008) Determining important parameters in the spread of malaria through the sensitivity analysis of a mathematical model. *Bull Math Biol*.70(5):1272-96. doi: 10.1007/s11538-008-9299-0

Diekmann, O., Heesterbeek, J.A.P. and Roberts, M.G. (2010). The Construction of Next-Generation Matrices for Compartmental Epidemic Models. *Journal of The Royal Society Interface*. 7 (47), 873–885.

Diekmann, O. and Heesterbeek, J.A.P. (2000). *Mathematical Modelling of Infectious*

Disease:Model Building, Analysis and Interpretation. New York, NY: John Wiley and Son, Inc

Elijah B. Baloba and Baba Seidu (2022). A mathematical model of anthrax epidemic with behavioural change. *Journal of Mathematical Modelling*,2(4): 243–256 DIO:http://dx.doi.org/10.3934/mmc.2022023 and Control.

Osman, S., Makinde, O. D., Theuri, M. D. (2018) Mathematical modelling of the transmission dynamics of anthrax in human and animal population. *Mathematical Theory and Modeling*, 8: 47–67

Shahram Rezapour, Sina Etemad and Hakimeh Mohammadi (2020). A mathematical analysis of a systemof Caputo–Fabrizio fractional differential equations for the anthrax disease model in animals. *Advances in Difference Equations* 2020:481 https://doi.org/10.1186/s13662-020-02937-x

Saad-Roy CM, van den Driessche P, Yakubu A.A. (2017). A Mathematical Model of Anthrax Transmission in Animal Populations. Bull Math Biol. 2017 Feb;79(2):303-324. doi: 10.1007/s11538-016-0238-1.

Sinkie, Z. M. and Murthy, N. S. (2016). Modeling and simulation study of anthrax attack On environment, *Journal of Multidisciplinary Engineering Science and Technology*, 3, 4574–4578.

World Health Organization, (2016) https://www.who.int/europe/news-room/questions -and-answers/item/anthrax. Retrieved 20, January 2024

APENDIX

$$A_0 = 1$$

$$A_1 = r_1 + r_2 + r_3 + r_4 + r_5 + r_6 + r_7 + r_8$$

$$\begin{aligned} A_2 = {} & (r_6(r_2 + r_3 + r_4 + r_5) + r_3(r_1 + r_2) - \alpha_1\alpha_2 - \varepsilon_1\varepsilon_2 - b_1c_2r_1r_2 \\ & + r_7(r_1 + r_2 + r_3 + r_4 + r_5 + r_6) + r_4(r_1 + r_2 + r_3) \\ & + r_8(r_1 + r_2 + r_3 + r_4 + r_5 + r_6 + r_7) + r_5(+r_1 + r_2 + r_3 + r_4)) \end{aligned}$$

$$\begin{aligned} A_3 = {} & (r_6(r_3(r_1 + r_2) - \alpha_1\alpha_2 + r_1r_2 + r_4(r_1 + r_2 + r_3) + r_5(r_1 + r_2 + r_3 + r_4) \\ & + r_4(r_3(r_1 + r_2) - \alpha_1\alpha_2 + r_1r_2) + r_5(r_3(r_1 + r_2) - \alpha_1\alpha_2 + r_1r_2 \\ & + r_4(r_1 + r_2 + r_3)) - r_3(\alpha_1\alpha_2 - r_1r_2) + r_7(r_6(r_1 + r_2 + r_3 + r_4 + r_5) \\ & + r_3(r_1 + r_2) - \alpha_1\alpha_2 - \varepsilon_1\varepsilon_2 + r_1r_2 + r_4(r_1 + r_2 + r_3) + r_5(r_1 + r_2 + r_3 + r_4)) \\ & + r_8(r_6(r_1 + r_2 + r_3 + r_4 + r_5) + r_3(r_1 + r_2) - \alpha_1\alpha_2 - \varepsilon_1\varepsilon_2 - b_1c_1 \\ & + r_1r_2 + r_7(r_1 + r_2 + r_3 + r_4 + r_5 + r_6) + r_4(r_1 + r_2 + r_3) + r_5(r_1 + r_2 + r_3 + r_4)) \\ & - \varepsilon_1\varepsilon_2(r_1 + r_2 + r_3 + r_4 + r_5) + \varepsilon_1\varepsilon_2r_5 + b_1c_2r_3 - b_1c_2(r_1 + r_2 + r_3 + r_4 + r_5 + r_6)) \end{aligned}$$

$$
\begin{aligned}
A_4 = (&r_8(r_6(r_3(r_1+r_2)-\alpha_1\alpha_2+r_1r_2+r_4(r_1+r_2+r_3)\\
&+r_5(r_1+r_2+r_3+r_4))+r_4\left(r_3\left(r_1+r_2\right)-\alpha_1\alpha_2+r_1r_2\right)\\
&+r_4\left(r_3\left(r_1+r_2\right)-\alpha_1\alpha_2+r_1r_2+r_4\left(r_1+r_2+r_3\right)\right)-\\
&r_3\left(\alpha_1\alpha_2-r_1r_2\right)+r_7(r_6\left(r_1+r_2+r_3+r_4+r_5\right)+r_3\left(r_1+r_2\right)\\
&-\alpha_1\alpha_2-\varepsilon_1\varepsilon_2+r_1r_2+r_4\left(r_1+r_2+r_3\right)+r_5\left(r_1+r_2+r_3+r_4\right))\\
&-\varepsilon_1\varepsilon_2\left(r_1+r_2+r_3+r_4+r_5\right)+\varepsilon_1\varepsilon_2r_5+b_1c_2r_3\\
&-b_1c_2\left(r_1+r_2+r_3+r_4+r_5+r_6\right))+r_7(r_6(r_3\left(r_1+r_2\right)-\alpha_1\alpha_2\\
&+r_1r_2+r_4\left(r_1+r_2+r_3\right)+r_5\left(r_1+r_2+r_3+r_4\right))\\
&+r_4\left(r_3\left(r_1+r_2\right)-\alpha_1\alpha_2+r_1r_2\right)+r_5(r_3\left(r_1+r_2\right)-\alpha_1\alpha_2+r_1r_2\\
&+r_4\left(r_1+r_2+r_3\right))-r_3\left(\alpha_1\alpha_2-r_1r_2\right)-\varepsilon_1\varepsilon_2\left(r_1+r_2+r_3+r_4+r_5\right)\\
&+\varepsilon_1\varepsilon_2r_5)+r_5(r_4(r_3\left(r_1+r_2\right)-\alpha_1\alpha_2+r_1r_2)-r_3\left(\alpha_1\alpha_2-r_1r_2\right))\\
&+r_6(r_4\left(r_3\left(r_1+r_2\right)-\alpha_1\alpha_2+r_1r_2\right)+r_5(r_3\left(r_1+r_2\right)-\alpha_1\alpha_2+r_1r_2\\
&+r_4\left(r_1+r_2+r_3\right))-r_3\left(\alpha_1\alpha_2-r_1r_2\right))-b_1c_2(r_6\left(r_1+r_2+r_3+r_4+r_5\right)\\
&+r_3\left(r_1+r_2\right)-\alpha_1\alpha_2-\varepsilon_1\varepsilon_2+r_1r_2+r_4\left(r_1+r_2+r_3\right)+r_5\left(r_1+r_2+r_3+r_4\right))\\
&-\varepsilon_1\varepsilon_2{r_5}^2-\varepsilon_1\varepsilon_2(r_3\left(r_1+r_2\right)-\alpha_1\alpha_2+r_1r_2+r_4\left(r_1+r_2+r_3\right)\\
&+r_5\left(r_1+r_2+r_3+r_4\right))-b_1c_2{r_3}^2-r_3r_4\left(\alpha_1\alpha_2-r_1r_2\right)\\
&+b_1c_2r_3\left(r_1+r_2+r_3+r_4+r_5+r_6\right)+\varepsilon_1\varepsilon_2r_5\left(r_1+r_2+r_3+r_4+r_5\right))\\
A_5 = (&r_7(r_5\left(r_4\left(r_3\left(r_1+r_2\right)-\alpha_1\alpha_2+r_1r_2\right)-r_3\left(\alpha_1\alpha_2-r_1r_2\right)\right)+r_6(r_4\left(r_3\left(r_1+r_2\right)-\alpha_1\alpha_2+r_1r_2\right)\\
&+r_5\left(r_3\left(r_1+r_2\right)-\alpha_1\alpha_2+r_1r_2+r_4\left(r_1+r_2+r_3\right)\right)-r_3\left(\alpha_1\alpha_2-r_1r_2\right))-\varepsilon_1\varepsilon_2{r_5}^2-\varepsilon_1\varepsilon_2(r_3\left(r_1+r_2\right)-\\
&\alpha_1\alpha_2+r_1r_2+r_4\left(r_1+r_2+r_3\right)+r_5\left(r_1+r_2+r_3+r_4\right)-r_3r_4\left(\alpha_1\alpha_2-r_1r_2\right)+\varepsilon_1\varepsilon_2r_5\left(r_1+r_2+r_3+r_4+r_5\right))\\
&+r_8(r_7(r_6\left(r_3\left(r_1+r_2\right)-\alpha_1\alpha_2+r_1r_2+r_4\left(r_1+r_2+r_3\right)+r_5\left(r_1+r_2+r_3+r_4\right)\right)+r_4\left(r_3\left(r_1+r_2\right)-\alpha_1\alpha_2+r_1r_2\right)\\
&+r_5\left(r_3\left(r_1+r_2\right)-\alpha_1\alpha_2+r_1r_2+r_4\left(r_1+r_2+r_3\right)\right)-r_3\left(\alpha_1\alpha_2-r_1r_2\right)-\varepsilon_1\varepsilon_2\left(r_1+r_2+r_3+r_4+r_5\right)+\varepsilon_1\varepsilon_2r_5)\\
&+r_5\left(r_4\left(r_3\left(r_1+r_2\right)-\alpha_1\alpha_2+r_1r_2\right)-r_3\left(\alpha_1\alpha_2-r_1r_2\right)\right)+r_6(r_4\left(r_3\left(r_1+r_2\right)-\alpha_1\alpha_2+r_1r_2\right)+r_5(r_3\left(r_1+r_2\right)\\
&-\alpha_1\alpha_2+r_1r_2+r_4\left(r_1+r_2+r_3\right))-r_3\left(\alpha_1\alpha_2-r_1r_2\right))-b_1c_2(r_6\left(r_1+r_2+r_3+r_4+r_5\right)+r_3\left(r_1+r_2\right)\\
&-\alpha_1\alpha_2-\varepsilon_1\varepsilon_2+r_1r_2+r_4\left(r_1+r_2+r_3\right)+r_5\left(r_1+r_2+r_3+r_4\right))-\varepsilon_1\varepsilon_2{r_5}^2-\varepsilon_1\varepsilon_2(r_3\left(r_1+r_2\right)-\\
&\alpha_1\alpha_2+r_1r_2+r_4\left(r_1+r_2+r_3\right)+r_5\left(r_1+r_2+r_3+r_4\right))-b_1c_2{r_3}^2-r_3r_4\left(\alpha_1\alpha_2-r_1r_2\right)\\
&+b_1c_2r_3\left(r_1+r_2+r_3+r_4+r_5+r_6\right)+\varepsilon_1\varepsilon_2r_5\left(r_1+r_2+r_3+r_4+r_5\right))+r_6(r_5(r_4\left(r_3\left(r_1+r_2\right)-\alpha_1\alpha_2+r_1r_2\right)\\
&-r_3\left(\alpha_1\alpha_2-r_1r_2\right))-r_3r_4\left(\alpha_1\alpha_2-r_1r_2\right))+\varepsilon_1\varepsilon_2{r_5}^3+b_1c_2{r_3}^3-b_1c_2(r_6(r_3\left(r_1+r_2\right)-\alpha_1\alpha_2+r_1r_2\\
&+r_4\left(r_1+r_2+r_3\right)+r_5\left(r_1+r_2+r_3+r_4\right))+r_4\left(r_3\left(r_1+r_2\right)-\alpha_1\alpha_2+r_1r_2\right)+r_5(r_3\left(r_1+r_2\right)-\alpha_1\alpha_2+r_1r_2\\
&+r_4\left(r_1+r_2+r_3\right))-r_3\left(\alpha_1\alpha_2-r_1r_2\right)-\varepsilon_1\varepsilon_2\left(r_1+r_2+r_3+r_4+r_5\right)+\varepsilon_1\varepsilon_2r_5)-\varepsilon_1\varepsilon_2(r_4\left(r_3\left(r_1+r_2\right)-\alpha_1\alpha_2+r_1r_2\right)\\
&+r_5\left(r_3\left(r_1+r_2\right)-\alpha_1\alpha_2+r_1r_2+r_4\left(r_1+r_2+r_3\right)\right)-r_3\left(\alpha_1\alpha_2-r_1r_2\right))-\varepsilon_1\varepsilon_2{r_5}^2\left(r_1+r_2+r_3+r_4+r_5\right)\\
&r_3r_4r_5\left(\alpha_1\alpha_2-r_1r_2\right)+b_1c_2r_3(r_5\left(r_1+r_2+r_3+r_4+r_5\right)+r_3\left(r_1+r_2\right)-\alpha_1\alpha_2-\varepsilon_1\varepsilon_2+r_1r_2\\
&+r_4\left(r_1+r_2+r_3\right)+r_5\left(r_1+r_2+r_3+r_4\right))+\varepsilon_1\varepsilon_2r_5(r_3\left(r_1+r_2\right)-\alpha_1\alpha_2+r_1r_2+r_4\left(r_1+r_2+r_3\right)\\
&+r_5\left(r_1+r_2+r_3+r_4\right))-b_1c_2{r_3}^2\left(r_1+r_2+r_3+r_4+r_5+r_6\right))
\end{aligned}
$$

$$A_6 = (r_7(r_6\left(r_5\left(r_4\left(r_3\left(r_1+r_2\right)-\alpha_1\alpha_2+r_1r_2\right)-r_3\left(\alpha_1\alpha_2-r_1r_2\right)\right)-r_3r_4\left(\alpha_1\alpha_2-r_1r_2\right)\right)+\varepsilon_1\varepsilon_2{r_5}^3$$
$$-\varepsilon_1\varepsilon_2\left(r_4\left(r_3\left(r_1+r_2\right)-\alpha_1\alpha_2+r_1r_2\right)+r_5\left(r_3\left(r_1+r_2\right)-\alpha_1\alpha_2+r_1r_2+r_4\left(r_1+r_2+r_3\right)\right)-r_3\left(\alpha_1\alpha_2-r_1r_2\right)\right)$$
$$\varepsilon_1\varepsilon_2{r_5}^2\left(r_1+r_2+r_3+r_4+r_5\right)-r_3r_4r_5\left(\alpha_1\alpha_2-r_1r_2\right)+\varepsilon_1\varepsilon_2r_5(r_3\left(r_1+r_2\right)-$$
$$\alpha_1\alpha_2+r_1r_2+r_4\left(r_1+r_2+r_3\right)+r_5\left(r_1+r_2+r_3+r_4\right)))+r_8(r_7(r_5(r_4(r_3\left(r_1+r_2\right)$$
$$-\alpha_1\alpha_2+r_1r_2)-r_3\left(\alpha_1\alpha_2-r_1r_2\right))+r_6(r_4\left(r_3\left(r_1+r_2\right)-\alpha_1\alpha_2+r_1r_2\right)+r_5(r_3\left(r_1+r_2\right)-\alpha_1\alpha_2+r_1r_2$$
$$+r_4\left(r_1+r_2+r_3\right))-r_3\left(\alpha_1\alpha_2-r_1r_2\right))-\varepsilon_1\varepsilon_2{r_5}^2-\varepsilon_1\varepsilon_2(r_3\left(r_1+r_2\right)-\alpha_1\alpha_2+r_1r_2+r_4\left(r_1+r_2+r_3\right)$$
$$+r_5\left(r_1+r_2+r_3+r_4\right))-r_3r_4\left(\alpha_1\alpha_2-r_1r_2\right)+\varepsilon_1\varepsilon_2r_5\left(r_1+r_2+r_3+r_4+r_5\right))+r_6(r_5(r_4(r_3\left(r_1+r_2\right)$$
$$-\alpha_1\alpha_2+r_1r_2)-r_3\left(\alpha_1\alpha_2-r_1r_2\right))-r_3r_4\left(\alpha_1\alpha_2-r_1r_2\right))+\varepsilon_1\varepsilon_2{r_3}^3+b_1c_2r_3{}^3-b_1c_2(r_6(r_3\left(r_1+r_2\right)-$$
$$\alpha_1\alpha_2+r_1r_2+r_4\left(r_1+r_2+r_3\right)+r_5\left(r_1+r_2+r_3+r_4\right))+r_4\left(r_3\left(r_1+r_2\right)-\alpha_1\alpha_2+r_1r_2\right)+r_5(r_3\left(r_1+r_2\right)-\alpha_1\alpha_2$$
$$+r_1r_2+r_4\left(r_1+r_2+r_3\right))-r_3\left(\alpha_1\alpha_2-r_1r_2\right)-\varepsilon_1\varepsilon_2\left(r_1+r_2+r_3+r_4+r_5\right)+\varepsilon_1\varepsilon_2r_5)$$
$$-\varepsilon_1\varepsilon_2(r_4\left(r_3\left(r_1+r_2\right)-\alpha_1\alpha_2+r_1r_2\right)+r_5\left(r_3\left(r_1+r_2\right)-\alpha_1\alpha_2+r_1r_2+r_4\left(r_1+r_2+r_3\right)\right)-r_3\left(\alpha_1\alpha_2-r_1r_2\right))$$
$$-\varepsilon_1\varepsilon_2{r_5}^2\left(r_1+r_2+r_3+r_4+r_5\right)-r_3r_4r_5\left(\alpha_1\alpha_2-r_1r_2\right)$$
$$+b_1c_2r_3\left(r_6\left(r_1+r_2+r_3+r_4+r_5\right)+r_3\left(r_1+r_2\right)-\alpha_1\alpha_2-\varepsilon_1\varepsilon_2+r_1r_2+r_4\left(r_1+r_2+r_3\right)+r_5\left(r_1+r_2+r_3+r_4\right)\right)$$
$$+\varepsilon_1\varepsilon_2r_5\left(r_3\left(r_1+r_2\right)-\alpha_1\alpha_2+r_1r_2+r_4\left(r_1+r_2+r_3\right)+r_5\left(r_1+r_2+r_3+r_4\right)\right)-b_1c_2r_3{}^2\left(r_1+r_2+r_3+r_4+r_5+r_6\right))$$
$$-\varepsilon_1\varepsilon_2{r_5}^4-b_1c_2r_3{}^4-\varepsilon_1\varepsilon_2\left(r_5\left(r_4\left(r_3\left(r_1+r_2\right)-\alpha_1\alpha_2+r_1r_2\right)-r_3\left(\alpha_1\alpha_2-r_1r_2\right)\right)-r_3r_4\left(\alpha_1\alpha_2-r_1r_2\right)\right)$$
$$-b_1c_2(r_5\left(r_4\left(r_3\left(r_1+r_2\right)-\alpha_1\alpha_2+r_1r_2\right)-r_3\left(\alpha_1\alpha_2-r_1r_2\right)\right)$$
$$+r_6(r_4\left(r_3\left(r_1+r_2\right)-\alpha_1\alpha_2+r_1r_2\right)+r_5(r_3\left(r_1+r_2\right)-\alpha_1\alpha_2+r_1r_2+r_4\left(r_1+r_2+r_3\right))$$
$$-r_3\left(\alpha_1\alpha_2-r_1r_2\right))-\varepsilon_1\varepsilon_2{r_5}^2-\varepsilon_1\varepsilon_2(r_3\left(r_1+r_2\right)-\alpha_1\alpha_2+r_1r_2+r_4\left(r_1+r_2+r_3\right)$$
$$+r_5\left(r_1+r_2+r_3+r_4\right))-r_3r_4\left(\alpha_1\alpha_2-r_1r_2\right)+\varepsilon_1\varepsilon_2r_5\left(r_1+r_2+r_3+r_4+r_5\right))+b_1c_2r_3(r_6(r_3\left(r_1+r_2\right)-$$
$$\alpha_1\alpha_2+r_1r_2+r_4\left(r_1+r_2+r_3\right)+r_5\left(r_1+r_2+r_3+r_4\right))+r_4\left(r_3\left(r_1+r_2\right)-\alpha_1\alpha_2+r_1r_2\right)+r_5(r_3\left(r_1+r_2\right)$$
$$-\alpha_1\alpha_2+r_1r_2+r_4\left(r_1+r_2+r_3\right))-r_3r_4\left(\alpha_1\alpha_2-r_1r_2\right)-\varepsilon_1\varepsilon_2\left(r_1+r_2+r_3+r_4+r_5\right))++\varepsilon_1\varepsilon_2{r_5}^3$$
$$-\varepsilon_1\varepsilon_2\left(r_4\left(r_3\left(r_1+r_2\right)-\alpha_1\alpha_2+r_1r_2\right)+r_5\left(r_3\left(r_1+r_2\right)-\alpha_1\alpha_2+r_1r_2+r_4\left(r_1+r_2+r_3\right)\right)-r_3\left(\alpha_1\alpha_2-r_1r_2\right)\right)$$
$$-\varepsilon_1\varepsilon_2{r_5}^2\left(r_1+r_2+r_3+r_4+r_5\right)-r_3r_4r_5\left(\alpha_1\alpha_2-r_1r_2\right)+\varepsilon_1\varepsilon_2r_5(r_3\left(r_1+r_2\right)$$

$$A_7 = +\Big(b_1c_2r_3^5 - r_8(\varepsilon_1\varepsilon_2r_5^4 - r_7(r_6(r_5\big(r_4\big(r_3\big(r_1+r_2\big)-\alpha_1\alpha_2+r_1r_2\big)-r_3\big(\alpha_1\alpha_2-r_1r_2\big)\big)-r_3r_4\big(\alpha_1\alpha_2-r_1r_2\big)\Big)$$

$$+\varepsilon_1\varepsilon_2r_5^3-\varepsilon_1\varepsilon_2\begin{pmatrix} r_4\big(r_3\big(r_1+r_2\big)-\alpha_1\alpha_2+r_1r_2\big)+r_5\big(r_3\big(r_1+r_2\big)-\alpha_1\alpha_2+r_1r_2+r_4\big(r_1+r_2+r_3\big)\big)\\ -r_3\big(\alpha_1\alpha_2-r_1r_2\big)\end{pmatrix}$$

$$+\varepsilon_1\varepsilon_2r_5^3-\varepsilon_1\varepsilon_2\begin{pmatrix} r_4\big(r_3\big(r_1+r_2\big)-\alpha_1\alpha_2+r_1r_2\big)+r_5\big(r_3\big(r_1+r_2\big)-\alpha_1\alpha_2+r_1r_2+r_4\big(r_1+r_2+r_3\big)\big)\\ -r_3\big(\alpha_1\alpha_2-r_1r_2\big)\end{pmatrix}$$

$$+\varepsilon_1\varepsilon_2r_5\big(r_3\big(r_1+r_2\big)\alpha_1\alpha_2+r_1r_2+r_4\big(r_1+r_2+r_3\big)+r_5\big(r_1+r_2+r_3+r_4\big)\big)$$

$$+b_1c_2r_3^4+\varepsilon_1\varepsilon_2\Big(r_5\big(r_4\big(r_3\big(r_1+r_2\big)-\alpha_1\alpha_2+r_1r_2\big)-r_3\big(\alpha_1\alpha_2-r_1r_2\big)\big)-r_3r_4\big(\alpha_1\alpha_2-r_1r_2\big)\Big)$$

$$+b_1c_2(r_5\big(r_4\big(r_3\big(r_1+r_2\big)-\alpha_1\alpha_2+r_1r_2\big)-r_3\big(\alpha_1\alpha_2-r_1r_2\big)\big)+r_6(r_4\big(r_3\big(r_1+r_2\big)-\alpha_1\alpha_2+r_1r_2\big)$$

$$+r_5(r_3\big(r_1+r_2\big)-\alpha_1\alpha_2+r_1r_2+r_4\big(r_1+r_2+r_3\big))-r_3\big(\alpha_1\alpha_2-r_1r_2\big))-\varepsilon_1\varepsilon_2r_5^2-\varepsilon_1\varepsilon_2(r_3\big(r_1+r_2\big)$$

$$-\alpha_1\alpha_2+r_1r_2+r_4\big(r_1+r_2+r_3\big)+r_5\big(r_1+r_2+r_3+r_4\big)-r_3r_4\big(\alpha_1\alpha_2-r_1r_2\big)+\varepsilon_1\varepsilon_2r_5\big(r_1+r_2+r_3+r_4+r_5\big)$$

$$-b_1c_2r_3(r_6(r_3\big(r_1+r_2\big)-\alpha_1\alpha_2+r_1r_2+r_4\big(r_1+r_2+r_3\big)+r_5\big(r_1+r_2+r_3+r_4\big)$$

$$+r_4\big(r_3\big(r_1+r_2\big)-\alpha_1\alpha_2+r_1r_2\big)+r_5(r_3\big(r_1+r_2\big)-\alpha_1\alpha_2+r_1r_2+r_4\big(r_1+r_2+r_3\big))$$

$$-r_3\big(\alpha_1\alpha_2-r_1r_2\big)-\varepsilon_1\varepsilon_2\big(r_1+r_2+r_3+r_4+r_5\big)+\varepsilon_1\varepsilon_2r_5)-\varepsilon_1\varepsilon_2r_5^3\big(r_1+r_2+r_3+r_4+r_5\big)$$

$$-\varepsilon_1\varepsilon_2r_5\Big(r_4\big(r_3\big(r_1+r_2\big)-\alpha_1\alpha_2+r_1r_2\big)+r_5\big(r_3\big(r_1+r_2\big)-\alpha_1\alpha_2+r_1r_2+r_4\big(r_1+r_2+r_3\big)\big)-r_3\big(\alpha_1\alpha_2-r_1r_2\big)\Big)$$

$$-b_1c_2r_3^3\big(r_1+r_2+r_3+r_4+r_5+r_6\big)+b_1c_2r_3^2(r_5\big(r_1+r_2+r_3+r_4+r_5\big)+r_3\big(r_1+r_2\big)-\alpha_1\alpha_2$$

$$-\varepsilon_1\varepsilon_2+r_1r_2+r_4\big(r_1+r_2+r_3\big)+r_5\big(r_1+r_2+r_3+r_4\big))+\varepsilon_1\varepsilon_2r_5^2(r_3\big(r_1+r_2\big)$$

$$-\alpha_1\alpha_2+r_1r_2+r_4\big(r_1+r_2+r_3\big)+r_5\big(r_1+r_2+r_3+r_4\big))+r_3r_4r_5r_6\big(\alpha_1\alpha_2-r_1r_2\big))$$

$$-b_1c_2(r_6\Big(r_5\big(r_4\big(r_3\big(r_1+r_2\big)-\alpha_1\alpha_2+r_1r_2\big)-r_3\big(\alpha_1\alpha_2-r_1r_2\big)\big)-r_3r_4\big(\alpha_1\alpha_2-r_1r_2\big)\Big)$$

$$+\varepsilon_1\varepsilon_2r_5^3-\varepsilon_1\varepsilon_2\begin{pmatrix} r_4\big(r_3\big(r_1+r_2\big)-\alpha_1\alpha_2+r_1r_2\big)+r_5\big(r_3\big(r_1+r_2\big)-\alpha_1\alpha_2+r_1r_2+r_4\big(r_1+r_2+r_3\big)\big)\\ -r_3\big(\alpha_1\alpha_2-r_1r_2\big)\end{pmatrix}$$

$$-\varepsilon_1\varepsilon_2r_5^2\big(r_1+r_2+r_3+r_4+r_5\big)-r_3r_4r_5\big(\alpha_1\alpha_2-r_1r_2\big)+\varepsilon_1\varepsilon_2r_5(r_3\big(r_1+r_2\big)-\alpha_1\alpha_2+r_1r_2+r_4\big(r_1+r_2+r_3\big)$$

$$+r_5\big(r_1+r_2+r_3+r_4\big)))-r_6(\varepsilon_1\varepsilon_2r_5^4+\varepsilon_1\varepsilon_2(r_5\Big(r_4\big(r_3\big(r_1+r_2\big)-\alpha_1\alpha_2+r_1r_2\big)-r_3\big(\alpha_1\alpha_2-r_1r_2\big)\Big)$$

$$
\begin{aligned}
A_8 = \; & \alpha_1\alpha_2 + r_1r_2 + r_4\left(r_1 + r_2 + r_3\right) + r_5\left(r_1 + r_2 + r_3 + r_4\right)) - b_1c_2r_3^2 - r_3r_4\left(\alpha_1\alpha_2 - r_1r_2\right) \\
& (r_7(r_5\left(r_4\left(r_3\left(r_1 + r_2\right) - \alpha_1\alpha_2 + r_1r_2\right) - r_3\left(\alpha_1\alpha_2 - r_1r_2\right)\right) + r_6(r_4\left(r_3\left(r_1 + r_2\right) - \alpha_1\alpha_2 + r_1r_2\right) \\
& + r_5\left(r_3\left(r_1 + r_2\right) - \alpha_1\alpha_2 + r_1r_2 + r_4\left(r_1 + r_2 + r_3\right)\right) - r_3\left(\alpha_1\alpha_2 - r_1r_2\right)) - \varepsilon_1\varepsilon_2r_5^{\,2} - \varepsilon_1\varepsilon_2(r_3\left(r_1 + r_2\right) - \\
& \alpha_1\alpha_2 + r_1r_2 + r_4\left(r_1 + r_2 + r_3\right) + r_5\left(r_1 + r_2 + r_3 + r_4\right)) - r_3r_4\left(\alpha_1\alpha_2 - r_1r_2\right) + \varepsilon_1\varepsilon_2r_5\left(r_1 + r_2 + r_3 + r_4 + r_5\right)) \\
& + r_8(r_7(r_6\left(r_3\left(r_1 + r_2\right) - \alpha_1\alpha_2 + r_1r_2 + r_4\left(r_1 + r_2 + r_3\right) + r_5\left(r_1 + r_2 + r_3 + r_4\right)\right) + r_4\left(r_3\left(r_1 + r_2\right) - \alpha_1\alpha_2 + r_1r_2\right) \\
& + r_5\left(r_3\left(r_1 + r_2\right) - \alpha_1\alpha_2 + r_1r_2 + r_4\left(r_1 + r_2 + r_3\right)\right) - r_3\left(\alpha_1\alpha_2 - r_1r_2\right) - \varepsilon_1\varepsilon_2\left(r_1 + r_2 + r_3 + r_4 + r_5\right) + \varepsilon_1\varepsilon_2r_5) \\
& + r_5\left(r_4\left(r_3\left(r_1 + r_2\right) - \alpha_1\alpha_2 + r_1r_2\right) - r_3\left(\alpha_1\alpha_2 - r_1r_2\right)\right) + r_6(r_4\left(r_3\left(r_1 + r_2\right) - \alpha_1\alpha_2 + r_1r_2\right) + r_5(r_3\left(r_1 + r_2\right) \\
& - \alpha_1\alpha_2 + r_1r_2 + r_4\left(r_1 + r_2 + r_3\right)) - r_3\left(\alpha_1\alpha_2 - r_1r_2\right)) - b_1c_2(r_6\left(r_1 + r_2 + r_3 + r_4 + r_5\right) + r_3\left(r_1 + r_2\right) \\
& - \alpha_1\alpha_2 - \varepsilon_1\varepsilon_2 + r_1r_2 + r_4\left(r_1 + r_2 + r_3\right) + r_5\left(r_1 + r_2 + r_3 + r_4\right)) - \varepsilon_1\varepsilon_2r_5^{\,2} - \varepsilon_1\varepsilon_2(r_3\left(r_1 + r_2\right) - \\
& + b_1c_2r_3\left(r_1 + r_2 + r_3 + r_4 + r_5 + r_6\right) + \varepsilon_1\varepsilon_2r_5\left(r_1 + r_2 + r_3 + r_4 + r_5\right)) + r_6(r_5(r_4\left(r_3\left(r_1 + r_2\right) - \alpha_1\alpha_2 + r_1r_2\right) \\
& - r_3\left(\alpha_1\alpha_2 - r_1r_2\right)) - r_3r_4\left(\alpha_1\alpha_2 - r_1r_2\right)) + \varepsilon_1\varepsilon_2r_5^{\,3} + b_1c_2r_3^{\,3} - b_1c_2(r_6(r_3\left(r_1 + r_2\right) - \alpha_1\alpha_2 + r_1r_2 \\
& + r_4\left(r_1 + r_2 + r_3\right) + r_5\left(r_1 + r_2 + r_3 + r_4\right)) + r_4\left(r_3\left(r_1 + r_2\right) - \alpha_1\alpha_2 + r_1r_2\right) + r_5(r_3\left(r_1 + r_2\right) - \alpha_1\alpha_2 + r_1r_2 \\
& + r_4\left(r_1 + r_2 + r_3\right)) - r_3\left(\alpha_1\alpha_2 - r_1r_2\right) - \varepsilon_1\varepsilon_2\left(r_1 + r_2 + r_3 + r_4 + r_5\right) + \varepsilon_1\varepsilon_2r_5) - \varepsilon_1\varepsilon_2(r_4\left(r_3\left(r_1 + r_2\right) - \alpha_1\alpha_2 + r_1r_2\right) \\
& + r_5\left(r_3\left(r_1 + r_2\right) - \alpha_1\alpha_2 + r_1r_2 + r_4\left(r_1 + r_2 + r_3\right)\right) - r_3\left(\alpha_1\alpha_2 - r_1r_2\right)) - \varepsilon_1\varepsilon_2r_5^{\,2}\left(r_1 + r_2 + r_3 + r_4 + r_5\right) \\
& r_3r_4r_5\left(\alpha_1\alpha_2 - r_1r_2\right) + b_1c_2r_3(r_5\left(r_1 + r_2 + r_3 + r_4 + r_5\right) + r_3\left(r_1 + r_2\right) - \alpha_1\alpha_2 - \varepsilon_1\varepsilon_2 + r_1r_2 \\
& + r_4\left(r_1 + r_2 + r_3\right) + r_5\left(r_1 + r_2 + r_3 + r_4\right)) + \varepsilon_1\varepsilon_2r_5(r_3\left(r_1 + r_2\right) - \alpha_1\alpha_2 + r_1r_2 + r_4\left(r_1 + r_2 + r_3\right) \\
& + r_5\left(r_1 + r_2 + r_3 + r_4\right)) - b_1c_2r_3^2\left(r_1 + r_2 + r_3 + r_4 + r_5 + r_6\right))
\end{aligned}
$$