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Modeling and Simulation of The Dynamics of Monkeypox (Mpox), in Nigeria

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ABSTRACT
Monkeypox (Mpox) is a Zoonotic disease transmitted via contact with infected rodents or contaminated bodies/bodily fluids. Mpox has caused significant setbacks globally, particularly in Africa. Despite continuous monitoring and interventions, the lack of timely detection and inadequate access to effective control measures hinders efforts to combat the Mpox outbreaks. In this paper, we develop and analyse a deterministic model for transmission dynamics of mpox, integrating early screening and therapy, isolation, and treatment as control interventions. The model is segmented into two interacting populations: humans and rodents population. The model is applied to daily reported cases of Mpox in Nigeria from January, 2023 to November 2024, using non-linear least square methods.
The numerical simulation of the model was derived using the fourth order Runge-Kutta iterative methods implemented in MATlAB. We investigated the effect of each control parameter on the infected individuals. Results reveal the double control strategies have great impact on reducing the outbreak and modification parameter play a significant role in reducing the rate of interaction between susceptible individuals and infected rodents.

Keywords:
Mpox Transmission;
Control Intervention;
Mathematical Modeling;
Early Screening;
Nigeria.

INTRODUCTION

Mpox, is categorized into the family of orthopoxvirus. It is a Zoonotic disease that is caused by Monkeypox virus (MPXV) (CDC, 2003; Heskin, et al., 2022; Rahman, et al., 2020,). Mpox is a transmissible disease, mostly found in rural settlement, with Central and West Africa region being the most affected, (Jezek *et al.*, 1988, Rizk, et al., 2022, Railian, et al., 2023, Valavan & Meryer, 2022).

MPXV is spread through, Animal-Human (A2H) transmission, Human-Human (H2H) transmission and Human-Animal (H2A) through contact with an infected rodent/person, contaminated environment or surface, (Alakunle *et al.,* 2020 CNBC, 2023, WOAH, 2023, CDC, 2022, Murphy & Ly, 2022, Titanji, et al., 2022, Beeson, et al., 2023). The window period of MPXV is usually 7-10 days (also for up to 21 days), then signs and the symptoms of MPXV begin to manifest, such as lymph node enlargement, fever, myalgia, back pain, severe headache, sweating, etc. appear after the latent period. (Esshauer *et al.*,2010, CDC-Africa, 2022, Hraib, et al., 2022, Luo & Han, 2022, Shaheen, et al., 2022).

Bhunu & Mushayabasa, (2011), set the frame for mathematical model of mpox, using the pox like virus as a case study. Usman & Adamu, 2017 and Peter, *et al.*, 2021 extended the work in (Bhunu & Mushayabasa, 2011) incorporating the exposed and isolated compartment, to study the impact of treatment and isolation.

Olapade *et al.*, (2024), developed a mathematical model study the early detection of infected individuals, with sole aim of reducing or possibly mitigate the disease spread.

Sefiu, *et al.*, (2024), formulated a mathematical model using the SIR-SI type model for the humans and rodents population, in the presence of public enlightenment and quarantine to predict the spread and enhanced public health policies on the spread of Mpox.

Bolaji, et al., (2024), developed a deterministic model of Mpox infection, considering the human population to access the impacts of vaccination and treatment.

Singo, et al., (2024), constructed a mathematical model for the transmission of Mpox, to analyzed and evaluate the effectiveness of vaccination and personal hygiene of control interventions.

Ikhsani, et al., (2025), formulated a mathematical model, for the transmission and control of mpox, incorporating low and high risk infected compartments with and without control functions.

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Karma et al (2025), developed and analysed a mpox infection model, integrating early screening and therapy, isolation and treatment as control interventions.

In the current study, we performed numerical simulation to validate the analytical results presented in Karma et al., (2025)., capturing early screening and therapy, isolation and treatment as control interventions.

MATERIALS AND METHODS

Formulation of Mpox Model

A model of Mpox dynamics is split into two interacting hosts: Humans and rodents. The human population is divided into five sub-compartments by using the general SEIHR-type (S-Susceptible, E-Exposed, I-Infectious H-Isolation and R-Recover) model for human population and the SEI (S-Susceptible, E-Exposed, I-Infectious) for rodent population.

Where the total population for both humans, rodents and force of infection of MPXV, are defined in equations (1)-(4), respectively

$$N_h = S_h + E_h + I_h + H + R_h \quad (1)$$

$$N_n = S_n + E_n + I_n \quad (2)$$

$$\lambda_h = \frac{\beta_h I_h}{N_h} + \frac{\epsilon \beta_n I_n}{N_n} \quad (3)$$

$$\lambda_n = \frac{\beta_n I_n}{N_n} \quad (4)$$

In equations (3)-(4), β_h, β_n is the transmission rate for human and rodents population, ϵ, is species barrier control rate to account for barrier jump across the two host population define as $0 \leq \epsilon \leq 1$.

And we present a deterministic model to describe the mathematical of Mpox infection capturing early screening and therapy, isolation and treatment as

$$\frac{dS_h(t)}{dt} = \Pi_h - (\lambda_h + \delta_{h0})S_h(t) \quad (5)$$

$$\frac{dE_h(t)}{dt} = \lambda_h S_h(t) - (\alpha + \delta_{h0})E_h(t) \quad (6)$$

$$\frac{dI_h(t)}{dt} = \alpha(1-\rho)E_h(t) - (\theta_1 + \delta_{h0} + \delta_{h1})I_h(t) \quad (7)$$

$$\frac{dH}{dt} = \theta_1 I_h(t) - (\theta_2 + \delta_{h0} + \delta_h)H(t) \quad (8)$$

$$\frac{dR_h(t)}{dt} = \alpha\rho E_h(t) + \theta_2 H(t) - \delta_{h0} R_h(t) \quad (9)$$

$$\frac{dS_n(t)}{dt} = \Pi_n - (\lambda_n + \delta_{n0})S_n(t) \quad (10)$$

$$\frac{dE_n(t)}{dt} = \lambda_n S_n(t) - (\gamma + \delta_{n0})E_n(t) \quad (11)$$

$$\frac{dI_n(t)}{dt} = \gamma E_n(t) - \delta_{n0} I_n(t) \quad (12)$$

With initial condition as

$$S_h(0) \geq 0, E_h(0) \geq 0, I_h(0) \geq 0, H(0) \geq 0,\ R_h(0) \geq 0, S_n(0) \geq 0, E_h(0) \geq 0, I_n(0) \geq 0, \quad (13)$$

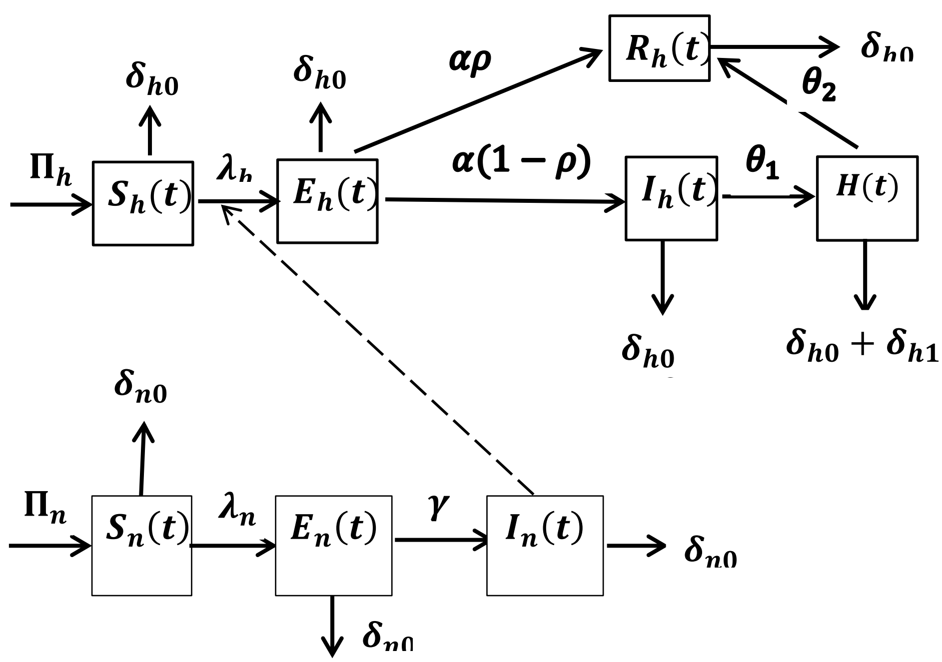


Figure1: Schematic Description of Mpox Disease Model

Table1: Description of Variable and Parameter

Variable/Parameter	**Description**
$N_h(t)$	The total Humans Population at time t
$N_n(t)$	The total Rodents Population at time t
$S_h(t)$	The total number of Susceptible humans at time t
$E_h(t)$	The total number of Exposed humans at time t
$I_h(t)$	The total number of infected humans at time t
$H(t)$	The total number of isolated humans at time t
$R_h(t)$	The total number of Recovered humans at time t
$S_n(t)$	The total number of Susceptible Rodents at time t
$E_n(t)$	The total number of Exposed Rodents at time t
$I_n(t)$	The total number of Infected Rodents at time t
β_h	Transmission rate of Human
β_n	Transmission rate of Rodents
π_h/π_n	Recruitment rate for Humans/ Rodents
ρ	Early screening and therapy
α	Progression rate of the exposed
θ_1	Rate of Isolation of Infected Human
θ_2	Recovery rate due to treatment
ϵ	Species barrier control rate
γ	Progression rate of Exposed Rodents to infected Compartment
δ_{h0}/δ_{h1}	Natural death/Death rate due to Mpox of Human
δ_{n0}	Natural Death rate in Rodents

BASIC PROPERTIES OF THE MODEL

In karma et al., (2025), we presented the mathematical analysis and analytical results of our model in equations (5)-(12), here we state the properties for clarity.

POSITIVITY OF THE SOLUTION, (karma et al., 2025).

Lemma 1: The initial condition $\{S_h(0), E_h(0), I_h(0), H(0), R_h(0) \geq 0\} \in \phi_h$ and $\{S_n(0), E_n(0), I_n(0) \geq 0\} \in \phi_n$ in equation (13), then the solution $\{S_h(t), E_h(t), I_h(t), , H(t), R_h(t)\}$ and $\{S_n(t), E_n(t), I_n(t)\}$ of equations (5)-(12) is nonnegative for all $t > 0$

THE FEASIBLE REGION, (karma et al., 2025).

Lemma 2:

Let $\phi_h = \left\{(S_h, E_h, I_h, H, R_h) \in \mathbb{R}_+^5 : N_h(t) \leq \frac{\Pi_h}{\delta_{h0}}\right\}$ and $\phi_n = \left\{(S_n, E_n, I_n) \in \mathbb{R}_+^3 : N_n(t) \leq \frac{\Pi_n}{\delta_{n0}}\right\}$, so that $\phi = \left\{\phi_h \times \phi_n \middle| N_h(t) \leq \frac{\Pi_h}{\delta_{h0}} ; N_n(t) \leq \frac{\Pi_n}{\delta_{n0}}\right\}$ then the region ϕ is positively invariant with respect to equations (5)-(12), see proof in (karma et al 2025)

Existence of Disease Free Equilibrium (DFE) and Stability Analysis, (karma et al.,2025).

At the disease free equilibrium (DFE) state (i.e. no infected individual from the community), particularly $E_h(t) = I_h(t) = I_n(t) = 0$, in equation (5)-(12).

Hence, we denote the mpox disease free equilibrium by E_0 and

$$E_0 = (S_h{}^*, E_h{}^*, I_h{}^*, H^*, R_h{}^*, S_n{}^*, E_n{}^*, I_n{}^*) = \left(\frac{\Pi_h}{\delta_{h0}}, 0,0,0,0, \frac{\Pi_n}{\delta_{n0}}, 0,0\right) \quad (17)$$

Endemic Equilibrium (EE) State (karma et al., 2025)

For endemic equilibrium state i.e. $I_h \neq 0$ and $I_n \neq 0$ in equations (5)-(12), solving yields $E_1 = (S_h{}^{**}, E_h{}^{**}, I_h{}^{**}, H^{**}, R_h{}^{**}, S_n{}^{**}, E_n{}^{**}, I_n{}^{**})$ and represented as

$$E_1 = \begin{pmatrix} S_h^{**} \\ E_h^{**} \\ I_h^{**} \\ H^{**} \\ R_h^{**} \\ S_n^{**} \\ E_n^{**} \\ I_n^{**} \end{pmatrix} = \begin{pmatrix} \frac{N_h^{**} M_1 M_3}{\beta_h M_2} \\ \frac{\Pi_h M_3}{\beta_h M_2}\left[\left[\frac{\beta_h M_2}{M_1 M_3} - 1\right] - \frac{\varepsilon \beta_n \delta_{n0}}{\beta_n \delta_{h0}}\left[\frac{\gamma \beta_n}{\delta_{n0}(\gamma+\delta_{n0})} - 1\right]\right] \\ \frac{\Pi_h}{\beta_h}\left[\left[\frac{\beta_h M_2}{M_1 M_3} - 1\right] - \frac{\varepsilon \beta_n \delta_{n0}}{\beta_n \delta_{h0}}\left[\frac{\gamma \beta_n}{\delta_{n0}(\gamma+\delta_{n0})} - 1\right]\right] \\ \frac{\theta_1 \Pi_h}{M_4 \beta_h}\left[\left[\frac{\beta_h M_2}{M_1 M_3} - 1\right] - \frac{\varepsilon \beta_n \delta_{n0}}{\beta_n \delta_{h0}}\left[\frac{\gamma \beta_n}{\delta_{n0}(\gamma+\delta_{n0})} - 1\right]\right] \\ \left[\left[\frac{\beta_h M_2}{M_1 M_3} - 1\right] - \frac{\varepsilon \beta_n \delta_{n0}}{\beta_n \delta_{h0}}\left[\frac{\gamma \beta_n}{\delta_{n0}(\gamma+\delta_{n0})} - 1\right]\right]\frac{1}{\delta_{h0}}\left[\frac{\alpha \rho \Pi_h M_3}{\beta_h M_2} + \frac{\theta_1 \theta_2 \Pi_h}{M_4 \beta_h}\right] \\ \frac{\delta_{n0}(\gamma+\delta_{n0}) N_n^{**}}{\beta_n \gamma} \\ \frac{\delta_{n0} \Pi_n}{\gamma \beta_n}\left[\frac{\gamma \beta_n}{\delta_{n0}(\gamma+\delta_{n0})} - 1\right] \\ \frac{\Pi_n}{\beta_n}\left[\frac{\gamma \beta_n}{\delta_{n0}(\gamma+\delta_{n0})} - 1\right] \end{pmatrix} \quad (18)$$

Where $M_1 = (\alpha + \delta_{h0}), M_2 = \alpha(1-\rho),\ M_3 = (\theta_1 + \delta_{h0} + \delta_{h1}), M_4 = (\theta_2 + \delta_{h0} + \delta_{h1})$

Basic Reproduction Number (R_0), (karma et al., 2025)
The basic reproduction number denoted by (R_0) is the average number of reported cases that arise as a result of an initial case within a community (Diekmann, et al., 1990, Van Den Driessche & Watmough, 2002).
We divide our model in (5)-(12) into new infection terms as F and transition terms as V, represented by the following compartments as E_h, I_h, E_n, I_n.
We use the next generation matrix method which yields the Jacobian matrix as

$$F = \begin{pmatrix} 0 & \frac{\beta_h S_h}{N_h} & 0 & \frac{\beta_{nh} S_h}{N_n} \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & \frac{\beta_n S_n}{N_n} \\ 0 & 0 & 0 & 0 \end{pmatrix} \ and\ V = \begin{pmatrix} (\alpha+\delta_{n0}) & 0 & 0 & 0 \\ -\alpha(1-\rho) & (\theta_1+\delta_{h0}+\delta_{h1}) & 0 & 0 \\ 0 & 0 & (\gamma+\delta_{n0}) & 0 \\ 0 & 0 & -\gamma & \delta_{n0} \end{pmatrix}$$

Hence the basic reproduction number of the model in (5)-(12) is denoted as $R_0 = \rho F V^{-1}$ where ρ spectral radius of the matrix
And

$$R_0 = \max(R_{0h}, R_{0n}) == \max\left\{\frac{\beta_h \alpha(1-\rho)}{(\alpha+\delta_{n0})(\theta_1+\delta_{h0}+\delta_{h1})}, \frac{\gamma \beta_n}{(\gamma+\delta_{n0})\delta_{n0}}\right\} \quad (19)$$

Where $R_{0h}\ and\ R_{0n}$ in equation (19) is the basic reproduction number of humans and rodents respectively.

RESULTS AND DISCUSSION

Parameter Estimation and Data Fitting

Parameter estimation is essential tool that gives precise prediction and meaning to mathematical model in the study of epidemiology. This is performed by fitting our model with real life data to give some degree of accuracy and validation of the model's proficiency in forecasting realistic outcome. Here we parameterized our model in equation (5)-(12) to study the dynamics of Mpox using real-life data of reported cases in Nigeria from January 1st 2023 to November 2nd 2024 (i.e. for a period of 22 months), assessed through the Nigeria Center for Disease Control (NCDC) dashboard. The number of cumulated confirmed monthly reported cases for this period is presented below in Table 2 and the curve fitting in figure 2

Table 2: Daily Reported cases of Mpox in Nigeria from 2023 to 2024

Month(s)	1	2	3	4	5	6	7	8	9	10	11	12
Cumulative of Infected	27	45	67	69	76	77	77	77	77	79	88	95
Month(s)	13	14	15	16	17	18	19	20	21	22		
Cumulative of Infected	97	101	107	115	119	125	132	151	175	211		

The natural death rate in human is denoted by $\delta_{h0} = \frac{1}{\tau_1}$, where τ_1 is average life expectancy in Nigeria and 54.46 years is the life expectancy in Nigeria (Macrotrends, n.d.). Nigeria's total population is projected at 227,882,945 in 2023 (Macrotrends, n.d.).
For the model fitting procedures, we used the least square nonlinear minimization method via the Fmincon function on MATLAB optimization toolbox to obtain the best parameter values that minimize each residual. The estimation procedure which minimizes the error is given by

$$\xi = argmin \sum_{i=1}^{n} (X_i - \dot{X}_i)^2 \quad (20)$$

Where X_i is actual data set and $\dot{X}_i$ fitted data, n is number of possible data points.
Figure 2 shows the Mpox reported cases in Nigeria in red check boxes and model fitted data in the blue check boxes. For the estimated parameters and initial condition

presented in table 2, it reveals that the cumulated reported cases and the model fitted data gives a reliable calibration for Mpox transmission dynamics.

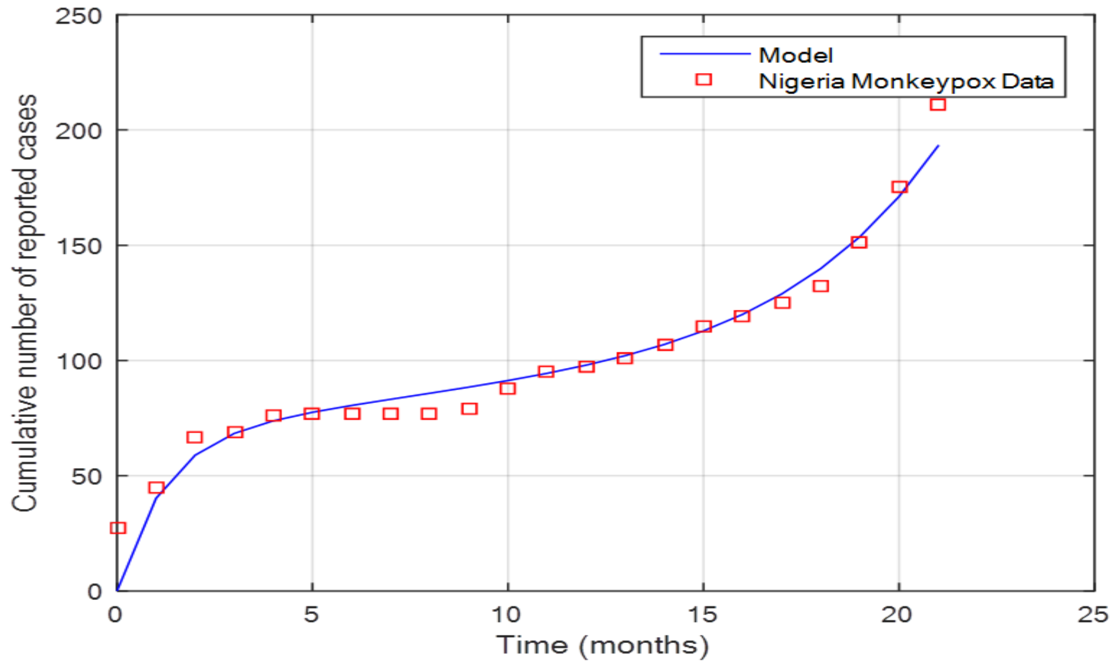


Figure 2: Cumulative confirmed Monkeypox cases in Nigeria.

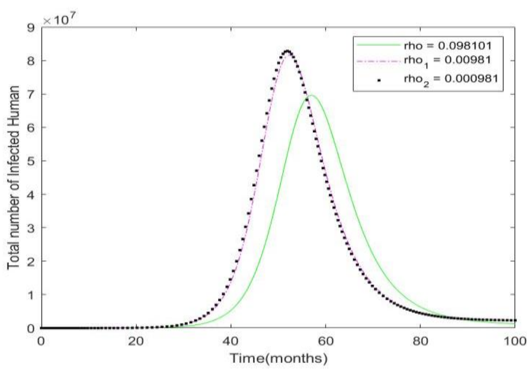
Table 3: Parameter/Initial Value of MPOX Model

PARAMETER/VARIABLE	VALUE	SOURCE
Π_h	348701	Estimated
Π_n	4167	Estimated
β_h	0.666244	Fitted
β_n	2.72948e-05	Fitted
ρ	0.0981012	Fitted
θ_1	0.067	Estimated
θ_2	6.62645e-07	Fitted
α	0.46	Estimated from Africa CDC, (2022)
ε	0.5	Assumed
δ_{h0}	0.0015302	Estimated from Macrotrends, n.d.
δ_{h1}	0.51	Estimated
δ_{n0}	0.08333	Estimated from Bing,n.d.
γ	0.3452051	Estimated from Bing,n.d.
$N_h(t)$	227882945	Macrotrends, n.d.
$N_n(t)$	50000	Peter et. al. (2024)
$S_h(t)$	227800000	Fitted
$E_h(t)$	870	Fitted
$I_h(t)$	10	Fitted
H	27	NCDC, dash board
$R_h(t)$	62	Fitted
$S_n(t)$	40000	Peter et al. (2024)
$E_n(t)$	0	Assumed
$I_n(t)$	2000	Peter et al. (2024)

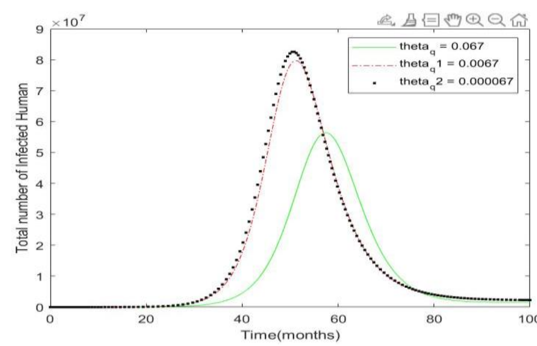
Numerical Simulation

In this section, we used the initial conditions and parameter values presented in table 3 to perform the numerical simulation of model presented in equations (5)-(12). These numerical results will validate the analytical results presented in (karma et al., 2025). We investigate the dynamical behavior of the control parameters on the infected human population and effect of human contact rate and modification parameter for zoonotic jumps on the susceptible human population. We use MATLAB ODE45 Solver to simulate our model in equations (5)-(12).

In fig. 3 (a-f), we demonstrate the effect of singe control interventions (i.e. early screening and therapy (ρ), Isolation rate (θ_1) and Treatment rate(θ_2)) on the infected and isolated individuals by decreasing and increasing each control parameter, it reveal that decrease on the control parameter (i.e. $\rho = 0.0981, \rho_1 = 0.00981, \rho_2 = 0.000981, \theta_q = 0.067, \theta_{q1} = 0.0067, \theta_{q2} = 0.00067, \theta_p = 6.626e-07, \theta_{p2} = 3.313e-07, \theta_{p2} = 1.656e-07$)increases the number of infected individuals as depicted in fig. 3(a-c) and increasing the value of each control parameter (i.e. $\rho = 0.0981, \rho_1 = 0.15, \rho_2 = 0.25, \theta_q = 0.067, \theta_{q1} = 0.095, \theta_{q2} = 0.15, \theta_p = 6.626e-07, \theta_{p2} = 6.626e-04, \theta_{p2} = 6.626e-01$) shows significant effect in reducing the number infected and isolated individuals as shown in fig. 3(d-f). In fig. 4 (a-g), we Illustrate the effect of double control interventions on the infected human population by varying each control parameter, it reveal a decrease on the control parameters increases the number of infected individuals within the shortest possible time and increasing the paired control parameter decreases the number of infected individuals with $\rho_2 = 0.25$ & $\theta_{q2} = 0.15, \rho_2 = 0.25$ & $\theta_{P2} = 6.626e-01$ and $\theta_{P2} = 6.626e-01$ & $\theta_{q2} = 0.15$ almost flatten the curve. In fig 5(a-b)., we Illustrate the effect of triple control interventions on the infected individuals by decreasing and increasing each control parameter, results reveal some increase in the number of individuals when the control parameters are decrease and decrease in the number of individuals when we increase the control parameters. From the results the double control has great significant impact in decreasing the number of infected individuals within the population see numerical values against time in table 4(a-f), table 5(a-g) and table 6(a-b), chosen at the peak points of each plot.



(a)



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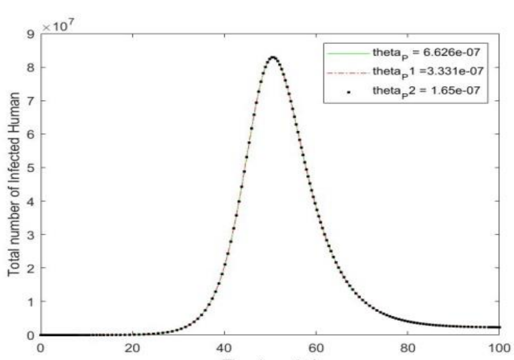
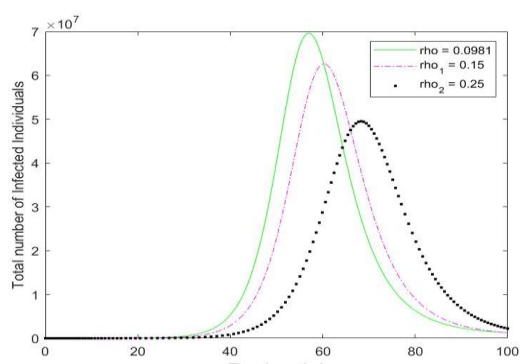


(c)



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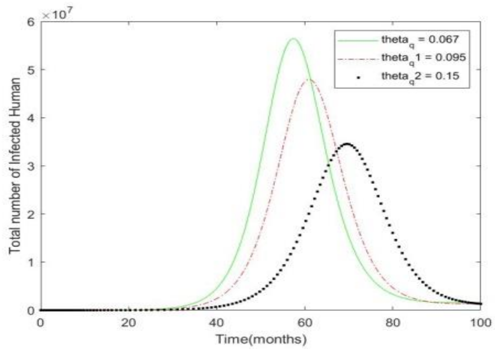

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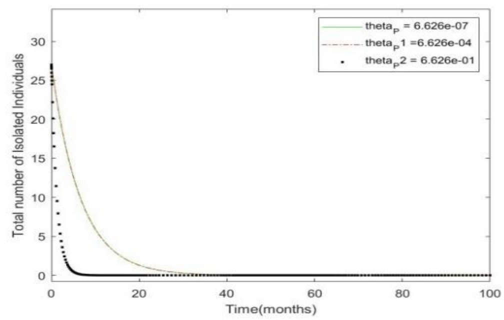
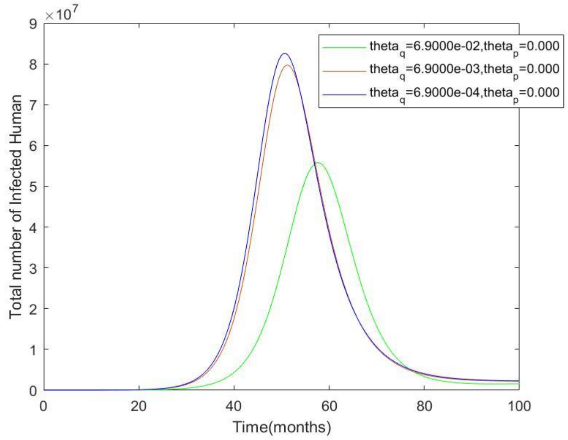
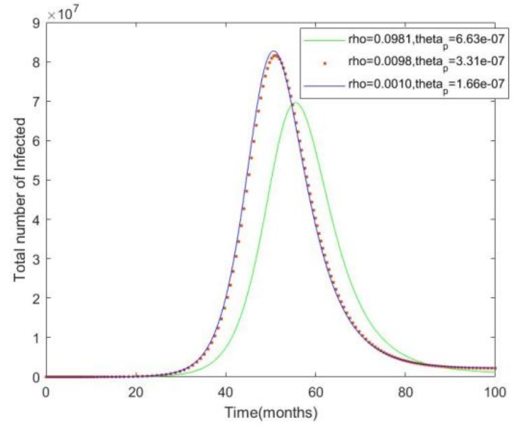


(f)

Figure 3(a-f): Simulation Plots for Single Control (by decreasing and increasing each control parameter)



(a)



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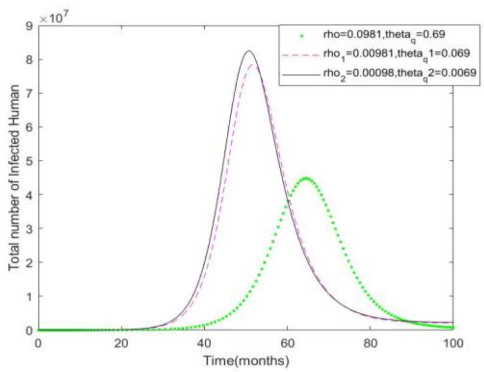

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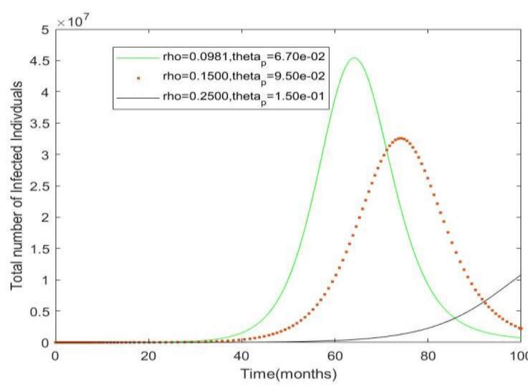

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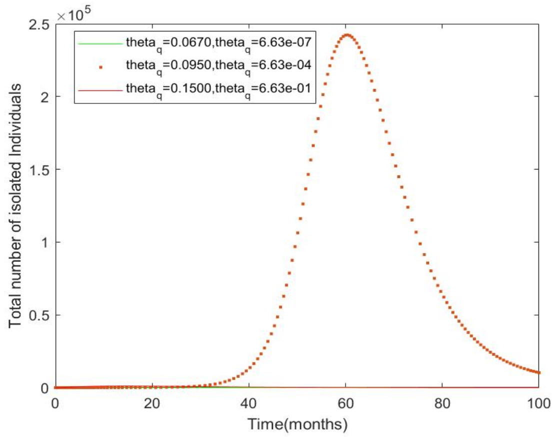

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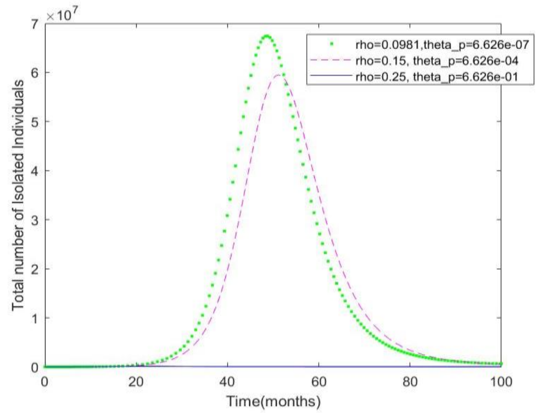

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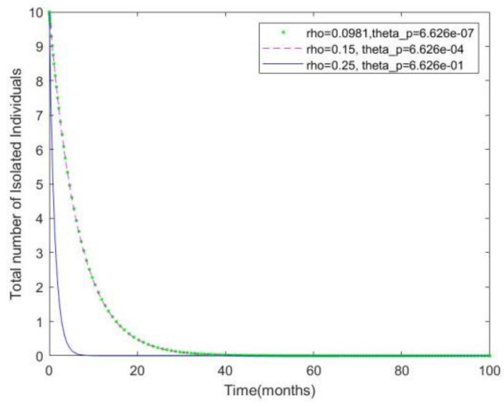
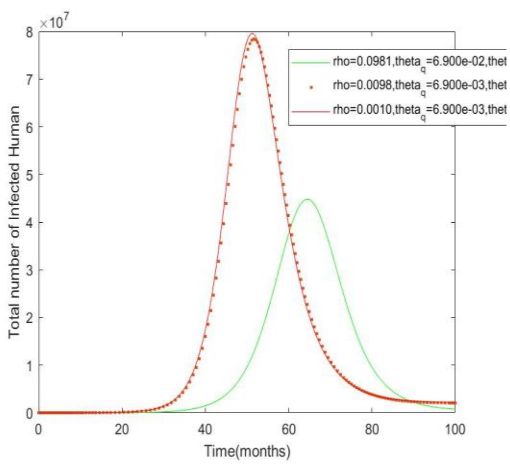
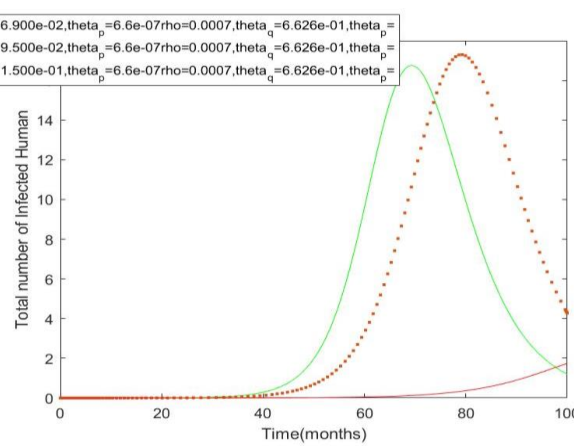


(g)

Figure 4(a-g): Simulation plots of Double Control (by decreasing and increasing each control parameter)



(a)



(b)

Figure 5(a-b): Simulation Plots of Triple Control (by decreasing and increasing each control parameter)

Fig. 6., demonstrate the trajectory on the effect of the human transmission rate (β_h) (i.e $\beta_h = 0.6662, \beta_{h1} = 0.3331, \beta_{h2} = 0.1665, \beta_{h3} = 0.00$). on the susceptible individuals, it shows a decrease on the transmission rate increase the degree of interaction of the susceptible individuals and the infected individuals, which reveal high risk of the susceptible been exposed to MPXV. Fig. 7., also demonstrates the effect of modification parameter ϵ on the interaction between the susceptible individuals and infected rodent, a decrease in it, increases the probability of the susceptible human becoming infected to mpox, this reveals increasing the modification parameters also serves as immunity to the susceptible individuals see numerical in table 7, chosen at the peak points of each plot.

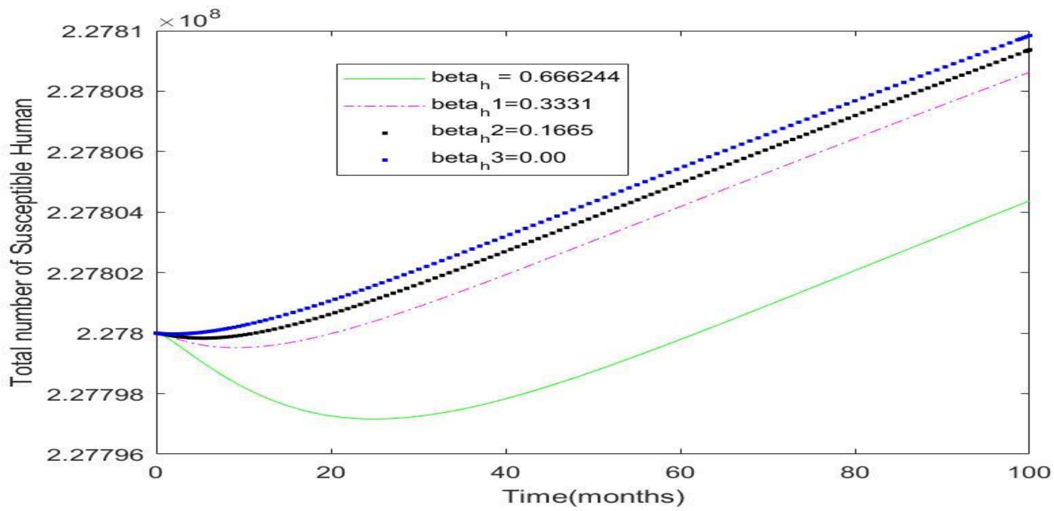


Figure 6: Effect of Contact rate on Susceptible Human Population

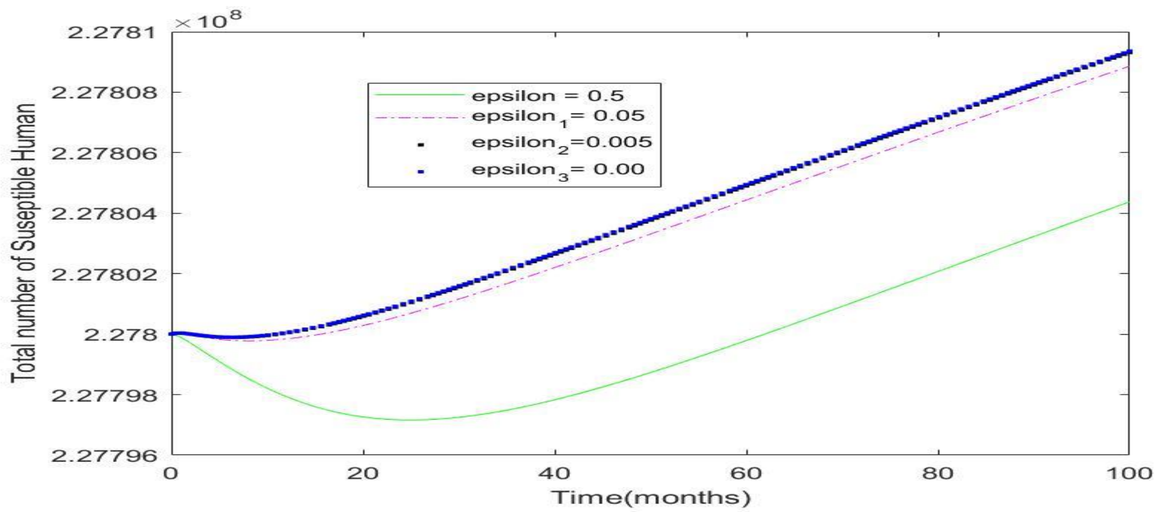


Figure 7: Effect of species barrier transmission parameter on the Susceptible Population

Table 4: Numerical Values for plots in Figure 3(a-f)

Parameter	No. of Infected (Decreasing)	Time(Months)	No. of Infected (Increasing)	Time (Months)
Rho	69409600	57	69624200	57
Rho_1	81608200	52	62146400	57
Rho_2	82623800	51	49407400	62
Theta_q	55686000	56	56439300	57
Theta_q1	76978200	50	49009700	53
Theta_q2	82573200	50	34436400	55
Theta_p	Flatten	-	-	-
Theta_p1	82535000	51	82708400	51
Theta_p2	Flatten	-	-	-

Table 5: Numerical Values for plots in Figure 4(a-g)

Parameter	No. of Infected (Decreasing)	Time(Months)	No. of Infected (increasing)	Time(Months)
Rho-theta_p	67389700	48	67427400	48
Rho_1- theta_p1	80980300	44	56591700	48
Rho_2- theta_p2	82785800	44	flatten	
Theta_q- theta_p	72816600	52	73810400	53
Theta_q1- theta_p1	81940800	50	69486600	54
Theta_q2- theta_p2	82803600	50	flatten	-
Rho-theta_q	37288400	57	45400900	54
Rho_1- theta_q1	78498100	51	32574800	50
Rho_2- theta_q2	82433500	50	163220	41

Table 6: Numerical Values for plots in Figure 3(a-b)

Parameter	No. of Infected (Decreasing)	Time (Months)	No. of Infected (Increasing)	Time (Months)
Rho-theta_p- Theta_q	40668700	55	45234000	61
Rho_1- theta_p1 Theta_q1	78498100	59	32523800	63
Rho_2- theta_p2- Theta_q2	82433500	62	1731760	67

Table 7: Numerical Values for plots in Figure 6 & 7

Parameter	No. Susceptible(Decreasing)	Time(Months)
Beta_h	227970000	12
Beta_h1	227800000	12
Beta_h2	227800000	12
Beta_h3	227800000	12
epsilon	227797000	12
Epsilon_1	227800000	12
Epsilon_2	227801000	12
Epsilon_3	227854000	12

CONCLUSION

This study demonstrates the effectiveness of a mathematical model in understanding the Mpox transmission dynamics and evaluating control interventions in Nigeria. The results highlighted the importance of combining early screening and therapy, Isolation and treatment to reduce the outbreak. Results show double control strategies have great impact in reducing the outbreak and modification parameter play a significant role in reducing the rate of interaction between susceptible individuals and infected rodents.

Further research can build on these findings to inform policy decisions and optimize control measures.

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