Mathematical Modeling of Chikungunya Fever

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1 Introduction

Chikungunya fever is an acute infection transmitted through Chikungunya virus(CHIKV) following a bite of an infected *Aedes aegypt* and *Aedes albopictus* mosquitoes . Chikungunya fever was first reported in 1952 on the Makonde plateau in Tanzania and CHIKV isolated in 1953. Recently, the disease has affected many populations in East and Central Africa, South America and South East Asia. Between 2005 and 2006, an outbreak was reported that involved 1.35 million suspected cases in India. In 2004, 13,500 cases of the disease were reported in Lamu, Kenya which spread to Indian ocean Islands causing outbreaks of an unprecedented magnitude, particularly in La Reunion. As of today, more than 100 countries have reported the circulation of CHIKV with more than 10 million cumulative cases of Chikungunya fever. An estimated 1.3 billion people are at risk of Chikungunya fever globally. Below, is a latest report on a three-month Chikungunya virus disease case notification rate per 100,000 population, September-December 2024.

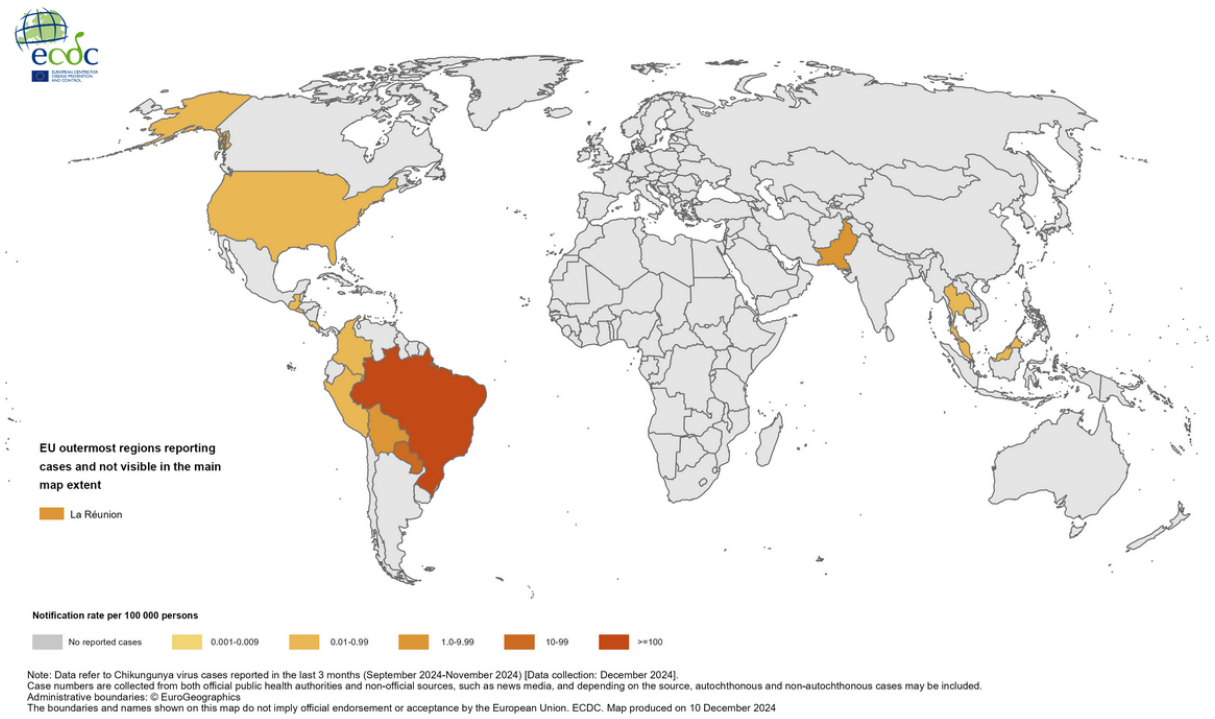


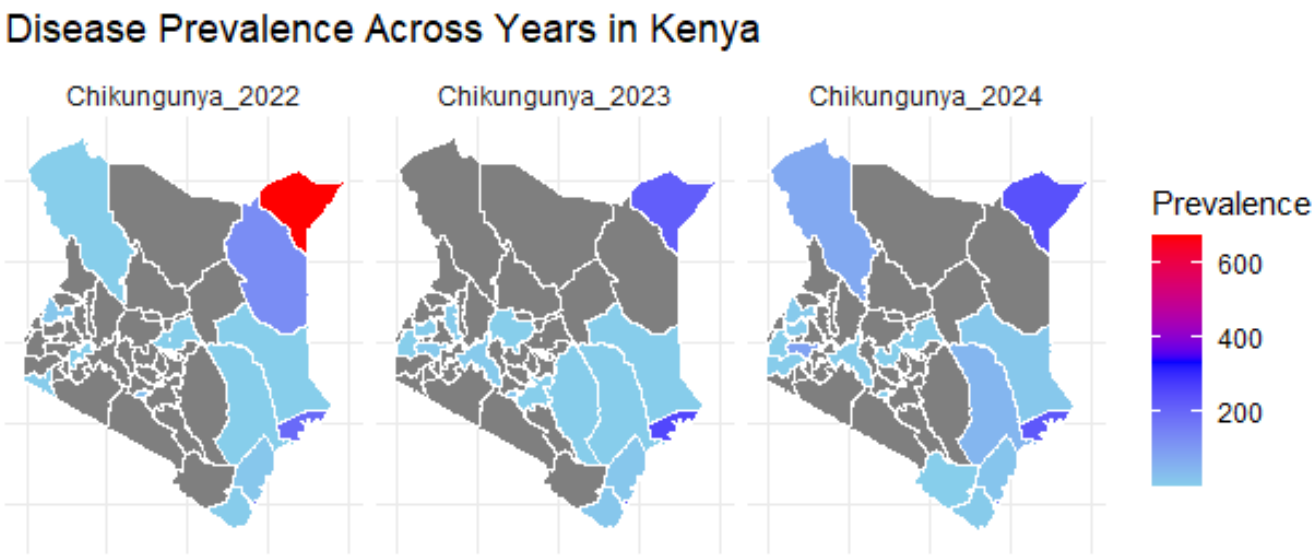
Fig 1: From the European Center for Disease Control

The disease is characterized by Rash, fever and joint pains. At early stages, the infection is characterized by high level viraemia which is accompanied by a robust innate immune response, driving an abrupt onset of fever after a 4 to 7 days incubation period. Although infection is self-limiting, it can be chronic and debilitating to those infected. Hospitalization and mortality of CHIKV infection range from 0.6% to 13% and from 0.024% to 0.8% respectively. However, more than 50% of the patients

report resolution of a period of 1 Month. Chikungunya fever has been recognized as a potential pandemic disease and CHIKV has been listed as a priority pathogen by the Coalition for Epidemiological Preparedness Innovation (CEPI). In 2018, CHIKV was added to the WHO shortlist for priority research and development.

Fatal cases have been reported making it a public health disease. Severe cases occur in the elderly, newborns, and individuals with immunocompromised bodies. There are no pathological information, effective vaccine and specific treatment. The available interventions focus on avoiding mosquito bites and controlling the mosquito vector.

Below, is a latest report on a 3 year Chikungunya virus prevalence in Kenya. The data was obtained on the Kenya Health Information System(KHIS)



Epidemiology

CHIKV is transmitted to humans by the bite of a female *Aedes* mosquito. It was believed that the virus was maintained in a sylvatic cycle(cyclical transmission between non-human animal hosts and insects) involving non-human primates and forest-dwelling mosquitoes of genus *Aedes* mostly *Aedes aegypt* with occasional transmission into humans. Mother-to-child CHIKV transmission does occur.

The risk of mother to child transmission is more than 15.5% with an increased risk of 50% infection during intrapartum period. Neonates with vertical chikungunya infection may present with clinical sepsis in the first few days of life. The rate of symptomatic disease among neonates with CHIKV infection was estimated at 50% while confirmed CHIKV antepartum fetal death has been reported at a rate of 0.3%. Stusies have evaluated the neurodevelopment of exposed children to CHIKV report a rate of development delay of 50% in symptomatic infants. In 2005 -2006 outbreak in La Reunion, vertical transmission occurred in 50% of peripartum maternal infection.

Phylogenetic analysis identified 3 distinct lineages which corresponds to their respective geographic origin; West Africa, East Central South Africa(ECSA) and the Asian lineage. The ECSA lineage was further divided into two clades: ECSA1 and ECSA2. The ECSA1 consists mainly of the ancestral CHIKV sequences and ECSA2 consists sequences from Central Africa Republic, Cameroon, Gabon and Republic of Congo.

2 Existing Literature

Diego Ruiz - moreno et al.,2012 modelled climate-based mosquito population dynamics stochastic SEIR model with an epidemiological model to identify temporal windows that have epidemic risks.

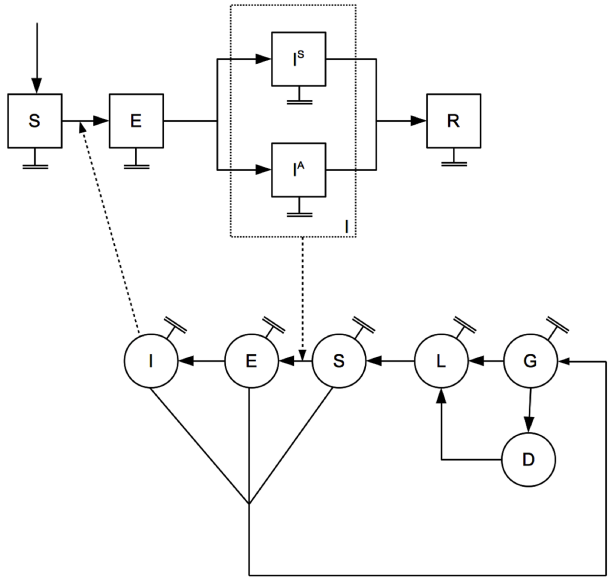


Fig 2: The model

Human population was divided into susceptible (S), exposed (E), symptomatic (I^S) and asymptomatic (I^A) infective, and recovered (R) individuals. Mosquito population is divided into immature eggs (G), larvae (L) and eggs under a diapause (D) state, and mature susceptible (S), exposed (E) and infected (I) states. Full arrows represent transition from one state to the other. Lines with parallel end represent natural mortality. Dotted lines represent infection dynamics

The model was ran on temperature data from different locations in the United states to study the geographic sensitivity of the epidemic potential. In their study, they found that in locations with marked seasonal variation in temperature showed seasonal variation of the epidemic risk.

Key assumption made in the model included: homogenous mixing CHIKV extrinsic incubation period was assumed to be reduced with increasing temperature (up to 32^0C) with a minimum of 2days and a maximum of 4 days.The parameters used in the model included : the percentage of eggs entering diapause, the rate of the survival of eggs, the duration of eggs development,the percentage of eggs leaving diapause, the survival percentage of larvae, duration of larvae development and median adult life span in days.

Laith et al., 2013 developed a simple SEIR mathematical model to describe the transmission of Chikungunya virus between humans and mosquitoes in Reunion Island.

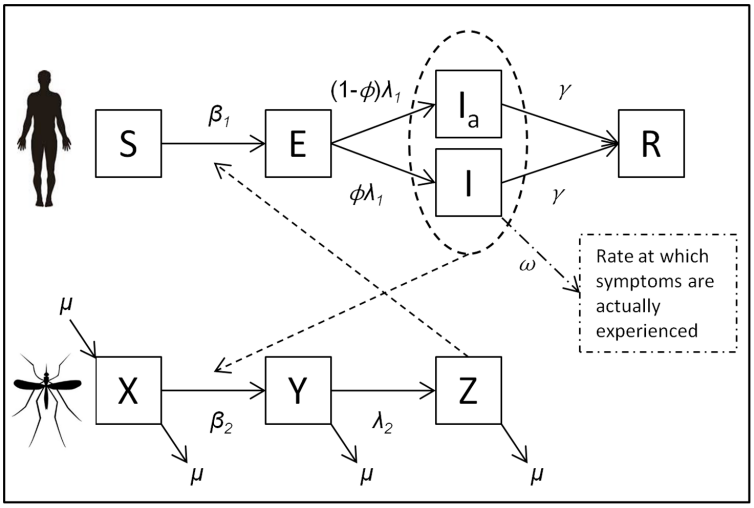


Fig 3: model

The model was based on a system of ordinary differential equations simulating the dynamics of virus transmission between humans and mosquitoes. The basic reproductive number (R_0) was calculated using the next-generation matrix.

Sensitivity analysis was conducted using Monte Carlo simulation to determine the influence of the latent period of infection in humans and the pre-patent period on the model outcomes of the Chikungunya fever.

Several assumptions were made in constructing the model. The recovery period in humans was assumed to range from 1 to 7 days, while the latent period ranged from 2 to 6 days. Additionally, mosquito births were assumed to balance mosquito deaths, resulting in a stable mosquito population.

The model incorporated several parameters, including the mosquito-to-human transmission rate, which represents the number of mosquito bites per human per day adjusted for imperfect pathogen transmission. Similarly, the human-to-mosquito transmission rate accounted for the per-day bite rate, also considering imperfect transmission. Other parameters included the proportion of infected hosts

that develop symptoms, the host latent period (time from infection to becoming infectious, measured in days), the mosquito latent period (time from infection to becoming infectious, measured in days), the host recovery rate (per day), the host pre-patent period (time from infection to symptom development, measured in days), and the mosquito lifespan (measured in days).

Folashade B. Agusto et al.,2016 developed an age structured SEIR model for the transmission dynamics of the CHIKV. The aim of the study was to investigate the effects of age on the Chikungunya transmission dynamics. They incorporated three different human age classes in the model that is juveniles, adults and senior human population. The model also involved two infectious human classes that is symptomatic and asymptomatic classes. Therefore, human population consisted of the following compartments ; susceptible, exposed, asymptomatic, symptomatic and recovered. On the other hand, mosquito population was divided into 3 compartments that is susceptible, exposed and infected.

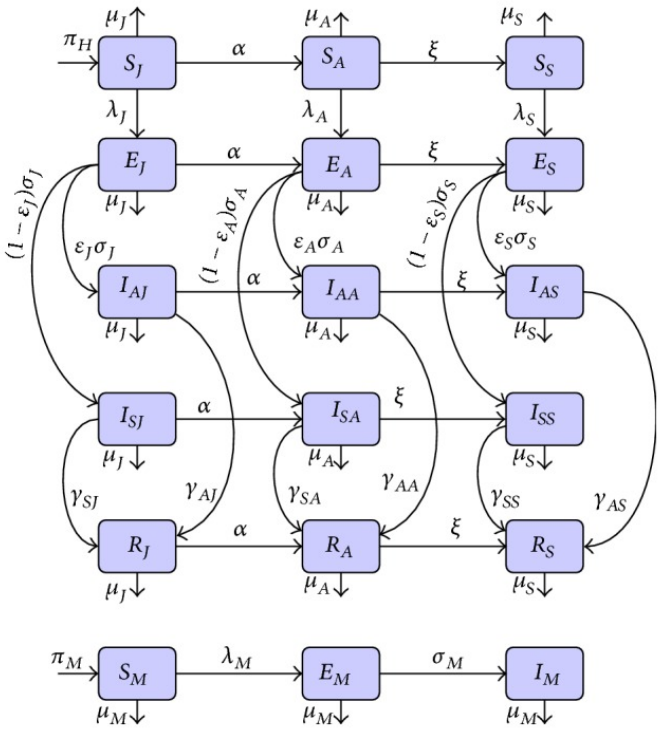


Fig 4: model

Key assumptions included: they assumed that there was no vertical transmission or immigration of infectious humans and thus no inflows into the infectious classes. They also assumed that recovery rates from adults asymptomatic and symptomatic classes are greater than those from juveniles classes which in inturn are greater than those from senior classes. The other assumption was that seniors progress more quickly to the asymptomatic and symptomatic classes than juveniles and adults.

They incorporated the following parameters in the model: Recruitment rate of juvenile humans, Recruitment rate of mosquitoes, Juvenile and adult maturation rates, Transmission probability

per, contact for susceptible humans, Transmission probability per contact for susceptible mosquitoes Mosquito biting rate, Natural death rate of juvenile, adult,and senior humans, Natural death rate of mosquitoes,Fraction of exposed humans becoming asymptomatic and symptomatic,Progression rate of exposed juvenile, adult, and senior humans, Recovery rate of asymptomatic and symptomatic juvenile humans, Recovery rate of asymptomatic and symptomatic adult humans,Recovery rate of asymptomatic and symptomatic senior humans and Progression rate of exposed mosquitoes. The model was formulated, basic reproductive number computed as well as stability analysis and Sensitivity analysis of the model was investigated.

Xiaomei F et al., 2019 modified a SEIR mathematical model to incorporate the virus mutation dynamics in the transmission of the CHIKV among human and mosquito populations in North-Eastern Italy. The study investigated whether the new variant of CHIKV with shorter extrinsic incubation period in the contaminated mosquitoes have an influence on the spread of Chikungunya fever.

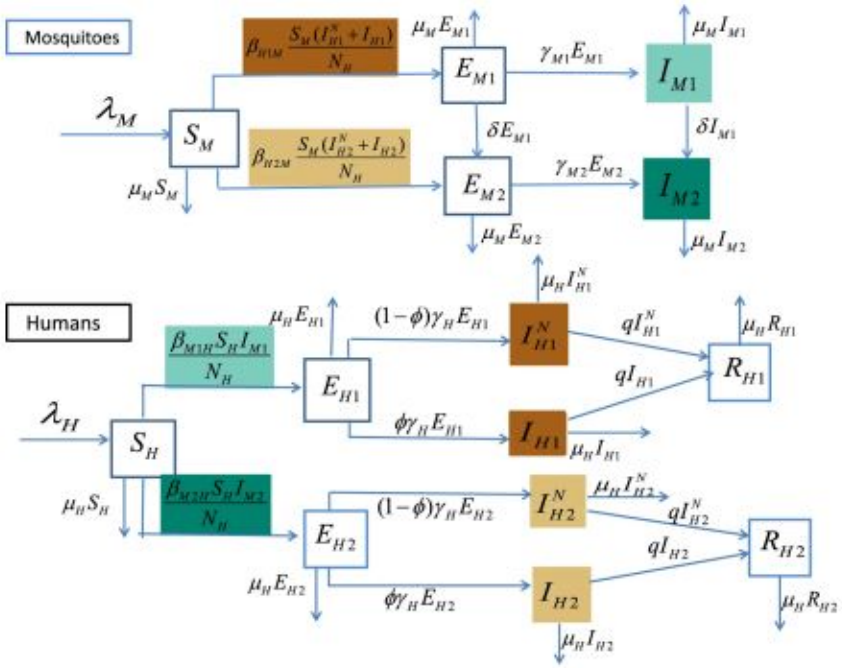


Fig 5: model

Subindices 1 and 2 correspond to the non-mutant and mutant strains, human populations stratified into exposed, asymptomatically/symptomatically infected and recovered compartments.

Numerical simulation was conducted and Markov chain monte carlo sampling method was used to fit the model outbreak. Sensitivity analysis was done to show how the transmission rate of the mutant strain from the mosquitoes to human has an influence on the basic reproductive number(R_0) than the shortened extrinsic incubation period. They stratified infected mosquitoes and human populations into non-mutant and mutant strains to describe the mutation dynamics.

Key assumptions in the model included: The virus mutates in the contaminated mosquitoes all through their life time. They also made an assumption that the proportion of the exposed individuals will become symptomatic after the latent period and that both symptomatic and asymptomatic individuals have the same probability of transmitting the virus to mosquitoes via each bite. Other assumptions were, the virus only mutates in the mosquito population because of the selective pressure that has been demonstrated in the mosquito bodies but not been found human and also that people who recover from one strain are immune of the other strain for life time.

The model incorporated many parameters including, recruitment rate of mosquitos,average lifespan of mosquitoes, Average biting rate of mosquitoes,probability of transmission from humans with nonmutant strain to mosquitoes, probability of transmission from humans with mutant strain to mosquitoes, mutation rate of virus inside mosquitoes per day, extrinsic incubation period in mosquitoes with nonmutant strain (days) , extrinsic incubation period in mosquitoes with mutant strain (days), probability of transmission of nonmutant strain from mosquito to human, probability of transmission of mutant strain from mosquito to human, intrinsic incubation period (days), proportion of symptomatic individuals and infectious period in humans (days)

Gilberto.C.G et al., 2019 developed a SEIR mathematical model of the Chikungunya epidemic at a population level to investigate and understand the importance of some specific model parameters in Colombia. They considered a special chronic subpopulation who are not infected by the disease into their model but have some types of chronic rheumatic symptoms.

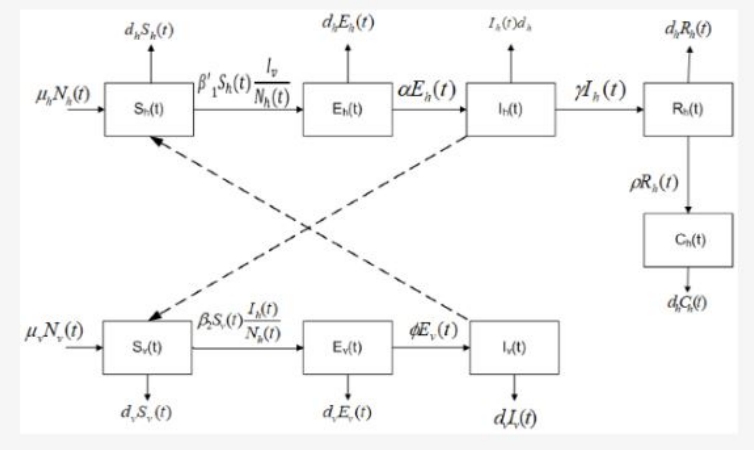


Fig 6: model

Some of the key assumptions in the model included: human and mosquito populations were assumed to be constant, the CHIKV spreads by effective contact between a infected mosquito with a human and vice versa. The model also assumed a constant season and populations variability. Other assumptions were, birth rate of the mosquitoes was assumed to be equal to their death rate and homogeneous mixing of the populations. The population was divided into five compartments; susceptible, latents, infected, recovered and ones with rheumatic symptoms.

The parameters used in the model were: birth rate of humans,mortality rate increase due to the disease is a real fact, the bite rate of an infected mosquito on susceptible people, birth rate of the mosquitoes, death rate of mosquitoes,rate of latent mosquitoes who goes through to infected mosquitoes, rate of recovered humans who moves to the chronic class, rate of recovery of humans, and rate of latent humans who passes to infected by the virus.

Bijal M., 2020 developed the SEIR model, a dynamical nonlinear mathematical model designed to describe the transmission of Chikungunya in both human and mosquito populations. The model was divided into six compartments: susceptible humans, exposed humans, infected humans, recovered humans, susceptible vector populations, and infected vector populations.

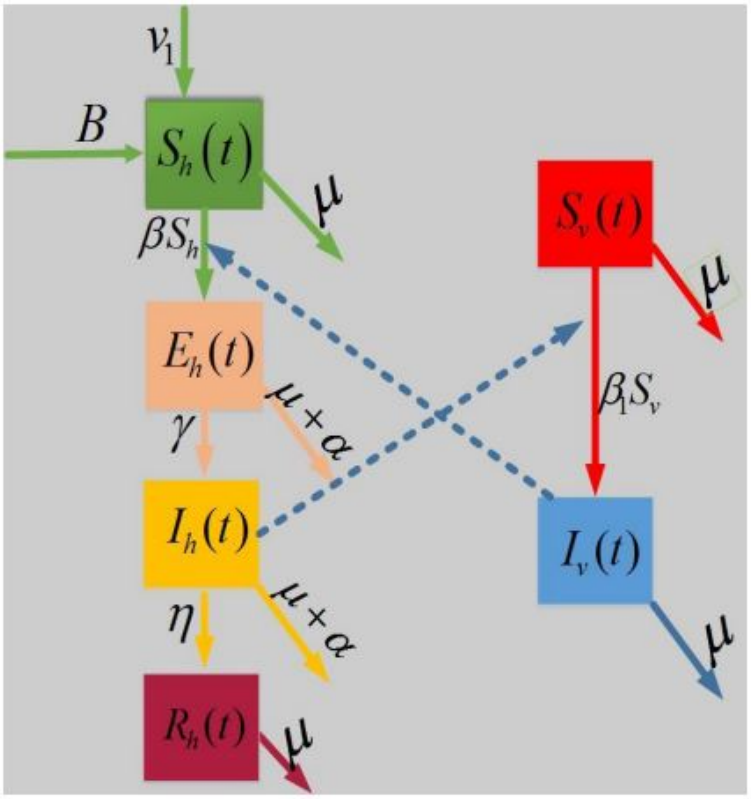


Fig 7: model

The basic reproductive number (R_0) was calculated, and stability analysis was performed. The local and global stability of the disease-free equilibrium and the endemic equilibrium points were analyzed to determine whether the model could effectively describe the dynamics of Chikungunya transmission in both human and mosquito populations.

The parameters used in the model included the transmission rate, mosquito bite rate, parasite transmission rate, the ratio of mosquitoes to humans, the rate at which humans infect mosquitoes, the transmission rate from exposed humans to infected humans, the recovery rate, the natural mortality

rate, disease-induced death rate, and the vertical transmission rate.

Ruchi et al.,2020 modified existing SEIR model by introducing a new section of human population which is the recuperation stage. The study investigated how the existing SEIR model could be modified to account for a long recuperation period which is observed in Chikungunya virus infections and the implications of the modification on the stability of disease free equilibrium, endemic equilibrium and on the basic reproduction number(R_0).They introduced a new compartment between the compartments of the infected and the recovered human population within the SEIR model to form a SEIR'R, where R' is the new recuperation compartment.

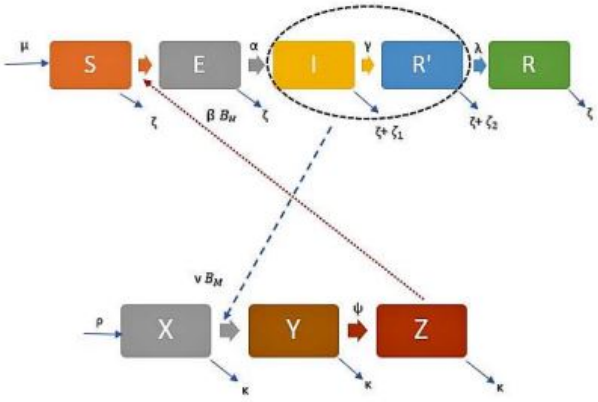


Fig 8: model

The total human population $N_H(t)$ was divided into five groups: susceptible (S), exposed (E), infected (I), population in recuperation (R'), and population fully recovered (R).

At a given time t,

$$N_H(t) = S(t) + E(t) + I(t) + R'(t) + R(t)$$

They assumed a constant birth and death rates as well as a constant rate of infections.

The parameters used in the model included: human birth rate,mosquito biting rate for the transfer of infection from the infectious mosquito class (Z) to the susceptible human population (S), progression rate of exposed to infected human population,Progression rate of infected to recuperated human population,progression rate of recuperated to fully recovered human population,mosquito birth rate, mosquito biting rate for the transfer of infection from the infected human population (I) or the population under the recuperation phase (R') to the susceptible mosquito population (X),progression rate from exposed to infectious mosquito population, natural death rate for the human population, human death rate in the infected stage due to viral infection, human death rate due to infection under the recovery phase, natural death rate for the mosquito population, transmission probability per contact in

susceptible humans,and transmission probability per contact in susceptible mosquitoes.
Their study showed that disease free equilibrium was locally and globally asymptotically stable whenever $R_0 < 1$ otherwise unstable. They also showed that the endemic equilibrium existed whenever $R_0 > 1$ and was asymptotically stable. This implied that the introduction of the recuperation compartment in the model was justifiable.

M.A. Haque et al., 2021 developed a compartmental SIR model to describe the transmission dynamics of chikungunya disease in Bangladesh. The study incorporated a nonlinear incidence rate to model the transmission of the disease and utilized a system of nonlinear differential equations to represent the dynamics. The primary goal of the study was to investigate how the model could enhance the understanding of chikungunya transmission dynamics in Bangladesh and to explore the insights or policies that could be derived from the analysis to mitigate the disease's impact.

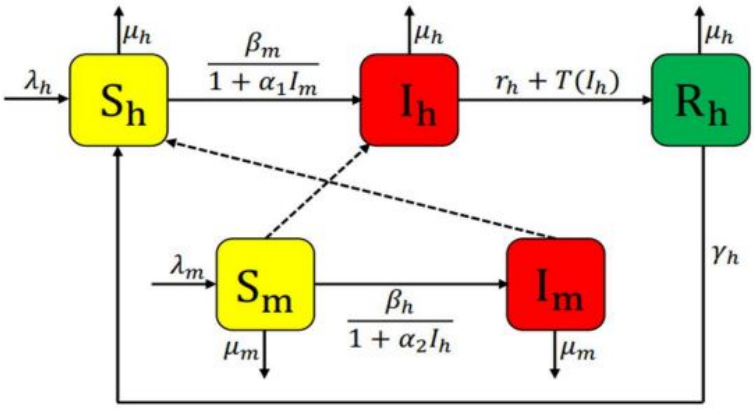


Fig 9: model

The basic reproductive number (R_0) was calculated using the next-generation matrix. The disease-free and endemic equilibrium points were computed, and the stability of the model was analyzed in terms of R_0. Numerical simulations were performed based on real data collected from health institutes in Bangladesh.

The model incorporated several parameters, including the disease contact rate of the susceptible human population due to the infected mosquito population, the disease contact rate of the susceptible mosquito population due to the infected human population, the birth rate of the human population, the birth rate of the mosquito population, the transmission rate from the infected human population to the recovered class, the transmission rate from the recovered class to the susceptible class, the natural death rates for both the human and mosquito populations, Holling type II functional response parameters for interactions between human and vector populations, and the capacity for treatment of infective individuals.

Key assumptions in the study included the following: the interaction between human and vector populations was assumed to occur in a homogeneously mixed environment, and all newborns were

considered infection-free. The model did not account for disease-related deaths. Furthermore, the mosquito infection rate was assumed to be equal to the human infection rate, and the birth and death rates of mosquitoes were assumed to be 100 times those of humans.

Mlyashimbi et al., 2022 introduced a nonlinear fractional order SEIR Chikungunya disease model based on the caputo derivative. The model incorporated asymptomatic infectious individuals whose main goal was to investigate the role of memory effects on the dynamics of the disease. They also investigate the role of asymptomatic infectious patients on the short and long term dynamics of the disease.

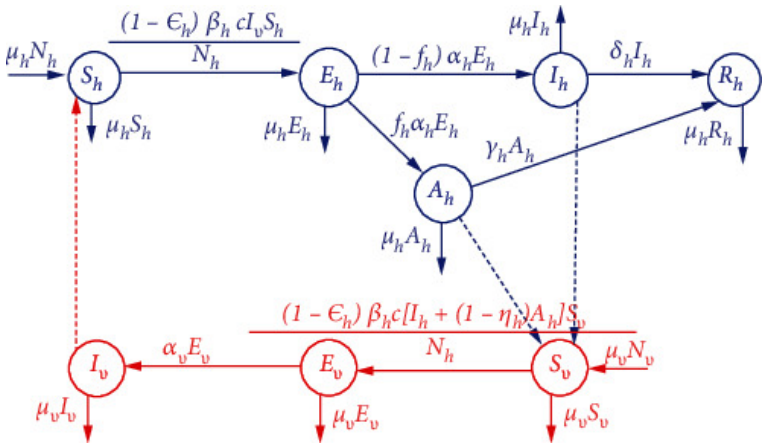


Fig 10: model

Key assumptions included: Once infected, vectors were assumed to remain infectious for their entire life span. Disease transmission was assumed to occur solely when there was interaction between the host and vector. Thus, all new recruits in the both the host and vector are assumed to be susceptible to infection. They assumed a constant size population in both the host and vector with a recruitment and non-disease-related mortality rate.

The parameters used in the model included: natural mortality rate of humans, Incubation period of in humans , Biting rate of human by female mosquito ,Proportion of asymptomatic patients,Infectious period for asymptomatic patients ,Infectious period for symptomatic patients,The number of mosquitoes per individuals,Reduction of infectivity from asymptomatic patients to susceptible mosquito,Efficacy of preventative strategies,Probability of infection to be transmitted from humans to mosquito per bite ,Probability of infection to be transmitted from an infectious to a susceptible human per bite,Life expectancy of mosquitoes,Incubation of mosquitoes and Basic reproduction number .

Seema Singla et al.,2022 introduced SEIR model to Chikungunya. The study aimed at determining the conditions under which SEIR model can achieve globally asymptotically stable disease-free equilibrium or stable endemic equilibrium and if R_0 may influence the dynamics of the infection and recovery rates of Chikungunya.
The parameters used in the model included: Rate of transmission,Rate of vaccination, Birth rate and

Recovery rates
Numerical analysis was performed to determine the current state of Chikungunya in India, Europe and Tanzania by comparing the computed eigenvalues with the basic reproductive number for each country using the 5 parameters. The results showed that India is unstable, Europe was asymptotically stable and Tanzania asymptotically unstable.

Key Assumptions: The interaction between two populations(human vector) and the entire human and vector populations are homogenously mixing with one another. It is assumed that all newborns are infection free and the model didnt consider any disease related death. It is assumed mosquito infection rate equal human infection rate and that its birth and death rates are hundred times as human birth and death rates.

Joseph Yangla et al.,2023 introduced caputo-sense fractional derivative SEIR model a modification of existing integer derivative models. In this model, the integer derivative is replaced by caputo derivative operator to obtain the asymtotic stability of the equilibrium points. Numerical simulations were performed using the parameter values from the Chikungunya epidemic in Chad. This study aimed to determine whether caputo-sense fractional derivatives can obtain different results about the asymptotic stability of the equilibrium points. The offspring reproduction number and basic reproduction number were computed.

The populations involved in the study were human and vector populations. Human population was divided into four compartments that is susceptible, exposed, infectious and recovered while vector population was divided into three compartments that is, (Egg, larvae, Pupae) and adult mosquitoes divided into susceptible, exposed and infectious.

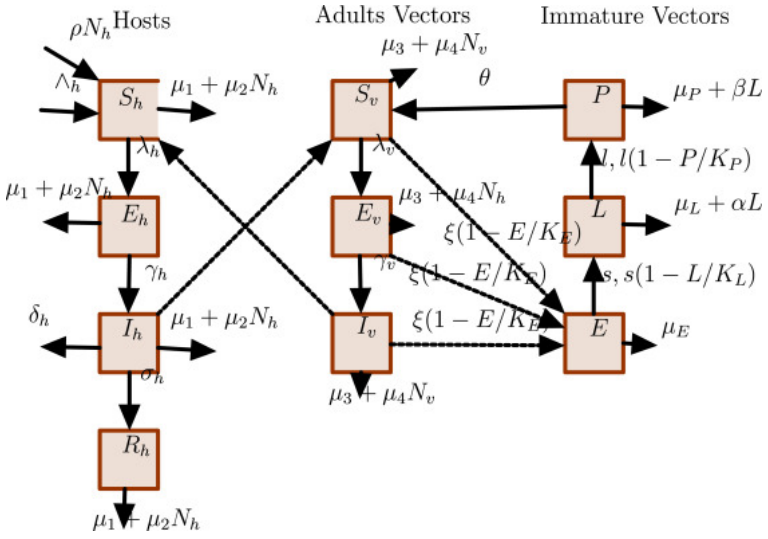


Fig 11: model

The key assumption in the model was that the infected mosquitoes remain infected through their lives and the parameters used in the model were: the average numbers of mosquito bites, probability

of infection transmission from an infectious vector to a susceptible human,e transition rate between compartments,death rate induced by the disease,e recovered rate of infectious humans, rate at which pupae become adult females (susceptible mosquitoes),mortality rates of adult female mosquitoes, average number of eggs laid by each adult female, at each deposit,natural death rates of eggs,larvae and pupae, additional death rate of larvae and pupae, due to the density.

2.1 Objective

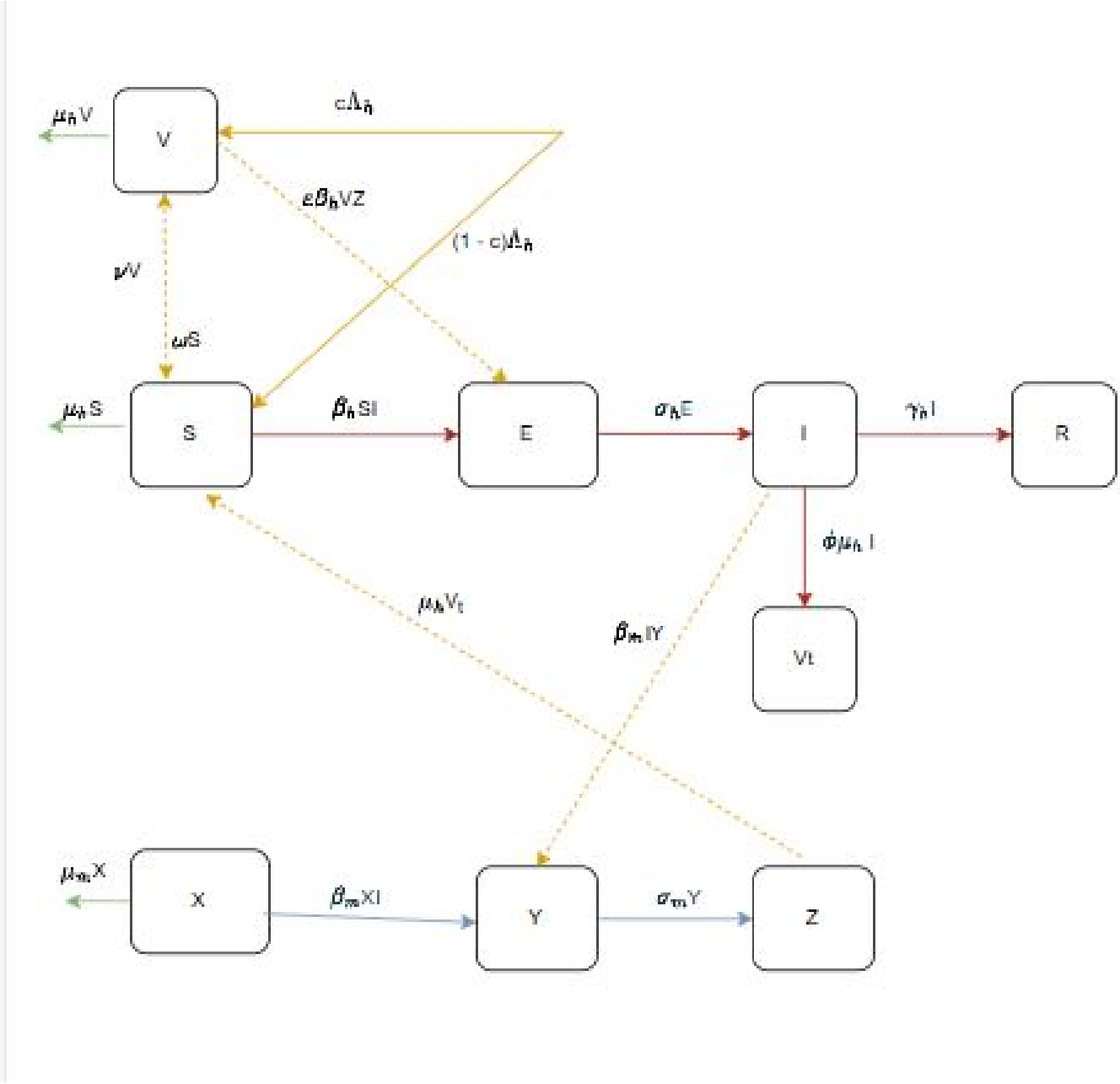
The main objective of this study is to determine the optimal level of vaccination coverage and vaccine efficacy that can achieve elimination of chikungunya virus disease in the endemic chikungunya virus zones in Kenya

In this study, we evaluate the transmission dynamics of the Chikungunya fever with the introduction of vertical transmissions in the model.

3 Model Formulation

We formulate a simple SEIR mathematical model for the transmissions of Chikungunya disease infection in human and mosquito populations. The proposed model includes vertical transmissions which is to the best of our knowledge has not been considered in other mathematical models.

Human population is divided into five subpopulations, **Susceptible(S)**: individuals who are at risk of infection, **Exposed humans(E)**: those who are likely to be infected, **Infected(I)**: Individuals infected with the virus, **Perinatal infected humans(V)**: a population infected through vertical transmission, **Recoverd humans(R)**: a population fully recovered with immunity. Mosquito population is divided into three subpopulations that is **Susceptible mosquitoes(X):** uninfected mosquitoes, **Exposed mosquitoes(Y):** mosquitoes likely to be infected and **Infectious mosquitoes(Z):** mosquitoes infected with the virus



3.1 Ordinary differential equations

The corresponding equations that describe the infection dynamics are:

Human Population Dynamics

1. **Susceptible humans (S):**

$$\frac{dS}{dt} = \Lambda_h - \mu_h S - \beta_h \frac{S}{N} Z - \nu S + \omega V$$

2. **Exposed humans (E):**

$$\frac{dE}{dt} = \beta_h \frac{S}{N} Z - \sigma_h E - \mu_h E$$

3. **Infected humans (I):**

$$\frac{dI}{dt} = \sigma_h E - \gamma_h I - \mu_h I$$

4. **Recovered humans (R):**

$$\frac{dR}{dt} = \gamma_h I - \mu_h R$$

5. **Vaccinated humans (V):**

$$\frac{dV}{dt} = \nu S - \omega V - \mu_h V - \epsilon \beta_h \frac{V}{N} Z$$

6. **Vertically infected humans (V_t):**

$$\frac{dV_t}{dt} = \phi \mu_h I - \mu_h V_t$$

Mosquito Compartments

1. **Susceptible mosquitoes (X):**

$$\frac{dX}{dt} = \Lambda_m - \mu_m X - \beta_m \frac{X}{N} Z$$

2. **Exposed mosquitoes (Y):**

$$\frac{dY}{dt} = \beta_m \frac{X}{N} Z - \sigma_m Y - \mu_m Y$$

3. **Infected mosquitoes (Z):**

$$\frac{dZ}{dt} = \sigma_m Y - \mu_m Z$$

Model Parameters

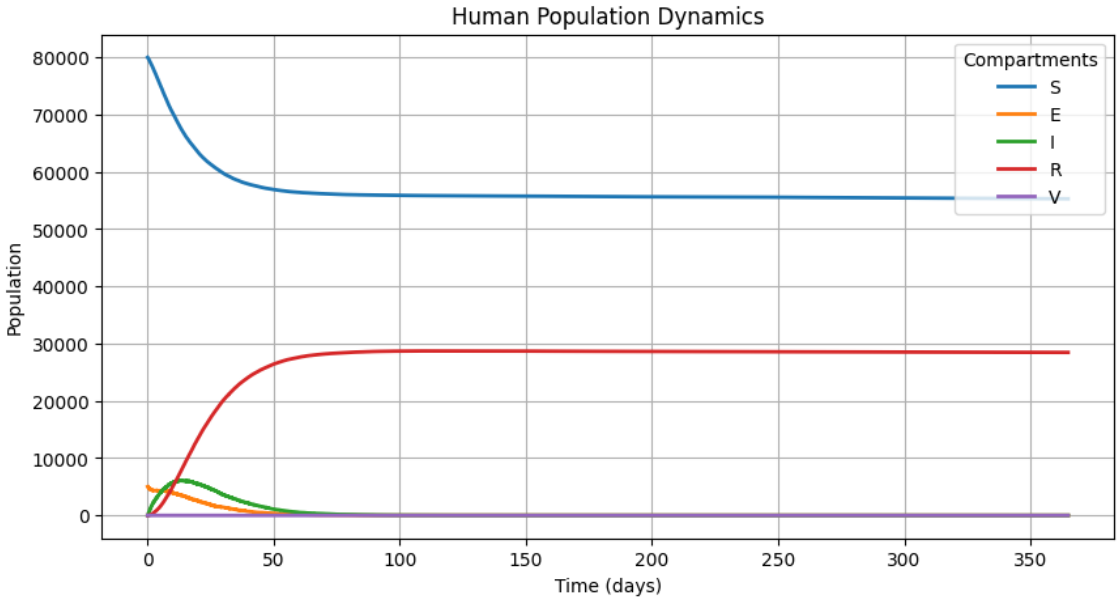
Table 1: Model Parameters

Symbol	Description	Value
b	mosquitoes biting rate	0.25
m	Mosquito-to-human ratio	3
p_h	Transmission probability from mosquito to human	0.24
p_m	Transmission probability from human to mosquito	0.25
$\beta_h = b.m.p_h$	Effective transmission rate from mosquitoes to human	0.18
$\beta_m = b.p_m$	Effective transmission rate from humans to mosquitoes	0.06
σ	Progression rate of exposed humans to infectious humans (1/incubation period in humans)	0.25
σ_1	Progression rate of exposed mosquitoes to infectious mosquitoes (1/latent period in mosquitoes)	0.2
γ_h	Recovery rate of infectious humans (1/recovery period in humans)	0.22
ϕ	Vertical transmission rate in humans	0.25
μ_h	Natural death rate in humans	0.00022
μ_m	Natural death rate in mosquitoes	0.0714
Λ	Recruitment rate of susceptible mosquitoes	83.75
N_H	Total human population in Lamu	101539
N_M	Total mosquito population	50000

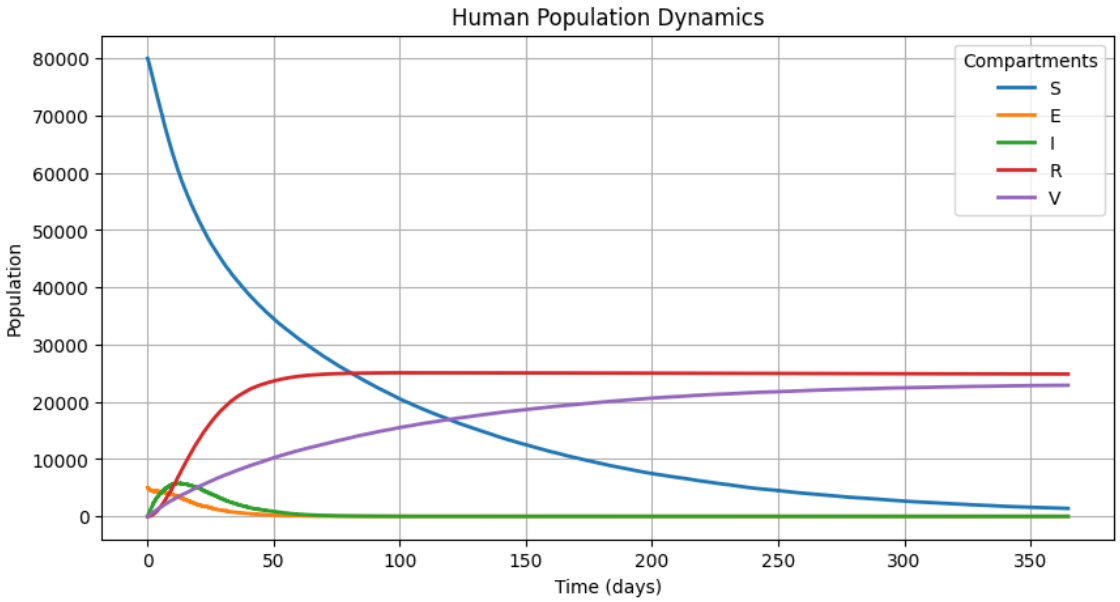
Using the above parameters obtained from literature to model chikungunya virus transmissions, we have the following human and mosquito population dynamics

Gillespie Methodology on compartmental modeling

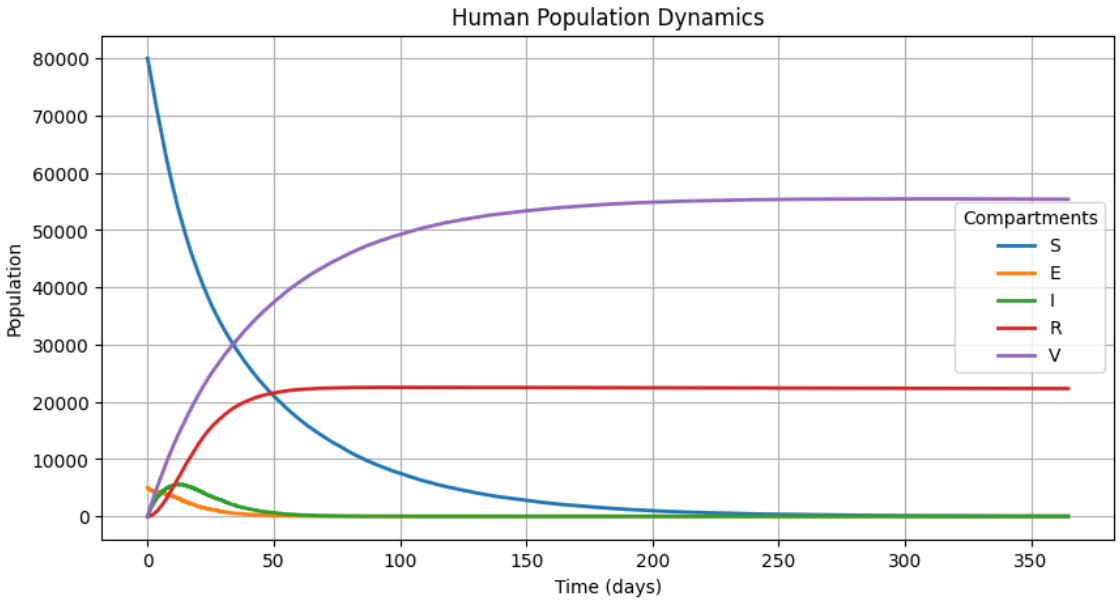
0% vaccination coverage



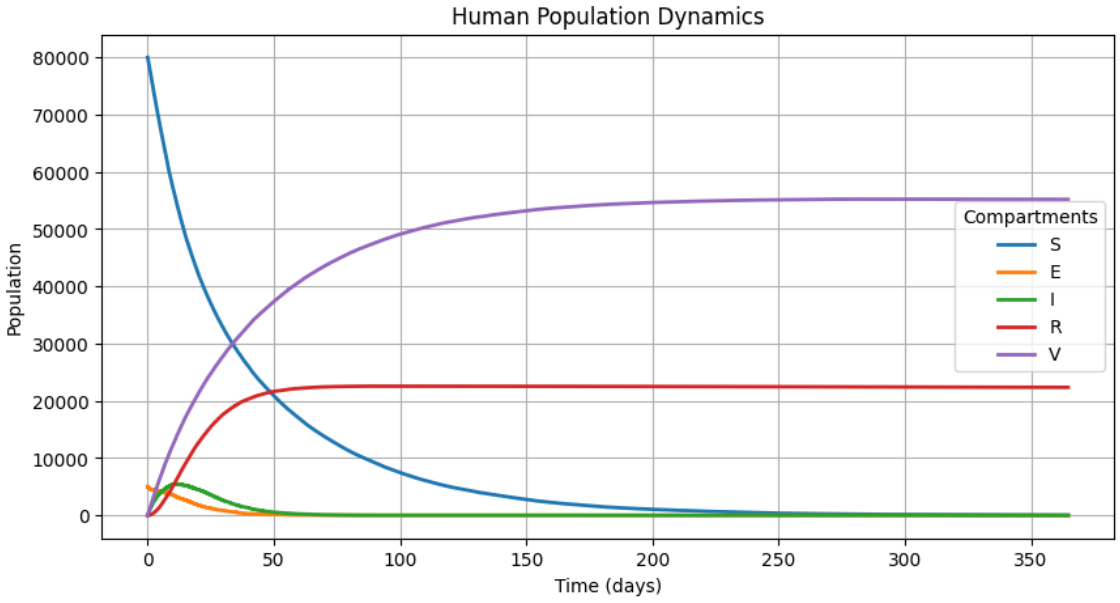
20% vaccination coverage and 40% vaccine efficacy



60% vaccination coverage and 90% vaccine efficacy



80% vaccination coverage and 90% vaccine efficacy



Agent Based Modeling

Model Formulation
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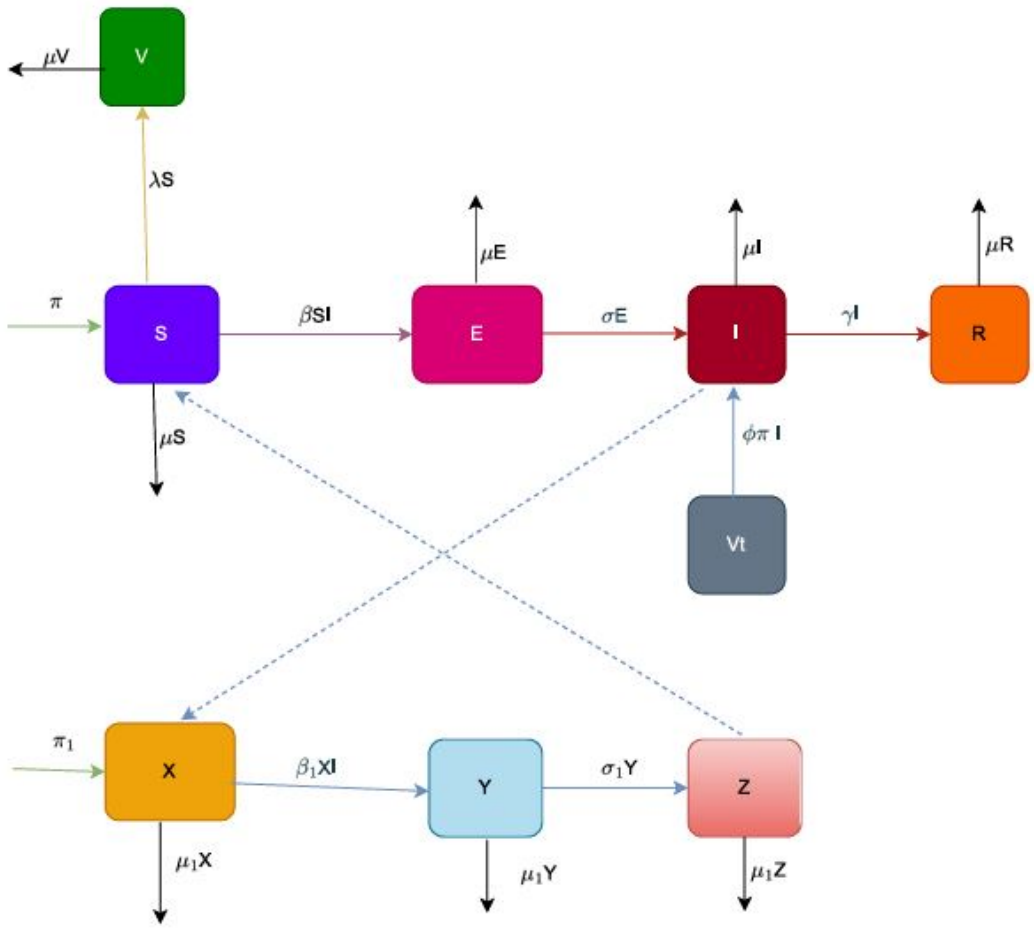
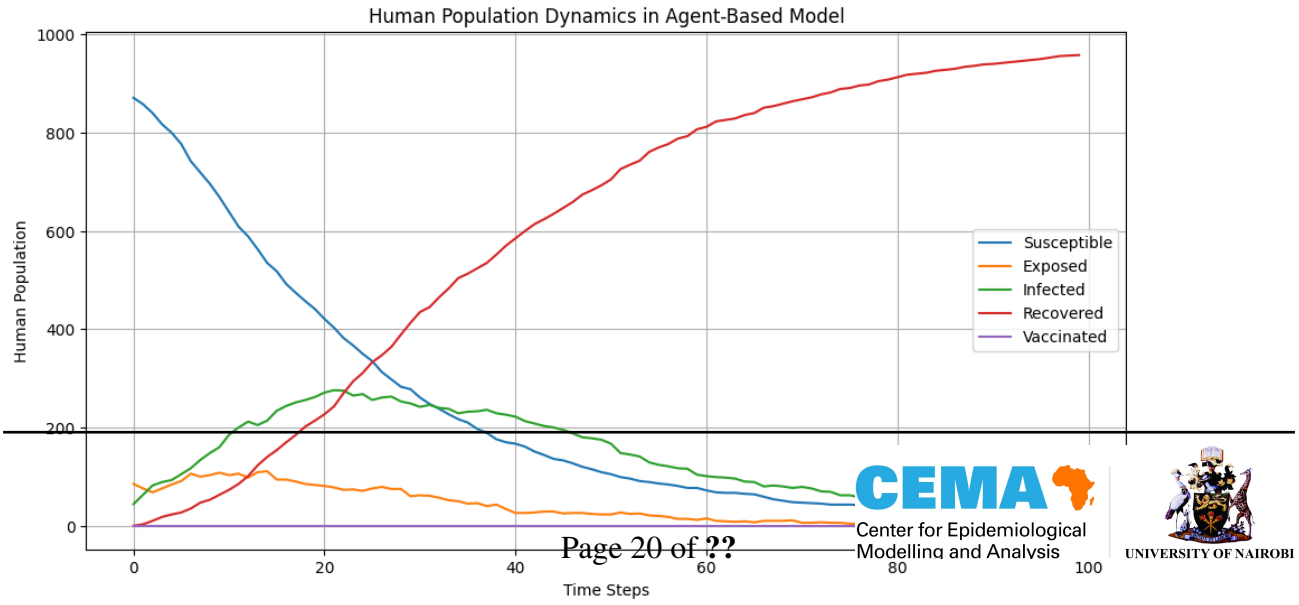
Model Structure



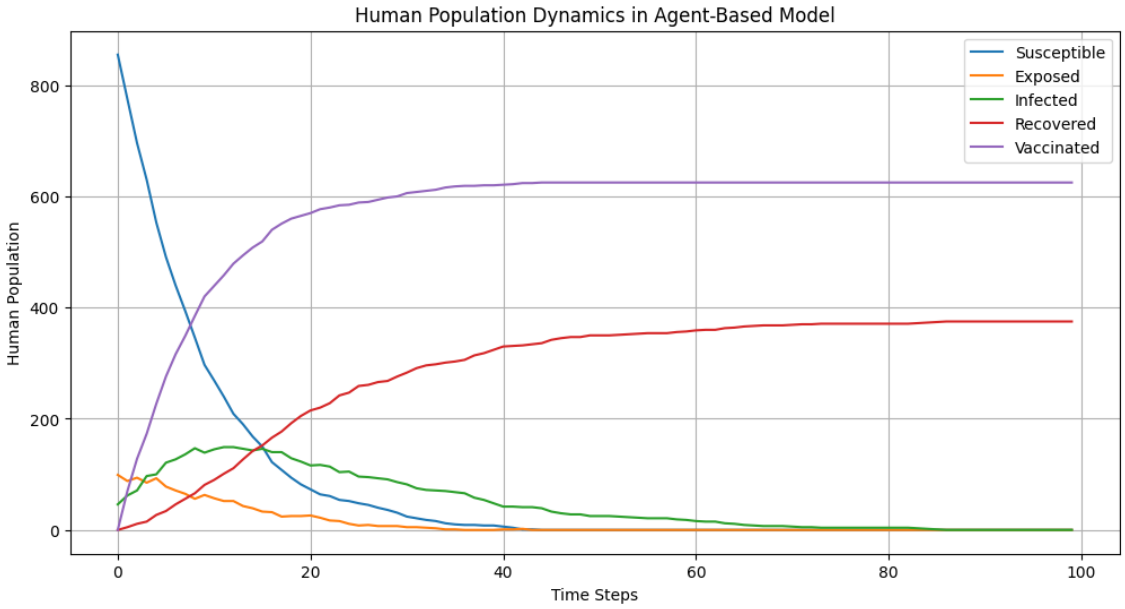
0% vaccination coverage and 0% vaccine efficacy

Table 2: Model Parameters

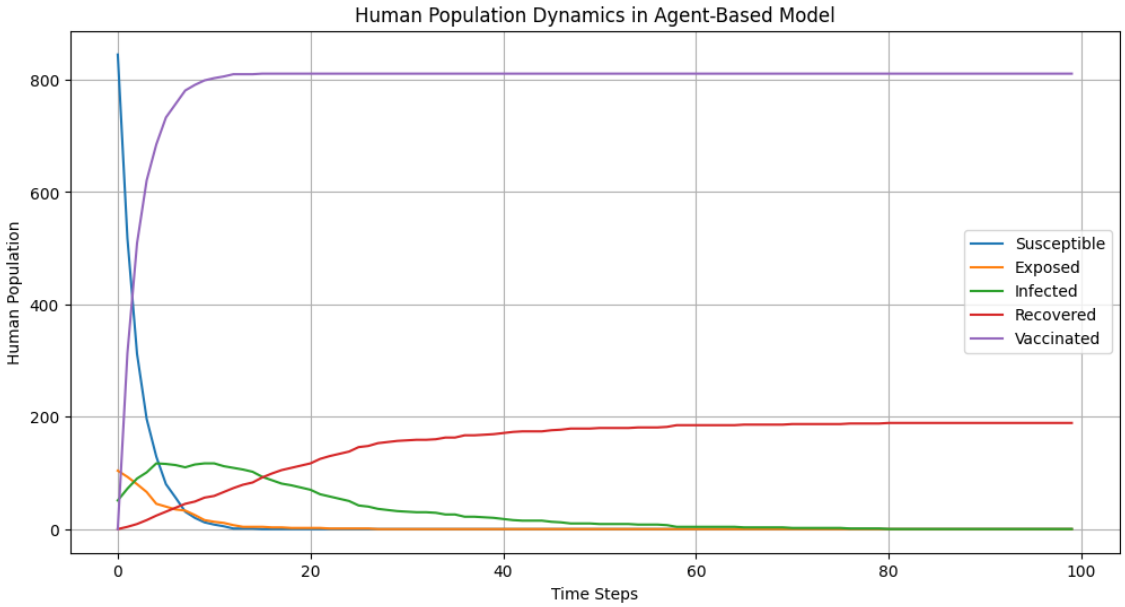
Symbol	Description	Value
b	mosquitoes biting rate	0.25
m	Mosquito-to-human ratio	5
p_h	Transmission probability from mosquito to human	0.24
p_m	Transmission probability from human to mosquito	0.25
$\beta_h = b.m.p_h$	Effective transmission rate from mosquitoes to human	0.3
$\beta_m = b.p_m$	Effective transmission rate from humans to mosquitoes	0.06
σ	Progression rate of exposed humans to infectious humans (1/incubation period in humans)	0.2
σ_1	Progression rate of exposed mosquitoes to infectious mosquitoes (1/latent period in mosquitoes)	0.2
γ_h	Recovery rate of infectious humans (1/recovery period in humans)	0.0714
μ_h	Natural death rate in humans	0.000041
μ_m	Natural death rate in mosquitoes	0.0714
N_H	Total human population in Lamu	101539
N_M	Total mosquito population	50000



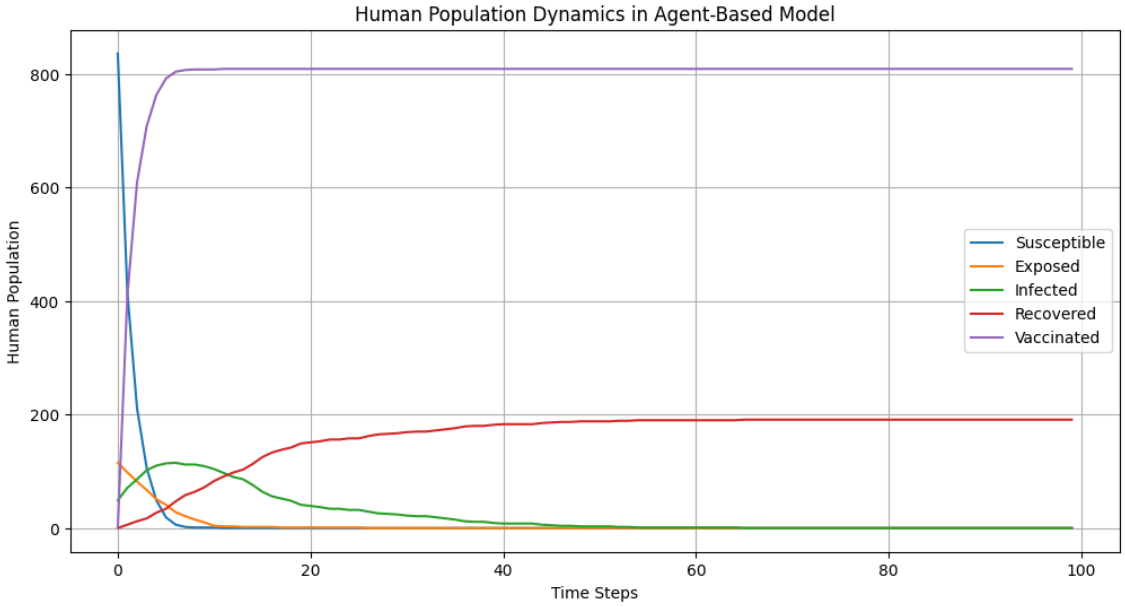
20% vaccination coverage and 40% vaccine efficacy



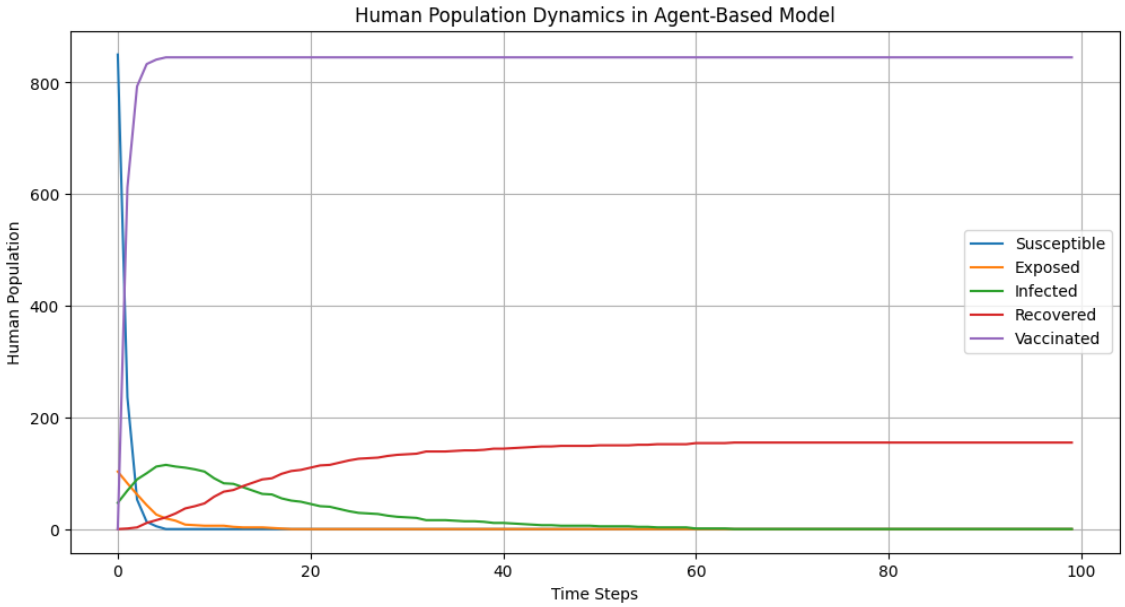
60% vaccination coverage and 60% vaccine efficacy



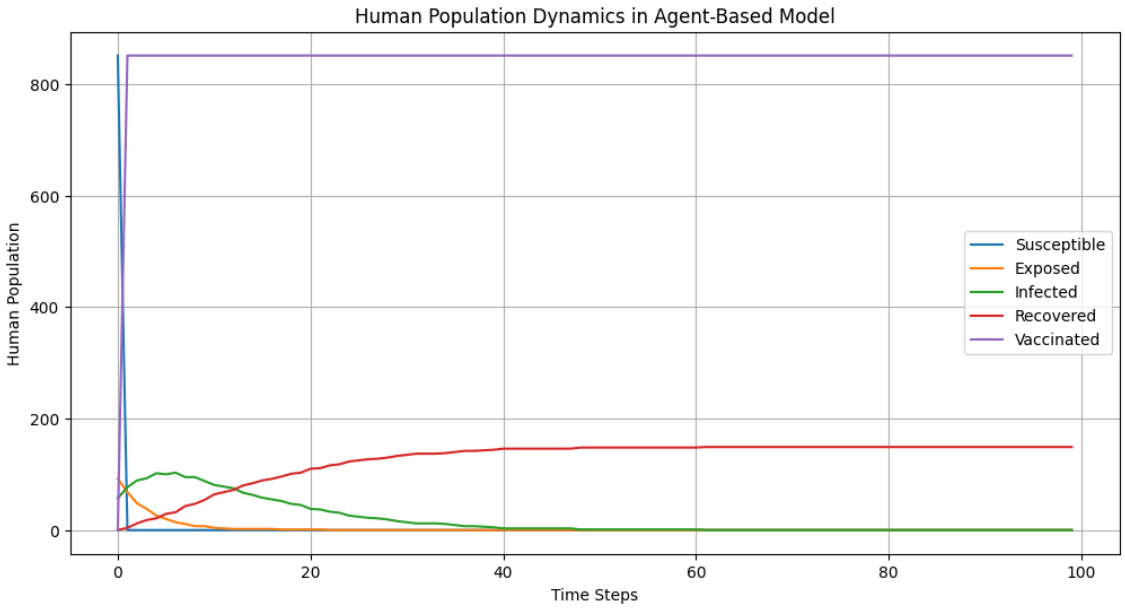
60% vaccination coverage and 80% vaccine efficacy



80% vaccination coverage and 90% vaccine efficacy



100% vaccination coverage and 100% vaccine efficacy



Vaccine	Phase 1	Phase 2	Phase 3
IXCHIQ	100%	ongoing	96.3 -98.6%
BBV87 â BBIL	No data		
MV-CHIK â Themis Bioscience		100%	
ChAdOx1 Chik â University of Oxford	100%		
PXVX0317	90%	98%	96.9 - 98.8%
mRNA-1388	100%		

Table 3: Vaccine efficacies

Symbol	Description	Range	Estimated
π	Human birth rate	1/67* 365	0.000039
μ	Human natural death rate	1/67*365	0.000039
β	Transmission rate of human to mosquito	0.02-0.94	0.2
υ	Vaccination rate	0.01 -0.1	0.01
σ	Progression rate from E to I humans	4, 2-6,2-4 ,2-4	0.25
π_1	Mosquito birth rate	To balance deaths	0.096
b_m	Mosquito biting rate	0.19-0.39, 0.3-1	0.2
β_1	Transmission rate of mosquito to human	0.005-0.35,	0.2
σ_1	Progression rate of E to I mosquitoes	1-14,2-6 ,2-6, 2-6	0.111
μ_1	Mosquito natural death rate	20-30,14-42,14-42	0.096
Ve	Vaccine efficacy	96.3 -98.6%	100%
γ	Recovery rate in humans	7 ,1-7,3-7 ,3-7	0.1667
	Symptomatic infection	60%,75% 83 -97%, 72-97% ,72-97% ,72-97%	0.6

Table 4: Model parameters

Table 5: Model Parameters

Symbol	**Description**
π	Birth rate
μ	Natural death rate
β	Transmission rate
υ	Vaccination rate
ϕ	Rate of becoming vaccinated immune
ω	Rate of waning immunity
σ	Progression rate from exposed to infected
ρ	Probability of symptomatic infection
Ve	Vaccine efficacy
γ	Recovery rate