

How to Cite:

Singla, S., & Rakshit, M. (2022). Mathematical analysis and control of chikungunya (CHIKV) virus by SEIR model. *International Journal of Health Sciences*, 6(S2), 8398–8407. <https://doi.org/10.53730/ijhs.v6nS2.7155>

Mathematical analysis and control of chikungunya (CHIKV) virus by SEIR model

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Abstract---Chikungunya is a re-emerging arboviral disease in Asia and Africa infected by Aedes mosquitoes which had posed a global threat in several countries. Vector borne diseases are the primary cause of death in most of the world countries, hence it becomes pertinent to control these vector borne diseases. In this paper a mathematical model is provided by dividing it in four components namely Susceptible human, Exposed human, Infected human, Recovered human. The study is carried out on basic reproduction number and stability analysis. A mathematical model is developed for globally asymptotically stable disease-free equilibrium, when the associated reproduction number is less than unity. The aim of this study is to formulate a model where number of infectives will not change and the infection rate equals to the recovery rate by reaching stable endemic equilibrium point.

Keywords---mathematical model, epidemic disease, stability, equilibrium point.

Introduction

Chikungunya is seasonal viral-infectious disease. It is an alphavirus infection and spread through bite from Aedes specially mosquitoes in humans population. The common symptoms of infection are fever and joint pain. Mostly symptoms are similar as dengue fever. The fever may be accompanied with headache, muscle pain, joint swelling or rashes. The infectious disease has affected approximately two million people, with some areas having attack rate as high as 68% [Roth et al. 2014]. Laith Y. et al. (2013) worked on Chikungunya and present a mathematical model of Chikungunya dynamics and control: The major epidemic on Reunion island. A simple, deterministic mathematical model of the transmission of the

virus between humans and mosquitoes was constructed and parameterised with the up-to-date literature on infection biology. In mathematical model, sensitivity analysis using Monte-Carlo simulation demonstrated the strong influence that both the latent period of infection in human and the pre-patent period have on these two epidemiological outcomes. Liu X. et al. (2014) analyzes vector borne disease chikungunya, transmitted by mosquitoes of the Aedes genus. Sujatha S. 2021, has been given the report on chikungunya virus (CHIKV) in India. CHIKV fever is an arbovirus disease caused by chikungunya virus, an alphavirus of Tgaviridae family. Symptoms appears after two to six days of incubation, including higher fever and severs arthralgia. The disease is self-limiting and usually resolve within two weeks. However, chronic disease can last up to several years with persistent polyarthralgia. Composition of some symptoms and common vector with dengue and malaria present many challenges for diagnosis and treatment of the disease.

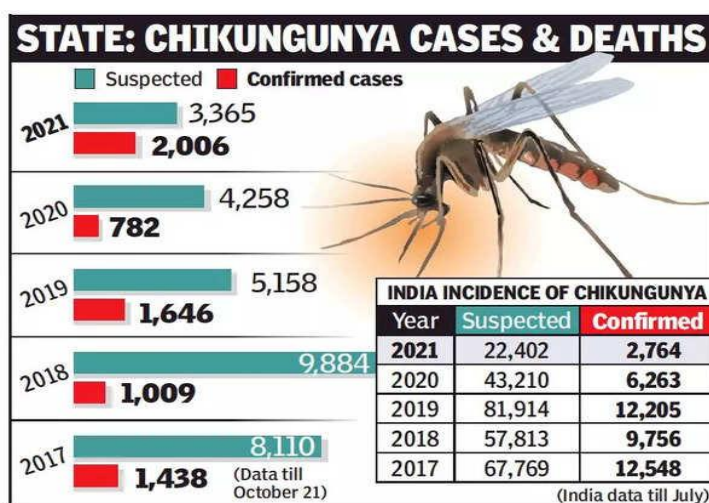


Figure 1: Data of Chikungunya in India

Chikungunya suspected and confirmed cases from year 2017 to 2021 in India and State taken from <https://timesofindia.indiatimes.com/city/mumbai/mumbai-5-yr-high-in-chikungunya-cases-in-state-but-count-under-reported/articleshow/87318886.cms>. Annual epidemiological report has been described and published online every year with all numerical facts. In this work ECDC (European Centre for Disease prevention and Control) surveillance report for the year 2018 to 2021 has been represented and used the numerical data for analysing the improved mathematical model on Chikungunya disease. Dileep M. et al. 2018 worked on increased mortality rate associated with Chikungunya epidemic, Ahmedabad India. Mortality rate data for Ahmedabad are consistent with investigation of other reported data that the virus may have mutated and becomes more dangerous than reported. Laurie A.S. et al. 2017 published research paper on Chikungunya virus (CHIKV). CHIKV is a mosquito-borne virus responsible for periodic and explosive outbreaks of a febrile disease that is characterized by severe and sometimes prolonged polyarthritis. The outcomes of CHIKV pathobiology indicates that CHIKV-elicited immune responses serve both

protective and pathogenic functions with several types of immune cells contributing to CHIKV induced rheumatic disease. Ruchi A. et al, 2020 presented the Mathematical modelling of chikungunya dynamics: stability and simulation. A new section of human population used in improved mathematical model SEIR, which is in the recuperation stage or in other words the human population that is no more representing acute symptoms but is yet to attain complete recovery. The outcome of the model is locally asymptotically stable because the basic reproduction number R_0 is less than 1. The numerical data of chikungunya disease is noted from January to November, 2021 through ECDC web-link.



Figure 2: Geographical distribution of Chikungunya cases reported worldwide

Chikungunya cases reported in India and South America from January to November 2021 <https://www.ecdc.europa.eu/en/publications-data/communicable-disease-threats-report-21-27-november-2021-week-47>. Several mutations have been identified in circulating strains of the virus resulting in better adaptations or increased fitness in the vectors, effective transmission and disease severity. CHIKV evolution has been a significant driver of epidemics in India, therefore the need to focus on proper surveillance, and implementation of prevention as well as control measure in the country.

Formulation of Mathematical Model

Kermack and McKendrick had developed an epidemic model in 1927, named as SIR Model, which is governed by the ordinary differential equations with sufficient numbers of variables and parameters. In this paper a mathematical model has been developed for obtaining reproduction number. SEIR is introduced for Chikungunya and is given as follows:

Where the variables and parameters are defined as

S(t): susceptible and individual who are uninfected

E(t): exposed class who received confirmation the symptoms against infection

I(t): infected individual who upon contact with S(t) class can infect the susceptible

R(t): recovered upon infection class

β = rate of transmission

ρ = rate of vaccination

μ = rate of death

Λ = birth rate

γ = recovery rate

$$\frac{dS}{dt} = \Lambda - \beta SE - \mu S \quad (2.1)$$

$$\frac{dE}{dt} = \beta SE - \rho E - \mu E \quad (2.2)$$

$$\frac{dI}{dt} = \rho E - \mu I - \gamma I \quad (2.3)$$

$$\frac{dR}{dt} = \gamma I - \mu R \quad (2.4)$$

Jacobian matrix is used to solve the governing equations

$$\text{Let } J = \begin{pmatrix} -\beta E - \mu & -\beta S & 0 & 0 \\ \beta E & \beta S - \rho - \mu & 0 & 0 \\ 0 & \rho & -\mu - \gamma & 0 \\ 0 & 0 & \gamma & -\mu \end{pmatrix}$$

Therefore, the characteristic equation is obtained as $|J - \lambda I| = 0$, we get

$$\begin{vmatrix} -\beta E - \mu - \lambda & -\beta S & 0 & 0 \\ \beta E & \beta S - \rho - \mu - \lambda & 0 & 0 \\ 0 & \rho & -\mu - \gamma - \lambda & 0 \\ 0 & 0 & \gamma & -\mu - \lambda \end{vmatrix} = 0$$

Which implies that,

$$(\mu + \gamma + \lambda)(\mu + \lambda)[A_0\lambda^2 + A_1\lambda + A_2] = 0 \quad (2.5)$$

Where $A_0 = 1$,

$$A_1 = -\beta S + \rho + 2\mu + \beta E$$

$$A_2 = \rho\beta E + \mu\beta E + \mu\rho - \mu\beta S + \mu^2.$$

Now from these characteristics equations we have two cases arises:

Case I: If all the values of eigen values λ 's are negative then the given system is stable for the epidemic disease.

Case II: If some or all the values of eigen values λ 's are positive then the given system is unstable for the epidemic disease.

The Basic Reproduction Number

The basic reproduction number (R_0) is defined for an epidemic disease by using SEIR model. If $R_0 < 1$, then the disease-free equilibrium point will be stable

otherwise, it will be unstable for $R_0 > 1$. From the above equation number, we have

$$\text{The basic reproduction number } (R_0) = \frac{\text{birth rate}}{\text{death rate}} = \frac{\Lambda}{\mu} \quad (3.1)$$

3.1 The observation of basic reproduction number $(R_0) = 2.32561 > 1$, by the definition the situation is unstable in India.

3.2 The observation of basic reproduction number $(R_0) = 0.88785 < 1$, by the definition the situation is asymptotically stable in Europe.

3.3 The observation of basic reproduction number $(R_0) = 1.0396 > 1$, by the definition the situation is asymptotically unstable in Tanzania.

Numerical Analysis

In this section numerical analysis of Chikungunya was done by using variables S_0, E_0, I_0, R_0 in comparing data of India, Europe and Tanzania. Data related to it is tabulated below.

Link For India: <https://timesofindia.indiatimes.com/city/mumbai/mumbai-5-yr-high-in-chikungunya-cases-in-state-but-count-under-reported/articleshow/87318886.cms>

For

Europe:

<https://www.google.com/search?q=birth+rate+of+population+of+europe&ei=rl>

For Tanzania: Wang, Y. and Liu, X., 2017. Stability and Hopf bifurcation of a within-host chikungunya virus infection model with two delays. Mathematics and Computers in Simulation, 138, pp.31-48.

Variables	Country 1: India		
	Cases in year 2021	Cases in year 2020	Cases in year 2019
S_0	22402	43210	81914
E_0	8806	7524	12890
I_0	2764	6263	12205
R_0	2663	5694	11709

Table 4.1: Chikungunya data for India

Variables	Country 2: Europe		
	Cases in year 2021	Cases in year 2020	Cases in year 2019
S_0	548	349936	693489
E_0	438	146914	37480
I_0	150	125678	32567
R_0	110	103022	28609

Table 4.2: Chikungunya data for Europe

Variables	Country 3: Tanzania		
	Cases in year 2020	Cases in year 2019	Cases in year 2018
S_0	191	281	294
E_0	13	101	14
I_0	11	30	6
R_0	03	13	3

Table 4.3: Chikungunya data for Tanzania

Parameters in different countries

In this section parameters value of three countries i.e India, Europe and Tanzania are obtained

Parameters	Numerical Values for country1:India	Numerical Values for country 2: Europe(ECDC-2018)	Numerical Values for country 3: Tanzania
β	0.1234	0.1511	0.1410
Λ	17.163	9.5	10.5
μ	7.380	10.7	10.1
ρ	54.4	9.34	12.41
γ	88.21	65.1	70.1

Table 4.1.1

Numerical Analysis of the Model

Case I: If all the values of eigen values λ 's are negative then the given system is stable for the epidemic disease.

Case II: If some or all the values of eigen values λ 's are positive then the given system is unstable for the epidemic disease.

Table 4.2.1: Eigen values λ 's for India

Eigen values λ 's	Numerical Values of cases in year 2021	Numerical Values of cases in year 2020	Numerical Values of cases in year 2019
λ_1	-95.59	-95.59	-95.59
λ_2	-7.38	-7.380	-7.380
λ_3	3530.77524	4488.12751	8530.7146
λ_4	1177.56316	1.97229	2.216015
Result of the Model	Asymptotically unstable	Asymptotically unstable	Asymptotically unstable

Table 4.2.2: Eigen values λ 'sfor Europe

Eigen values λ 's	Numerical Values of cases in year 2021	Numerical Values of cases in year 2020	Numerical Values of cases in year 2019
λ_1	-75.8	-75.8	-95.59
λ_2	-10.7	-10.7	-7.380
λ_3	17.5349	30649.8219	4488.12751
λ_4	-31.6539	-3.9377	1.97221

Result of the Model	Asymptotically unstable	Asymptotically unstable	Asymptotically unstable
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Table 4.2.3: Eigen values λ 's for Tanzania

Eigen values λ 's	Numerical Values of cases in year 2020	Numerical Values of cases in year 2019	Numerical Values of cases in year 2018
λ_1	-80.2	-80.2	-80.2
λ_2	-10.1	-10.1	-10.1
λ_3	0.42715	7.98998	16.0325
λ_4	-7.93915	-15.21998	-9.1625
Result of the Model	Asymptotically unstable	Asymptotically unstable	Asymptotically unstable

Graphical Representation

Graphical representation of the variables S_0 , E_0 , I_0 , R_0 in comparing data of India, Europe and Tanzania are depicted below:

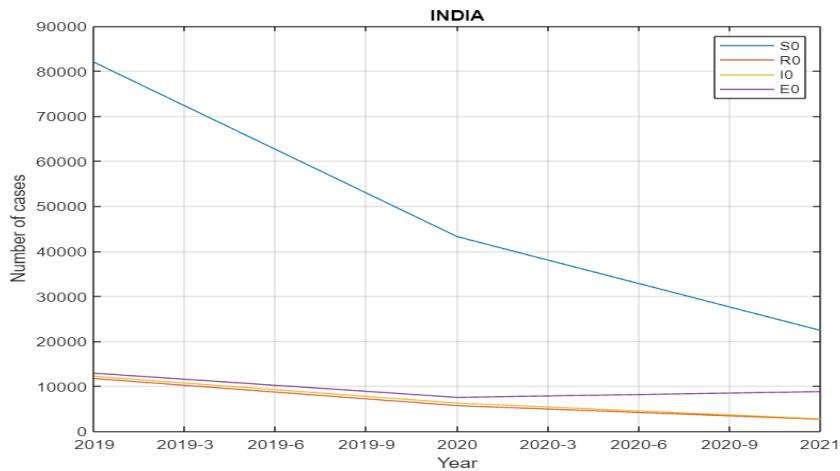


Figure 4.3.1: Graphical representation of CHIKV cases in year 2019 to 2021 in India

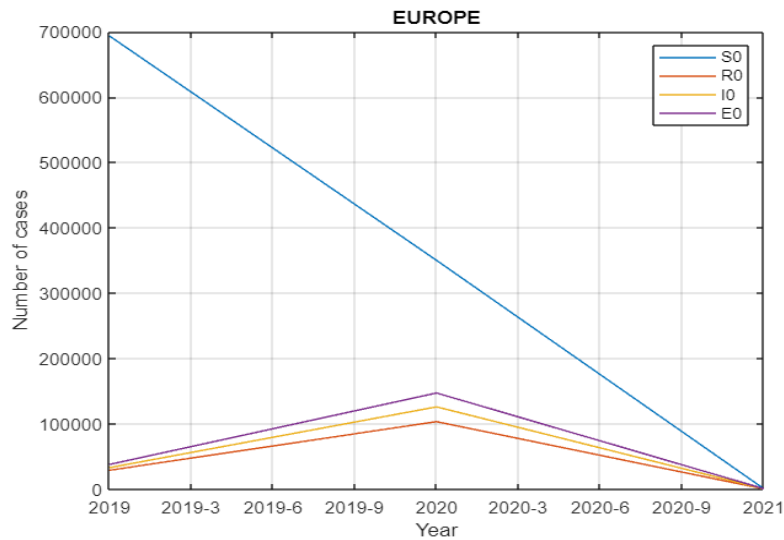


Figure 4.3.2: Graphical representation of CHIKV cases in year 2019 to 2021 in Europe

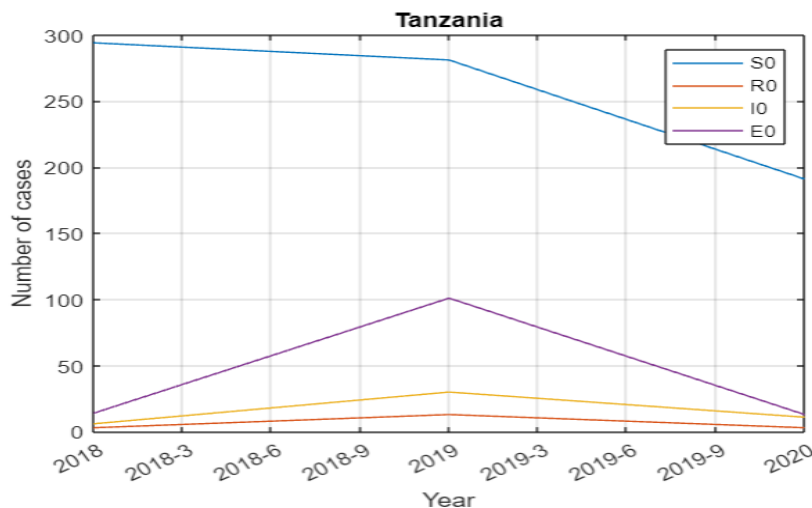


Figure 4.3.3: Graphical representation of CHIKV cases in year 2018 to 2020 in Tanzania

Conclusion

In this paper a SEIR mathematical model is developed on situation of Chikungunya disease by comparing the data of three countries i.e India, Europe and Tanzania, with the help of variables: $S(t)$: Susceptible, $E(t)$: Exposed, $I(t)$: Infected, $R(t)$: Recovered and parameters: β i.e rate of transmission, ρ i.e rate of vaccination, μ i.e rate of death, Λ i.e birth rate, γ i.e recovery rate. Table 4.2.1 to 4.2.3 provides the eigen values λ 's for India, Europe and Tanzania respectively and their conditions of asymptotically unstability. The SEIR model provides the

numerical analysis for three countries to discuss the present situation of Chikungunya. The observation of basic reproduction number (R_0) = 2.32561 > 1, $0.88785 < 1$ and $1.0396 > 1$ by the definition of R_0 the situation is unstable for India, asymptotically stable for Europe, asymptotically unstable for Tanzania respectively. The epidemic model on Chikungunya well explained graphically that India and Tanzania have to focus for the next coming years while Europe is in better situation.

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