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# Caputo fractional order derivative model of Zika virus transmission dynamics

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## Abstract

The Zika Virus (ZIKV) is a highly contagious disease, and several outbreaks have occurred since it emerged. It is transmitted from one to another human via a mosquito Aedes aegypti. There is no vaccine or established medicine available for ZIKV to date. There is an urgent need to enhance an understanding of the progression mechanism of the disease when drugs or vaccines are not available. Mathematical modeling is a tool that might be helpful to understand the progression dynamics of ZIKV which can enable us to make control strategies for invading the progression dynamics of disease. SEIR-SEI is a famous compartmental deterministic modeling based on integer-order derivative calculus. Nowadays, conversion from integer to fractional order-based derivative modeling is in trend, and it is a very effective and high degree of accuracy. In this paper, we proposed a Caputo fractional-order based susceptible-exposed-infected-recovered (SEIR) structure for hosts and a susceptible-exposed-infected (SEI) structure for mosquitoes for transmission dynamics of ZIKV. For this purpose, we modified the classical compartmental model used in the study of progression dynamics of the Zika fever outbreak in El-Salvador during 2015-16. The modified model involves nonlinear differential equations of fractional (non-integer) order which has an advantage over the classical model due to its memory effect property. Our study includes eight regions across the globe where the Zika outbreak has occurred during the year 2013-2016 including six major archipelagos of French Polynesia, i.e., Tahiti, Sous-le-vent, Moorea, Tuamotu, Marquises, and Australes. The other two regions included Costa Rica and Colombia. The outbreak in selected regions was studied first using a classical model and then compared by a fractional-order model. The data of outbreaks are best fitted with the fractional-order model which enables us to estimate the best parameters values for the outbreaks. Using this modeling, the epidemic threshold parameter $R_0$ was computed which is more accurate than the classical one. Hence, the fractional-order model for ZIKV transmission dynamics is much better prediction, analysis, and disease parameters estimation than the classical model. This modeling enhances the knowledge in the field of fractional order and understanding the ZIKV transmission accurately.

**Keywords:** Fractional-order, transmission dynamics, basics reproduction number, ZIKV.

**2020 MSC:** 92B05, 92D25, 92D30, 26A33.



## 1. Introduction

The Zika virus (ZIKV) belongs to the Flaviviridae family, and it was initially identified in Uganda, Africa, in 1947 in monkeys [28]. Zika disease is caused by a virus transmitted by the bite of a female *Aedes*

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*aegypti* mosquito during the day. Symptoms may include mild fever, rash, conjunctivitis, muscle and joint pain, malaise or headache and typically last for 2–7 days. ZIKV has been an emerging disease since 1952, and the first large outbreak occurred in Yap, Micronesia during April-July 2007 [21], followed by French Polynesia outbreak 2013-14 [10], and also in other Pacific countries [39, 46]. The local transmission was also reported during 2015 in South American countries, including Brazil [9, 38] and Colombia [36]. The emergence of ZIKV and other infectious diseases occurred by several mediums have caused an extremely significant impact on global health, and economies [7, 37]. Still, we have not established medicine and vaccine for ZIKV treatment. Hence, understanding the progression dynamics of the disease might have a tool as mathematical modeling. Mathematical modeling can tell us about the crucial parameters which are in the progression of the disease, and control strategies can develop for these parameters to invade the disease [1, 4–6, 8, 25].

Although much research based on mathematical modeling has been done contributing ZIKV disease, the most worrying aspect about it is that we are yet far-reaching from the accurate and high degree of prediction [12, 13, 22, 48]. Thus, it is important to increase our understanding of ZIKV transmission dynamics by introducing new techniques in the existing models. Developing control and prevention methods for the disease is an important issue in an epidemic situation. Mathematical modeling has a long history in providing insights into transmission and control of various viral infectious diseases across the world [4, 11, 14, 23, 27, 34, 50]. In particular, mathematical modeling plays an important role in investigating the transmission and interior of the ZIKV [25, 31, 41, 49]. Most of these studies focused on deterministic integer-order compartmental modeling techniques to investigate the dynamics. These models have been proposed with more assumptions and restrictions to achieve a goal. However, these are not appropriate to incorporate host and vector memory and learning behavior on transmission dynamics of vector-borne diseases. Recent studies on viral infections show the implementation of memory effect property through fractional-order differential equations (FDEs), which produce the better result as compared to the classical approach based on ordinary differential equations (ODE) [16, 17]. Researcher also attempted fractional order based mathematical modeling for ZIKA also such as [2, 3, 24, 29, 45]. In the paper [3], authors introduced the concept of fractional differentiation based on a non-local operator with non-singular and non-local kernel for ZIKA disease transmission. Further, they did equilibrium analysis and developed iterative approximation using Atangana-Baleanu fractional integral operator, they did a mathematical analysis of the solution, but the authors did not simulate any actual datasets. [29] described a model for ZIKA in the Caputo sense and analysis model, but they also did not simulate for any actual datasets. [45] proposed an epidemic model for Zika virus infection using delay differential equations with fractional order, and the numerical simulations confirmed that a combination of fractional order and time delays in the epidemic model effectively enriches the dynamics and strengthens the stability condition of the model. In this way, most of the research work based on fractional-order derivatives for ZIKA transmission did not consider a simultaneous analysis for fractional and integer order derivative based models and did not simulate actual datasets.

In the present investigation, we extended the concept of the ZIKV infection model to study the ZIKV outbreak. These outbreaks occurred in eight regions, including six major archipelagos of French Polynesia, i.e., Tahiti, Sous-le-vent, Moorea, Tuamotu, Marquises, and Australes during 2013-14, Colombia during 2016 and Cost Rica during 2016-17. We incorporated fractional-order derivatives for the transmission of ZIKV infection in the existing model, which was earlier examined the progression dynamics of El-Salvador outbreak of ZIKV disease during 2015-16 [32]. This modified model has been validated with the actual ZIKV outbreak data of French Polynesia (2013-14), Colombia (2016), and Costa Rica (2016-17). Further, the Adams-Bashforth-Moultan algorithm [18, 33] has been used to solve and simulate this fractional-order derivative-based model. The numerical solutions indicate that it has good quality of the approximation, providing a better agreement between actual and simulated data. This better approximation is helpful to determine the factor related to the disease. We also estimated key epidemiological parameter, i.e., the basic reproduction number ($R_0$), which has a massive literature devoted to it. Basic Reproduction Number ($R_0$) is an expected number of secondary infections produced by single infections in a population where

everyone is susceptible [15]. Generally, $R_0 > 1$ indicates the spreading of infections in a susceptible population. Although, this study could help to assist the outbreak planning, measure the transmission potential of disease, and investigate the association between ZIKV infection with other conditions. This study also argues that fractional-order derivatives might be more appropriate than integer-order. Thus, this approach can be further extended in modeling several vector-borne and other viral diseases like influenza, COVID-19, etc. This work will be helpful to plan for invading the disease before it reaches disasters condition.

## 2. Mathematical model

### 2.1. The classical mathematical model

This work utilizes SEIR compartmental model for hosts and SEI model for vectors developed to dynamics ZIKV infection. In this model whole human population is decomposed into different classes on the basis of infectious state of individuals. Each class represents the health condition of an individual at time t of the infection. We assumed here uniform mixing in host (human) and vector (mosquito) population. Further, each human as well as each mosquito has equal probability of transmitting and acquiring the infection in their respective population. Human population is divided into four mutually exclusive groups, i.e., susceptible ($S_h$), exposed ($E_h$), infected ($I_h$) and recovered ($R_h$), whereas mosquito population is splited into three groups, i.e., susceptible ($S_v$), exposed ($E_v$) and infected ($I_v$). The total human and mosquito population is denoted by $N_h(t)$ and $N_v(t)$, respectively. In this case, $N_h(t) = S_h(t) + E_h(t) + I_h(t) + R_h(t)$ and $N_v(t) = S_v(t) + E_v(t) + I_v(t)$. We considered this model for ZIKV which is defined by a system of non linear ODEs given in system of equations (2.1).

$$\begin{aligned}
&\frac{dS_h}{dt} = -\alpha_h S_h I_v, \qquad \frac{dE_h}{dt} = \alpha_h S_h I_v - \beta_h E_h, \qquad \frac{dI_h}{dt} = \beta_h E_h - \gamma_h I_h,\\
&\frac{dR_h}{dt} = \gamma_h I_h, \qquad \frac{dS'_v}{dt} = \mu_v - \mu_v S'_v - \alpha_v S'_v \frac{I_h}{N_h}, \quad \frac{dE'_v}{dt} = -\mu_v E'_v - \beta_v E'_v + \alpha_v S'_v \frac{I_h}{N_h},\\
&\frac{dI'_v}{dt} = \beta_v E'_v - \mu_v I'_v,
\end{aligned} \tag{2.1}$$

where, $S'_v(t)$, $E'_v$, and $I'_v$ signify proportion of vectors with the property $0 \leqslant S'_v, E'_v, I'_v \leqslant 1$ given in equation (2.2).

$$S'_v(t) = \frac{S_v}{N_v}, \qquad E'_v(t) = \frac{E_v}{N_v}, \qquad I'_v(t) = \frac{I_v}{N_v}. \tag{2.2}$$

In this system, $\alpha_h$ denotes the rate at which susceptible humans are exposed and is equal to $a \times b \times m$, where $a$ is the number of mosquitoes bites per day per human, $b$ is the transmission probability from infectious mosquito to suspected human per bite and $m$ is the average ratio of mosquito to human, $\beta_h$ is the rate at which exposed humans are become infected, and $\gamma_h$ is the rate at which infected humans get recovered. Similarly $\alpha_v$ is the rate at which susceptible mosquitoes are exposed and is equal to $a \times c$ (independent of vector to human ratio), where $c$ is the transmission probabilities from infected human to infected mosquitoes, $\beta_v$ is the rate at which exposed mosquitoes become infected. Moreover, the parameter $\mu_v$ is the mortality rate of vectors (mosquito life span). Finally, the rate from infected human population to recovered human population is denoted by $\gamma_h$. For the better understanding of parameters the above mentioned model (2.1) can be defined accordingly as in system of equations (2.3).

$$\begin{aligned}
&\frac{dS_h}{dt} = -abmS_hI_v, \quad \frac{dE_h}{dt} = abmS_hI_v - \beta_hE_h, \quad \frac{dI_h}{dt} = \beta_hE_h - \gamma_hI_h,\\
&\frac{dR_h}{dt} = \gamma_hI_h, \quad \frac{dS'_v}{dt} = \mu_v - \mu_vS'_v - acS'_v\frac{I_h}{N_h}, \quad \frac{dE'_v}{dt} = -\mu_vE'_v - \beta_vE'_v + acS'_v\frac{I_h}{N_h},\\
&\frac{dI'_v}{dt} = \beta_vE'_v - \mu_vI'_v.
\end{aligned} \tag{2.3}$$

We make following assumptions while formulating this model. (a) The transmission do not consider human-to-human transmission like sexual transmission, mother to baby, or through blood transmission, (b) Demo-graphical changes, migration, new births or deaths are not considered in human population, hence the total human population ($N_h$) is maintained constant, (c) The total vector population ($N_v$) is also maintained constant during the work by considering the birth and death rates identical.

### *2.2. Fractional order derivative based model*

Recently, FDEs have gained considerable attention in different fields of engineering, life sciences, physics, biology and many others. It is being observed that fractional-order derivatives can provide a better agreement between actual and simulated data as compared to classical models, which are based on integer-order derivatives [16, 17]. Therefore, it is reasonable to formulate the presented model using fractional-order derivatives, which has an advantage due to its memory effect property [40]. Memory effect property suggests that the future state does not depend only on its current state but also on its past states.

Leibniz predicted the concept of FDEs in a letter written in 1695 [35]. After that Pooseh et al. [44] attempted to introduce the notion of fractional derivative in the field of vector-borne transmission dynamics. They replaced all the first derivatives in a classical model by Riemann-Liouville type fractional derivative of order $\alpha \in (0,1)$. There are many exciting definitions of fractional derivatives that have been discussed in [30, 43], although the best known is the Riemann-Liouville definition. The Riemann-Liouville derivative of order $\alpha$ is defined as:

$$D^{\alpha}_{0+}f(t) = \frac{1}{\Gamma(n-\alpha)}\left(\frac{d}{dt}\right)^n \int_0^t \frac{f(s)}{(t-s)^{\alpha-n+1}}ds, \quad n = [\alpha]+1,$$

where, $0 < \alpha < 1$ for $\alpha \in R$, $n$ is an integer, $\Gamma$ represents the gamma function and $[\alpha]$ represents greatest integer value of $\alpha$. This approach leads to the following two issues. First is that, Riemann-Liouville does not hold differentiation of the constant [16], i.e.,

$$D^{\alpha}c = \frac{c}{\Gamma(1-\alpha)}t^{-\alpha} \neq 0, \quad c = \text{constant}.$$

Hence, it fails to solve the differential operators in case of their constant value when they get replaced by Riemann-Liouville differential operator of order $\alpha \in (0,1)$ [20]. Thus, the modified model will discard our assumption that a total human population ($N_h$) and a total number of mosquito populations ($N_v$) should keep constant. The second issue is that Riemann-Liouville type fractional derivative fails to combine with the initial conditions of the form defined here in the classical model [16, pp. 54–55].

Therefore, in this article, we considered Caputo type fractional derivative [16, Chap. 3], [26] instead of Riemann-Liouville. It can be defined as:

$$D^{\alpha}_{t}f(t) = \frac{1}{\Gamma(n-\alpha)}\int_0^t \frac{f^n(s)}{(t-s)^{\alpha-n+1}}ds, \quad n = [\alpha]+1.$$

Thus, by replacing the integer derivative in model (2.3) by Caputo derivative of order $\alpha$, the modified

model (2.4) is given as:

$$\begin{aligned}
&\frac{d^\alpha S_h}{d^\alpha t} = -abmS_hI_v, \quad \frac{d^\alpha E_h}{d^\alpha t} = abmS_hI_v - \beta_hE_h, \quad \frac{d^\alpha I_h}{d^\alpha t} = \beta_hE_h - \gamma_hI_h,\\
&\frac{d^\alpha R_h}{d^\alpha t} = \gamma_hI_h, \quad \frac{d^\alpha S'_v}{d^\alpha t} = \mu_v - \mu_vS'_v - acS'_v\frac{I_h}{N_h}, \quad \frac{d^\alpha E'_v}{d^\alpha t} = -\mu_vE'_v - \beta_vE'_v + acS'_v\frac{I_h}{N_h},\\
&\frac{d^\alpha I'_v}{d^\alpha t} = \beta_vE'_v - \mu_vI'_v,
\end{aligned} \tag{2.4}$$

where $\alpha \in (0,1]$ is the order of fractional derivative and the fractional operator $d^\alpha$ is identical to the classical first derivative for $\alpha = 1$.

Further, by a simple dimension analysis, we can note that model (2.4) have mismatching in the dimensions on the left hand and right-hand side of the equations. A simple dimensional analysis shows that the left-hand side of this model has dimension $(\text{time})^{-\alpha}$. The terms $a, \beta_h, \gamma_h, \mu_v, \beta_v$ on the right-hand side has the dimension $(\text{time})^{-1}$ and the other terms on right-hand side are dimensionless found by doing a close inspection. Therefore, the right-hand side of this model has the dimension $(\text{time})^{-1}$. We make sure that the right-hand side of the equations of the system must have the same dimension as the left-hand side. This drawback of "fractionalization" has been addressed by Diethelm where he formulated a fractional-order deterministic model [17]. Sardar et al. [47] used this method to analyze a similar model and achieved better results. Therefore, we tried to overcome the mismatching in dimensions using the procedure described by Diethelm [17]. Moreover, the mosquitoes and human population do not behave the same way, which gives more refinement to this model. Hence, the model (2.4) can become more realistic by introducing two different fractional differential operators $\alpha \in (0,1]$ and $\beta \in (0,1]$ for human and mosquitoes, respectively. Following the method given by Diethelm [17], modified and improved model (2.5) is given as:

$$\begin{aligned}
&\frac{d^\alpha S_h}{d^\alpha t} = -a^\alpha bmS_hI_v, \quad \frac{d^\alpha E_h}{d^\alpha t} = a^\alpha(b)(m)S_hI_v - \beta_h^\alpha E_h, \quad \frac{d^\alpha I_h}{d^\alpha t} = \beta_h^\alpha E_h - \gamma_h^\alpha I_h,\\
&\frac{d^\alpha R_h}{d^\alpha t} = \gamma_h^\alpha I_h, \quad \frac{d^\beta S'_v}{d^\beta t} = \mu_v^\beta - \mu_v^\beta S'_v - (a)^\beta(c)S'_v\frac{I_h}{N_h}, \quad \frac{d^\beta E'_v}{d^\beta t} = -\mu_v^\beta E'_v - \beta_v^\beta E'_v + (a)^\beta(c)S'_v\frac{I_h}{N_h},\\
&\frac{d^\beta I'_v}{d^\beta t} = \beta_v^\beta E'_v - \mu_v^\beta I'_v.
\end{aligned} \tag{2.5}$$

It is evident that as $\alpha \to 1$ and $\beta \to 1$, model (2.5) reduces to classical model (2.3). By a simple computation in model (2.5), the total population $N_h$ and $N_v$ in the modified system is observed to be constant. Therefore, this section deals with the mathematical formulation of the fractional-order initial value problem. The classical model (2.3) is an integer order system that is based on the deterministic, in which the present state do not carry any information from its previous all state where current state is just based on initial state. It is well defined that the state of many systems in biological science, viscoelastic study etc., depends on the properties of previous all states [42]. In order to get a better understandingof the transmission dynamics of mosquito-borne diseases, it is necessary to incorporate the memory and learning behavior of hosts and vectors. Therefore, we tried the generalization of the classical model, which carries information about its different previous states, to get better and more accurate results.

Furthermore, the Basic reproduction number $R_0$ is an important part of knowing infections' dynamics. A basic reproduction number is the average number of secondary infections from one infected to another susceptible population. We compute $R_0$ using the adopted methodology from [32] and resulted in the

form of equation (2.6) for fractional-order model (2.5).

$$R_0 = \sqrt{\frac{(a^\alpha bm)(a^\alpha c)\beta_v^\beta}{\gamma_h^\alpha \mu_v^\beta (\mu_v^\beta + \beta_v^\beta)}}. \tag{2.6}$$

## 3. Simulations

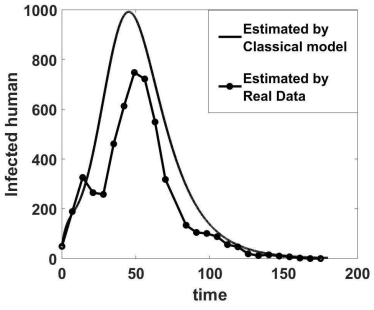
In this article, the data for ZIKV outbreaks occurred in French Polynesia (2013-14) has been obtained from the supporting information of Kucharski et al. [10], the data of Costa Rica (2016) outbreak has been obtained from Pan American Health Association (PAHO) from $17^{th}$ week of 2016 to $15^{th}$ week of 2017 and Colombia data has been extracted from a research article [36]. As the mathematical model depends on the parameters, the parameter can be calculated by two mode, one can be estimated from literature by doing certain calculation and other from the original data. Here, the range value of the parameter for the concerned data are obtained from the related literature and are shown in Table 1. The initial conditions for all the data with respect to the parameters are given in Table 2 depicting the healthy mosquito population. In this article, we first attempted to validate the classical model (2.3) for the defined set of parameters subjected to the initial conditions, showing the need of fractional order, as the solution for this model do not provide a good match with the actual number of infected humans. We simulated the model on the MATLAB platform using Runga-Kutta fourth order finding the plot between the simulated model and the actual number of reported cases as shown in Figures 1a to 1h for the respective regions. The comparison of two curves in the figures suggested that actual data of outbreak does not correspond well with the data generated from the model with the given values of parameters. The prediction of infected humans was somewhat over estimated by the model. Hence, we use the generalization of the model to get more better and accurate results.

Table 1: Range and baseline values chosen for model parameters.

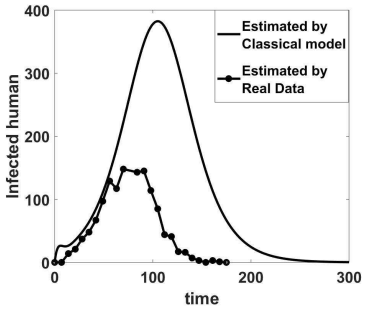
| Regions | **a** | **b** | **m** | **c** | $1/\gamma_h$ | $\beta_h$ | $\beta_v$ | $1/\mu_v$ |
|---|---|---|---|---|---|---|---|---|
| Tahiti | 0.4 | 0.6 | 2 | 0.7 | 5 | 0.05 | 0.9 | 16 |
| Sous-le-vent | 0.3 | 0.6 | 5 | 0.7 | 4 | 0.15 | 0.1 | 7.4 |
| Moorea | 0.3 | 0.6 | 5 | 0.7 | 2.5 | 0.25 | 0.17 | 7 |
| Tuamotu-Gambier | 0.3 | 0.6 | 5 | 0.7 | 2.5 | 0.25 | 0.17 | 7 |
| Marquises | 0.3 | 0.6 | 5 | 0.7 | 2.5 | 0.25 | 0.17 | 7 |
| Australes | 0.3 | 0.6 | 5 | 0.7 | 12.5 | 0.25 | 0.125 | 7 |
| Costa Rica | 0.3 | 0.4 | 5 | 0.6 | 8 | 0.03 | 0.1 | 17 |
| Colombia | 0.3 | 0.4 | 5 | 0.6 | 7 | 0.06 | 0.07 | 17 |
| Range | 0.3-1 | 0.1-0.75 | 1-10 | 0.3-0.75 | 3-14 | 0.01-0.75 | 0.01-0.75 | 4-35 |

Table 2: Initial values for state variables for ZIKV outbreak in concerned regions.

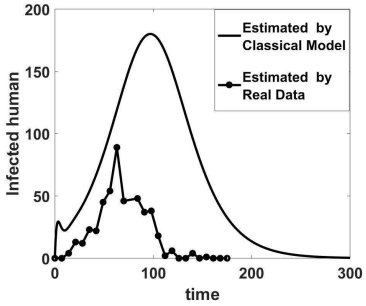
| Regions | $S_h$ | $E_h$ | $I_h$ | $R_h$ | $S_v$ | $E_v$ | $I_v$ |
|---|---|---|---|---|---|---|---|
| Tahiti | $10^4$ | $10^3$ | 49 | 0 | $10^5$ | 20 | 10 |
| Sous-le-vent | $10^4$ | 90 | 0 | 0 | $10^5$ | 20 | 10 |
| Moorea | $10^4$ | 100 | 0 | 0 | $10^5$ | 20 | 10 |
| Tuamotu-Gambier | $10^4$ | 10 | 0 | 0 | $10^5$ | 20 | 10 |
| Marquises | $10^4$ | 10 | 0 | 0 | $10^5$ | 20 | 10 |
| Australes | $10^4$ | 10 | 0 | 0 | $10^5$ | 20 | 10 |
| Costa Rica | $10^4$ | 100 | 4 | 0 | $10^5$ | 20 | 10 |
| Colombia | $10^5$ | $15^3$ | 2173 | 100 | $10^6$ | 200 | 100 |



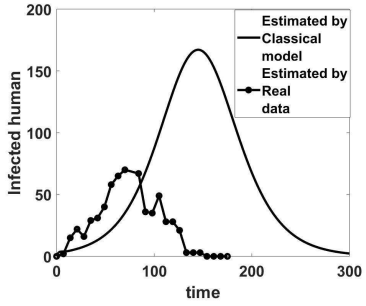

(a) Tahiti, French Polynesia 2013-14



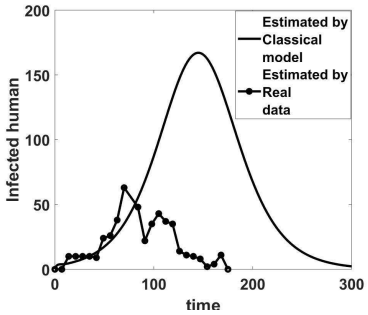

(b) Sous-le-vent, French Polynesia 2013-14



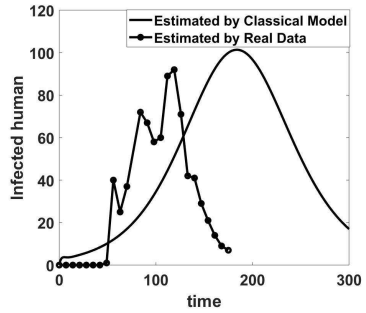

(c) Moorea, French Polynesia 2013-14



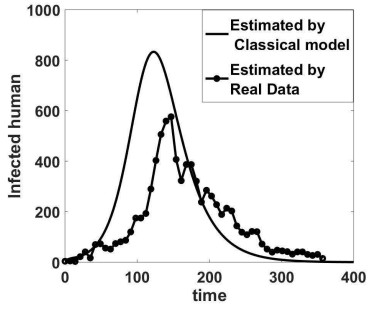

(d) Tuamotu-Gambier, French Polynesia 2013-14



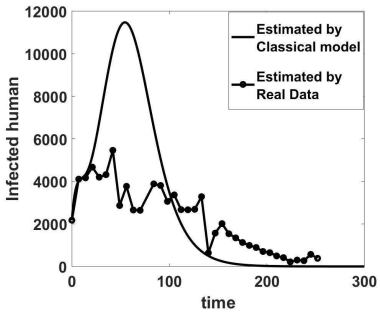

(e) Marquises, French Polynesia 2013-14




(f) Australes, French Polynesia 2013-14




(g) Costa Rica 2016




(h) Colombia 2016

Figure 1: Actual and estimated number of infected humans $I_h(t)$ in outbreak occured in (a) Tahiti, French Polynesia 2013-14, (b) Sous-le-vent, French Polynesia 2013-14, (c) Moorea, French Polynesia 2013-14, (d) Tuamotu-Gambier, French Polynesia 2013-14, (e) Marquises, French Polynesia 2013-14, (f) Australes, French Polynesia 2013-14, (g) Costa Rica 2016, (h) Colombia 2016: Comparison of results obtained by simulation via classical model 2.3 based on ODE with real data.

## 4. Results and discussion

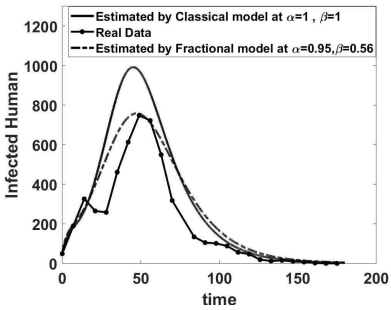
Fractional order model is used as a generalization to classical model to simulate the ZIKV transmission by establishing the model with memory in both the host and vector population. There is no analytical solution available to solve and analys the FDEs in our knowledge. We solved fractional order problem given in model (2.5) numerically using an effective predictor-corrector numerical scheme described briefly in [18, 19, 47]. The starting point in the Caputo fractional derivative is taken as zero. The step size has been taken as $10^{-2}$ days as it is considered appropriate for this system of equation as using smaller step sizes like $10^{-4}$ days do not give significantly different results [17]. Using the parameter values and initial values as given in Tables 1 and 2, respectively. We searched the fractional order that best fits the data on the reported number of cases. The value of the derivative order was obtained by a search on the interval $(0, 1]$, i.e., $\alpha, \beta \in i/100$: i=1,2,3,. . . ,100. We started with $\alpha = 1$ and successively lower its value until we find better solution, similarly we did with $\beta$ by varying it value on the interval (0, 1]. A good approximation was obtained for the values of $\alpha$ and $\beta$ given in Table 3 for the respective regions of ZIKV outbreak. The plot of numerical solutions of system of FDEs having fixed parameter values is shown Figure 2a to 2h. The figures depicted that the variation in values of $\alpha$ and $\beta$ can leads to better approximation of real outbreak data as compared to classical solution ($\alpha, \beta = 1$) when examined all of the regions. It can be seen that smaller value of $\alpha$ leads to slightly better approximations of the real data in early stage of the epidemic as compared to the larger values of $\alpha$. Moreover, we have also calculated the basic reproduction

Table 3: Reproduction number and fractional values for ZIKV outbreak in respective regions.

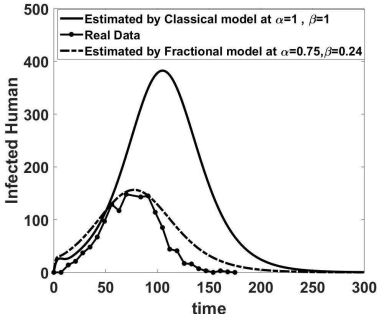
| **Region** | $\alpha$ | $\beta$ | $R_0$ |
|---|---|---|---|
| Tahiti | 0.95 | 0.565 | 1.9472 |
| Sous-le-vent | 0.75 | 0.24 | 1.1854 |
| Moorea | 0.6 | 0.495 | 1.1508 |
| Tuamotu-Gambier | 0.2 | 0.36 | 1.1169 |
| Marquises | 0.215 | 0.34 | 1.1417 |
| Australes | 0.4 | 0.7 | 1.2246 |
| Costa Rica | 1 | 0.47 | 1.8658 |
| Colombia | 0.99 | 0.05 | 1.1717 |

number for the fractional-order model using equation (2.6). The values of the basic reproduction number for the respective data are shown in Table 3. All the values of $R_0$ come out to be $> 1$, which indicates that the Zika virus is spreading. Also, through the previous studies of disease outbreaks, $R_0$ is found to be greater, i.e., $0.5 - 6.3$ in El-Salvador, Brazil and Columbia [25, 32] and $2.6 - 4.8$ in French Polynesia [31] when computed using classical model.

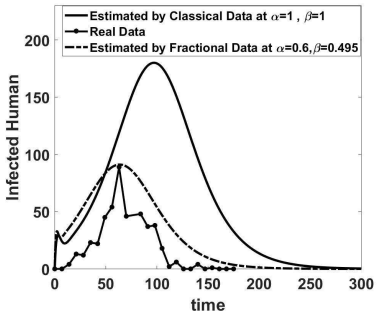
The behavior of Reproduction number $R_0$ with the variation in different parameters defined for the fractional epidemic model is shown in Figures 3a-3c for the ZIKV outbreak in Costa Rica in 2016. Figure 3a depicted that $R_0$ varies from 0-20 with respect to change in mosquitoes biting rate $a \in [0, 5]$ for different value of recovery rate, i.e., $\gamma_h \in [0.0714, 0.3333]$ for Costa Rica epidemic. It can be noticed through the figure that $R_0$ is directly proportional to mosquitoes biting rate with any value of $\gamma_h$. Further, we can notice that $R_0$ also depends on $\gamma_h$ (recovery rate) as it increases with a decrease in the value of $\gamma_h$ at any fixed value of a (mosquitoes biting rate). Figure 3b illustrated inversely proportionate behavior of Reproduction number ($R_0$) to the death rate of mosquitoes ($\mu_v$) with the change in values of mosquitoes biting rate, $a \in [0.3, 1]$. The range of $R_0$ comes out to be $[0.5, 6]$ for both the data concerning the $\mu_v$. Here, the relationship curve also indicates the upwards shift with the mosquito's biting rate value. Moreover, Figure 3c also showed that $R_0$ is in direct relationship with the mosquitoes biting rate with variation in the value of $\mu_v$. However, the curve showed the reciprocal behavior with the death rate of mosquito ($\mu_v$), i.e., the value of $R_0$ decreases with the increase in value of $\mu_v$.



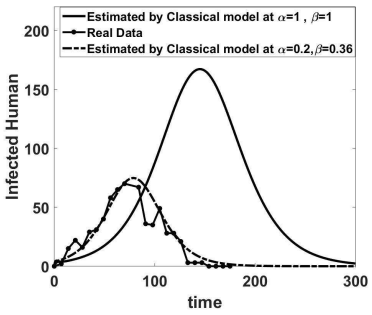

(a) Tahiti, French Polynesia 2013-14



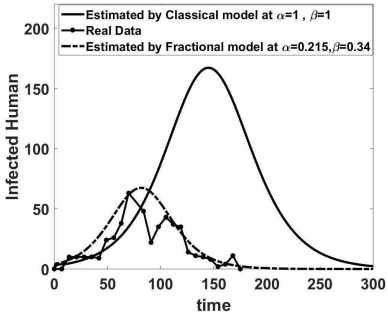

(b) Sous-le-vent, French Polynesia 2013-14



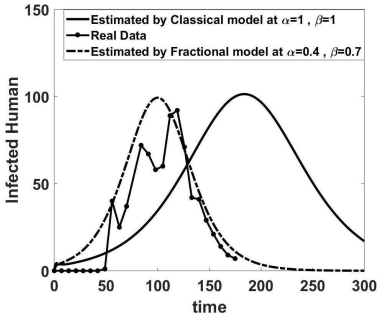

(c) Moorea, French Polynesia 2013-14



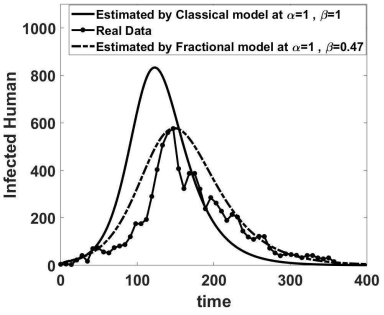

(d) Tuamotu-Gambier, French Polynesia 2013-14



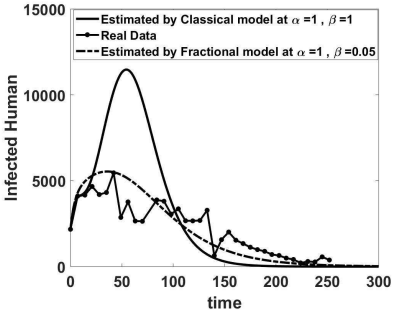

(e) Marquises, French Polynesia 2013-14




(f) Australes, French Polynesia 2013-14

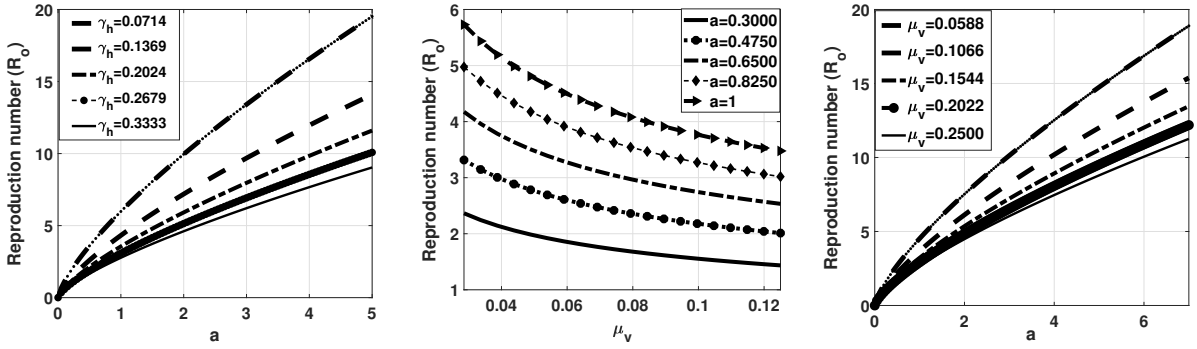



(g) Costa Rica 2016




(h) Colombia 2016

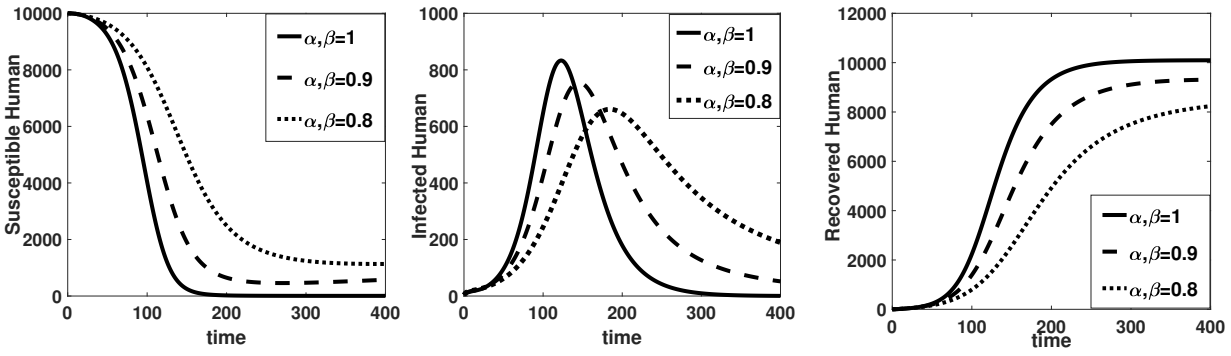
Figure 2: Comparison of infected/infectious individuals I(t): real data, classical model and the fractional model with the different values of $\alpha$ and $\beta$ as mentioned in Table 3 for ZIKV outbreak in Tahiti, Sous-le-vent, Moorea, Tuamotu-Gambier, Marquises, Australes, Costa Rica, and Colobia, respectively.




(a) (b) (c)

Figure 3: Behavior of basic reproduction number $(R_0)$ varying with different parameters involved in model for Cost Rica outbreak, (a) change in $R_0$ with respect to mosquitoes biting rate, $\alpha$ with variation $\gamma_h$; (b) change in $R_0$ with respect to $\mu_v$ with variation $\gamma_h$; (c) change in $R_0$ with respect to mosquitoes biting rate, $\alpha$ with variation $\mu_v$.

We have simulated $S_h$, $R_h$, and $I_h$ for different values of FDEs for Costa Rica outbreak for a better understanding of fractional order. Three different values of $\alpha$ are considered in each plot in Figures 4a-4c. When $\alpha = 1$, the system is the classical order. The variation of $S_h(t)$, $R_h(t)$, and $I_h(t)$ versus time $t$ is shown for different values of $\alpha = 1, 0.9, 0.8$ by fixing the parameter values. It is observed that the susceptible population drops significantly in a relatively short time with the same set of parameters which seems somewhat unrealistic in nature. Figures 4a-4c, shows that approximate solution implementing simple fractional model will provide surprisingly better results. However, transforming a classical model into a fractional one makes it sensitive to the order of differentiation as a small change in the value of fractional order leads to a big change in the final result. It can be clearly depicted that the approximate solutions depend continuously on the fractional derivative, $\alpha$ and $\beta$. Therefore, the obtained results show that we have improved the dynamics of SEIR model by implementing fractional derivatives.




(a) (b) (c)

Figure 4: Numerical solution of model (2.5) with the parameters mention in Table 1. (a) $S_h(t)$ of Costa Rica 2016-17 Zika outbreak at $\alpha = 1, 0.9, 0.8$; (b) $I_h(t)$ of Costa Rica 2016-17 Zika outbreak at $\alpha = 1, 0.9, 0.8$; (c) $R_h(t)$ of Costa Rica Zika 2016-17 outbreak at $\alpha = 1, 0.9, 0.8$.

## 5. Conclusion

Zika continues to be a disease with potential threats and burdens to humans worldwide. This research work is considered a generalization of a classical epidemic model by implementing fractional order. We constructed and analyzed a fractional-order derivative-based model for the progression of ZIKV infection during the outbreak in six major archipelagos of French Polynesia, i.e., Tahiti, Sous-le-vent, Moorea Tuamotu, Marquises and Australes, and Costa Rica and Colombia during the years 2013-16. Further, we evaluated the model with different values of the fractional operator and observed its effect at different values involving the same parameters as described initially in the classical model. By the simulation of infection through a linear and non-linear fractional model, it is concluded that a non-linear FDEs model provides more accurate results than ODEs models. We used the Adams-type predictor-corrector method to demonstrate numerically that the fractional-order model provides exciting and more accurate results. Specifically, it has been revealed that the human population follows a different order than the mosquito population. This model further might be extendable for in-homogeneity distribution of population and their contact using incorporation of network-based approach.

## Acknowledgments

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