Asian Journal of Probability and Statistics

15(4): 351-364, 2021; Article no.AJPAS.79173
ISSN: 2582-0230

Modelling by Simulations Monte Carlo of First Historical Zika Outbreak in Salta, Argentina, Occurred in 2017

Juan Carlos Rosales [a,b*], Juan Pablo Aparicio [c], Pablo Quintana [a], Celeste Herrera [d] and Betina Abad [e]

[a] *Department of Mathematic, Faculty of Exact Sciences, National University of Salta, Argentina.*
[b] *EPIFISMA, Epidemiología e Fisiología Matemática, IMECC, UNICAMP, Brasil.*
[c] *INENCO Faculty of Exact Sciences, National University of Salta, Argentina.*
[d] *Member of the Research Project 2515/0 CIUNSa, National University of Salta, Argentina.*
[e] *Faculty of Natural Sciences, National University of Salta, Argentina.*

Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

Article Information

DOI: 10.9734/AJPAS/2021/v15i430386
Editor(s):
(1) Dr. Dariusz Jacek Jakóbczak, Koszalin University of Technology, Poland.
Reviewers:
(1) Seema Sudhir Raut, G. H. Raisoni Institute of Engineering & Technology, India.
(2) Wachira Charles, Masinde Muliro University of Science and Technology, Kenya.
Complete Peer review History, details of the editor(s), Reviewers and additional Reviewers are available here : https://www.sdiarticle5.com/review-history/79173

Original Research Article

Received: 20 November 2021
Accepted: 18 December 2021
Published: 24 December 2021

Abstract

Scopes and Objectives: We analyzed some aspects of the first historical outbreak of Zika that occurred in Salta, Argentina, in the year 2017. We obtained elementary estimates, such as the prevalence ratio and describe the probabilistic behavior of the outbreak by simulation of type Monte Carlo.
Study Design: Retrospective-descriptive studies and stochastic computational experiment analysis.
Place and Duration of Study: Department of Mathematic, Faculty of Exact Sciences. National University of Salta, Argentina, from December 2020 to September 2021.
Methodology: Descriptive and computational experiment analysis. Estimates of parameters and Simulation of type Monte Carlo.
Results: We describe the probabilistic behavior through Monte Carlo simulation of the first historical outbreak of Zika in Salta Argentina, 2017. Based on the data of registered Zika cases,

**Corresponding author: E-mail: jcrmodeling@gmail.com;*

we estimate a probabilistic model for it. We also spatially describe the outbreak by estimating the prevalence ratio. Finally, by computational experiment we generate epidemic outbreaks with 10, 20 and 30 runs, determining the intrinsic growth rate and estimating the basic reproductive number R_0 for a generation time that takes into account both man and mosquito. We find that the estimates are significantly affected for the simulation type factor of 10 runs. The computational experiment shows that the descriptions of the outbreak and the estimates of R_0 obtained, if the number of repetitions of the experiment corresponds to 20 and 30 runs, are qualitatively acceptable.

Keywords: Models theoretical; basic reproduction number; simulation; Monte Carlo; Zika virus.

2010 Mathematics Subject Classification: 62P10; 62J05; 62-07; 65C20; 65C05.

1 Introduction

Zika fever is a mosquito-borne viral disease caused by Zika virus (ZIKV), consisting of mild fever, rash (mostly maculo papular), headaches, arthralgia, myalgia, asthenia, and non-purulent conjunctivitis, occurring about two to seven days after the mosquito vector bite [1]. However, many people infected with the Zika virus have no or only mild symptoms.

The ZIKV is an arbovirus (arthropod-borne virus) of the *Flaviviridae* family. Transmission is mainly vector, from infected mosquitoes, mainly of the genus *Aedes*. ZIKV has been isolated from 19 different *Aedes* species, but virus has been most frequently found in *Ae. aegypti* [2].

The ZIKV was first isolated in 1947 from a rhesus monkey in a tropical forest called Zika near Kampala, the capital of Uganda. Currently, not much information is available on this disease or on the virus that is causing explosive epidemics in different parts of the world associated with serious neurological disorders. That is why in 2016 the World Health Organization declared it an international public health emergency [3].

The first major outbreaks of ZIKV occurred on islands of the Federated States of Micronesia in 2007. Then the virus spread in the Pacific region and to the Caribbean and South and Central America . The first outbreaks of ZIKV arose in Yap and Micronesia between April and July of 2007, followed by an additional outbreak in French Polynesia between October 2013 and April 2014 [4],[5].

In 2015, ZIKV raised to prominence in American countries, more specifcally in Brazil and Colombia, the areas where the epidemic form of ZIKV was previously uncommon [6].

Recent associations with Guillain-Barré syndrome in adults and microcephaly in infants born to ZIKV-infected mothers have revealed that ZIKV could lead to more severe complications than the mild rash and flu-like symptoms that characterize the majority of symptomatic cases [2].

There is uncertainty surrounding about the time of introduction of the virus to the region, although epidemiological and genetic findings estimate that the Zika virus (ZIKV) arrived in Brazil between May and December 2013 [5]. However some authors point out that after spreading through the Pacific islands, the ZIKV begins its incursion into Brazil in 2015 led to a widespread epidemic in Latin America [5],[7],[8].

From there it begins to spread in a north-south direction through Brazil, Zika reaches Argentina [8],[9]. After entering South America in May 2015 through the Northeast of Brazil [9], the ZIKV enters Argentina between April and June 2016, and in 2017 in its continuous expansion, it has arrived in the province of Salta. In the case of Salta province, the situation of cases Zika is new, the first cases were reported in 2017 [10], and provide research opportunities of vital importance

in different epidemiological aspects. For example, the theoretical concept the basic reproduction number, R_0, of infectious diseases, could be related to the initial growth of an epidemic outbreak [11], [12]. Growth rate estimates for exponential and logistic models play a fundamental role and its estimates for a historical outbreak can be used for retrospective, modeling, and simulation studies.

Currently, there are no medicines or vaccines against ZIKV or specific antiviral treatment for clinical ZIKV infection. To address this medical need, novel ZIKV interventions suitable for prevention and therapeutic purposes are urgent [13]. All this, added to the poor sanitary infrastructures and the high rates of poverty in these regions of the country, mean that all diseases with similar potentialities, could be neglected by the governmental entities of the province of Salta and the country.

ZIKV has the potential to be transmitted in Argentina throughout the current geographic range of the mosquito vector. Although the transmission would be mainly seasonal [9]. Estimates of parameters related to the ZIKV will allow to make better decisions and optimize the design of plans for the provision and supply of treatments, prevention and control measures, by the Public Health authorities for the affected regions.

2 Materials and Methods

In the subsections that follow, we briefly comment on different aspects of the methods applied in this work.

Characterizing an outbreak in space implies describing the geographical or spatial distribution of the cases, based on the respective attack rates. The spatial distribution of cases can be described based on various characteristics that are considered relevant to document the geographical extension of the outbreak, as well as to clarify its etiology, exposure and spread. Outbreak spatial study in particular can benefit from the use of maps [14].

On the other hand, the basic instrument to characterize an outbreak in time is the epidemic curve. Characterizing an outbreak in time implies establishing the duration of the outbreak, defining its nature and estimating the probable period of exposure [14].

2.1 Parameters

Two of the classic measures of frequency of a disease are incidence and prevalence. Prevalence is not a dynamic measure, so a more appropriate name is prevalence ratio. The prevalence is directly defined as the proportion of the population suffering from the disease at a specific time [11],[14]. It is the measure of the total number of existing cases, called cases prevalent, of a disease at a point or period of time and in a given population, without distinguishing whether or not they are new cases. Prevalence is an indicator of the magnitude of the presence of a disease or other health event in the population [11], [14].

We estimate the prevalence by departments in the province of Salta with the data of human cases registered in the first outbreak in 2017 and using the projection of the populations obtained from Citypopulation [15], we estimated the prevalence ratio. With these values we design maps using shape files from Instituto Geográfico Nacional Argentino (IGN) [16] and QGIS Software Development Team [17], in this way we present a spatial model that approximately shows the region affected by Zika in Salta.

2.2 Definitions

In this subsection we present some definitions that were used in the present study, in order to highlight their application to the situation under analysis.

Taking into account the concept of endemic corridor and the epidemic curve of registered cases, we are going to define the silence phase, endemic phase and epidemic phase based on the following Definition 2.1 and we will describe the situation that presented the first historical outbreak of Zika in Salta.

A times series is a set of observations x_t, each one being recorded at a specific time t. In this case the observations are made at fixed time intervals. To allow for the possibly unpredictable nature of future observations it is natural to suposse that each observation x_t is a realized value of a certain random variable aleatoria X_t [18]. Let x_t be the number of Zika cases registered at time t, to analyze the impact of the outbreak and in order to estimate the limits for the silent, endemic and epidemic phases respectively, we consider the data recorded as a discrete time series. For this we introduce the following definition.

Definition 2.1. Let $\{X_t\}$ a sequence of random variables IID of which $\{x_t\}$ is postulated to be a realization, then the silence phase, endemic phase and epidemic phase are the intervals $[0, Q_1), [Q_1, Q_3)$ and $[Q_3, +\infty)$, respectively, where Q_1, Q_2 and Q_3 correspond to the first, second and third quartile of the observed data $\{x_t\}$. x_t correspond to number weekly news cases of Zika occurred in the localities of Department San Martín, Orán and Rivadavia in the province of Salta and $t = 1, 2, ...$ indicate each epidemiological week from 4 of 2017 to 23 of 2017.

For the modelling by simulations of the epidemic curve, we will define the random variable in a certain probability space.

Despite of we do not discuss in detail a probabilistic space $(\Omega, \mathcal{A}, P)$ associated to the random experiment ε, we precise the sample space and the random variable corresponding in the following Definition 2.2.

Consider an experiment ε where the number of observations of a particular time interval, *i-th epidemiological week*, in which cases of Zika have occurred, is of interest.

The triplet $(\Omega, \mathcal{A}, P)$ consisting of the sample space Ω, the $\sigma - algebra$ $\mathcal{A}$ of subsets of Ω, and a probability measure P defined on $\mathcal{A}$ is called a probability space [19]. We try to define succinctly the probability space for the analyzed situation in a brief and expressed as follows

Definition 2.2. Let $(\Omega, \mathcal{A}, P)$ a probabilistic space associated to random experiment ε, with $\Omega = \{\omega_i \mid i = 1, 2, ..., m; \omega_i =$ i-th epidemiological week, in which the cases registered that occurred in localities of Department San Martín, Orán and Rivadavia in the first historical outbreak of Zika in Salta$\}$. Let X a discrete random variable defined by $X : \Omega \to \mathbf{R}, X(\omega_i) = n_i$, number of times a case of Zika has occurred in the i-th epidemiological week, ω_i. Let $\mathcal{A} = \{\emptyset, \{\omega_1\}, \{\omega_2\}, ..., \{\omega_m\}, \Omega\}$, be the σ-algebra of events generated by assuming that $\{\omega_i\} \in \mathcal{A}$ for $i = 0, 1, 2, ..., m.$ and $P(\omega_i) = P_{n_i}(\omega_i) \approx f_r(\omega_i) = \frac{n_i}{N}$ be the probability of n_i cases results in the interval *i-th epidemiological week*, w_i , where f_r is the corresponding relative frequency provided by the data and N is the total number of cases of the outbreak.

It is assumed that the set $\mathcal{A}$ is a $\sigma - algebra$ which means that the following properties hold for $\mathcal{A}$,

1. $\Omega \in A$
2. If $A \in \mathcal{A}$, then $A^c \in \mathcal{A}$
3. If $\{A_i\}_{i=1}^{\infty}$, $A_i \in \mathcal{A}$, $\forall i = 1, 2, ...,$ then $\bigcup_{i=1}^{\infty} A_i \in \mathcal{A}$

where A^c is the complement of set A, more details of probability spaces in [19].

2.3 Statistical Analysis

The simplest boxplot is based on the following five-number summary: smallest x_i, lower fourth, median, upper fourth, largest x_i. We perform the analysis of the five-number through the construction of the box plot, to determine the of the smallest observation, the largest, the first quartile, the median and the third quartile in order to describe the set of data and the epidemic curve smoothed

by moving averages [18], with respect to the epidemic corridor and determine the limits of the epidemic phases.

The statistical program used was Statgraphics Centurion (version 16.1.03) [20] and the statistical analysis was performed in this software. For the simulations, we generate the cases in each run, perform several series of 10, 20, and 30 runs, and calculate the average to make comparisons with the real epidemic curve. The results thus obtained were analyzed using the Chi-Square goodness-of-fit test.

Regarding the type of simulations we carry out, to generate the epidemic curves of 10, 20 and 30 runs, in each of which 252 cases of Zika were randomly generated, we classify them in simulations of type A, B and C respectively. We denote this type of simulation simulations type A, STA for 10 runs. Similarly for 20 runs and 30 runs, Type B and Type C simulations, denoted STB and STC respectively.

To analyze whether the estimates of R_0, calculated using the expression of the Begon&Harper model [21] are influenced or not by the number of runs, we performed a multi-factor analysis of variance to determine which of the factors STA, STB, STC have a statistically significant effect on the values of R_0. We also use the plot of Means and 95% Fisher LSD to graphically interpret the significant effects.

2.4 Simulations

With the data of Zika number cases of the historical outbreak first occurred in Salta, we have estimated the relative and cumulative frequencies of cases submitted in each epidemiology week, so that, they can be described qualitative by making simulations of the Monte-Carlo type. In order to perform simulation experiments, an estimation for the empirical cumulative distribution function (c.d.f.), denoted by $F_X(\cdot)$, corresponding to each epidemiological week of the outbreak is necessary; i.e., that is, every epidemiological week where Zika cases have occurred. Where X be a discrete random variable with $P(X = x_i) = p_i$ con $i = 1, 2, ..., n$ with $\sum_{i=1}^{n} p_i = 1$ and $x_1 < x_2 <, ..., < x_n$, and the c.d.f., $F_X(\cdot)$ is given by $F_X(x) = \sum_{i:x_i \leq x} p_i$, [22].

Implementations of algorithms for the simulations, Monte Carlo type, were similar to those developed by Rosales *et al.* [23][24], in order to get estimates of the Zika weekly case number and obtain the approximate values of the number cases registered in the localities of province de Salta. We simulate various runs with random generations of weekly cases considering the period of duration of the epidemic outbreak and the total number of case registered in this historical irruption of ZIKV in Salta. Finally, we calculate the corresponding weekly averages for the epidemic curve approximation and make comparisons of the obtained scenarios.

2.5 Influence on the estimation of R_0 for different types of simulation

We could learn a great deal about an infection if an expression for its basic reproduction number R_0. For microparasites R_0 is defined as average number of secondary infections produced when one infected individual is introduced into a host population in which every host is susceptible [11].

As Zika is a vector-borne disease, we estimate R_0 from the data using the Begon&Harper's expression [21], with modifications for the Generation Time (T_g) [25], so that it takes into account both the human being and the mosquito. This T_g time is generated stochastically similar to what was done in work [12].

As we expressed before we carry out different simulations with different number of runs, for example, simulations with 10, 20 and 30 runs in which Zika cases are stochastically generated per weeks and the average of the cases generated in each week is taken and a probabilistic model is obtained for the first historical epidemic outbreak, occurred in Salta in 2017.

Simulated outbreaks can provide an intrinsic growth rates, and through the relationship between these rates and the expression of R_0 found by Begon&Harper [21] it is possible to obtain estimates of the basic reproductive number R_0. The quality of the estimates could depend on the type of simulations. To analyze the possible statistically significant effect of the type factors of runs in R_0, we carried out simulations, several tests and graphs that we exemplified.

3 Results

The spatial model that we estimate by the approximate calculation of the prevalence ratio is presented in Fig. 1. The prevalence map accurately shows the departments of the province of Salta that were actually affected by the first historical outbreak in Salta. The localities where the cases were registered belong to the departments of San Martín, Orán and Rivadavia. The estimated prevalence ratios were 90.07 x10E-5, 17.69x10E-5 and 13.42x10E-5, respectively.

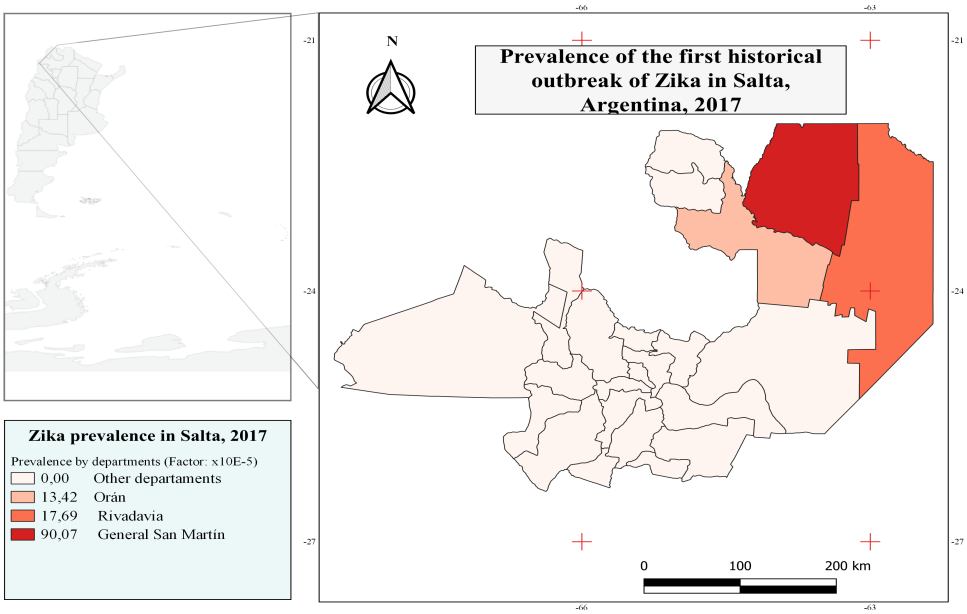

Fig. 1. Indication of the region of study, located in the Province of Salta, Argentina. The study area is composed of the departments of Orán, General San Martín and Rivadavia. The map show the prevalence ratio of Zika by Departments mentioned in the first historical outbreak and was designed by the authors with shape files from Instituto Geográfico Nacional Argentino [16] using QGIS Software Development Team (3.12) **[17].**

Fig. 2 shows the the number cases of this first historical outbreak of Zika, after entering South America in May 2015 through Northeast Brazil, this outbreak developed with a total of 252 cases distributed in localities of the Departments of the northern and northeastern of the Province of Salta, specifically in the Departments of Orán, General San Martín and Rivadavia, which were indicated with their respective prevalence ratios in Fig. 1.

Also, Fig. 2 represents the smoothed curve of human cases infected by ZIKV, during the first epidemiological outbreak registered in the province of Salta, Argentina, during the epidemiological weeks between EW 4 - EW 23, year 2017. The weeks were renumbered according to the origin of coordinates. It was obtained using the 4 EW moving average window technique. The yellow, red and black horizontal lines allow the delimitation of what could be considered as references of the

phases of silence, endemic and epidemic, for others events of occurrences of Zika that could occur in the future in the region. The box plot provides the following five-number summary: smallest 0, lower fourth 2.75, median 12, upper fourth 24.25, largest 29.

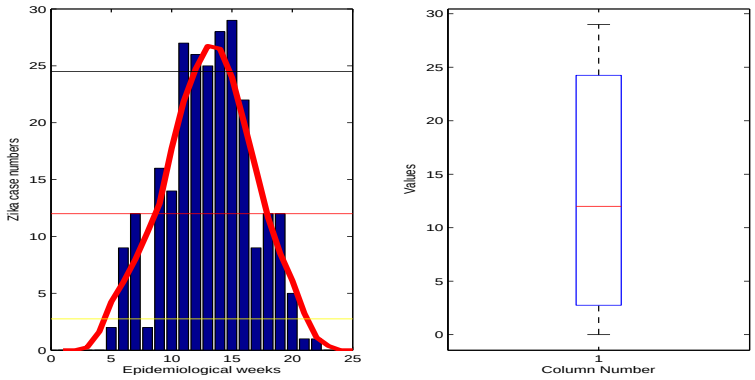

Fig. 2. Left: First historical outbreak of Zika in Salta, Argentina 2017. Developed between the epidemiological weeks *EW* 4 - *EW* 23, of year 2017, with a total of 252 cases distributed in localities in the northern and northeastern Departments of the Province of Salta, specifically in the Departments of Orán, General San Martín and Rivadavia. Rigth: Box plot for the outbreak. Source: BIV [10].

Table 1 shows the relative frequencies and the accumulated frequencies determined by the first historical outbreak of Zika, this allows us to estimate a probabilistic model for the situation presented in the North-Northeast region of the Salta Province.

The values in Table 1, based on the data from the first Zika outbreak in Salta, allow us to propose a probabilistic model, as specified in the following Proposition 3.1.

Proposition 3.1. *The estimation for the c.d.f., $F_X(x)$ based on the data corresponding to the historical outbreak first of ZIKV occurred in Salta, Argentina, 2017, in the Departments of San Martín, Orán and Rivadavia, provide the following probabilistic model, $F_X : \mathbf{R} \to [0,1]$,* defined with the assignment

$$x \mapsto F_X(x) = \begin{cases} 0.0000 & x \in (-\infty, 1] \\ 0.0079 & x \in (1, \ 2] \\ 0.0436 & x \in (2, \ 3] \\ 0.0912 & x \in (3, \ 4] \\ 0.0991 & x \in (4, \ 5] \\ 0.1626 & x \in (5, \ 6] \\ 0.2182 & x \in (6, \ 7] \\ 0.3253 & x \in (7, \ 8] \\ 0.4285 & x \in (8, \ 9] \\ 0.5277 & x \in (9, \ 10] \\ 0.6388 & x \in (10, 11] \\ 0.7539 & x \in (11, 12] \\ 0.8412 & x \in (12, 13] \\ 0.8769 & x \in (13, 14] \\ 0.9245 & x \in (14, 15] \\ 0.9721 & x \in (15, 16] \\ 0.9919 & x \in (16, 17] \\ 0.9959 & x \in (17, 18] \\ 0.9999 & x \in (18, 19] \\ 1.0000 & x \in (19, +\infty] \end{cases} \tag{3.1}$$

Table 1. Relative frequencies of weekly Zika cases number and its cumulative frequencies for the historical peak first of Zika ocurred from EW 4 to EW 23, Salta, Argentina, 2017.*

EW	Relative frequency	Cumulative frequency
1	0.0000	0.0000
2	0.0079	0.0079
3	0.0357	0.0436
4	0.0476	0.0912
5	0.0079	0.0991
6	0.0635	0.1626
7	0.0556	0.2182
8	0.1071	0.3253
9	0.1032	0.4285
10	0.0992	0.5277
11	0.1111	0.6388
12	0.1151	0.7539
13	0.0873	0.8412
14	0.0357	0.8769
15	0.0476	0.9245
16	0.0476	0.9721
17	0.0198	0.9919
18	0.0040	0.9959
19	0.0040	0.9999
20	0.0001	1.0000

*: Total number of Zika cases in the first historical outbreak in Salta, $N = 252$.

By simulation we generate rough estimates for the first historical outbreak of Zika in Salta. Several runs were performed each with 252 stochastically obtained Zika cases. The first historical outbreak that marked the arrival of Zika in Salta, in 2017, registered 252 human cases. Some examples of these results are presented in the figures. Figs. 3, 4 shows three examples of these runs, of type A and B, also to the right, the respective evaluations of the averages values of the number cases obtained for each run is compared to the actual outbreak that occurred in Salta.

The ANOVA table decomposes the variability of Value of R_0 into contributions due to different numbers of runs in the simulations, simulation type A, B and C; denoted STA, STB and STC respectively. The contribution of each type of simulation is measured by eliminating the effects of the other types. The P-values test the statistical significance of each of the STA, STB, and STC types. Since a P-value is less than 0.05, this factor has a statistically significant effect on R_0 with a 95.0% confidence level.

Table 2. ANOVA table, the F-tests allow to identify the significant factor Type A for the estimates of reproduction number, R_0 of first historical outbreak of Zika occurred in Salta, Argentina, 2017.*

Analysis of Variance for R_0	Sum of Squares	gl	Mean Square	F-Ratio	P-Value
Main Effects					
Type A (STA)	0.02002	2	0.01001	5.76	0.0083
Waste	0.04694	27			
Total(Corrected)	0.06696	29			

*: Based on simulations for generation times T stochastically obtained. All F-ratios are based on the mean square of the residual error.

The Fig. 5 shows the graph of means and of 95% Fisher LSD (Least Significant Difference) intervals corresponding to the types of runs in each simulation, STA, STB and STC. It is observed that the estimated values of the basic reproduction number, R_0, for the exponential model of Begon&Harper [21], differ significantly for the STA simulations factor, those where 10 runs are performed to obtain the probabilistic models of the epidemic curves for ZIKV.

4 Discussion

As Fajardo points out [26], the prevalence measures the proportion of people who are ill at the time of evaluating the condition in the population, therefore, there is no follow-up time. In this case, we measure the prevalence that occurred during the outbreak of the first historical outbreak of Zika in Salta. The estimates showed that the San Martín department, 90.07 x10E-5, was affected approximately 5 times more than the Orán department, 17.69x10E-5, while the prevalence in the Orán department was approximately 1.3 times more than in the Rivadavia department, 13.42x10E-5. The prevalence map, Fig. 1, shows the commented situation and the region affected by Zika and also the rest of the departments of the Province, in which no cases were registered can be observed with the spatial model.

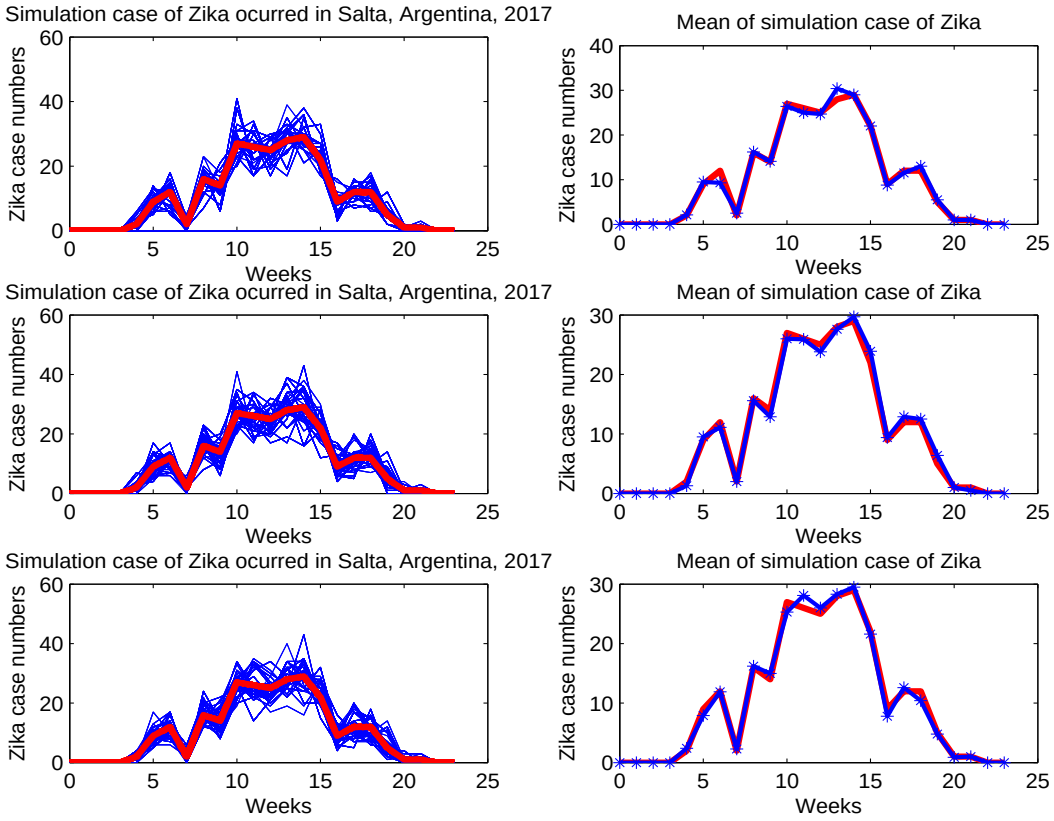

Fig. 3. Left, an example showing three simulations of 10 runs (- blue lines) and the actual outbreak of Zika in Salta, 2017 (-red line). Right, the corresponding average values of number cases of Zika stochastically obtained (*- blue lines) and the actual outbreak Zika in Salta, 2017 (-red line).

The Table 1 shows the relative frequencies of weekly Zika cases number and its cumulative frequencies for the historical peak first of Zika ocurred from EW 4 to EW 23, Salta, Argentina, 2017. On the other hand, the function given by (3.1) provides, the estimation for the c.d.f., $F_X(x)$ based on the data corresponding to the historical outbreak first of ZIKV occurred in Salta, Argentina, 2017, in the Departments of San Martín, Orán and Rivadavia, resulting like this the probabilistic model obtained.

Wiratsudakul et. al. points out that the compartmental model is still commonly used for the timely assessment of epidemics. However, much more complex modeling frameworks (metapopulation, network, and individual-based models) have been of increasing interest [27], here we present a simple method to obtain probabilistic qualitative descriptions to model epidemic outbreaks, which provide a different point of view from that of deterministic models, in this case applied to Zika, however the methodology could be applied to other diseases.

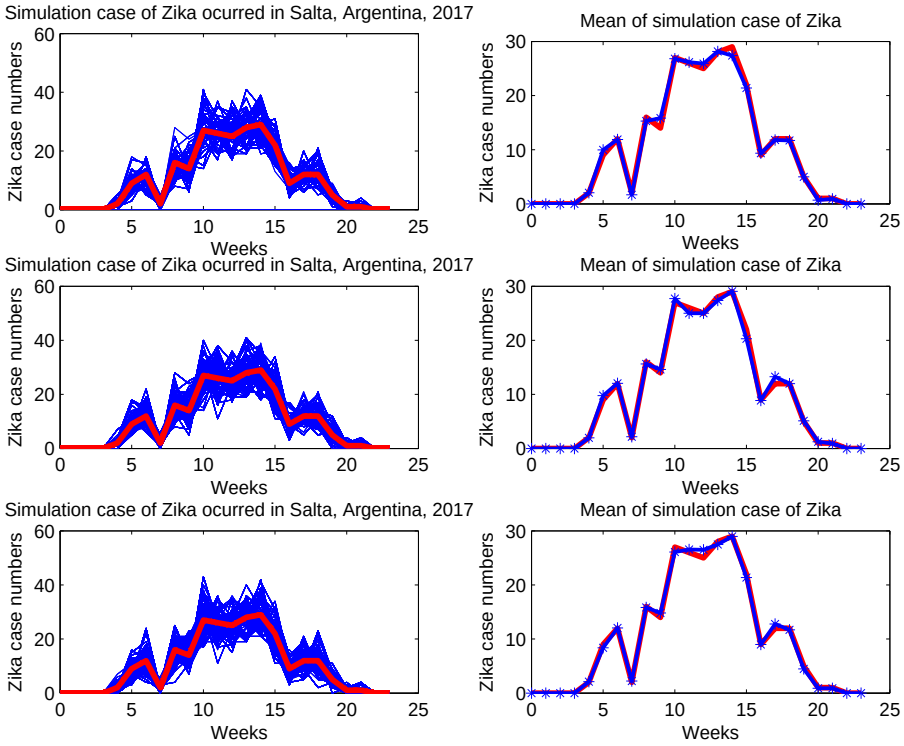

Fig. 4. Left, an example showing three simulations of 20 runs (- blue lines) and the actual outbreak of Zika in Salta, 2017 (-red line). Right, the corresponding average values of number cases of Zika stochastically obtained (*- blue lines) and the actual outbreak Zika in Salta, 2017 (-red line).

Figs. 3 and 4 show 10 and 20 simulated epidemic runs respectively from the model built based on the real data of the first historical outbreak of Zika in Salta, Argentina. On the left, it is observed that, the greater the number of runs, a certain convergence region is generated by the greater number of simulations, however, this makes it difficult to visually distinguish differences between them. On the right, the average values allow to observe less variability with respect to the true values that occurred during the first historical outbreak, because the distributions of the simulated sample means are considered.

Estimates of the basic reproductive number R_0 were made, according to the expression of Begón, et. al. [21] These estimates were obtained by varying the number of runs in 10, 20 and 30. Since a P-value (0.0083) is less than 0.05, this factor has a statistically significant effect on R_0 with 95.0% of confidence level. This value corresponds to the simulations of type A, STA, 10 runs to obtain the epidemic curve and compare it with the real epidemic, see Table 2, graphs of means Fig. 4 (right) and of Fisher LSD in Fig. 5. These descriptions were better when the number of experimental runs were 20 and 30, see Figs. 3, 4, right. Previous estimates of the basic reproduction number for the region, $R_0 \approx$ 1.10595%CI[1.104 − 1.106] and $R_0 \approx 1.111$ 95%CI[1.110 − 1.112] [12], small values, induce us to agree with what is expressed by Zhang et.al. that the ZIKV epidemic is characterized by slow growth [28].

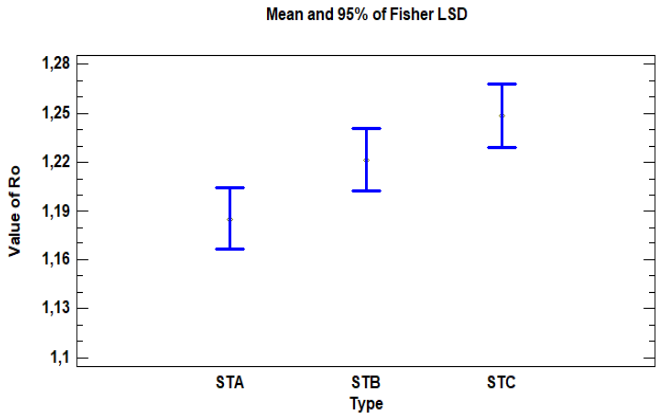

Fig. 5. Graph of means and of 95% Fisher LSD (Least Significant Difference) intervals corresponding to the types of runs in each simulation, STA, STB and STC. The estimated values of the basic reproduction number, R_0, differ significantly for the STA simulations factor.

Taking into account of means and of 95% Fisher LSD (Least Significant Difference) intervals corresponding to the types of runs in each simulation, STA, STB and STC, Fig. 5. It is observed that the estimated values of the basic reproduction number, R_0, differ significantly for the STA simulations factor, those where 10 runs are performed to obtain the probabilistic models of the epidemic curves for ZIKV. This suggests that our simulator would provide good descriptions of the epidemic curve when performing 20 or 30 runs. This detail would be important if, for example, it is necessary to obtain several intrinsic growth rates of the epidemic outbreak to be used in deterministic models.

5 Conclusions

In this work we have qualitatively described the first historical outbreak of Zika that occurred in Salta, in 2017, using Monte-Carlo simulations. The methodology proposed here is simple and we think that it can easily be applied to the description of epidemic outbreaks of other diseases. The model found to describe the probabilistic behavior for the first historical outbreak of Zika in Salta in its expansion through South America has been presented in Proposition 3.1. At present, after the outbreaks of 2017 and 2018, Zika has remained in a phase of silence in this region of Argentina.

On the other hand, a classic measure of the frequency of a disease, the prevalence ratio, was estimated. In this case, a map was constructed with the estimated prevalence values in the departments that were affected by ZIKV infection.

Our simulator provides probabilistic models of the epidemic outbreak that fit reasonably well if the number of randomized experiments is 20 and 30 replicates. Thus, the epidemic curves generated allows us to estimate their respective intrinsic growth rates. Therefore, using the Begon&Harper expression [19], it is possible to estimate R_0 using a generation time that includes both the human being and the mosquito. These R_0 estimates are affected by the simulation type factor STA, which correspond to 10 runs. However, if 20 or 30 runs are carried out, the scenarios obtained are quite acceptable and could generate rates to apply to deterministic models SIR and SEIR types.

Acknowledgement

This work has been partially supported by CIUNSa (Consejo de Investigaciones de la Universidad Nacional de Salta, Argentina - Councils of Investigation of National University of Salta, Argentina). Research Project 2515/0.

We would like to thank to Prof. Melani Quintana for her help with English language.

We thank the anonymous reviewers for their suggestions in order to improve the present work.

Competing Interests

The authors declare that the research was conducted in the absence of any financial relationships that could be construed as a potential conflict of interest.

References

[1] Pan American Health Organization PAHO; 2021. Topics. Zika.
Available:https://www.paho.org/en/topics/zika

[2] Messina JP, Moritz UG, Kraemer MUG, Oliver J, Brady OJ, David M, Pigott DM, Shearer FM, Weiss DJ, Golding, Ruktanonchai CW, Gething PW, Cohn E, Brownstein JS, Khan K, Tatem AJ, Jaenisch T, Murray CJL, Marinho F, Scott TW, Hay SI. Mapping global environmental suitability for Zika virus. eLife. 2016;1-19.
DOI: 10.7554/eLife.15272

[3] Academia Nacional de Medicina (ANM). Historia natural de tres enfermedades emergentes y reemergentes en la Argentina: ZIKA, CHIKUNGUNYA Y DENGUE. Buenos Aires, Argentina; 2018.

[4] Faria NR, et al. Zika virus in the Americas: Early epidemiological and genetic findings. Science. 2016;352:345-349.

[5] Duffy MR, Chen TH, Hancock WT, Powers AM, Kool JL, Lanciotti RS. Pretrick M, Marfel M, Holzbauer S, Dubray C, Guillaumot L, Griggs A, Bel M, Lambert AJ, Laven J, Kosoy O, Panella A, Biggerstaff BJ, Fischer M, Hayes EB. Zika virus outbreak on Yap Island, Federated States of Micronesia. The New England Journal of Medicine. 2009;360:2536-2543.

[6] Rahman M, Bekele-Maxwell K, Cates L, Banks HT and Vaidya NK. Modeling Zika Virus Transmission Dynamics: Parameter Estimates, Disease Characteristics, and Prevention. Scientific Reports. 2019;9:10575.
Available:https://doi.org/10.1038/s41598-019-46218-4

[7] German Advisory Committee Blood (Arbeitskreis Blut), Subgroup 'Assessment of Pathogens Transmissible by Blood'. Zika Virus. Transfusion Medicine Hemotherapy. 2016;43:436-446.

[8] Pan American Health Organization PAHO. 2016: The year Zika evolved from an emergency into a long-term public health challenge; 2016.
Available:https://www.paho.org/hq/index.php?option=com_content&view=article&id=12861:2016-zika-evolved-from-emergency-into-long-term-public-health-challenge&Itemid=1926&lang=en

[9] Wong SSY, Rosana Wing-Shan Poon RWS, Sally Cheuk-Ying Wong SCY. 'Zika virus infection the next wave after dengue?'. Journal of the Formosan Medical Association. 2016;115:226-242.

[10] Boletín Integrado de Vigilancia (BIV). Dirección Nacional de Epidemiología y Análisis de la Salud. Ministerio de la Salud. Presidencia de la Nación. 2018;394-SE 02.
ISSN 2422-698X.

[11] Scott M, Smith G. Parasitics and Infectious Deseases. Epidemiology and Ecology. Academic Press; 2000.

[12] Rosales JC, Acosta NA and Herrera C. Estimates of Intrinsic Growth Rates and Basic Reproduction Number (R_0) for the First Historical Zika Outbreak in Salta, Argentina. Asian Journal of Probability and Statistics. 2020;8(4):48-60.

[13] Nguyen CQ, Nguyen THM, Nguyen TTT, Bui TBH, Nguyen TT, Huynh NT, Le TD, Nguyen TMP, Nguyen DT, Nguyen MT, Pham MQ, Tran QD, et.al. Designs, Synthesis, Docking Studies, and Biological Evaluation of Novel Berberine Derivatives Targeting Zika Virus. Journal of Chemistry; 2021. Article ID 5567111.

[14] MOPECE. Medición de las condiciones de salud y enfermedad en la población. Unidad 3. Organización Panamericana de la Salud Oficina Sanitaria Panamericana; 2002.

[15] Thomas Brinkhoff: City Population.

`Available:https://www.citypopulation.de/php/argentina-admin_s.php?adm1id=66`

[16] Instituto Geográfico Nacional (IGN), Argentina.
Available:http://www.ign.gob.ar/.Geodatos

[17] QGIS Software Development Team (QGIS 3.1.12).
Available:https://qgis.org/es/site/

[18] Brockwell PJ and Davis RA. Introduction to times series and forescasting. Springer text in statistics. Springer-Verlag; 2002.

[19] Allen E. Modeling with Itô Stochastic Differential Equations. MATHEMATICAL MODELLING: Theory and Applications. Springer. 2007;22.

[20] Statgraphics Centurion 16.1.03. StatPoint Technologies Inc; 2010.

[21] Begon M, Townsend CR, and Harper JL. Ecology, From Individuals to Ecosystems. Blackwell Publising, Oxford UK; 2006.

[22] Meyer P. Introductory Probability and Statistical Applications. Addison Wesley Longman, México; 1998.

[23] Rosales JC, Avila Blas OJ, and Yang HM. Monte Carlo simulation of American Tegumentary Leishmaniasis epidemic. The case in Orán, Salta, Argentina. 1985-2007. Applied Mathematical Sciences. 2017;11:1-14.
DOI: 10.12988/ams.2017.610255

[24] Rosales JC, Davies D. Population Dynamics of Biomphalaria tenagophila Snails: Simulations Using the Square-Wave Carrying Capacity Model. Biostastistics Biometrics Open Acc J. 2019;9(2): 555758.
DOI: 10.19080/BBOAJ.2019.09.555758

[25] Wallinga J and Lipsitch M. How generation intervals shape the relationship between growth rates and reproductive numbers. Procedings Royal Society B. 2007;274:599-604.
DOI: 10.1098/rspb.2006.3754

[26] Fajardo-Gutiérrez A. Measurement in epidemiology: prevalence, incidence, risk, impact measures. Revista Alergia México. 2017;64 (1):109-120.

[27] Wiratsudakul A, Suparit P and Modchang C. Dynamics of Zika virus outbreaks: an overview of mathematical modeling approaches. PeerJ. 6:e4526.
DOI: 10.7717/peerj.4526

[28] Zhang Q, Sun K, Chinazzi M, Pastore y Piontti A, Dean NE, Rojas DP, Merler S, Mistry D, Poletti P, Rossi L, Bray M, Halloran E, Longini Jr. IM and Vespignani A. Spread of Zika virus in the Americas. Spread of Zika virus in the Americas. PNAS; 2017.

Peer-review history:
The peer review history for this paper can be accessed here (Please copy paste the total link in your browser address bar)
https://www.sdiarticle5.com/review-history/79173