Asociación Argentina
de Mecánica Computacional

Mecánica Computacional Vol XLII, pp. 1441-1445
A. Caggiano, G. Etse, P. Folino, M. Goldschmit, M. Pucheta, M. Storti (Eds.)
R. Lima, M. Piovan, G. Ruano, R. Sampaio (Issue eds.)
Buenos Aires, November 11-14, 2025

ANALYZING THE IMPACT OF MASS VACCINATION ON DISEASE SPREAD: A STOCHASTIC PERSPECTIVE

Beatriz Borges, Roberta Lima and Rubens Sampaio

Pontíficia Universidade Católica do Rio de Janeiro, Laboratório de Dinâmica e Vibrações. Rua Marquês de São Vicente, 225, Gávea, Rio de Janeiro, Brasil.

Keywords: Stochastic modeling, Uncertainties propagation, Branching process, Epidemiology, Vaccination.

Abstract. This work adopts a stochastic approach to analyze the impact of mass vaccination on the spread of an epidemiological disease. The number of individuals each infected person can transmit the disease to, referred to as contagion, is modeled as a discrete random variable following a binomial distribution. The progression of infections over time is represented by a stochastic branching process. The primary goal is to investigate how the percentage of vaccinated individuals and the efficacy of the vaccine affect both the spread of the disease and the probability of extinction. The analysis is based on sample statistics such as the mean and variance of the number of infections over time, as well as histograms of their distributions. The statistical models are constructed using Monte Carlo simulations under various scenarios combining different levels of vaccine coverage, efficacy, and contagion parameters. Specifically, six levels of vaccinated population percentage, four values for vaccine efficacy, and 21 different parameter sets for the binomial contagion distribution are considered. For each scenario, 4000 realizations of the branching process were simulated, totaling 2.1 million realizations. This scale of data characterizes the study as a big data problem.

ISSN: 2591-3522 DOI: 10.70567/mc.v42.ocsid8615

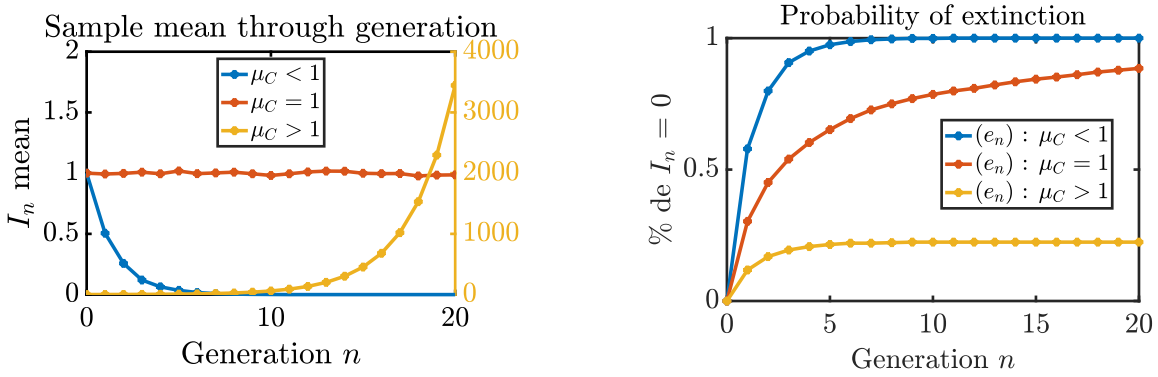
1 CONSTRUCTION OF PROBABILISTIC MODELS TO THE CONTAGION AND SPREAD OF A DISEASE

The spread of infectious diseases is a subject of interest in many different research areas Borges et al. (2020, 2021b,a). The knowledge of spread behavior over time can help governments plan and implement the best control strategies. Accurate predictions of the evolution of the number of infected individuals over time can help, for example, in the organization of hospital supplies.

In this paper, one model the contagion and the spread of an infectious disease is constructed. For that, let us consider that an infection begins with a single infected individual, $i_0 = 1$. This individual comes into contact with m people, and the number of those who receive a sufficient viral load is given by a realization of the binomial random variable C. For each of these potentially infected contacts, we then evaluate two conditions: first, whether the person has been vaccinated, modeled by the Bernoulli variable V with probability p_V; and second, if vaccinated, whether the vaccine was effective, modeled by another Bernoulli variable E with probability p_E. To illustrate the process, suppose that the initial infected person, $i_0 = 1$, transmits a sufficient viral load to three individuals, so that $C = 3$. Among these three, one was not vaccinated and became infected. The other two were vaccinated, but while had effective protection and was spared, the other had ineffective vaccination and became infected. Thus, in the first generation we obtain $i_1 = 2$ newly infected individuals. In the second generation, each of these two infected individuals contacts m new people. Suppose that their realizations of C are 2 and 3, respectively, totaling 5 potential new infections. For each of these five, we ask ourselves if they were vaccinated, and if so, if the vaccine was effective. For that scenario, three were effectively vaccinated and avoided the disease, one was vaccinated but not protected, and the other was not vaccinated at all. This results in $i_2 = 2$ new infections in the second generation. In the third generation, each of these two individuals once again spreads the disease according to the same probabilistic rules. If their realizations of C are, for instance, 1 and 0, we would obtain one potential new infections. If that individual is properly vaccinated, then the contagion is over. If not, the process continues this way, with variables C, V, and E determining, at each step, how many individuals are infected in the next generation. The stochastic process described with this scenario is called Branching Process.

To analyze the impact of a mass vaccination on the spread of a disease, we first take a look at how the contagion and spread of a disease in an unvaccinated population would be characterized by this model. For that we take the percentage of the vaccinated population and the vaccine efficacy and take it to zero, as in $p_V = p_E = 0$. Among all the results obtained with the simulations, in Figure 1 we highlight the results of the scenarios considered critical to the mean of C, given by $\mu_C = m * p$, showing the average number of infected individuals in each generation during the spread of the disease, as well as the probability of extinction across generations e_n. For $\mu_C < 1$ we have $p = 0.16$; for $\mu_C = 1$ we have $p = 0.33$; and for $\mu_C > 1$ we have $p = 0.50$.

To investigate the impact of the vaccination on the number of infections per generation, on a disease propagation and on an probabilities of extinction, we conducted Monte Carlo simulations and developed statistical models for disease spread using 21 parameter values from the binomial family of random variables for C. For each of these 21 cases, 6 different levels of vaccination coverage were considered (2%, 10%, 20%, $50\%, 75\%$ and 100%), combined with 4 vaccine efficacy rates (50.4%, 62.1%, 70.4% and 95%). Each scenario involved 4000 realizations of the branching process from generation $n = 0$ to $n = 20$, generating a total of



(a) Sample mean for the critical values of μ_C.

(b) probability of extinction for the critical μ_C values.

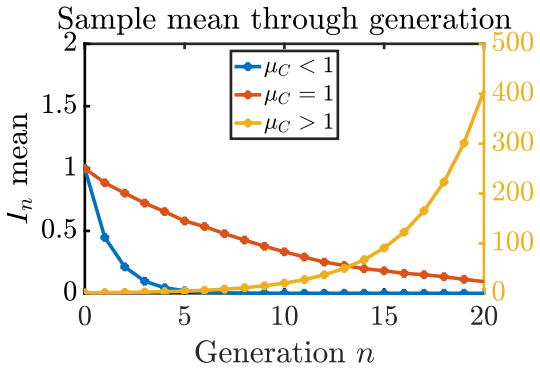
Figure 1: Graphics constructed with 4000 realizations of the branching process in an unvaccinated population.

2.1 million simulations. Running all computations required approximately 100 hours of CPU time. The substantial computational demand in both time and data volume classifies the problem as big data. A convergence study was conducted to determine the appropriate number of realizations Souza and Sampaio (2012); Sampaio and Lima (2018b,a, 2012). From these simulations, sample statistics (mean, variance, and probability of extinction) as well as histograms were derived.

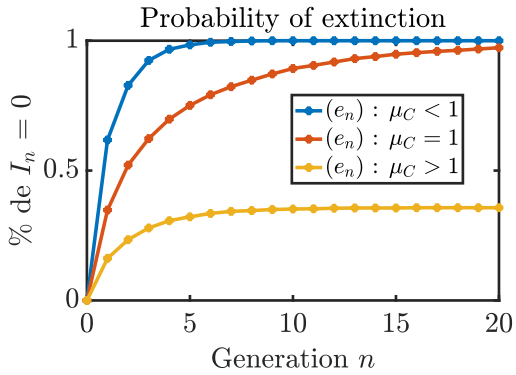
The first analysis was the influence of the percentage of the population that was vaccinated. Figure 2 and Figure 3 presents the results obtained for two of the scenarios analyzed. In Figure 2 it is assumed that 20% of the population was vaccinated with a vaccine of proven efficacy of 50.4%, and that individual contact C is modeled by a binomial$(3, p)$, with the values of p established above. In Figure 3, it is assumed that 50% of the population was vaccinated, with the same other parameters as in Figure 2. A comparison between the two sets of graphs in Figures 1 and Figures 2 and 3 shows that when $\mu_C < 1$, the epidemic dies more rapidly; when $\mu_C = 1$, the mean ceases to fluctuate around 1 and instead behaves similarly to the case in which $\mu_C < 1$, meaning that the average number of infected individuals declines across successive generations. Furthermore, when comparing Figures 2 and 3 with Figure 1, which depicts the progression of the epidemic in a non-vaccinated population, it becomes clearer that for $\mu_C > 1$, vaccination accelerates the decrease in the mean of the sample of infected individuals per generation. In addition, the probability of disease extinction by the twentieth generation, which previously converged to approximately 23.6%, increases to 35.7% when 20% of the population got vaccinated, and 67.4% when you have 50% of the people with the vaccine.

The second analysis takes into account the efficacy of the vaccine applied during the vaccination process. Figure 4 illustrates the scenario in which 50% of the population is vaccinated with a vaccine with 70.4% efficacy. The results indicate a clear reduction in the average number of infected individuals. In this case, for all critical values, the models converge toward a scenario in which the epidemics eventually die out. That is, with a more efficient vaccine, the more likely it is to control the epidemic.

The final set of scenarios analyzed represents a society in which 75% of the population is vaccinated. For each of the three critical cases ($\mu_C < 1$, $\mu_C = 1$, and $\mu_C > 1$), the expected result was obtained: in each scenario, the mean number of infected individuals decreases over generations and the probabilities of extinction converged to $e = 1$. Figure 5, with 75% of the population vaccinated with a vaccine with an efficacy of 50.4%, was chosen to represent this

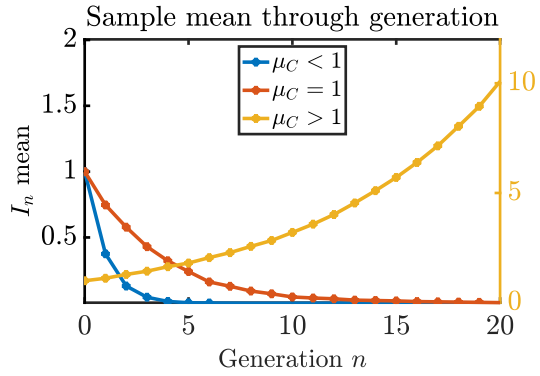


(a) Sample mean for the critical values of μ_C.

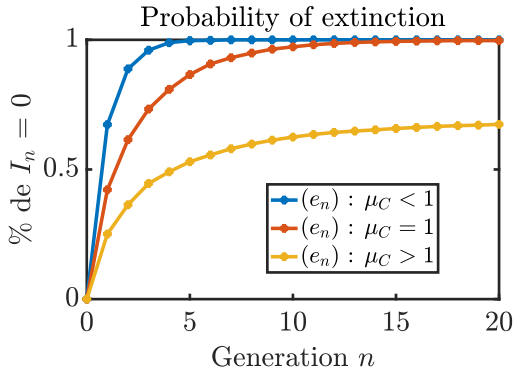


(b) probability of extinction for the critical μ_C values.

Figure 2: Graphics constructed with 4000 realizations of the branching process in in a 20% vaccinated population.

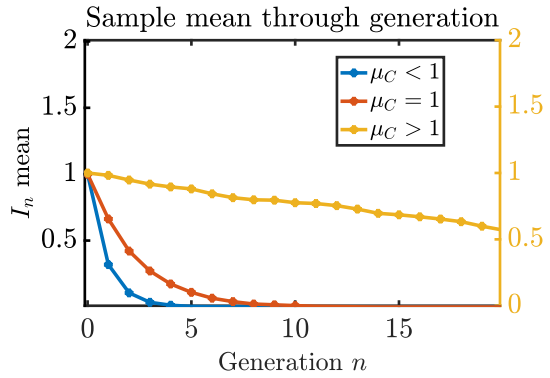


(a) Sample mean for the critical values of μ_C.

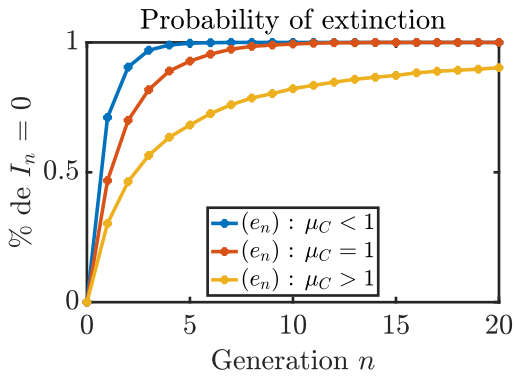


(b) probability of extinction for the critical μ_C values.

Figure 3: Graphics constructed with 4000 realizations of the branching process in a 50% vaccinated population.



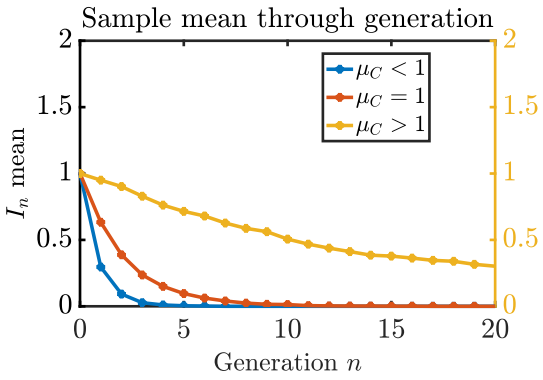
(a) Sample mean for the critical values of μ_C.



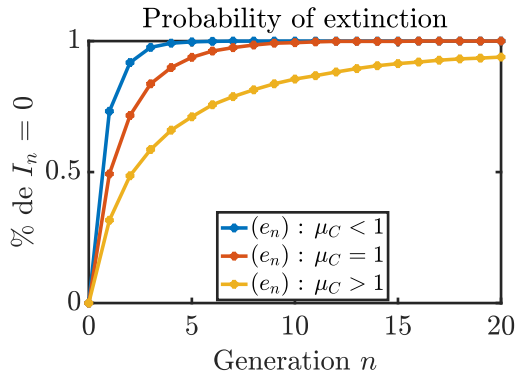
(b) probability of extinction for the critical μ_C values.

Figure 4: Graphics constructed with 4000 realizations of the branching process in a 50% of the population vaccinated with a 70.4% efficacy vaccine.

result.



(a) Sample mean for the critical values of μ_C.



(b) probability of extinction for the critical μ_C values.

Figure 5: Graphics constructed with 4000 realizations of the branching process in a 75% of the population vaccinated with a 50.4% efficacy vaccine.

2 CONCLUSIONS

The results obtained demonstrate that vaccination plays a decisive role in the mitigation and eventual extinction of an epidemic, provided that both the coverage and the efficacy of the vaccine reach adequate levels. The stochastic branching process allowed us to quantify the uncertainties inherent in disease propagation and to characterize how vaccination alters the expected number of infections across generations. The analysis showed that even moderate vaccination coverage significantly increases the probability of extinction and, when combined with vaccines of higher efficacy, the epidemic can be effectively controlled. In particular, scenarios with 75% vaccination coverage consistently resulted in a probability of extinctions approaching 100%, corroborating the idea that large-scale vaccination is a robust strategy for epidemic control. Thus, this work highlights that a joint consideration of vaccine efficacy and coverage is fundamental for the design of public health policies capable of suppressing outbreaks under diverse epidemiological conditions.

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