Identifying the complex underlying transmission network of COVID-19 in México from 2020 to 2024

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Has been demonstrated that the interaction of individuals in a social network can be modeled using the complex networks theory. In this sense, we believe that knowing at least approximately the underlying network of interaction among the individuals in a society could help to understand the dynamic of diseases transmission among the individuals and elucidate the most effective mechanisms to contain the spread and minimize negative effects like the over-saturation of health systems, such as hospitals and medical clinics. In this work, we study the spread of COVID-19 in Mexico from 2020 to 2024 using the statistical data available in the public health departments of Mexico. Through stochastic simulations we found a complex network that could represent a simplification of the real underlying network of interaction among the Mexican population, in particular we found that the network has degree distribution following a power law $P(k) \sim k^{-\gamma}$ with exponent close to $\gamma \approx 2.5$. As mentioned before it could help to understand the spread of future diseases through stochastic simulations using a network structure closer to reality and consequently implement best healthy policies.

Keywords: Covid 19; complex network topology; social interaction network; quarantine; stochastic modeling.

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1. Introduction

The COVID-19 pandemic led to the publication of numerous works recently [1–6]. Mainly focusing on the study of classical epidemiological models like the well known Susceptible-Infected-Removed(SIR) model over networks with different topological characteristics with the aim of study the influence of the network structure on the diseases spread among individuals in a population. Particularly, focused in random networks built with the classical Erdös-Rényi (*ER*) [7,8] and Barabási-Albert (*BA*) [9] growth models. Assuming that these models reproduce the interactions among the individuals in real populations. However, in real documented networks [10–15] the interaction among its components exhibit distinct properties than the generated by those models. For example, the degree distribution follows a power-law $P(k) \sim k^{-\gamma}$ with exponent γ starting from one, indicating the existence of individuals with more interactions than others. Moreover, as stated by Timár *et.al.* [15] social networks like Facebook exhibit dense property and power-law exponent γ close to one. In this sense, a network growth model able to build networks with γ tunable from 1 to ∞ was proposed by Esquivel-Barájas recently [16]. It is important to mention that in recent works addressing Covid-19 transmission behaviors in several countries have been investigated following different approaches [17, 18] and analyzing the effectiveness of non-pharmaceutical interventions like border restrictions and strict stay-at-home orders with the aim to contain the Covid-19 spread [19, 20]. However, in the major not take into account the effect of the network structure. We believe that knowing the underlying network of interaction among individuals in a society would help to understand the dynamic of virus transmission and elucidate the most effective mechanisms to contain the spread of future diseases and minimize negative effects like the over saturation of health systems. In this sense, we find it interesting to use the available statistical data of the last Covid-19 pandemic in the public health departments of México with the aim of finding a representation of the underlying network of interaction among the Mexican population.

Because the social distancing and quarantine policies was used to contain the virus spread in the last Covid-19 pandemic, in this work, we investigate the behavior of the *SIQR* epidemic model including statistical data of the Mexican population, like the age distribution and Covid-19 infected individuals by age distribution. Through statistical simulations we found that the best approximation to the fraction of infected individuals classified by age in the period from 2020 to 2024 is obtained simulating the Covid-19 spread in a complex network with degree distribution following a power law in the form $P(k) \sim k^{-2.5}$. It is an important result because as mentioned before it could help to understand the spread of future diseases, leading to find the best healthy policies through stochastic simulations or mathematical modeling considering network structures closer to reality.

This paper is organized as follows. In Sec. 2, statistical data retrieved from the public health department of México are presented. Features of the network model are outlined in Sec. 3. Details and results of the *SIQR* epidemic model on complex networks with different values of γ are presented in Sec. 4. Approximations of the proposed *SIQR* model to statistical data of Covid-19 in Mexican population from 2020

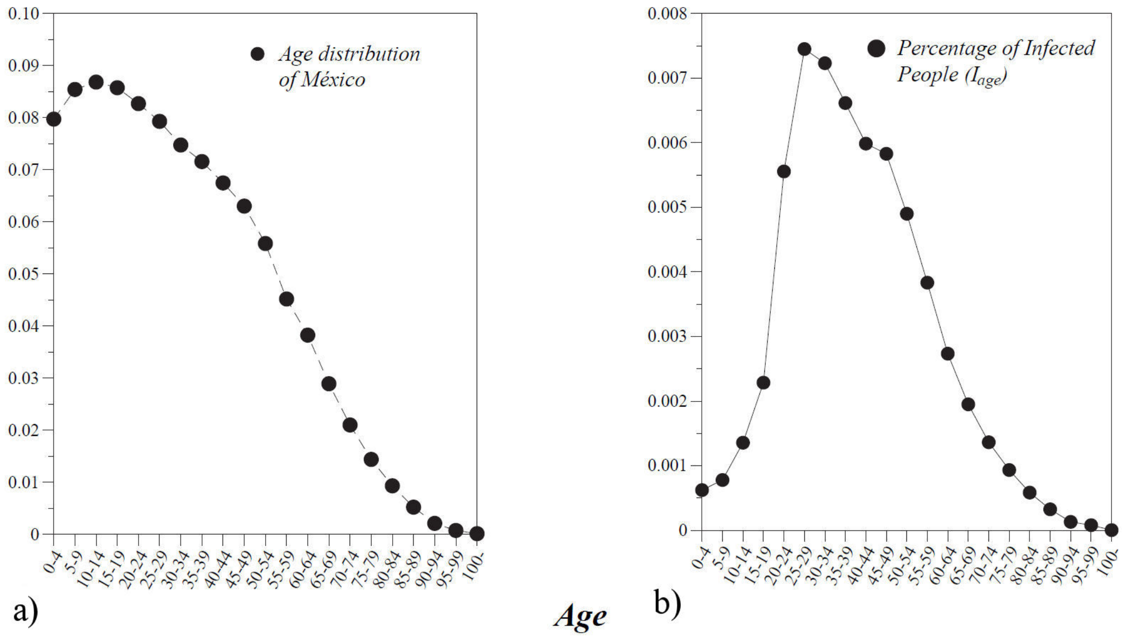

FIGURE 1. In figure are shown a) the age distribution in Mexican people and b) Covid-19 confirmed cases by age distribution in México from 2020-2024.

to 2024 are outlined in Sec. 5. Finally, the discussion and conclusion are given in Secs. 6 and 7, respectively.

2. Covid-19 data in México

As mentioned before, in order to attempt to elucidate a probably representation of the underlying interaction network among the population in México, we use the statistical data available in several Mexican organisms like the Instituto Nacional de Estadística y Geografía (INEGI) [21] from which we obtained the age distribution of Mexico, depicted in Fig. 1a). As shown, the majority of the people is young. Also, we use the Covid-19 confirmed cases by age distribution of México from 2020-2024 available in the public health department of México [22]. As shown in Fig. 1b), the majority of confirmed cases of Covid-19 occurred in people around twenty and forty years old. This is expected because the social interaction of individuals ranging on this age usually is very active, because of a variety of activities, like work, studies or leisure. Additionally, the amount of confirmed cases from 2020 to 2024 was $7,633,355$ and the total population in México was about $126,014,024$ in 2020. That is, the fraction of confirmed cases was about $I_{\text{total}} \approx 0.060$.

3. Network model

In this work we study the effect of the network topology on the spread of diseases among the individuals in a network. In particular, focusing on networks with degree distribution following a power law $P(k) \sim k^{-\gamma}$ with different γ values. In this sense, we implement the network growth model proposed by Esquivel and Barajas [16]. The model considers that initially the network comprises m_0 fully connected nodes and new nodes n_{new} with μ links are added subsequently. The value of μ is determined considering two cases: with probability p, $\mu = m$ links, where $m \leq m_0$ and with complementary probability $1 - p$, $\mu = \nu$ where ν is the degree of a randomly selected node in the network. To connect its μ links to another nodes in the network, n_{new} use the following attachment rule: $\Pi(k_i) = (k_i + \alpha)/(\sum_j (k_j + \alpha))$ where k_i and α represent the degree and initial attractiveness of one node n_i in the network, with $\alpha \geq 0$. Thus, $\Pi(k_i)$ describes the probability that n_{new} connects to n_i. This model build networks with $P(k) \sim k^{-\gamma}$ where γ can be tuned from 1 to ∞ changing the values of p, α and m as it is showed in Fig. 2.

4. *SIQR* model on power law networks

One of the most effective control action to contain the spread of infectious diseases is the quarantine policy, that consists in isolating several infected nodes to reduce the emergence of new infected nodes. In this section, we implement the *SIQR* model (see Fig. 3) and analyze its behavior in scale-free networks with different degree distributions. In the model, it is assumed that the network size is fixed, that is, consists in N nodes and the births and deaths are not taken into account. Also, we consider that the probability for a node becoming infected depends directly on its degree k. Additionally, since the network connectivity is heterogeneous, the presence of nodes with different degrees have to be considered. As such, it is convenient to assume that the population is organized into classes. In particular, we will consider that within each class, all nodes have the same degree k, with $k \in [m : k_{\max}]$, where $k_{\max}$ is the highest node degree value for the entire

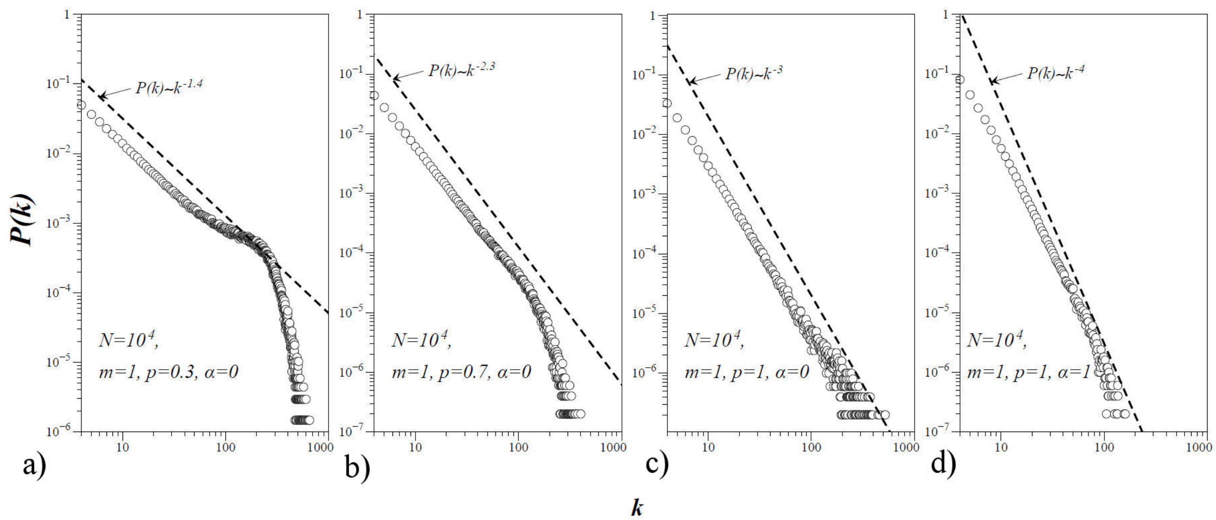

FIGURE 2. Degree distributions of networks built with the model proposed by Esquivel and Barajas [16]. Defining $m = 1$, $n = 10^4$ nodes and different values for p and α as follows: a) $p = 0.3$, $\alpha = 0$, b) $p = 0.7$, $\alpha = 0$, c) $p = 1$, $\alpha = 0$ and d) $p = 1$, $\alpha = 1$. With that values, degree distributions with power law exponents $\gamma \sim 1.4$, $\gamma \sim 2.3$, $\gamma \sim 3$ and $\gamma \sim 4$ are obtained respectively.

network. Also, within each class, the nodes can be in only one of the four different compartments according to its health condition and degree, $S_k(t)$, $I_k(t)$, $Q_k(t)$, and $R_k(t)$, which represent the densities of susceptible, infected, quarantined and recovered nodes with degree k at time t, respectively. Furthermore, the density of susceptible, infected, quarantined and recovered nodes in the entire network is defined as $S(t) = \Sigma_k S_k(t)P(k)$, $I(t) = \Sigma_k I_k(t)P(k)$, $Q(t) = \Sigma_k Q_k(t)P(k)$ and $R(t) = \Sigma_k R_k(t)P(k)$. Under the assumptions described above, the mean-field reaction rate dynamical equations for class k in *SIQR* model is described bellow.

$$\begin{aligned}
\frac{dS_k(t)}{dt} =& -\beta k S_k(t)\theta(t),\\
\frac{dI_k(t)}{dt} =& \beta k S_k(t)\theta(t) - \sigma I_k(t) - \eta I_k(t),\\
\frac{dQ_k(t)}{dt} =& \sigma I_k(t) - \varepsilon Q_k(t),\\
\frac{dR_k(t)}{dt} =& \varepsilon Q_k(t) + \eta I_k(t),
\end{aligned} \tag{1}$$

where the fraction $\theta(t)$ of links pointing to infected nodes is given by

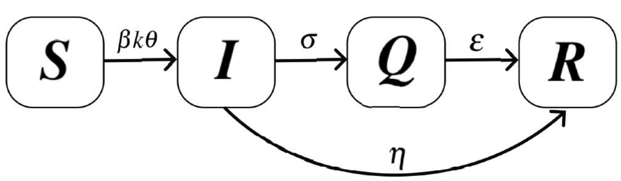

FIGURE 3. Flow diagram of the *SIQR* epidemic model. As shown, the degree k of nodes is considered in the chance to get infected. Additionally, β, σ and ε represent the infection, quarantine and recovery in quarantine rates respectively. Also, is considered the case in which an infected individual recovers without have been quarantined, denoted by η.

$$\theta(t) = \frac{\Sigma_k k P(k) I_k(t)}{\Sigma_s s P(s)} = \frac{1}{\langle k \rangle} \Sigma_k k P(k) I_k(t), \tag{2}$$

where $P(k)$ is the degree distribution and $\langle k \rangle$ is the average degree within the network and denotes the normalization factor. This formulation of the dynamical equations for heterogeneous networks was introduced by Y. Moreno, R. Pastor-Satorras, A. Vespignani [23].

In order to investigate the behaviour of the proposed *SIQR* model in networks with different degree distributions, in particular, degree distributions following a power-law with different exponent value γ. We perform stochastic simulations on networks built with the model outlined in Sec. 3. The procedure similar to that proposed by Yutaka Okabe and Akira Shudo [1], is as follows:

1. Generate the network and compute the average degree $\langle k \rangle$. After the network is built, the spread of the disease will be simulated from $t = 0$ to $t = 100$ time steps.

2. At $t = 0$, I_0 individuals (nodes) are chosen randomly to be infected.

3. A susceptible individual will be infected with a probability β if one of its k connecting individuals is infected.

4. An infected individual will be recovered in $1/\eta$ days on average without having been quarantined. Another case, is that an infected individual could be quarantined between $1/\sigma$ days due to a positive test of infection.

5. A quarantined individual will be recovered in $1/\varepsilon$ days.

6. At each time step t, the processes 3, 4 and 5 are repeated.

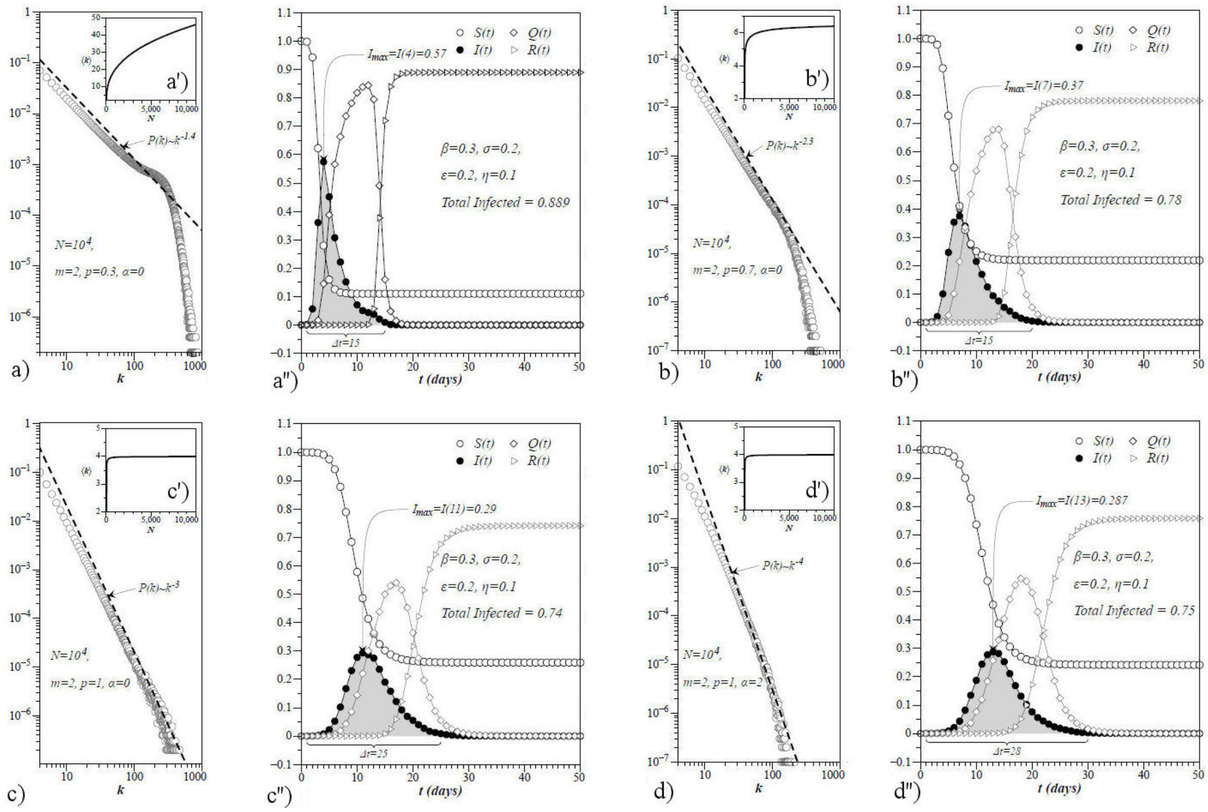

FIGURE 4. a), b), c), d), Degree distributions of the networks used for the stochastic simulations. a'), b'), c'), d') Average degree value respect to the size of the network. a"), b"), c"), d") Quantities S, I, Q and R derived from the stochastic simulations with the *SIQR* model.

- The steps $1-5$ produce a single sample. Simulations are performed one thousand times and averaged to get the final results.

For all simulations, networks with $N=10^4$ were considered, defining $m=2$ and different values for p. The rate of infection was fixed to $\beta=0.3$, quarantine rate $\sigma=0.2$, recovery rate after quarantine $\varepsilon=0.2$ and recovery rate without quarantine fixed to $\eta=0.1$. In Fig. 4 are shown the results of the stochastic simulations. Figures 4a), 4b), 4c) and 4d) show the degree distribution $P(k)$ of the networks built with the model outlined in Sec. 3. As illustrated, generated networks have power-law degree distributions with $\gamma\sim 1.4$, 2.3, 3 and 4. In addition, the average degree grows significantly as the value of γ decreases bellow 3 [see Figs. 4a'), 4b'), 4c'), 4d')], that is, the networks become to be more densely connected as reported by Esquivel and Barajas [16]. As shown in Figs. 4a"), 4b"), 4c"), 4d"), the topology of the network in which the *SIQR* model was simulated, in this case for different γ values, have a high influence on the dynamic of S, I, Q and R quantities. In particular, the following two cases:

- As the value of γ decreases, the amount of infected individuals and the maximum value of infected individuals ($I_{\max}$) also increase.
- The time Δt represents the amount of days in which the disease have been present in the population. As shown, Δt increase as the value of γ increases. This can be a convenient behavior because it prevents over saturation of health systems.

The behaviors described above are expected because as the value of γ decrease, the networks become to be more densely connected and the amount of nodes with a higher number of connections, frequently called Hub-nodes increases and these nodes act as superspreaders nodes, causing the rapid spread of the disease in the network. However, the quarantine implementation helps to contain the spread of the disease reducing the time in which the disease is present in the population.

5. Approximating the density of Covid Infected individuals in México from 2020 to 2024

As showed in the Sec. 4, the topology of a network, or in other words, the interaction of individuals in a population plays a significant role in the spread of diseases. In this sense, if the underlying interaction network of the individuals in a population is known, it would be possible to determine how quickly or slowly a virus spreads on the network and study

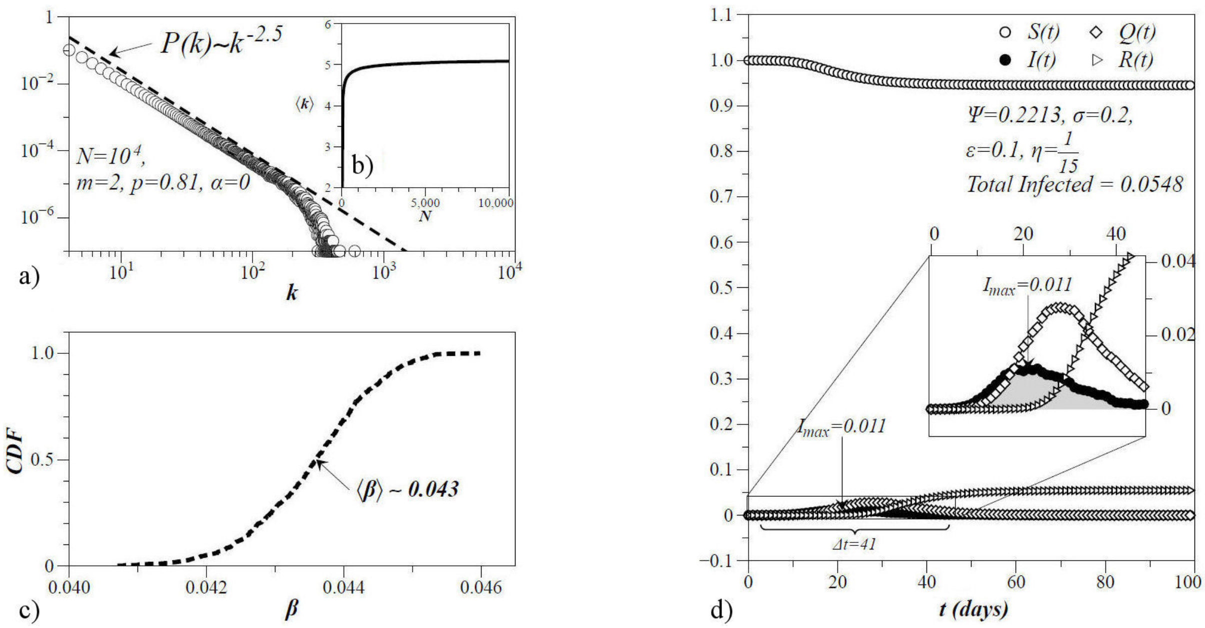

FIGURE 5. a) Degree distribution of the network. b) Average degree value respect to the network size. c) Cumulative distribution function of β. d) Quantities S, I, Q and R. The depicted values are obtained averaging the results from one thousand stochastic simulations of the *SIQR* model.

the effect of different containment policies to prevent the over saturation of health systems and reduce the number of deaths.

In order to attempt to elucidate a probably representation of the underlying interaction network among the population in Mexico, we use the statistical data presented in Sec. 2. That is, the age distribution in Mexican population (depicted in Fig. 1a) and the Covid-19 confirmed cases by age distribution of México from 2020-2024 [Fig. 1b)]. From the Covid-19 pandemic, Y. Alimohamadi *et.al.* [24] found that the reproductive number $R_0 \approx 3.32$, also it is known that

$$R_0 = \frac{\psi}{\eta},$$

where ψ and η represent the infection and recovery rates. Raveendran *et.al.* [25], found that infected individuals with SARS-CoV-2 virus commonly develop symptoms 4-5 days after exposure. Then, we consider that infected individuals could be quarantined among the first 5 days, *i.e.*, $\sigma = 1/5$.

Additionally, recovery from mild SARS-CoV-2 infection commonly occurs within 7-10 days after the onset of symptoms in mild disease and in severe/critical illness could take 3-6 weeks. We consider only the mild disease cases, that is, ten days for recovery after quarantine $\varepsilon = 1/10$. Additionally, with these data, we can consider that $\eta = 1/15$ that is, the recovery period without intervention was approximated to 15 days in mild infection cases. Then, we can approximate the value of $\psi \approx 0.2213$. However, for the $SIQR$ model studied in this work it is necessary to consider that $\psi = \beta k$ in order to take into account the heterogeneity of the underlying interaction network.

In order to attempt to reproduce the Covid-19 confirmed cases by age distribution of México from 2020-2024 [Fig. 1b)] using the *SIQR* model, we perform stochastic simulations on networks with different degree distribution. The procedure similar to the outlined in Sec. 4.

1. Generate the network using the model outlined in Sec. 3 comprising $N = 10^4$ nodes and considering that the age of each node in the network is based on the age distribution shown in Fig. 1a). Additionally, at the end of the growth $\langle k \rangle$ is computed. After that, the spread of the disease will be simulated from $t = 0$ to $t = 100$ time steps.

2. At $t = 0$, $I_0 = 1$ individual (node) is chosen randomly to be infected.

3. A susceptible individual with degree k will be infected with a probability $\beta = \psi/\langle k \rangle$ if one of its k connecting individuals is infected.

4. An infected individual will be recovered in fifteen days on average without have been quarantined. Another case, is that an infected individual could be quarantined around five days due to a positive test of infection.

5. A quarantined individual will be recovered in ten days on average.

6. At each time step t, the processes 3, 4 and 5 are repeated.

7. The steps $1-5$ produce a single sample. Simulations are performed two thousand times and averaged to get the final results.

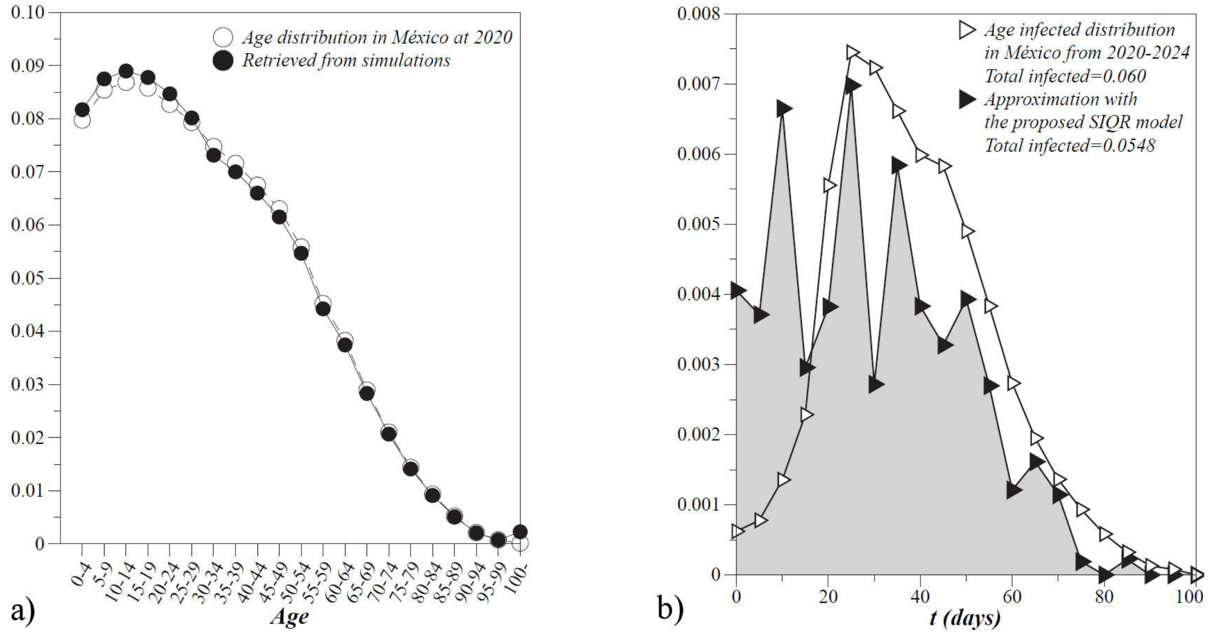

FIGURE 6. a) Age distribution in Mexican population and b) Age infected distribution in Mexican population from 2020 to 2024. In both, the comparison of real data and the obtained from stochastic simulations is showed.

The best approximation to the Covid-19 confirmed cases by age distribution of México from 2020-2024 [Fig. 1b)] using the *SIQR* model, was obtained using a complex network with degree distribution $P(k) \sim k^{-2.5}$. As shown in Fig. 5a) that topology was obtained using the network growth model outlined in Sec. 3 with $m = 2$, $p = 0.81$ and $\alpha = 0$. In Fig. 5c) is shown the Cumulative Distribution Function (*CDF*) of β retrieved from $\psi = \beta\langle k\rangle$ with $\psi = 0.2213$ and $\langle k\rangle \approx 5$ got from the simulations [see Fig. 5b)]. Fig. 5d) depicts the values of S, I, Q, and R achieved from the *SIQR* stochastic simulation. As shown, the fraction of infected individuals was 0.0548 close to the calculated for México from 2020 to 2024 (I_{total} mentioned in Sec. 2). Additionally, Fig. 6 shows the comparison of the Age distribution [Fig. 6a)] and the Age infected distribution [Fig. 6b)] from the Mexican population and the retrieved from the stochastic simulations. As it can be seen, the Age infected distribution retrieved from the simulations (▶ symbol) not fit exactly to the real (▷ symbol). However, seems to be a good approximation and the fraction of total infected individuals is very close. Indicating that, the underlying network of interaction among the Mexican people could behave as a complex network with degree distribution close to $P(k) \sim k^{-2.5}$.

6. Discussion

In this work, we investigate the dynamic of disease spread on networks using the *SIQR* model. Particularly, in networks exhibiting scale-free property in which the degree distribution follows a power-law $P(k) \sim k^{-\gamma}$. We found that, the amount of infected individuals increase steeply for γ values close to one. This is expected since this type of networks are more densely connected and they have more hub-nodes which play the super spreader role, because of this, $I_{\max}$ emerges in fewer days and the total amount of infected individuals is concentrated in fewer days also. Additionally, we attempt to reproduce the Covid-19 confirmed cases by age distribution of México from 2020-2024, finding the best results with a complex network with degree distribution $P(k) \sim k^{-2.5}$. Although the results of the stochastic simulations not fit exactly to the real data, it seems to be a good approximation, since the total amount of infected individuals and the age distribution among the individuals in the network are very similar. It is important to mention that this model not implement complicated processes in the growth of the network and in the spread of the disease among the individuals because the goal is to offer a simple model to attempt elucidate a probably representation of the underlying interaction network of the Mexican population.

7. Conclusion

With the aim to find a probably representation of the underlying interaction network of the Mexican population, in this paper we have investigated through stochastic simulations the effect that different network topology have on the dynamic of the epidemiological *SIQR* model focusing in networks with scale-free property. We found that the best approximation is achieved using a complex network with degree distribution $P(k) \sim k^{-2.5}$. It is an important result because using that network topology it would be possible study the spread behavior in future diseases and investigate the effect of different containment policies and its rigor in implementation, achieving that the amount of infected individuals grow slowly preventing the overcrowding of health systems. Or even to avoid future pandemics.

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