Numerical simulations on scale-free and random networks for the spread of COVID-19 in Pakistan

Muhammad Rafiq [a,*], **Abdul Rauf Nizami** [a], **Dumitru Baleanu** [b,c,d], **Nadeem Ahmad** [e]

[a] *Department of Mathematics, University of Central Punjab, Lahore, Pakistan*
[b] *Department of Mathematics, Cankaya University, Ankara, Turkey*
[c] *Department of Medical Research, China Medical University Hospital, China Medical University, Taichung, Taiwan*
[d] *Institute of Space Sciences, Magurele, Bucharest, Romania*
[e] *Technical Education and Vocational Training Authority, Government of the Punjab, Lahore, Pakistan*

Abstract Epidemiology is the study of how and why an infectious disease occurs in a group of people. Several epidemiological models have been developed to get information on the spread of a disease in society. That information is used to plan strategies to prevent illness and manage patients. But, most of these models consider only random diffusion of the disease and hence ignore the number of interactions among people. To take into account the interactions among individuals, the network approach is becoming increasingly popular. It is novel to consider the dynamics of infectious disease using various networks rather than classical differential equation models. In this paper, we numerically simulate the Susceptible-Infected-Recoverd (SIR) model on Barabási-Albert network and Erdös-Rényi network to analyze the spread of COVID-19 in Pakistan so that we know the severity of the disease. We also show how a situation becomes alarming if hubs in a network get infected.

1. Introduction

The coronavirus (later known as COVID-19) was originated in Wuhan, China, in December 2019 [34], and soon became a life-threatening disease [1]. The virus spread over the world so rapidly that the World Health Organization (WHO) declared this outbreak as a health emergency of international concern in January 2020 and in March 2020 declared it as a pandemic [9,37]. As a result, most countries imposed mitigation and suppression strategies, such as lockdowns and social distancing, to control the spread of the disease. To ensure the effectiveness of these strategies, several epidemiological models were used to predict the spread of the virus [8,13,39].

The most common epidemiological models used to study the dynamics of COVID-19 are: The Susceptible-Infected-Recovered (SIR) model [2,20]. According to this model, an infected individual can only transmit the virus to susceptible

* Corresponding author.
E-mail addresses: m.rafiq@ucp.edu.pk (M. Rafiq), arnizami@ucp.edu.pk (A.R. Nizami), dumitru@cankaya.edu.tr (D. Baleanu), nadeemahmadap@gmail.com (N. Ahmad).

individuals. Once an infected individual is recovered (or passed away) it cannot infect others and cannot be reinfected. The SIR model was extended to Susceptible-Exposed-Infectious-Recovered (SEIR) model. According to this model, a susceptible get exposed (E) to virus but does not become contagious [12,30,38]. To increase the predictive power of SIR and SEIR models, several additional parameters were considered, as clustering [21], age heterogeneity [4,30], change in policy and control measures [31,39], and meteorology [15].

However, these models do not take account of social interactions, thus limiting the possible mitigation strategies [22]. To consider interactions in human society we need social networks. Interactions among individuals can be described collectively by a network where the individuals are represented by nodes (vertices) and the interactions are represented by edges. The number of edges incident to a node is called the degree of the node. A node with a large degree (usually greater than a fixed number) is called a hub.

The importance of social networks have been pointed out in [6,19,23,28]. In connection with the coronavirus, simulations of epidemic models on a scale-free network have been studied in [14]. The dynamics of the coronavirus with quarantines have been modeled on social networks in [5].
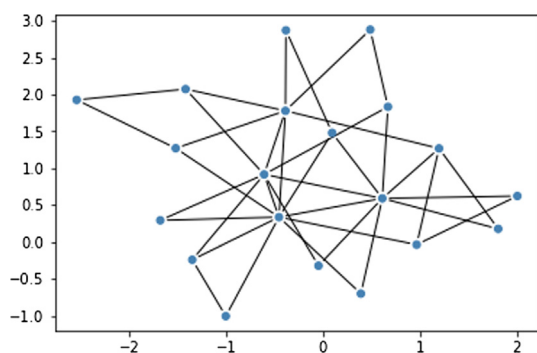

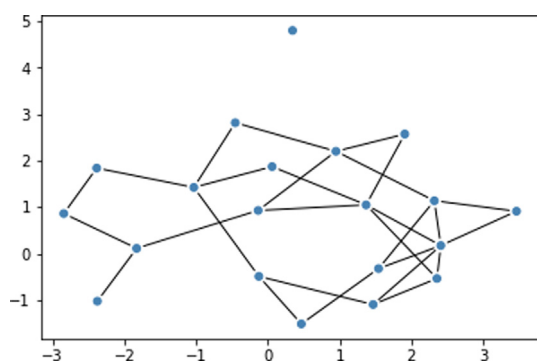**Fig. 1**   BA network with 20 nodes and average degree 3.7.

Fig. 2   ER network with 20 nodes.

In this paper, we consider two types of networks, Barabási-Albert network and Erdös-Rényi network, and numerically simulate the SIR model on them to analyze the spread of COVID-19 in Pakistan. Also, we compare the dynamics of the disease on both networks and make a prediction for the future concern.

2. Networks

A (social) network is a group of interactive persons. The persons are represented by nodes (vertices) and an interaction between two persons is represented by an edge. A network is said to be *scale-free network* if its degree distribution follows a power law, which describes a relationship between two quantities such that one varies as a power of the other. In networks, this property arises when there are few nodes with many edges and many nodes with few edges [14]. A network is said to be *random network* if its degree distribution follows the Poisson law. To learn more about networks, please see [3,19,27].

2.1. Barabási-Albert Network

The Barabási-Albert (BA) network is a scale-free network, i.e., the degrees of nodes are heterogeneous. The algorithm to generate the BA network is as follows: Begin with some initial nodes. Add a new node to the existing nodes until we get the required number of nodes. A new node is added to the existing nodes with some fixed probability. That probability should be proportional to the degree of each node to which the new node is being connected.

Fig. 1 shows an example of the BA network of 20 nodes, initialized with 2 nodes. The average degree of nodes is $k = 3$. It is generated in Python using the command **igraph. Graph.Barabasi()**.

2.2. Erdös-Rényi Network

The Erdös-Rényi (ER) network is a random network, where edges are chosen completely at random with equal probability. The construction algorithm is as follows: Create n nodes. Create an edge between a pair of nodes with some probability; this edge-creating probability is independent of the probability of the existence of other edges. The average degree of a node is approximately the product of edge-creating probability and the total number of nodes.

An example of ER network is given in Fig. 2. It is generated in Python using the command **igraph.Graph.Erdos_Renyi()**. The number of nodes is 20 and the average degree is $k = 3$.

3. The SIR Model

The SIR model was proposed by Kermack and McKendrick to study dynamics of infectious diseases[20]. The model has some
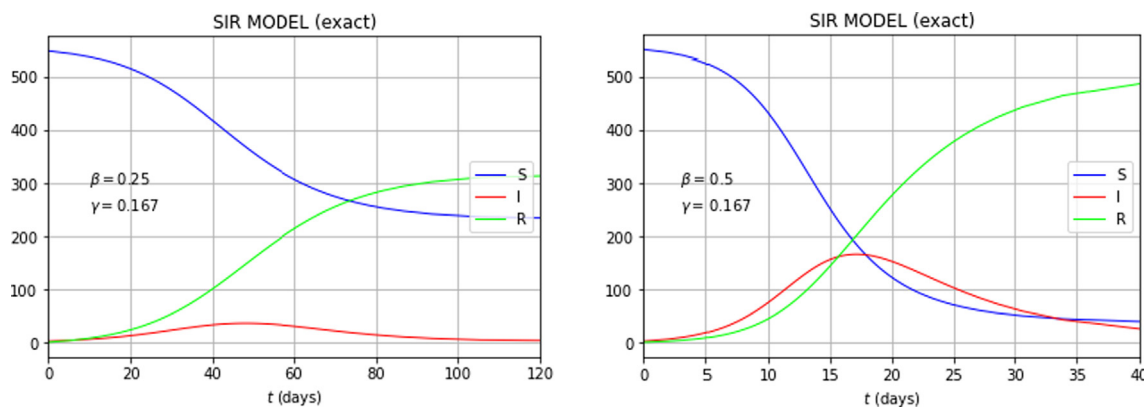

Fig. 3   The SIR model.

Fig. 4 $N = 550, I = 2$, and $k = 5$.

assumptions. First, the whole population, say N, can be divided into three parts, the susceptible people, say S, the infected people, say I, and the recovered people, say R. Second, only susceptible people can receive the infection. Third, if an infected person gets recovered, he/she does not get the infection again. Finally, the total number of people in the population remains the same, that is, $S + I + R = N$. The SIR model is illustrated in Fig. 3.

The following is the SIR model in the form of differential equations; all three variables S, I, and R are functions of time. β and γ are respectively rates of infection and recovery.

$$\frac{dS}{dt} = -\frac{\beta}{N} SI \qquad (3.1)$$

$$\frac{dI}{dt} = \frac{\beta}{N} SI - \gamma R \qquad (3.2)$$

$$\frac{dR}{dt} = -\gamma R \qquad (3.3)$$

Although a numerical solution of the differential equations of the SIR model is sufficient to study the dynamics of infectious disease, some people gave its exact solutions. For example, Harko et al. gave an analytical solution by expressing the system into a differential equation (actually a Bernoulli differential equation) in a single variable $S(t)$ [10] while Okabe and Shudo solved the system using two variables, $S(t)$ and $I(t)$ [26]. The results of the exact solution given by [26] of the SIR model are shown in Fig. 4.

In this paper, we will simulate the SIR model on the BA and ER networks and compare the results of the dynamics of COVID-19.

4. COVID-19 Data of Punjab

Since the situation of the coronavirus in all provinces of Pakistan is almost the same, we take Punjab as a sample. The dynamics of the disease in Punjab will reflect the dynamics of the disease in the whole of Pakistan. The data of the confirmed and recovered cases of COVID-19 in Punjab during January 2022 are as follows: The total population of Punjab is 110 million, and the total number of confirmed and recovered cases of COVID-19 are respectively 0.454 and 0.431 million; the source of data is *https://covid.gov.pk/stats/punjab*. The percentages of the confirmed and recovered cases are respectively 0.413 and 0.392; see Fig. 5.

5. Numerical Simulations

We perform microscopic simulations of the SIR model on Barabási-Albert network, a scale-free network, and on Erdös-Rényi network, a random network.

For a fast simulation of the data, we reduce the total population of Punjab to 0.2 million times. So, the total population and infected cases reduce to 550 and 2, respectively.
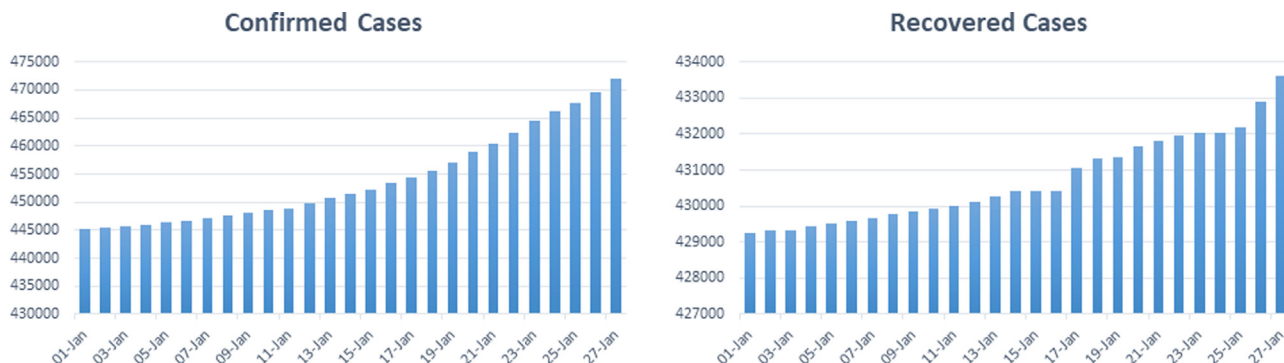

Fig. 5   Confirmed and recovered cases of COVID-19.

5.1. Algorithm

The algorithm we follow is the same as is given in [27]. However, instead of computing the average number of recovery days ($\frac{1}{\gamma}$) from the Poisson distribution we fix $\frac{1}{\gamma} = 6$, which is the average number of recovery days for the present variant (i.e., omicron) of coronavirus in Pakistan. The algorithm is:

Step 1 Generate a network.

Step 2 Fix the number of recover days, that is $\frac{1}{\gamma}$.

Step 3 At $t = 0$, take the number of infected persons as I.

Step 4 A healthy person receives infection with some fixed probability p if he/she meets with an infected person. Please note that $\beta = k \times p$.
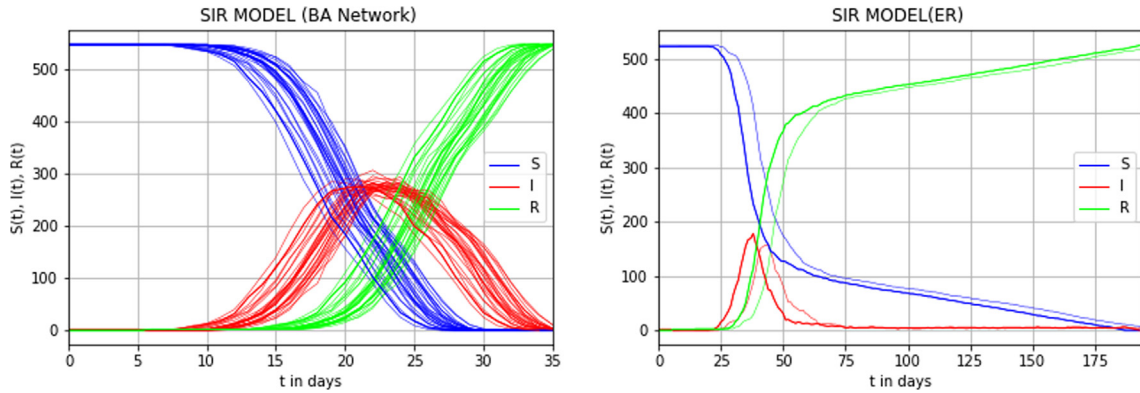

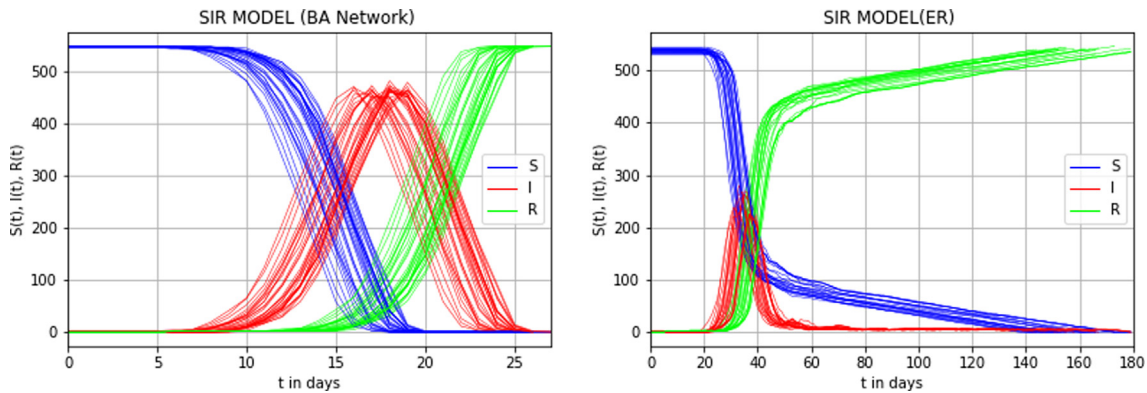**Fig. 6** $N = 550, I = 2, k = 3$ and $p = 0.05$.

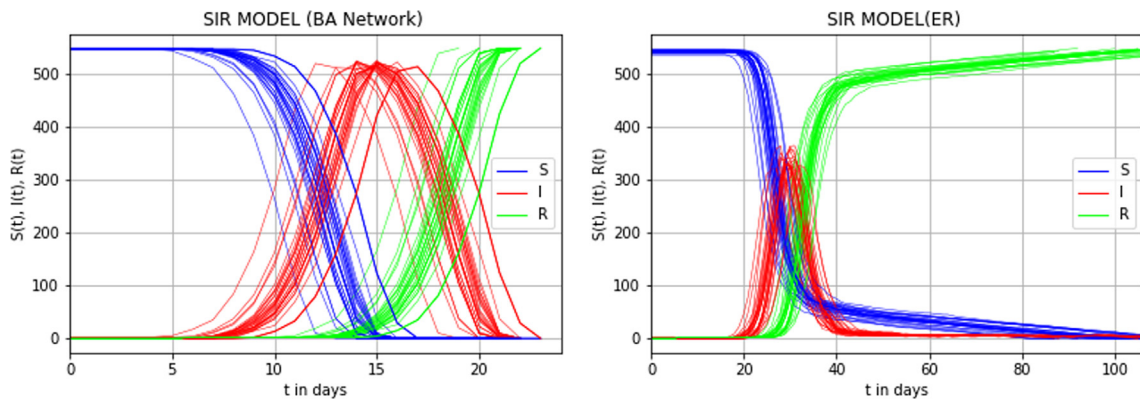**Fig. 7** $N = 550, I = 2, k = 4$ and $p = 0.05$.

Fig. 8 $N = 550, I = 2, k = 5$ and $p = 0.05$.

Step 5 The time sequence obtained from the above proce-
dure is regarded as a single sample. Simulations are
performed for several samples.

5.2. Comparison of Disease Dynamics

To compare the dynamics we plot the simulated results on BA
and ER networks by taking the total population as $N = 550$

and the initial number of infected people as $I = 2$. To get a
clear picture of the disease dynamics we take several values
of the average connectivity, k, and the infection probability, p.

5.2.1. ($k = 3, 4, 5$ and $p = 0.05$)

Due to randomness in generating the networks and choosing
the infected people, we plot 30 samples in each simulation to
understand the average behavior of the disease dynamics.
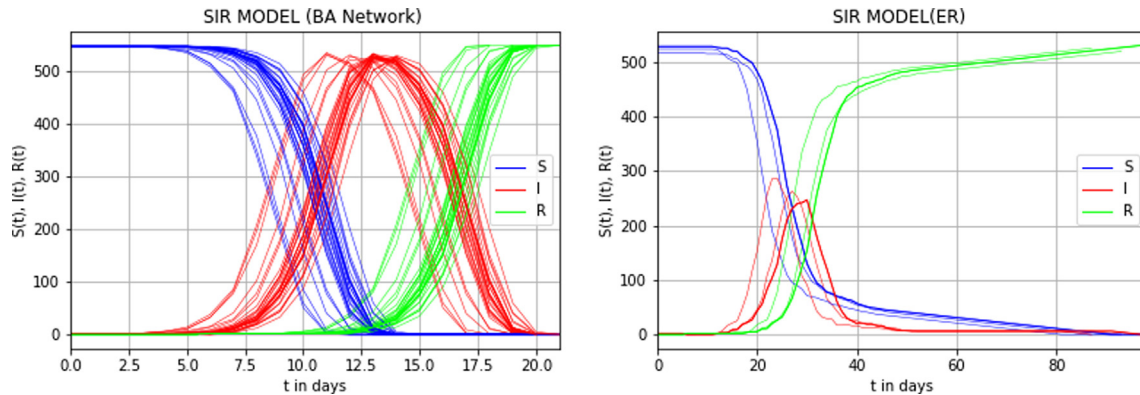The dynamics on both networks indicate that the number of

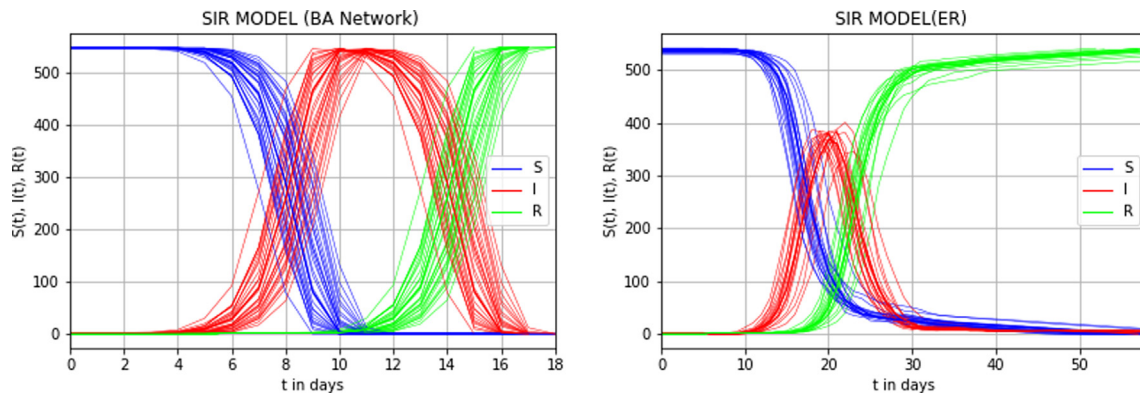**Fig. 9** $N = 550, I = 2, k = 3$ and $p = 0.1$.

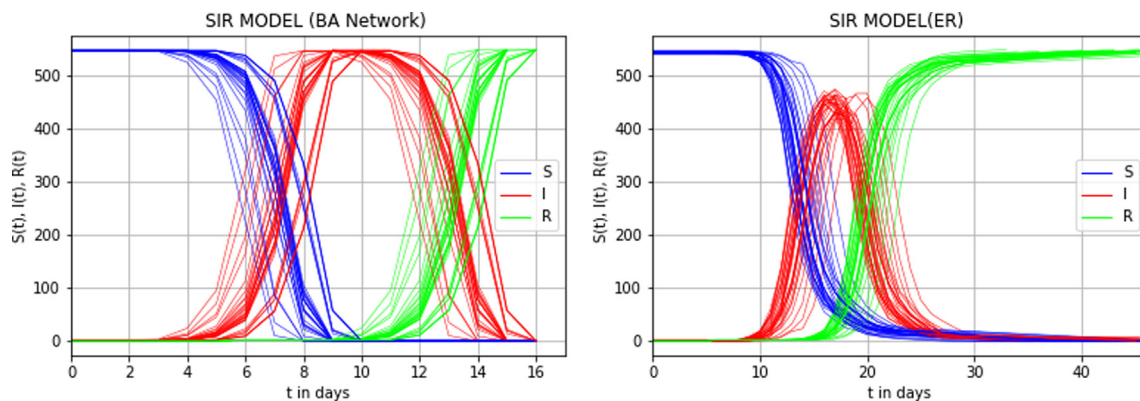**Fig. 10** $N = 550, I = 2, k = 4$ and $p = 0.1$.

Fig. 11 $N = 550, I = 2, k = 5$ and $p = 0.1$.

infected persons increases with time, gets a peak, and finally decreases, which reflects the true behavior of the Susceptible-Infected-Recovered model; see Fig. 3. However, the speeds of getting an infection and getting recovered on both networks are different. The infection spreads more rapidly on the BA network than on the ER network. The reason is that the BA network is always a connected network while the ER network is not; that is, the ER network can have some isolated nodes. Also, the peak of infection is higher on the BA network than on the ER network; it seems almost all people get infection in the case of the BA network. Finally, the infected individuals get recovered sooner on the BA network than on ER network. For instance, Fig. 6 indicates that the infected take less than
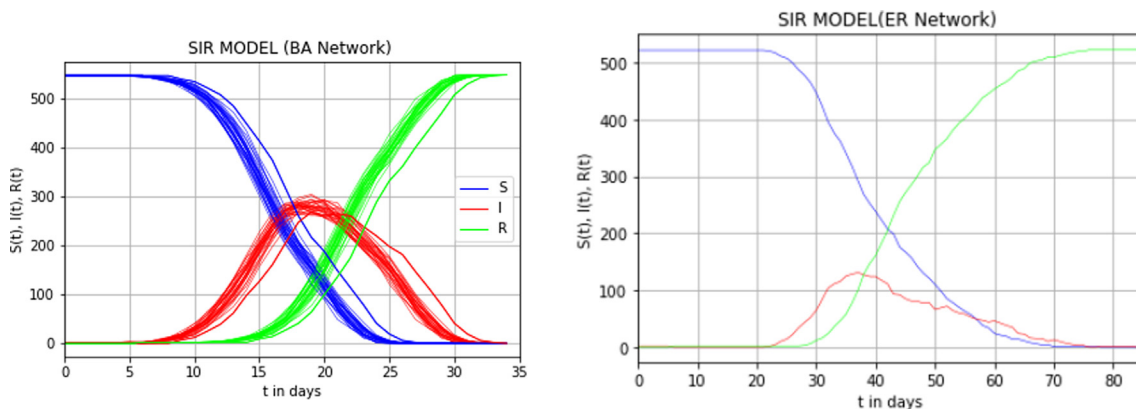

Fig. 12   Hub: $k = 3$ and $p = 0.05$.
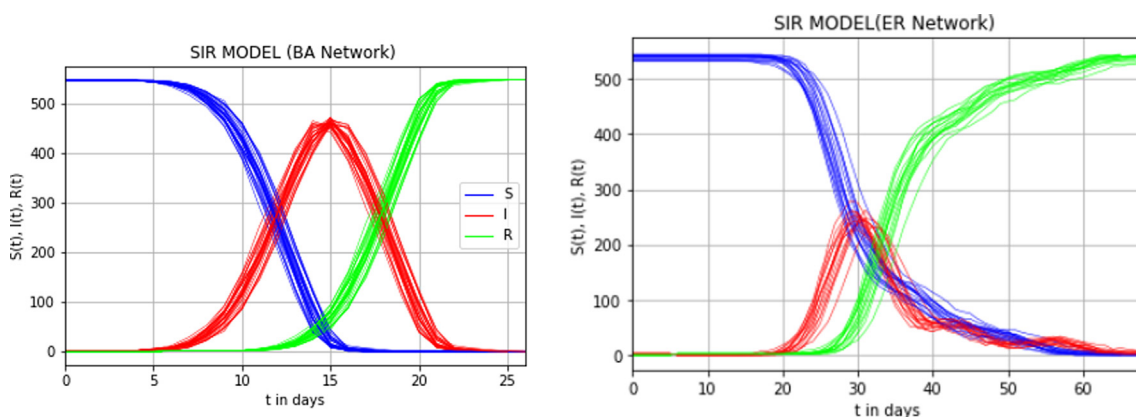
Fig. 13   Hub: $k = 4$ and $p = 0.05$.
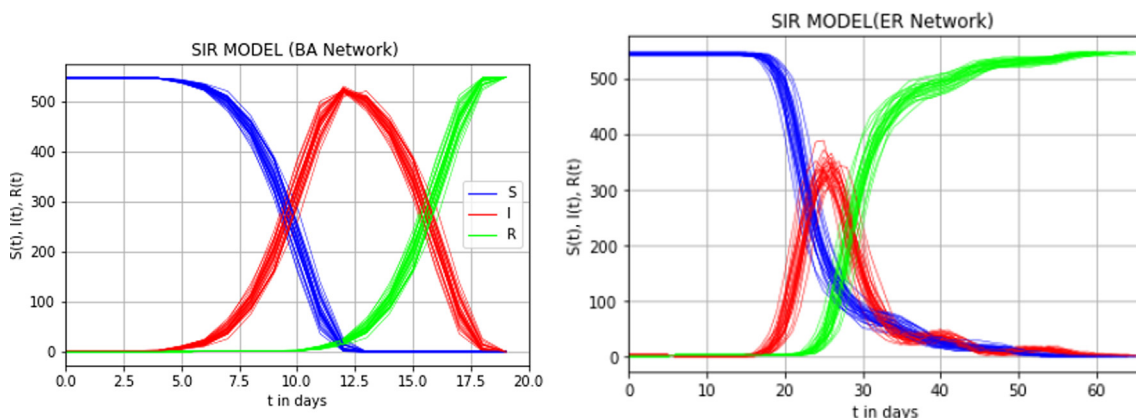
Fig. 14   Hub: $k = 5$ and $p = 0.05$.

40 days to get recovered in the case of BA networks and take more than 175 days in the case of ER network.

5.2.2. (k = 3, 4, 5 and p = 0.1)

(see Figs. 7–10).

5.3. Hub Consideration

Here we study the disease dynamics on both networks taking into account the role of hubs, the nodes that have very large degrees. In the BA network, some nodes receive very large

Fig. 15   Hub: $k = 3$ and $p = 0.1$.

Fig. 16   Hub: $k = 4$ and $p = 0.1$.

Fig. 17   Hub: $k = 5$ and $p = 0.1$.

degrees, so we consider a hub with a degree greater or equal to $8k$, while in ER network a hub has a degree greater or equal to $2k$. We observe that if the initially infected individuals come from hubs, then the dynamic of the disease changes drastically. The infection spreads more rapidly and, interestingly, the recovery is also fast on both 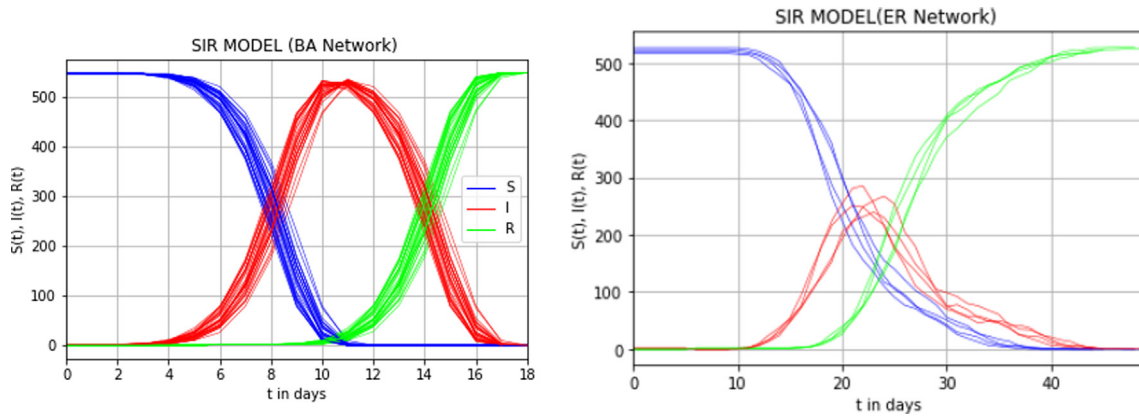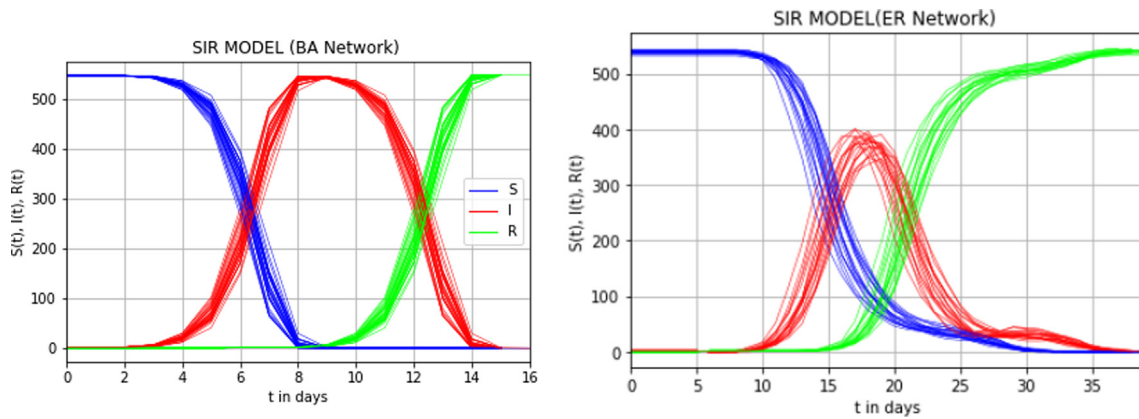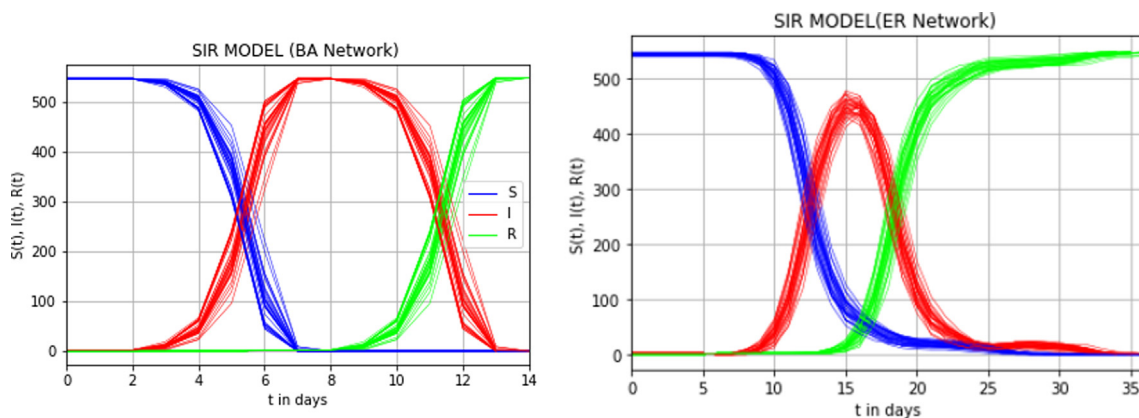networks. For instance, on comparing the results of the BA network in Figs. 6 and 11 we observe that the peak of infection is obtained in 18 days if the infected persons are from a hub while the peak is obtained in 22 days if the infected persons are not from a hub. In case of ER network, the peak of infection is obtained in 37 days if the initial infected come from the hubs while the peak is obtained in 40 days if the infected persons are not from a hub. (see Figs. 12–17).

6. Conclusion

In this paper, we took the data of COVID-19 for January 2022 in the province of Punjab, Pakistan, and numerically simulated the Susceptible-Infected-Recovered model on both BA and ER networks to study the dynamics of the disease. The dynamics on both networks indicated that the number of infected individuals increased with time, reached a peak, and then gradually decreased so that the disease disappeared from the society. However, the rates of getting the infection and getting recovered on the BA network are faster than the corresponding rates on ER network.

We considered the role of hubs for spreading the disease. We figured out that the infection spread drastically fast if the initial infected people lie inside hubs.

Based on our study, we suggest immediate isolation of the infected individuals from susceptible ones, paying special attention to those who lie inside hubs. This strategy should be applied not only to Punjab but also to all provinces of Pakistan to fight against the pandemic. Although testing is important to identify the infected individuals, simulations on close networks provide a quick way to know the dynamics and severity of the disease in the society.

Our future plan is to implement the network techniques to analyse the models governed by fractional, delay, and stochastic differential equations as are discussed in [7,11,16–18,24,25,29,32,33,35,36,40].

7. Data availability

The data regarding COVID-19 in Pakistan is available on *https://covid.gov.pk/stats/pakistan*.

Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

References

[1] Roy M. Anderson, Hans Heesterbeek, Don Klinkenberg, T. Déirdre Hollingsworth, How will country-based mitigation measures influence the course of the COVID-19 epidemic? The Lancet, 395(10228):931–934, 2020. Publisher: Elsevier.

[2] Norman T.J. Bailey, et al., The mathematical theory of infectious diseases and its applications. Charles Griffin & Company Ltd, 5a Crendon Street, High Wycombe, Bucks HP13 6LE., 1975.

[3] Guido Caldarelli, Michele Catanzaro, Networks: A very short introduction, volume 335, Oxford University Press, 2012.

[4] Sheryl L. Chang, Nathan Harding, Cameron Zachreson, Oliver M. Cliff, Mikhail Prokopenko, Modelling transmission and control of the COVID-19 pandemic in Australia, Nat. Commun., 11(1):1–13, 2020. Publisher: Nature Publishing Group.

[5] K. Choi, Hoyun Choi, B. Kahng, Covid-19 epidemic under the K-quarantine model: Network approach. arXiv preprint arXiv:2010.07157, 2020.

[6] Zoltán Dezs\Ho, Albert-László Barabási, Halting viruses in scale-free networks, Phys. Rev. E, 65(5):055103, 2002. Publisher: APS.

[7] C. Dineshkumar, R. Udhayakumar, V. Vijayakumar, Kottakkaran Sooppy Nisar, Anurag Shukla, A note on the approximate controllability of Sobolev type fractional stochastic integro-differential delay inclusions with order $1 < r < 2$, Math. Comput. Simul., 190:1003–1026, 2021. Publisher: Elsevier.

[8] Neil M. Ferguson, Daniel Laydon, Gemma Nedjati-Gilani, Natsuko Imai, Kylie Ainslie, Marc Baguelin, Sangeeta Bhatia, Adhiratha Boonyasiri, Zulma Cucunubá, Gina Cuomo-Dannenburg, et al. Impact of non-pharmaceutical interventions (NPIs) to reduce COVID-19 mortality and healthcare demand. 2020. Publisher: Imperial College COVID-19 Response Team London.

[9] Harapan Harapan, Naoya Itoh, Amanda Yufika, Wira Winardi, Synat Keam, Haypheng Te, Dewi Megawati, Zinatul Hayati, Abram L. Wagner, Mudatsir Mudatsir, Coronavirus disease 2019 (COVID-19): A literature review, J. Infect. Public Health, 13(5):667–673, 2020. Publisher: Elsevier.

[10] Tiberiu Harko, Francisco S.N. Lobo, MK3197716 Mak, Exact analytical solutions of the Susceptible-Infected-Recovered (SIR) epidemic model and of the SIR model with equal death and birth rates, Appl. Math. Comput., 236:184–194, 2014. Publisher: Elsevier.

[11] T.E. Harris, Contact Interactions on a Lattice, Annals Probab., 2(6):969–988, 1974. Publisher: Institute of Mathematical Statistics.

[12] Xi He, Eric H.Y. Lau, Peng Wu, Xilong Deng, Jian Wang, Xinxin Hao, Yiu Chung Lau, Jessica Y. Wong, Yujuan Guan, Xinghua Tan, et al. Temporal dynamics in viral shedding and transmissibility of COVID-19, Nat. Med/, 26(5):672–675, 2020. Publisher: Nature Publishing Group.

[13] Joel Hellewell, Sam Abbott, Amy Gimma, Nikos I Bosse, Christopher I Jarvis, Timothy W Russell, James D Munday, Adam J Kucharski, W John Edmunds, Fiona Sun, and others. Feasibility of controlling COVID-19 outbreaks by isolation of cases and contacts. The Lancet Global Health, 8(4), e488–e496, 2020. Publisher: Elsevier.

[14] Helena A. Herrmann, Jean-Marc Schwartz, Why COVID-19 models should incorporate the network of social interactions. Phys. Biol., 17(6):065008, 2020. Publisher: IOP Publishing.

[15] Jiwei Jia, Jian Ding, Siyu Liu, Guidong Liao, Jingzhi Li, Ben Duan, Guoqing Wang, Ran Zhang, Modeling the control of COVID-19: impact of policy interventions and meteorological factors. arXiv preprint arXiv:2003.02985, 2020.

[16] Kasthurisamy Jothimani, Kalimuthu Kaliraj, Sumati Kumari Panda, Kotakkaran Sooppy Nisar, Chokkalingam Ravichandran, Results on controllability of non-densely characterized neutral fractional delay differential system. Evol. Eqs. Control Theory, 10(3):619, 2021. Publisher: American Institute of Mathematical Sciences.

[17] K. Kavitha, V. Vijayakumar, Anurag Shukla, Kottakkaran Sooppy Nisar, R. Udhayakumar. Results on approximate controllability of Sobolev-type fractional neutral differential inclusions of Clarke subdifferential type. Chaos, Solitons & Fractals, 151:111264, 2021. Publisher: Elsevier.

[18] K. Kavitha, V. Vijayakumar, R. Udhayakumar, C. Ravichandran, Results on controllability of Hilfer fractional differential equations with infinite delay via measures of noncompactness, Asian J. control, 24(3):1406–1415, 2022. Publisher: Wiley Online Library.

[19] Matt J. Keeling, Ken T.D. Eames, Networks and epidemic models, J. Roy. Soc. Interface, 2(4):295–307, 2005. Publisher: The Royal Society London.

[20] William Ogilvy Kermack, Anderson G. McKendrick, A contribution to the mathematical theory of epidemics, Proc. Royal Soc. London. Series A, Contain. Papers Mathematical Phys. Charact., 115(772):700–721, 1927. Publisher: The Royal Society London.

[21] Xiaofeng Luo, Shanshan Feng, Junyuan Yang, Xiao-Long Peng, Xiaochun Cao, Juping Zhang, Meiping Yao, Huaiping Zhu, Michael Y. Li, Hao Wang, et al. (Eds.), Analysis of potential risk of COVID-19 infections in China based on a pairwise epidemic model, Publisher: Preprints, 2020.

[22] Gianluca Manzo, Complex social networks are missing in the dominant COVID-19 epidemic models, Sociologica 14 (1) (2020) 31–49.

[23] Mark E.J. Newman., Spread of epidemic disease on networks, Phys. Rev. E, 66(1):016128, 2002. Publisher: APS.

[24] Kottakkaran Sooppy Nisar, K. Jothimani, K. Kaliraj, C. Ravichandran, An analysis of controllability results for nonlinear Hilfer neutral fractional derivatives with non-dense domain, Chaos, Solitons & Fractals, 146:110915, 2021. Publisher: Elsevier.

[25] Kottakkaran Sooppy Nisar, V. Vijayakumar, Results concerning to approximate controllability of non-densely defined Sobolev-type Hilfer fractional neutral delay differential system, Math. Methods Appl. Sci., 44(17), 13615–13632, 2021. Publisher: Wiley Online Library.

[26] Yutaka Okabe, Akira Shudo, A mathematical model of epidemics—a tutorial for students. Mathematics, 8(7):1174, 2020. Publisher: Multidisciplinary Digital Publishing Institute.

[27] Yutaka Okabe, Akira Shudo, Microscopic numerical simulations of epidemic models on networks. Mathematics, 9 (9):932, 2021. Publisher: Multidisciplinary Digital Publishing Institute.

[28] Romualdo Pastor-Satorras, Alessandro Vespignani, Epidemic spreading in scale-free networks, Phys. Rev. Lett., 86(14):3200, 2001. Publisher: APS.

[29] Olumuyiwa J. Peter, Amjad S. Shaikh, Mohammed O. Ibrahim, Kottakkaran Sooppy Nisar, Dumitru Baleanu, Ilyas Khan, Adesoye I. Abioye, Analysis and dynamics of fractional order mathematical model of COVID-19 in Nigeria using atangana-baleanu operator, 2021.

[30] Anca Radulescu, Cassandra Williams, Kieran Cavanagh, Management strategies in a SEIR-type model of COVID 19 community spread, Scient. Rep., 10(1):1–16, 2020. Publisher: Nature Publishing Group.

[31] Reza Sameni, Mathematical modeling of epidemic diseases; a case study of the COVID-19 coronavirus. arXiv preprint arXiv:2003.11371, 2020.

[32] Amjad Shaikh, Kottakkaran Sooppy Nisar, Vikas Jadhav, Sayed K. Elagan, Mohammed Zakarya, Dynamical behaviour of HIV/AIDS model using fractional derivative with Mittag-Leffler kernel. Alexandria Eng. J., 61(4), 2601–2610, 2022. Publisher: Elsevier.

[33] Amjad Salim Shaikh, Iqbal Najiroddin Shaikh, Kottakkaran Sooppy Nisar, A mathematical model of COVID-19 using fractional derivative: outbreak in India with dynamics of transmission and control, Adv. Diff. Eqs., 2020(1), 1–19, 2020. Publisher: Springer.

[34] Jiumeng Sun, Wan-Ting He, Lifang Wang, Alexander Lai, Xiang Ji, Xiaofeng Zhai, Gairu Li, Marc A. Suchard, Jin Tian, Jiyong Zhou, et al. COVID-19: epidemiology, evolution, and cross-disciplinary perspectives, Trends Mol. Med., 26(5):483–495, 2020. Publisher: Elsevier.

[35] N. Valliammal, C. Ravichandran, Results on fractional neutral integro-differential systems with state-dependent delay in Banach spaces, Nonlinear Stud. 25 (1) (2018).

[36] V Vijayakumar, Chokkalingam Ravichandran, Kottakkaran Sooppy Nisar, Kishor D. Kucche, New discussion on approximate controllability results for fractional Sobolev type Volterra-Fredholm integro-differential systems of order 1 < r < 2. Numer. Methods Partial Differ. Eqs., 2021. Publisher: Wiley Online Library.

[37] Joseph T. Wu, Kathy Leung, Mary Bushman, Nishant Kishore, Rene Niehus, Pablo M. de Salazar, Benjamin J. Cowling, Marc Lipsitch, Gabriel M. Leung, Estimating clinical severity of COVID-19 from the transmission dynamics in Wuhan, China, Nat. Med., 26(4):506–510, 2020. Publisher: Nature Publishing Group.

[38] Joseph T. Wu, Kathy Leung, Gabriel M. Leung. Nowcasting and forecasting the potential domestic and international spread of the 2019-nCoV outbreak originating in Wuhan, China: a modelling study, The Lancet, 395(10225), 689–697, 2020. Publisher: Elsevier.

[39] Shilei Zhao, Hua Chen, Modeling the epidemic dynamics and control of COVID-19 outbreak in China. Quant. Biol., 8(1):11–19, 2020. Publisher: Springer.

[40] Yong Zhou, V. Vijayakumar, C. Ravichandran, R. Murugesu, Controllability results for fractional order neutral functional differential inclusions with infinite delay, Fixed Point Theory 18 (2) (2017) 773–798.