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Epidemic Spread Analysis in Social Communication Networks With Sir Model

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Abstract: Compartmental mathematical models are frequently used in epidemiology. These models are based on certain assumptions to mathematically model real-life events. However, these assumptions have some limitations. One of these limitations is that they assume that the community is homogeneous, although communities are often heterogeneous. For example, a community may have people or super-spreaders who are not in contact with anyone infected with the virus. In case of limited opportunities, the rate of disease spread can be reduced by vaccinating super-spreaders instead of normal individuals. In the study, centrality values of each individual in the community are determined using a real data set. Vaccinated (immune) and infected individuals are then selected according to certain criteria, and disease spread is simulated. Finally, results are produced using the SIR model, which is the basis of compartmental models. According to the results obtained, the minimum amount of vaccine required to prevent disease spread is calculated. As a result, it was concluded that using the recommended method instead of traditional methods to prevent the spread of disease in the community will result in a 14.39% reduction in vaccine usage.

Sır Modeli ile Sosyal İletişim Ağlarında Salgın Yayılım Analizi

Anahtar Kelimeler
Merkezilik ölçüleri, Sosyal ağ analizi, Topluluk tespiti, SIR modeli

Öz: Bölmeli matematiksel modeller epidemiyolojide sıklıkla kullanılmaktadır. Bu modeller, gerçek hayattaki olayları matematiksel olarak modellemek için belirli varsayımlar üzerine kuruludur. Ancak, bu varsayımların bazı sınırlamaları vardır. Bu sınırlamalardan biri, gerçekte toplulukların genellikle heterojen olmasına karşın, topluluğun homojen olduğunu varsaymalarıdır. Örneğin, bir toplulukta virüs bulaşmış herhangi bir kişiyle temas halinde olmayan kişiler veya süper yayıcılar bulunabilmektedir. Kısıtlı imkanların olması durumunda normal bireyler yerine öncelikle süper yayıcıların aşılanmasıyla hastalık yayılım hızı azaltılabilmektedir. Yapılan çalışmada gerçek bir veri seti kullanarak topluluktaki her bireyin merkezilik değerlerini belirlenmektedir. Daha sonra aşılanmış (bağışıklıklı) ve enfekte olmuş bireyler belirli kriterlere göre seçilmekte ve hastalık yayılımı simüle edilmektedir. Son olarak kompartıman modellerinin temeli olan SIR modelini kullanarak sonuçlar üretilmektedir. Elde edilen sonuçlara göre hastalık yayılımının önlenmesi için kullanılması gereken asgari aşı miktarı elde edilmektedir. Sonuç olarak, toplumda hastalık yayılımını önlemek için geleneksel yöntemler yerine önerilen yöntemin kullanmasıyla aşı kullanımında % 14,39'luk bir azalma sağlayacağı sonucuna varılmıştır.

1. INTRODUCTION

Mathematical models used in the field of epidemiology can produce useful outputs to make predictions about the possibility of emerging diseases turning into epidemics, mortality rate, effectiveness of the measures taken, etc. and to prepare for possible scenarios. The studies that began in 1766 with Daniel Bernoulli's mathematical model of smallpox [1] were first developed by Hamer in 1906, considering the assumption that the number of new

cases depends on the number of infected individuals and the number of individuals susceptible to the disease [2]. In 1911, Ross developed a differential model of the number of cases and epidemic control [4]. The model called SIR (Susceptible – Infectious – Removed / Recovered), created by Kermack – McKendrick in 1927, constitutes the basic logic of compartment models of the spread of infectious diseases in communities by assuming that there is no new individual entry [3]. The SIR model is based on some assumptions such as that community is closed, the population is fixed, individuals are homogeneous, there are no birth or death (except infectious diseases), and the disease is only contagious from person to person. In the studies on the constraints in the SIR model, new models such as SIS, SEIS, SIRS, SEIRS, SEIR, MSIR, MSEIR, and MSEIRS were created. In the Kermack–McKendrick basic epidemic model, it is assumed that each individual is in equal contact. However, in epidemics, it is often observed that there are few "super spreaders" that cause the disease to spread in the community. At the same time, most of the sick individuals do not transmit the disease at all or infect a minimal number of individuals [6]. In the Netherlands, 96% of the population was vaccinated against measles, but in 1999 a 5-person case of measles in a small school turned into an epidemic of 3000 people [7]. In 2003, one of two SARS individuals who traveled to Canada infected five more people in Toronto, causing an outbreak of 200 people in total [8]. The difference in the contact rates of individuals may vary according to their social environment, age, gender, environment, and behavior. This type of heterogeneity can be seen at any scale and in every epidemic. These conditions may cause differences in variables such as contagiousness and susceptibility to the disease [9]. Thanks to such advances, there are studies in epidemiology that focus on individual-based approaches and network modeling to avoid assumptions that are incompatible with real life in order to simplify mathematical equations in compartment models [10, 27]. However, there may be some difficulties in the addition of a dynamic network structure in compartment models [28]. In this study, instead of the assumption that the population structure is homogeneous, a heterogeneous population structure that is more representative of the actual community was used. Basically, in order to prevent the spread of the disease to the maximum extent with the minimum amount of vaccine, the prevention of the spread of the disease was simulated by immunizing the individuals who make up the community according to their degree of centrality in the network.

The study consists of the following sections. In the introduction, basic information about the pandemic, compartment models, constraints, and social networks is given. In the literature review section, studies on the use of compartment models and social networks in the field of epidemiology are included. In the Materials and Method section, the basic SIR model, basic degrees of centrality and calculation methods used in the feature inference of the nodes that make up the networks, and basic information about the data set used in the application are presented. In the findings section, the effects of a total of 7 different infected and immune individual communities on disease spread in networks are presented numerically and visually on the sample data set. In the conclusion section, the contribution of the study to the literature and some limitations are emphasized.

2. MATERIAL AND METHOD

New models such as SIR [5], SEIR ([12] [13][14]), SIRS ([15] [16] [17] [18]), SEIRS ([19][20][21]), MSIR ([22][23][24]), MSEIR [25], etc., which are shown as the basis of compartment models, were created by adding new compartments according to the need. Additionally, efforts have been made to address some of the drawbacks of compartment models. Saeedian et al. [31] believed that individual experiences had a direct bearing on how the epidemic evolved and introduced memory to the SIR basic model to account for these impacts. A fractional SIR model with birth and death rates in heterogeneous complex networks was developed in the paper of Huo and Zao [26]. Studies on the presumption that the population in the models is homogeneous are also available [27]. It was underlined that statically built networks gave inaccurate data concerning infection spread paths compared to dynamic networks in the study by Isella et al. [29] to explore the spreading behavior of diseases in networks. The impact of population structure on infectious diseases has also been the subject of numerous studies [30]. Bansal et al. used heterogeneous network models rather than homogeneous network models in compartment models used in the field of epidemiology to conduct investigations on disease spread variability [27]. There has been researching on how disease knowledge affects the spread of diseases in static networks [32]. Additionally, employing random regular networks on the SIR and SIS models, which serve as the foundation for compartment models, the impacts of network parameters on epidemic propagation were investigated [33]. Olinky and Stone [34] reached the conclusion that the traditional compartment-type models' assumption that the disease will end when the transmission rate falls below a particular threshold is invalid in heterogeneous networks and that the spread of epidemics is correlated with the properties of the networks. A thorough investigation into the dynamic behavior of epidemics in large and diverse networks was carried out by Barthélemy et al. [35].

In addition to the number of nodes and edges, networks can also show different characteristics according to the relationships between nodes. Different studies have been conducted to determine the value of nodes according to their location in networks [36][37][49][50]. Wang et al. proposed a new measure of centrality called effiency centrality (EffC) [38]. The results obtained by simulating the spread of the epidemic in 4 real networks with the SIR model showed that the proposed method was effective and feasible. In the SIR model, it was noted that heterogeneous contact patterns compared to homogeneous scenarios caused earlier and larger outbreaks for a wide range of parameter values, with smaller outbreaks occurring in some parameter combinations [40].

2.1. Material and Method Subheading

2.1.1. Data Set

Data from the 2009 exhibit "Infectious: Stay Away" at the Science Gallery in Dublin were used to create the data set that serves as a representation of the sample population [41]. Visitors to the exhibition were knotted together, and an edge was created to represent the face-to-face contact between these visitors that lasted at least 20 seconds. Many edges between two nodes could signify multiple points of contact between the nodes. Data from the day with the most interactions is present in the network. The data were obtained between the hours of 10.00-14.00, when the interaction was high. Table 1 displays the dataset's basic numerical data.

Table 1. Basic information of the dataset

Property	Value
Node number	410
Number of links	17,298
Median distance	4
p-value	0.8790
Number of unique edges	2,765
Average edge multiplicity	6.2560
Maximum spoke size	410
Average distance	3.5679
Diameter	9

2.1.2. SIR Model

The model, which Kermack and McKendrick introduced to the literature in 1927, includes a total of 3 compartments (Figure 1) [3]. It is presumed that people in the first compartment, S (Susceptible – Sensitive), do not already have the disease but are susceptible to it. People who have the disease, which is present in the S compartment as well and spreads at a consistent rate, go on to the I (Infectious) compartment. The final compartment of the model, R (Removed / Recovered - Death / Immunity), contains individuals from compartment I who have endured the sickness at a constant rate, developed immunity, or perished as a result of the disease.

Figure 1. SIR Model [3]

When developing the SIR model, some presumptions were made. The population is fixed, there is no other cause of death besides birth or disease, those who have developed an immunity to the disease do not relapse, each person spreads the disease equally, and the disease only spreads between people in these situations where society is homogeneous (in terms of age, social position, geography, etc.) and closed to outside influences.

$$\frac{dS(t)}{dt} = -\beta S(t) I(t) \quad (1)$$

$$\frac{dI(t)}{dt} = \beta S(t) I(t) - \gamma I(t) \quad (2)$$

$$\frac{dR(t)}{dt} = \gamma I(t) \quad (3)$$

If the β and γ used in the equations of the SIR model (Equations 1-3) are patient and recovery constant values t, respectively, indicate time [31]. The sum of the values S(t), I(t), and R(t) at any given stage is equal to the population size (N). An important parameter in epidemiology is the parameter R0, which is the basic coefficient of reproduction. It is defined as the average number of secondary cases transmitted by a single infected individual placed in a fully favorable population. In other words, R0 shows us the initial rate of spread of the disease. Therefore, if R0 is > 1, there will be an outbreak, and if R0 is < 1, infected infected persons will recover (or die) before they can replace them with newly infected people. For the SIR model, the value R0 is calculated as in Equation 4:

$$R_0 = \frac{\beta}{\gamma} \quad (4)$$

2.1.3. Graph Analysis

A graph is a type of structure where different objects are represented as nodes and their connections as edges. In the literature, the letter "G" is typically used to symbolize the graph, the letter "V" for the nodes that make up the graph, and the letter "E" for the edges ([42][43]). There are numerous ways to think about the network structure that emerges from a graph illustrating the connections between nodes and edges. He describes the edges that depict the relationship between these nodes as the connection between social beings, in accordance with Wasserman and Faust [44]. In addition, according to Katz et al., the relationship between individuals can represent different structures such as work, friendship, kinship [45]. Centrality criteria is a criterion that is used to specify the degree of importance relative to the interrelationships of the nodes that make up the network structure. Freeman noted that degree centrality could be used to measure information transfer and communication, centrality between to measure mediation status or control of interest, and proximity centrality could be used to estimate the level of efficiency and appropriateness [47][50]. Studies on these centrality measures were based on Freeman ([46], [47], [48]) in the 1970s [49]. The measure of centrality of intervalence [48] and the measure of the centrality of proximity [53] can produce better results with their low calculation cost. Degree Centrality is calculated according to the sum of the relationships of the nodes that make up the network structure directly with each other [50], [51]. It is formulated using the neighborhood matrix ($A = (a_{ij})$) as shown in Equation 5. σ_D degree centrality, j degree centrality is the desired node, n is the total number of nodes in the network, and a_{ij} refers to the distance between i and j nodes in the neighborhood matrix.

$$\sigma_D(j) = \sum_{i=1}^{n} a_{ij} \quad (5)$$

Closeness Centrality is used to specify the total distances of one node to other nodes. The smaller the distance

between one node in the network and the other nodes, the higher the proximity center [44], [52]. The proximity used in the centralization calculation is shown in Equation 6, σ_C closeness centrality, j closeness centrality value is the node to be calculated, n is the total number of nodes in the network, and $d_G(j,i)$ denotes the shortest distance between i and j nodes.

$$\sigma_C(j) = \frac{1}{\sum_{i=1}^{n} d_G(j,i)} \quad (6)$$

Betweenness Centrality In a network, a node's ability to serve as an intermediary and make connections between other nodes who do not already have them is known as centrality. A node must be significant and probably have a high Betweenness Centrality if it discovers the only path via which other nodes such as communication, connectivity, transportation, or transaction must travel [46]. The Betweenness Centrality is used to calculate the centrality shown in Equation 7 σ_B the Betweenness Centrality, j is the node whose Betweenness Centrality value is to be calculated, n is the total number of nodes in the network, g_{ix} is the shortest distance between nodes i and x, and the $g_{ix}(j)$ denotes the shortest distance between nodes i and x that passes through node j.

$$\sigma_B(j) = \sum_{i=1, i\neq j}^{n} \sum_{x=1, x<i, x\neq j}^{n} \frac{g_{ix}(j)}{g_{ix}} \quad (7)$$

3. RESULTS

Using the community network obtained using the sample dataset shown in Figure 2 to demonstrate the importance of the degree of centrality of the nodes in the networks representing the community in the disease spread, the nodes with the characteristics of 41 nodes infected and 41 nodes with immune characteristics, which is 10% of the total population, are selected before determining the input parameters to the SIR model. Then, if the nodes selected as infected transmit the disease instantly, the total number of infected individuals is reached at the end of the exhibition. The 41 randomly infected nodes in State 1, State 2, and State 3 are the same. The 41 randomly selected nodes in State 1, State 4, and State 5 are the same.

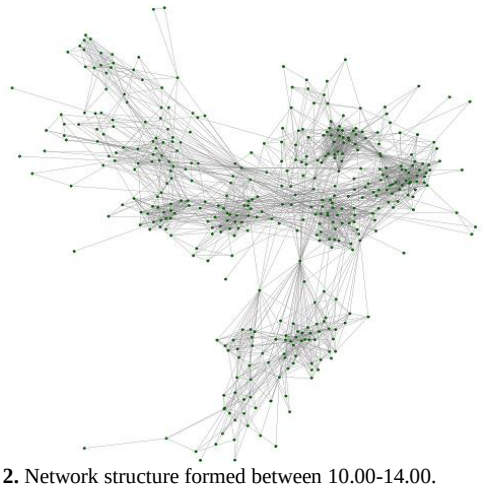

Figure 2. Network structure formed between 10.00-14.00.

The numerical values of the infected individuals obtained as a result of the simulation of the sample cases are shown in Figure 3.

Table 2. Selection patterns of nodes used in the sample cases

Cases	Infected node selection method	Recovered node selection method
Case 1	Random	Random
Case 2	Random	Closeness Centrality
Case 3	Random	Betweenness Centrality
Case 4	Closeness Centrality	Random
Case 5	Betweenness Centrality	Random
Case 6	Closeness Centrality	Betweenness Centrality
Case 7	Betweenness Centrality	Closeness Centrality

In Case 1, infected and recover nodes are randomly selected in the network. Then, as a result of the spread of the disease to the nodes that are infected throughout the exhibition and the nodes that do not have immune characteristics and then infects the other nodes with which the nodes that are infected with the disease interact, the number of 41 infected individuals, which initially corresponds to 10% of the total population, reached 294 at the end of the exhibition, infecting approximately 72% of the population. In Case 2, infected individuals were randomly selected. The top 41 individuals with the highest proximity centrality value were selected as immune. In this case, the number of infected individuals reached 291 at the end of the exhibition, infecting about 71% of the population. In Case 3, infected individuals were randomly selected. The first 41 individuals with the highest centrality values among them were selected as immune. In this case, the number of infected individuals reached 280 at the end of the exhibition, infecting about 68% of the population.

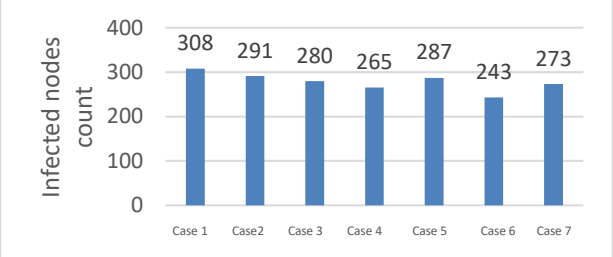

Figure 3. Infected individual values from cases

In Case 4, infected individuals consisted of the top 41 individuals with the highest closeness centrality value. Immune individuals were randomly selected. In this case, the number of infected individuals reached 265 at the end of the exhibition, infecting about 64% of the population. In Case 5, the top 41 individuals with the highest betweenness centrality value among infected individuals were selected. Immune individuals were randomly selected. In this case, the number of infected individuals reached 287 at the end of the exhibition, infecting 70% of the population. In Case 6, infected individuals consisted of the top 41 individuals with the highest closeness centrality value. The group of immune individuals consists of the top 41 individuals with the highest betweenness centrality value among them. In this case, the number of infected individuals reached 287 at the end of

the exhibition, infecting approximately 59% of the population. Finally, in Case 7, the top 41 individuals with the highest centrality value among infected individuals were selected. The group of immune individuals consists of the top 41 individuals with the highest value of closeness centrality. In this case, the number of infected individuals reached 273 at the end of the exhibition, infecting about 66% of the population.

Table 3. Percentage infected distribution rates

%	Case 1	Case 2	Case 3
10	71,71	70,98	68,29
20	61,95	60,24	56,83
30	50,98	48,05	46,34
40	43,17	36,83	33,66
50	35,37	29,51	20,98
60	27,80	20,00	14,15
70	21,22	14,15	8,78
80	13,66	7,80	4,39
90	9,27	2,93	1,95

In Table 3, when vaccination is carried out, the changes in the ratio of infected individuals to the total population as a result of the percentage of vaccinated are shown if the people to be vaccinated are randomly selected (Case 1) and if they are made by taking into account centrality criteria such as betweenness centrality values (Case 3) and closeness centrality values (Case 2) according to their location in the network. As can be seen in Table 3, in case 10% of the randomly selected individuals from the total population are immunized by administering vaccine, the randomly selected 10% infected individuals infect approximately 71% of the total population at the end of the exhibition.

Table 4. Differences between percentile results for situations

%	Case 1 - Case 2	Case 1 - Case 3	Case 2 - Case 3
10	0,73	3,41	2,68
20	1,71	5,12	3,41
30	2,93	4,63	1,71
40	6,34	9,51	3,17
50	5,85	14,39	8,54
60	7,80	13,66	5,85
70	7,07	12,44	5,37
80	5,85	9,27	3,41
90	6,34	7,32	0,98

In case 2, in the same conditions, it is seen that if the 41 individuals with the highest closeness centrality value corresponding to 10% in the total population are immunized by administering vaccine, the randomly selected 10% infected individual infects approximately 70.98% of the total population at the end of the exhibition. In case 3, if the 41 individuals with the highest betweenness centrality value of 10% of the total population are immunized by administering the vaccine under the same conditions, the randomly selected 10% infected individual infects approximately 70.98% of the total population at the end of the exhibition. In Table 4, the largest difference between the 3 cases is 14.39% of the 50% vaccination rate between Case 1 and Case 3. According to this result, if 205 individuals, corresponding to 50% of the total population, are randomly selected and immunized by being vaccinated, 41 infected individuals, of which 10% are randomly selected at the beginning, infect 35.37% of the total population at the end of the exhibition. If 205 individuals, corresponding to 50% of the total population, are selected from among the individuals with the highest intervalence centrality value instead of randomly, 41 infected individuals of 10% randomly selected at the beginning infect 20.98% of the total population at the end of the exhibition. The largest proportional difference between the criteria of intervalence and closeness centrality is seen in the vaccination rate of 8.54% and 50%. It is seen that if the betweenness centrality values are used instead of the closeness centrality values as the selection criterion of individuals corresponding to 50% of the total population, the infection spread rate will be 8.54% less.

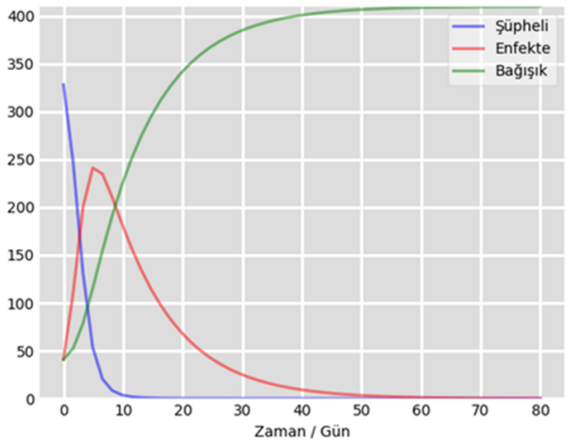

Figure 4. SIR model output

Covid-19 spread analysis was performed by applying the SIR model to the existing data set and the result graph is shown in Figure 4. Studies show that the R0 value varies between 2.2-2.6 ratio. The disease is transmitted from person to person through cough or sneeze droplets. The incubation period from the person's exposure to the virus lasts 2-14 days [55][56][57]. SIR is one of the model parameters (value is 1 / 14, (value is 1.2, S value is 410, I and R values are 41. When the result graph is examined, the number of infected patients reaches its peak with approximately 250 individuals infected in the first 10 days and then shows that the spread will decrease and end in an average of 50 days.

4. DISCUSSION AND CONCLUSION

As a result of the studies carried out, compartment-type estimation models frequently used in the field of epidemiology have limitations [28] and one of the most important of these limitations is the assumption that all the individuals constituting the society have the same characteristics [27][41]. In real life, it is seen that the individuals who make up the society have different characteristics such as profession, age, education, social environment and these characteristics have a significant impact on the spread of the disease. Today, it is necessary to use the assets in the best way for the rapid solution against the infectious diseases that develop suddenly and spread to many parts of the world at a level that can be called a pandemic. A vaccine is used as the primary treatment method to prevent and control infectious diseases that have rapidly reached the level of a pandemic. In the absence of existing solutions in new pandemics,

vaccine development studies gain importance. For example, the time it took to find the first vaccine and control the disease was approximately one year during the most recent Covid-19 pandemic [39]. Two years after the first effective vaccine is available, access to the vaccine is still limited in some countries. In this case, it is also important that the vaccines obtained are used systematically and consciously in order to control the spread of the pandemic in countries with limited access to vaccines due to economic reasons. With this awareness, many countries have developed different strategies to use the available vaccines effectively and efficiently by identifying priority groups in vaccination. In the study, sample cases were simulated on the selection of individuals to be vaccinated. According to the results obtained, the rate of infected individuals is 14.39% less if the individuals to be vaccinated are selected according to their degree of centrality instead of being randomly selected. Considering the population of Turkey, it means that approximately 12 million vaccines are used less and financial savings in order to stop the spread of the epidemic.

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