

EPIDEMIC SPREADING IN GEOMETRIC NETWORK WITH MOBILE AGENTS

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In recent time, an infectious disease spreads by making the contact with the infected agent in a population. This contact may be affected by the movement of the infected agents in any geographical region. Most of the studies are done by considering underlying static network topology. The movement of agents is important to consider the underlying network topology, which in this work is assumed random. Therefore, a new model is desired to analyze the spreading behavior of infected disease due to the random movement of infected agents. In this paper, we propose a geometric network with mobile agents by considering the random movement of some fraction of the nodes, while remaining nodes are stationary. Dynamics of epidemic spreading is studied using the SIS and SIR models. A rest time t_{rest} of an agent is introduced during its movement, and its effect on the epidemic is studied. We simulate the modified epidemic model on underlying network topologies of the geometric network with mobile agents. It represents the real-world scenario, where agents constantly create new connections with their movements in their regions. We also evaluate our model using real dataset from Brightkite. The simulation results are in accordance with our theoretical findings which show that the random geometry of the agents, as well as the t_{rest} , affect dynamics of epidemic spreading. The simulation on the dataset also shows the effectiveness of our proposed framework.

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1. Introduction

As technological development increases, it leads to the new class of problems for which solutions are thought not trivial due to the complexity of the system, *e.g.*, complex networks, random geometric network *etc.* Nowadays

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many phenomena and incidents have been modeled as a network to analyze the behavior of the system, *e.g.*, rumor spreading, epidemic spreading, opinion dynamics [1, 2]. In recent time, many phenomena and incidents are modeled as a network to analyze the behavior of the system [3]. Epidemic spreading can also be analyzed by using the concept of a complex network [4]. The relationship between the dynamics of epidemic spreading and the structure of the underlying network is crucial in many real cases, such as the spreading of worms in a computer network, viruses in a human population, or rumors in a social network [5, 6]. Recently, we have seen a panic situation due to random virus attack on the technological network, and Zika and Ebola viruses spread in the human population due to the human movement from one location to another. In the human population network, agents may be mobile due to their respective velocities and affect the epidemic spreading in a given spatial region. The epidemic spreading in human population may be modeled by considering random geometry of the nodes in which a change of position is non-uniform as each node moves with unequal velocity. A human makes connections with another human when both come under the vicinity of connectivity radius of each other. Most of the time, infected nodes can be immunized and become susceptible again and then infected.

One of the important questions that may be raised for the spreading process of the viruses in the complex network is how epidemics spread in a random geometric network with mobile nodes. Various researches were proposed with different facts of the virus spreading problem [7–9]. Human interactions among individuals determine the properties and the behavior of a human connection network. These types of interactions give rise to various ecological networks and their mathematical representations as graphs. We use the network for epidemic propagation in the human population.

In recent years, a lot of techniques and methods have been developed by using mean-field theories that show new quantitative understanding of the dynamics of epidemic processes in networks [7]. Therefore, researchers need to focus on exploring the geometric network with mobile agents to model the epidemic spreading in human population.

In this paper, we propose a network model with mobile nodes, based on random waypoint mobility [10]. In random waypoint mobility, the topology of the network is updating due to a random change of position of nodes against the time. Therefore, it may also be called geometric network with mobile nodes (GNMN) as geometry of the nodes is changing with the random movement of the nodes. It is also important to study the epidemic spreading over this GNMN. Here, any infected node should stay for some time to infect the neighboring nodes in the given connectivity region r . If infected mobile nodes will not stay for some time, then they may not be affecting

the neighboring nodes in their connectivity region r . Therefore, an infected node i affects the susceptible nodes in the given connectivity region r if it stays for a time, t_{rest_i} , during its movement. In this work, it is also studied how this t_{rest_i} time effects epidemic spreading over the network with moving nodes. The main contribution of the work may be summarized as:

1. Every node in the population of the network may exist in any of the states: (a) static, (b) moving with $t_{\text{rest}} = 0$, and (c) moving with t_{rest} . The connections between them are established only during the rest condition of the respective nodes. The mobile nodes cannot establish connections in any case.
2. t_{rest} plays an important role in the epidemic spreading. Structure of the geometric network depends upon the velocity of a nodes V and its rest time t_{rest} , respectively. Velocity V and t_{rest} affect the number of neighbors of a node with which it will make connections in the given region and which it may infect as shown in Fig. 1.

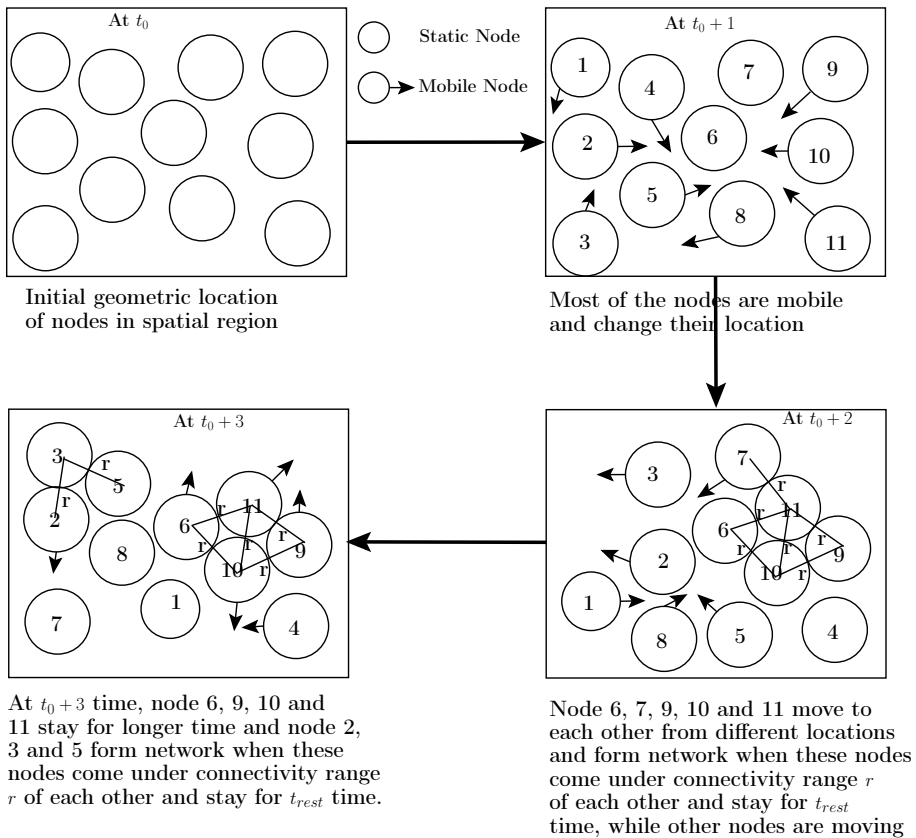


Fig. 1. Mobility and interaction with nodes.

Time of rest, t_{rest} , plays a crucial role in the network formation. The structure of network depends upon the velocity of the nodes, V , its rest time, t_{rest} , and connectivity region, r , respectively. The velocity V affects the number of neighbors of a node by which it will make connections with the other nodes and which it may infect. If t_{rest} increases then the average degree of network is increased. By considering the GNMN, we find out the various properties of the network as degree distribution, average degree $\langle K \rangle$ and clustering coefficient for the proposed model. We also simulate the epidemic models SIS and SIR for multiple instances of the network to show the spreading of disease in the human population. The dataset of human movement is used provided by SNAP [11] to generate a human connection network in the spatial region. After that epidemic models SIS and SIR are evaluated on the human connection network to validate our proposed model.

The remainder of this paper is organized as follows: Section 2 explains the related work regarding the traditional disease model and underlying network topology. Section 3 describes the proposed methodology. This section explains “how the nodes move from one location to another and make contacts with others”. Section 4 presents a simulation and result analysis. In this section, simulations leading to the result for the proposed model for the number of times are performed. Finally, Section 5 describes the conclusions and outlines of future work.

2. Background and related work

In this section, we discuss two streams of relevant literature at the intersection of which our work lies. First, we explore the literature of human movement and their contact network. After that, we describe the epidemic spreading process by considering different types of underlying networks.

There are many factors that provoke the human movement such as job, medical facility, outing, *etc.* This kind of a human movement takes place in predefined geographical region. Human movements are generally modeled by using random walk or diffusion-based concept [12, 13]. Viswanathan *et al.* [14] proposed the model by analyzing the monkeys and marine predators movement and explained it as a Lévi flight. However, a problem with this model is that it assumes a human must have long-range connection that is not true, even some animal movements do not follow the Lévi flight [15]. Bettstetter *et al.* [10] proposed a random waypoint mobility model for wireless *ad hoc* networks in which human can connect to the nearest sink to transfer the data. In this model, connections can be established even if human is moving that also is not true. González *et al.* [16] proposed a hybrid model by combining the Lévi flight with random walk to describe the human movement. Again, this model needs some improvement as connection establishment cannot take place in moving condition, that will help to find the epidemic spreading due to a local contact. In the course of research

and development, Anderson and May, Kermack and McKendrick [8, 17] defined the modern mathematical approach of infectious diseases. In recent years, researchers and scientists are working on the real-world accuracy of the models used in epidemiology by the integration of large-scale data sets and the explicit simulation of entire populations down to the scale of single individuals. These models have gained importance in the public health domain, especially in infectious disease epidemiology. Many researchers are supporting the use of these models as real-time ones [18, 19]. At the center of all epidemic, modeling strategies consider the structure of human interactions, mobility, and contact patterns that help to represent it in the form of network.

The epidemic process is network-driven so it requires the understanding of the interactions between epidemic processes and networks [20]. Traditional epidemic disease models are called compartmental models, in which the population is divided into compartments. Recently, extensive researches exposed that the most real-world networks are dynamic, self-organized and heterogeneous. Singh *et al.* [21] proposed a method to find the influential nodes in the networks by considering structural centrality. Based on this, authors studied the robustness of network using targeted attack. Singh *et al.* [22] studied the rumor spreading and inoculation strategy in networks. They derived the critical inoculation value for targeted inoculation and random inoculation. Kumar *et al.* [23] presented an immunization technique in which highly connected neighbors of overlapping nodes are immunized in the network. Arquam *et al.* [24] propose a delayed SIR model that consider the delay in the infection process. They derive the critical threshold of infection using various underlying network structures. Singh *et al.* [25] studied the impact of degree-degree correlation on the rumor dynamics and on the inoculation strategies in the scale-free networks. Authors suggested that a rumor threshold in random inoculation scheme is greater than the rumor threshold in the proposed model without any inoculation scheme.

Vespignani *et al.* [4] proposed the epidemic spreading model on the scale-free network to analyze the absence of epidemic threshold and its associated critical behavior. Their proposal was based on computer virus spreading on communication and social networks. Moreno *et al.* [2] presented a new epidemiological framework characterized by a highly heterogeneous response of the system to the introduction of infected individuals with different connectivity considering the underlying scale-free network. In this course of development, Singh *et al.* [26] proposed the nonlinear spread of the rumor by introducing two parameters named nonlinear exponent and degree-dependent tie strength exponent in the SIR model. Arquam *et al.* [27, 28] presented a modified SIR model, integrating temperature and considering both types of network as homogeneous network as well as heterogeneous network. Authors derived the basic reproduction number for both types of networks.

Barthélemy *et al.* [20] presented the model that shows the effect of the connectivity pattern of complex networks on the propagation dynamics of epidemics with a network degree fluctuation, signaling that spreading of epidemics takes place almost instantly in scale-free networks. Mickens *et al.* [29] proposed a probabilistic queuing method that explains the spreading of the virus in the mobile environment in which they consider only the spreading during mobility. There are many types of research done for epidemic spreading by considering a spatial network with a different measure as a proximity network [30], while Lang *et al.* [31] proposed an analytical model for SIR disease spread on the random spatial network. Buscarino *et al.* [32] show the effect of the mobility of node on epidemic spreading by considering the Lévy flight model for human movement. Therefore, researches on epidemic spreading are mostly done on the spatial network by considering only moving nodes. Blyuss [33] proposed a model considering traveling of a node between 1-dimensional regions (migrating model) without movement. He has not considered any underlying network. Enright and Kao [34] studied the epidemic spreading on dynamic network considering underlying temporal network, where the underlying networks are formed with the appearing and disappearing of the link with some rate against the time. They have not considered any parameters for the network formation.

Due to stochastic, the connecting process of the nodes shows the large-scale variations, clustering, and communities, characterizing the connectivity patterns of real-world systems [35, 36]. Hence, intensive research is required for these stochastic processes on the network by considering the mathematical and computational model [37]. There are two most studied network models named random graph and random geometric graph.

- I. **Random graph:** Classical random graph was proposed by Erdős and Rényi [38]. A random graph is created when a node is connected with another node with connecting probability. It is represented by $G(N, p)$, where N is the number of nodes and p is connection probability.
- II. **Random geometric graph:** A random geometric graph (RGG) is created by randomly distributed nodes in the space and two nodes are connected if the distance between two nodes is in a given range, called connectivity region. A random geometric graph (RGG) [39], denoted $G(N, r)$, is an undirected graph created by randomly distributed N nodes in the space and two nodes are connected if the distance between two nodes is in a given range r .

3. Proposed methodology

The random geometric graph is not able to explain how the positions of nodes are changing randomly and a change of positions may be uniform or non-uniform. Based on this assumption, Bettstetter *et al.* [10] proposed random waypoint mobility model in which each node of the network may exist in any of the following three categories in the population: (a) static, (b) moving, and (c) rest during movement. This model was used mainly in wireless routing, in which cellular node changes its position due to its mobility. On the other hand, static components are also connected with each other in human mobility — the connection cannot be established between moving nodes. Therefore, it is proposed that connections are established between nodes when they are in a static state or in the rest position during movement as mentioned in Fig. 1. Here, the node is not making any connection with other nodes while it is moving. Topology changes when a node moves to other geometric location and makes contact with other neighboring nodes within connectivity region r of each other and within a given time interval.

3.1. Node distribution of GNMN

Let us consider N nodes uniformly distributed over a two-dimensional space/region $[0, a] \in \mathbb{R}^2$. Some nodes in this region may choose a new destination point during the course of movement with velocity V . The velocity is random for every moving node, and a node moves in any direction. The node moves from one random point to another in a given spatial region. Let two random points (X_1, Y_1) and (X_2, Y_2) be i.i.d. in the region $[0, a]$ and their difference be also i.i.d. Therefore, the expected distance between two random points is derived as [10, 40]

$$E[d] = \int_0^a \int_0^a \int_0^a \int_0^a \sqrt{(X_1 - X_2)^2 + (Y_1 - Y_2)^2} dX_1 dX_2 dY_1 dY_2. \quad (1)$$

The expected distance is the quadruple integral of the distance formula. It is nontrivial to find. First, we simplify it into two random variables by focusing on a variable for the x -distance as $|\Delta X|$ and a separate one for the y -distance as $|\Delta Y|$, where $|\Delta X| = X_1 - X_2$ and $|\Delta Y| = Y_1 - Y_2$ [41] (Fig. 2). Therefore, the pdf of $|\Delta X|$ and $|\Delta Y|$ is defined as

$$f_{\Delta X}(x) = \begin{cases} 2(a-x), & 0 \leq x \leq a \\ 0 & \text{otherwise} \end{cases}, \quad (2)$$

$$f_{\Delta Y}(y) = \begin{cases} 2(a-y), & 0 \leq y \leq a \\ 0 & \text{otherwise} \end{cases}. \quad (3)$$

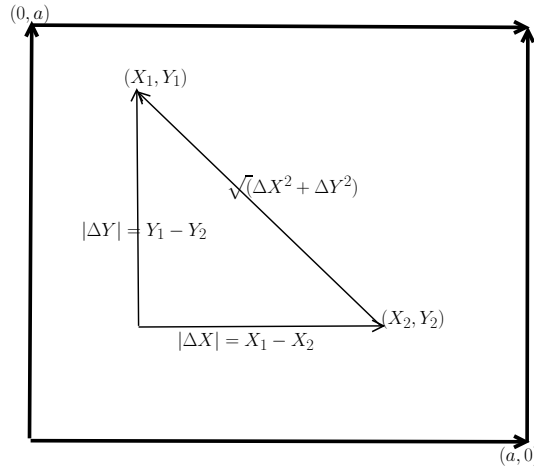


Fig. 2. Distance between the points (X_1, Y_1) and (X_2, Y_2) is given by $\sqrt{(X_1 - X_2)^2 + (Y_1 - Y_2)^2}$.

The expected distance between two random points is calculated by multiplying pdfs mentioned in Eq. (3), and the integral becomes the following [42]:

$$E[d] = \int_0^a \int_0^a 4(a-x)(a-y) \sqrt{x^2 + y^2} dx dy. \quad (4)$$

Therefore, the expected distance $E[d]$ between any two random points in two-dimensional area $[0, a] \in \mathbb{R}^2$ is given by $0.521 \times a$ [10]. When any node reaches the destination point, then there is a chance that it will rest for a certain time, t_{rest} , and again start moving (Fig. 3). The transmission of epidemic takes place through an infected moving node, when it will stay for some time, t_{rest} .

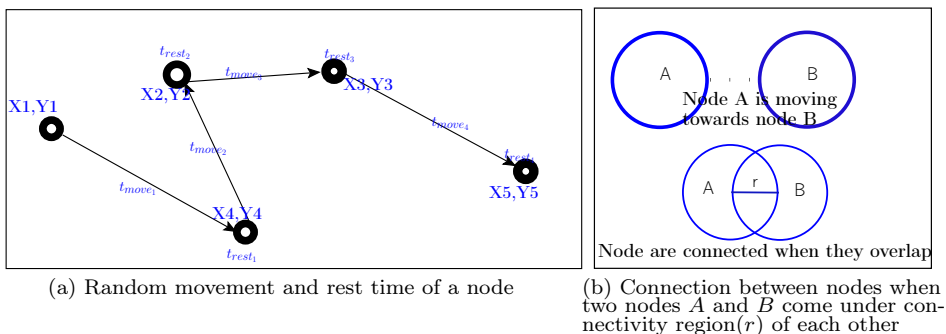


Fig. 3. Mobility and connectivity pattern of a node in geometric space in the Random Mobile Network Model.

A node may remain in the stationary state with a probability, p_{stat} . Therefore, $(1 - p_{\text{stat}})$ is the probability of a node to be in the mobile state. An example is when some fraction of humans is spread in a given geographical region by using some communicating mediums or stays at a fixed location. It is important to define the spatial distribution of the nodes in a network. In the proposed model, the movement of nodes is considered to be Brownian [43]. In the Brownian motion, a particle moves in any direction with random velocity, likewise, human mobility is also in any direction with random velocity. In this mobility model, the mobility of each node is independent of the others, and nodes move with the random velocity V . The duration of the movement time of the node, represented by t_{move} , depends on the distance between the starting and ending point of the movement and the velocity of a moving node, as shown in Fig. 4.

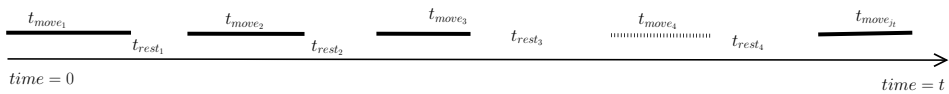


Fig. 4. Movement of a node from a source to destination and how a node changes from the moving state to rest state.

Hence, expected movement time is $E[t_{\text{move}}] = \frac{E[d]}{E[V]}$. Let $m(t)$ denote the total number of movement completed just before time t , where t is very large, and t_{move_j} denotes the duration of j^{th} movement of a node with velocity V , therefore, probability that any node is resting at time t_{rest} is given by

$$p_{\text{rest}} = \lim_{t \rightarrow \infty} \frac{\sum_{j=1}^{m(t)} \frac{t_{\text{rest}}}{t_{\text{rest}} + t_{\text{move}_j}}}{m(t)}. \quad (5)$$

By the law of large numbers,

$$\begin{aligned} p_{\text{rest}_i} &= \lim_{t \rightarrow \infty} \frac{t_{\text{rest}} \sum_{j=1}^{m(t)} \frac{1}{t_{\text{rest}} + t_{\text{move}_j}}}{m(t)} \\ &= \lim_{t \rightarrow \infty} \frac{t_{\text{rest}} \left(\left(\frac{1}{t_{\text{rest}} + t_{\text{move}_1}} \right) + \left(\frac{1}{t_{\text{rest}} + t_{\text{move}_2}} \right) + \dots + \left(\frac{1}{t_{\text{rest}} + t_{\text{move}_{m(t)}}} \right) \right)}{m(t)} \\ &= \lim_{t \rightarrow \infty} \frac{t_{\text{rest}} m(t) \frac{1}{t_{\text{rest}_i} + E[t_{\text{move}}]}}{m(t)} \\ &= \frac{t_{\text{rest}}}{t_{\text{rest}} + E[t_{\text{move}}]}, \end{aligned}$$

$p_{\text{rest}} = \frac{t_{\text{rest}}}{t_{\text{rest}_i} + \frac{E[d]}{E[V]}}$, where, $E[t_{\text{move}}] = \frac{E[d]}{E[V]}$. Hence, spatial distribution of nodes moving in $\mathbb{R}^2$ with a parameter p_{stat} , t_{rest} and velocity V_i is given by random waypoint mobility model [10].

The node may be in any state either in static or in moving state. Initially, all nodes are static as geometric locations are assigned to nodes. After that, certain nodes start moving. Hence, the node distribution in geometrical region has three components: static, rest and mobile. The static component f_{stat} can be determined from the initial uniform distribution by observing that a node remains static with probability p_{stat} . Thus, we have $f_{\text{stat}}(x, y) = p_{\text{stat}} \times f_{(X,Y)}(x, y)$ independent of the time t at which the node is static. If p_{stat} is the probability of a node to be static, then probability of a node to be in rest during movement will be $(1 - p_{\text{stat}})p_{\text{rest}}$. Hence, probability of the moving node is $(1 - p_{\text{stat}})(1 - p_{\text{rest}})$. Then distribution of a node to be mobile is dependent on probability of a moving node. Hence, the combined node distribution is given as

$$f_{X,Y}(x, y) = \begin{cases} \underbrace{p_{\text{stat}} \times f_{(X,Y)}(x, y)}_{f_{\text{stat}}} + \underbrace{(1 - p_{\text{stat}})p_{\text{rest}}}_{f_{\text{rest}}} & X, Y \in [0, a] \\ + \underbrace{(1 - p_{\text{stat}})(1 - p_{\text{rest}}) 36 \frac{xy}{a^4} \left(1 - \frac{x}{a}\right) \left(1 - \frac{y}{a}\right)}_{f_{(X,Y)_{\text{move}}}(x, y)} \\ \underbrace{\hspace{10em}}_{f_{\text{move}}} \\ 0 & \text{otherwise.} \end{cases} \quad (6)$$

The component f_{stat} gives the pdf of the stationary component, while the component f_{move} gives the pdf of the mobile component. The pdf defined in Eq. (6) reflects the spatial structure of the real-world problem of human movement. We assume that during the movement any node cannot spread the epidemic while it comes within a connectivity region (r) of other nodes also called connecting radius. Therefore, we are not considering any connection during the movement of nodes. The probability of a node to be within the connectivity region, r , with respect to another random node during movement, when any node i is at location (x_i, y_i) is

$$\Pr_M(x_i, y_i) = \int_{y_i-r}^{y_i+r} \int_{x_i-\sqrt{r^2-(y-y_i)^2}}^{x_i+\sqrt{r^2-(y-y_i)^2}} f_{X,Y_{\text{move}}}(x, y) dx dy. \quad (7)$$

We are not considering the edges created during movement of nodes. Hence, the probability of a node to be within connectivity region, r , with respect

to another random node when node is static is

$$\Pr_s((x_i, y_i)) = 1 - \Pr_M(x_i, y_i). \quad (8)$$

The probability of having k neighbors of a node at location (x_i, y_i) is calculated as

$$\Pr(x_i, y_i, k) = \binom{N-1}{k} (\Pr_s(x_i, y_i))^k (1 - \Pr_s(x_i, y_i))^{N-k-1}, \quad (9)$$

where k is the degree of a node while a node is in static or in rest during the movement of a node with random geometry, where $k \in [0, N-1]$. If a node is moving for a time span, its degree is kept changing with its motion. The average probability of a node over the entire area that a node has k neighbors is

$$\Pr(k) = \frac{\int_0^a \int_0^a \Pr(x_i, y_i, k) dx dy}{A}, \quad (10)$$

where area $A = a^2$. Only those nodes participate in creating network that are either in rest or in the static state within a given time interval. Hence, the topology of network existing in the given spatial region keeps changing against the time. The method to create GNMN is given in Algorithm 1, in which we choose N nodes uniformly distributed in the two-dimensional geometrical region $(a \times a)$. Certain nodes are static with probability p_{stat} . Contacts are created when a node is in a static state and other nodes are in the connectivity region of the static node. The geometry of nodes is changed by the movement of nodes from one location to another.

3.2. Epidemic spreading in GNMN

The spread of infectious disease is a complex phenomenon depending on various interacting factors such as environment in which the pathogen and hosts are living that may help in growth of pathogens, population density exposed that may have high probability to get infected, inter- and intra-dynamics of the population that causes the spread of disease from one to other location. The two most widely studied models are: (i) susceptible–infected–recovered (SIR) [17] and (ii) susceptible–infected–susceptible (SIS) models [44]. The theoretical approach of the epidemiological model is based on the compartmental concept, in which the whole population is categorized into compartments. In SIR model, there are three compartments: (i) Susceptible (S), (ii) Infected (I), and (iii) Recovered (R), while in SIS there are only two compartments — Susceptible (S) and Infected (I). Individuals in the susceptible compartment represent the group of healthy persons that can be infected when getting in contact with infected persons. If a person

Algorithm 1: Algorithm to create GNMN

Input: Number of nodes (N), velocity (V), time of rest (t_{rest}), connectivity region (r), p_{stat} , time of movement (t_{move}), dimensions ($a \times a$) $\in \mathbb{R}^2$, d is the travel distance of a node when it is moving

Output: Network (G) is created

Method:

$two_dim = \text{len}(\text{dimensions})$, $positions = \text{empty}(N, two_dim)$;
 $u = \text{empty}(N, two_dim)$;

while ($True$) **do**

while ($i \leq N$) **do**

$X_1, Y_1 = \text{Current position of nodes}$;

$X_2, Y_2 = \text{Next position of nodes}$;

$d = 0.521 * a$;

$t_{\text{move}} = \frac{d}{V}$;

$p_{\text{rest}} = \frac{t_{\text{rest}}}{t_{\text{rest}} + t_{\text{move}}}$;

$q_0 = p_{\text{rest}}$;

if ($d \neq 0$ $\&\&$ $q_0 = 0$) **then**

 Node is moving ;

break ;

else

$positions[i] = X_1, Y_1$;

$New_positions[i] = X_2, Y_2$;

 if a node stays at any position during movement from
 (X_1, Y_1) to (X_2, Y_2) ;

$u = \text{rand}(*positions.shape)$;

u is the position of a node during movement between
 (X_1, Y_1) and (X_2, Y_2) ;

$positions = u * positions + (1 - u) * New_positions$;

 To find contacts ;

while ($j \leq \text{length}(positions)$) **do**

$l = \sqrt{((y - y[j])^2 + (x - x[j])^2)}$;

l is the distance between position of two nodes ;

if ($l \leq r$) **then**

 contacts is created ;

$j++$

gets infected, it is transferred into the infected compartment. Finally, after recovery, an infected person is moved into the recovered compartment, which cannot be further moved into another compartment. Susceptible nodes may be infected with the rate of β , while infected nodes become recovered with the rate of μ , where $\beta, \mu \in [0, 1]$. Human's behavior, *e.g.*, mobility pattern and their social interactions, cannot be captured by the available classical epidemiological models alone. We are using the SIS and SIR models to generalize the epidemic spreading in the human population considering the GNMN. As already explained in the available literature, epidemic outbreak happens when the infection rate, β , exceeds the recovery rate μ [4].

3.2.1. SIS model

The rate equation for the basic SIS model without considering the network topology, if the number of nodes in population is N , then the fraction of susceptible is represented by S and the fraction of infected node by I [44] reads

$$\frac{\partial S}{\partial t} = -\beta SI + \mu I, \quad (11)$$

$$\frac{\partial I}{\partial t} = \beta SI - \mu I. \quad (12)$$

Let us consider a node is moving in a region where many other nodes exist. Any node i takes rest for t_{rest} time during its movement from the source to next points during t_{move} time. A node will transmit the infection to its neighbors created during t_{rest} time in the course of the movement. Moving nodes cannot make interactions with other nodes. Therefore, infection rate of a node at t_{rest} time will be $\beta k \text{Pr}(k) t_{\text{rest}}$. Let N_1 nodes be in rest during movement, where $N_1 = N(1 - p_{\text{stat}})p_{\text{rest}}$. Total infection rate will be $\sum_{k=1}^{N_1-1} \beta k \text{Pr}(k) t_{\text{rest}}$. Based on these assumptions, epidemic spread, if the following condition occurs, is given as

$$\sum_{k=1}^{N_1-1} \beta k \text{Pr}(k) t_{\text{rest}} > \mu t_{\text{rest}}.$$

In this duration, infected nodes will come out with their infectious contact. Applying the network parameter into equations (11), (12), we obtain

$$\frac{\partial S}{\partial t} = -\beta k \text{Pr}(k) t_{\text{rest}} SI + \mu I t_{\text{rest}}, \quad (13)$$

$$\frac{\partial I}{\partial t} = \beta k \text{Pr}(k) t_{\text{rest}} SI - \mu I t_{\text{rest}}. \quad (14)$$

Equations (13) and (14) give the rate of change in susceptible and infected populations respectively. Based on this model, simulation has been done and the result is concluded.

3.2.2. SIR model

The rate equation for the SIR model without considering the network topology, if the number of nodes in population is N , then $S + I + R = 1$, where S , I , and R are the fraction of susceptible, infected and recovered population, respectively, is as follows:

$$\frac{\partial S}{\partial t} = -\beta S(t)I(t), \quad (15)$$

$$\frac{\partial I}{\partial t} = \beta S(t)I(t) - \mu I(t), \quad (16)$$

$$\frac{\partial R}{\partial t} = \mu I(t), \quad (17)$$

$$\frac{\partial S}{\partial t} = -\beta k \text{Pr}(k) t_{\text{rest}} SI, \quad (18)$$

$$\frac{\partial I}{\partial t} = \beta k \text{Pr}(k) t_{\text{rest}} SI - \mu I t_{\text{rest}}, \quad (19)$$

$$\frac{\partial R}{\partial t} = \mu I t_{\text{rest}}. \quad (20)$$

Equations (18), (19) and (20) give the rate of change in susceptible, infected and recovered populations, respectively. Based on this model, simulation has been done and the result is concluded.

4. Simulation and results

To study the dynamics of epidemics in GNMN, modified SIS and SIR models are used. First, we simulate the proposed model by considering the mobility and epidemic parameters. After that, we analyze the dataset of human movement to validate our proposed model.

4.1. Simulation setup

Simulations for the proposed model are done in a 2-D region of 2500 meter square. Nodes movement is guided by the GNMN based on the random waypoint model [10]. To emphasize the impact of mobility on network modeling, we typically use rest times, t_{rest} , of a node; connectivity region, r , for each node is taken 2 m.

The simulations done in paper are categorized as follows:

1. RGG model and proposed GNMN.
2. SIS and SIR models on proposed GNMN.
3. SIS and SIR models using real dataset which support human network with mobile human network created from dataset.

The list of parameters taken in the simulations is presented in Table I.

TABLE I

Simulation parameters for GNMN.

Name of parameter	Value
Nodes	2000
Simulation area ($a \times a$)	2500 m $\times$ 2500 m
Square length (a)	2500 m
Connectivity region (r)	2 m
Spreading rate (β)	0.8
Recovery rate (μ)	1
Time of rest (t_{rest})	Random (3,50) s
Threshold time for connectivity ($t_{\text{threshold}}$)	3 s
p_{stat}	0.2
Expected length between two random points	$0.521 \times a$
Velocity (V)	Random (1.0) m/s

Initially, a GNMN is generated by using parameters mentioned in Table I. We run the simulation for 1000 time steps for 100 network configurations for a single experiment, where the average degree and clustering coefficient of each configuration is recorded after each 10-time steps. We performed 50 independent experiments and analyzed the average degree and clustering coefficient of each experiment.

4.2. Result and analysis of proposed model

In simulations, it is found that geometric positions of nodes are changing due to the random mobility of the nodes with random velocity V . The connectivity between nodes changes due to nodes' movement. Time of rest (t_{rest}) during movement is also randomly selected for every mobile node. Due to the randomness in V , the structure of the network changes. The reason for changing the network is that a geometry of each node is changing with random velocity. It is similar to the position of a node in a random geometric graph, where geometry of a node is random. Here, the network with mobile nodes becomes equivalent to random geometric graph at any instant of time. The mobility of a node with random velocity is the reason for a node's random geometry. Hence, the proposed model is named a geometric network with mobile nodes (GNMN). It creates the perturbation in the degree distributions of the network, which is calculated at different times. Degree distribution (DD) for GNMN for two different time instances at 3rd and 7th instances is plotted to show the effect of random movement of the nodes and t_{rest} on the network structure. It looks like a Poisson

distribution with perturbations. In Fig. 5 (a), a degree distribution is shown when velocity is 21 m/s and t_{rest} is 15 s, while, in Fig. 5 (b), the degree distribution is shown when velocity is 10 m/s and t_{rest} is 45 s. It seems that patterns of degree distribution of GNMN are not similar and always change due to different velocities and t_{rest} . A change in the velocity and time of rest affects the average degree of the network. However, the degree distribution remains the same. If the value of t_{rest} is high, then the number of connection increases, as shown in Fig. 5 (a) and (b).

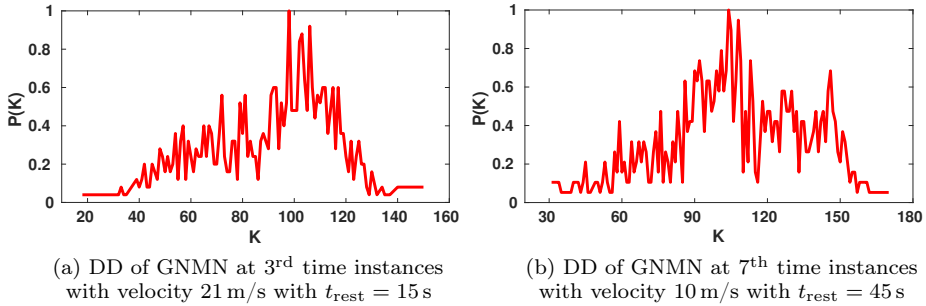


Fig. 5. Degree distribution (DD) of GNMN at different time instances.

The simulations are performed for 100 instances of random movement of nodes to generate the network topology at each instance and to see the effects of mobility and time of rest on network properties. Average degree, $\langle K \rangle$, of the network is plotted against the velocity, V , of nodes and parameter t_{rest} in Fig. 6. It is observed that $\langle K \rangle$ increases with the increase of time of rest as more nodes come in contact with the resting nodes within that time. Velocity helps to change the position of nodes resulting in the change

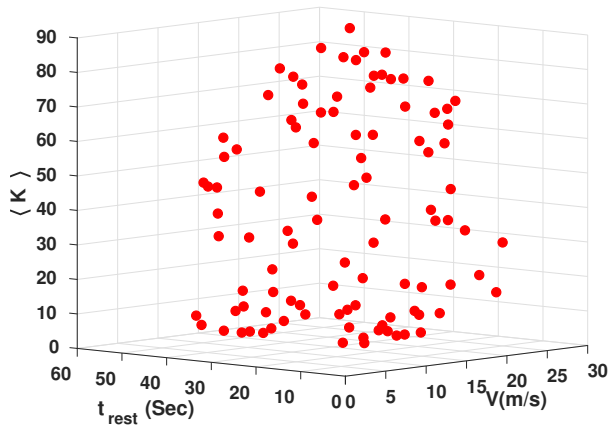


Fig. 6. $\langle K \rangle$ with respect to V and t_{rest} at each time instance.

of the network structure. Hence, $\langle K \rangle$ is also affected by velocity. t_{rest} is responsible for the network to be dense or sparse. A node resting for longer t_{rest} has more acquaintances than a node resting for smaller t_{rest} .

Further, simulations are performed for 50 times by considering 100 instances of random movement to find the ensemble results. In Fig. 7, we plot two properties of the formed network with mobile agents: average degree $\langle K \rangle$ and the clustering coefficient, which is stochastic with respect to the network structure that changes with the change in V and t_{rest} . $\langle K \rangle$ for GNMN vary with high variance with time instances. At some time instances, $\langle K \rangle$ is low and at some instances, $\langle K \rangle$ is high due to the high density of the nodes present in connectivity region r due to random movement of nodes as well as t_{rest} which ranges from 33 to 43. The average degree, $\langle K \rangle$ of each experiment is plotted in Fig. 7 (a). The clustering coefficient of a node is defined as a measure of the degree to which nodes form tightly knit groups. The clustering coefficient of the network is also changing with respect to the network structure in GNMN, due to variation in average degree as clustering coefficient is inversely proportional to the average degree [45]. The average clustering coefficient of each experiment is plotted in Fig. 7 (b). It ranges from 0.52 to 0.54.

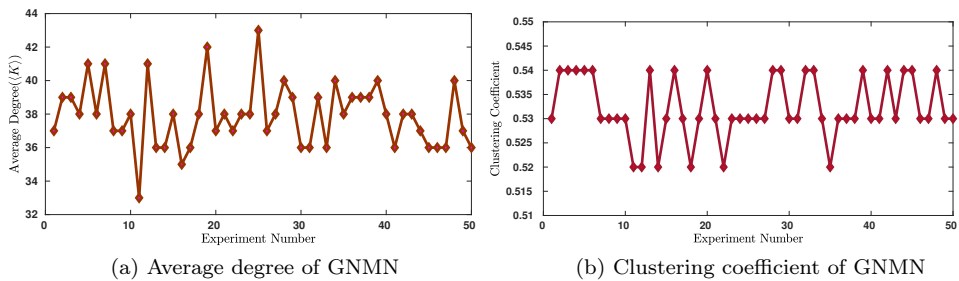


Fig. 7. Network characteristics of GNMN after 50 experiments.

In Fig. 8 (a), error bars are plotted to show the variance in degree of geometric network with mobile nodes. The variance in average degree is very high at some time instance and sometimes it is low due to a random movement and time of rest of nodes. Error bars are also plotted in Fig. 8 (b) to show the effect of mobility on the clustering coefficient.

Average degree $\langle K \rangle$ and clustering coefficient of RGG for 50 independent experiments are plotted in Fig. 9 for the same number of nodes. Average degree of RGG ranges from 204 to 215, while clustering coefficient ranges from 0.650 to 0.658. It is observed that average degree and clustering coefficient of RGG are greater than GNMN since in RGG, all nodes are statically positioned at geometric location, while in GNMN, some nodes are mobile. Therefore, remaining static nodes participate in creating the network in GNMN.

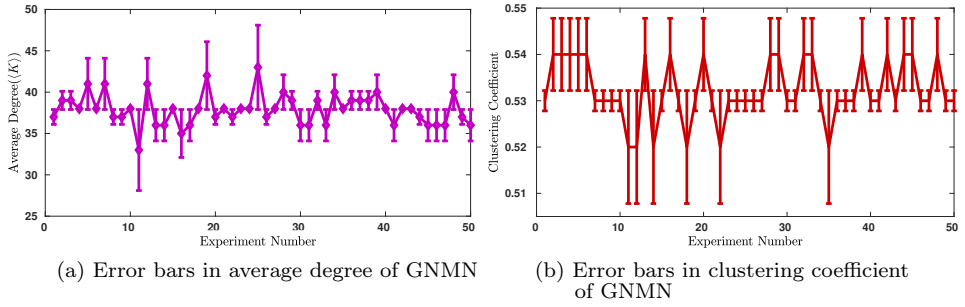


Fig. 8. Error bars showing the fluctuation on network characteristics of GNMN after 50 experiments.

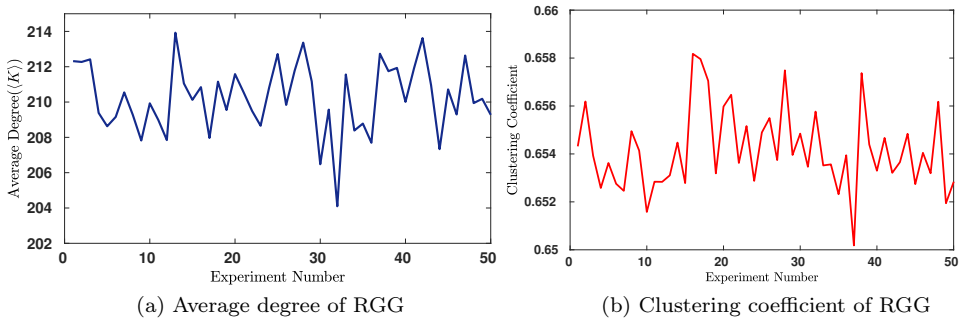


Fig. 9. Network characteristics of RGG after 50 experiments.

We list the result of RGG and GNMN in Table II. The table shows that the average degree of RGG is 210, while the average degree of GNMN is 38. It is found that GNMN is more sparse than RGG in nature as the number of connections in GNMN is less than RGG. The average clustering coefficient of GNMN is also less than RGG as it is 0.654 in the case of RGG, while ensemble clustering coefficient of GNMN is 0.533.

TABLE II

Average degree and clustering coefficient of RGG and GNMN.

Name of parameter	RGG	GNMN
Average degree	210	38
Clustering coefficient	0.654	0.533

4.3. Analysis of real-world dataset

To validate this proposed work, dataset named **Brightkite** is taken from the Stanford Large Network Dataset Collection — SNAP: Stanford [11]. This data allows for studying human mobility. In the broader context, modeling the human movement based on geographic location has many applications such as urban planning, understanding human migration patterns and the spread of diseases. Total human movement data is for 2 years and 58 228 number of person. They provide data in the format shown in Table III.

TABLE III

Brightkite dataset details.

user	check_in time	latitude	longitude	location_id
58186	2008-12-03T21:09:14Z	39.633321	-105.317215	ee8b88dea22411
58186	2008-11-30T22:30:12Z	39.633321	-105.317215	ee8b88dea22411
58186	2008-11-28T17:55:04Z	-13.158333	-72.531389	e6e86be2a22411
58186	2008-11-26T17:08:25Z	39.633321	-105.317215	ee8b88dea22411
58187	2008-08-14T21:23:55Z	41.257924	-95.938081	4c2af967eb5df8
58187	2008-08-14T07:09:38Z	41.257924	-95.938081	4c2af967eb5df8
58187	2008-08-14T07:08:59Z	41.295474	-95.999814	f3bb9560a2532e
58187	2008-08-14T06:54:21Z	41.295474	-95.999814	f3bb9560a2532e
58188	2010-04-06T06:45:19Z	46.521389	14.854444	ddaa40aaa22411
⋮	⋮	⋮	⋮	⋮

We process this dataset according to check-in behavior of users. We are interested in understanding how people move from one to another location and how much time they rest during the movement. The dataset is divided into 10 parts based on the check-in times. Data is further processed by splitting the region based on the area of $25\,000\text{ m} \times 25\,000\text{ m}$. We are not considering such a type of nodes in network formation which belongs to two regions simultaneously. This creates 7 network structures in a given spatial region. According to the dataset, we infer the information listed in Table IV.

When we analyze the dataset, a node is considered in rest if its velocity is less than 1 km/h . After analysis of rest time t_{rest} during the movement, we find that t_{rest} ranges from 2 days to 115 days. That is randomly distributed as shown in Fig. 10 (a). Most of the nodes are in rest with rest time 12 days. Distribution of velocity of nodes is shown in Fig. 10 (b). The velocity of nodes (V) lies between 3 km/h to 200 km/h that is similar to proposed quantitative analysis. Very few nodes are moving with a velocity of more than 100 km/h . Most nodes are moving with a velocity ranging from 3 to 50 km/h .

TABLE IV

Brightkite dataset statistics after processing.

Name of parameter	Value
Total nodes	58228
Time of rest (t_{rest})	(2–115) days
Velocity (V)	(3–200) km/h
Connected nodes in each network	570, 483, 328, 184, 149, 165, 144
Edges in each network	3282, 2166, 1083, 736, 894, 656, 574
Spatial region taken ($a \times a$)	25 000 m $\times$ 25 000 m
Connectivity region r	20 m
Average degree $\langle K \rangle$ in each region	6, 5, 3, 4, 6, 4, 4

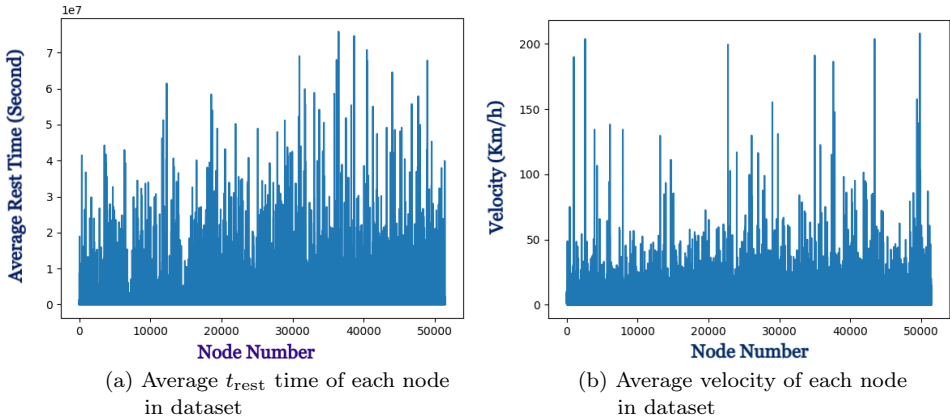


Fig. 10. Average t_{rest} time and velocity V of nodes extracted from Brightkite dataset.

The network is created by using the proposed model within a spatial region and taking the value of connectivity region, r , and time of rest, t_{rest} , from Table IV. The degree distribution of the 6-network topology of a given spatial region defined in Table IV is plotted in Fig. 11. The degree distribution of each network structure is not fixed due to mobility of nodes with random velocity V and random t_{rest} time. Hence, each plot is different. It is also found that the number of nodes in each network is different. Therefore, the average degree $\langle K \rangle$ also varies as listed in Table IV. We, moreover, claim that due to the movement of nodes with random velocity and smaller t_{rest} time in a given spatial region, the network will be sparse and degree distribution will vary in each network. Since the density of nodes depends upon the t_{rest} time when a node is staying for longer t_{rest} , then at the same time, other nodes from other locations move to the locations that come under the connectivity region of the respective node.

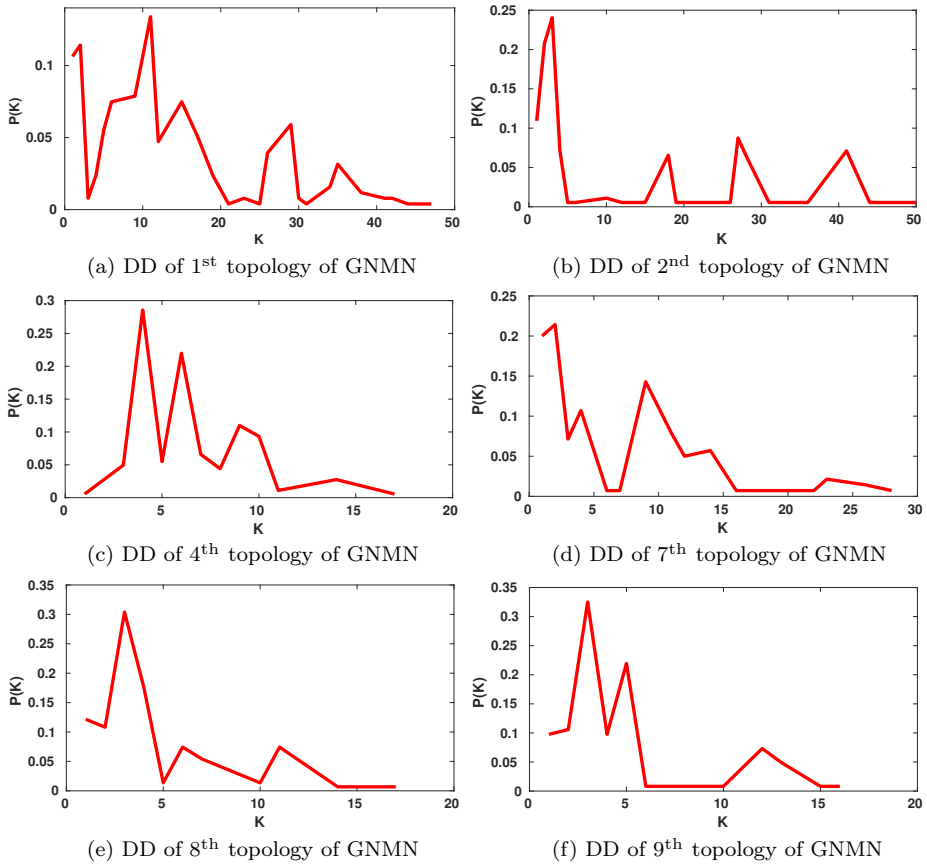


Fig. 11. Degree distribution (DD) of 6-human connection network created using Brightkite dataset.

4.4. Analysis of SIS and SIR epidemic models on GNMN

The simulations are performed for epidemic spreading by using the SIS model considering GNMN for human interaction. It clearly shows that epidemic spreading is greatly affected by t_{rest} time as shown in Fig. 12. The value of t_{rest} is chosen as 5, 10, 15, 20 seconds to see the effect of increasing value of t_{rest} . As t_{rest} increases, the epidemic spreads much faster. It is due to staying of an infected person for t_{rest} longer then it is necessary to make connections with the persons who are existing under connectivity region. In the meantime, some more nodes move and come closer to the proximity of infected person and catch the infection. It means that if in the human population an infected person gets in more contacts with the susceptible person for the longer t_{rest} time, it increases the epidemic spread at large scale instantly. To analyze the impact of mobility on epidemic spreading, we typically used equal rest times, t_{rest} , for all nodes.

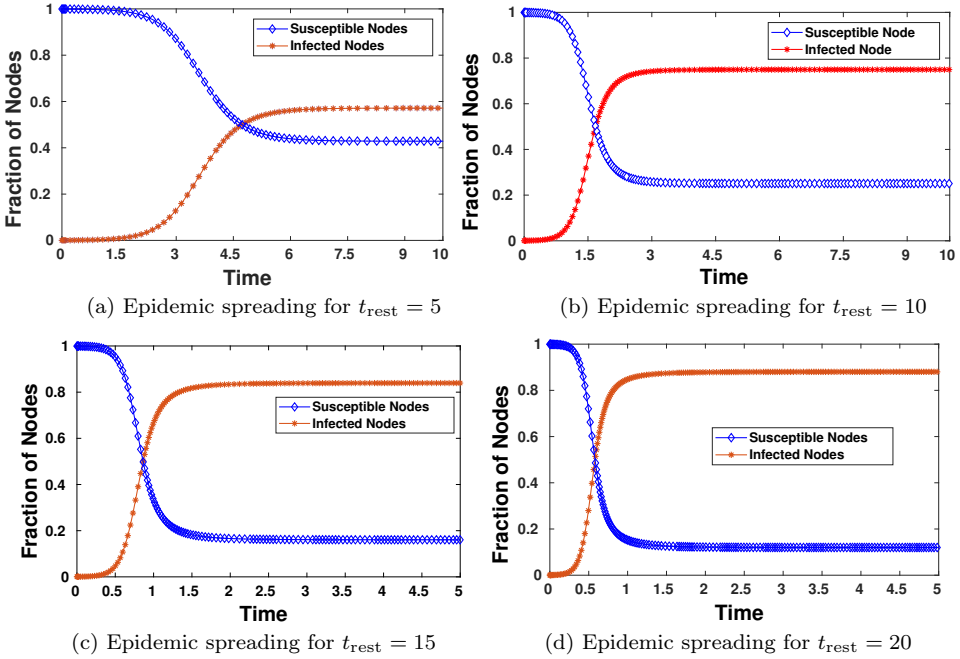


Fig. 12. Effect of t_{rest} time in epidemic spreading (SIS model).

Mobile nodes do not play any role in connectivity because during movement nodes cannot make contact with other nodes. Mobility just changes the positions of nodes. Therefore, nodes get connected with other nodes only after being stationary for at least t_{rest} time. We take the value of velocity V from 1 m/s to 30 m/s and simulate the result until the steady state of S_{∞} and I_{∞} for 20 network structures in given spatial region. We found that mobility and t_{rest} also affect S_{∞} and I_{∞} as shown in Fig. 13. It means that an infected person cannot spread the epidemic during movement. The healthy person will be affected by an infected person when they both get in contact in the t_{rest} time.

The simulation of SIS epidemic model is performed by considering 20 network structures in a given geometric region as topology is stochastic with respect to time due to the movement of nodes with random velocity. In mobility mode, at $t = 0$, nodes are static in a given spatial distribution. After that, some nodes start moving with velocity, V . Here, to get the final spread over the network, multiple network structure of GNMN is considered.

We show the effect of the mobility of nodes on the susceptible population and infected population in each topology in Fig. 13 (a) and (b). For the first network topology at $t = 1$, the value of saturation state of S_{∞} is 0.0582, while I_{∞} is 0.9418. It suddenly changes at $t = 2$ in the next network topology, *i.e.*, the second, as the infected population increases to 0.9614 and

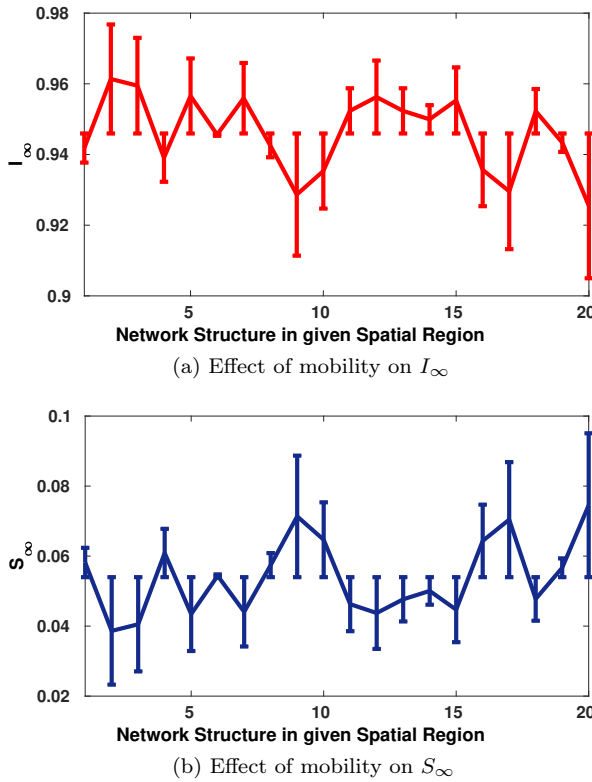


Fig. 13. Effect of mobility in epidemic spreading (SIS model).

healthy population decreases to 0.0386 due to the mobility of nodes, as the degree of nodes varies. For the third network topology at $t = 3$, the infected and susceptible population again changes. In this way, we plot the saturated value of infected and susceptible population for 20 network topology. For the network topology at $t = 12, 13, 14$ and 15 , the change in saturated value of infected and susceptible population is low and equals 0.0463, 0.0437, 0.0477 and 0.05 for susceptible population, and 0.9537, 0.9563, 0.9523 and 0.95 for infected population respectively. The error bars are plotted to show the variation in the susceptible population and infected population from the mean value on a different network topology of GNMN in a given spatial region. The length of an error bar explains the uncertainty of the value from the mean value. If the length of the error bar is longer then the mean collection of values is low of which mean value is calculated. A small error bar shows the certainty of mean value as the concentration of values is high. Therefore, it should be advised from the error bars plot that immunization should be taken immediately to cure the epidemic. Otherwise, in GNMN, epidemic spreads out more quickly at certain time instances as shown in Fig. 13 (a).

Figure shows that at the 9th network structure, when the epidemic is not controlled on time, spreading will increase in 12th network structure in a given region.

Further, the simulations are performed for epidemic spreading by using the SIR model considering GNMN for human interactions. This model also shows that epidemic spreading is greatly affected by t_{rest} time as shown in Fig. 14. The value of t_{rest} is taken as 3, 6, 10, 15 seconds to see the effect of increasing value of t_{rest} . As t_{rest} increases, the epidemic spreads quickly. It is due to residing of an infected person for t_{rest} longer, then it will make connections with the persons who are existing under connectivity region. In the meantime, some more nodes move and come closer to the vicinity of infected person and catch the infection. The increasing value of t_{rest} decreases the steady state time as well as increases the value of I_{max} . The values of I_{max} are 0.72, 0.78, 0.82 and 0.86 for the value of t_{rest} 3, 6, 10, 14, respectively. The steady state time values are 3, 1.2, 0.7 and 0.6 for the corresponding t_{rest} time. It means that in the human population, if an infected person gets in more contacts with the susceptible person for the longer t_{rest} time, it increases the epidemic spread at large scale instantly.

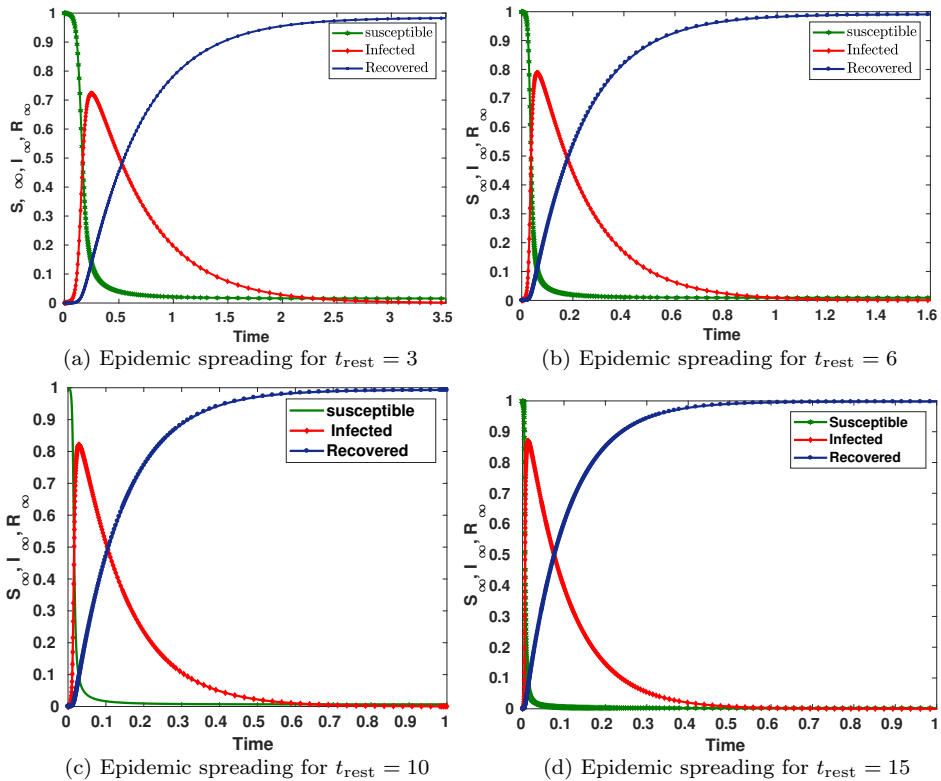


Fig. 14. Effect of t_{rest} time in epidemic spreading (SIR model).

Mobile nodes only change its position, hence topology changes respectively. These nodes do not play any role in connectivity. Therefore, nodes get connected with other nodes only after being stationary for at least $t_{\text{threshold}}$ time. The value of velocity V is taken from 1 m/s to 30 m/s and we simulate the result until the steady state of I_{max} for 20 network instances. We found that mobility as well as t_{rest} affect I_{max} as shown in Fig. 15. It means that an infected person cannot spread the epidemic during movement. The healthy person will be affected by an infected person when both get in contact in the t_{rest} time.

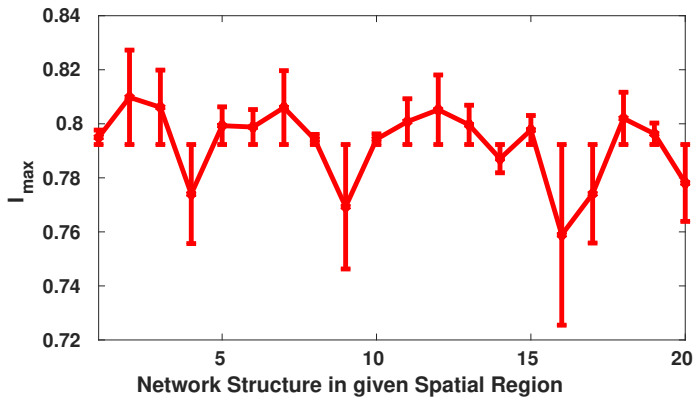


Fig. 15. Effect of mobility in epidemic spreading (SIR model).

We perform the simulation using SIR epidemic model by considering 20 different networks as topologies changing randomly with respect to time due to the random movement of nodes in a given spatial region. In Fig. 15, we show the effect of the mobility of nodes on the infected population in a network topology at each time instance. For the network topology, at time $t = 0$, the maximum value of the infected population I_{max} is 0.7950. In the next time instance at time $t = 1$, again, the network topology changes, as the infected population increases to 0.8098 due to the mobility of nodes, as the degree and clustering coefficient of nodes vary. For the network topology, at the third time instance, the infected population again changes. In this way, the maximum value of the infected population I_{max} is plotted for the network topology of 20-time instances. The error bars are also plotted to show the variation in the infected population from the mean value of network at each instances. The length of an error bars explains the uncertainty of the value from the mean value. Error bar shows the intensity of epidemic spreading on each network based on average degree. Therefore, it should be advised from the error bar plot that immunization should be taken immediately to cure the epidemic. Otherwise, in GNMN, epidemic spreads out more quickly at

certain time instances as shown in Fig. 15 because number of acquaintances is high at respective time. Figure 15 shows that the network at time instances 4, 9 and 16 infection is low and it should be controlled as soon as possible, otherwise spreading will increase in the network created at the next time instances, *i.e.*, 5, 10 and 17 because a number of acquaintances increases due to movement of nodes and t_{rest} .

4.5. Analysis of SIS and SIR models on Brightkite dataset

A network is formed using the proposed model with parameter t_{rest} and V . Further, SIS and SIR epidemic models are used over it to study the epidemiological dynamics. It is found that the increasing the t_{rest} time of a node also increases the epidemic spreading faster as shown in Fig. 16. The value of t_{rest} is taken in days as 5, 10, 15, and 20. We see that spreading at $t_{\text{rest}} = 20$ is much faster than $t_{\text{rest}} = 5$.

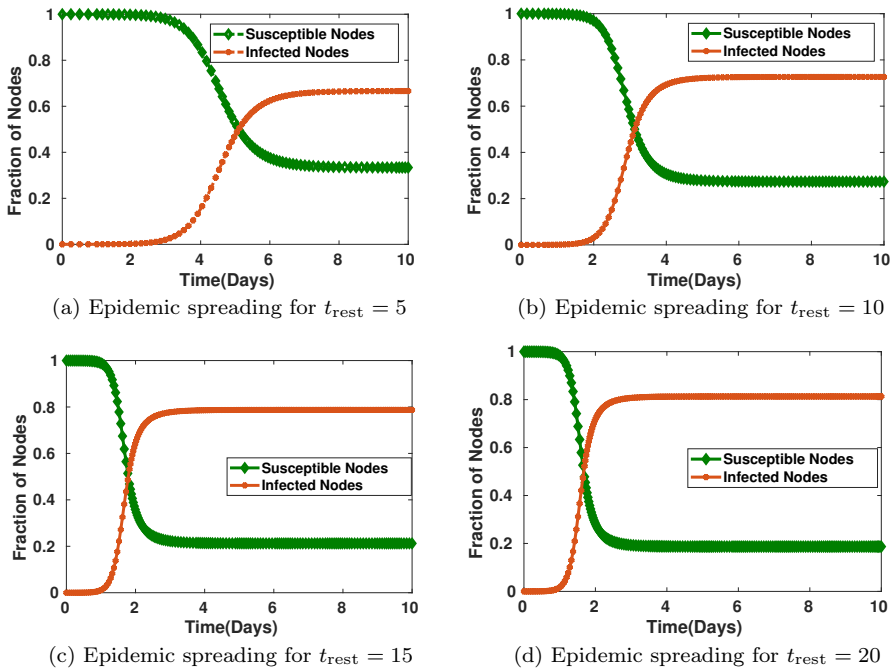


Fig. 16. Effect of t_{rest} time in SIS epidemic spreading model considering human connection network from Brightkite dataset.

SIS model is applied over a human network with mobility of humans to see its effect. We analyze the spreading pattern on various network topologies using mobile nodes in a given spatial region. We conclude the value of I_{∞} and S_{∞} . For the first network structure of dataset, the value of satu-

ration state of S_∞ is 0.1871, while I_∞ is 0.8129 as per degree of nodes. In the second network structure, infected population decreases to 0.78734 as a number of acquaintances of infected nodes is low hence healthy population increases to 0.21266. For the third network, infected and susceptible population again changes because an average degree of nodes vary. In this way, we plot the saturated value of infected and susceptible population for 6th network structure of defined spatial region from Table IV in Fig. 17. For 4th, 5th and 6th network structure, the saturated value of infected and susceptible population changes as 0.2735, 0.32245 and 0.35915 for susceptible population, and 0.7265, 0.67755 and 0.64085 for infected population, respectively. This change in infected and susceptible population depends upon average degree of nodes.

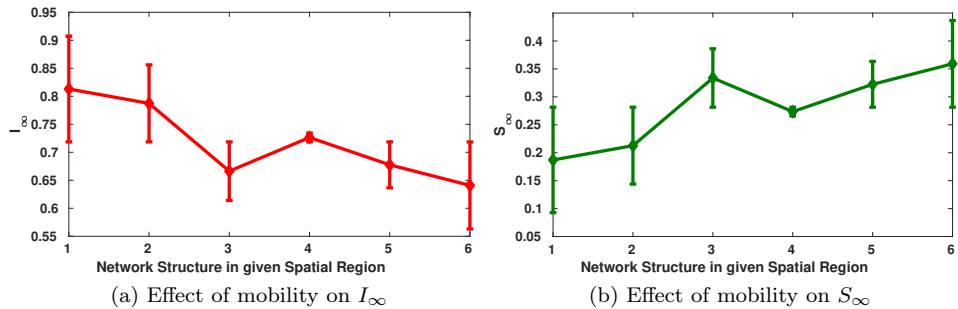


Fig. 17. Effect of mobility on SIS epidemic spreading model in human connection network from Brightkite dataset.

By considering underlying network, formed by static nodes with the node at t_{rest} time during movement, we apply the SIR epidemic model to show the effect of t_{rest} of a node. It is found that the increasing the t_{rest} time of a node also increases the epidemic spreading faster as shown in Fig. 18. We consider 4 value of t_{rest} in days as 3, 5, 8, and 10. We see that spreading at $t_{\text{rest}} = 10$ is much faster than $t_{\text{rest}} = 3$ — an infection threshold also increases.

To find the effect of mobility of human population on epidemic spreading by using SIR model, we analyze the spreading pattern in 6th network structure formed in a spatial region and find that mobility also effects the epidemic spreading as shown in Fig. 19. We analyze the value of I_{max} . By considering the first network structure, the value of I_{max} is 0.5188. In the second network structure, infected population decreases to 0.4932 as average degree is low compared to the first network. In this way, we plot the maximum value of infected population for 6th network structure. For 4th, 5th and 6th network structure, maximum value of infected population changes as 0.3902, 0.3215 and 0.2822, respectively, due to change in average degree.

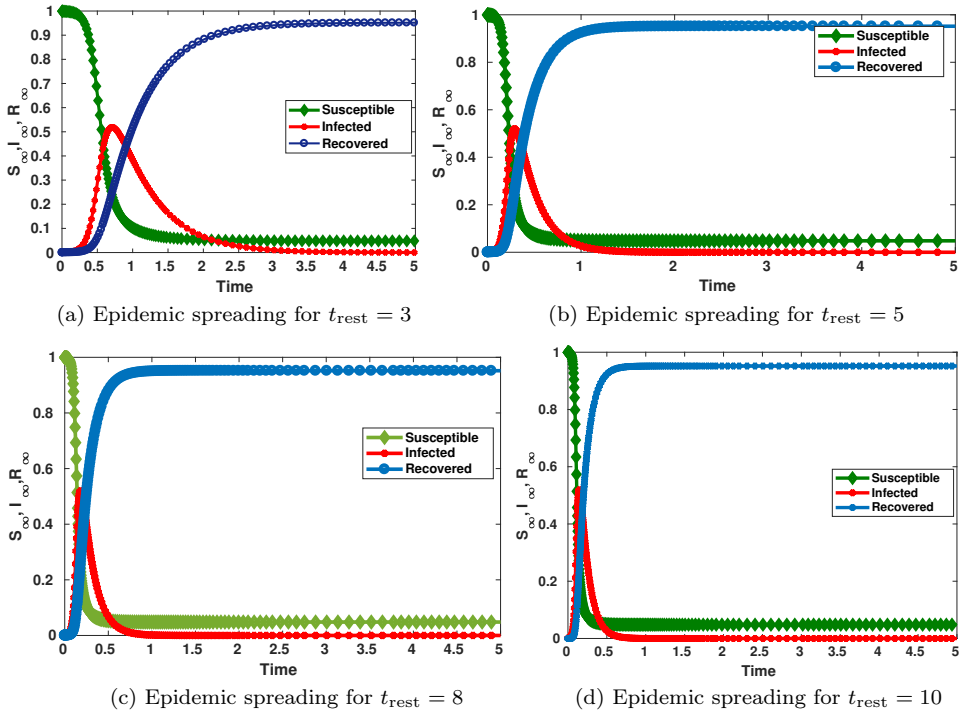


Fig. 18. Effect of t_{rest} time in SIR epidemic spreading model by considering human connection network from Brightkite dataset.

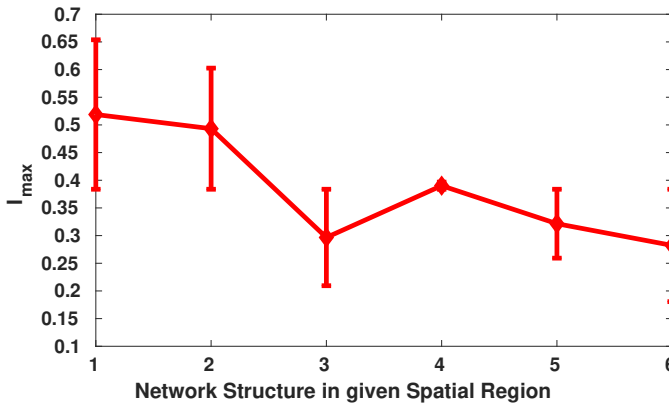


Fig. 19. Effect of mobility on SIR epidemic spreading model in human connection network from Brightkite dataset.

5. Conclusions and future work

In this paper, we have proposed a GNMN. The acquaintances of each node in the connectivity region (r) keep changing due to mobility of a node with random velocity in a given spatial region and their stay for $t_{\text{rest}_i} > t_{\text{threshold}}$ time. Therefore, statistical properties of the network in this model are not fixed. The variation in statistical properties affect the dynamics of epidemics. The dynamics of epidemics is studied by considering the parameter t_{rest} , and simulations show that epidemics spread out quickly if an infected node remains for the longer t_{rest} time. If t_{rest} of a node is longer, then there is a chance that more nodes will appear in connectivity region of the respective node. Hence, dense acquaintances are found with longer t_{rest} because when a node is in rest for longer t_{rest} , then at the same time, some other nodes move from different locations to the connectivity region of that node and epidemics spread out quickly as compared to smaller t_{rest} , where longer and smaller t_{rest} is greater than $t_{\text{threshold}}$. We vary the velocity V and t_{rest} of nodes to analyze the epidemic spreading in the human connection network. Our proposed model is validated by using the dataset of human movement, which also shows that t_{rest} and V of nodes play an important role in the dynamics of network. Simulation with human movement dataset also shows that the mobility changes the topology of network and statistical properties as produced in different geometric region. The generated network by the dataset of human movement validates the varying statistical properties of the network as degree distribution of network varies in each geometric region. Simulations of epidemic on synthetic data and real data show a similar type of result that t_{rest} affects the spreading of epidemics while, due to mobility, epidemics spread from one region to another region.

There are other important areas for future work based on the random mobility, such as the effect of the mixing rate and the connectivity fluctuation parameter. There are a lot of areas where time delay should be considered in the propagation process.

I would like to thank Mr. Abhishek Saroha for helping in simulation on the dataset.

Appendix

TABLE V

Symbols and variables used in the paper.

Symbol	Description
N	Total number of nodes
t_{rest}	Time of rest of a node during movement
$E[d]$	Expected distance between two random points
r	Connectivity radius
β	Spreading rate
μ	Recovery rate
p_{rest}	Probability of a node to be in rest during movement
p_{stat}	Probability of a node to be stationary
$m(t)$	Total number of movement of a node
V	Velocity of node
t_{move_j}	Duration of j^{th} movement of a node with velocity V
$f_{X,Y}(X, Y)$	Spatial density function
(X, Y)	Random variable of geometric points

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