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DJIBRIL MBOUP, Université Gaston Berger de Saint-Louis, Saint-Louis, Saint-Louis, Senegal

CHÉRIF DIALLO, Université Gaston Berger de Saint-Louis, Saint-Louis, Saint-Louis, Senegal

MOUSSA LÔ, Université Gaston Berger de Saint-Louis, Saint-Louis, Saint-Louis, Senegal

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Mobility and Epidemic Process in Temporal Networks

Djibril Mboup
Laboratoire Algèbre Cryptographie Codes et Applications (ACCA)
UFR de Sciences Appliquées et de Technologie
Université Gaston Berger, BP 234, Saint-Louis, Senegal
mboup.djibril@ugb.edu.sn

Cherif Diallo
Laboratoire Algèbre Cryptographie Codes et Applications (ACCA)
UFR de Sciences Appliquées et de Technologie
Université Gaston Berger, BP 234, Saint-Louis, Senegal
cherif.diallo@ugb.edu.sn

Moussa Lo
Laboratoire Analyse Numérique et Informatique (LANI)
UFR de Sciences Appliquées et de Technologie
Université Gaston Berger, BP 234, Saint-Louis, Senegal
moussa.lo@ugb.edu.sn

ABSTRACT

Complex networks are distinguished to have a particular structure due to its large dimension and its many interactions, which play an important role in its characteristic. In fact, these networks are the locus of many dynamical phenomena such as birth of community, opinion formation, information diffusion, and rumors or epidemic spreading and so on. User mobility is of critical important when you want to know how disease spreads in network. The synthetic models represents a good alternative to describe how humans move. In this paper, we study the dynamics of epidemic spreading in temporal network generated by synthetic mobility model such as Random Waypoint (RWP), Gauss Markov (GM) and Truncated Levy Walk (TLW). Then, we show how proximity in terms in distance could impact a spreading process like droplet or airborne modes of pathogen spreading. Finally, we will statistically evaluate the number of infected nodes by scaling the spreading rate depending on the proximity between agents.

CCS CONCEPTS

• **Computer systems organization → Embedded systems**; *Redundancy*; Robotics; • **Networks** → Network reliability;

KEYWORDS

Complex Networks, Temporal Networks, Dynamic Process, Epidemic Spreading, Mobility

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1 INTRODUCTION

Complex networks are distinguished to have a particular structure due to its large number of nodes and its many interactions, which play an important role in its characteristic. In fact, these networks are the locus of many dynamical phenomena such as birth of community, opinion formation, information diffusion, and rumors or epidemic spreading and so on [25]. Understanding these phenomena and being able to predict their behaviors represent an exciting challenge in scientific research. In fact, the recent studies in complex networks show that the dynamism of the human being has key role in how epidemics spread in some networks [29][10][4]. The GLEAMviz (Global Epidemic and Mobility Model) project combines real-world data on population and human mobility in order to design new models which allow to forecast disease transmission and to help in minimizing the impact of potentially devastating epidemics [1]. Ebola is the recent famous example of epidemic spreading such that transmission mode is based on physical contact or proximity between individuals, and the mobility has played a key role in its expansion [11]. However, the synthetic models represent a good alternative to describe how humans move. In this paper, we try to understand the relationship which exists between mobility and epidemic process. For this reason, we study the dynamics of epidemic spreading in temporal network generated by synthetic mobility model such as Random Waypoint (RWP), Gauss Markov (GM) and Truncated Levy Walk (TLW). Then, we show how distance-proximity impact the spreading process like droplet or airborne modes of pathogen spreading and statistically we evaluate the number of infected nodes by scaling the spreading rate depending on the proximity between agents.

To carry out our work, this paper is organized in four sections as follow: firstly, we will introduce the notion of temporal networks in section 2. Next, in section 3, we give a review of epidemic models and a brief description in some synthetic mobility models which we are using in our simulation model. Finally, we exhibit in section 4 the simulation and results.

2 TEMPORAL NETWORKS

The study of complex networks are based on graph theory but this is not sufficient to know how dynamical phenomena work on the networks. That is the reason why researchers invent new tools to complete the complex networks analysis. Understanding at the same time the topological and dynamical aspect of complex networks still remain an important challenge [20]. Because, many complex systems are not static but consisting of contacts that are off and on as time progresses [14]. To do a deep analysis of the temporal structure of complex network, researchers have recently introduced the concept of temporal networks. In the real life, most of data are collected in time intervals that are more or less irregular

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(mobile phones records, online social networks, GPS, sensors, Bluetooth traces and so on). To give a motivation taking into account the temporal information in complex temporal networks modeling, let us consider the static graph in [Fig. 1(b)], there exists a path between A and F via (A, B, C, D, E, F), however, if we take into account the time-order showing in the temporal graph [Fig. 1(a)], A can't reach F. This fact is very important if we want to know the infected nodes in epidemic spreading, for example, a pathogen can spread from A to B, from B to C, from C to D, but not from D to E or F. Because, the transitive nature does not exist in temporal networks. Therefore, the temporal or time varying graph can represent more accurately the dynamics of a complex evolving system. In this section, we will give some essential concepts in Temporal networks.

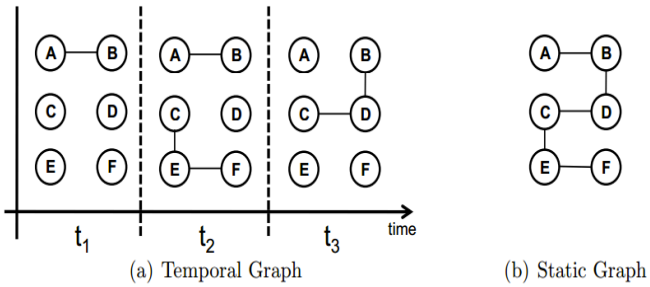


Figure 1: a)Temporal Network b) Aggregated Static Graph [31].

2.0.1 Definition. Temporal networks or Time varying graphs (TVG) are defined as sequences of snapshots of static graphs evolving at each time step t_i. In spite of the difficulty to take into account the dynamics in a complex network, this type of graph is an adaptable mean to study the dynamic evolving in networks. In the literature, we encounter different ways to define the temporal networks but we will focus here on those which correspond to the representations shown in [Fig. 1 and 2].

In the first case, According to Tang [31], a temporal network $\mathcal{G}$ is defined as an ordered sequence of static graph $(G_0, G_1, ..., G_{\tau-1})$ such that $G_t = (V_t, E_t)$, where V_t and E_t are respectively the set of nodes and edges in a time window t, there exists a link between node i and node j in E_t if there is some link in the real network between i and j during a time window interval (see Figure 1). In this definition, the author assumes that the set of nodes is fixed, $V_t = V, \forall t \in [0, \tau)$ and $\mid V \mid = N$.

In the second case, If we consider the triplet $(V, E, \mathbb{T})$ such that V represents the set of vertices, E is the set of edges and $\mathbb{T}$ the time-scale, then a temporal network can be define as a *contact sequence i.e* a set of C contacts, triples (i, j, t) where $i, j \in V$ and $t \in \mathbb{T}$ (see an example of this definition in Figure 2) [13]. This representation is appropriate in the context where the duration of the contact is less important such as communication data (sets of e-mails, phone calls, text messages, etc.) or physical proximity data (e.g. sexual networks) [13]. In the other hand, when the duration of the contact δt is taken into account, the temporal network is represented by a quadruplet $(i, j, t, \delta t)$ and it is called *interval graph*. As example, δ may correspond to the duration of a flight in an air transport network or the duration that two users are communicating.

In this paper, to generate a temporal network, we use the contact sequences provided by synthetic mobility models (Random Waypoint, Gauss Markov,Truncated Levy Walk).

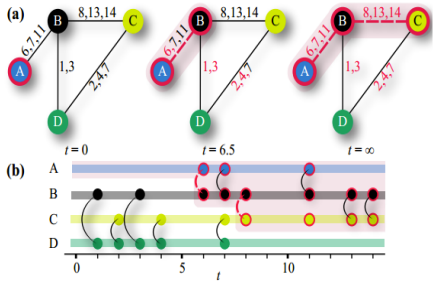


Figure 2: Two representations of temporal networks [13].

2.1 Paths, connectivity

In static network, the reachability condition is based on the concept of *path*. We say that the node j is reachable from i, if there exists a path which starts at i and ends up at j. Here, the concept of *path* depend only the connectivity between nodes. Unlike the static graph, in the temporal networks the notion of path depends on the time-order of links. That is to say "*time-respecting path*" [13]. Thus, one can define a "*time-respecting path*" between a source node v and a target node w to be any sequence of time-stamped links (or sequences of contacts):

$$(v_0, v_1, t_1), (v_2, v_3, t_2), ..., (v_{l-1}, v_l, t_l)$$

, such that $v_0 = v$, $v_l = w$ and the sequence of time-stamps is increasing, *i.e.* $t_1 < t_2 < ... < t_l$. For example, in [Fig. 2], there exists a time-respecting path from A to C, $(A, B, 7), (B, C, 8)$, but there is no path from A to D. In the literature, time-respecting path is also called "*journey*" [8] or "*temporal path*" [23] [31]. Like static networks, the notions of *connectedness* and *connected components* are very important in TVG. Moreover, we can define a node i is *temporally connected* to a node j if there exists a time-respecting path going from i to j. As the relation of connectivity is not symmetric in temporal networks, so the *strongly connectedness* is used to say two nodes i and j are temporally connected in both directions. In [24], Nicosia et *al.* give more details about connectedness and component in temporal networks. This give us the opportunity to define a certain number of concepts such as *temporal path length*, *shortest path*, *fastest path*, *temporal distance*.

Different from the (topological) time-respecting path, the *temporal path length* or *duration* can be measured as the time interval between the first and the last contact in the path i.e. $t_l - t_1 + 1$. We can also define the *shortest time-respecting* path between two nodes v and w as the time-respecting path with the smallest (topological) length while the *fastest time-respecting* path is the time-respecting path with the smallest (temporal) duration. Furthermore, if we consider two nodes i and j, the temporal distance τ_{ij}, called also latency, is the shortest time it takes to reach j from i at time t along

temporal paths. Similarly, it is the the temporal length of the temporal shortest path from i to j. From the temporal distance, Tang [31] define the *characteristic* or *average temporal path length* $\mathcal{L}$, similar to that defined by Watts & Strogatz [35].

$$\mathcal{L} = \frac{1}{N(N-1)} \sum_{ij} \tau_{ij} \tag{1}$$

The author define, in the context of disconnected time-varying graph, the measure of *temporal global efficiency* [31].

$$\mathcal{E} = \frac{1}{N(N-1)} \sum_{ij} \frac{1}{\tau_{ij}} \tag{2}$$

The concept of clustering observed in static graphs have been extended in Temporal network by Tang et *al.* [31]. They called it *temporal-correlation coefficient C* [31].

$$C_i = \frac{1}{T-1} \sum_{t=1}^{T-1} \frac{\sum a_{ij}(t) a_{ij}(t+1)}{\sqrt{\left(\sum a_{ij}(t)\right)\left(\sum a_{ij}(t+1)\right)}} \tag{3}$$

$$C = \frac{1}{N} \sum C_i \tag{4}$$

where $a_{ij}(t) \in \mathcal{A}^t$, the adjacent matrix of the graph G_t. In [9], the authors give another definition of temporal coefficient. This Measure is important to extend the nature of small-world on Temporal networks.

3 MOBILITY MODELS AND EPIDEMIC PROCESS

3.1 Mobility Models

The mobility in networks is a theme that has mostly interested the MANETs (*Mobile Ad hoc Networks*) area in which first models have been developed. The suggested models can be separated by two main classes: the synthetic models based on mathematical equations that try to capture the mobile motion in a simulation area [18] [22] [19] [5], and the models based on traces (logs, traceroute, geolocation etc.) obtained from systems deployed in the environment [26] [17] [32]. Here, we are interested in synthetic models such as *Random Waypoint (RW)*, *Gauss Markov (GM)*, *Truncated Levy Walk (TLW)* to generate temporal network that allow us to investigate the dynamic process which take place on it.

Random Waypoint (RW). The Random Waypoint was first proposed by Johnson and Maltz [18] and has become the main mobility model used for simulations in academic research, in particular to test routing algorithms. Iteratively, the mobile nodes chose randomly a destination in the simulation area and a speed that is uniformly distributed between $[v_{min}, v_{max}]$. At the destination, each mobile takes a certain period of time (i.e., a *pause-time*) chosen between 0 and w_n before moving another location. Bettstetter and Wagner have shown that the probability density function (pdf) of the spatial node distribution of the RWP model in a square area is given by the formula 5 [6]:

$$f(x,y) \approx f(x)f(y) = \frac{9}{16x_m^3 y_m^3}(x^2 - x_m^2)(y^2 - y_m^2) \tag{5}$$

where $0 \le x \le x_m$ and $0 \le y \le y_m$. In certain case this model suffers from some issues. For example, the case where nodes are concentrated in the middle of a bounded area. Additionally, the model suffers from the fact that the transient (i.e., non-stationary) regime may last for a very long time[21]. It is also proved that the RWP exhibits speed decay over time [16]. Despite the problems raised above, this model is still very used in opportunistic networks.

Gauss Markov (GM). This model tries to imitate the famous Gauss-Markov random process. In continuous time, a stationary Gaussian process $v(t)$ is a Gauss-Markov process if it has the auto-correlation function [28]

$$R_v(\tau) = E[v(t)v(t+\tau)] = \sigma^2 e^{-\gamma|\tau|} \tag{6}$$

where σ^2 is the variance of $v(t)$ and γ determines the degree of memory in the mobility pattern. The authors found that the speed and the direction at the *n-th* instance of the discrete Gauss-Markov process are calculated based on the value of the speed and the direction at the *(n-1)-th* instance, and a random variable using the following equations [28]

$$v_n = \alpha v_{n-1} + (1-\alpha)\mu_v + \sqrt{1-\alpha^2} w_{v_{n-1}} \tag{7}$$

$$\theta_n = \alpha \theta_{n-1} + (1-\alpha)\mu_\theta + \sqrt{1-\alpha^2} w_{\theta_{n-1}} \tag{8}$$

where v_n and θ_n are, respectively, the new speed and the new direction of the mobile station at each time n, the running parameter α verifying the following condition $0 \le \alpha \le 1$ handles the randomness, the constants μ_v and μ_θ represent the mean value of the velocity and direction and finally the terms $w_{v_{n-1}}$ and $w_{\theta_{n-1}}$ are random variables following the Normal distribution. Now, the position of the mobile at each time interval is calculated based on the current location, speed, and direction of movement. It is obtained by the equation below [28]

$$x_n = x_{n-1} + v_{n-1} \cos\theta_{n-1} \tag{9}$$

$$y_n = y_{n-1} + v_{n-1} \cos\theta_{n-1} \tag{10}$$

where (x_n, y_n) and (x_{n-1}, y_{n-1}) are the x- and y-coordinates of the mobile's position at the *n-th* and *(n-1)-th* time intervals, respectively, and v_{n-1} and θ_{n-1} are the speed and direction of the mobile node, respectively, at the *(n-1)-th* time interval.

Truncated Levy Walk (TLW). Truncated Levy Walk is a model developed by Rhee et *al.* in order to reproduce human behaviors on mobility model [27]. These behaviors include heavy-tail flight, pause-time distributions and the super-diffusive nature of mobility. Therefore, authors defined TLW to be a random walk that uses truncated Pareto distributions for flight and pause-time distributions to emulate mobility within a confined area [27]. Mathematically, we can consider a random walk defined by a sequence of step such that every step is represented by $S = (l, \theta, \Delta t_f, \Delta t_p)$ where $l > 0$ is flight length, θ is the direction of the flight, $\Delta t_f > 0$ is the duration of the flight or *flight time*, and $\Delta t_p > 0$ the pause time. At each step, a walker chooses a random direction from a uniform distribution of angle within $[0, 360]$, a finite flight time randomly based on some distribution, its flight length and pause time from probability distributions $p(l)$ and $\psi(\Delta t_p)$, respectively [27]. In TLW model, $p(l)$ and $\psi(\Delta t_p)$ follow Levy distributions with coefficients α and β, respectively. The distribution of Levy in terms of Fourier

Transformation with a scale factor c and exponent α can be written as follow [27]:

$$f_X(x) = \frac{1}{2\pi} \int_{-\infty}^{\infty} e^{itx - |ct|^{\alpha}} \tag{11}$$

From the parameters c, α and β, the model generates synthetic (truncated) Levy-walk mobility traces with truncation factors τ_l and τ_p flight lengths and pause times, respectively, in a confined area [27]. For every step S, if l and Δt_p are negative $l > \tau_l$ or $\Delta t_p > \tau_p$, then S is discarded and a new step is generated. This process is repeated after the step time $\Delta t_f + \Delta t_p$. It is worth to precise that when a flight crosses a boundary of the predefined area, then it is allowed to be reflected off the wall.

3.2 Epidemic process

The dynamic processes modeling remains a crucial problematic in complex networks community. Epidemiologists, computer and social scientists share a common interest in studying spreading phenomena. Many works rely on very similar models for the description of the diffusion of viruses, knowledge, and innovation [2]. Early, many approaches, in different fields, have proposed to know how epidemic spreads in a population. Basically, the most classical mathematical approach used in this area is the compartmental methods. This approach considers the population of individuals divided into different groups or classes according to the stage of the disease. For instance, *susceptibles*, denoted by S, represent the healthy individuals who can contract the disease, *infectious* (I), those who have contracted the disease and are contagious, and recovered (R), those who have recovered from the disease *i.e* immune or died. In fact, the choice of which compartments to include in a model depends on the characteristics of the particular disease being modeled and the purpose of the model. Here, we focus on the simplest model widely used in the scientific community: Susceptible-Infected-Susceptible (SIS).

The SIS model classifies the individuals in two states, susceptible or Infected, in any given time. Individuals can contract disease with probability $\beta\Delta t$ within a short time interval, but an infected nodes may recover and become susceptible again with probability $\mu\Delta t$. The parameters β and μ are transition rates for infection and recovery, respectively, and Δt is defined to be a discrete simulation time step. It is important to note that, in this model, the transmission process is cyclic, hence the name Susceptible-Infected-Susceptible (SIS) [25].

If we consider a population N, the evolution of the SIS model is therefore completely defined by the number of infected individuals $I(t)$ or equivalently the corresponding density $i(t) = I(t)/N$. We can also define $s(t) = S(t)/N$, and the number of infected individuals in contact with any susceptible individual. As a first approximation, let us consider that each individual/vertex has the same number of contacts/edges, $k \simeq \langle k \rangle$, under the homogenous mixing assumption. The continuous and deterministic reaction rate equation describing the evolution of the SIS model is given by [2]:

$$\frac{di(t)}{dt} = \beta\langle k \rangle i(t)s(t) - \mu i(t) \tag{12}$$

The usual normalization condition $s(t) = 1 - i(t)$ has to be valid at all times. Therefore, the number of infected nodes nodes evolving in times given by the above equation is describing in the [Fig. 3]. As we can see, at large t the epidemic reaches an *endemic state*, that's mean the number of infected individuals becomes constant [Fig. 3]. In SIS model, at the endemic state only a finite fraction of individuals are infected.

In the literature, we encounter various model depending compartmental methods, for instance SIS, SIR, SIRS, SEIR, etc.[25]. The new challenge is to understand the impact of human behaviors in the process of disease spreading. Human mobility plays a key role in interaction and/or contact between individuals. Several works have been carried out to understand how social or physical interaction impact the process of epidemic spreading. In [30], Stopczynski et *al.* have shown the critical impact that has distance proximity on disease transmission. They studied contact networks between two level: the network of intimate interactions defined as distance $d \lesssim 1$ meter, and the ambient network which includes all interactions $d \lesssim 10$ meters [30]. By using data set collected in one month, they found the spreading processes across proximity networks is highly sensitive to the distance of the interactions. In this work, the authors did not take into account the influence of the interaction distance for each user. In [12], authors tried to explain the fact that healthy people reduce contact with its infected neighbors and tend to restore those contacts when they are cured by using a weighted time-varying graph. They pointed out that a greater interacting strength leads to a higher epidemic threshold, lower average disease density of steady-state and shorter epidemic prevalent decay time [12]. Otherwise, they have shown that nodes reacting with local infected information will restrict the outbreak of disease comparing to the ones with global infective information [12]. However, this model ignored the influence of geometric distance between nodes. Valler et *al.* studied the epidemic threshold in the context of mobile ad hoc networks, they have shown that the node velocity in mobility models does not affect the epidemic threshold. However, this study did not care about the nodes proximity in the infection transmission [33]. Recently, Vestergaard and Génois use a temporal Gillespie algorithm to simulate SIS and SIR contagion process on time-varying network [34]. In [15], authors used Random Waypoint Model to show the impact of several network parameters, such as covering radius, moving velocity, and node density on the number of infected nodes in SEIR model.

In the rest of the paper, we will investigate how SIS model works in temporal networks and how proximity plays a key role on disease transmission, by using mobility model.

4 SIMULATIONS

4.1 Methodology

To study the evolution of the dynamic process of the SIS model on mobile network, we consider the temporal graph $\mathcal{G} = \{G_1, G_2, ...G_T\}$ where $G_t = (V, E_t)$ is generated at every time step by using each of these three mobility models (Random Waypoint, Gauss-Markov and Truncated Levy Walk) with 1000 nodes moving in an area of 100×100. Temporally, the nodes are located by their positions. Hence, to draw G_t we consider the following assumptions:

- Simply, two nodes are considered to be connected each other if their proximity is less than a given threshold distance d_{th}.

Table 1: Simulation parameters

Parameter	value	Description
N	1000	Number of nodes
dth	4 m	the distance maximum between two nodes to catch a tie
ρ	0.1	The initial infected ratio
β	0.2	spreading rate
μ	0.3	recovery rate
wt_{max}	1	The max waiting time
v_{min}, v_{max}	0.1, 1	max and min velocity in *RWP* mobility
v_{mean}	1	The velocity mean in GM mobility
fl_{exp}	-2.6	The exponent of the flight length distribution in TLW
wt_{exp}	-1.8	The exponent of the waiting time distribution in TLW

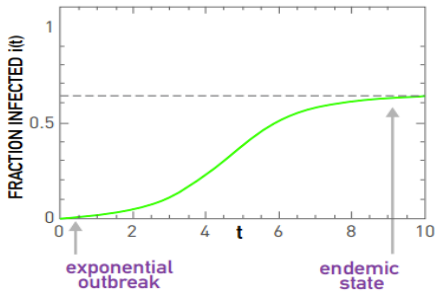


Figure 3: Time evolution of the fraction of infected nodes in the SIS model [3].

For every step Δt, we generate a snapshot of undirected network $G_{t_{i+i}}$ with $t_{i+1} = t_i + \Delta t, i = 1 \cdots T-1$. To be more precise, the distance considered here is the physical distance.

- In the second case, we generated a temporal weighted graph by taking into account the proximity distance between nodes. We define a weight to be the distance d_{ij} over the threshold distance d_{th}.

$$w_{ij} = \frac{d_{ij}}{d_{th}} \tag{13}$$

Since,

$$0 \leq d_{ij} \leq d_{th}$$

Then,

$$0 \leq w_{ij} \leq 1$$

By using the weight measure, one can define the strength of the proximity between two nodes i and j, denoted s_{ij}, as follows

$$s_{ij} = \frac{1}{(w_{ij})^{\alpha}}$$

where α is a scaling parameter.

In our model, for every time step a susceptible node is sick with probability β and becomes infected while an infected node is recovered with μ. Here, we distinguish two cases in our simulation. In the first case, the likelihood that an infected node selects its neighbors is completely random and the second case, we define this probability as follow:

$$p_{ij} = \frac{s_{ij}}{\sum_{l \in \Gamma(i)} s_{il}} \tag{14}$$

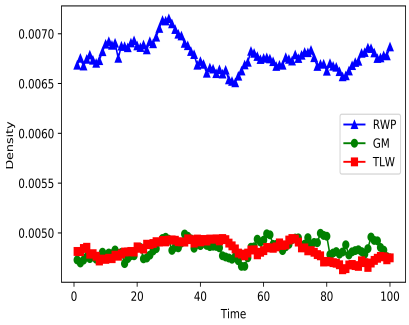
where $\Gamma(i)$ is the set of the neighbors of the node i and s_{ij} is the strength between i and j. In both cases, our aim is to know how mobility and proximity impact the epidemic spreading on network. Simulation parameters are summarized in [Table 1].

4.2 Results and Discussion

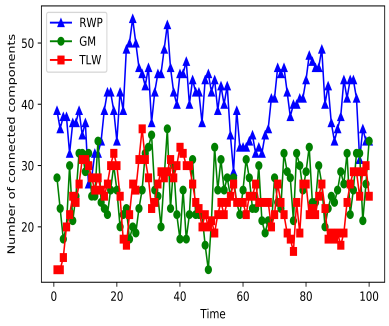
After several runs, we see that the temporal graphs generated by the mobility models (RWP, GM, TLW) show a very high percentage of disconnection. This fact depends essentially on the mobility models used as we explained above [7]. In [Fig. 4b], the first observation made on the results show that all generated graphs show a high number of disconnected components. The structure of $\mathcal{G}_{RWP}$ is less sparse than $\mathcal{G}_{GM}$ and $\mathcal{G}_{TLW}$ but it has more connected components, [Fig. 4a]. This means that we have more isolated and tightly connected cluster in $\mathcal{G}_{RWP}$ than the temporal networks generated by Gauss-Markov model and Truncated Levy Walk.

In the first case of our SIS model, the likelihood to be selected by infected nodes does not depend on the strength of interaction of the distance, so as we can see, the disease spreads rapidly in $\mathcal{G}_{RWP}$ than $\mathcal{G}_{GM}$ and $\mathcal{G}_{TLW}$ and reaches the endemic state at t=8 with 60% of infected. Nevertheless, the number $\mathcal{G}_{TLW}$ of infected nodes grows slowly reaching a constant value at the time t = 40.

In the second case, the probability to be selected by infected node depends on the parameter p_{ij} defined the formula 14. Here, we test our hypothesis by using different values of the scaling parameter α. When $\alpha = 0, p_{ij}$ depends only on the degree of the node i. In [Fig. 6b], the number of infected nodes increases faster than $\mathcal{G}_{RWP}$ and $\mathcal{G}_{TLW}$ before reaching the threshold value of 70% at the time t=12. With different values of alpha, the number of infected node tend to converge to the same value. In $\mathcal{G}_{RWP}$ and $\mathcal{G}_{TLW}$, the values of α has an influence on the epidemic spread rate [Fig. 6a] and [Fig. 6c]. These results point out the high impact of physical



(a) Density



(b) Number of connected components

Figure 4: (a) Density and (b) Number of connected components of the temporal networks, $\mathcal{G}_{RWP}, \mathcal{G}_{GM}, \mathcal{G}_{TLW}$, generated by RWP, GM, TLW, respectively.

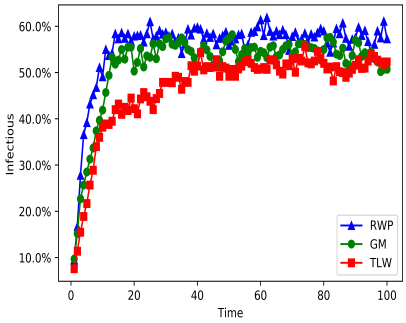
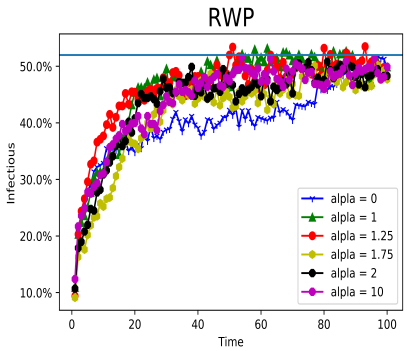
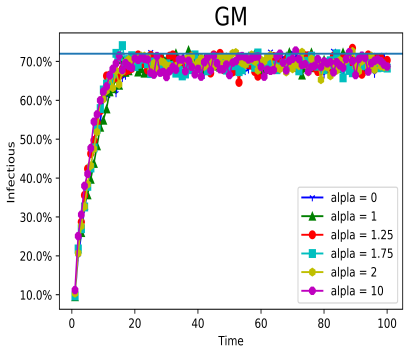


Figure 5: (a) Fraction of Infected nodes in $\mathcal{G}_{RWP}, \mathcal{G}_{GM}, \mathcal{G}_{TLW}$..

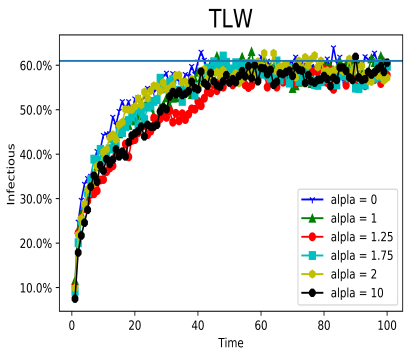
proximity in the process of transmission of airborne and droplet diseases.



(a) Fraction of Infected nodes



(b) Fraction of Infected nodes



(c) Fraction of Infected nodes

Figure 6: Fraction of Infected nodes in $\mathcal{G}_{RWP}, \mathcal{G}_{GM}, \mathcal{G}_{TLW}$ in the case where the probability to be infected depends on p_{ij}

5 CONCLUSIONS

In complex networks, it generally occurs many emergent phenomena. To understand these phenomena and to be able to predict their behaviors represent a crucial issue in scientific community. Our goal was to understand a spreading process like SIS model in a temporal graph, and how the mobility and proximity of the nodes

impact the transmission processes. As we can see, the graphs generated by the RWP, GM and TLW models are sparse and disconnected which impacts on the rate of propagation and the fraction of infected nodes. Moreover, we also show that proximity between two individuals can increase the probability to get an infection.

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