Dynamical Processes in Time-Varying Networks

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Abstract and Keywords

Networks in almost any domain are dynamical entities. New nodes join the system, others leave it, and links describing their interactions are constantly changing. However, due to the absence of time-resolved data and mathematical challenges, the large majority of research in network science neglects these features in favor of static or mean-field representations. While such approximations are useful and appropriate in some systems and processes, they fail in many others where the co-occurrence, duration, and order of contacts are crucial ingredients. This chapter presents a review of recent developments in the study of temporal networks and dynamical processes unfolding on their fabrics. It focuses in particular on activity-driven networks as an empirically motivated and analytically tractable class of models of the time-varying network. Within this framework the chapter studies the effects of temporal connectivity patterns in random walks, the epidemic model, and the rumor spreading model. The results highlight the striking impact that temporal correlations have on dynamical processes taking place over time-varying networks. The chapter ends by considering future research directions and challenges in this important area.

Keywords: Time-varying networks, social networks, dynamical processes, temporal networks, random walks, epidemic model, rumor spreading model

1. Introduction

The modern world lives and breathes connections: an email to a distant contact, a flight to a faraway land, a railroad to a neighboring city, a road to a different neighborhood, or a phone call to a loved one. The properties of such connections, how they come together to form cohesive networks that knit together our societies, technologies, and thoughts, has been the subject of much scrutiny in recent decades (Barrat et al., 2008; Newman, 2010; Cohen and Havlin, 2010; Barabási, 2016) from researchers in both the physical and social sciences.

Such networks are interesting not only for their own sake, but perhaps even more fundamentally because they form the backbone through which many other processes take place. Ideas (Weng et al., 2013) and memes (Goel et al., 2015) diffuse through emails and phone calls (Onnela et al., 2007), people and the viruses (Pastor-Satorras and Vespignani, 2001) they carry move through transportation networks, economic activity relies on the networks connecting financial institutions, and so on.

The intense research in this area has shown how the structural features observed in real networks affect dynamical processes taking place on their fabric. In particular, heterogeneity in the number of contacts (Albert et al., 2000; Pastor-Satorras and Vespignani, 2001; Vespignani, 2012), the presence of hierarchies (Kitsak et al., 2010; Fortunato, 2010), and different types of correlations between nodes and links (Onnela et al., 2007; Newman, 2002) have been proven to be nontrivial effects on spreading phenomena.

Traditional approaches have focused, in turn, on each of the two aspects mentioned: modeling the network itself and taking a given network and modeling a dynamical process occurring on top of it. These two approaches can be thought of as corresponding to opposite limits of the typical timescale of network evolution, τ_G, which is much faster or much slower with respect to the typical timescale of the dynamical process τ_P. In either case, the two timescales are separated, resulting in an annealed ($\tau_G \ll \tau_P$) or a static network ($\tau G \gg \tau P$).

While such approximations have proven their usefulness and validity in many circumstances such as cascading failures in power grids or the diffusion of data over the Internet, they have also come up short (Butts, 2009, 2008) on the study of many important processes in which the two timescales are comparable (Stehlé et al., 2010) ($\tau_G \sim \tau_P$), as is the case for sexually transmitted diseases (Moody, 2002; Morris, 1993; Rocha et al., 2011), short-lived memes (Miritello et al., 2011; Panisson et al., 2011), and face-to-face interactions (Isella et al., 2011; Stehlé, Voirin, Barrat, Cattuto, Colizza, et al., 2011; Stehlé, Voirin, Barrat, Cattuto, Isella, et al., 2011). This intermediate regimen has become known as temporal networks (Holme, 2015; Holme and Saramäki, 2012) and has been the focus of much recent research (Perra, Baronchelli, et al., 2012; Perra, Gonçalves, et al., 2012; Ribeiro et al., 2013; Karsai et al., 2014; Liu et al., 2014; Tomasello et al., 2014; Scholtes et al., 2014; Lambiotte et al., 2014; Sun et al., 2015).

This chapter provides an overview of recent developments in the study of dynamical processes on time-varying networks. We consider explicitly the case in which spreading occurs on a timescale comparable to the changes of the network in which it takes place. Common examples of this situation are the transmission of sexually transmitted diseases, information spreading through phone calls, and any other process in which edges are active only at specific times. From this vantage point we analytically and numerically study the effects of time-varying topologies on different types of diffusion processes, such as random walks, epidemic spreading, and rumor spreading.

2. Time-Varying Networks

Network modeling stems from sociology, psychology, and graph theory (Albert and Barabási, 2002; Boccaletti et al., 2006; Bollobas, 1998; Newman, 2010). Erdős-Rényi, Logit, and p*-models, and exponential random graphs (Erdős and Rényi, 1959; Molloy and Reed, 1995; Holland and Leinhardt, 1981; Frank and Strauss, 1986; Wasserman and Pattiston, 1996) are examples of the frameworks proposed and adopted over the years. Most recently, research in statistical physics and computer science has led to the development of a new class of models, exemplified by the preferential attachment model (Barabási et al., 1999; Barabási and Albert, 1999; Dorogovtsev et al., 2000; Dorogovtsev and Mendes, 2003; Fortunato et al., 2006; Boguña and Pastor-Satorras, 2011). Although very different in nature, these frameworks can all be classified as “connectivity driven.” Indeed, the goal is reproducing the final aggregated topology of networks obtained through their evolution and growth over time. In other words, such approaches do not explicitly consider the temporal nature of networks and are concerned just with their static properties.

As mentioned, virtually any network evolves in time. The importance of developing modeling frameworks able to account for and reproduce this fundamental feature is clear. Over the last decade various approaches have been put forward (Holme, 2015; Holme and Saramäki, 2012). The problem has been tackled using field dependence. For example, social scientists are traditionally inclined to adopt exponential random graphs (Wasserman and Pattiston, 1996). These models infer from data the importance of the structural element deemed relevant. Recently, this modeling framework has been generalized to consider the dynamical evolution of connections (Hanneke and Xing, 2006; Kolar et al., 2010). In the physics and computer science communities several other models have been introduced that are based on different intuitions and approaches. Some, which consider explicitly face-to-face interactions, model group dynamics starting from the observation that the more a node remains engaged in a group, the less likely it is to leave it (Zhao et al., 2011; Stehlé et al., 2010). Others focus on the timing of contacts, considering multiple timescales and extending mechanisms typically used in the classic static models, such as triadic closure and tie strength reinforcement mechanisms (Jo et al., 2011; Laurent, Saramäki, & Karsai, 2015). Others, motivated by modeling the spreading of infectious diseases, consider a turnover of peers in time or generate contact patterns within a specific time window given a certain mixing function (Volz and Meyers, 2007; Kretzschmar and Morris, 1996).

2.1. Representations

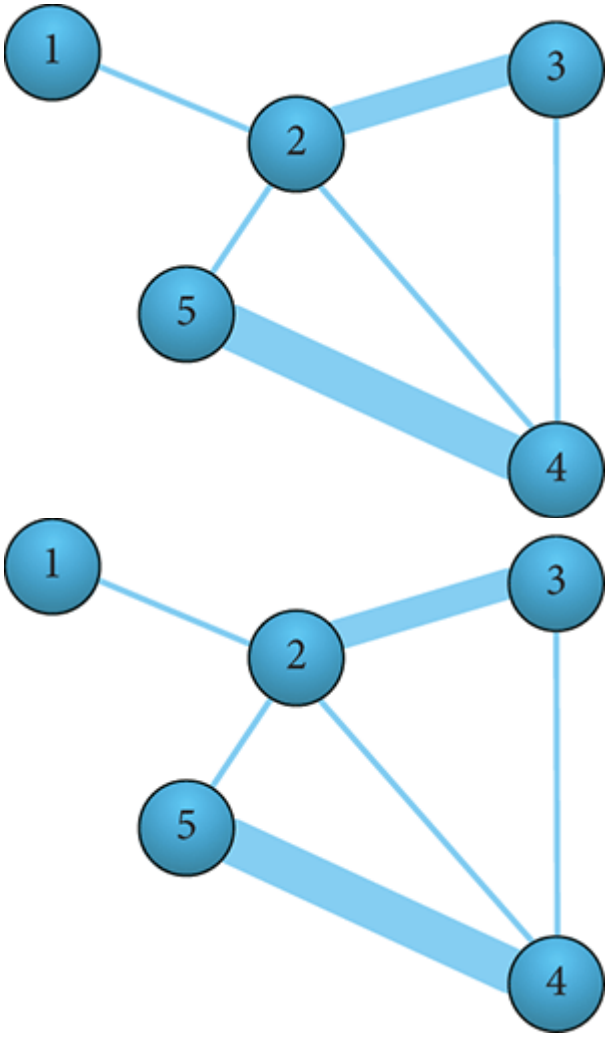

Figure 1. A simple weighted network.

The structure of a static network can be fully specified by just a few pieces of information: node labels, the list of connections between nodes, and the weight of each connection. In the case of weighted or directed networks, a weight or direction can also be assigned to each edge (see Figure 1).

One mathematically convenient way to represent an unweighted network is as a matrix A, known as the adjacency matrix, in which each element, a_{ij}, is zero if there is no edge between nodes i and j and is one otherwise. From this representation we can obtain several network properties by using matrix algebra. For example, a vector containing the in-(out-)degree of each node can be obtained by simply taking the left (right) product of the matrix and a vector of 1s. It is also easy to see that, since a_{ij} is only non-zero when there is a path between i and j, the product

$$a_{ij}\,a_{jk}$$

1.1

will only be non-zero when there is a path from i to j and from j to k. Therefore, by summing over j we obtain the total number of paths between i and k in two steps. In matrix form, this corresponds to the $a_{ij}^{(2)}$ element of the square of the adjacency matrix. This same argument can be justified for further powers of A, such that the $a_{ij}^{(n)}$ gives us the number of paths connecting nodes i and j in n steps. Also, the number of connected components is given by the number of zero eigenvalues of the Laplacian matrix, L = K − A, where K is a diagonal matrix of the node degrees. Weighted networks can be represented by simply replacing each value of 1 by the corresponding weight:

$$A_{ij} = \begin{pmatrix} 0 & 1 & 0 & 0 & 0 \\ 1 & 0 & 2 & 1 & 1 \\ 0 & 2 & 0 & 1 & 0 \\ 0 & 1 & 1 & 0 & 3 \\ 0 & 1 & 0 & 3 & 0 \end{pmatrix}$$

Unfortunately, in the ever more common case of extremely large networks, this representation is not numerically convenient due to the large number of zero elements. In these cases, we represent the network as an edge list:

i	j	w_{ij}
1	2	1
2	3	3
2	4	1
2	5	1
3	4	1
4	5	3

where we simply list one edge per line with the corresponding weight. Now the out-(in-)degrees can be obtain by simply counting how many times each node is listed in the first (second) column, and it is easy to see how we may recover the above matrix representation from this more space-efficient version.

In order to be able to handle the case of temporal networks, we must extend these simple representations. The simplest way to achieve this is to include one extra temporal dimension (see Figure 2). In this case, the adjacency matrix becomes an adjacency tensor:

$$A_{ij}^{(t)} = \begin{pmatrix} 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 \\ 0 & 1 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 1 \\ 0 & 0 & 0 & 1 & 0 \end{pmatrix}^{(1)} \begin{pmatrix} 0 & 1 & 0 & 0 & 0 \\ 1 & 0 & 0 & 1 & 1 \\ 0 & 0 & 0 & 1 & 0 \\ 0 & 1 & 1 & 0 & 1 \\ 0 & 1 & 0 & 1 & 0 \end{pmatrix}^{(2)} \begin{pmatrix} 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 \\ 0 & 1 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 1 \\ 0 & 0 & 0 & 1 & 0 \end{pmatrix}^{(3)}$$

where we have a full adjacency matrix for each time step t, with all the numerical issues that this representation implies. On the other hand, the edge list must also be extended to indicate at which time steps that specific edge is active:

i	j	w_{ij}	t
2	3	1	1
4	5	1	1
1	2	1	2
2	4	1	2
3	4	1	2
2	5	1	2
4	5	1	2
2	3	1	3
4	5	1	3

If we keep the edges in chronological order, we can simply replay the entire history of the system by processing the list one time step at a time.

Thus far we have considered only the common case in which each connection has the duration of a single time step or can be represented as a multiple of individual time steps. This is the case with SMS, email, online chatting, phone calls, and so on. Simple changes can be made to include varying contact lengths.

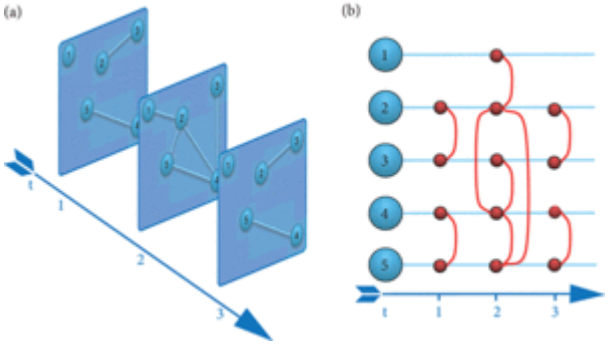

Figure 2. Temporal network representations.

2.2. Properties

The representation changes previously introduced, while apparently trivial, have some deep and nonobvious consequences that require some further formalism modifications and the introduction of new metrics/quantities.

2.2.1. Time-Respecting Path

It is clear that the properties of the adjacency matrix at each time step depend strongly on the size of the time step. For example, if the time step is sufficiently small, it is possible that A^t matrix is fully disconnected, with just a few isolated edges. In turn, this implies that equation 1.1 now becomes

$$a_{ij}^{t} a_{jk}^{t+1}$$

2.1

since we require that the edge between i and j be active at time t and that the connection between j and k be active at t + 1. The adjacency matrix is different from time step to time step, making it clear that any process that takes place on the network is now strongly dependent on the temporal sequence of steps taken: if the aij edge is present only at time t and the ajk edge is present only at time t + 1, then we are able to reach node k from node i (passing through node j) only if we start our journey at time t. As a consequence, there is no static representation of the network that is exactly equivalent to the full temporal sequence.

We define a time-respecting path to be a path that connects two nodes i and k through a sequence of link activations that follow each other in time.

2.2.2. Connectivity and Latency

In general, time-respecting paths are directed, regardless of the directionality of the network at each time step. As in the previous example, it might be possible to go from node i to node k at time t while still being impossible to go from node k to node i at the same time. We can then define a temporal network as strongly or weakly connected if there are

directed or undirected paths between each pair of nodes, respectively. The diameter of the network can be defined in a similar fashion.

Also, the distance between each two nodes will generally change in time. We can define the average distance between two nodes as the number of steps necessary to travel between them averaged over all possible initial times. As temporal paths have an intrinsic duration, we can similarly define the average time necessary to travel between any two nodes. This is necessarily different from the number of steps because we might have to "wait" several time steps for the next necessary edge to be present. The shortest connection time between two nodes is called the latency.

2.2.3. Burstiness

The concept of latency becomes particularly important when we consider temporal networks derived from human activity. Humans are notorious for following complex dynamical patterns that introduce highly not trivial temporal correlations in edge activation sequences. Consider, for example, the case of an individual who reserves a specific time each day to respond to emails and ignores email the rest of the time. Over the short period of time in which he is active, many edges will be activated, one following the other, but this burst of activity will be followed by a long period of inactivity (Jo et al., 2012). This type of behavior results in strong temporal correlations that can have an important impact on the observed properties of the network and on any processes. Such correlations can be easily detected by measuring the distribution of the time interval between two consecutive activations of the same edge or node, the so-called inter-event time distribution. Indeed, the observation in 2005 (Barabási, 2005) of broad-tailed inter-event time distributions in human communications such as emails and letters spurred a flurry of research in models of human dynamics that might be able to account for this observation at the individual level.

Individuals also vary widely in their activity levels. The vast majority of email (Vázquez et al., 2006), Twitter (Kwak et al., 2010), and cell phone (González et al., 2008) users have relatively low activity levels, while the few most active individuals account for the overwhelming proportion of the total activity. As a result, the individual activity distribution is broad tailed and can typically be well approximated by a power-law (Perra, Gonçalves et al., 2012) of the form $P(a) \propto a^{-\beta}$. Such activity heterogeneity is a fundamental aspect of human activity and underlies many different kinds of behavior.

2.2.4. Memory

This brief discussion of some of the fundamental properties of temporal networks is lacking just one final aspect, a user's preference of some edges over others. When an individual becomes active and decides whom to contact, there is a much higher probability of her contacting, say, a boyfriend or a child than, say, a mechanic or a public information line. This phenomenon is usually accounted for by introducing the concept of memory (Gonçalves et al., 2011). Users "remember" whom they contacted in the past (and how often) and then choose accordingly, resulting in a higher chance of connecting to someone who has recently been connected to (as you might call someone back after a few minutes

to confirm an appointment time) as well as to someone you contact often (such as a significant other or a family member). This results in strong and weak ties, in the language of Granovetter (1973), and explains the seminal observations of Moreno (1953) about how individuals choose to spend their social capital differently from others.

2.3. Activity-Driven Networks

Having introduced some of the fundamental concepts and ideas relating to temporal networks, we now turn to an analytically tractable approach, the so-called activity-driven modeling framework (Perra, Baronchelli, et al., 2012; Perra, Gonçalves, et al., 2012; Karsai et al., 2014; Liu, Baronchelli, & Perra, 2013; Liu, Perra, Karsai, & Vespignani, 2014; Tomasello et al., 2014). This approach has the advantage of keeping the number of assumptions to a minimum and has proven to be able to explain several properties observed in empirical networks.

The activity-driven approach starts from the observation that the propensity of individuals to be engaged in social acts is highly heterogeneous and then gradually adds new details to obtain an increasingly realistic model that remains tractable while allowing us to study analytically the effects of time on spreading phenomena.

In activity-driven networks N nodes are characterized with an activity rate a_i, defined as the probability per unit of time to create new contacts or interactions with other individuals. The activity of each node is assigned from a probability distribution F (a) that can be defined a priori or determined from empirical observations.

From a given activity distribution the network can be generated, in its simplest form, as follows:

- At each time step t the network Gt starts with N disconnected nodes.
- With probability $a_i\Delta t$ each vertex i becomes active and connected to m randomly selected vertices. Nonactive nodes can still receive connections from other active vertices.
- At the next time step t +Δt, all the edges in the network Gt are deleted.

It should be noted that in its simplest incarnation, this model generates a Markovian process with no burstiness or memory. Indeed, nodes do not have memory of the previous time steps and do not recollect with whom they interacted. The full dynamics of the network are encoded in the activity distribution F (a). In the common case where F (a) ~ $a^{-\gamma}$, the network generated at each iteration is a simple random graph with low average connectivity. However, by integrating the links generated over a large time window of size T, the model generates a broad-tailed degree distribution, P_T (k), due to the wide variation of activity rates in the system.

It is crucial to note the different interpretation of the formation of hubs in this case in respect to different growing network models as the preferential attachment. While in activity-driven networks the creation of hubs is driven by the presence of highly active nodes

that repeatedly engage in more interactions than typical nodes, in preferential attachment models hubs are the result of different forms of positional advantage (older nodes are more likely to have large numbers of connections) and a passive attraction of connections (the rich get richer).

At each time step, the average number of active nodes is N<a>. Since each active node creates m links, the average degree at each time t can be written as:

$$\langle k \rangle_t = \frac{2E_t}{N} = 2m \langle a \rangle$$

2.2

Interestingly, in the limit of small k/N and k/T, the degree distribution of the integrated network, defined as the union of the links generated at each time step, can be written as PT (k) ~ F [k/Tm], meaning that the degree distribution of the integrated network follows the same functional form of the activity distribution (Starnini and Pastor-Satorras, 2013). Remarkably, this theoretical prediction is approximately observed in empirical data (Perra, Gonçalves et al., 2012), giving us the first indication that despite their simplicity, activity-driven networks are able to accurately reproduce important features observed in real networks.

The simplicity of the model, however, comes with a cost. As described so far, these models are unable to capture the lifetime distribution of links and the memory of nodes as previously described. To be able to account for them, we must introduce a simple reinforcement mechanism in how each of the m connections at each time step t is chosen. We define the probability, p(k), that the next communication event of a node currently having k social ties will result in the establishment of a new $(k + 1)^{th}$ link (Karsai et al., 2014; Ubaldi et al., 2016) and introduce a crucial difference to the model previously described: a node with k previously established social ties will connect randomly a new node with probability p(k). Otherwise, with probability 1 − p(k) she will interact with a node already contacted, thus reinforcing earlier established ties. In this case, the selection is done randomly among the k neighbors. Empirical studies have shown that p(k) is well approximated by

$$p(k) = 1 - \frac{k}{k - c} = \frac{c}{k + c}$$

2.3

where c is a constant that does not depend on the degree of the node considered and can be defined to be c = 1 without loss of generality. The behavior of p(k) with k suggests that the larger the number of people with whom a node interacted, the smaller the probability that a new tie will be activated. In other words, the activity of nodes is distributed most likely toward a small number of strong ties.

We refer here to the original model as ML, meaning memory less, and to this modified version as WM. A comparison between time-aggregated networks generated by the two models allows us to better understand the effects of memory (Karsai et al., 2014). The ML dynamics induce an aggregated network with a degree distribution following the same functional form of the activity and a weight distribution decaying exponentially (Perra, Gonçalves et al., 2012; Starnini and Pastor-Satorras, 2013). In case of the WM dynamics, memory induces a considerably different structure. In particular, the degree distribution is more skewed in the WM model than in the ML. Furthermore, the WM model generates a heterogeneous weight distribution capturing observations in real data (Karsai et al., 2014).

3. Dynamical Processes on Activity-Driven Networks

The following discussion analytically and numerically explores different spreading phenomena unfolding on ML and WM activity-driven networks. In particular, we will explore diffusive processes (i.e. random walks), as well as simple (i.e. epidemic spreading) and social contagion phenomena.

3.1. Random Walks

Random walks are fundamental diffusion processes (Newman, 2010; Noh and Rieger, 2004; Barrat et al., 2008; Baronchelli and Pastor-Satorras, 2010) with applications in a wide variety of disciplines, ranging from economics and genetics to physics and the arts. They also form part of the secret behind the success of modern search engines such as Google (Brin and Page, 1998; Page et al., 1999). The basic idea behind random walks is a simple one: a set of particles or individuals at each time step randomly choose their next move based on their current location and a probability distribution over future states. In the context of networks, the future states correspond to the nearest neighbors of the current node and result in a random path through the graph. Clearly the behavior of random walkers is determined by the topological features of the underlying network and as such can provide fundamental clues about the structure of often unknown media through the way they diffuse.

In network science, the large majority of research has taken place within one of the two limits previously discussed, considering either quenched or annealed graphs (Newman, 2010; Noh and Rieger, 2004; Barrat et al., 2008; Baronchelli and Pastor-Satorras, 2010). More recently, these studies have been extended to consider random walks diffusing at the same timescale as the one ruling network evolution (Perra, Baronchelli et al., 2012; Ribeiro et al., 2013; Lambiotte et al., 2014; Masuda, Porter, and Lambiotte, 2017). Indeed, these phenomena are the perfect example test bed for the effects of time-varying topologies on diffusion processes.

Before diving into the most recent results, let us formulate the problem with some mathematical rigor and briefly revise some classic results involving annealed networks. This will provide us with a theoretical framework we can later expand on to include activity-driven networks. Let us consider a generic graph, G, with degree distribution, P(k). If we want to be as generic as possible, all we need is to define the conditional probability P(k'|k) that a node of degree k' is found at the end of an edge emanating from a node of degree k. With this definition, all nodes of the same degree class k are statistically equivalent. This is known as the configurational or Molloy-Reed model (see Molloy and Reed, 1995).

Let us consider a number W of walkers diffusing uniformly (one edge at a time) in the network. The average number of walkers in a given degree class is then $W_k = \sum_{i|k_i=k} W_i/N_k$, with Nk being the number of nodes with degree k. The variation of Wk in time is given by

$$\frac{dW_k}{dt} = -W_k + k\sum_{k'} P(k'|k)\frac{W_{k'}}{k'}$$

3.1

The first term on the right-hand side (r.h.s.) of this expression takes into account the number of walkers moving out of each node of degree k, while the second term describes the number of walkers reaching nodes of degree k from nodes of any other degree class. For uncorrelated networks, the probability that a node of degree k is connected to a node of degree k' is a function of just k', so that the stationary state of the above equation is given by

$$W_k = \frac{k}{<k>}\frac{W}{N}$$

3.2

Interestingly, after an initial transient the number of walkers in each degree class reaches a dynamical equilibrium that scales linearly with the degree. In other words, nodes of higher degree will tendentially obtain a larger number of walkers. It is possible to prove that this holds for any undirected network (Noh and Rieger, 2004). Furthermore, we find p_k =Wk/W is the probability that a random walker visits a given node of degree This quantity preserves the linear scaling with the degree, that is, p_k = k/<k>N. As a consequence, nodes with larger degree are characterized by a large probability of discovery (Newman, 2010; Noh and Rieger, 2004; Barrat et al., 2008).

Let us now consider the same processes unfolding on an ML activity-driven network. In this case, the spreading phenomenon proceeds as follows: at each time step t an activity-driven network G_t is generated, and walkers diffuse on it for a time Δt. After diffusion, at time t + Δt, a new network $G_{t+\Delta t}$ is generated. It is important to note that dynamics of the random walker and the network take place at the same timescale, introducing a unique

feature not found on static or annealed networks: walkers can get trapped in temporarily isolated nodes for an extended period of time, as described in our previous discussion of burstiness. As we will see, it is now convenient to consider activity classes instead of degree classes, by assuming that all nodes within degree class a are statistically equivalent. It can be shown (Perra, Baronchelli et al., 2012) that the number of walkers, W_a, in a given node of activity class a is given by

$$\frac{dW_a}{dt} = -\mathrm{a}W_a + amw - m < a > W_a + \int a' W_{a'} F(a')\, da'$$

3.3

where w ≡ W/N is the average number of walkers per node, and we have taken the continuous a limit. The first two terms on the right-hand side are due the activity of the nodes in class a, which release all the walkers they have and receive walkers originating from the nodes they connect to. The last two terms describe the activity of the nodes in all the other activity classes that connect to nodes of activity class a. The stationary state of the process is then

$$W_a = \frac{amw + \phi}{a + m < a >}$$

3.3

where $\varphi = \int aF\ (a) W_a da$ is the average number of walkers moving out of active nodes. Interestingly, in the stationary state this quantity is constant, and can be evaluated self-consistently as shown in Ref. [25].

It should be noted that the behavior of time-varying networks is strikingly different than that of static and annealed networks (see Figure 3). Indeed, in time-varying networks the number of walkers is not a linear function of the activity, but rather saturates at sufficiently large values of a. The origin of this difference is deeply rooted in the properties of the instantaneous network. Nodes with high activity have on average k ~ m connections at each time step, resulting in a limited capacity for collecting new walkers, a feature that is not present in time-aggregated views of dynamical networks (Perra, Baronchelli et al., 2012). These results highlight the importance of an appropriate consideration of the time-varying feature of networks in the study of exploration and spreading processes in dynamical complex networks.

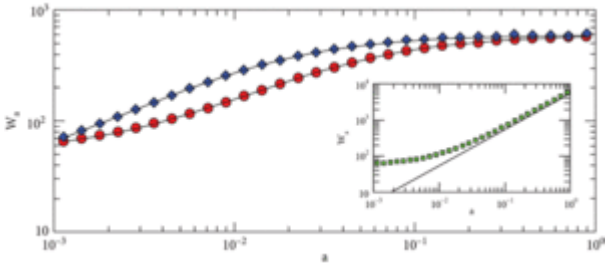

Figure 3. Diffusion dynamics in networks.

Note: In the main panel W_a is shown as a function of a for random walkers diffusing on activity driven networks with activity distribution $F(a) \sim a^{-\gamma}$. $\gamma = 2$ (circles) and $\gamma = 2.8$ (diamonds). Solid lines describe the analytical prediction equation 3.3. In the inset W_a is shown as a function of a random walks on top of an activity driven network with $F(a) \sim a^{-2}$, integrated over $T = 50$ time steps. The solid line corresponds to the curve $W_a \sim a$, fitting the simulation points for large value of a. In all the cases $N = 10^5$, $m = 6$, $\varepsilon = 10^{-3}$, and $w = 10^2$. Averages performed over 10^3 independent simulations.

3.2. Epidemic Spreading

From the diffusion of individuals or walkers between nodes we now proceed to consider the way in which information or viruses spread and infect the nodes of a network. Not surprisingly, due to its practical importance, the modeling of the spreading of infectious diseases has a long tradition that dates back to the work of Bernulli in 1760 (Bernulli, 1760). When considering illness that spreads from human to human, it is clearly of crucial importance consider the way we interact. For this reason, one of the most relevant applications of network science is devoted to the understanding of our contact patterns and how these affect the spreading of infectious diseases (Newman, 2010; Barrat et al., 2008; Keeling and Rohani, 2008). In this case, although contact networks are highly dynamical in nature (Morris and Kretzschmar, 1997; Morris, 2007; Isella et al., 2011), the large majority of research has been done on quenched or annealed networks. While these approximations are well suited to model influenza-like Illnesses, they fail to capture more complex diseases such as sexually transmitted diseases, where the concurrency, frequency, duration, and order of contacts are crucial ingredients (Morris and Kretzschmar, 1997; Morris, 2007; Rocha et al., 2011; Isella et al., 2011; Perra, Goncalves et al., 2012).

As before, let us start by reviewing some classic results obtained on annealed networks before proceeding to the activity-driven case. In the susceptible-infected-susceptible (SIS) epidemic compartmental model (Barrat et al., 2008; Kermack and McKendrick, 1927; Keeling and Rohani, 2008; Pastor-Satorras, Castellano, Van Mieghem, and Vespignani, 2015), the population is divided into two classes of individuals: susceptible individuals, who are healthy, and infected individuals, who have the disease and are able to spread it. The disease propagates from infected to susceptible neighbors with probability λ per contact, while infectious individuals spontaneously recover with rate μ, rejoining the ranks of

susceptible individuals. The infection and recovery process can be described by the following transitions:

$$S + I \rightarrow 2I$$

3.4

$$I \rightarrow S$$

In a well-mixed population the behavior of the epidemics is controlled by the reproductive number R0 = β/μ, where β = λ <k> is the per capita spreading rate that takes into account the rate of contacts, <k> of individuals. The reproductive number provides the average number of secondary infections generated by a primary case in a fully susceptible population (Keeling and Rohani, 2008). As such, it is easy to see that an epidemic can only occur when R0 > 1, which implicitly defines the epidemic threshold. Above this value epidemics can reach an endemic state and be sustained by the population. Indeed, it is easy to show that the SIS dynamics are characterized by a dynamic equilibrium defined by a finite fraction of individuals in the infected state, that is, an endemic state (Keeling and Rohani, 2008).

Over the last fifteen years the well-mixed population approximation has been gradually relaxed through the inclusion of more realistic and data-driven connectivity networks and mobility schemes. This has highlighted new and interesting results showing clearly the importance of accounting for complex topologies when modeling spreading phenomena (Lloyd and May, 2001; Balcan et al., 2009; Wang et al., 2003; Chakrabarti et al., 2008; Castellano and Pastor-Satorras, 2010; Wang et al., 2016). In particular, the epidemic threshold has been found to depend on the topological properties of the networks (Castellano and Pastor-Satorras, 2010; Pastor-Satorras et al., 2015). In the case of static networks, the threshold is given by the principal eigenvalue of the adjacency matrix (Wang et al., 2003; Chakrabarti et al., 2008). For annealed networks, the epidemic threshold is a function of the first and second moments of the degree distribution (Barrat et al., 2008; Vespignani, 2012):

$$\frac{\beta}{\mu} > \frac{< k >^2}{< k^2 >}$$

3.5

It is important to note that the heterogeneities observed in real networks induce second moments significantly larger than the first moment. In other words, the heterogeneity in the number of contacts pushes the epidemic threshold to small values, facilitating the spread of the disease. While the scenario emerging from this observation is rather scary, it suggests extremely efficient methods to protect ourselves from the diffusion by means of targeted vaccinations (Barrat et al., 2008; Vespignani, 2012).

How do the network dynamics affect a disease spreading at the same timescale? It is very easy to understand the importance of time in this case. Indeed, a disease characterized by a small infectious period, μ^{-1}, will have time to explore a time-aggregate network, but it might not have time to spread on the dynamic instantaneous networks whose union defines the time-aggregated one (Moody, 2002; Morris and Kretzschmar, 1997; Morris, 2007; Isella et al., 2011). In fact, if the disease spreads on aggregated networks, all edges will be readily available to carry the contagion process, disregarding the fact that the edges may be active or not according to a specific time sequence defined by the agents' activity. This intuitive observation can be precisely quantified by calculating analytically the epidemic threshold. Let us consider an SIS process unfolding on ML activity-driven networks. The epidemic dynamic can be characterized by studying the number of infected individuals in the class of activity rate a (Perra, Goncalves et al., 2012). The variation of this quantity is described by the following equation:

$$\frac{dI_a}{dt} = -\mu I_a + \lambda m \left(N_a - I_a\right) a \int da' \frac{I_{a'}}{N} + \lambda m \left(N_a - I_a\right) \int da' \frac{a' I_{a'}}{N}$$

3.6

where Na represents the total number of individuals in activity class a. In equation 3.6 the first term on the r.h.s describes the recovery process, while the second takes into account the probability that a susceptible individual of class a is active and acquires the infection through a connection with any other infected individual. Finally, the last term considers the probability that a susceptible is contacted by any infected active individual. The equation can be solved yielding the epidemic threshold (Perra, Goncalves et al., 2012; Rizzo, Frasca, & Porfiri, 2014; Starnini & Pastor-Satorras, 2014):

$$\frac{\beta}{\mu} > \frac{2 < a >}{< a > + \sqrt{< a^2 >}}$$

3.7

The threshold is then a function of the first and second moment of the activity-driven distribution. It considers the activity rate of each node while taking into account the actual dynamics of the interactions. We note that this formula does not depend on the time-aggregated network representation used. The spreading process is characterized considering the interplay between the timescale of the network and spreading process evolution. As shown in Figure 4, in the case when the two dynamics unfold at comparable timescales, the epidemic threshold, predicted by equation 3.7 is significantly larger than the threshold of the same process taking place on a time-aggregated representation of the same network (Perra, Goncalves et al., 2012). This implies that neglecting the evolution of connectivity patterns might induce an underestimation of the spreading potential of an infectious disease.

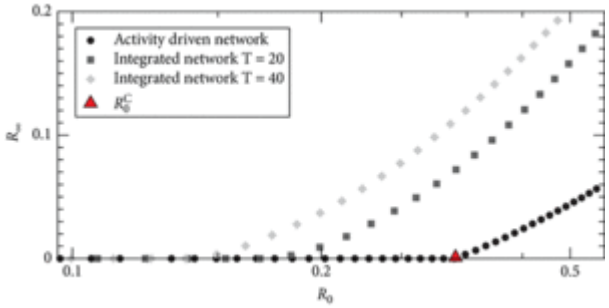

Figure 4. Epidemic dynamics in networks.

Note: Density of infected nodes, i_∞, in the stationary state, obtained from numerical simulations of the SIS model on a network generated according to the activity driven model and two other networks resulting from an integration of the model over 20 and 40 time steps, respectively. $N = 10^6$, $m = 5$, $\eta = 10$, $F(x) \propto x^{-\gamma}$ with $\gamma = 2.1$ and $\varepsilon \leq x \leq 1$ with $\varepsilon = 10^{-3}$. Each point represents an average over 10^2 independent simulations. The red triangle marks the epidemic threshold as predicted by equation 3.7

Highly active nodes engage repeatedly in social interactions and can drive the spreading process. Indeed, it has been proved that immunizing a small fraction of such nodes will result in complete protection for the entire population (Liu et al., 2014).

3.3. Rumor Spreading

Epidemic spreading can be considered a simple version of the way in which information spreads. The field of rumor spreading takes the lessons learned from the way viruses diffuse among nodes and modifies and extends them to the more general case of diffusion of information.

Rumor spreading is responsible for the adoption of innovations and the spreading of ideas, information, or rumors in a population (Barrat et al., 2008), and while it is sometimes referred to as “viral,” the manner in which rumors spread through a social network has significant differences from epidemic spreading. Indeed, the spreading of an idea is induced by a sequence of intentional and deliberate acts, while the spreading of a disease is passive and can occur just by being in proximity to others, despite our intentions. Also, multiple exposures to the same rumor might be required before “infection” occurs, and different individuals will naturally have a different propensity to adopt and or diffuse an idea or a piece of information (Barrat et al., 2008). All these properties make the modeling and description of social contagion extremely challenging. However, it is intuitive to understand that the features of the connectivity patterns describing the interactions of individuals play a crucial role on the unfolding of social contagion. As for the other dynamical processes, the large majority of research in the past considered the timescale separation limit. We first formulate the problem and revise some classic results in this limit, then discuss these dynamics in time-varying networks.

In the most fundamental rumor spreading process (Daley and Kendall, 1964), each node can be in three possible states according to its status with respect to the rumor: ignorant (I) nodes are unaware of the rumor, spreaders (S) are aware and actively spread it, and stiflers (R) are aware of the rumor but have since decided to no longer spread it. The dynamic of the models can be described by the following transitions:

$$\mathrm{I} + \mathrm{S} \xrightarrow{\lambda} 2\mathrm{S}$$

$$\mathrm{S} + \mathrm{R} \xrightarrow{\alpha} 2\mathrm{R}$$

$$\mathrm{S} + \mathrm{S} \xrightarrow{\alpha} 2\mathrm{R}$$

Here λ and α describe the transition rates into the states of spreader or stifler, respectively. While the contagion transition in this case is mathematically equivalent to the one we considered for the epidemic process, spreaders recover to become stiflers when they come in contact with other spreaders or stiflers. In other words, the recovery process is not spontaneous but is instead mediated by interactions, a property that has critical effects on the spreading patterns.

We can better understand this point by considering a rumor diffusing on a simple Watts and Strogatz (WS) network (Watts and Strogatz, 1998). In the WS model, nodes are arranged in a circle, and the links are static. Each node has k links connecting it to the closest nodes on the left, and k links connecting to the closest nodes on the right. Each edge is then randomly rewired with probability p. As p varies between 0 and 1, the network changes character from a regular graph to an Erdős-Rényi network (Erdős and Rényi, 1959). At intermediate values of p the resulting networks are simultaneously characterized by a small diameter, due to the random shortcuts, and high values of clustering, due to the local initial ordered arrangement (Watts and Strogatz, 1998). This topology is extremely useful to understand the dynamics of rumor spreading models. At small values of p the high level of clustering results in a localization of the spreaders that in time transition to stiflers, stopping the overall spreading of the rumor (Zanette, 2001). As p increases, the number of shortcuts increases, reducing the localization of connections and the annihilation of spreaders with a phase transition occurring at a point that depends on the value of k (Zanette, 2001). These results show clearly the difference between rumor and epidemic spreading. In this case the repetition of contacts induces an early termination of the spreading.

Armed with this understanding of the classical rumor spreading model, we are now able to better understand the effect that the temporal dynamics of ML and WM activity-driven networks (Karsai et al., 2014; Ubaldi et al., 2016) can have on this process. Numerical simulations on the subject (Karsai et al., 2014) show a clear difference between the two cases. The repetition of contacts that is characteristic of WM dynamics results in a strong reduction on the final fraction of nodes aware of the rumors with respect to the ML case (see Figure 5). In order to understand the biases induced in the dynamical properties of rumor spreading processes by the time-aggregated representation of the networks, Kar-

sai et al. (2014) considered the topologies generated by a time-aggregated view of ML and WM models and compared the results with their time-varying counterparts. The results obtained showed striking differences between the velocity of spreading. The time for a rumor to reach a consistent fraction of nodes can vary by four orders of magnitude between the two cases, with very slow spreading dynamics in time-varying networks. These results further illustrate the clear difference between the dynamical properties of processes taking place on time-aggregated or time-resolved networks and confirm once again that when the timescale of the processes is comparable with the evolution of the network, static representations of the system might introduce strong errors into the characterization of the phenomenon.

Figure 5. Rumor spreading processes.

Note: Panel (a) visualizes spreading in ML activity driven networks; panel (b) visualizes spreading in WM activity driven networks. Node colors assign their states as ignorant (blue), spreader (red), and stifler (yellow) states. Node sizes, color, and width of edges represent the corresponding degrees and weights. The parameters of the simulations are the same for the two processes: $N = 300$, $T = 900$, $\lambda = 1.0$, and $\alpha = 0.6$. The process was initiated from a single seed with maximum strength.

4. Discussion

The era of big data is revolutionizing our technology and how we communicate and interact. As our social interactions become more reliant on technology through email, cell phones, online social networks, and so on, they also become more amenable to large-scale analysis, creating unprecedented opportunities for the social sciences and also unique theoretical and practical challenges.

Our social interactions are naturally represented as temporal connections taking place over an underlying social network. Despite a wealth of recent progress, the field of temporal networks is just now coming of age, and much still remains to explore. The quenched and annealed limits of network dynamics are well understood, but the intermediate regime where $\tau_G \sim \tau_p$ is mostly unexplored.

In this short chapter we have reviewed some recent theoretical results using the activity-driven framework for three classical dynamical processes: random walks, epidemic spreading, and rumor spreading. These processes are the most prototypical examples of dynamical processes and cover three important aspects of human behavior: mobility, public health, and information spreading. They also have a long and venerable history of theoretical, analytical, and simulation results that can guide us to better understand how our changing social landscape can impact our lives.

The WP and ML network dynamical models we have explored are just the first steps toward the modeling of real-world social dynamics. For instance, they still do not take into account burstiness or different classes of nodes (say, male and female). They are also not able to directly explain the latency, connectivity, and clustering properties of real networks, both social and technological. Much remains to be done in this emerging field, and we hope that this chapter can contribute to raising the interest of other researchers in this interesting and promising field of research.

While simple, the results introduced here demonstrate the fundamental importance of understanding the way the different timescales interact in the real world, resulting in more complex and realistic models. Any process that relies on the explicit activation of an edge (as a phone conversation relies on the recipient picking up the phone) must be analyzed in light of a temporally explicit framework such as this if we are to properly understand and model real-world phenomena. In many cases, the timescale of contact is given by the process itself (like the duration of a phone call), while in others it must be explicitly chosen by the researcher. Methods to determine the optimal timescale are a subject of ongoing research.

The rise of passive data collection that we are currently witnessing in the form of the World Wide Web and the “Internet of Things” will undoubtedly result in an unprecedented increase in the number of processes for which detailed temporal information is available. The development of methodologies that are able to correctly account for the inherent temporal characteristics and correlations is an important step in furthering our understanding of the modern world and of our place within it.

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