Diffusive Phenomena in Dynamic Networks: a data-driven study

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Abstract. Everyday, ideas, information as well as viruses spread over complex social tissues described by our interpersonal relations. So far, the network contexts upon which diffusive phenomena unfold have usually considered static, composed by a fixed set of nodes and edges. Recent studies describe social networks as rapidly changing topologies in which interactions are bursty and node presence is not stable. In this work – following a data-driven approach – we compare the behaviors of classical spreading models when used to analyze a same social network whose topological dynamics are observed at different temporal-granularities. Our goal is to shed some light on the impacts that the adoption of a static topology has on spreading simulations as well as to provide an alternative, dynamic-aware, formulation of two classical diffusion models.

Keywords: Diffusion processes, Information Spreading, Dynamic Networks

1 Introduction

Since the last decade we are accustomed to living two lives at the same time: one offline and one online. Indeed, one of the most immediate facilities the WWW has granted us is the dismantle of physical distances, thus impacting the way diffusive phenomena evolve.

In the real world, we are used discussing the spread of viruses, such as influenza, or diseases, *passive* contagion processes that do not require active agents to unfold. The diffusion of ideas, conversely, is an example of *active* process: each individual can choose to adopt a new idea or not, to advertise it or not. When we move to the online world we can experience both *passive* diffusions as well as *active* ones. Diffusion processes occur on top of social structures that, so far, have been often considered static in analytical studies. However, both passive and active processes require a direct contact for a content to spread from an already *infected* person to a susceptible one. Social interactions have a limited duration so that they dynamically shape the topology of our social graph – indeed, we are not constantly in contact with all our friends.

In this work, we tackle the problem of understanding if, and how, dynamic network topology affects the diffusion of information. Is a static social network

representation enough to correctly simulate information spreading? Must topology dynamics be taken into account in order to better understand the real diffusive phenomena?

2 Related Works

In order to better approach the analysis of diffusive phenomena on time evolving social graphs two different, yet related, topics need to be reviewed and discussed: information spreading and dynamic social networks analysis.

Information Spreading. Commonly, when we use the word *"spreading"* we think to contagious diseases caused by biological pathogens, like influenza, measles or sexually transmitted diseases. However, a plethora of phenomena can be linked to the concept of epidemic: think about the spread of computer viruses [1], or the spread of mobile phone virus [2,3], or the diffusion of knowledge, innovations, products in an online social network [4]. In this paper, we focus on the diffusion of a particular content: innovations/ideas. The diffusion of innovation theory was developed by Rogers in 1962 [5]: it aims to explain how an idea or product gains momentum and diffuses through a specific population or social system. Rogers found that people who adopt an innovation early have different characteristics than people who adopt an innovation later.

Although often treated as similar processes diffusion of information and epidemic spreading can be easily distinguished by a single feature: the degree of *activeness* of the subjects they affect.

Dynamic Social Networks. Since its beginning, complex network analysis has been approached by researchers through the definition of specific mining problems. Among them community discovery [6], link-based object ranking [7], frequent pattern mining [8] are only examples of analytical tasks originally defined on networks *"frozen in time"*.

However, with the explosion of human-generated data, time has started representing a non-negligible entity. During the last decade, several works have tried to cope with such important dimension providing novel interpretations of known problems, porting them from static networks to temporal networks: motifs mining [9], Link prediction [10], community discovery [11] are only few examples.

Indeed, it has been shown that networks inferred from social ties can be used to observe, characterize and forecast different aspects of human activities and that, in order to correctly describe social phenomena, it is mandatory to consider different granularity of temporal abstraction [12]. Once understood the importance of ties dynamics for the overall network topology it becomes natural to study how they affect spreading phenomena.

Spreading on Dynamic Networks. Information spreading on social networks has always produced a considerable attention from various disciplines. Most of the works on such subject mainly focus on studying the effect of diffusion processes on static networks, but as we already discussed, the structure of social networks continuously change as time goes by. Recently, the analysis of diffusive processes in dynamic networks has started to capture the attention of the

research community, such as in [13] where the authors used a SI-type spreading process or in in [14] where they used the SIR model in dynamic contests

One of the few investigations of how dynamic networks affects the spread of information is found in [15] where features of time-varying social networks are measured empirically using a dataset of phone calls. In [16] the authors investigated empirically link formation mechanisms that are driven by the information generating behavior of individuals. One common theme of investigation relates network topology evolution as response to spreading processes. In [17] the authors applied Independent Cascade Model and Linear Threshold Model on Twitter showing that their lack in capturing diffusion in dynamic contexts. Finally, in [18] a data driven study similar to ours was performed. However due to the short timespan of the analyzed data, the authors was forced to synthesize network topology evolution thus making impossible to observe the impact of characteristic phenomenon events on the diffusive process.

3   Problem definition

In this work, we tackle a particular typology of network spreading: the diffusion of innovation. Innovation diffusion is a term often used to describe an active process: each agent autonomously decide to adopt/publicize a given behavior/idea, the sole exposition to it is not sufficient to get infected. Our analysis will be focused on answering the following questions:

Q1: can analyzing spreading phenomena on a static social graph lead to an overestimate of the real volume of its diffusion?

Q2: do the choices made to keep track of topology dynamics impact the speed of diffusive processes?

Q3: is it safe to assume that spreading phenomena on a dynamic network topology unfold at a constant rate? Do the variations, as the diffusion progresses, of the number of nodes/edges impact the overall diffusion process?

To address such questions, we define three scenarios each capturing a different temporal granularity of topology evolution and observe their impact on the evolution of spreading phenomena. To do so, we model a network as an undirected graph denoted as $G = (V, E)$, where V is the set of the nodes and E is a set of interactions (edges), i.e., a set of triple (u, v, t) where $u, v \in V$ are nodes and $t \in \mathbb{N}$ identify the time at which an *interaction* occurs between nodes u to v. Since we will analyze dynamic social interaction graphs we allow the presence of multiple interactions among the same pair of nodes. Moreover, in the following, we will denote with E_{t_j} the set of interactions that appears in the graph at time t_j. We can formalize the problem in the following way:

Definition 1 (Spreading problem). *Given a network $G = (V, E)$ observed for k consecutive snapshots (i.e., $\forall (u, v, t)$, $t \in \{t_1, t_2, ..., t_k\}$), a diffusion model $\mathcal{D}$, and a set $I_{t_0} = \{n_1, n_2, ..., n_j\} \subseteq V$ identifying the initial infected nodes we define the result of $\mathcal{D}(G, I_{t_0})$ as the ordered sequence $\mathcal{I} = \{I_{t_1}, ..., I_{t_k}\}$ of the nodes infected during each network snapshot.*

The scenarios we will analyze in our data-driven investigation are:

- *S1 – Static topology.* In this first scenario for each time t_i with $i = 1, ..., k$, we applied $\mathcal{D}$ to the full network $G = (V, E)$ using as infected node set at time t_i the result of $\mathcal{D}(G, I_{t_{i-1}})$. In this case the set of edges will be $E = E_{t_1} \cup E_{t_2} \cup ... \cup E_{t_k}$.
- *S2 – Snapshot Evolution.* In this second scenario for each time t_i with $i = 1, ..., k$ we compute $\mathcal{D}(G_{t_i}, I_{t_{i-1}})$ where $G_{t_i} = (V, E_{t_i})$.
- *S3 – Interaction Dynamics.* In this last scenario for each time t_i with $i = 1, ..., k$ we apply $\mathcal{D}$ incrementally to the ordered stream of interaction in E_{t_i}.

The difference between **S2** and **S3** lies in the temporal granularity used to track topology dynamics. To better understand how they differ let us consider as graph snapshot unit a single day. In **S1** a network will be built flattening all the interactions occurred during the observed time span in a single one, thus describing dynamic phenomena with a static structure. In **S2** a network will be built for each day and the spreading process computed on each one of them starting, incrementally, from the previous infection status. Finally, in **S3** all the interactions among nodes that occur during each day will be analyzed in their natural, temporal, ordering: no network will be explicitly built, the spreading process will be simulated considering only a single one-to-one contact at a time.

4 Data Driven Study

To address our research questions, we carried out a data-driven investigation involving two interaction graphs. In particular, we used the following datasets: **WEIBO**[3]: this dataset is built upon the logs of the popular Chinese micro-blog service WEIBO[4]. An interaction represents a direct message from two users. We selected the first 90 days from the year 2011.
Facebook: the FB07 network is a sample of the WOSN2009 [19] dataset and describes online interactions between Facebook users during 2007.
In Table 1 are reported the main statistics of the networks.

On such datasets, we simulated two classical compartmental models SI and SIR detailed in 4.1. For each scenarios, in 4.2 we compared the diffusion trends obtained while varying network dynamic and the model's parameters; in 5 we discuss our results and underline their relations with the topology dynamic.

4.1 Diffusion models

To understand how network dynamics impact spreading processes, we focus our attention on two well-known compartmental models: SI and SIR. These models were chosen to describe two slightly different information diffusion scenarios:
D1 – Continuous advertising: after having adopted an idea/innovation an

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[3] http://www.wise2012.cs.ucy.ac.cy/challenge.html
[4] http://weibo.com

Network	Nodes	Interactions	Edges	CC	#Observation
WEIBO	1 656 615	6 759 012	3 394 566	152	90 days
FB07	19 561	304 392	67 077	13	365 days

Table 1. Base statistics of the analyzed interaction graphs. CC identifies the number of connected components.

agent continue to advertise it to its neighbors during each interaction;

D2 – Diminishing advertising: after having adopted an idea/innovation an agent can decide to stop advertising it to its neighbors.

Since both models have been described for complete networks and static graphs, we will describe the modifications to apply them to the S2 and S3 scenarios.

SI: this epidemic model was introduced in 1927 by Kermack [20]. During the epidemics an individual can belong to two stages, *infected* (I) and *susceptible* (S): we adopt SI to simulate diffusion scenario D1. SI assumes that if a susceptible node comes into contact with an infected one, it becomes infected with probability β. The model can be described by the transition rule $S \rightarrow I$, where the arrow indicates that once an individual becomes infected, it stays infected.

S1: Static network. In this scenario, the temporal dimension is collapsed into a single static network composed of all the nodes and interactions in that appear in the dataset. As a first step, an initial set of nodes are considered *infected* and thus assigned to the I set while the others belong to the susceptible set S. For every day t_i, with $i = 1, ..., k$, each node $u \in V$ having at least an infected neighbor is evaluated in order to decide if it will become infected or not. SI sets the probability of infection for a node having n infected neighbors as $n\beta$: the more the infected neighbors a node has the higher its chance to join the I set.

S2: Snapshot-based evolution. To adapt the classical formulation to the snapshot based topology evolution we updated the network structure during each iteration. The model applied at day t_i will then use as starting infected set $I_{t_{i-1}}$, the result of the iteration performed on the interaction graph of the day t_{i-1}, and as social structure the current one. Such choice implies that not only the interactions of consecutive snapshot could vary but that the node sets can also differ. Naturally, the nodes not present during the snapshot t_i not take part to the diffusion process at time t_i; they can't infect the neighbors, and they can't change their status. In this scenario the probability of infection for a node u is computed not as $n\beta$ with n the number of *total* infected neighbors, but as $n_{t_i}\beta$ with $n_{t_i} \leq n$ restricting the set of infected neighbors to the ones that are present at time t_i.

S3: Interaction-based evolution. In this dynamic scenario, the network structure falls apart, being substituted by a stream of instantaneous interactions. We can imagine such scenario as a word of mouth spreading phenomena in which an idea or a behavior can be shared/adopted only through a direct contact. To simulate such behavior during each single interaction with an infected node an actor decides to adopt the idea/innovation or not with probability β. We implement

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Algorithm 1 Interaction-based SI

Require: I_{t_0}: set of initial infected node
1: **for each** t_i in {1,...,k} **do**
2:     $I_{t_i} = I_{t_{i-1}}$
3:     **for each** interaction (u, v, t_i) in E_{t_i} **do**
4:         **if** v in $I_{t_{i-1}}$ **then**
5:             $p = rand(0, 1)$ ▷ Random value in [0,1]
6:             **if** $\beta > p$ **then**
7:                 add u to I_{t_i}
8:             **end if**
9:         **end if**
10:     **end for**
11:     **yield** I_{t_i} ▷ Return daily status
12: **end for**

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streaming SI as shown in Algorithm 1. In this model an actor u involved into m interactions with infected nodes during the day t_i has a probability of infection during such day equal to $\sum_{i=1}^{m} \beta$ due to the independence of the m contacts.

SIR: this model represents a variation of the previous one. Each node belongs to three stages during the epidemics: the state *infected* I, the *susceptible* state S and the *removed* stage R, describing actors that successfully recovered from the infection. We adopt SIR to simulate diffusion scenario D2. The model can be described by the transition rule $S \rightarrow I \rightarrow R$, where the arrow indicates that once an individual becomes infected it can only change its status to removed.

S1: Static network. As for SI in the S1 scenario, we applied the classical formulation of the model on the flattened static graph. In SIR the idea/innovation is adopted with a $n\beta$ probability. Moreover, during each iteration, the probability that an infected node decides to stop advertising to its neighbors the previously adopted idea/innovation – thus joining the R set – is γ.

S2-S3: Dynamic networks. In order to comply with the topology dynamics described by S2 and S3, we adopted the SIR model the same rationales used for SI. We omit the pseudocode for the interaction-based version of SIR since it differs from the one reported in Algorithm 1 solely for the evaluation of the removal probability γ (which is performed on daily iteration basis one time for each node having at least one interaction during such time frame).

4.2 Diffusion Analysis

To extensively compare the diffusion scenarios described by D1 and D2 while varying their level of topology dynamic we organized our simulations as follow:

  i. for each dataset we randomly selected 10 disjoint sets of nodes each one covering 5% of the V: such sets identify, for each scenario and model, 10 different initial infection starting points, e.g., I_{t_0};
 ii. for each dataset, scenario and initially infected status we executed the SI and SIR models while setting their parameters;
iii. we build the infection trend over the observed period for each scenario, model, initially parameter configuration and dataset as the iteration wise
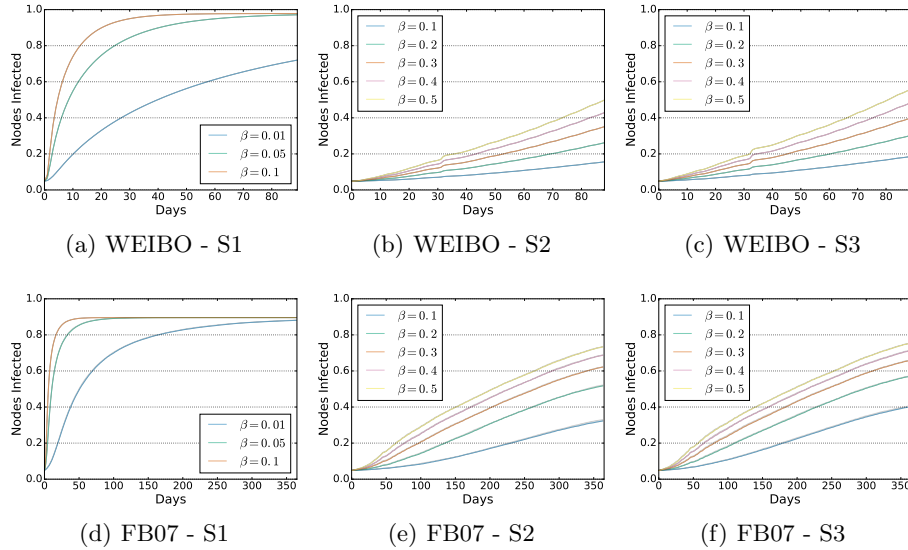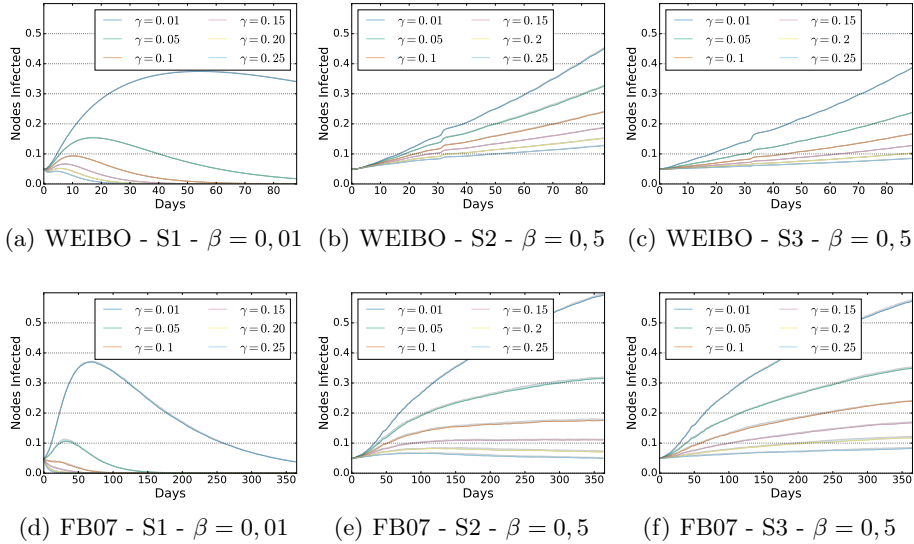
Fig. 1. Simulation of SI models on both WEIBO and FB07: the curve represent the average percentage of infected nodes over time while varying the model parameter. Due to the number of connected components (as shown in Table 1), the number of infected nodes never reaches the 100%.

average of the runs over the 10 executions performed varying the initially infected nodes.

D1 - Continuous advertising. Figure 1 shows the results obtained by the simulation of the SI model on the two datasets while varying both the value of the β parameter and the topology dynamicity.

Scenario S1. The diffusion process on the complete, static, graph results in a sharp increase in the percentage of infected nodes even for low values of β. In WEIBO, Figure 1(a), setting $\beta = 0,01$ leads at the end of the simulation to an epidemic state covering almost 70% of the nodes in the network (half of the population is infected after the first 40 iterations). While increasing the values of the infection parameter a significative speed up in the diffusion process allows reaching almost the 80% of the nodes, after only 15-20 iterations. In FB07, Figure 1(d), the impact of β on the diffusion trend is more evident: a slight increase from a value of 0.01 to 0.05 almost double the number of nodes infected after the first 50 iterations leading to a complete saturation within the 4th month.

Scenario S2. Considering during each step the network built over the interactions established during a single day leads to a significative reduction of the diffusion speed. In both WEIBO and FB07 the infection trends do not reach saturation. Observing the FB07 trend, Figure 1(e), we note that only for $\beta = 0.5$ we are able to reach a final percentage of infected nodes "comparable" to the lowest one obtained by the same model on the static scenario: 50 times the β-value of the *"worst"* performing SI model in S1. In WEIBO, Figure 1(b), the pattern

Fig. 2. Simulation of SIR models on both WEIBO and FB07: the curve represent the average percentage of infected nodes over time while varying the model parameters.

is similar although even considering $\beta = 0.5$ no more than 50% of the overall nodes become infected after 90 days, 20% less than using $\beta = 0.01$ in S1.

Scenario S3. Moving to the interaction-based evolution we observe a behavior similar to the one identified in S2; however, in this scenario the infection trends grow always faster than the ones having the same β value in the S2 scenario (on average $5 - 10\%$ on both WEIBO and FB07, as shown in Figure 1(c-f)). Such speed up is due to the different way the probability of infection is calculated in the two scenarios. Where given the interactions occurred during a day t_i, in S2 a node having n infected neighbors is subject to a $n\beta$ probability of being infected, in S3 the probability equals to $\sum_{i=1}^{m} \beta$ (where $m \geq n$ since during the same day multiple interactions can occur among the same pair of nodes).

D2 - Diminishing advertising. Figure 2 shows the results obtained by the simulation of the SIR model on the two datasets while varying both the value of the β and γ parameters and the topology dynamicity.

Scenario S1. In the simulation with SI model, we observed that the final reach in the three different scenarios are comparable only selecting different values of β. In particular the diffusion reached in S1 with $\beta = 0.01$ is, almost, reachable in S2 and S3 when $\beta = 0.5$: for this reason, we chose to instantiate SIR on the static networks built upon our datasets by fixing $\beta = 0.01$ and varying only the γ parameter value. In both WEIBO and FB07 we observe, Figure 2(a-d), the classic decay experienced by the infection trend in a SIR model. With lower values of γ (i.e., $\gamma = 0.01$) we found a rapidly grow in the first observation period (around 50 days in FB07) followed that a rapidly decreased. Such two-phase trend is expected when $\beta \leq \gamma$: at first the susceptible nodes start to become infected
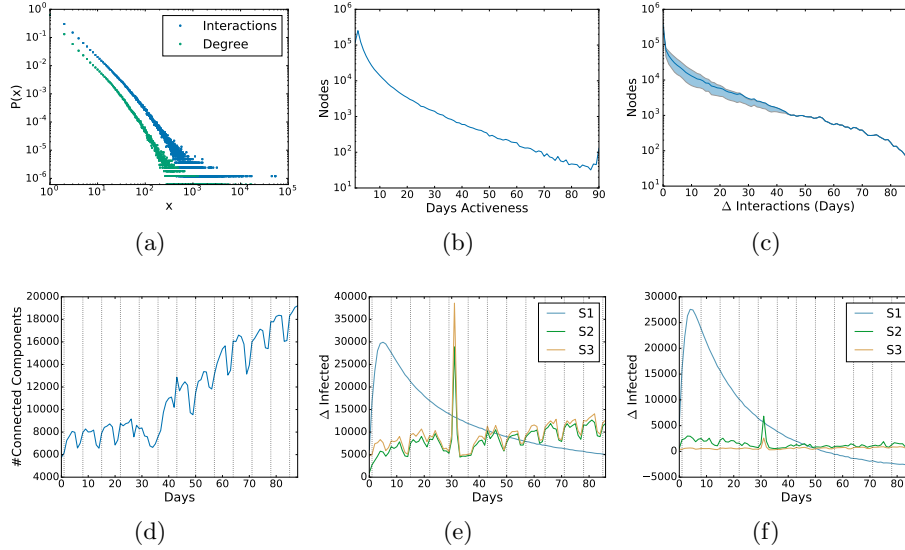
Fig. 3. WEIBO statistics: (a) distribution of node degrees and interactions, (b) distribution of nodes' activity, (c) distribution of delay among consecutive interactions of a same user, (d) connected components trend and delta infection trend in SI (e) and SIR (f). In (e) and (f) the trends compare models having the following parameter settings - SI: S1 $\beta = 0.01$, S2-S3 $\beta = 0.5$; SIR: S1 $\beta = 0.01$ $\gamma = 0.01$, S2-S3: $\beta = 0.5$ $\gamma = 0.01$

leading to an increase in the trend, then infected nodes are gradually removed and stop their spreading activity causing, on the long run, the disease to die out. For $\gamma >> \beta$ the growing phase is likely to not be present since all the initial infected nodes are more likely to being removed than to spread the infection (e.g., in Figure 2(a-d) the trends having $\gamma \in [0.15 - 0.25]$).

Scenarios S2-S3. In Figure 2(b-c-e-f) we report for S2 and S3 the infection trends for $\beta = 0.5$ (other values of β behaving alike). Similar to what happened in S1, for values of γ comparable to the β ones the trend curves steadily die out. However, the velocity of both infection and recovery diffusions are extremely lower w.r.t. the ones observed in S1. Even setting a β-value equals to 50 times the one used in S1 we can compare to the diffusion peaks of such scenarios (almost 36% in FB07 and 39% in WEIBO reached respectively on the 60th and 50th simulation days) only after a longer simulation period (at the 200th and 160th days in FB07 for S2 and S3 respectively, at the 69th and 90th days in WEIBO for S2 and S3 respectively).

5 Discussion

We have observed how the introduction of topology dynamics impacts two different spreading phenomena definitions. Indeed our results suggest that the particular characteristics possessed by a dynamic system deeply affect the way a

(a) WEIBO dataset   (b) FB07 dataset
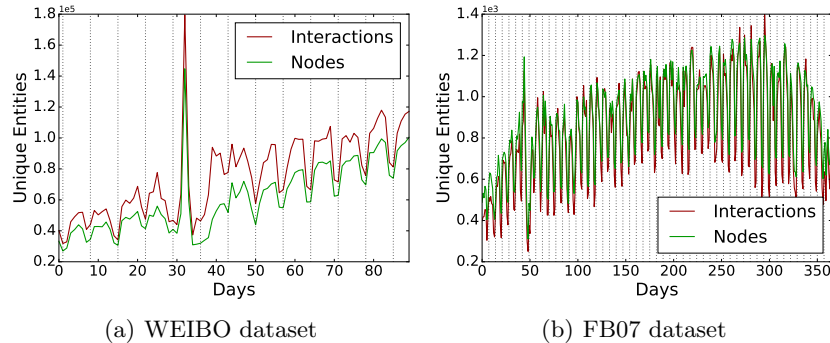
Fig. 4. (a) Daily trends in the WEIBO dataset. The peak on the 34th day capture the increase of contacts and presences happened during the Chinese New Year. (b) Daily trend of nodes and edges in the FB07 dataset. (a-b) Vertical lines identify Sundays.

word of mouth diffusion of an idea/innovation will spread. We now focus to better understand how the topology expressed by the adopted data sources work to favor/against the simulated diffusion processes. Figure 3 shows some distributions computed on the WEIBO dataset (FB07 behaving alike). In Figure 3(a) we observe the degree and interaction distributions describing respectively the "flattened" overall connectivity and the real interaction one. Both distributions are heavy tailed: however, the interaction one is heavier, meaning that, on average, active nodes tend to exploit multiple times their connections. As we have discussed in 4.2, in a dynamic topology a node is not necessarily present during all the observed snapshots: in Figure 3(b) is reported the distribution of active days per user. We can observe that only a few hundreds of nodes (less than the 1%) are active for all the observed 90 days, while the majority of users interacts only during 3-4 days. Moreover, as shown in Figure 3(c) the average interval between two consecutive interactions of the same user (disregarding the endpoint) is likely to be low: users seem to concentrate their service usage for short-bounded time frames. Such contact patterns affect the overall connectivity of the graph: as shown in Figure 3(d) the number of connected components highly vary as time goes by. Conversely, as highlighted in Table 1, considering an aggregate view of the network we get only 152 components (one of them composed by 98% of the nodes). In Figure 4(a) are shown the patterns of daily interactions and node presences of the WEIBO interaction network. Such trends show an overall increase of the number of interactions and nodes, day after day. In such plot, we identify the Sundays with vertical lines: the WEIBO users tend to diminish their presence (and usage) of the service during the weekends. Moreover, we can also observe a sharp peak in the number of interactions and nodes on the 34th day of our sample: such day, 3 February 2011, identified the Chinese New Year. If we examine the 34th day of the WEIBO diffusion trends for the SI and SIR models, shown respectively in Figures 1(a-b-c) and 2(a-b-c),

we can notice a peculiarity: in both S2 and S3, for all the tested parameters, a "small" jump highlight a sudden increase in the infected nodes while in S1 such behavior is not present. Therefore, adopting a flattened graph as done in S1, not only we get an overestimate of the percentage of infected nodes but also we do not capture the presence of special events. Such observations are confirmed by the *prevalence* plots shown in Figure 3(e-f) where are reported for each day the number of novel infected nodes for SI and SIR respectively. Even in the case of diminishing advertising, SIR we are still able to identify Chinese New Year day in both S2 and S3 even if the diffusion rate appears to be almost uniform.

The same analysis performed on the FB07 dataset is shown in Figure 4(b). The interactions and node presences trends are similar the one observed in WEIBO, however, the temporal pattern is shifted: Facebook users, are more active during the weekends. Another difference is the absence of a single day that generates a dominant peak in the observed trends. Such absence could be due to the limited number of users observed during the 365 days.

Once compared the diffusion trends in the three identified scenarios we can now provide answers to the research questions raised in Section 3:

A1: Yes, reducing the dynamic unfolding of a social interaction phenomena to an aggregate, static, snapshot necessarily lead to an overestimate of the real network connectivity and, as a consequence, of all the diffusion processes that on such topology take place.

A2: Yes, different temporal granularities for topology dynamics aggregation (e.g., snapshots and interactions) - at least for the analyzed diffusion models - cause different spreading velocity. Such result is primarily due to the specific choices that need to be made to adapt diffusive models to the available dynamic structure. Both SI and SIR were originally defined for complete network topology then adapted to general static networks. We introduced a novel reinterpretation in which the topology changes at each step (S2) and another one in which the network topology is completely absent (S3).

A3: No, peculiar topology evolution patterns or the chosen diffusion model deeply affect the rate of infection. In particular, cyclic patterns (weekend/weekdays) or special events (e.g., the Chinese New Year) have shown to deeply characterize the rate at which diffusion occurs in SI, while the former loses their relevance if a SIR model is applied.

6 Conclusions

In this work, we analyzed diffusive phenomena on dynamic social interaction graphs. Moving from the observation that studying how information spread in a static social context could lead to inconsistent results, we performed a data-driven study aimed to underline the real impact of network dynamics. After having modeled three different evolutive scenarios, we studied their impact on the outcome produced by classical compartmental models (SI and SIR), models we redefined to handle topology dynamics[5]. Our results show that analyzing

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[5] All methods were made available within the ndlib library: `https://goo.gl/1tstvG`.

diffusive phenomena not considering topology dynamic lead to relevant over estimate of the real speed and amplitude of the spreading. Moreover, dynamic-aware approaches enables the identification of context-dependent events as well as activity patterns that may severely affect diffusion dynamics.

As future work, we plan to study the other side of the problem, namely the impact diffusive processes have on network topology. Finally, another research theme remains open: the definition of novel analytical diffusion frameworks tailored to integrate the competing dynamic processes *on* and *of* networks.

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