



An analytical model for multi-epidemic information dissemination

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ABSTRACT

Contemporary distributed systems usually involve the spreading of information by means of ad-hoc dialogs between nodes (peers). This paradigm resembles the spreading of a virus in the biological perspective (epidemics). Such abstraction allows us to design and implement information dissemination schemes with increased efficiency. In addition, elementary information generated at a certain node can be further processed to obtain more specific, higher-level and more valuable information. Such information carries specific semantic value that can be further interpreted and exploited throughout the network. This is also reflected in the epidemical framework through the idea of virus transmutation which is a key component in our model. We establish an analytical framework for the study of a multi-epidemical information dissemination scheme in which diverse 'transmuted epidemics' are spread. We validate our analytical model through simulations. Key outcomes of this study include the assessment of the efficiency of the proposed scheme and the prediction of the characteristics of the spreading process (multi-epidemical prevalence and decay).

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1. Introduction

In this paper we focus on a distributed computing setting with the following characteristics:

- An unstructured network of a large number of nodes.
- Nodes send and receive information.
- Nodes can relay information to other nodes.
- Nodes have specific neighbours either due to communication constraints or some logical organization.
- Exchanged information carries certain semantic value and presents dependencies to other pieces of information.
- Semantic dependencies can be further exploited by nodes to more accurately tune their behaviour.

We propose an analytical model for disseminating pieces of information in various levels of detail. The considered model is probabilistic, so that each node decides with a given probability whether to transmit/relay information or not. We capitalize on the similarity between information dissemination and the epidemic model, mostly in the abstractions of virus spreading, virus severity, virus interdependencies and possible transmutations.

The great advantage of epidemic-inspired communication is that dissemination proceeds on a local basis, without any central

coordination [12]. Such communication is highly reliable, efficient, and resilient to sudden failures of communication links and nodes. However, the study on dissemination of dependent pieces of information is a major challenge. For instance, consider the dissemination of fragments of files in a peer-to-peer overlay, news updates and semantic multimedia meta-data updates in a social network, more accurate and up-to-date measurements in a wireless sensor network. Specifically, the dependent pieces of information that have been disseminated can be further processed by receiving nodes to obtain more up-to-date, specific, higher-level and more valuable information. In this paper we adopt the epidemics-based dissemination model, which reliably and efficiently handles the information dissemination issue.

Information dissemination is handled by a simple, message passing protocol to fulfil certain information diffusion requirements, i.e., spatio-temporal constraints. A piece of information should reach potential recipients within a certain time horizon (e.g., in less than 2 min). Moreover, such piece may be considered valid only in the neighbourhood of the node (in specific geographical area or within a certain number of hops). This means that, not all information needs to be propagated everywhere. Through this paper we show that the stochastic nature of epidemic spreading achieves very high coverage (even) for low forwarding probability: probability of a message passing to a neighbour. The similarity of our model to epidemics extends beyond the spreading scheme.

The basic scheme: A disseminated piece of information matches an epidemic in the sense that, a node carrying a piece of information becomes infected; otherwise it is susceptible. An infected node

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can disseminate information to its neighbours in an opportunistic way. When a node carries information, which has become invalid, e.g., beyond the scope, then it becomes susceptible and can be probably re-infected at a later stage.

The extended scheme: The severity of epidemics is included in our abstraction. We introduce the metaphor of a stronger epidemic than the one, which has previously infected a given node. Stronger epidemics abstract more detailed information, i.e., information which is valued more by the receiving node. To be able to assess the value of the incoming piece of information, each node provides a mechanism which unambiguously specifies interdependencies among pieces of information and evaluates them. In addition, some nodes provide a mechanism to generate/infer information. We can figure out the following scenarios:

- the incoming piece of information, denoted as p , is of *better quality* than the one previously received (e.g., more up-to-date message), or p is *more detailed* than the one previously received by the node (e.g., incoming p refers to more accurate position), and,
- the incoming p can act as a *seed* thus enabling the receiving end to generate/infer additional information. For instance, the incoming p covers the missing elements needed for generating extra information; the combination of location, time and information about the scheduled lectures of a conference could be exploited by a personal conference assistant application. We adopt the term ‘information completion’ for this case, where some vital pieces of information are missing (until reception of incoming p) in order to generate new information of higher semantic value. Since, in any of these cases, the derived information (i.e., after the reception of new information from the neighbourhood) is deemed more valuable for the receiving node, we abstract them as ‘epidemic aggravation’.

The last part of the abstraction is related to the dissemination of derived/inferred information. Imagine that the derived information is not kept locally in the node, but further treated as a virus and propagated to the neighbourhood as new information. A new virus starts spreading and will possibly infect nodes in the proximity. Hence, in a group of nodes multiple pieces of information circulate, thus, leading to the need of studying a multi-epidemic information dissemination scheme. The contribution of this paper is the study of the multi-epidemic information dissemination. Our objective is to develop a mathematical model that deals with:

- the multi-epidemic spreading in the light of information completion and aggravation, and,
- the multi-epidemic thresholds, which are quantitative indicators on the spreading dissemination, e.g., the infection rates that turns the epidemic into a pandemic or causes the epidemic to fade out.

To this purpose,

- we first abstract the problem of multi-epidemics assuming that nodes are capable of deciding whether to replace existing pieces of information with more valuable incoming information or not.
- we use a graph-based representation in order to formulate multi-epidemic propagation through a spatio-temporal random process based on interactions among nodes.
- we make use of a discrete-time model and network topology information to describe the spatial and temporal statistical dependencies among diverse epidemics in arbitrary network topologies. The temporal dependency is modelled as a Markov process.
- we consider conditional probability independence among neighbouring infected nodes; the assumption of such independence introduces an exact joint probability distribution

depending on one-node marginal probabilities. The proposed model only allows one event, i.e., Susceptible \rightarrow Infected, or Infected \rightarrow Susceptible, in a single discrete time step focusing on the transient behaviour of multi-epidemic propagation.

- we generalize the Markov model in [25] (w.r.t. mathematical model), which deals with mono-epidemic spreading.
- we apply our model to describe the final size of infection, which corresponds to the equilibrium solution and characterizes the potential distribution of the epidemics over a network.
- the proposed model emphasizes the steady-state solution and the epidemic threshold for each epidemic. The model captures the impact of the underlying topology but is not limited to it. The viral propagation is largely determined by the intrinsic characteristics of the network. We show that, the multi-epidemic threshold is closely related to the eigenvalues of the network adjacency matrix and decays exponentially over time.
- we study the significance of the topology in determining epidemic thresholds and the speed of propagation for each transmuted epidemic.

The article is organized as follows: Section 2 discusses related work and Section 3 introduces the concept of multi-epidemic information dissemination. In Section 4 we analyse the corresponding mathematical model. Section 5 reports analytical and simulation results. Finally, in Section 6 we discuss possible exploitation and adoption of the proposed model with other relevant models, and conclusions and directions for future work are presented in Section 7.

2. Related work

Several approaches have been proposed to model and simulate mono-epidemic spreading in networks. Therefore, considerable research related to reliable epidemic-based information dissemination in ad-hoc networks has been studied in [19]. The work in [11] presented a model which analyses the epidemic spreading in random graphs. The authors in [5] studied epidemic spreading in complex networks and the authors in [22] proposed a spreading model for arbitrary network topologies. In [25] the authors analyse a Markov process-based framework that characterizes the spreading of epidemics through the SIS model and the impact of the underlying topology on propagation. In that work, a mono-epidemic propagation model is introduced based on temporal and spatio-temporal dependency of the infected nodes (an Independent and Markov model, respectively). However, the concept of transmutation of an epidemic is not considered since there is no information processing (e.g., information completion). Additionally, the architecture discussed in [16] proposed an approach for dissemination among groups of nodes. Such architecture takes into account the reliability of information in the dissemination process. Nevertheless, the information spreading adopts a simple flood-based model. The performance handicap of a flood-based approach with respect to epidemic spreading is studied in [1] and in this paper, too. The work in [13] deals with the application of the *Susceptible-Infected* (SI) epidemiological model across ad-hoc networks. Nonetheless, the SI model cannot be considered appropriate for multi-epidemic information dissemination, since infected nodes cannot recover or get reinfected (see Section 3). Moreover, the autonomous gossiping algorithm in [8] refers to the selectivity attribute of the epidemic spreading. However, such an algorithm does not consider any information process, thus, nodes cannot generate new information and, consequently, cannot augment knowledge. The model in [10] refers only to spatially constrained information dissemination. The authors in [22] investigate the threshold of a mono-epidemic propagation exploiting the eigenvalue of the adjacency matrix of the network. Our model generalizes the model in [22] investigating the behaviour of

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