

# Intelligent Immunization Strategies: RDF Graph and ABC Algorithm

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**Abstract**—Spreading processes are strongly interacting with huge flow of quantitative social, demographic and behavioral data that may be used to improve immunization strategies. The existing immunization strategies are limited by their computational requirements and still have the problem of scaling in large networks. The topology of the pattern of contacts between individuals plays a fundamental role in determining the spreading patterns of epidemic processes embedding the mechanism of diverse infection periods and is an impact on the dynamical spreading process behaviors properties. An important challenge is to define an immunization strategy that identify a meaningful group (community) of nodes that are strongly related to the disease and who cannot catch nor transmit the disease. Artificial Bee Colony (ABC) is widely used as an optimization algorithm that performs community detection. To immunize intelligently, ABC asks the node related ontology and changes the strategy evolution consequently by combining many efficient strategies for each node. This paper presents an Ambient Intelligence (AmI) based approach that designs a semantic temporal network as an RDF graph and implements the ABC algorithm as a novel intelligent and immunization strategy accordingly.

**Index Terms**— Semantic Temporal Network, ABC Algorithm, Intelligent Immunization Strategy, Community Detection.

## I. INTRODUCTION

Kang & Fu [1] describe the effects of uniform and targeted immunization schemes on scale-free networks. However, they argue that, in reality, the spread of many epidemic diseases exhibits heterogeneity, in particular, small-world and scale-free property. Great research attentions about complex networks are attracted in such a way. However, these strategies are limited by their computational requirements and still have the problem of scaling in large networks.

Ki & al [2] constructed diverse infection periods on a random mobile network, to address the influence on its epidemics from diverse infection periods. To explore extra realistic spreading process, random mobile individuals moving at a square plane have been considered. As different people may have different infection periods due to their different physique, they focused on random mobile dynamical networks with diverse infection periods due to people's different constitutions and external circumstances. This means that each individual as a node in the network needs to be specified with more semantics. In addition, the links must provide more information.

Yan & al [3] introduce some parameters to investigate the evolution of vaccinated nodes during iterations, and find that some nodes in the network were selected for multiple times, although not always continuously. As epidemic season continues, the selection of vaccinated individuals tends to be stable. Those nodes include both global hubs, who possess most connections, and local hubs, who are influential in their communities. In addition, they also present some numerical

results of their strategy on certain real social networks. Consequently, the immunization strategy must select intelligently the best individuals.

Starnini & al [4] investigated the structural properties of networks and the relative importance of their constituents but they did not provide any constituents knowledge. They consider simple disease spreading processes on empirical time-varying networks of contacts between individuals and compare the effect of several immunization strategies on these processes. The choice of nodes is performed according to a certain ranking of the nodes of the contact network. They consider various ranking strategies, focusing in particular on the role of the training window during which the nodes' properties are measured in the time-varying network: longer training windows correspond to a larger amount of information collected and could be expected to result in better performances of the immunization strategies. They find instead an unexpected saturation in the efficiency of strategies based on nodes' characteristics when the length of the training window is increased, showing that a limited amount of information on the contact patterns is sufficient to design efficient immunization strategies. This finding is balanced by the large variations of the contact patterns, which strongly alter the importance of nodes from one period to the next and therefore significantly limit the efficiency of any strategy based on an importance ranking of nodes. They also observe that the efficiency of strategies that include an element of randomness and are based on temporally local information do not perform as well but are largely independent on the amount of information available. Therefore, the efficiency of strategies have to perform well in any circumstances. To do so, ranking must be computed more realistically with artificial intelligence supports.

In these previous works, the size of the networks is very small. Alternatively, some small cities may have more than 100 000 citizens. Individuals' characteristics must be semantically based to support complex networks that exhibit heterogeneity and mobility. The used strategies are typically data based but they, really, need to perform intelligently to rank nodes more realistically. Therefore, we have to consider big data and complex network with best-designed specification that require distribution and real-time interoperability.

Let us conclude that the dynamics of many social, technological and economic phenomena are driven by individual human actions, turning the quantitative understanding of human behavior into a central question of modern science. These findings have led to a large modeling effort and stimulated the study of the impact of a network's dynamics on the dynamical processes taking place on top of it. Contacts within populations are better described in terms of semantic networks with a non-trivial structure that exhibits the fact that connections appear, disappear, or are rewired on various timescales, corresponding to the creation and

termination of relations between pairs of individuals including individual diversity of susceptibility and infectivity. Spreading processes are strongly interacting with huge flow of quantitative social, demographic and behavioral data that may be used to improve the immunization strategy. The topology of the pattern of contacts between individuals plays a fundamental role in determining the spreading patterns of epidemic processes embedding the mechanism of diverse infection periods and is an impact on the properties of the dynamical behaviors of the spreading process. The existing immunization strategies are limited by their computational requirements and still have the problem of scaling in large networks. Optimal immunization strategies shed light on how the role and importance of nodes depend on their properties and can yield importance rankings of nodes.

An important challenge is to define an immunization strategy that identify a meaningful group of nodes (community) that are strongly related to the disease and who cannot catch nor transmit the disease. As a solution, when working on big data, we need to change the network topology to a graph that can be semantically handled. Graphical modeling provides many advantages and offers rich information in a simple readable format model (RDF). Especially, interaction networks have become an area of great interest for applying Artificial Intelligence and Data Mining tools to analyze, understand, extract information and knowledge, and finally to apply immunization strategies intelligently.

Ambient Intelligence (AmI) based on constrained devices and their communication protocols helps handling such information into semantic temporal networks and spreading processes as RDF graphs. In addition, it addresses the sharing information in a semantic format through RDF graph (ontology) as a common virtual shared space. Communities, related to immunization, need to be automatically identified and the strategy needs to evaluate intelligently each node before immunizing.

Artificial Bee Colony is widely used as an optimization algorithm that performs community detection. It will provide best performance when applied as an immunization strategy. As long as application developers use standard ontologies, different applications using the same spaces will interact automatically. Hence, many strategies can be applied simultaneously. A strategy has to collect all information needed to decide whether to immunize or not. A node and its entire links are specified as an ontology. The global graph is an ontology of ontologies. To immunize intelligently, the strategy must ask the node related ontology and changes the strategy evolution consequently.

This paper presents an AmI based approach of a semantic temporal network. Artificial Bee Colony (ABC) algorithm is applied as a novel intelligent and dynamical immunization strategy. Contacts positions, social and environment information are dynamically gathered as and when applying any strategy. Nodes and links are designed as specific ontologies. ABC detects the appropriate contacts by asking their specific ontologies to decide to immunize the contact. ABC may combine more efficient strategies for each node. The bees decide at each node, which politic is the best.

We hope this method is better when discovering communities and applying immunization strategies comparing with previous solutions. Data mining technologies can be applied as knowledge discovery tools to enhance ontologies.

Finally, this paper shows the designing of temporal networks as RDF graph and implements the ABC algorithm accordingly. Section II provides related works. We describe the semantic temporal network as RDF graph in Section III. The spreading model using the ABC Algorithm as an immunization strategy is introduced in detail in Section IV. The DEVS implementation of a Tuberculosis simulation is presented in Sections V, respectively. This TB is fully detailed in (Mokaddem, in press). Finally, conclusion is drawn in Section VI and relevant prospect is discussed.

## II. RELATED WORK

Dynamical networks can describe plenty of complex systems. A typical network comprises nodes and links, where the nodes represent different individuals (contacts) of a real system and each link represents the connection between two nodes. In many studied epidemic dynamical networks, their topological structures are often assumed to have static connections [5,6]. It is well known that there is great necessity to study the spreading mechanics and dynamical behaviors of epidemic diseases, which has attracted much attention [7].

Kang & Fu [1] present an SIS model with delay on scale-free networks, calculate its epidemic threshold and describe the effects of uniform and targeted immunization schemes. Initially proposed by Kermack and Mckendrick [8], SIS and SIR were established on homogeneous networks. However, in reality, the spread of many epidemic diseases exhibits heterogeneity, in particular, small-world and scale-free property. Since, great research attentions about complex networks are attracted by these two concepts. In fact, many study results have indicated that the mobility of individuals (inducing time-varying topological structure) can play an important role in the epidemic spreading process [9–10]. For example, the moving of individuals among cities has a great impact on the epidemic threshold when one of the cities has been infected [11, 12].

The individual diversity of susceptibility and infectivity is also an important factor when addressing the spreading behavior on networks [11, 13]. In general, the susceptibility and infectivity of individuals are heterogeneous, which may be caused by age, sex, or other intrinsic differences. Recent research findings [14] have shown that the heterogeneity of individual susceptibility and infectivity can increase the epidemic threshold. By embedding the mechanism of diverse infection periods into a random mobile epidemic network, Li & al [2] investigated the epidemic dynamics affected by individual diversity of susceptibility and infectivity. The theoretical analysis results of their considered epidemic model show that the shorter the individual's infection period is, the larger its epidemic threshold will be. Moreover, the epidemic threshold of the random mobile network with diverse infective periods is larger than the counterpart with the same infection period [14].

The topology of the pattern of contacts between individuals plays a fundamental role in determining the spreading

patterns of epidemic processes. The first predictions of classical epidemiology were based on the homogeneous mixing hypothesis, assuming that all individuals have the same chance to interact with each other. This assumption and its results were challenged by the empirical discovery that the contacts within populations are better described in terms of networks with a non-trivial structure. Subsequent studies were devoted to understand the impact of network structure on the properties of the spreading process. The main result obtained concerned the large susceptibility to epidemic spread shown by networks with a strongly heterogeneous connectivity pattern, as measured by a heavy-tailed degree distribution  $P(k)$  (defined as the probability distribution of observing one individual connected to  $k$  others) with a diverging second moment [15].

The original studies considered the interaction networks as static entities, in which connections are frozen or evolve at a time scale much longer than the one of the epidemic processes. This static view of interaction networks hides however the fact that connections appear, disappear, or are rewired on various timescales, corresponding to the creation and termination of relations between pairs of individuals [16]. Longitudinal data have traditionally been scarce in social network analysis, but, thanks to recent technological advances, researchers are now in a position to gather data describing the contacts in groups of individuals at several temporal and spatial scales and resolutions. The empirical data analysis on several types of human interactions (in particular phone communications or physical proximity) has unveiled the presence of complex temporal patterns in these systems [16-18]. In particular, the heterogeneity and burstiness of the contact patterns are revealed by the study of the distribution of the durations of contacts between pairs of agents, the distribution of the total time in contact of pairs of agents, and the distribution of gap times between two consecutive interactions involving a common individual. All these distributions are indeed heavy-tailed (often compatible with power-law behaviors), which corresponds to the burstiness of human interactions [19].

Current models of human dynamics, used from risk assessment to communications, assume that human actions are randomly distributed in time and thus well approximated by data mining and statistical processes. In contrast, an increasing evidence is that the timing of many human activities, ranging from communication to entertainment and work patterns, follows non-Poisson statistics, characterized by bursts of rapidly occurring events separated by long periods of inactivity. The bursty nature of human behavior is a consequence of a decision-based queuing process: when individuals execute tasks based on some perceived priority, the timing of the tasks will be heavy tailed, with most tasks being rapidly executed, whereas a few experiences very long waiting times. In contrast, random or priority blind execution is well approximated by uniform inter-event statistics. These findings have important implications, ranging from resource management to service allocation, in both communications and retail. They have led to a large modeling effort [20-21] and stimulated the study of the impact of a network's dynamics on the dynamical processes taking place on top of it. The processes studied in this context include synchronization [22], percolation [23], social consensus [24],

or diffusion [25]. Epidemic-like processes have also been explored, both using realistic and toy models of propagation processes [26-28]. The study of simple schematic spreading processes over temporal networks helps indeed expose several properties of their dynamical structure: dynamical processes can in this context be conceived as probing tools of the network's temporal structure [18].

The study of spreading patterns on networks is naturally complemented by the formulation of immunization strategies tailored to the specific topological (and temporal) properties of each network and most previous literature of this field have focused on the selection of vaccinated nodes before the outbreak of an epidemic [29-32]. Optimal strategies shed light on how the role and importance of nodes depend on their properties and can yield importance rankings of nodes. In the case of static networks, this issue has been particularly stimulated by the fact that heterogeneous networks with a heavy-tailed degree distribution have a large susceptibility to epidemic processes, as represented by a vanishingly small epidemic threshold. In such networks, the simplest strategy consisting in randomly immunizing a fraction of the nodes is ineffective. Numerous immunization strategies have been proposed such as uniform immunization (nodes are vaccinated randomly) [29-31] or targeted immunization (vaccinate the most highly connected nodes) [29-31]. Targeted immunization is highly effective [33], but it requires global information about the network thus making it impractical in real cases. Cohen et al. proposed acquaintance immunization strategy [34], based on the immunization of a small fraction of random neighbors of randomly selected nodes. Its principle can be described as a node with higher degree is easier to be chosen from a random link. Without specific knowledge of the network, this method is efficient for networks of any broad-degree distribution and allows for a relatively low threshold of immunization. Besides, some other novel immunization strategies have been proposed in the last decade [31-32] and have their applications in different cases. More complex strategies, in which nodes with the largest number of connections are immunized, turn out to be effective but rely on the global knowledge of the network's topology. This issue is solved by the previous acquaintance immunization strategy. Few works have addressed the issue of the immunization strategies design and their respective efficiency in the case of dynamical networks [28,35-36]. However, many infectious diseases outbreak seasonally, which is not fully discussed in previous literature as far as we know [37-38]. The periodic change of temperature, humidity profiles, or even the succession of school terms and holidays, can lead to periodic phenomena of epidemics. Previous data have shown that rubella, whooping cough, and influenza reveal obvious seasonality [39]. Here is a simple explanation of epidemics with seasonal phenomena: After spreading extensively, a virus dies out because infected individuals have recovered and produced antibodies. Yet, in the next epidemic season, the mutated virus propagates again, rendering a new outbreak of the epidemic. This process then occurs repeatedly. Yan & al [3] propose an immunization strategy for seasonal epidemics to give a better description of this phenomenon. They merely adopt uniform immunization on the network at first. Before the start of the next epidemic season, they adjust the vaccinated nodes according to the

infection status of their neighbors in the previous epidemic season. This process does not need global information of the network and achieves better performance than uniform and acquaintance immunizations under the same circumstances.

In particular, Lee & al [35] consider datasets describing the contacts occurring in a population during a time interval  $[0, T]$ ; they define and study strategies that use information from the interval  $[0, \Delta T]$  to decide which individuals should be immunized in order to limit the spread during the remaining time  $[\Delta T, T]$ . Specifically, the authors introduce two strategies, called Weight and Recent. In the Weight strategy, a fraction  $f$  of nodes is selected randomly: for each of these nodes, his/her most frequent contact in the interval  $[0, \Delta T]$  is immunized. In the Recent strategy, the last contact before  $\Delta T$  of each of the randomly chosen individuals is immunized. Both strategies are defined in the spirit of the acquaintance immunization, insofar as they select nodes using only partial (local) information on the network. Using a large  $\Delta T = 75\%T$ , they show that these strategies perform better than random immunization and that this is related to the temporal correlations of the dynamical networks. The scenario they used is indeed the possibility to implement a real-time immunization strategy for an ongoing social event, in which the set of individuals to be immunized is obtained by strategies based on preliminary measurements up to a given time  $\Delta T$ . The immunization problem takes thus a two-fold perspective: the specific rules (strategy) to implement and the interval of time over which preliminary data are collected. Obviously, a large  $\Delta T$  will lead to more complete information, and a more satisfactory performance for most targeting strategies, but it incurs in the cost of a lengthy data collection. On the other hand, a short  $\Delta T$  will be cost effective, but yield a smaller amount of information about the observed social dynamics. In order to investigate the role of the training window length on the efficiency of several immunization strategies, they considered a simple snowball susceptible-infected (SI) model where individuals can be either in the susceptible (S) state, indicating that they have not yet been infected, or in the infectious (I) state, meaning that they have been infected by the disease and can further propagate it to other individuals. Infected individuals do not recover, i.e., once they transit to the infectious state they remain indefinitely in it. Despite its simplicity, this model has indeed proven to provide interesting insights into the temporal structure and properties of temporal networks. They focused on the SI model dynamics over empirical time-varying social networks. The considered networks describe time-resolved face-to-face contacts of individuals in different environments and were measured by the SocioPatterns collaboration using wearable proximity sensors (<http://www.sociopatterns.org>) [17] **table 1**. They considered SI model spread effects by immunizing a fraction of nodes, chosen according to different strategies based on different information amounts of the contact sequence. They found a saturation effect in the increase of the efficiency of strategies based on nodes characteristics when the length of the training window is increased. The efficiency of strategies that include an element of randomness and are based on temporally local information do not perform as well but are largely independent on the amount of information available.

**TABLE 1**

Some properties of the SocioPatterns datasets under consideration: number  $N$  of different individuals engaged in interactions; total duration  $T$  of the contact sequence, measured in intervals of length  $\Delta t = 20$ s; average degree  $\langle k \rangle$  (number of different contacts) and average strength  $\langle s \rangle$  (total time spent in face-to-face interactions) of the network of contacts aggregated over the whole sequence; average number of interactions  $f$  at each time step.

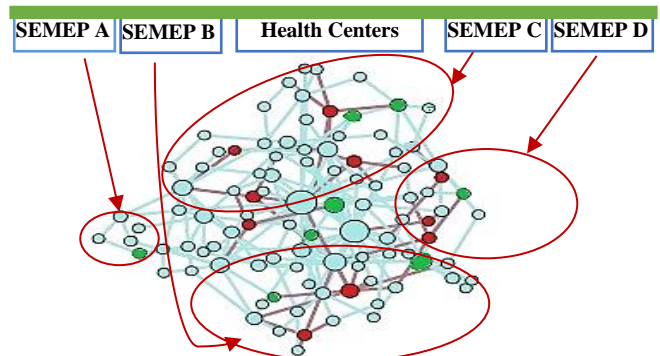
| Dataset | $N$ | $T$    | $\langle k \rangle$ | $\langle s \rangle$ | $\langle f \rangle$ |
|---------|-----|--------|---------------------|---------------------|---------------------|
| Eswc    | 173 | 4703   | 50                  | 370                 | 6.8                 |
| ht      | 113 | 5093   | 39                  | 366                 | 4.1                 |
| hosp    | 84  | 20,338 | 30                  | 1145                | 2.4                 |
| sfhh    | 416 | 3834   | 54                  | 502                 | 27.2                |

### III. INTELLIGENT TEMPORAL NETWORK

#### A. Temporal Network as RDF Graph

We consider a typical network (Fig. 1) that comprises nodes and links, where the nodes represent different individuals of a real system and each link represents the connection between two nodes. Since the mobility of individuals can play an important role in the epidemic spreading process, we must gather such information using constrained devices as smartphones and sensors. From recent technological advances, we are now in a position to gather data describing the contacts in groups of individuals at several temporal and spatial scales and resolutions. Contacts are connected to the system via constrained devices such as Smartphones with GPS and sensors. These devices communicate with the system in a remote invocation mode which is widely used in applications all over the Internet in SOAP or RESTful [40] approaches (Fig. 2). Regarding REST, its use in resource constrained devices is a current trend defended by the WoT initiative [41]. WoT proposes to embed web servers in everyday things. These objects expose their capabilities following the REST principles. In this way, they fully integrate with the web and positions, moving, temperature, climate, etc. are gathered online. Many smartphone applications are ready to catch tracks and routes, which may be stored locally in an SQL Lite database or remotely in a NoSQL store. Every individual is related to many stores.

Health information is stored in each store where the contact was administered his vaccine or getting a health control. May be the same store, which means that he always reached the same Health Center (HC), or many stores if he has been in many health centers. Previous contact information such as health and social information is retrieved from his related stores.



**Fig 1.** Global Network Dispatching

Fig. 1 shows the relation between contacts and their respective stores. Some contacts are stored in 4 Health Centers stores (HC A, HC B, HC C, HC D). A city may have many HCs. For example, a contact X is born in a city A where he is vaccinated for some vaccines in HC A and HC B of that city and lives now in a city B where he has a job and is vaccinated for many other vaccines in HC C. He has been admitted for some disease in a public hospital of a city D. To gather all this contact information, we have to connect to these remote stores and retrieve each related information. This information is retrieved as RDF triples via REST web services invocation and collected in a virtual shared space that holds the related RDF graph as an ontology. Each data is time dependent that means that this data is efficient only from this time. A gathered position is given by a longitude  $L$  and a latitude  $l$  at time  $t$ . Individual routes are the sequence of positions visited by that individual. Routes intersections define contacts and links that compose a network. Route intersection design a pair of participating individuals which were in face-to-face close proximity ( $\approx 1-2m$ ), with a temporal resolution of 20 s inside the radius of the designed area.

We must investigate the network dynamics affected by individual diversity of susceptibility and infectivity that may be caused by individuals' intrinsic differences that may lead in infections periods. To address the heterogeneous connectivity, we measure two important degrees  $\tau_i(t)$  and  $i_i(t)$  and the state  $S_i(t)$ , this state may be 'S', 'I', 'R' to correspond to a SIR model (Fig. 1, blue ='S', red ='I', green ='R'). Since it is computed dynamically, we can adopt any other model SI, SIS or SEIR.  $\tau_i(t)$ ,  $i_i(t)$  and  $S_i(t)$  correspond to the contamination and the immunization degrees and the state for each node  $i$ .

We compute dynamically two thresholds  $\tau(t)$  and  $i(t)$ , the disease contamination threshold and the disease immunization threshold.  $\tau_i(t) > \tau(t)$  means  $i$  has a strong contamination otherwise he has a weak contamination and  $i_i(t) < i(t)$  means  $i$  has a weak immunity otherwise he has a strong immunity. In the case of strong contamination, the contamination degree of a susceptible individual is strongly affected and in the case of a weak contamination, it is weakly affected. A strong immunity means a susceptible individual will not be infected but his immunity degree will decrease and a weak immunity means a susceptible individual will be infected. Each disease is associated to rules that change states of its related individuals, its thresholds and the degrees of its individuals. For example, if  $\tau_i(t) > \tau(t)$  and  $i_i(t) < i(t)$  and  $S_i(t) = 'S'$  then  $S_i(t) = 'I'$ . Some others rules change the thresholds values of  $\tau(t)$  and  $i(t)$  respectively. Some other rules compute the values of  $\tau_i(t)$ ,  $i_i(t)$  for each node  $i$ . A full example will be given when applying the ABC algorithm to show how bees compute these parameters. These degrees are dependent of environmental, social and health parameters like sex, age, weight, climate, humidity, etc. Data Mining tools help discretize these parameters more efficiently. The periodic change of temperature, humidity profiles, or even the succession of school terms and holidays, can lead to periodic phenomena of epidemics and affect these parameters. Some mutated virus propagates again, rendering a new outbreak of the epidemic. This process then occurs repeatedly, the immunization strategy needs to handle this phenomenon to give a better description of these seasonal epidemics.

We need to collect the network topology global knowledge to apply more efficient acquaintance immunization strategies. We consider datasets describing the contacts occurring in a population during a time interval  $[T_B, T_E]$  and a space area defined by a center and a radius.

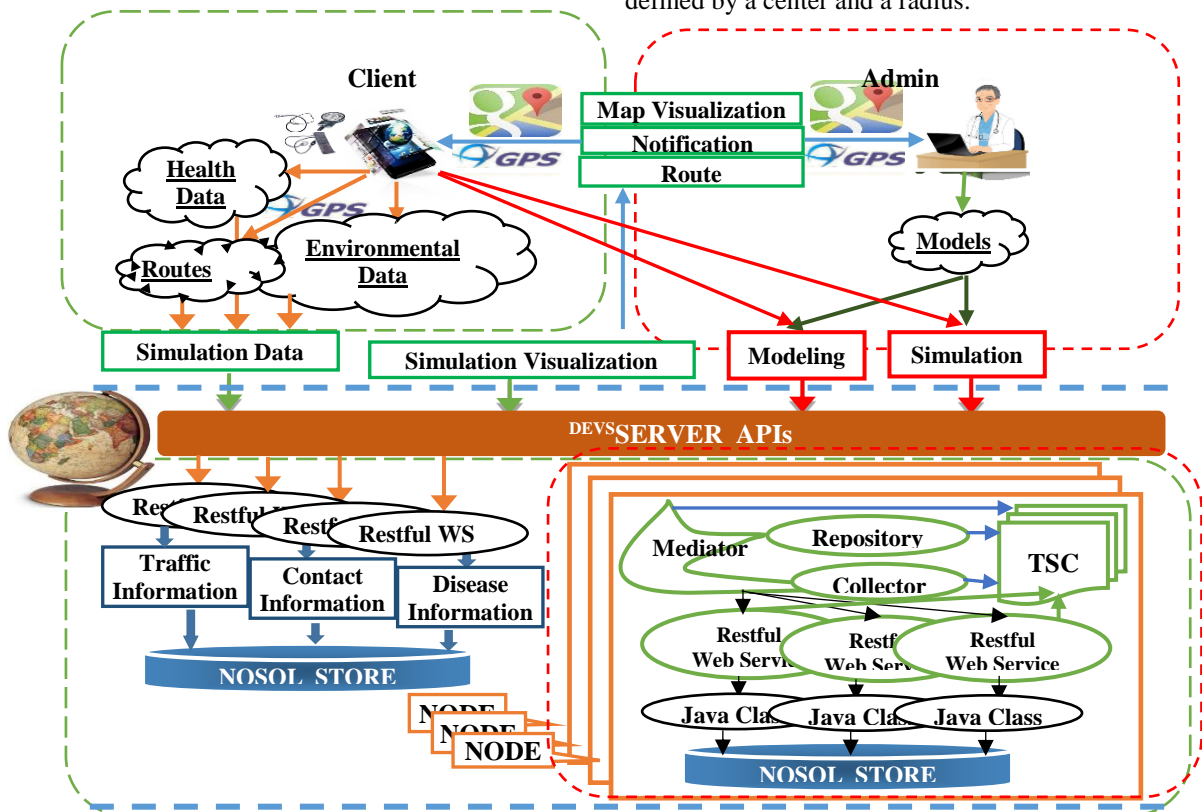
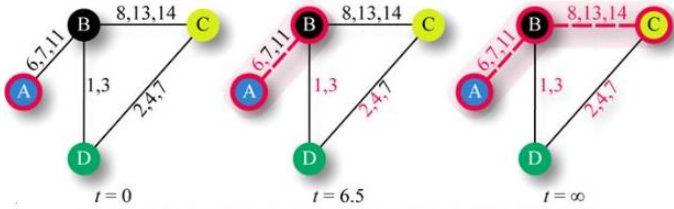


Fig 2. DEVServer architecture.



**Fig. 3.** Illustration of the reachability issue and the intransitivity of temporal networks (more specifically a contact sequence). The times of the contacts between vertices A–D are indicated on the edges. Assume that, for example, a disease starts spreading at vertex A and spreads further as soon as a contact occurs. The dashed lines and vertices show this spreading process for four different times. The spreading will not continue further than what is indicated in the  $t = \infty$  picture, i.e. D cannot get infected. However, if the spreading started at vertex D, the entire set of vertices would eventually be infected. Aggregating the edges into one static graph cannot capture this effect that arises from the time ordering of contacts [16].

Only contacts found inside these area and time interval are included in the temporal network. Contacts can dynamically reach or leave the area and the time interval. Such information is gathered via contacts smartphones and collected using REST web services deployed on the related HCs. This network is fully distributed over many platforms. Each platform builds its own subgraph. The full network is obtained by assembling these subgraphs into a common virtual space. Semantic is embedded in the RDF triples of each node and its links.

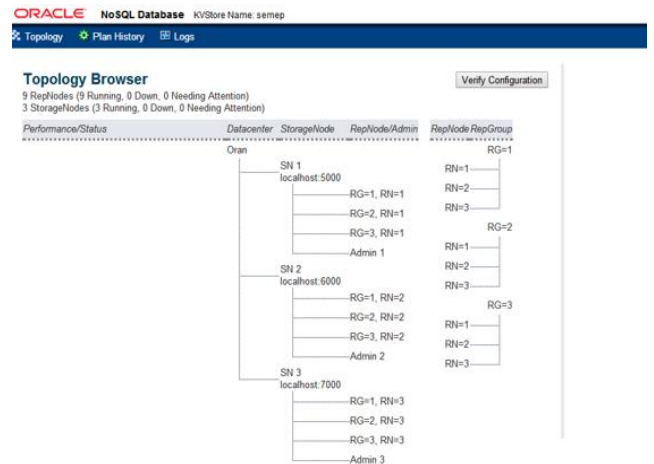
Fig. 3 is extracted from the global network of Fig. 1, corresponding to the subnet of HC A. Fig. 4 shows the store topology of this datacenter.

To apply the chosen immunization strategy, we use and increment the global time between  $T_b$  and  $T_e$ . The time of the next discrete event (next move) may be used as the increment step. When a move occurs, we must compute the system state changes (individuals' state and degrees).

We can use a fixed step  $\Delta T$  to compute the time advance. At each step, each bee applies rules to compute the previous parameters.

In static networks, whether directed or not, if A is directly connected to B and B is directly connected to C, then A is indirectly connected to C via a path over B. However, in temporal networks, if the edge (A, B) is active only at a later point in time than the edge (B, C), then A and C are disconnected, as nothing can propagate from A via B to C (Fig. 3). Thus, the time ordering can matter a lot, and the timings of connections and their correlations do have effects that go beyond what can be captured by static networks. Accordingly, we focus on rules that do not ignore the consequences of the time and space ordering by e.g. projecting out the interaction times [16]. Fig. 5 is an example of RDF triples describing the contact 'Abou Falak' and some of his moving. The set of all RDF triples of any contact defines his RDF graph (his ontology). This ontology includes his vaccinations with dates, nurses, centers, virus related to that vaccination, weights, heights, type of home including humidity, climate, temperature, pressure, etc. All these data are required to compute individuals' degrees and disease thresholds. Some of these data are temporal, which means that they are not significant after a deadline time.

The temporal network of concerned contacts defines the full intelligent temporal network.



**Fig. 4.** Store topology of HC A

## B. RDF Building Tool

AmI applications need to integrate and coordinate heterogeneous data sources or service providers. The data applications usually exchange is diverse and application domain dependent. This implies that data will not be meaningful in other domains unless a specialized system converts and reinterprets them. A way to solve this problem is annotating the data semantically as proposed by [42].

Triple Space Computing (TSC) is a coordination paradigm, which promotes communication style and uses semantic data [43-45]. The way it works is simple: each application writes semantically annotated information in a shared space, and other applications or nodes can query for it and even take it

Fig. 1 depicts 4 datacenters in the significance of Fig. 4. Each one is implemented as an MVC (Model-View-Controller) application (Fig. 2.) to allow interoperability over REST web services. Each MVC is used as a node in the whole system. A node (Fig. 2.) is designed as <sup>DEV</sup>S<sub>Server</sub> simulation server which is fully described in [44-45]. <sup>DEV</sup>S<sub>Server</sub> implements the TSC paradigm by defining a Mediator, a Collector, and a Repository. The Mediator handle the TSC. When an epidemiologist connects to the system to apply an immunization strategy, he begins by creating the shared space (TSC) on his own node by calling its *createTSC()* primitive. When introducing the area and the time interval data, his own Mediator puts this information inside the TSC in RDF form, using the *writeToTSC()* primitive. The Mediator executes its *constructTemporalGraph()* primitive to ask the Repository to retrieve all concerned Mediators URLs. Once getting Mediators URL, the Mediator allows these Mediators to access its own TSC using the *readFromTSC()* and *writeToTSC()* primitives. Each Mediator invokes its own *findAllContactsAroundPosition()* primitive to collect its subgraph forwarding this to its own Collector which invokes its *getContactInfo()* and *getContactRoutes()* primitives to get information and routes of each contact in the given area and time interval. Finally, the temporal network is ready to use in the TSC. The system can now apply its selected immunization strategy.

For instance, consider two epidemiologist mobile applications. The first one consumes information from its TSC on HC A using standard ontologies to link epidemiologists working jointly on some epidemic.

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<u:Birth_270000> <u:hasPosition> <<u:position_1>
<u:Birth_270000> <u:hasRoute> <u:route_29>
<u:Birth_270000> <u:hasPosition> <<u:position_2>
<u:position_1> <u:hasAddress> <station_urbaine>
<u:position_1> <u:hasEndDate> <Fri Jan 01 23:42:22 WAT 2016^^http://www.w3.org/2001/XMLSchema#string>
<u:position_1> <u:hasLongitude> <0.092078^^http://www.w3.org/2001/XMLSchema#decimal>
<u:position_1> <u:hasStartDate> <Fri Jan 01 23:19:22 WAT 2016^^http://www.w3.org/2001/XMLSchema#string>
<u:position_1> <u:hasLatitude> <35.931482^^http://www.w3.org/2001/XMLSchema#decimal>
<u:position_2> <u:hasAddress> <universite_kharouba>
<u:position_2> <u:hasLongitude> <0.099867^^http://www.w3.org/2001/XMLSchema#decimal>
<u:position_2> <u:hasEndDate> <Sat Jan 02 01:01:22 WAT 2016^^http://www.w3.org/2001/XMLSchema#string>
<u:position_2> <u:hasLatitude> <35.951777^^http://www.w3.org/2001/XMLSchema#decimal>
<u:position_2> <u:hasStartDate> <Sat Jan 02 00:57:22 WAT 2016^^http://www.w3.org/2001/XMLSchema#string>
<u:position_3> <u:hasEndDate> <Sat Jan 02 03:00:22 WAT 2016^^http://www.w3.org/2001/XMLSchema#string>
<u:position_3> <u:hasStartDate> <Sat Jan 02 02:40:22 WAT 2016^^http://www.w3.org/2001/XMLSchema#string>
<u:position_3> <u:hasAddress> <boulevard_benghettat_mohamed>
<u:position_3> <u:hasLatitude> <35.932759^^http://www.w3.org/2001/XMLSchema#decimal>
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<u:position_4> <u:hasAddress> <station_urbaine>
<u:position_4> <u:hasStartDate> <Sat Jan 02 03:09:22 WAT 2016^^http://www.w3.org/2001/XMLSchema#string>
<u:position_4> <u:hasLongitude> <0.092078^^http://www.w3.org/2001/XMLSchema#decimal>
<u:position_4> <u:hasEndDate> <Sat Jan 02 03:43:22 WAT 2016^^http://www.w3.org/2001/XMLSchema#string>
<u:position_4> <u:hasLatitude> <35.931482^^http://www.w3.org/2001/XMLSchema#decimal>

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**Fig. 5.** A snapshot of a random contact generation with his route.

Since the application uses Triple Spaces, this information is available for the Mediators in the shared space from HC B, HC C, HC D nodes. The Mediators in the same party (session) populate dynamically the contacts moving in the case of real time immunization. The second epidemiologist independent application, which try to immunize another disease, may notify the first epidemiologist when the two diseases have common contacts moving which means that immunization strategies can affect each other. The second application may populate the first shared space by dumping information retrieved from its TSC [44-45].

Prior to the dump, the application semantizes the information according to the ontology. Finally, it periodically looks into the space to check the contacts leaving the space area and remove them from the network. The interoperability is achieved when the second strategy, which does not support the first one, discovers and update automatically contacts moving in the first application. This is possible because both applications share information in common spaces.

As was previously stated, in TSC paradigm information is stored in RDF. Three key concepts are important at this point: agents (Mediators) share information in a common space. A

space is identified by an URI. Therefore, all the operations in TSC are performed against a particular space. By default, all applications connect to a common standard space, but they can optionally choose to connect to a particular private space. Within a space, the information is stored in sets of triples called graphs. Each graph can also be identified by an URI.

The RDF triples are the underlying concept of all the Semantic Web (SW) languages. Operations supported by the TSC paradigm attempt to add or remove graphs, as well as to query for graphs or for sets of triples retrieved from different graphs.

TSC provides space decoupling, so applications do not know where the information is physically located. They just access the space requesting, removing and providing information. Therefore, the conceptual scheme the developer should have in mind is that multiple nodes interact through different spaces (represented by clouds). Each space contains multiple graphs (represented by temporal networks). These graphs are composed by a set of triples represented by nodes and links within each HC and corresponding to the area and time interval provided.

However, AmI environments are mainly populated by mobile devices and sensors. These devices frequently join and leave the spaces and the information they hold constantly changes. Thus, AmI environments are highly dynamic. As a consequence, we decided to adopt a distributed strategy which locally stores, or even generates on demand, the information necessary to answer a query. Doing so, we ensure the freshness of the responses regarding the sensed data. The main drawback is that whenever a node is temporarily unavailable its contents become unavailable for the rest of the nodes too. However, this faithfully represents the actual state of the space.

Our TSC design does this by allowing each node, no matter how complex or simple it is, to manage its own information. Besides, it establishes a communication channel with the space it wants to join to, i.e. with each of the nodes belonging to it. Queries are propagated to other nodes which previously joined that space (regardless of who they are at each moment). Possible responses are received from them using the same communication channel. In this scheme, each node actually has the sets of graphs locally allowing knowledge distribution strategies.

#### IV. ABC COLONY AS AN IMMUNIZATION STRATEGY

An immunization strategy is defined by the choice of the set  $V$  of nodes to be immunized. Different strategies efficiencies can be compared by measuring their  $\tau_{i \in V}(t)$  and  $t_{i \in V}(t)$ . More precisely, for each contact sequence of duration  $T$ , strategies consider a space area and an initial temporal window  $[T_B; T_E]$  over which various nodes properties can be measured. A fraction  $f$  of the nodes, chosen according to different possible rules, is then selected and immunized (it forms the set  $V$ ). Finally,  $\tau_{i \in V}(t)$  and  $t_{i \in V}(t)$  are computed by simulating the epidemiological model with and without immunization and averaging over starting seeds and times. For each selection rule, the two relevant parameters are  $f$  and  $\Delta T$ . The most popular rules are the following:

1. Compute, for each node  $i$ ,  $K_i$ , the number of different other individuals with whom  $i$  has been in contact during  $[T_B; T_E]$ . [4,6,16]. Sort  $\{K_i\}$ .

2. Compute, for each node  $i$ ,  $B_i$ , Betweenness centrality (Barycenter) over  $[T_B; T_E]$ . Sort  $\{B_i\}$  [4,16].

3. Compute, for each node  $i$ ,  $L_i$ , the latest contacts of  $i$  in  $[T_B; T_E]$ . Sort  $\{L_i\}$  [4,16,35].

4. Compute, for each node  $i$ ,  $F_i$ , the frequency over  $[T_B; T_E]$ . The most frequent nodes in  $[T_B; T_E]$ . Sort  $\{F_i\}$  [4,16,35].

The immunization strategy can be modeled as a problem of community detection in interaction networks. Community detection is considered with great attention for pattern recognition in a graph and is closely related to graph partitioning. This detection (or partitioning) allows us to find the closely related groups that form the nodes to be immunized. To ensure a best development of automatic community detection algorithms, let us say that a community (group to be immunized) is usually defined as a part of network (graph) that includes a finite number of vertices (nodes) with similar functions or characteristics. The existence of communities in network is presented as groups of nodes with important fitness than the other nodes in the graph. They are the related classes with the best rules application in the entire graph. The identification of such structure is interesting from several points of view.

During the last decade, many approaches based on physics, mathematics, computer science, etc. principles, have been proposed for studying community structures in complex networks. These approaches may be grouped into three different categories: hierarchical, optimization, and the Swarm Intelligence.

The first one is based on hierarchical methods that aim to use a tree of communities, called dendrogram. Communities merging or partitioning are performed according to similarity function or distance. The most important characteristic is the nature of the distance or similarity function. To obtain the optimal partition, a cut in the dendrogram must be provided. Newman and Girvan [46-47] introduced the most famous algorithm in this category. The applied method is a hierarchical division of community based on pulling out network links iteratively. Deleted links are selected using Betweenness measures [47]. Quick Method version based on the same strategy is described in [48]. An agglomerative hierarchical method for clustering large linked networks is proposed in [49]. It is used to identify stable or natural cluster. In this same family, another algorithm [50] identifies such communities. Based on the concept of *edge-clustering coefficient*, this algorithm is a divisive hierarchical method which works similarly as the one proposed in [46].

The second category considers an optimization function to estimate the quality of partition. Once again, the method of Newman is applied to determine the optimal partition [47]. The common algorithm of this category considers three steps: first, it proposes several partitions of the network (randomly or by following a function), secondly it retains the best one according to the quality measure. Finally, this partition is refined in order to get a better quality. The optimization of this general form algorithm is specified by several algorithms described in [51-52]. Fast Unfolding Algorithm (FUA) is explained in [53], Label Propagation Algorithm (LPA) in [54], and hub-based algorithms in (Costa, 2004) [55].

The last family contains different nature inspired approaches. These approaches use the ant-based algorithms



(ABA) for community detection [56-60]. ABA is based on the mechanism of the ant colony. Some other approaches are based on Genetic Algorithms [61-62] where a GA algorithm uses a fitness function as the previous similarity function. As a survey, more comprehensive and detailed proposed approaches are presented by Fortunato [63].

Also based on nature-inspired ideas, the last few decades have witnessed the introduction of several optimization algorithms [64-66]. Most of them are meta-heuristic techniques and generally considered as multipurpose optimization algorithms due to their applicability to a wide range of problems. In a similar context, Artificial Bee Colony algorithm (ABC) was initially published by Karaboga [67]. ABC simulates the intelligent behavior of the real honeybees. Based on population optimization, ABC seems to be very simple. The colony of artificial bees contains three groups of bees: employed bees, onlooker bees and scout bees [67]. The employed bees comprise half of the colony while the other half consists of the onlookers and scouts. The food sources detection cycle of the ABC algorithm consists of three special rules (three different behaviors): sending the employed bees to find food source and evaluate its quality of nectar; the onlooker bees choose food sources from employed bees based on a probability (employees dance) and then try to improve its quality of nectar; the scout bees determine potential new food source to place it instead of the abandoned solution.

The probability for a food source to be selected increases with the increase of its quality. Therefore, the food source with the highest quality of nectar has more chance of being selected. The position of a food source means a promising solution of the problem, while the quality of the food source nectar represents the fitness cost associated to that solution [67].

Prior to algorithm description, some basic principles and terminology on partitions are useful.

#### A. Basic Principles

Consider a graph  $G = (V, E)$  with  $|V| = n$  vertices and  $|E| = m$  edges. Let  $P = \{V_1, V_2, \dots, V_p\}$  be a partition of  $V$  into  $p$  classes. Each  $V_i$  may be a group of nodes to be immunized according to one of the previous rules. Most of the works cited above take as input a graph  $G$  whose vertices  $V$  are people and edges  $E$  are the observed relationships (disease characteristics) between these people. The result of this work is a partition  $P$  of the graph  $G$  so that each individual belongs to a community that is the nodes to be immunized according to a specific strategy. The retained immunization strategy will be the best solution.

#### B. Schema principle of the algorithm

We are interested in identifying rules to detect existing communities when partitioning the network (graph). The population consists of bees looking for an optimal partitioning of the graph. The general outline of such ABC community detection algorithm is as follow:

##### 1) Step 1 - Initialization and generation of solutions :

First, ABC parameters and solutions initialization are very important for quick convergence of the ABC algorithm. In this step, we define all necessary parameters such as the number of bees in the hive, the number of visits allowed to a

source of food (the number of iteration to improve the solution), the total number of the algorithm cycles, the number of employed bees, onlookers and scouts, finally the maximum number of communities. This is completed by the generation of a primer solution of each employed bee. The algorithm proposes a solution for each chosen rule. This solution, presented as vector of nodes, affects each node with its degrees (contamination and immunity) to a community. An example of 4 rules means 4 communities. Proposed solution is accepted or rejected according to the connection between nodes, which could lead to a bad solution. In such case, this bad solution means that we do not know how infection occurred between nodes of the same community. Yet, to fit our objectives, a better generation phase is required. Two nodes in a same community must have at least one direct or transitive connection (infection occurred between nodes). After randomly identifying communities to nodes, we choose some nodes and give their identifiers to nodes that are their infected, it is a way to avoid bad solutions, and after each generation of solutions, a verification process is performed to check whether the solutions are acceptable, otherwise new solutions are generated to replace the bad solutions. The initialization and verification process guided the ABC algorithm to avoid a beginning with uninteresting partitions of graph; this will give a quick convergence because the space of possible solution is promising from the beginning and will eliminate unnecessary iterations. So, at the end of this step, the ABC has an initial population randomly distributed to find the optimal solution and the number of cycles is initialized as  $C=0$ .

##### 2) Step 2: Move the employed bees (local search )

We consider the first half of the colony as employed bees. In this step, each solution is treated as a food source for the employed bee to explore. Employed bees calculate the quality of their solutions using the contamination and immunization thresholds, and then they propose changes to improve these solutions. Next, each employed bee produces new solution in the neighborhood of its solution, taking into account local information of the vector solution. The production of solutions in the surrounding area of the original solution lead to a better local search (may give a better partition of the graph). At the end, the bee calculates the quality of the new solution (the rule of the new proposed partition). In case the new quality is higher than the previous one, the bee memorizes the new position and forgets the old one. Otherwise, the bee always keeps the position of the previous solution in its memory and increments the number of visits. In case the number of visit reaches its maximum, the employed bee of this solution becomes scout and proposes a random solution.

##### 3) Step 3: Selection and improvement (global search)

After all employed bees have completed the process of improving local solutions; they share this information with onlookers in a place called the dance area. Onlookers bees evaluate the information of all solutions of the employed bees and choose one source of food (solution) with a probability related to its quality. As in the case of employed bees, each onlooker bee produces a modification to the selected solution and checks its quality. After that, the bee keeps in its memory the solution with higher quality.

#### 4) Step 4: Moving the scouts

In ABC, the solution that cannot be improved by a predetermined number of visits by the employed bees is considered as an abandoned solution. The predetermined value of the number of visits is an important parameter. If the employed bee uses all visits to the solution and this solution did not improve, this solution becomes an abandoned one. Finally, this solution is replaced by a new solution and the employed bees become scouts (scout offers a new random solution following the steps of the initialization phase). This is simulated by generating a new random position and replacing the abandoned one. Scout bee discovers a new food source when exploring other locations. After the generalization of the solution, the bee evaluates its quality.

In a strong search algorithm, exploration and exploitation process must be carried out simultaneously. In the ABC algorithm, employed bees and onlookers perform the operation of search process; the scouts control the exploration process. The performance of the local search depends in the ABC algorithm of the neighborhood searches and the mechanisms of the greedy selection made by employed bees and onlookers. The performance of the global search depends on random search process performed by scouts' bees.

#### C. Main Steps Of The ABC Algorithm

##### 1. Load the data set and initialize the parameters

##### 2. Generate the initial solutions

For each solution

Check the existence of efficient connection  
in the proposed partitioning.

If there is a bad generation solution

Then propose a new solution instead.

##### 3. Evaluate the quality of all solutions using the rules.

##### 4. Repeat

###### 1. Employed bees phase

For each employed bee

Produce a change in the  $n_i$  solution

Calculate the modularity of this new solution

Apply the greedy selection mechanism.

###### 2. Calculate the probability $p_i$ of the value of each solution.

###### 3. Onlookers bees phase

For each onlooker bee

Choose a food source depending on  $p_i$  of employed bee

Produce a new food solution from the one that has been chosen

Calculates the value according to the rule function.

Apply the greedy selection mechanism.

###### 4. Scouts bees phase

If there is an abandoned solution by an employed bee

Then replace it with a new solution generated randomly

###### 5. Save the best solution.

###### 6. Cycle $C = C + 1$ .

##### 5. Until the maximum number of cycle is reached.

**Fig. 6:** ABC Pseudo code for community detection.

#### V. DEVS SPECIFICATION OF THE IMMUNIZATION STRATEGY

As previously stated (fig. 1), four SEMEPs and an HC are interconnected, each one has its own <sup>DEVS</sup>Server node and let's say that the HC is the main <sup>DEVS</sup>Server node (Mokaddem

and al., in press). Simulation is initiated at the main node. The User Interface (UI) starts the UI DEVS model which initiates the simulation. The UI model takes as inputs (X) such that:

$X = \{T_B, T_E, Radius, InitialPosition, EpidemyName, Start, Stop\}$ .

$T_B$ : Simulation start time.

$T_E$ : Simulation end time.

$Radius$ : the radius of the area to simulate the immunization.

$InitialPosition$ : the position (the center) of the area where the epidemic is propagated.

$EpidemyName$ : the simulated epidemic.

$Start$ : start the simulation.

$Stop$ : stop the simulation.

The UI executes its  $DeltaExt()$  function that performs :

–  $DeltaExt(T_B, T_E, Radius, InitialPosition, EpidemyName, Start)$ :

1. write information into its TSC.

2. ask the repository for the related nodes URI.

3. write nodes URI into the TSC.

4. invoke each node to pick its information.

5. invoke each node to start simulation

–  $DeltaExt(T_B, T_E, Radius, InitialPosition, EpidemyName, Stop)$ :

1. ask each node to stop its simulation.

2. ask each node to report results into the global TSC.

The  $DeltaInt()$  function of the UI, checks if new results have been generated by nodes. This generation is provided by the temporal network updates or the ABC algorithm computation. Each time a generation or a contact computation occurs, the related node reports this as an internal event. When immunizing, these internal events become related to ABC (bees) computation.

The  $Out()$  function of the UI reports results from TSC to screen to have real-time results.

On each node, the selected epidemic DEVS model (e.g. TB model) performs two tasks, the real-time updates of the temporal network (network dynamic) and the ABC execution (moves of the bees).

The Tuberculosis characteristics and attributes (dataset) are described in (Mokaddem and al, in press) (fig. 5). These attributes are: weight, age, smoking, alcoholism, HIV, corticoid therapy, previous TB, itinerancy, physical activity, IDU (Injecting Drug User), chronic stress, diabetes, cancer, social level, malnutrition, immunity degree, contamination degree, and state.

#### A. Dynamic of the Temporal Network

Some of these variables moves slowly such as age, weight, etc. and others moves more quickly such as physical activities, social level, etc. the generation is closely related.

Some contacts enter the area and are then added to the network others instantly leave the area and the network.

##### 1) TB attributes generation :

The TB generator model is continuously generating data until the end of the simulation. The main role of this model is to update temporal network data.

Each contact model has its own generator.

## B. ABC DEVS Representation

When invoked to start:

1. write information into its local TSC.
2. load the local temporal net according to parameters.
3. for each contact in its local temporal net do;
  1. start its parameters Generator DEVS model
  2. start the contact DEVS model.
4. start the ABC DEVS model

. When invoked to stop:

1. for each contact into its local temporal net do:
  1. stop Generator
  2. stop Contact
2. ask ABC to stop.

## VI. CONCLUSION

DSS (Disease Surveillance Systems) with Epidemic Modeling deal with a large number of contacts moving dynamically and temporally. Each contact is using AmI devices to join/disjoin the distributed structure dynamically at run time. Therefore, we need to use a middleware such as <sup>DEVS</sup>Server that adapts itself to AmI environments and provides a distributed simulation among different types of nodes in a dynamic way.

In this paper, we proposed a new algorithm for community detection based on the ABC and <sup>DEVS</sup>Server principles, which seeks to optimize the modularity of the network. The main contribution of this study is the introduction of the ABC to the problem of the community detecting that does not require any information on the number of communities in the network. The detection of the community in complex networks is an NP-hard problem. The ABC algorithm is often an effective way to solve these problems, each bee is trying to spread its solution using a process that maximizes the immunity degree locally through different types of groups and contamination. Our proposal is superior to traditional approaches of the state of art since it acts over large scale network and provide a distribution of the ABC algorithm.

The temporal network generation and dynamic updates process is still hard since it requires local distributed multiprocessors architectures or a <sup>DEVS</sup>Server cloud implementation.

Next to that, exploring and optimization of the network is now a partial operation. In future work, we will improve these two aspects. Firstly, we will improve the exploring procedure in order to make it more sensitive than before. Then we will also create a more powerful strategy of optimization by adding some new manipulations rather than transferring nodes in communities. Finally, we also intend to apply the ABC algorithm to several real-world diseases networks that have an overlapping community to interpret their significant structures.

Also, a new concept and ideas for a distributed simulation is implemented using <sup>DEVS</sup>Server <sup>DEVS</sup>Server principles (TSC paradigm, Mediator, Collector, and Repository). This can achieve immunization strategies configuration and execution more powerfully.

The considered immunization strategies style at the Web level (RWS) allows take advantage of <sup>DEVS</sup>Server as new

Web-based features or technologies. On the other hand, <sup>DEVS</sup>Server provides better interoperability applying RWS principles among the TSC paradigm.

We aim to consider implementing the visualization process with its web interface. A real-time simulation with on-line data under AmI assistance to show the ABC algorithm over <sup>DEVS</sup>Server ability to a wide range of interaction and pursue its intelligent interoperability aspect is to be considered. We hope choosing testbed of volunteers' people to validate this ability.

We also consider integration in the immunization strategies of other contacts states such as 'Ill', 'Under Treatment', 'Recovered' and 'Healthy' so that 'Ill' recovers soon, 'Under treatment' does not relapse nor abundant his treatment, and 'Recovery' does not relapse. Such proposals are related to Artificial Intelligence and are part of actual AmI systems.

The Tuberculosis example with its ABC application is still under work and will be an apart paper to be submitted soon in the next ISSPM simulation conference. Others diseases are under study to make ABC algorithm over <sup>DEVS</sup>Server a fully Epidemic Modeling solution.

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## REFERENCES

- [1] H. Kang, X. Fu. Epidemic spreading and global stability of an SIS model with an infective vector on complex networks. *Com Nonlinear Sci Num Sim* 27 (2015) 30–39, Elsevier.
- [2] K. Li, H. Yu, Z. Zeng, Y. Ding, Z. Ma. Epidemic transmission on random mobile network with diverse infection periods. *Com Nonlinear Sci Num Sim.* 22 (2015) 596–604. Elsevier.
- [3] S. Yan, S. Tang, S. Pei, S. Jiang, Z. Zheng. Dynamical Immunization Strategy for Seasonal Epidemics. *Phys. Rev. E* 90(2014), 022808.
- [4] M. Stamini, A. Machens, C. Cattuto, A. Barrat, R. Pastor-Satorras. Immunization strategies for epidemic processes in time-varying contact networks. *Journal of Theoretical Biology* 337 (2013) 89–100. Elsevier.
- [5] Liu SY, Baronchelli A, Perra N. Contagion dynamics in time-varying metapopulation networks. *Phys Rev E* 2013;87:032805.
- [6] R. Pastor-Satorras and A. Vespignani, *Epidemic dynamics in finite size scale-free networks*, *Phys. Rev. E* **65**:036104 (2002);
- [7] Bailey NTJ. The mathematical theory of infectious disease. 2nd ed. New York: Hafner; 1975.
- [8] W.O. Kermack, A.G. McKendrick. Contributions to the math. theory of epidemics. *Proc R Soc* 1932;A138:55–83.
- [9] J. Zhou, N.N. Chung, L.Y. Chew. Epidemic spreading induced by diversity of agents' mobility. *Phys Rev E* 2012;86:026115.
- [10] V. Coliza, A. Vespignani. Epidemic modeling in metapopulation systems with heterogeneous coupling pattern: Theory and simulations. *J Theor Biol* 2008;251:450–67

- [11] B. Wang, L. Cao, H. Suzuki, K. Aihara. Safety-information-driven human mobility patterns with metapopulation epidemic dynamics. *Sci Rep* 2012;2:887.
- [12] E. Vergu, H. Busson, P. Ezanno. Impact of the infection period distribution on the epidemic spread in a metapopulation model. *PLoS ONE* 2010;5:e9371.
- [13] P. Rodrigues, A. Margheri, C. Rebelo, M. Gomes. Heterogeneity in susceptibility to infection can explain higher infection rates. *J Theor Biol* 2009;259:280–90
- [14] X. Li, L. Cao, G.F. Cao. Epidemic prevalence on random mobile dynamical networks: individual heterogeneity and correlation. *Eur Phys J B* 2010;75:319–26.
- [15] Newman, M.E.J., 2002. The spread of epidemic disease on networks. *Phys. Rev. E* 66, 016128.
- [16] Holme, P., Saramäki, J., 2012. Temporal networks. *Phys. Reports* 519, 97–125.
- [17] Cattuto, C., van den Broeck, W., Barrat, A., Colizza, V., Pinton, J.F., Vespignani, A., 2010. Dynamics of person-to-person interactions from distributed RFID sensor networks. *PLoS ONE* 5, e11596.
- [18] Karsai, M., Kivela, M., Pan, R.K., Kaski, K., Kertész, J., Barabási, A.L., Saramäki, J., 2011. Small but slow world: how network topology and burstiness slow down spreading. *Phys. Rev. E* 83, 025102.
- [19] Hill, S., Braha, D., 2010. A dynamic model of time-dependent complex networks. *Phys. Rev. E* 82, 046105.
- [20] Stehlé, J., Barrat, A., Bianconi, G., 2010. Dynamical and bursty interactions in social networks. *Phys. Rev. E* 81, 035101
- [21] Starnini, M., Baronchelli, A., Pastor-Satorras, R., 2013. Modeling human dynamics of face-to-face interaction networks. *Phys. Rev. Lett.* 110, 168701.
- [22] Fujiwara, N., Kurths, J., Díaz-Guilera, A., 2011. Synchronization in networks of mobile oscillators. *Phys. Rev. E* 83, 025101.
- [23] Parshani, R., Dickison, M., Cohen, R., Stanley, H.E., Havlin, S., 2010. Dynamic networks and directed percolation. *Europhys. Lett.* 90, 38004.
- [24] Baronchelli, A., Díaz-Guilera, A., 2012. Consensus in networks of mobile communicating agents. *Phys. Rev. E* 85, 016113.
- [25] Starnini, M., Baronchelli, A., Barrat, A., Pastor-Satorras, R., 2012. Random walks on temporal networks. *Phys. Rev. E* 85, 056115.
- [26] Rocha, L.E.C., Liljeros, F., Holme, P., 2011. Simulated epidemics in an empirical spatiotemporal network of 50,185 sexual contacts. *PLoS Comput. Biol.* 7, e1001109.
- [27] Rocha, L.E.C., Blondel, V.D., 2013. Bursts of vertex activation and epidemics in evolving networks. *PLoS Comput. Biol.* 9, e1002974.
- [28] Masuda, N., Holme, P., 2013. Predicting and controlling infectious disease epidemics using temporal networks. *F1000Prime Reports* 5, 6.
- [29] Liu, Z., Lai, Y. C., & Ye, N. (2003). Propagation and immunization of infection on general networks with both homogeneous and heterogeneous components. *Physical Review E - Statistical, Nonlinear, and Soft Matter Physics*, 67(3 1), [031911].
- [30] N. Madar, T. Kalisky, R. Cohen R, ben-Avraham. D, and S. Havlin. Immunization and epidemic dynamics in complex networks. *Eur. Phys. J. B*, 38, 269 (2004).
- [31] JC Miller, JM Hyman. Effective vaccination strategies for realistic social networks. *Physica A: Statistical Mechanics and its Applications* 386 (2), 780-785, 2007.
- [32] Y. Chen, G. Paul, S. Havlin, F. Liljeros, and H. E. Stanley, "Finding a Better Immunization Strategy," *Phys. Rev. Lett.* 101, 058701 (2008).
- [33] S. Pei and H. A. Makse, *J. Stat. Mech.* Spreading dynamics in complex networks. *J. Stat. Mech.*, P12002(2013).
- [34] R. Cohen, S. Havlin, and D. ben-Avraham. Efficient immunization strategies for computer networks and populations, *Physical Review Letters* **91**, 247901 (2003).
- [35] Lee, S., Rocha, L.E.C., Liljeros, F., Holme, P., 2012. Exploiting temporal network structures of human interaction to effectively immunize populations. *PLoS ONE* 7, e36439.
- [36] Takaguchi, T., Sato, N., Yano, K., Masuda, N., 2012. Importance of individual events in temporal networks. *New J. Phys.* 14, 093003.
- [37] J.E. Augeraud-Véron and N. Sari. Seasonal dynamics in an SIR epidemic system, *J. Math Biol.*, 68(3), 701-725 (2014).
- [38] H. W. Hethcote. **The Mathematics of Infectious Diseases**. *SIAM Rev.*, 42(4), 599-653 (2000).
- [39] Clancy D. SIR epidemic models with general infectious period distribution. *Stat Probab Lett* 2014;85:1–5.
- [40] Fielding, R. T. (2000). Architectural styles and the design of network-based software architectures. Ph.D. Thesis. Irvine: University of California.
- [41] Guinard, D. (2011). A web of things application architecture integrating the real-world into the web. Ph.D. ETH Zurich.
- [42] Berners-Lee, T., Hendler, J., & Lassila, O. (2001). The semantic web. *ScientificAmerican*, 284, 3443.
- [43] Aitor Gómez-Goiri, Pablo Orduña, Javier Diego, Diego López-de-Ipiña. Otsopack: Lightweight semantic framework for interoperable ambient intelligence applications. *Computers in Human Behavior* 30 (2014) 460–467. Elsevier.
- [44] Mokaddem, M., Atmani B., Boularas A., (2016) DevsServer : Ambient Intelligence and DEVS Modeling Based Simulation Server, SpringSim-MSCIAAS 2016, April 3-6, 2016, Pasadena, CA, USA. Copyright 2016 Society for Modeling & Simulation International (SCS).
- [45] Mokaddem, M., Atmani B., Boularas A., Mokaddem C. (2018) "DEVS"Server: Ambient Intelligence and DEVS Modelling Based Simulation Server for Epidemic Modelling", *Int. J. Simulation and Process Modelling*, Vol. XX, No. Y4, pp.000–000 (under revision).
- [46] M. Girvan, M.E.J. Newman, "Community structure in social and biological networks". *Proc. National. Academy of Science. USA* 99, 7821–7826 (2002)
- [47] M.E.J. Newman, M. Girvan, "Finding and evaluating community structure in networks". *Physical Review E* **69** (2004) 026113.
- [48] M.E.J. Newman, "Fast algorithm for detecting community structure in networks". *Physical Review E* 69, 066133 (2004)
- [49] J.E. Hopcroft, O. Khan, B. Kulis, B. Selman, "Natural communities in large linked networks". In: *Proc. International Conference on Knowledge Discovery and Data Mining (KDD 2003)*, pp. 541–546 (2003)
- [50] F. Radicchi, C. Castellano, F. Cecconi, V. Loreto, D. Parisi, "Defining and identifying communities in networks". *Proc. Natl. Acad.Sci. USA (PNAS 2004)* , 2658–2663 (2004)
- [51] M.E.J. Newman, "The structure and function of complex networks". *SIAM Review* 45, 167–256 (2003)
- [52] J. Duch, A. Arenas, "Community detection in complex networks using extremal optimization". *Physical Review E* 72 (2005) 027104
- [53] V. D. Blondel, J. L. Guillaume, R. Lambiotte, and E. Lefebvre, "Fast unfolding of communities in large networks". *J. Stat. Mech.* 2008, P10008.
- [54] U. N. Raghavan, R. Albert, and S. Kumara, "Near linear-time algorithm to detect community structures in large-scale networks", *Phys. Rev. E.* 76 (2007) 036106.
- [55] L. D. F. Costa, "Hub-based community finding", 2004, e-print cond-mat/0405022.
- [56] Y. Liu, Q. X. Wang, Q. Wang, Q. Yao, and Y. Liu, "Email community detection using artificial ant colony clustering". in *Proc. Joint 9th Asia-Pacific Web Conference and 8th International Conference on Web-Age Information Management Workshops (APWeb/WAIM'07)* (Huang Shan, China, 2007), pp.287-298.
- [57] Y. Liu, J. Y. Luo, H. J. Yang, and L. Liu, "Finding closely communicating community based on ant colony clustering model". in *Proc. Int. Conference on Artificial Intelligence and Computational Intelligence (AICI '10)* (Sanya, China, 2010), pp.127-131.
- [58] S. Sadi, Ş. Etaner-Uyar, and Ş. Gündüz-Öğüdücü, "Community detection using ant colony optimization techniques". in *Proc. Int. Conference on Soft Computing (MENDEL '09)* (Brno, Czech Republic, 2009), pp.206-213.
- [59] S. Sadi, Ş. Öğüdücü, and A. Ş. Uyar, "An efficient community detection method using parallel clique-finding ants". in *Proc. IEEE Congress on Evolutionary Computation (CEC '10)* (Barcelona, Spain, 2010), pp. 1-7.
- [60] D. Jin, D. Y. Liu, B. Yang, J. Liu, and D. X. He, "Ant colony optimization with a new random walk model for community detection in complex networks". *Adv. Complex Syst.* 14 (2011) 795-815.
- [61] M. Tasgin, A. Herdagdelen, A. Bingol, "Communities detection in complex networks using genetic algorithms". oai:arXiv.org:0711.0491v1 [physics.soc-ph] (2007).
- [62] A. Firat, S. Chatterjee, M. Yilmaz, "Genetic clustering of social networks using random walk". *Computational Statistics and Data Analysis* 51, 6285–6294 (2007).
- [63] S. Fortunato. "Community detection in graphs". *Complex Networks and Systems Lagrange Laboratory, ISI Foundation, Viale S. Severo* 65, 10133, Torino, Italy (2009).
- [64] M. Dorigo, M. Birattari, and T. Stutzle. "Ant colony optimization". *Computational Intelligence Magazine, IEEE*, 1(4):28–39, 2006.
- [65] J. Kennedy and R. Eberhart. "Particle swarm optimization. In *Neural Networks*", 1995. Proceedings., IEEE International Conference on, volume 4, pages 1942–1948. IEEE, 1995.
- [66] Z.W. Geem, J.H. Kim, and GV Loganathan. "A new heuristic optimization algorithm: harmony search. *Simulation*", 76(2):60, 2001.
- [67] D. Karaboga. "An idea based on honey bee swarm for numerical optimization". *Techn. Rep. TR06, Erciyes Univ. Press, Erciyes*, 2005.

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